

MSL No. 20351
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Y 1020 1030 1040 1050 1060 1070
cry1a-105-pe EAYSOERCPGEGVILRVAYKEVGEGCVTHIEINNTDELKFSNCVEEIVPNNTV
40282 EAYSOEVRPFGVYLIVRVAYKEVGEGCVTHIEINNTDELKFSNCVEEIVPNNTV

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cry1a-105.pe      TCNDYTVNCEYGCATTSNRGNEEA,PSVPDYACVVEKSYTDGRRENPCFNKGYRD      1086 1099 1100 1110 1120 1130
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
TCNNYATQCEEHGNTSNRGNYEAYEAMSSVHAAVVEKSYTDGRRENPCSNRGYD
40282

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cry1a-105.pe	YTPLPVGYVKTELYFPETDKWVIEIGSTEGTFFI	1130	1135	1140	1145	1150	1155	1160	1165	1170	1175	1180	1185	1190	1195	1200	1205	1210	1215	1220	1225	1230	1235	1240	1245	1250	1255	1260	1265	1270	1275	1280	1285	1290	1295	1300	1305	1310	1315	1320	1325	1330	1335	1340	1345	1350	1355	1360	1365	1370	1375	1380	1385	1390	1395	1400	1405	1410	1415	1420	1425	1430	1435	1440	1445	1450	1455	1460	1465	1470	1475	1480	1485	1490	1495	1500	1505	1510	1515	1520	1525	1530	1535	1540	1545	1550	1555	1560	1565	1570	1575	1580	1585	1590	1595	1600	1605	1610	1615	1620	1625	1630	1635	1640	1645	1650	1655	1660	1665	1670	1675	1680	1685	1690	1695	1700	1705	1710	1715	1720	1725	1730	1735	1740	1745	1750	1755	1760	1765	1770	1775	1780	1785	1790	1795	1800	1805	1810	1815	1820	1825	1830	1835	1840	1845	1850	1855	1860	1865	1870	1875	1880	1885	1890	1895	1900	1905	1910	1915	1920	1925	1930	1935	1940	1945	1950	1955	1960	1965	1970	1975	1980	1985	1990	1995	2000	2005	2010	2015	2020	2025	2030	2035	2040	2045	2050	2055	2060	2065	2070	2075	2080	2085	2090	2095	2100	2105	2110	2115	2120	2125	2130	2135	2140	2145	2150	2155	2160	2165	2170	2175	2180	2185	2190	2195	2200	2205	2210	2215	2220	2225	2230	2235	2240	2245	2250	2255	2260	2265	2270	2275	2280	2285	2290	2295	2300	2305	2310	2315	2320	2325	2330	2335	2340	2345	2350	2355	2360	2365	2370	2375	2380	2385	2390	2395	2400	2405	2410	2415	2420	2425	2430	2435	2440	2445	2450	2455	2460	2465	2470	2475	2480	2485	2490	2495	2500	2505	2510	2515	2520	2525	2530	2535	2540	2545	2550	2555	2560	2565	2570	2575	2580	2585	2590	2595	2600	2605	2610	2615	2620	2625	2630	2635	2640	2645	2650	2655	2660	2665	2670	2675	2680	2685	2690	2695	2700	2705	2710	2715	2720	2725	2730	2735	2740	2745	2750	2755	2760	2765	2770	2775	2780	2785	2790	2795	2800	2805	2810	2815	2820	2825	2830	2835	2840	2845	2850	2855	2860	2865	2870	2875	2880	2885	2890	2895	2900	2905	2910	2915	2920	2925	2930	2935	2940	2945	2950	2955	2960	2965	2970	2975	2980	2985	2990	2995	3000	3005	3010	3015	3020	3025	3030	3035	3040	3045	3050	3055	3060	3065	3070	3075	3080	3085	3090	3095	3100	3105	3110	3115	3120	3125	3130	3135	3140	3145	3150</
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cryla-105.pap
NRRA:295866

295866 source="GENBANK_PROT" crystal protein [Bacillus
thuringiensis]gi|27436034|gb|AAO13295.1| crystal delta
thuringiensis}

```

SCORES      Init1: 2880      Initn: 5043      Opt: 5318      z-score: 6036.7      E(): 0
>NRAA:295866
Initn: 5043      Init1: 2880      Opt: 5318      z-score: 6036.7      expect(): 0
Smith-Waterman score: 5318; 68.8% identity in 1187 aa overlap
(1-1177:1-1174)

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[illegible]

```
cryla-105.pe VDIWIGFQSDAFLVQIQEQLINRIEFARNQAISRLGLSNLYQIYAFSFEWAD      70    80    90    100    110    120
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
FDLWIGFTIPSPWSLFLLIQLEEQRIETERNRAITTLGKLADESYEVYALREWEEN
295866
```

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cryla-105.pe  F T N P A L R E M R I O F N D M N S A L T T A P L F A V Q N Y V P L S V V Q A A N L H S L V R D V S F V Q
: | | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
P N N A Q L R E D V R F A N T D A L I N N F T I T S F E P L L S V V Q A A N L H S L V R D V S F V Q
295866
120 130 140 150 160 170 180

```

```
cryla-105.pe      190      200      210      220      230      240
|||:::|||||
GWGFDAATNSRYNDLTGLIGNYTDHAWMYNTGLERWVGSDSDWTIRNQFRRELLTV
GWLGIATVNNHYLNRLNIHRYTEHCFLDTYNGLELRGNITFQMSRFNQRRELLTV
```

```

250      260      270      280      290
cry1a-105.pe LDIVSLFPNVDKSTPIRTVSQLTREYTNVPLEN--FDGSGRGSAGTIEGSTRSPHLM
295866        LDIVLFPNVDKSTPIRTVSQLTREYTNVPLEN--FDGSGRGSAGTIEGSTRSPHLM

```

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

2295866
FMNSLFVTAETVRSQTWGGH--LVSSRNTAGNPNFPIYGIF-NPGGAIWIAEDPRPF
300 310 320 330 340 350

```

cry1a-105.pe      360      370      380      390      400      410
YRTLSSTLYRFFWIGNNQQLSV-LDGTFAAYGTSNLSFSAVYRGTGVDLSDEIPQP
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
YRTLSDPVEVRG--GFGNPHYVLGRGVAFOQ-TGYN-HTRFRNSGTGVDLSDEIPQP
295866            360      370      380      390      400      410

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[illegible][illegible]

```
cryla-105.pe      540    550    560    570    580    590
::: : : : : : : : : : : : : : : : : : : : : :
YIVVAGERIFAGQNKMTGDTPLTFQSFSATINNTAFPPMSQSFVTGADTPSSNE
FPRINGTVNGCNFGFTMRMGNLESGNFRTAGTFFSFAQAQTFLGTGAQSN-QE
925866            530    540    550    560    570
```

600 610 620 630 640 650
 CY1a.105.1e YIDRPELPVATLAEYLNLEAKAVNALPSTNSGLKNTVYDHYDQVSNLVLTYS
 VYIDRPEFPVPAEYFESLSLEAKAVNALPSTNSGLKNTVYDHYDQVSNLVLACLS
 229566

~~660 670 680 690 700 710
 DEFLCDEKESKRYUAKLSLERNLLODSNFKDINRQPERGMSGSTITIGGGDVFK
 295866 DEFLCDEKESKRYUAKLSLERNLLODSNFKDINRQPERGMSGSTITIGGGDVFK
 DEFLCDEKESKRYUAKLSLERNLLODSNFKDINRQPERGMSGSTITIGGGDVFK
 DEFLCDEKESKRYUAKLSLERNLLODSNFKDINRQPERGMSGSTITIGGGDVFK~~

778 730 740 750 760 770
 ENTVTTGGTPECYPTVWKNIDSKRPFQYQUGVIEDSDLEIYSIRYNKHETWN
 ENTVTTGGTPECYPTVWKNIDSKRPFQYQUGVIEDSDLEIYSIRYNKHETWN
 ENTVTTGGTPECYPTVWKNIDSKRPFQYQUGVIEDSDLEIYSIRYNKHETWN
 ENTVTTGGTPECYPTVWKNIDSKRPFQYQUGVIEDSDLEIYSIRYNKHETWN
 710 720 730 740 750 760

~~cryIIa-105.pe~~

VPTGSLWPLSPQKIGPKCSNRPSAPHELENPDLSCDGGSKCAHHHSHFLSDIDVGC	780	790	800	810	820	830
:: :	:	:	:	:	X	
VPTGSLWPLSVENQIQGPCENRCAPIELNFDLHGCDGGCKCVHSHSHFLSDIDVGC	770	780	790	800	810	820

~~L295866~~

~~TDLNEDLGWVIFKIKTQDGHARGLNLEFLEKPIVCSALRYVKRAEKWKDRKKRLANE~~
840 850 860 870 880 890
~~TDLNEDLGWVIFKIKTQDGHARGLNLEFLEKPIVCSALRYVKRAEKWKDRKKRLANE~~
920 930 940 950 960 970 980 990

	900	910	920	930	940	950
cryla-105.pe	TNIVYKEAKESVDALFVNSOVDLOQADTNIAHIAADKRVHVSREAYLPELSITFVNAA					
295866	TNIVYKEAKESVDALFVNSOYDLQADTNIAHIAADKRVHVSREAYLPELSIVGNAA					

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960 970 980 990 1000 1010
crt1a-105.pe IFEELEGRIFTAFCHYDARNVTKNGDFNNCLSCWNVKGHVDEQNNORSVLVYPEWEAE

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[illegible][illegible]

8469133 cry1a-105.pe LDI VALPFPNDARAVPIOTSSQLTREIYTSVIEDSPVSAIPNGFNRAEFVVRPHPLMD
240 250 260 270 280 290
cry1a-105.pe LLSNITIIYDARGEYVSGHQMASPVGSGPEFFLYIGTMGNAAPQORIVAGUGGV
300 310 320 330 340 350
8469133 FNNLSFVTAETAGVQVWGGH--LVSSRNAGNPINFIYGVF-NPGGAIWADEPRPF
300 310 320 330 340 350
cry1a-105.pe YRTLSSTLYRPNENGINNOOLSV-LDGEFAVGTSSNLPASVYKSTVDSLEIPON
360 370 380 390 400 410
8469133 YRTLSDFVVRG--GFCNPHVVLGLGVGQQ-IGTN-HRTFNSGTIDSLDELPD
360 370 380 390 400 410
cry1a-105.pe NNVPFQGSFRLSHVSMFR-SGFSNSSVSIIRAPMFWSIHRSAEFNIIASITQIPL
420 430 440 450 460 470
8469133 NSGAPNDYSHVNLHVTVRWPGEGAGSDW-RAPMFWSIHRSAEFNIIASITQIPL
420 430 440 450 460 470
cry1a-105.pe VKAHTLSQSTTVVRGPGFTGGDLIRRTSGSPAYIIVNINQLPQRYRIRIYASTNLR
480 490 500 510 520 530
8469133 VKAHTLSQSTTVVRGPGFTGGDLIRRTSGSPAYIIVNINQLPQRYRIRIYASTNLR
470 480 490 500 510 520
cry1a-105.pe IYVTVAGERIFAGQFNKMTDGPFLQSFVSATINTAFTPPMSQSFVVGADTSSGNE
540 550 560 570 580 590
8469133 IYVTVAGERIFAGQFNKMTDGPFLQSFVSATINTAFTPPMSQSFVVGADTSSGNE
530 540 550 560 570 580 590
cry1a-105.pe VYIDRELIPTAEAEYNYRAQKAVNAFTSTQGLKNTVYDHIQVSNLVTYLS
600 610 620 630 640 650
8469133 VYIDRELIPTAEAEYNYRAQKAVNAFTSTQGLKNTVYDHIQVSNLVTYLS
590 600 610 620 630 640 650
cry1a-105.pe DEFCLDERSELSEKVKVKAQV--KRNLLQDNFRCINRQPDHGRGSDITTIQGGDDVFK
660 670 680 690 700 710
8469133 DEFCLDERSELSEKVKVKAQV--KRNLLQDNFRCINRQPDHGRGSDITTIQGGDDVFK
650 660 670 680 690 700 710
cry1a-105.pe ENVTVLSGTFECYPTLYKIDSKLKEFYVARGVIESQLEIYIRYNAKHETVN
720 730 740 750 760 770
8469133 ENVTVLSGTFECYPTLYKIDSKLKEFYVARGVIESQLEIYIRYNAKHETVN
710 720 730 740 750 760 770
cry1a-105.pe VPGTGLMPLSAQSPICKCEPNRCAPHLEWNPDLSCSDGEKCAHSHVSLDQVGC
780 790 800 810 820 830
8469133 VPGTGLMPLSAQSPICKCEPNRCAPHLEWNPDLSCSDGEKCAHSHVSLDQVGC
770 780 790 800 810 820 830
cry1a-105.pe TDLNEDLGWVIFKIKTQDGHARLGNLFLEKPLVGEALARYKRAEKKAKKKEWE
840 850 860 870 880 890
8469133 TDLNEDLGWVIFKIKTQDGHARLGNLFLEKPLVGEALARYKRAEKKAKKKEWE
830 840 850 860 870 880 890
cry1a-105.pe TINVYKEKESVDALFVNSQYDQADTNIAHAAKRVHSREAYLPSELSVPGVNA
900 910 920 930 940 950
8469133 TINVYKEKESVDALFVNSQYDQADTNIAHAAKRVHSREAYLPSELSVPGVNA
890 900 910 920 930 940 950

8469133 cry1a-105.pe VSOQVRVCGRGYVLAIVYKGGCVTHREIENNTDELKFNCEVEEYFNNTVTGN
1080 1090 1100 1110 1120 1130
2982744 VSOQVRVCGRGYVLAIVYKGGCVTHREIENNTDELKFNCEVEEYFNNTVTGN
1080 1090 1100 1110 1120 1130
cry1a-105.pe VSOQVRVCGRGYVLAIVYKGGCVTHREIENNTDELKFNCEVEEYFNNTVTGN
1080 1090 1100 1110 1120 1130
2982744 VSOQVRVCGRGYVLAIVYKGGCVTHREIENNTDELKFNCEVEEYFNNTVTGN
1080 1090 1100 1110 1120 1130
cry1a-105.pe DY--NKNHGANACSSRNRGYDESYESSNIPADYGVLEWYATDGGNACEFNRGH--
1070 1080 1090 1100 1110 1120
2982744 DY--NKNHGANACSSRNRGYDESYESSNIPADYGVLEWYATDGGNACEFNRGH--
1070 1080 1090 1100 1110 1120
cry1a-105.pe YTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVSGVGLMEE
1130 1140 1150 1160 1170 1180
2982744 YTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVSGVGLMEE
1130 1140 1150 1160 1170 1180
cry1a-105.pe -TFLPAGYVTALEYFPETDVVWEIGETEGTFIVDSVELLMES
1130 1140 1150 1160 1170 1180
2982744 -TFLPAGYVTALEYFPETDVVWEIGETEGTFIVDSVELLMES
1130 1140 1150 1160 1170 1180
cry1a-105.pe
SW:8469133

8469133 description="PESTICIDIAL CRYSTAL PROTEIN CRY1EB (INSECTICIDAL
DELTA-ENDOTOXIN CRY1F(B)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (132 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar morrisoni"
source="swissprot_prot version=NA type=PR"

SCORES Initl: 3052 Initn: 4791 Opt: 5288 z-score: 6002.6 E(1): 0
>>SW:8469133
initn: 4791 initl: 3052 opt: 5288 z-score: 6002.6 expect(1):
Smith-Waterman score: 5288; 68.4% identity in 1186 aa overlap
(1-1177:1-1169)

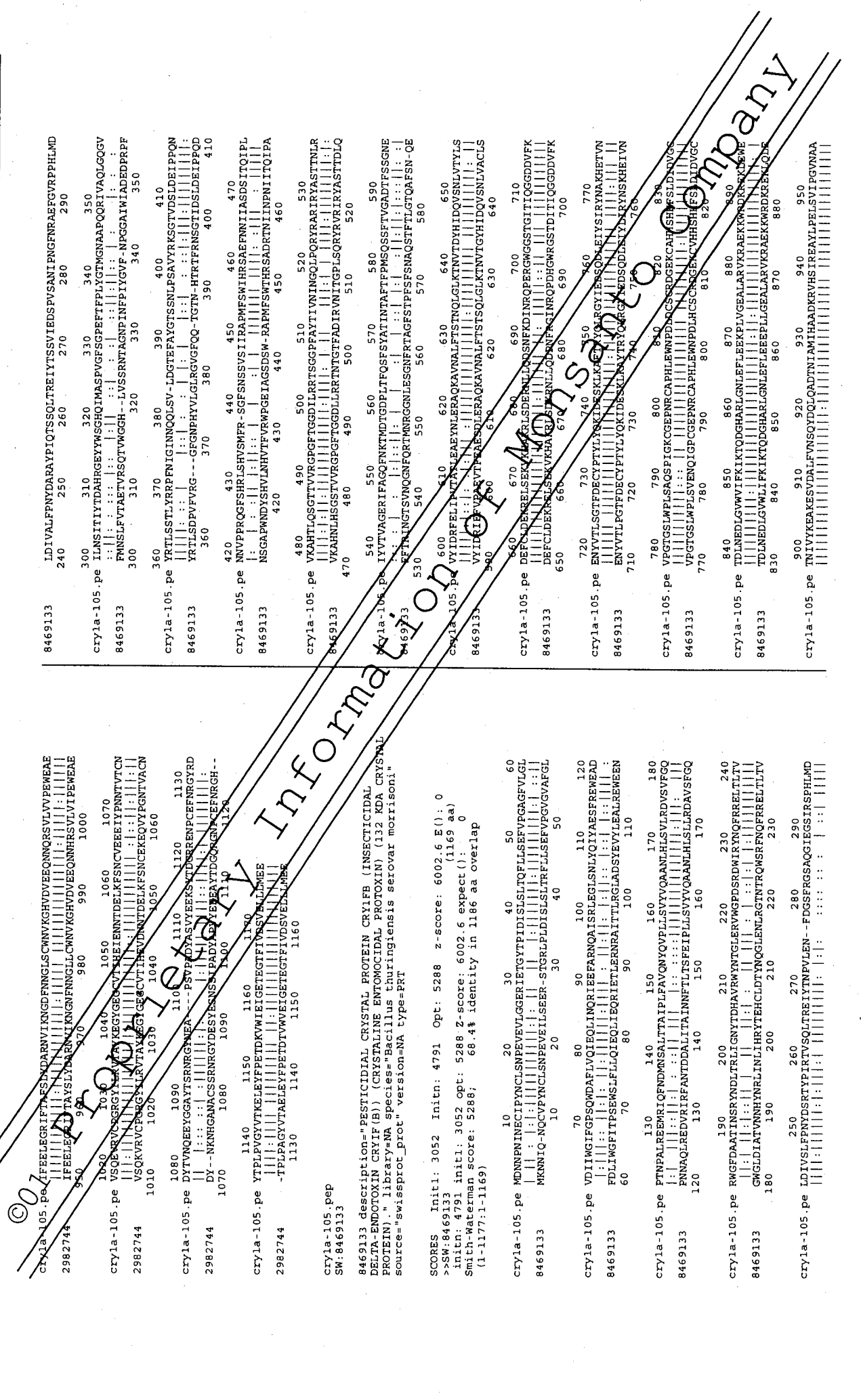
cry1a-105.pe MDNPNINECIPYCNLSNPEVGLGGERIETGYTPIDISLSLTQFLLSFVFGAGVLGL
10 20 30 40 50 60
8469133 MKNNIQ-NOCVPYCNLSNPEVGLSEER-STGRPLDLSLSLTQFLLSFVFGAGVLGL
10 20 30 40 50 60

cry1a-105.pe VDIIMGIFGQSDAFVQIQLIMORIEEPARNOAISRLGLSNLYIYAESFWEAD
70 80 90 100 110 120
8469133 FDLINGFITPSEMSFLQIQLIEORIEETERNHAITTLRGADSTVLEALREMEEN
60 70 80 90 100 110 120

cry1a-105.pe PTNPALREEMRIQFMDNMSALTTAIPFAVQYQVPLLSVYVQAANLHLSVLRDVSFVGQ
130 140 150 160 170 180
8469133 PNPALREEMRIQFMDNMSALTTAIPFAVQYQVPLLSVYVQAANLHLSVLRDVSFVGQ
120 130 140 150 160 170 180

cry1a-105.pe RWGFDAAINRNDLTRLIGNVTHAVRWYNTGLERWPGDSRDWRVNOQFRELITV
190 200 210 220 230 240
8469133 RWGFDAAINRNDLTRLIGNVTHAVRWYNTGLERWPGDSRDWRVNOQFRELITV
180 190 200 210 220 230 240

cry1a-105.pe LDIVSLFVNSDRTYPIRTVSQLTREIYNPVLN--FDGSPGSAQGIIEGSIPLMD
250 260 270 280 290
8469133 LDIVSLFVNSDRTYPIRTVSQLTREIYNPVLN--FDGSPGSAQGIIEGSIPLMD
240 250 260 270 280 290




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8469133      TNIVYKEAKESVDALFVNSQVDRLOADTNIAHIAADKRVHRIREAYLPESLVIQVNA
890          900      910      920      930      940
cryla-105.pe IFEELGRIFTAFLSYDARNVILKQDFNGLSCWNVKGVHDVEEQNQNSVLLVPEWEAE
960          970      980      990      1000      1010
8469133      IFEELGRIFTAFLSYDARNVILKQDFNGLSCWNVKGVHDVEEQNQNSVLLVPEWEAE
950          960      970      980      990      1000
cryla-105.pe VSOEVRVCPGRGYILRVTAKEGYGEGCVTITHEINNTDELKFS-NCVEEELPNNTVTC
1020         1030      1040      1050      1060      1070
8469133      VSOEVRVCPGRGYILRVTAKEGYGEGCVTITHEINNTDELKFS-NCVEEELPNNTVTC
1010         1020      1030      1040      1050      1060
cryla-105.pe NDYTVNQBEYGAATSNRNGYNEA----PSVPADYASVYEEKSYTDGRENPCFENGYR
1080         1090      1100      1110      1120      1130
8469133      NDY--NKHGANACSSRNGGYDESYESNSIPADYAPVYEEAYTDQGRNCFENRGH-
1070         1080      1090      1100      1110      1120
cryla-105.pe DYTLPVGVTKLEYFETDKVWEIGETGTFVDSVLLMEE
1140         1150      1160      1170
8469133      --TELPAGVITAELEYFETDKVWEIGETGTFVDSVLLMEE
1130         1140      1150      1160
cryla-105.pep
NRAA:6650206
6650206 source="GENBANK_PROT" crystal protein CryIb [Bacillus thuringiensis
serovar morrisonii|gi|8469133|sp|O66377|CRLFB_BACTM Pesticidal crystal protein
CryIb (insecticidal delta-endotoxin CryIb(b)) (Crystalline entomocidal protoxin)
(132 kDa crystal protein)
SCORES      Initl: 3052      Initn: 4791      Opt: 5288      z-score: 6002.6      E(): 0
>>NRAA:6650206
initn: 4791      initl: 3052      opt: 5288      z-score: 6002.6      expect(): 0
Smith-Waterman score: 5288;      68.4% identity in 1186 aa overlap
(1-1177:1-1169)
cryla-105.pe      MNPNINECIPNCLSNPEVEVLGGERIETGTPIDISLSTQFLLSEFVPGAGFVLGL
10          20      30      40      50      60
6650206      MNKNIQ-NQCVPNCLSNPEVEVLSEER-STGRPLDLSLSTFLLSEFVPGVAFGL
10          20      30      40      50
cryla-105.pe      VDIWGIFGSQMDAFLVQLEOLINORIEEFARNQAIISRLGLSLXLYOIAESFREWEAD
70          80      90      100      110      120
6650206      FDLWGFTTSEMSFLQLEQLIEQRIETERNRAITTLRGLADSYEVLEALREWEEN
60          70      80      90      100      110
cryla-105.pe      PTNPALREEMRIQFNDMNSALTAIPLFAVQNVQVPLLSVYQAAHLHSLVLRDVSVFQ
130         140      150      160      170      180
6650206      PNAQLREDVRIRFANTDALLITAINNFTLSFEIPLLSVYQAAHLHSLVLRDVSFQ
120         130      140      150      160      170
cryla-105.pe      RWGFDAAITNSRINDLTRLIGNYTHAVRWNTGLEVWGPDSDRWIRYQFRRELTLV
190         200      210      220      230      240
6650206      GWGLDIATVNNHYNRLINLHRYTEHCLDITYNQGLENLGRNTWQMSFNFQFRRELTLV
180         190      200      210      220      230
```

```
cryla-105.pe      LDIVSFPPNYSRYPRTVQSQTRITRYINPVLEN--FDGSRGSAQGIEGSIRSPHLM
250         260      270      280      290
6650206      LDIVSFPPNYSRYPRTVQSQTRITRYINPVLEN--FDGSRGSAQGIEGSIRSPHLM
240         250      260      270      280      290
cryla-105.pe      ILNSITIVTDARGEYVMSGHQIMASPVGFCSPETFLYGTMGNAAPQORIVAQLGQGV
300         310      320      330      340      350
6650206      FMSLSFVTAETVRSQTVWGGH--LVSSRTAGNPINPIFYGVF-NFGGAIWIADDEPRPF
300         310      320      330      340      350
cryla-105.pe      YRTLSSTLYRRFPFNGINNOQLSV-LDGTETAYGTSNLPASVVRKSGTVDSLDEIPPN
360         370      380      390      400      410
6650206      YRTLSSTLYRRFPFNGINNOQLSV-LDGTETAYGTSNLPASVVRKSGTVDSLDEIPPN
360         370      380      390      400      410
cryla-105.pe      NVVPPRQGESHRSLHSMFR-SGFSNNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPL
420         430      440      450      460      470
6650206      NSGAPWNDSYHVLNHRVTFVRWPGEIAAGDSW-RAPMFSWTHRSADRNTINPNITQIPA
420         430      440      450      460      470
cryla-105.pe      VKAHTLQSGTTVVRGPGFTGCDILRTSGGPFAYTIVNINGOLPORVARIKYSTNLR
480         490      500      510      520      530
6650206      VKAHTLQSGTTVVRGPGFTGCDILRTSGGPFAYTIVNINGOLPORVARIKYSTNLR
470         480      490      500      510      520
cryla-105.pe      IYTVAGRIIFAGQFNKMTDGTDFTFOSFYATINTAFTFPMSSQSFVAGDTFSSGNE
540         550      560      570      580      590
6650206      IYTVAGRIIFAGQFNKMTDGTDFTFOSFYATINTAFTFPMSSQSFVAGDTFSSGNE
530         540      550      560      570      580
cryla-105.pe      VVIDRFLIPVATLEAEYNLBRACKAVNALFTSINOLGLKNTVTHIDQVSNLVYLS
600         610      620      630      640      650
6650206      VVIDRFLIPVATLEAEYNLBRACKAVNALFTSINOLGLKNTVTHIDQVSNLVYLS
590         600      610      620      630      640
cryla-105.pe      DEFCLDEKRELSEKVKHAKELSDERNLLQDSNFKDINRQPERGWSGTGTTIQGDDVFX
660         670      680      690      700      710
6650206      DEFCLDEKRELSEKVKHAKELSDERNLLQDSNFKDINRQPERGWSGTGTTIQGDDVFX
650         660      670      680      690      700
cryla-105.pe      ENYVTLSTDFECYPTLYQKIDESKLAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVN
720         730      740      750      760      770
6650206      ENYVTLSTDFECYPTLYQKIDESKLAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVN
710         720      730      740      750      760
cryla-105.pe      VPGTGLSWPLSEVNGQIPGCPENRCAPIHLEWNPDLHSCDRDGEKCVHSHHFLSDIDVGC
780         790      800      810      820      830
6650206      VPGTGLSWPLSEVNGQIPGCPENRCAPIHLEWNPDLHSCDRDGEKCVHSHHFLSDIDVGC
770         780      790      800      810      820
cryla-105.pe      TDNLNEDLGWVIFKIKITQGHARLGNLEFLEKPLVGEALARKVAKKWKDKREKLEWE
840         850      860      870      880      890
6650206      TDNLNEDLGWVIFKIKITQGHARLGNLEFLEKPLVGEALARKVAKKWKDKREKLEWE
830         840      850      860      870      880
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MSL No. 20351
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©01

cr1a-105.pe TNAVYKADSVDAIWNSSDLOADNTNIAHAAKRVHISREAVLPSELSVIFGVNAA
6650206 TNAVYKADSVDAIWNSSDLOADNTNIAHAAKRVHISREAVLPSELSVIFGVNAA

cr1a-105.pe IFEELGRTFASLSDARVATAGDFNGSCNNKGHVDVEONNORSVLVWPEWAE
6650206 IFEELGRTFASLSDARVATAGDFNGSCNNKGHVDVEONNORSVLVWPEWAE

cr1a-105.pe VSOEVRVCPGRGVLRTAYKREGSEGNTHIEKATPELKFS-NVSEVEIYVNNVTVC
6650206 VSOEVRVCPGRGVLRTAYKREGSEGNTHIEKATPELKFS-NVSEVEIYVNNVTVC

cr1a-105.pe NDYVNVQEEVGCAYTSNRNGNEA----PSPADYASVYKSTDGRNPNPVRNGYR
6650206 NDYVNVQEEVGCAYTSNRNGNEA----PSPADYASVYKSTDGRNPNPVRNGYR

cr1a-105.pe DYTLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVVELLIMEE
6650206 DYTLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVVELLIMEE

cr1a-105.pep
NRAA:61252381

61252381 source: "GENBANK PROT" Pesticidal crystal protein cr1aA (insecticidal
delta-endotoxin cr1aAa) (Crystalline entomocidal protoxin) (133 kDa crystal
protein)gi|551713|gb|AA2252.1| insecticidal crystal
protein|gi|224474|prf|1106181A protein, insecticidal crystal

SCORES Initl: 2659 Initn: 5117 Opt: 5206 z-score: 5910.9 E(): 0
>NRAA:61252381
Initn: 5117 Initl: 2659 Opt: 5206 z-score: 5910.9 expect(): 0
Smith-Waterman score: 5206; 83.5% identity in 937 aa overlap
(1-935:1-934)

cr1a-105.pe MDNPNINCEIPYCNLSNPEVEVLGGERIETGTPIDISLSLTOFLSEVPVAGVGLG
61252381 MDNPNINCEIPYCNLSNPEVEVLGGERIETGTPIDISLSLTOFLSEVPVAGVGLG

cr1a-105.pe VDIIMGIPGSDQAFVQIEQLINQRIEFAFNQASRLGSLNLYQIYAESFREWAD
61252381 VDIIMGIPGSDQAFVQIEQLINQRIEFAFNQASRLGSLNLYQIYAESFREWAD

cr1a-105.pe PTNPALREHRIQFNDMSALTTAIPFAVQNVQVPLLSVYVQAAHLSLVLDVSFVQ
61252381 PTNPALREHRIQFNDMSALTTAIPFAVQNVQVPLLSVYVQAAHLSLVLDVSFVQ

cr1a-105.pe RWGFDAAATNSRWDLTFLIGNVTDHVRWYNTGLERVGPDSDMTIRYNQFRRLTLTV
61252381 RWGFDAAATNSRWDLTFLIGNVTDHVRWYNTGLERVGPDSDMTIRYNQFRRLTLTV

cr1a-105.pe LDIVSLFNFYDSRTYPIRTYSQTLTTRIYNTPVLENFDCSFRGSAQIEGSRSHPLMDIL
61252381 LDIVSLFNFYDSRTYPIRTYSQTLTTRIYNTPVLENFDCSFRGSAQIEGSRSHPLMDIL

cr1a-105.pe NSITIYDAHRGEYWSGHQIMASPVGFSGFPTFPLXGTMGNAAPQORIVAOIGGVIR
61252381 NSITIYDAHRGEYWSGHQIMASPVGFSGFPTFPLXGTMGNAAPQORIVAOIGGVIR

cr1a-105.pe TLSSTLYRRP-FNIGINNQQLSVLDGTEPAYGT-SSNLPSSAVRKSGTVDLSDEIPPQNN
61252381 TLSSTLYRRP-FNIGINNQQLSVLDGTEPAYGT-SSNLPSSAVRKSGTVDLSDEIPPQNN

cr1a-105.pe NVPPQGFSHRLSHVMSFRSGNSVSIIIPAPMFHRSAEFNIIASDSITQIPLVK
61252381 NVPPQGFSHRLSHVMSFRSGNSVSIIIPAPMFHRSAEFNIIASDSITQIPLVK

cr1a-105.pe STNDSGNTVGVGPGTGGDLRLRTSGPFAYTININGQLPQRYRIRYASTTNLRIY
61252381 STNDSGNTVGVGPGTGGDLRLRTSGPFAYTININGQLPQRYRIRYASTTNLRIY

cr1a-105.pe VIVAGEIIPAQOFNTVNDGDLPTFOSFYATINTAFTFPMSSOSTVGAUTFFSGNEVY
61252381 VIVAGEIIPAQOFNTVNDGDLPTFOSFYATINTAFTFPMSSOSTVGAUTFFSGNEVY

cr1a-105.pe IDREFLIPVAFANFAEYNFEAKAVNALETSNOLGLKNTVDYHIDVSNLVYLSDE
61252381 IDREFLIPVAFANFAEYNFEAKAVNALETSNOLGLKNTVDYHIDVSNLVYLSDE

cr1a-105.pe FCIDKEKELSEKVKAKLSDERNLQSNFQDARQARGGKSGNLTGOGGDVFKEN
61252381 FCIDKEKELSEKVKAKLSDERNLQSNFQDARQARGGKSGNLTGOGGDVFKEN

cr1a-105.pe YVTLSGTFDECYPTLYOKIDESKKAFTRYQLRGYIEDQODLEIYVYANETVNVY
61252381 YVTLSGTFDECYPTLYOKIDESKKAFTRYQLRGYIEDQODLEIYVYANETVNVY

cr1a-105.pe GTGSLWFLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDVGCTD
61252381 GTGSLWFLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDVGCTD

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cryla-105.pe LNEGLGVWVIFKIKTDGCHARLGNLEFLEKPLVGEALARVRAEKWRDKREKLEWETN
61252381 LNEGLGVWVIFKIKTDGCHARLGNLEFLEKPLVGEALARVRAEKWRDKREKLEWETN
840 850 860 870 880 890
cryla-105.pe IYVKEAKESVDALFVNSQYDRLQADNTINIAHAAKRVHSIREAYLPESLVIPGVNAALF
900 910 920 930 940 950
61252381 IYVKEAKESVDALFVNSQYDRLQADNTINIAHAAKRVHSIREAYLPESLVIPGVNAALF
900 910 920 930
cryla-105.pe EELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNORSVLVVPWEAEVS
960 970 980 990 1000 1010
cryla-105.pep
SW:117534
117534 description="130 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALINE
ENTOMOCIDAL PROTOXIN)." library=NA species="Bacillus thuringiensis serovar
Smith-Waterman score: 5206; 83.5% identity in 937 aa overlap
(1-935:1-934)
SCORES Initl: 2659 Initn: 5117 Opt: 5206 z-score: 5910.9 E(): 0
>>SW:117534
Initn: 5117 initl: 2659 opt: 5206 Z-score: 5910.9 expect(): 0
Smith-Waterman score: 5206; 83.5% identity in 937 aa overlap
(1-935:1-934)
cryla-105.pe MDNPNNEICIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGFVLGL
10 20 30 40 50 60
117534 MDNPNNEICIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGFVLGL
10 20 30 40 50 60
cryla-105.pe VDIWGIFGSPQMDAFLVQIEQLINQRIEFAFNQAEISRLGSLNLYIYAESFREWEAD
70 80 90 100 110 120
117534 VDIWGIFGSPQMDAFLVQIEQLINQRIEFAFNQAEISRLGSLNLYIYAESFREWEAD
70 80 90 100 110 120
cryla-105.pe PTPNALREEMRIQFNDWNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLVDVSFVGQ
130 140 150 160 170 180
117534 PTPNALREEMRIQFNDWNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLVDVSFVGQ
130 140 150 160 170 180
cryla-105.pe RWGFDAAATNSRNDLTRLIGNYTHAVRWYNTGLERWVGSDSDWIRYNOFRRELITV
190 200 210 220 230 240
117534 RWGFDAAATNSRNDLTRLIGNYTHAVRWYNTGLERWVGSDSDWIRYNOFRRELITV
190 200 210 220 230 240
cryla-105.pe LDIVSLFPNVDRTPIRTVSQLTREIYTNVPLENDFGSGAQQEGSIRSPHMDIL
250 260 270 280 290 300
117534 LDIVSLFPNVDRTPIRTVSQLTREIYTNVPLENDFGSGAQQEGSIRSPHMDIL
250 260 270 280 290 300
cryla-105.pe NSIITYDARGEYWSGHQIMASPVGSGFEFTFPLTYMGNAAPQRIAGLQGVYR
310 320 330 340 350 360
117534 NSIITYDARGEYWSGHQIMASPVGSGFEFTFPLTYMGNAAPQRIAGLQGVYR
310 320 330 340 350 360
cryla-105.pe NRITYTDVHRGFWGNSGHQITASPVGSGFEFTFPLTYMGNAAPQRIAGLQGVYR
370 380 390 400 410
117534 NRITYTDVHRGFWGNSGHQITASPVGSGFEFTFPLTYMGNAAPQRIAGLQGVYR
370 380 390 400 410
```

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cryla-105.pe TLSSLTLYRRP-FNIGINNQLSVLDGTEFAYGT-SSNLPSAVYRKSGTVDSLDLEIPQWN
117534 TLSSLTLYRRP-FNIGINNQLSVLDGTEFAYGT-SSNLPSAVYRKSGTVDSLDLEIPQWN
360 370 380 390 400 410
cryla-105.pe NYPYRQGFSHRSLSHVSMFSGFSNVSIIIRAPMFVHRSFAFNIIASDSITQIPLVK
420 430 440 450 460 470
117534 NYPYRQGFSHRSLSHVSMFSGFSNVSIIIRAPMFVHRSFAFNIIASDSITQIPLVK
420 430 440 450 460 470
cryla-105.pe AHTLQSGTIVVRGPGFTGGDILRLRTSGGPFAYTVININGOLPORVRIYASVTNLRVY
480 490 500 510 520 530
117534 AHTLQSGTIVVRGPGFTGGDILRLRTSGGPFAYTVININGOLPORVRIYASVTNLRVY
480 490 500 510 520 530
cryla-105.pe VTVAGERIFAGOFNKTMDTGDLPTFQSFYATINTAFTPMSSQSFVVGADTFSSGNEVY
540 550 560 570 580 590
117534 VTVAGERIFAGOFNKTMDTGDLPTFQSFYATINTAFTPMSSQSFVVGADTFSSGNEVY
540 550 560 570 580 590
cryla-105.pe IDRELPVATILEAEYNLERAQAVNALFTSTNQLGKTVYDHYDQVSNLVTYLSDE
600 610 620 630 640 650
117534 IDRELPVATILEAEYNLERAQAVNALFTSTNQLGKTVYDHYDQVSNLVTYLSDE
600 610 620 630 640 650
cryla-105.pe FCLDEKRELSEKVKHAKRUSDERNLQDSNFKDINRQPERGMGSGTITIGQDDVFKEN
660 670 680 690 700 710
117534 FCLDEKRELSEKVKHAKRUSDERNLQDSNFKDINRQPERGMGSGTITIGQDDVFKEN
660 670 680 690 700 710
cryla-105.pe YVTLGTFDECYPTLYQKIDSKLKAFTRYQLAGYIEDSQLEIYIRYNAKHETVNP
720 730 740 750 760 770
117534 YVTLGTFDECYPTLYQKIDSKLKAFTRYQLAGYIEDSQLEIYIRYNAKHETVNP
720 730 740 750 760 770
cryla-105.pe GTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTD
780 790 800 810 820 830
117534 GTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTD
780 790 800 810 820 830
cryla-105.pe LNEGLGVWVIFKIKTDGCHARLGNLEFLEKPLVGEALARVRAEKWRDKREKLEWETN
840 850 860 870 880 890
117534 LNEGLGVWVIFKIKTDGCHARLGNLEFLEKPLVGEALARVRAEKWRDKREKLEWETN
840 850 860 870 880 890
cryla-105.pe IYVKEAKESVDALFVNSQYDRLQADNTINIAHAAKRVHSIREAYLPESLVIPGVNAALF
900 910 920 930 940 950
117534 IYVKEAKESVDALFVNSQYDRLQADNTINIAHAAKRVHSIREAYLPESLVIPGVNAALF
900 910 920 930 940 950
cryla-105.pe EELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNORSVLVVPWEAEVS
960 970 980 990 1000 1010
117534 EELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNORSVLVVPWEAEVS
960 970 980 990 1000 1010
cryla-105.pep
SW:61252381
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MSL No. 20351
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61252381 description="Pesticidal crystal protein cryIaA (Insecticidal
delta-endotoxin CryIaA)) (Crystalline entomocidal protein) (133 kDa crystal
protein) library=20 species="Bacillus thuringiensis serovar sotto"
source="swissprot_prot" version=NA type=PRT

SCORES Initl: 2659 Initn: 2864 Opt: 5266 z-score: 5910.9 E(I): 0
>>SW:61252381
initn: 5117 initl: 2659 opt: 5266 z-score: 5910.9 expect(1): 0
Smith-Waterman score: 5266; 83.6% identity to 997 aa overlap
(1-935:1-934)

cryIa-105.pe MDNNPINECIPNCLSNPEVLSGRIETCTPTDLSLSLTOFLSEFFVPGAGFVLGL
61252381
10 20 30 40 50 60
MDNNPINECIPNCLSNPEVLSGRIETCTPTDLSLSLTOFLSEFFVPGAGFVLGL

cryIa-105.pe VDIWIFGFSQMDAFLVOIEQLINORIEEPARNQALRDSLSLVOYLAESPFEWQ
61252381
70 80 90 100 110 120
VDIWIFGFSQMDAFLVOIEQLINORIEEPARNQALRDSLSLVOYLAESPFEWQ

cryIa-105.pe PTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYQAAHLHLSVNDVAFQO
61252381
130 140 150 160 170 180
PTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYQAAHLHLSVNDVAFQO

cryIa-105.pe RWGFDAAATINSRVNDLRLIGNYTHAVRWNTGLERWGPDSRDWRYNQFRELTLV
61252381
190 200 210 220 230 240
RWGFDAAATINSRVNDLRLIGNYTHAVRWNTGLERWGPDSRDWRYNQFRELTLV

cryIa-105.pe LDIVLFPNYSRTPIRTVSQLTREIYNPVLNFDGSRGSAQIEGSRPHMDIL
61252381
250 260 270 280 290 300
LDIVLFPNYSRTPIRTVSQLTREIYNPVLNFDGSRGSAQIEGSRPHMDIL

cryIa-105.pe NSITITDHRGEYWSHQIMASPVGSGPEFTFPLXGTMGNAAPQORIVAQOGQVVR
61252381
310 320 330 340 350
NSITITDHRGEYWSHQIMASPVGSGPEFTFPLXGTMGNAAPQORIVAQOGQVVR

cryIa-105.pe TLSSLYRRP-FNIGINNQOLSVDGTEFAYGT-SSNLPASVAVKSGTVDSDLEPPQNN
61252381
370 380 390 400 410
TLSSLYRRP-FNIGINNQOLSVDGTEFAYGT-SSNLPASVAVKSGTVDSDLEPPQNN

cryIa-105.pe NVPPRGFSHRLSHVSMFRSGFSNVSIIIRAPMFSWTHRSAEFNNIADSDIOTPLVK
61252381
420 430 440 450 460 470
NVPPRGFSHRLSHVSMFRSGFSNVSIIIRAPMFSWTHRSAEFNNIADSDIOTPLVK

cryIa-105.pe AHTLQSGTIVRGFGFTGGDILRTSGGPFAYTVINGQLPQRYRIRVASTINLRIY
61252381
480 490 500 510 520 530
AHTLQSGTIVRGFGFTGGDILRTSGGPFAYTVINGQLPQRYRIRVASTINLRIY

cryIa-105.pe VTVAGERIFAGQFNKNTWDGDLPTFCQSRYATINTATTFPMSQSSFTVCADTFSSGNEVY
61252381
540 550 560 570 580 590
VTVAGERIFAGQFNKNTWDGDLPTFCQSRYATINTATTFPMSQSSFTVCADTFSSGNEVY

cryIa-105.pe IDRFELIPVATLAEAYNLERAKAVNALFTSTNQLGLKNTVTDVHIDQVSNLYTILSDE
61252381
600 610 620 630 640 650
IDRFELIPVATLAEAYNLERAKAVNALFTSTNQLGLKNTVTDVHIDQVSNLYTILSDE

cryIa-105.pe FCLDEKRELSKVKHAKRUSDERNLLQDSNFKDINRQPERGSGSTGITIQGGDDVFKEK
61252381
660 670 680 690 700 710
FCLDEKRELSKVKHAKRUSDERNLLQDSNFKDINRQPERGSGSTGITIQGGDDVFKEK

cryIa-105.pe VYTLGTFDECYTYLYQKIDSKLKAFTRYQLRGVIEDSODLEIYSIRYNAKHETVNP
61252381
720 730 740 750 760 770
VYTLGTFDECYTYLYQKIDSKLKAFTRYQLRGVIEDSODLEIYSIRYNAKHETVNP

cryIa-105.pe GTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLSDIDVGCCTD
61252381
780 790 800 810 820 830
GTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLSDIDVGCCTD

cryIa-105.pe LNEELGFWYFKTKTQDGHARGLNLEFLEKPLVGEALARKVRAEKKWRDKREKLEWETN
61252381
840 850 860 870 880 890
LNEELGFWYFKTKTQDGHARGLNLEFLEKPLVGEALARKVRAEKKWRDKREKLEWETN

cryIa-105.pe IVYNAKESVDALFYQYDLSQADNMIHAADR
61252381
900 910 920 930
IVYNAKESVDALFYQYDLSQADNMIHAADR

cryIa-105.pe EELEGRIFTALSLYDARNVITQSDNNGLSCHVAVSHVDVEEQNNQSVLVVPEWEAEVS
61252381
960 970 980 990 1000 1010
EELEGRIFTALSLYDARNVITQSDNNGLSCHVAVSHVDVEEQNNQSVLVVPEWEAEVS

8469137 description="PESTICIDIAL CRYSTAL PROTEIN CRYIaA (INSECTICIDAL
DELTA-ENDOTOXIN CRYIaA)) (CRYSTALLINE ENTOMOCIDAL PROTEIN) (133 kDa crystal
protein)" library=NA species="Bacillus thuringiensis serovar aizawa"
source="swissprot_prot" version=NA type=PRT

SCORES Initl: 2864 Initn: 4526 Opt: 5185 z-score: 5885.5 E(I): 0
>>SW:8469137
initn: 4526 initl: 2864 opt: 5185 z-score: 5885.5 expect(1): 0
Smith-Waterman score: 5244; 67.6% identity in 1188 aa overlap
(1-1177:1-1174)

cryIa-105.pe MDNNPINECIPNCLSNPEVLSGRIETCTPTDLSLSLTOFLSEFFVPGAGFVLGL
8469137
10 20 30 40 50
MDNNPINECIPNCLSNPEVLSGRIETCTPTDLSLSLTOFLSEFFVPGAGFVLGL

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cry1a-105.pe VDIWICPGSQWDAFLVQIEQLINORIEEFARNQASIRLEGSLNLIQIYAESFREHEAD 70 80 90 100 110 120
8469137 FDIWGAIGPGSQWDAFLVQIEQLINORIEEFARNQASIRLEGSLNLIQIYAESFREHEAD 70 80 90 100 110 120

cry1a-105.pe PTPALREEMRIQFNDMSALTTAIPFAVQNYQVPLLSVVQAAHLNLSVLDRDVSFVGQ 130 140 150 160 170 180
8469137 PTPALREEMRIQFNDMSALTTAIPFAVQNYQVPLLSVVQAAHLNLSVLDRDVSFVGQ 130 140 150 160 170 180

cry1a-105.pe RWGFDAAITNSRYNDLTRILIGNYTDHAWRYNTGLERV-MGPSRDMIRYNGFRRELTLT 190 200 210 220 230
8469137 RWGFDAAITNSRYNDLTRILIGNYTDHAWRYNTGLERV-MGPSRDMIRYNGFRRELTLT 190 200 210 220 230

cry1a-105.pe VLDIVSLPNVDSRTYPIRVQSOLTREIYTNVLENFDGSRGSAQIEGS-IRSPHLM 240 250 260 270 280 290
8469137 VLDIVSLPNVDSRTYPIRVQSOLTREIYTNVLENFDGSRGSAQIEGS-IRSPHLM 240 250 260 270 280 290

cry1a-105.pe ILNSITITDHRGEYVMSGHQIMASPVGSGPEFTFLYGTMGNAAPQORIVAQLGQGV 300 310 320 330 340 350
8469137 ILNSITITDHRGEYVMSGHQIMASPVGSGPEFTFLYGTMGNAAPQORIVAQLGQGV 300 310 320 330 340 350

cry1a-105.pe ---YRILSTLYRRPFNIGINNQOLSVDLGTFAFGTSNLPSSAVKSGTVDSDLEIPP 360 370 380 390 400 410
8469137 ---YRILSTLYRRPFNIGINNQOLSVDLGTFAFGTSNLPSSAVKSGTVDSDLEIPP 360 370 380 390 400 410

cry1a-105.pe QNNVPPROGFSHRLSHVSMFRSGFSNSVSIIRAPMFSHSAEFNNIIASDSITQIP 420 430 440 450 460 470
8469137 QNNVPPROGFSHRLSHVSMFRSGFSNSVSIIRAPMFSHSAEFNNIIASDSITQIP 420 430 440 450 460 470

cry1a-105.pe LVKAHTLQSGTTVVRGPGFTGGDILARTSGGPFATVIVNNGQLPQRYRARIYASITNL 480 490 500 510 520 530
8469137 LVKAHTLQSGTTVVRGPGFTGGDILARTSGGPFATVIVNNGQLPQRYRARIYASITNL 480 490 500 510 520 530

cry1a-105.pe RIVTVAGERIFAGQFNKMTDGLTDFOSFSYATINTAFTFPMQSSFTVGADTFSSGN 540 550 560 570 580 590
8469137 RIVTVAGERIFAGQFNKMTDGLTDFOSFSYATINTAFTFPMQSSFTVGADTFSSGN 540 550 560 570 580 590

cry1a-105.pe EVVIDRFELIPVTALAEVNLERAQKAVNALFTSTNOLGLKTNVTDYHIDOVSNLTVYL 600 610 620 630 640 650
8469137 EVVIDRFELIPVTALAEVNLERAQKAVNALFTSTNOLGLKTNVTDYHIDOVSNLTVYL 600 610 620 630 640 650

cry1a-105.pe SDFCLDEKRELSEKVKHAKLSDEERNLLQDSNFKDINRQPERGWGSGTGITIQGGDVF 660 670 680 690 700 710
8469137 SDFCLDEKRELSEKVKHAKLSDEERNLLQDSNFKDINRQPERGWGSGTGITIQGGDVF 660 670 680 690 700 710
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cry1a-105.pe KENYVTLSTGTFDECPYLYOKIDESKKAFTRYOLRGYIEDSODLEIYISRYNAKHETV 720 730 740 750 760 770
8469137 KENYVTLSTGTFDECPYLYOKIDESKKAFTRYOLRGYIEDSODLEIYISRYNAKHETV 720 730 740 750 760 770

cry1a-105.pe NVFGTCSLWPLSAGSPIKCGENRCAPHLNPNLDSCSRDGEKCAHSHHSHFSLDIDVG 780 790 800 810 820 830
8469137 NVFGTCSLWPLSAGSPIKCGENRCAPHLNPNLDSCSRDGEKCAHSHHSHFSLDIDVG 780 790 800 810 820 830

cry1a-105.pe CTDLNEDLGVWVIFKIKITQDGHARLGNLEFLEEKPLGEALARVRAEKKKWRDKREKLEW 840 850 860 870 880 890
8469137 CTDLNEDLGVWVIFKIKITQDGHARLGNLEFLEEKPLGEALARVRAEKKKWRDKREKLEW 840 850 860 870 880 890

cry1a-105.pe ETRNIVYKEAKESVDALFVNSQYDQLQADNTNIAHIAADKRVHSIREAYLPESLVIPGVNA 900 910 920 930 940 950
8469137 ETRNIVYKEAKESVDALFVNSQYDQLQADNTNIAHIAADKRVHSIREAYLPESLVIPGVNA 900 910 920 930 940 950

cry1a-105.pe AIFEELEGRIPTAFSLYDARNVINKGDFNNGLSQWNVKGVHDVEEQNNQORSVLVVPWEA 960 970 980 990 1000 1010
8469137 AIFEELEGRIPTAFSLYDARNVINKGDFNNGLSQWNVKGVHDVEEQNNQORSVLVVPWEA 960 970 980 990 1000 1010

cry1a-105.pe EVSQEVVPCPGRGYILRVATYKSGYGGCVTHIEENNTDELAFSNCVBEETYPNNVTYC 1020 1030 1040 1050 1060 1070
8469137 EVSQEVVPCPGRGYILRVATYKSGYGGCVTHIEENNTDELAFSNCVBEETYPNNVTYC 1020 1030 1040 1050 1060 1070

cry1a-105.pe NDVYVQOEYGCAT--SRNRGNYEA---PSVPADYASVYVEEKSYPDGRNCPCFNRG 1080 1090 1100 1110 1120
8469137 NDVYVQOEYGCAT--SRNRGNYEA---PSVPADYASVYVEEKSYPDGRNCPCFNRG 1080 1090 1100 1110 1120

cry1a-105.pe YRDYTPLPVGYVTKLEYFPPTDKWIEIGETEGTFIVDSVELLMEE 1130 1140 1150 1160 1170
8469137 YRDYTPLPVGYVTKLEYFPPTDKWIEIGETEGTFIVDSVELLMEE 1130 1140 1150 1160 1170

cry1a-105.pe YVNYRFPAGYVTKLEYFPPTDKWIEIGETEGTFIVDNVELLMEE 1180 1190 1200 1210 1220
8469137 YVNYRFPAGYVTKLEYFPPTDKWIEIGETEGTFIVDNVELLMEE 1180 1190 1200 1210 1220

CRYIA-105.pep
NRAA:8469137
8469137 source="GENBANK_PROT" Pesticidal crystal protein cryIEb (Insecticidal
delta-endotoxin CryIE(b)) (Crystalline entomocidal protoxin) (134 kDa crystal
protein)[gi|142754|gb|AAA22346.1| cryIE(b)]
SCORES Initl: 2864 Initn: 4526 Opt: 5185 Z-score: 5885.5 E(): 0
>NRAA:8469137
Initn: 4526 Initl: 2864 Opt: 5185 Z-score: 5885.5 expect(): 0
Smith-Waterman score: 5244; 67.6% identity in 1188 aa overlap
(1-1177:1-1174)
cry1a-105.pe MDNPNINECIPNCLNSPEVEVLGGRIETGYTPTIDISLSLTQFLSFEVPGAGFVLGL 10 20 30 40 50 60
```

8469137 MENNIFDCCIPYCNNDVEILGTERSNNVAA-EIGLGSRLSVSR-IPLDGFIILG
cryla-105.pe VALLIGFSPSWAALVOIEQLNORFEARNOAISRLGSLNLYQIYAESFREWAD
8469137 FDTWNGGPSOWDLPFEOALIGRIETEFANOAISRLGSLNLYQIYAESFREWAD
cryla-105.pe PINPALREEMRIQFNDMNSALTAIPSAVAVNOVPLLSVUQAANLHLSVLROVSFVQ
8469137 PINPALREEMRIQFNDMNSALTAIPSAVAVNOVPLLSVUQAANLHLSVLROVSFVQ
cryla-105.pe RWGFDAAINSRYNDLTRIGNYTHAVRWYNLGEVWSPDSRWINKNOFRELKIT
8469137 RWGFDVATINSRYNDLTRIGEDYAVRWYNLGEVWSPDSRWINKNOFRELKIT
cryla-105.pe VLDIVSLFPNYDSRTYPIRTVSQLTRELYTNPLENDFSGFRGSAQEGS-IESPHND
8469137 VLDIISFQNYDSRLYPIRTVSQLTRELYTNPLENDFSGFRGSAQEGS-IESPHND
cryla-105.pe ILNSTIYTDHRGEYVWGHQIMASPVGFGPEFTPLPYGTMGNAAPQOIRVAQLQGV
8469137 FLNNIIDTLIRGVHVWAGHRVTSHTG-SQVSSPQIGITANAEPSRTIAPSTFPL
cryla-105.pe ---YELSSLYLRPNIGINNQQLSVLDCTERAYGTSNLSAVRKSQVDSLDIIPP
8469137 NLFYTLSDPFPRKSDNI-MPTLGINVQGVGFQPNNGEV---LYRRGTVDSLDLP
cryla-105.pe QNNVPPRQGFSEHLSHVSMFRSGFSNSVSIIRAPMFSIHRSAEFNNIIASDSITOIP
8469137 DGEN-SLVGYSHLSHVTLTSLNTNITSL---PTFVWTHSATDRNIIYPDVITQIP
cryla-105.pe LUKATLOSCTTVRPGFTGGDILRRTSQGFAYTIVNINQOLPORVRAIRVASTNL
8469137 LVKFSLTSGTSVVRGFTGGDILRRTSQGFAYTIVNINQOLPORVRAIRVASTNL
cryla-105.pe RIYVTVAGERIFAGQFNKMTDGLTFQSPSYATINTAFTFPMSSQSTVGTGDTSSGN
8469137 VMRVNNGSTTFQGFPSMTSANGSLTSQSPFAEPFVGISTSGSQTA-GISISNPRQ
cryla-105.pe EYVIDREFLIPVATLEAEVNERAQKAVNALFTSTNQLGLKTNVTDVHDOVSNLVYL
8469137 TPLDRIFEIFVDTAEAEVNERAQKAVNSLFTSSNQIELKTDVTDVHDOVSNLVYL
cryla-105.pe SDEFCLDEKRELSEKVKHAKRUSDRNLLQDSNFKDINRQPERGWSGTGTIGQDDVF

8469137 SDEFCLDEKRELSEKVKHAKRUSDRNLLQDSNFKDINRQPERGWSGTGTIGQDDVF
cryla-105.pe KENYVILSGTDECTPYLYQKIDSKLAKATRYQLRGYIEDSQOLEIYSIRYNAKHETV
8469137 KENYVILSGTDECTPYLYQKIDSKLAKATRYQLRGYIEDSQOLEIYSIRYNAKHETV
cryla-105.pe NYPGTGSLWPLSASPIGKCGEPNRCAPHLNPDLDCCRCDEKCAHSHHSHFLDIDVG
8469137 NYPGTGSLWPLSASPIGKCGEPNRCAPHLNPDLDCCRCDEKCAHSHHSHFLDIDVG
cryla-105.pe CTDLNEDLGWVWIFPKIKTQGHARLGNLEFLEEXPLVGEALARKVRAEKWRDKREKLEW
8469137 CTDLQEDLGWVWIFPKIKTQGHARLGNLEFLEEXPLVGEALARKVRAEKWRDKREKLEW
cryla-105.pe ETNYVYKESVDSALFVANSOYDQLOADNTNAMIHAADKRVHSIREAYLPESLVIPGVNA
8469137 ETNRYVTEAKEAVDAULFVDSQYDRLOADNTNAMIHAADKRVHSIREAYLPESLVIPGVNA
cryla-105.pe EYVGEVCPGRTSTVAYAYGEGVGTIHEIENNTDELKFSNVEEYIYNNVTVC
8469137 EYVGEVCPGRTSTVAYAYGEGVGTIHEIENNTDELKFSNVEEYIYNNVTVC
cryla-105.pe NDYVNSEFSGATVSRPRVNEA---FVDPADVASVVEKSVTDGRNPFENRG
8469137 NDYTAHQTAGSDSSNSRNIRFETEMWNTTACVNYKPYEEERYITDQGNHCEYDRG
cryla-105.pe YRDYTPPLGVVTKLEYFPEKVNIEIGSTFVNDSDVSLMSE
8469137 YVNYRFPVAGVTKLEYFPEKVNIEIGSTFVNDSDVSLMSE
cryla-105.pe
NRAA:8469134
8469134 sources="GENBANK PROT" Pesticidal crystal protein cryIa (insecticidal
delta-endotoxin CryIc(b)) (Crystalline entomocidal protoxin) 1133-1176 aa
protein)
SCORES Init1: 3092 Initn: 4578 Opt: 5094 z-score: 5782.1 E(): 0
>>NRAA:8469134
Initn: 4578 Init1: 3092 Opt: 5094 z-score: 5782.1 expect(): 0
Smith-Waterman score: 5288; 67.9% identity in 1195 aa overlap
(1-1177.1-1176)

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cry1a-105.pe MDNNPINECPYCNLSNPEVEVLGERIETGYPIDISLSITOPILSEFFVPGAGVLGL 60
8469134 MENNIQ-NQCPYNCLSNPEFEILGGERISTGSSIDISLSVQLLVNPNFVPGGFLVLGL 50
10 20 30 40 50
cry1a-105.pe VDIINGIFGSPQMDAFLVOIEQLINQRIIEEPARNOAISRLGSLNLIQIVAESPREWEAD 120
8469134 LDFVINGIVGSPQMDAFLVOIEQLINERIAAARSAAISNLEGLGNFNFIYVEAFKEWEAD 110
70 80 90 100 110
cry1a-105.pe PTNPALREEMRIQFNDMSALTATPILFAVQNYOVPLLSVYQAAHLHLSVLRDVSVFQ 180
8469134 PNPVTRVVDPRILDLGLLERDIPSFRIAGFEVPLLSVYQAAHLHILIRDSIFGA 170
130 140 150 160 170
cry1a-105.pe RWGFDAAITNSRYNDLTRILIGNYTDHAVRWYNTGLEWVGPPSDRWISYNOFRELTIV 240
8469134 RWGLTTINVENYNRILIRHIDEYANHCAITYNGLNMLPKSTYQDWIYTNREDLTLIV 230
190 200 210 220 230 240
cry1a-105.pe LDIVSLFNDSDRTYPIRTVSQLTREIYTNVPLENFDGFRSAQG----IEGS-IRSP 290
8469134 LDIAAFPSVDNRRYPIQSVGLTREIYTDPLI-TFNPOLQSVVAQLPTFNWESNAIRTP 280
250 260 270 280 290
cry1a-105.pe HMDILASITIIYTDHR-GE-YWNGHIMASPVGSGFEFFPPIYGTMGNAAPQRIVA 350
8469134 HLDVFNLLIIFIDWFSGVGRNFGYGHVSNRIG--GGNITSPYIGREANQEPFRSFT- 340
300 310 320 330 340 350
cry1a-105.pe QLGQGVRTLSSTLYR---RPFNIGINNQOLSVDLGTETAYGTSSNLPSVAVRKSQTVDS 400
8469134 -FNGVPFRTLSNPTFPPLQPPWAPPFN--LRGVGVGF---STPLNSFTYRGRTVDS 390
360 370 380 390 400
cry1a-105.pe LDEIPPNNVPPRQGFSHLSHVSMP-RSGFNSSVSIIRAPMFSWTHRSAPFNIIAS 460
8469134 LTELPPEDNSVPPREGYSRHLCHATFVQRSG---TPFLTTPGVFSWTHRSATDRNIYP 450
410 420 430 440 450 460
cry1a-105.pe DSITQILPVKAHTLOSQTVVGRGFTGGDLIRARTSGGFATYIYINGQLPQRYARIR 520
8469134 DVINGQLPVKAFLNLSIGTSVVRGFGFTGGDLIRTNVGSVLSMSLNFSNTLQRYRVR 510
470 480 490 500 510 520
cry1a-105.pe YASTNLRIVTVVAGERIFAGQFNKTMIDGDLTQFSFSYATINTAFPFMSQ--SSFTVG 580
8469134 YAAQTVMVSVTVGSGTTCNQGFSTMSANGALTSQSFRAEFPIVGTISASCSGASIS 570
530 540 550 560 570 580
cry1a-105.pe ADTFSSNGNEVY-IDREFELIPVATLEAFYNLRAQKAVNALFTSTNQLGKTNVTDYHID 640
8469134 NNV---GRQMFHLDRIEFLPVTSTFEBEYDLERAQAVNALFTSTNQLGLKTDVTDYHID 630
590 600 610 620 630 640
```

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cry1a-105.pe QVSNLVITLSDEPCIDEXKRELSEKVKHAKRLSDERNLLQDSNPKDINRQPERGGSGTGI 700
8469134 QVSNLVECLSDPECLDEKRELSEKVKHAKRLSDERNLLQDRNFRSINGQLDRGWRGSTD 690
650 660 670 680 690 700
cry1a-105.pe TIQGGDVFKENVYVTLGGTFDSCYPTLYIQIDESKLFKAFTRVYOLRGVIEDSQLEIYSI 760
8469134 TIQGGDVFKENVYVTLGGTFDSCYPTLYIQIDESKLFKAFTRVYOLRGVIEDSQLEIYLI 750
710 720 730 740 750 760
cry1a-105.pe RYNAKHETVNVPGTGSILWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSH 820
8469134 RYNAKHETVNVPGTGSILWPLSLTENSIGPCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSH 810
770 780 790 800 810 820
cry1a-105.pe HFSLDIDVGCTDLNEDLGWVWIFKIKTODGHARLGNLEFLEKPLVGALARVRAEKKW 880
8469134 HFSLDIDVGCTDLNEDLGWVWIFKIKTODGHARLGNLEFLEKPLVGALARVRAEKKW 870
830 840 850 860 870 880
cry1a-105.pe RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAHDAKRVHSIREAVLPE 940
8469134 RDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAHDAKRVHRIEAVLPE 930
890 900 910 920 930 940
cry1a-105.pe LSVIPGVNAIFEELEGRIFTAFSLYDARNVKNKGDFNNGLSQWNVKGVHVDVEQNNQRS 1000
8469134 LSVIPGVNAGIFEELGRIFTAYSILYDARNVKNKGDFNNGLLCNLKGHVHVDVEQNNHRS 990
950 960 970 980 990 1000
cry1a-105.pe VLVVPEMAEVSQEVRCVGRGYILRTAYKEGEGCVTHIEIENNTDELKSNVCEE 1060
8469134 VLVVPEMAEVSQEVRCVGRGYILRTAYKEGEGCVTHIEIEDNTDELKSNVCEE 1050
1010 1020 1030 1040 1050 1060
cry1a-105.pe IYPNNTVTCDYTVNOEYGGAYTSRNRGYNEA---PSVPADYASVVEEKSVDGRREN 1120
8469134 VYPNNTVTCDYATATOEYGGAYTSRNRGYNEA---PSVPADYASVVEEKAQTDGRDN 1110
1070 1080 1090 1100 1110 1120
cry1a-105.pe PCFENRGYRDTPLPVGYVTKLEYFPTDKWIRIGETEGTFIVDSVELLMEE 1170
8469134 HCESNRGYGDTPLPVGYVTKLEYFPTDKWIRIGETEGTFIVDSVELLMEE 1160
1130 1140 1150 1160 1170
cry1a-105.pe pep
SW:8469134
```

8469134 description="PESTICIDIAL CRYSTAL PROTEIN CRY1CB (INSECTICIDAL DELTA-ENDOTOXIN CRY1C(8)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (133 KDA CRYSTAL PROTEIN)." library="NA species="Bacillus thuringiensis serovar galleriae" source="swissprot_prot" version="NA type="PRT"

SCORES Initl: 3092 Initn: 4578 Opt: 5094 z-score: 5782.1 E(): 0

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[illegible]

cryla-105.pe ADTFSSGNEVY-IDRFELIPVATLEAEYINLERAQKAVNALFTSTNQLGKTNVTDYHH
8469134 NNW---GRQPHLDRIEFLPVTSTFEFEYDLERAQEAVALFTSTNQLGKTDVTDYHH
650 590 600 610 620 630 640
cryla-105.pe QVSNLVTVTSLDEFLCEKRESEKVKHAKSLDERNNLLQDSNFDVQINRQFSGWGSGTGI
8469134 QVSNVLECLSDFCLEKRESEKVKHAKSLDERNNLLQDSNFRFSINGQLDGRWGSDTI
650 660 670 680 690 700
cryla-105.pe TIQGGDDVFKENVTITSGTFDECYPTLYQKIDESKLAFTRYQLRGYIEDSDQLEIYSI
8469134 TIQGGDDVFKENVTITSGTFDECYPTLYQKIDESKLAFTRYQLRGYIEDSDQLEIYLI
710 720 730 740 750 760
cryla-105.pe RYNAKHETVNPVGTGSLMPLSAQSPISKCEPNRCAPHLEWPNPLDCSRDGEKCAHSH
8469134 RYNAKHETVNPVGTGSLMPLSTIENSIGPCPNRCAPHLEWPNPLDCSRDGEKCAHSH
770 780 790 800 810 820
cryla-105.pe HFSLDIDVGCIDLNEDLGVWIFIKITQDCHARLGNLFELEKPLGEALARKVRAEKW
8469134 HFSLDIDVGCIDLNEDLGVWIFIKITQDCHARLGNLFELEKPLGEALARKVRAEKW
830 840 850 860 870 880
cryla-105.pe RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIMHAADKRVHRIEAYLPE
8469134 RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIMHAADKRVHRIEAYLPE
890 900 910 920 930 940
cryla-105.pe LSVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 LSVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
950 960 970 980 990 1000
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
1010 1020 1030 1040 1050 1060
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
1070 1080 1090 1100 1110 1120
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
1130 1140 1150 1160 1170 1180
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
1190 1200 1210 1220 1230 1240
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
1250 1260 1270 1280 1290 1300
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
1310 1320 1330 1340 1350 1360
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
1370 1380 1390 1400 1410 1420
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
1430 1440 1450 1460 1470 1480
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
1490 1500 1510 1520 1530 1540
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
1550 1560 1570 1580 1590 1600
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
1610 1620 1630 1640 1650 1660
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
1670 1680 1690 1700 1710 1720
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
1730 1740 1750 1760 1770 1780
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
1790 1800 1810 1820 1830 1840
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
1850 1860 1870 1880 1890 1900
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
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1910 1920 1930 1940 1950 1960
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
1970 1980 1990 2000 2010 2020
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
2030 2040 2050 2060 2070 2080
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
2090 2100 2110 2120 2130 2140
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
2150 2160 2170 2180 2190 2200
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
2210 2220 2230 2240 2250 2260
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
2270 2280 2290 2300 2310 2320
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
2330 2340 2350 2360 2370 2380
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
2390 2400 2410 2420 2430 2440
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
2450 2460 2470 2480 2490 2500
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
2510 2520 2530 2540 2550 2560
cryla-105.pe VLVVPEWAEVSGQEVNVAEENGRITAFSLYDARNVIKNGDFNNGSLCWNVKGHVDEEONNRS
8469134 VLVVPEWAEV

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source="swissprot_prot" version=NA type=PRI

```
SCORES   Initl: 4688   Initn: 5153   Opt: 4702   z-score: 5336.7   E(): 0
>SW:117533
Initn: 5153   Initl: 4688   Opt: 4702   z-score: 5336.7   expect(): 0
Smith-Waterman score: 6896;   88.7% identity in 1181 aa overlap
(1-1177:1-1155)

cry1a-105.pe MDNPNINECIPNCLSNPEVEVLGGRIETGYTPIDISLSLTOFLISEFVPGAGVLGL
117533      10 20 30 40 50
MDNPNINECIPNCLSNPEVEVLGGRIETGYTPIDISLSLTOFLISEFVPGAGVLGL
10 20 30 40 50

cry1a-105.pe VDIWIFGFSQWDALFQIEQLINQRIIEFAFNOAISRLEGLSNLYQIYAESFREWEAD
117533      70 80 90 100 110 120
VDIWIFGFSQWDALFQIEQLINQRIIEFAFNOAISRLEGLSNLYQIYAESFREWEAD
70 80 90 100 110 120

cry1a-105.pe PTNPALREEMRIQFNDMSALTTAIPFAVQNYQVPLSVYVQAANHLVLRDVSFVQ
117533      130 140 150 160 170 180
PTNPALREEMRIQFNDMSALTTAIPFAVQNYQVPLSVYVQAANHLVLRDVSFVQ
130 140 150 160 170 180

cry1a-105.pe RWGFDAAITNSRINDTLRLIGNYTHAVRWNTGLERVMGPDSDWIRYNQFRRLTLV
117533      190 200 210 220 230 240
RWGFDAAITNSRINDTLRLIGNYTHAVRWNTGLERVMGPDSDWIRYNQFRRLTLV
190 200 210 220 230 240

cry1a-105.pe LDIVSLFPNDSRTYPIRTVSQLTREIYNTPVLENDFSGFRGAGGIEGIRSPHLMIDL
117533      250 260 270 280 290 300
LDIVSLFPNDSRTYPIRTVSQLTREIYNTPVLENDFSGFRGAGGIEGIRSPHLMIDL
250 260 270 280 290 300

cry1a-105.pe NSITIIYDAHRGEYWSGHQIMASPVGSGPEFTPLPGTGMGNAAPQORIVAQLGGVYR
117533      310 320 330 340 350 360
NSITIIYDAHRGEYWSGHQIMASPVGSGPEFTPLPGTGMGNAAPQORIVAQLGGVYR
310 320 330 340 350 360

cry1a-105.pe TLSSTLYRRFPNIGINNQLSVLDGTEFAFGTSSNLPNAVYKSGTVDSDLEIPPNQNV
117533      370 380 390 400 410 420
TLSSTLYRRFPNIGINNQLSVLDGTEFAFGTSSNLPNAVYKSGTVDSDLEIPPNQNV
370 380 390 400 410 420

cry1a-105.pe PPROGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWIRSAEFNIIASDSITQIPLVRAH
117533      430 440 450 460 470 480
PPROGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWIRSAEFNIIASDSITQIPLVRAH
430 440 450 460 470 480

cry1a-105.pe TLQSGTIVVRGPGFTGGDILARTSGGPPAYTIININGQLPQRYRARIYASTNLRIYVT
117533      490 500 510 520 530 540
TLQSGTIVVRGPGFTGGDILARTSGGPPAYTIININGQLPQRYRARIYASTNLRIYVT
490 500 510 520 530 540

cry1a-105.pe VAGERIFAGQFNKMTDGLTDFQSFYATINTAFTFPMSSQSFVGNADTFSSGNEVID
117533      550 560 570 580 590 600
VAGERIFAGQFNKMTDGLTDFQSFYATINTAFTFPMSSQSFVGNADTFSSGNEVID
550 560 570 580 590 600
```

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117533      IDGRPINQGNFSATMSSGNSLQSGSFYTGFTTFPNFNGSSVFTLSAHVFNSGNEVYID
550 560 570 580 590 600

cry1a-105.pe RFELIPVTATLEAEYMLRAQKAVNALFTSTNQLGKTNVDYHIDQVSNLVTYLSDFEC
117533      610 620 630 640 650 660
RIEVPVAFETFAEYDLERAKAVNELFTSSNQIGLKTVDYHIDQVSNLVTYLSDFEC
610 620 630 640 650 660

cry1a-105.pe LDEKREUSEKVKHAKRLSDERNLLQDSNFKDINRQPERGSGSTGITIQGDDVFKENTV
117533      670 680 690 700 710 720
LDEKREUSEKVKHAKRLSDERNLLQDSNFKDINRQPERGSGSTGITIQGDDVFKENTV
670 680 690 700 710 720

cry1a-105.pe TLSGTFDECYPTVLYOKIDESKLAFTYQYRGYIEDSQDLEIYSIRYNAKHETVNPCT
117533      730 740 750 760 770 780
TLLGTFDECYPTVLYOKIDESKLAFTYQYRGYIEDSQDLEIYSIRYNAKHETVNPCT
730 740 750 760 770 780

cry1a-105.pe GSLWPLSAQSPIGKCEPNRCAPHLWNPDLCSCRDGKCAHSHHFLSLDIDVGCTDLN
117533      790 800 810 820 830 840
GSLWPLSAQSPIGKCEPNRCAPHLWNPDLCSCRDGKCAHSHHFLSLDIDVGCTDLN
790 800 810 820 830 840

cry1a-105.pe EDLGVWVIFKIKTQGHARLGNLFLEEKPLVGEALARKVKAEEKWRDKREKLEWETNIV
117533      850 860 870 880 890 900
EDLGVWVIFKIKTQGHARLGNLFLEEKPLVGEALARKVKAEEKWRDKREKLEWETNIV
850 860 870 880 890 900

cry1a-105.pe YKEAKESVDALFVNSQYDLOQADNIIAMIIHAADKRVHSIREAYLPESVIPGVNAAIFEE
117533      910 920 930 940 950 960
YKEAKESVDALFVNSQYDLOQADNIIAMIIHAADKRVHSIREAYLPESVIPGVNAAIFEE
910 920 930 940 950 960

cry1a-105.pe LEGRIFTAFSLYDARNVKNKGDFNNGLSQWNVKGVHDVEEQNNQNRSLVLPWEAEVSQOE
117533      970 980 990 1000 1010 1020
LEGRIFTAFSLYDARNVKNKGDFNNGLSQWNVKGVHDVEEQNNQNRSLVLPWEAEVSQOE
970 980 990 1000 1010 1020

cry1a-105.pe VRVCPGRGYILRVYAKGEGGCVTTHEIENNTDELKFSNCVEEIIYPNNTVTCNDIYV
117533      1030 1040 1050 1060 1070 1080
VRVCPGRGYILRVYAKGEGGCVTTHEIENNTDELKFSNCVEEIIYPNNTVTCNDIYV
1030 1040 1050 1060 1070 1080

cry1a-105.pe NOBEYGAITYSRNRGVNEA----PSVPADYASVYEKSYTDGRRNCFNFRGYDYTPL
117533      1090 1100 1110 1120 1130
TOBEYGTITSNRNGYDGAYESNSSVSPADYASAYEKA YTDGRRNCFNFRGYDYTPL
1090 1100 1110 1120 1130

cry1a-105.pe PVGVTKLEYFPETDKVMIEIGETGTFIVDSVELLMEE
117533      1140 1150 1160 1170
PAGVTKLEYFPETDKVMIEIGETGTFIVDSVELLMEE
1140 1150 1160 1170

cry1a-105.pe
117533      1180 1190 1200 1210 1220 1230
SW:61221643
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612121643 description="Pesticidial crystal protein cryIAb (Insecticidal
612121643 SW:612121643) (Crystalline entomocidial protoxin) (130 kDa crystal
612121643 library=NA Species="Bacillus thuringiensis serovar kurstaki"
612121643 library="PDB" Species="Bacillus thuringiensis serovar kurstaki"
612121643 source="swissprot.pdb" version=NA type=PRT

SCORES Init1: 4688 Init2: 5153 Opt: 4702 z-score: 5336.7 E(): 0
SW:612121643
initn: 5153 init1: 4688 opt: 4702 z-score: 5336 Eexpect(): 0
Smith-Waterman score: 6896; 88.7% identity in 1181 aa overlap
(L:1177:I:1155)

10 20 30 40 50 60
MNNPNINEICIPNCLNSPEVEVLGGENTGTGTDIALSLITQFLSEWPGAGFVLGL
|||||
612121643 MNNPNINEICIPNCLNSPEVEVLGGENTGTGTDIALSLITQFLSEWPGAGFVLGL
|||||

```

10	20	30	40	50	60
70	80	90	100	110	120
VDIIWGIFGFSQDAFLVOIEQLINQRIEFARNQAISRLEGLSNVOYVAESPENEAR					
70	80	90	100	110	120
VDIIWGIFGFSQDAFLVOIEQLINQRIEFARNQAISRLEGLSNVOYVAESPENEAR					
130	140	150	160	170	180
PTNPALREEMRIQFNDMNSALTAIPFAVQYQVPELVSVVQAAANHLHLSVJRDVGPQSO					
130	140	150	160	170	180
PTNPALREEMRIQFNDMNSALTAIPFAVQYQVPELVSVVQAAANHLHLSVJRDVGPQSO					
190	200	210	220	230	240
RWGFDAATINSRYNDJTRILIGNYTDHARVWNTGLERVWGPDSRDRIRYNQFRRELTUV					
190	200	210	220	230	240
RWGFDAATINSRYNDJTRILIGNYTDHARVWNTGLERVWGPDSRDRIRYNQFRRELTUV					

61221643	VDIIIGIFGFSQWDAFLVOIEQLINQRIEFARQAISRLEGLSNVYQVAESPENEAR	70	80	90	100	110	120
61221643	PTNPALREEMRIQFNDMNSALTTAIPFAVQYQVPLLSVTVQAANHLHLSVRDVSFG	130	140	150	160	170	180
61221643	PTNPALREEMRIQFNDMNSALTTAIPFAVQYQVPLLSVTVQAANHLHLSVRDVSFG	130	140	150	160	170	180
61221643	RGWFDAAITNSRYNDJTRIIGNYTDHAVRWNTGLEFVWGPDSRDWRVYQRFRELLTV	190	200	210	220	230	240
61221643	RGWFDAAITNSRYNDJTRIIGNYTDHAVRWNTGLEFVWGPDSRDWRVYQRFRELLTV	190	200	210	220	230	240
61221643	LDIVLFPNDSTRYPIRTVQSGLTREITYTPVLNFNDSFRGSAQGTGESSIRSPHLMDDIL	250	260	270	280	290	300

61221643	PINPALREEMKIQFNDMSNAITAIPIFAVONTQVPELUSVYQQAANHLHLSVLRSDVSFVGQ	130	140	150	160	170	180
61221643	RGWFDAAATINSRYNDJLTRILIGNYTHAVRWNTGLERVWGPDSRDRIRYNQFRRELTUTV	190	200	210	220	230	240
61221643	RGWFDAAATINSRYNDJLTRILIGNYTHAVRWNTGLERVWGPDSRDRIRYNQFRRELTUTV	190	200	210	220	230	240
61221643	LDIVSLFPNDYSRTYPIRTVSQLTREITNPLVLENFDSFRGSAQGIEGSIIRSPHLMJIL	250	260	270	280	290	300
61221643	LDIVSLFPNDYSRTYPIRTVSQLTREITNPLVLENFDSFRGSAQGIEGSIIRSPHLMJIL	250	260	270	280	290	300
61221643	NSIITITVDHURGEVYWSHOIMASFGSPFETPLXTGMNAAPOORITVAQLQGQGVYR	310	320	330	340	350	360
61221643	NSIITITVDHURGEVYWSHOIMASFGSPFETPLXTGMNAAPOORITVAQLQGQGVYR	310	320	330	340	350	360

ryia-105.pe	LDIVSLPNDSRTYPIRTVSQLTREIYTPVLENFDSFRGSAQGIESIRSPHMDIL	250	260	270	280	290	300
61221643	LDIVSLPNDSRTYPIRTVSQLTREIYTPVLENFDSFRGSAQGIESIRSPHMDIL	250	260	270	280	290	300
ryia-105.pe	NSITTYDAHRGEVYMSGHOIMASVFGSCPEPTPLGTGMNAPQOIRIVAQLGQGYR	310	320	330	340	350	360
61221643	NSITTYDAHRGEVYMSGHOIMASVFGSCPEPTPLGTGMNAPQOIRIVAQLGQGYR	310	320	330	340	350	360
ryia-105.pe	TLSSLTRRPFNIGINQQLSVLDGTFAYGTSSNLPASVYKSGTVDSLEIPQNNNV	370	380	390	400	410	420
61221643	TLSSLTRRPFNIGINQQLSVLDGTFAYGTSSNLPASVYKSGTVDSLEIPQNNNV	370	380	390	400	410	420
		430	440	450	460	470	

6161221643	PPROGFSHRUSHVMFRSGFNSSVSIIRAPMFSWIKHRSAEFNNIIRASUSITTOIPLVKAH	430	440	450	460	470	480
6161221643	PPROGFSHRUSHVMFRSGFNSSVSIIRAPMFSWIKHRSAEFNNIIRASUSITTOIPLTKST	430	440	450	460	470	480
6161221643	TLQSGITTVRGPFGTGDIILRRTSGFPFAYITVINGOLPORVEARIRVASTTNIRIVYT	490	500	510	520	530	540
6161221643	NLGSGTSVVKGPFGTGDIILRRTSGFQISITLVRNITAPLSORIVRIRVASTTNLQPHFHS	490	500	510	520	530	540

NSIIYTDARHEGYYSCHQIMASVPFGSPETPLVGTWGNAPQQRIVLAQLQGYYIR	310	320	330	340	350	360
TLSSTLVRRPFGNINNOQLSVLDGFAYGTSSNLPSAVYKSGTVDSLEIPQNNNV	370	380	390	400	410	420
TLSSTLVRRPFGNINNOQLSVLDGFAYGTSSNLPSAVYKSGTVDSLEIPQNNNV	370	380	390	400	410	420
PPRQGFSHRSHVSMFRSGFNSSVSIIRAPMFSIHRSAFNNIITASDITQIPLVKAH	430	440	450	460	470	480
PPRQGFSHRSHVSMFRSGFNSSVSIIRAPMFSIHRSAFNNIIPSSQITQIPLTKST	430	440	450	460	470	480
TLQSQITVWRGPGTGGDILRRTSQGFAYTIVINGOLPORVEAIRVASTNLIIRIVYT	490	500	510	520	530	540

161221643 NLGSGTSVVKGPFGTGGDILLRSTSPGQISLIRVNIITADLSORIVRVIRVASTINLQPHTS 540

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MSL No. 20351
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cryla-105.pep
SW:61221646

61221646 description="Pesticidal crystal protein cryIAb (Insecticidal
delta-endotoxin CryIA(b)) (Crystalline entomocidal protoxin) (130 kDa crystal
protein)." library="NA species="Bacillus thuringiensis serovar berliner"
source="swissprot_prot" version="NA type="PRT

SCORES   Initl: 4688   Initn: 5153   Opt: 4702   z-score: 5336.7   E(): 0
>>SW:61221646
Initn: 5153   Initl: 4688   Opt: 4702   Z-score: 5336.7   expect(): 0
Smith-Waterman score: 6896;   88.7% identity in 1181 aa overlap
(1-1177:1-1155)

cryla-105.pe  MDNPNINECIPNCLSNPEVEVLGGERITGYTPIDISLSLTQFLISEFVPGAGFVLGL
10 20 30 40 50 60
MDNPNINECIPNCLSNPEVEVLGGERITGYTPIDISLSLTQFLISEFVPGAGFVLGL
10 20 30 40 50 60
70 80 90 100 110 120
VDIWIIGFQSQWDAFLVQIQLINQRIEFARNQAIISRLGSLNLYQIVAESFREWEAD
cryla-105.pe  VDIIWIIGFQSQWDAFLVQIQLINQRIEFARNQAIISRLGSLNLYQIVAESFREWEAD
10 20 30 40 50 60
VDIIWIIGFQSQWDAFLVQIQLINQRIEFARNQAIISRLGSLNLYQIVAESFREWEAD
70 80 90 100 110 120
130 140 150 160 170 180
PTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAAHLHSLVRDVSFVQ
cryla-105.pe  PTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAAHLHSLVRDVSFVQ
10 20 30 40 50 60
PTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAAHLHSLVRDVSFVQ
130 140 150 160 170 180
190 200 210 220 230 240
RWGFDAAATINSRYNDLTRILGNYTDHVAWRWYNTGLERWGPDDSRDWIRYNQFRRELTIV
cryla-105.pe  RWGFDAAATINSRYNDLTRILGNYTDHVAWRWYNTGLERWGPDDSRDWIRYNQFRRELTIV
10 20 30 40 50 60
LDIVSLFPNYDSRTYPIRTVSQLTREIYTPVLENDFSGFRGAGQEGGIRSHPMDIIL
61221646      LDIVSLFPNYDSRTYPIRTVSQLTREIYTPVLENDFSGFRGAGQEGGIRSHPMDIIL
250 260 270 280 290 300
LDIVSLFPNYDSRTYPIRTVSQLTREIYTPVLENDFSGFRGAGQEGGIRSHPMDIIL
250 260 270 280 290 300
310 320 330 340 350 360
NSITIYDHAHGEYVWSGHQIMASGVFGSGPEFTFLYXGTGMGNAAPQORIVAGLGGVYR
cryla-105.pe  NSITIYDHAHGEYVWSGHQIMASGVFGSGPEFTFLYXGTGMGNAAPQORIVAGLGGVYR
10 20 30 40 50 60
NSITIYDHAHGEYVWSGHQIMASGVFGSGPEFTFLYXGTGMGNAAPQORIVAGLGGVYR
310 320 330 340 350 360
370 380 390 400 410 420
TLSSTLYRRFPNIGINNQLSVLDGTGFAYGTSNNLPAAVRKSGTVDLSDEIIPQNNNV
cryla-105.pe  TLSSTLYRRFPNIGINNQLSVLDGTGFAYGTSNNLPAAVRKSGTVDLSDEIIPQNNNV
10 20 30 40 50 60
TLSSTLYRRFPNIGINNQLSVLDGTGFAYGTSNNLPAAVRKSGTVDLSDEIIPQNNNV
370 380 390 400 410 420
430 440 450 460 470 480
PARGFSHRLSHVSMRSGFNSSVSIIRAPMFSWTHRSASFNNIITASDSTIOTPLVXAH
cryla-105.pe  PARGFSHRLSHVSMRSGFNSSVSIIRAPMFSWTHRSASFNNIITASDSTIOTPLVXAH
10 20 30 40 50 60
PARGFSHRLSHVSMRSGFNSSVSIIRAPMFSWTHRSASFNNIITASDSTIOTPLVXAH
430 440 450 460 470 480
490 500 510 520 530 540
PARGFSHRLSHVSMRSGFNSSVSIIRAPMFSWTHRSASFNNIITASDSTIOTPLVXAH
61221646      PARGFSHRLSHVSMRSGFNSSVSIIRAPMFSWTHRSASFNNIITASDSTIOTPLVXAH
430 440 450 460 470 480
490 500 510 520 530 540

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cryla-105.pe PVGVVTELEYNEPDKWIEGTEGTFIVDSVELLMEE
61221646 PAGVYVTELEYNEPDKWIEGTEGTFIVDSVELLMEE
1120 1130 1140 1150
cryla-105.pep
NRAA: 40273
40273 source="GENBANK_PROT" unnamed protein product [Bacillus
thuringiensis]gi|216280|dbj|BA000711.1|CryIIA-endotoxin [Bacillus thuringiensis
serovar kurstaki]gi|3746545|gb|AAC4003.2|CryIIA-endotoxin [Bacillus
thuringiensis serovar kurstaki]gi|2736100|gb|AA013302.1|CryIIA-endotoxin
CryIAb [Bacillus thuringiensis]gi|2390452|gb|AA016494.1|CryIIA-endotoxin
[Bacillus thuringiensis]gi|61221643|sp|P04370|CryIAB-CTK Pectinidial crystal .

SCORES Initl: 4688 Initn: 5153 Opt: 4702 Z-score: 5336.7 E(1): 0
>NRAA:40273
Initn: 5153 Initl: 4688 Opt: 4702 Z-score: 5336.7 expect(1): 0
Smith-Waterman score: 6896; 88.7% identity in 1181 aa overlap
(1-1177:1-1155)

cryla-105.pe MDNPNNECIPYCNLSNPEVEVLGGERIETGYTPIDISLTQFLSEFVFGAGVLSA
40273 MDNPNNECIPYCNLSNPEVEVLGGERIETGYTPIDISLTQFLSEFVFGAGVLSA
10 20 30 40 50
70 80 90 100 110 120
cryla-105.pe VDIWIFGFSQWDAFLVQIQLINQRIEFAFNAQISLEGLSNLVQIAESFREWEAD
40273 VDIWIFGFSQWDAFLVQIQLINQRIEFAFNAQISLEGLSNLVQIAESFREWEAD
70 80 90 100 110 120
cryla-105.pe PTNPALEEMRIQFNDMSALTTPILFANVQYOVLLSVYVQANHLHSLVLRDVSFQ
40273 PTNPALEEMRIQFNDMSALTTPILFANVQYOVLLSVYVQANHLHSLVLRDVSFQ
130 140 150 160 170 180
cryla-105.pe RMGFDAATINSRYNDLRLIGNYTHAVRWNTGLERVGPDSRDWRVYNOFRRELTIV
40273 RMGFDAATINSRYNDLRLIGNYTHAVRWNTGLERVGPDSRDWRVYNOFRRELTIV
190 200 210 220 230 240
cryla-105.pe LDIVSLFPNDSTYPIRTVSQLTREITVPLVLENDGFRGSAQIEGSIIRSPHMDIL
40273 LDIVSLFPNDSTYPIRTVSQLTREITVPLVLENDGFRGSAQIEGSIIRSPHMDIL
250 260 270 280 290 300
cryla-105.pe NSIITYDAHRGEYVWSGHQIMASPVGFSGPETFFLYGTMGNAAPQRIVAQLGGGVYR
40273 NSIITYDAHRGEYVWSGHQIMASPVGFSGPETFFLYGTMGNAAPQRIVAQLGGGVYR
310 320 330 340 350 360
cryla-105.pe TLSLTVRRFPNIGINNQLSVLDGTFEYAGTSSNIPSAVYRKSQGVDSDEIPPQNNV
40273 TLSLTVRRFPNIGINNQLSVLDGTFEYAGTSSNIPSAVYRKSQGVDSDEIPPQNNV
370 380 390 400 410 420
430 440 450 460 470 480

cryla-105.pe PPROGFSHRLSHVSMFRSGFNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPLVKAH
40273 PPROGFSHRLSHVSMFRSGFNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPLVKAH
430 440 450 460 470 480
cryla-105.pe TLQSGTTVVRGPGFTGGDILRLRTSGGPFAYTVININGQLPORRYARIRYASTTNLRIYVT
40273 TLQSGTTVVRGPGFTGGDILRLRTSGGPFAYTVININGQLPORRYARIRYASTTNLRIYVT
490 500 510 520 530 540
cryla-105.pe VAGERIFAGFNKMTMDTGLPTFQSFYSYATINTAFTFPMSSSFTVGADTFSSGNEVYID
40273 VAGERIFAGFNKMTMDTGLPTFQSFYSYATINTAFTFPMSSSFTVGADTFSSGNEVYID
550 560 570 580 590 600
IDGRPINOQNFSAATMSSGSLQSGSFRIVGFTTFFNFNSGSSVFTLSAHVFNSEVYID
40273 IDGRPINOQNFSAATMSSGSLQSGSFRIVGFTTFFNFNSGSSVFTLSAHVFNSEVYID
550 560 570 580 590 600
cryla-105.pe RFELIPVATLEAEYMLERAKAVNALFTSNOLGLKTNVTDYHIDQVSNLVYLSDFEC
40273 RFELIPVATLEAEYMLERAKAVNALFTSNOLGLKTNVTDYHIDQVSNLVYLSDFEC
610 620 630 640 650 660
cryla-105.pe LDEKRELSEKVKHAKSLSDERNLLQDNFVDINRQPERGCMGSGTITIOGDDVFKENVY
40273 LDEKRELSEKVKHAKSLSDERNLLQDNFVDINRQPERGCMGSGTITIOGDDVFKENVY
670 680 690 700 710 720
cryla-105.pe TLSTTFDECYPTLYQKIDESKXAFTRYQLRGYIEDSQLEIYSIRYNAKHETVNPVT
40273 TLSTTFDECYPTLYQKIDESKXAFTRYQLRGYIEDSQLEIYSIRYNAKHETVNPVT
730 740 750 760 770 780
cryla-105.pe SLSLDYSAKSNVICKCEPNCAPHELNWPNLDCSCRDGEKCAHSHHFSLDIDVGCTDLN
40273 SLSLDYSAKSNVICKCEPNCAPHELNWPNLDCSCRDGEKCAHSHHFSLDIDVGCTDLN
790 800 810 820 830 840
cryla-105.pe EDLGVVWIFKIKTOSCHALSNLDEKFLVGESEARVYRAEKKKWRDKREKLEWETNV
40273 EDLGVVWIFKIKTOSCHALSNLDEKFLVGESEARVYRAEKKKWRDKREKLEWETNV
850 860 870 880 890 900
cryla-105.pe YKEAKESVDALFVNSQYDQLQADTNIAADRVHSIREAYDPELSVPGVNAAFIEE
40273 YKEAKESVDALFVNSQYDQLQADTNIAADRVHSIREAYDPELSVPGVNAAFIEE
910 920 930 940 950 960
cryla-105.pe LEGRIFFATSLYDARVINKGDNNGSLCNVKGHVDEKNNRSESLVAKPEIYEVSOE
40273 LEGRIFFATSLYDARVINKGDNNGSLCNVKGHVDEKNNRSESLVAKPEIYEVSOE
970 980 990 1000 1010 1020
cryla-105.pe VRVCPGRIYLRVTAKEGEGCVTTHEIENNTDLKESCNVEEYIPNNTVTCNDYTA
40273 VRVCPGRIYLRVTAKEGEGCVTTHEIENNTDLKESCNVEEYIPNNTVTCNDYTA
1030 1040 1050 1060 1070 1080
1090 1100 1110 1120 1130 1140

Monsanto Company
Final Report
Product Characterization Center

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cry1a-105.pe NOEYGGAYTSRNGYNEA---PSVPADYASVVEEKS YTDGRRENPCFNGRYDYTPVL
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
40273  TOEEYEGYTSRNGYDGAYESNSSVPADYASVVEEKA YTDGRRENPCFNGRYDYTPVL
1060 1070 1080 1090 1100 1110

cry1a-105.pe PVGYVKELEYFETDKVWIEIGETEGTFIVDSVELLMEE
1140 1150 1160 1170
40273  PAGYVKELEYFETDKVWIEIGETEGTFIVDSVELLMEE
1120 1130 1140 1150

cry1a-105.pep
SW:61221650

61221650 description="Pesticidal crystal protein cry1Ab (Insecticidal
delta-endotoxin CryIA(b)) (Crystalline entomocidal protoxin) (130 kDa crystal
protein)." library="NA species="Bacillus thuringiensis serovar aizawai"
source="swissprot_prot" version="NA type="PRT

SCORES Init1: 4688 Initn: 5153 Opt: 4702 z-score: 5336.7 E(): 0
>>SW:61221650
Init1: 5153 Initn: 4688 Opt: 4702 Z-score: 5336.7 expect(): 0
Smith-Waterman score: 6896; 88.7% identity in 1181 aa overlap
(1-1177:1-1155)

cry1a-105.pe MDNPNINECIPYNCLSNPEVEVLGGERIETGTPIDISLSLTQFLSEFVPGAGFVLGL 60
10 20 30 40 50
61221650 MDNPNINECIPYNCLSNPEVEVLGGERIETGTPIDISLSLTQFLSEFVPGAGFVLGL
10 20 30 40 50 60

cry1a-105.pe VDIWIFGFSQWDAFLVQIQLINQRIEFPARNQAIKSLGSLNLYQIYAESFREWAD 120
70 80 90 100 110
61221650 VDIWIFGFSQWDAFLVQIQLINQRIEFPARNQAIKSLGSLNLYQIYAESFREWAD
70 80 90 100 110 120

cry1a-105.pe PTNPALREEMRIQFNDMNSALTATPILFAVQNVQVPLLSVYVQAANHLHSLRDVSVFGQ 180
130 140 150 160 170
61221650 PTNPALREEMRIQFNDMNSALTATPILFAVQNVQVPLLSVYVQAANHLHSLRDVSVFGQ
130 140 150 160 170 180

cry1a-105.pe RWGFDATINRSYNDLTRILIGNYTHAVRWYNTGLERWGPDSRDWRYNQFRRELTIV 240
190 200 210 220 230
61221650 RWGFDATINRSYNDLTRILIGNYTHAVRWYNTGLERWGPDSRDWRYNQFRRELTIV
190 200 210 220 230 240

cry1a-105.pe LDIVSLFPNDYSRTYDITVTSQLTREIYTPVLENDFGFRSAGIEGSIKSPHLMIDL 300
250 260 270 280 290 300
61221650 LDIVSLFPNDYSRTYDITVTSQLTREIYTPVLENDFGFRSAGIEGSIKSPHLMIDL
250 260 270 280 290 300

cry1a-105.pe NSITIIYDAHRGEYVWSHQIMASPVGFSGPETFPFLYGTMGNAAPQRIVAQLGGGVYR 360
310 320 330 340 350
61221650 NSITIIYDAHRGEYVWSHQIMASPVGFSGPETFPFLYGTMGNAAPQRIVAQLGGGVYR
310 320 330 340 350 360

cry1a-105.pe TILSSTLYRRFPNIGINNQLSVLDGTEFAYGTSNPLPSAVYRKSGTVDLSLDEIPPNQNNV 420
370 380 390 400 410
61221650 TILSSTLYRRFPNIGINNQLSVLDGTEFAYGTSNPLPSAVYRKSGTVDLSLDEIPPNQNNV
370 380 390 400 410 420
```

```
61221650 TILSSTLYRRFPNIGINNQLSVLDGTEFAYGTSNPLPSAVYRKSGTVDLSLDEIPPNQNNV
370 380 390 400 410 420

cry1a-105.pe PPROGFSHRLSHVSMFRSGFNSSVSIIRAPMFWSIHRSAEFNNIIASDSITQIPLVKAH 480
430 440 450 460 470
61221650 PPROGFSHRLSHVSMFRSGFNSSVSIIRAPMFWSIHRSAEFNNIIASDSITQIPLVKAH
430 440 450 460 470 480

cry1a-105.pe TLOSGTIVRGPGFTGDDILRRTSQGFAYTIVNINGQLPQRYRARIYASTTNLRIYVT 540
490 500 510 520 530
61221650 TLOSGTIVRGPGFTGDDILRRTSQGFAYTIVNINGQLPQRYRARIYASTTNLRIYVT
490 500 510 520 530 540

cry1a-105.pe VAGERIFAGQFNKMTMDTQPLTFQSFYSATINTAFTFPMSSQSFVTGADTFSSGNEVYID 600
550 560 570 580 590
61221650 VAGERIFAGQFNKMTMDTQPLTFQSFYSATINTAFTFPMSSQSFVTGADTFSSGNEVYID
550 560 570 580 590 600

cry1a-105.pe RPELIPVTATLEAEYNLERAQKAVNAUFTSTNQLGKTNVTYHIDQVSNLVTVLSDFEC 660
610 620 630 640 650
61221650 RPELIPVTATLEAEYNLERAQKAVNAUFTSTNQLGKTNVTYHIDQVSNLVTVLSDFEC
610 620 630 640 650 660

cry1a-105.pe LDEKREISEKVKHAKLSLDERNLLQDNFQINRQPERGCGSGTITIQGGDDVFKENYV 720
670 680 690 700 710
61221650 LDEKREISEKVKHAKLSLDERNLLQDNFQINRQPERGCGSGTITIQGGDDVFKENYV
670 680 690 700 710 720

cry1a-105.pe TILSGTFDECPTLYQKIDESKIAFTRYQLRGYIEDSDLEIYSIRYNAKHETVNVPGT 780
730 740 750 760 770
61221650 TILSGTFDECPTLYQKIDESKIAFTRYQLRGYIEDSDLEIYSIRYNAKHETVNVPGT
730 740 750 760 770 780

cry1a-105.pe GSLWPLSAQSPICKGCEPNRCAPHLEWNPDLDCSDRDKCAHSHHPSLIDIDVGCTDLN 840
790 800 810 820 830
61221650 GSLWPLSAQSPICKGCEPNRCAPHLEWNPDLDCSDRDKCAHSHHPSLIDIDVGCTDLN
790 800 810 820 830 840

cry1a-105.pe EDLGWVWIFKIKTODGHARLGNLEFLEKPLVGEALARKRAEKKWRDKREKLEWETNV 900
850 860 870 880
61221650 EDLGWVWIFKIKTODGHARLGNLEFLEKPLVGEALARKRAEKKWRDKREKLEWETNV
850 860 870 880 900

cry1a-105.pe YKEAKESVDALFVNSQYDQLQADTNIAHIAADKRVHSIREAYLPESLVIPGVNAAIFEE 960
910 920 930 940
61221650 YKEAKESVDALFVNSQYDQLQADTNIAHIAADKRVHSIREAYLPESLVIPGVNAAIFEE
910 920 930 940 960

cry1a-105.pe LEGRIFTAFSLYDARNVIKNGDFNGLSCWNKGVHDVEEQNNHRSVLVPEWEAEVSQE 1020
970 980 990 1000
61221650 LEGRIFTAFSLYDARNVIKNGDFNGLSCWNKGVHDVEEQNNHRSVLVPEWEAEVSQE
970 980 990 1000 1020

cry1a-105.pe VRVPCPGRYILRTVATYKEGSGCVTTHETENNTDELKFSNCVEEYIPNNTVTCNDYTV 1080
1030 1040 1050 1060
61221650 VRVPCPGRYILRTVATYKEGSGCVTTHETENNTDELKFSNCVEEYIPNNTVTCNDYTV
1030 1040 1050 1060 1080
```

61221650 VAVCPGRIYILNTRAKYEGGEGCVTHIENNTDELKFCNVEEVEVNNVTVCNDYTA
1000 1010 1020 1030 1040 1050
cryla-105.pe NOEYGGANSPARVNEA--PSAPAYASVVEEKSVDGRENPCFNRGVDYTP
1090 1100 1110 1120 1130
61221650 TOEEYEGTISRNGDGVESNSVADYASAVEEKAYTDGRENPCFESNGYGDYTP
1060 1070 1080 1090 1100 1110 1120 1130
cryla-105.pe PVGYTKELEFFENKWEIGETEFQIVDSVLLMEE
1140 1150 1160 1170 1180 1190 1200 1210
61221650 PAGYVTELEFFETDKVNEIGETEFQIVDSVLLMEE
1120 1130 1140 1150 1160 1170 1180 1190 1200 1210
cryla-105.pe
NRAA:225669
225669 source="GENBANK_PROT" insect control protein

SCORES Initl: 4688 Initn: 6611 Opt: 4702 z-score: 5336.7 (1156 aa)
>>NRAA:225669
initn: 6611 initl: 4688 opt: 4702 z-score: 5336.7 expect (1): 0
Smith-Waterman score: 6866; 88.4% identity in 1182 aa overlap
(1-1177:1-1156)

cryla-105.pe MDNPNINECIPNCLSNPEVEVLGGERIETGYTPIDISLSTQPLLESEFVPGAGFVLGL
10 20 30 40 50 60
225669 MDNPNINECIPNCLSNPEVEVLGGERIETGYTPIDISLSTQPLLESEFVPGAGFVLGL
10 20 30 40 50 60
cryla-105.pe VDIWIFGFSQMDAFLVOIQLINRIEERFARNQISRLGSLNLIIVAESFREWED
70 80 90 100 110 120
225669 VDIWIFGFSQMDAFLVOIQLINRIEERFARNQISRLGSLNLIIVAESFREWED
70 80 90 100 110 120
cryla-105.pe PTNPALREEMRIQFNDMSALTTPAIFAVQNYQVPLLSVYVQAANLHLSVLRDVSFQ
130 140 150 160 170 180
225669 PTNPALREEMRIQFNDMSALTTPAIFAVQNYQVPLLSVYVQAANLHLSVLRDVSFQ
130 140 150 160 170 180
cryla-105.pe RWGFDAAITNSRYNDLTRIGNYTHAVRWNTCLERVWGPDSRDWIRYQFRRELTIV
190 200 210 220 230 240
225669 RWGFDAAITNSRYNDLTRIGNYTHAVRWNTCLERVWGPDSRDWIRYQFRRELTIV
190 200 210 220 230 240
cryla-105.pe LDIVSLFPNDSTYPIRTVSQLTREIYTNPVLNDFSGSAGQEGSIRSPHLMIDL
250 260 270 280 290 300
225669 LDIVSLFPNDSTYPIRTVSQLTREIYTNPVLNDFSGSAGQEGSIRSPHLMIDL
250 260 270 280 290 300
cryla-105.pe NSIITYDAHRGEYWSGHQIMASVFGSGPEFTPLGYTGMNAAPOQRIVAQLGGVYR
310 320 330 340 350 360
225669 NSIITYDAHRGEYWSGHQIMASVFGSGPEFTPLGYTGMNAAPOQRIVAQLGGVYR
310 320 330 340 350 360
cryla-105.pe TLSSTLYRPFNIGINNOQLSVLDGTEFAVGTSSNLPASVYKSGTVDLSDEIPPNNNV
370 380 390 400 410 420

225669 TLSSTLYRPFNIGINNOQLSVLDGTEFAVGTSSNLPASVYKSGTVDLSDEIPPNNNV
370 380 390 400 410 420
cryla-105.pe PPRQGFSHRLSHVMPRSGFSSNSSVSIIRAPMFSWHRGAENNIASDSITQPLVKAH
430 440 450 460 470 480
225669 PPRQGFSHRLSHVMPRSGFSSNSSVSIIRAPMFSWHRGAENNIASDSITQPLVKAH
430 440 450 460 470 480
cryla-105.pe TIQSGTIVRGPGFTGDIILRRTPGPFAYTIVNINQOLPORVRIYASTTNLRIYVT
490 500 510 520 530 540
225669 NLGSGTIVRGPGFTGDIILRRTPGPFAYTIVNINQOLPORVRIYASTTNLRIYVT
490 500 510 520 530 540
cryla-105.pe VAGERIFAGQPNMTGDPDLTFQSFYATINTAFTFPMSSQSFVGTADTFSSGNEVYID
550 560 570 580 590 600
225669 IDGRPIQNGFNSATMSGSGNSGSGFTVGTFTPFNFSGSVFTLSAHVFNSEVYID
550 560 570 580 590 600
cryla-105.pe REELIPVTATLEAYNLEPAKAVNALFTSNQGLKTNVTDYHIDQVSNLVYLSDFC
610 620 630 640 650 660
225669 RIEFVPAEIVFEAYEYDLEAKAVNALFTSNQGLKTNVTDYHIDQVSNLVYLSDFC
610 620 630 640 650 660
cryla-105.pe LDEKFESEKVKHAKLSERNLQDNFKNQINQPERGWSGSGTITQGGDDVFENYV
670 680 690 700 710 720
225669 LDEKFESEKVKHAKLSERNLQDNFKNQINQPERGWSGSGTITQGGDDVFENYV
670 680 690 700 710 720
cryla-105.pe TISGTECPYLYKQIDSEKAYTRYQIRGYIEDSODLEIYLRYNKAKHETVNPVT
730 740 750 760 770 780
225669 TISGTECPYLYKQIDSEKAYTRYQIRGYIEDSODLEIYLRYNKAKHETVNPVT
730 740 750 760 770 780
cryla-105.pe GSLWPLAQSSICKCKGQENRAPHLENNPDDSCDGEKCAHSHHPSLDIDVGCTDLN
790 800 810 820 830 840
225669 GSLWPLAQSSICKCKGQENRAPHLENNPDDSCDGEKCAHSHHPSLDIDVGCTDLN
790 800 810 820 830 840
cryla-105.pe EDLGVWVIFIKITQDCHERLGNLFESRAVGEASAKKWKREKLEWETNI
850 860 870 880 890
225669 EDLGVWVIFIKITQDCHERLGNLFESRAVGEASAKKWKREKLEWETNI
850 860 870 880 890
cryla-105.pe VYKAKESVDALFVANSQDRLQADTNIAHAAKRVHSIRENLPISLVIPKAFIPE
900 910 920 930 940 950 960 970 980 990
225669 VYKAKESVDALFVANSQDRLQADTNIAHAAKRVHSIRENLPISLVIPKAFIPE
900 910 920 930 940 950 960 970 980 990
cryla-105.pe ELEGRIFTAFSLYDARNVKNKNGDFNGLSCWNKGVHVEQNNORSLVLPVNEASO
960 970 980 990 1000 1010 1020 1030 1040 1050 1060 1070
225669 ELEGRIFTAFSLYDARNVKNKNGDFNGLSCWNKGVHVEQNNORSLVLPVNEASO
960 970 980 990 1000 1010 1020 1030 1040 1050 1060 1070
cryla-105.pe EVRVCPRGRIYLRVTAIRYEGYEGCVTHIENNTDELKFCNVEEVEIYPNNTVTCNDYT
1020 1030 1040 1050 1060 1070

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225669
1000 1010 1020 1030 1040 1050
EYVCPGRGYILRVATAYKEGYGCVTHIEIENNTDELAFNSCVEEVEYPPNVTNCNDYT
1080 1090 1100 1110 1120 1130
cry1a-105.pe VNOBEYGATSNRGYNEA----PSVPADYASVYEKSYTGDGRNCPENCFNRCYRDYTP
225669
1060 1070 1080 1090 1100 1110
ATQBEYEGTTSNRGYDGAYESNSSVPADYAYEAKAYTDGRDNPCESNRGYGYDTP
1140 1150 1160 1170
cry1a-105.pe LPVGVTKELEYFETDKVMIEIGETGTFIVDSVLLMEE
225669
1120 1130 1140 1150
LPAGVTKELEYFETDKVMIEIGETGTFIVDSVLLMEE
cry1a-105.pcp
NRAA:10440886
10440886 source="GENBANK_PROT" delta endotoxin [Bacillus thuringiensis]
SCORES Init1: 4681 Initn: 5146 Opt: 4695 z-score: 5328.7 E(): 0
>>NRAA:10440886
Initn: 5146 Init1: 4681 opt: 4695 z-score: 5328.7 expect(): 0
Smith-Waterman score: 6871; 88.4% identity in 1181 aa overlap
(1-1177:1-1155)

10 20 30 40 50 60
cry1a-105.pe MDNPNNECIPYNCLSNPEVEVLGGERIETGTPIDISLSLTQFLSEFPVAGFVLGL
10440886 MDNPNNECIPYNCLSNPEVEVLGGERIETGTPIDISLSLTQFLSEFPVAGFVLGL
70 80 90 100 110 120
cry1a-105.pe VDIIWGFQSPQWDAFLVQIEQLINQRIEFAFNQAIISLEGLSNLQIVAESFREWEAD
10440886 VDIIWGFQSPQWDAFLVQIEQLINQRIEFAFNQAIISLEGLSNLQIVAESFREWEAD
130 140 150 160 170 180
cry1a-105.pe PTNPALREEMRIQFNDMSALTTPALPFAVONYQVPLLSVYVQAANLHLSVLRDVSVFQ
10440886 PTNPALREEMRIQFNDMSALTTPALPFAVONYQVPLLSVYVQAANLHLSVLRDVSVFQ
190 200 210 220 230 240
cry1a-105.pe RWGFDAAITNSRYNDLTRIGNYTDHVRWYNTGLERVGPDSDRWIRYVQFRRELTIV
10440886 RWGFDAAITNSRYNDLTRIGNYTDHVRWYNTGLERVGPDSDRWIRYVQFRRELTIV
250 260 270 280 290 300
cry1a-105.pe LDIVSLFPNYDSRTPIRTVSQLTREIYTNPVLENFDSFRGSAQEGSIRSPHMDIL
10440886 LDIVSLFPNYDSRTPIRTVSQLTREIYTNPVLENFDSFRGSAQEGSIRSPHMDIL
310 320 330 340 350 360
cry1a-105.pe NSITIYTDARGEYWSGHQIMASPVGFSQPEFTPLFGTGMGNAPQQRIVAOLOGGVYR
10440886 NSITIYTDARGEYWSGHQIMASPVGFSQPEFTPLFGTGMGNAPQQRIVAOLOGGVYR
370 380 390 400 410 420

cry1a-105.pe TLSSTLYRRPPIGINNOQLSVLQGTGFAYGTSNLPASVYKSGCTVDSLDEIPQNNVV
10440886 TLSSTLYRRPPIGINNOQLSVLQGTGFAYGTSNLPASVYKSGCTVDSLDEIPQNNVV
370 380 390 400 410 420
cry1a-105.pe PPRQGFHRLSHVSMFRSGFNSSVSIIIRAPMFSWIHRSAEFNNIIASDSITQIPLVKAH
10440886 PPRQGFHRLSHVSMFRSGFNSSVSIIIRAPMFSWIHRSAEFNNIIASDSITQIPLVKAH
430 440 450 460 470 480
cry1a-105.pe TLQSGTIVVRGPGFTGCDILRRTSQGPAYTIVINQQLQPYRARIYASTTNLRIYVT
10440886 TLQSGTIVVRGPGFTGCDILRRTSQGPAYTIVINQQLQPYRARIYASTTNLRIYVT
490 500 510 520 530 540
cry1a-105.pe VAGERIPAGOFNKMTDGTPLTFOSFSYATINTAFTFPMSSQSFVAGDTFSSGNEVYID
10440886 VAGERIPAGOFNKMTDGTPLTFOSFSYATINTAFTFPMSSQSFVAGDTFSSGNEVYID
550 560 570 580 590 600
cry1a-105.pe RFEIIPVTATLEAEYNLERAQKAVNALFTSTNGLKTNVTDYHIDQVSNLVTYLSDEF
10440886 RFEIIPVTATLEAEYNLERAQKAVNALFTSTNGLKTNVTDYHIDQVSNLVTYLSDEF
610 620 630 640 650 660
cry1a-105.pe LDEKREISEKVKHAKSLDERNLQDNLNLRGINRQDLDRGSGTDTITQGGDDVFKENTV
10440886 LDEKREISEKVKHAKSLDERNLQDNLNLRGINRQDLDRGSGTDTITQGGDDVFKENTV
670 680 690 700 710 720
cry1a-105.pe TSLGTFDECYPTLYOKIDESKLAFTYRLGYIEDSODLEIYSIRYNAKHETVNVPGT
10440886 TSLGTFDECYPTLYOKIDESKLAFTYRLGYIEDSODLEIYSIRYNAKHETVNVPGT
730 740 750 760 770 780
cry1a-105.pe GSLWPLSAQSPFGKCEPNRCAPHLWNPDLCSCRDGKCAHSHHFLSLDIDVGCTDLN
10440886 GSLWPLSAQSPFGKCEPNRCAPHLWNPDLCSCRDGKCAHSHHFLSLDIDVGCTDLN
790 800 810 820 830 840
cry1a-105.pe EDLGVWVIFKIKTOGHARLGNLFLEKEPLVCEALARYKAERKWRDKREKLEWETNIV
10440886 EDLGVWVIFKIKTOGHARLGNLFLEKEPLVCEALARYKAERKWRDKREKLEWETNIV
850 860 870 880 890 900
cry1a-105.pe YKEAKESVDALFVNSQYDQLOADNTNIAMHAADKRVHSIREAYLPESLVPVGNAAIFEE
10440886 YKEAKESVDALFVNSQYDQLOADNTNIAMHAADKRVHSIREAYLPESLVPVGNAAIFEE
910 920 930 940 950 960
cry1a-105.pe LEGRIFFATSLYDARNVTKNGDFNNGLSVWVKGHVDVEEQNNQRSLVVPWEAEVSQ
10440886 LEGRIFFATSLYDARNVTKNGDFNNGLSVWVKGHVDVEEQNNQRSLVVPWEAEVSQ
970 980 990 1000 1010 1020
cry1a-105.pe LEGRIFFATSLYDARNVTKNGDFNNGLSVWVKGHVDVEEQNNQRSLVVPWEAEVSQ
10440886 LEGRIFFATSLYDARNVTKNGDFNNGLSVWVKGHVDVEEQNNQRSLVVPWEAEVSQ
990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090

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cryla-105.pe VVPCRGYDRTVYKEGVGGCVTHIEIENNTDELKSNCEVEEIPNNITVCNDYTV
10440886 VVPCRGYDRTVYKEGVGGCVTHIEIENNTDELKSNCEVEEIPNNITVCNDYTV
1000 1010 1020 1030 1040 1050

cryla-105.pe NOESGCVTSRNGNEA-----PSVNDQSVVEEKSYDGRNCPCEFRNGYDTPPL
10440886 TOEEYEGTYSRNGYDGTGSESNVAPADYASAVDEKAYTDGRNCPCEFRNGYDTPPL
1060 1070 1080 1090 1100 1110

cryla-105.pe PVGYVTELEYPFETDKVWEIGETEGTFVDSVLLMEE
10440886 PAGYVTELEYPFETDKVWEIGETEGTFVDSVLLMEE
1120 1130 1140 1150 1160

cryla-105.pep
NRAA:48734426

48734426 source="GENBANK_PROT" parasporal crystal protein (acifliss
thuringiensis)
SCORES Initl: 4680 Initn: 6928 Opt: 4694 z-score: 5327.6 E() 0
>>NRAA:48734426
Initn: 6928 Initl: 4680 Opt: 4694 Z-score: 5327.6 expect()
Smith-Waterman score: 6881; 88.6% identity in 1181 aa overlap
(1-1177;1-1156)

cryla-105.pe MDNPNINECIPNCLSNPEVEVLGGRIETGYTPIDISLSITOFLLSEVPAGVGLG
48734426 MDNPNINECIPNCLSNPEVEVLGGRIETGYTPIDISLSITOFLLSEVPAGVGLG
10 20 30 40 50 60

cryla-105.pe VDIWGFQSDAFVQIEQLINQRIEFARNQAISSLEGLSNLYQIYAESFREWED
48734426 VDIWGFQSDAFVQIEQLINQRIEFARNQAISSLEGLSNLYQIYAESFREWED
70 80 90 100 110 120

cryla-105.pe PTFPALREEMRIQFNDMNSALTTPALFAVQVPLLSVYVQAAHLHSLVLDVSVEGO
48734426 PTFPALREEMRIQFNDMNSALTTPALFAVQVPLLSVYVQAAHLHSLVLDVSVEGO
130 140 150 160 170 180

cryla-105.pe RWGFDAATINSRYNDLTRIGNYTDHVRWYNTGLERVWGPDSRDWIRYNQFRRELTIV
48734426 RWGFDAATINSRYNDLTRIGNYTDHVRWYNTGLERVWGPDSRDWIRYNQFRRELTIV
190 200 210 220 230 240

cryla-105.pe LDIVSLFPNVDSTPIRTYSQLTREIYNPVLNFDSPFGSQGIEGSIKSPHMDIL
48734426 LDIVSLFPNVDSTPIRTYSQLTREIYNPVLNFDSPFGSQGIEGSIKSPHMDIL
250 260 270 280 290 300

cryla-105.pe NSITITVDHRGEYVWSGHQIMASPVGFSEPTFPLXGTWGNAAFOQRLVLAQLGGYVR
48734426 NSITITVDHRGEYVWSGHQIMASPVGFSEPTFPLXGTWGNAAFOQRLVLAQLGGYVR
310 320 330 340 350 360

cryla-105.pe TLSSTLVRFPENIGINNQLSVLDGTEFAYCTSSNLPASVYKSGTVDLSDEIPQNNVV
48734426 TLSSTLVRFPENIGINNQLSVLDGTEFAYCTSSNLPASVYKSGTVDLSDEIPQNNVV
370 380 390 400 410 420

cryla-105.pe PPROQFHRSHVSMRPSGFSNVSIIIRAFPMFSWIHRSAEFNNIIASDSITQIPLVKAH
48734426 PPROQFHRSHVSMRPSGFSNVSIIIRAFPMFSWIHRSAEFNNIIASDSITQIPLVKAH
430 440 450 460 470 480

cryla-105.pe TLOSGTIVVRGPGFTGDDLARTSGGPFATVINGQLPQRYRARIYASTNNLRIYVT
48734426 NLGSGTIVVRGPGFTGDDLARTSGGPFATVINGQLPQRYRARIYASTNNLRIYVT
490 500 510 520 530 540

cryla-105.pe VAGERIFAGQFNKMTDGLPTTFQSFVATINTAFTFPMSSQSFVAGDTFSSGNEVYID
48734426 IDGRPIQNGNFSATMSSGNLQSGSFRVTGFTTFFNFNSGSSVFTLSARVFNSEVYID
550 560 570 580 590 600

cryla-105.pe RFLPIPTALEAEYNLEAKQAVNALFTSTNGLKTNVDYHIDQVSNLVTYLSDEFEC
48734426 RIEFVPAETFEAEYDLERAQAVNELFTSSNQIGLKTVDYHIDQVSNLVTYLSDEFEC
610 620 630 640 650 660

cryla-105.pe LDEKSELSEKVKHAKELSDERNLQDSNFKDINRPERGWSGSGTIGTIOGDDVFKENTV
48734426 LDEKSELSEKVKHAKELSDERNLQDSNFKDINRPERGWSGSGTIGTIOGDDVFKENTV
670 680 690 700 710 720

cryla-105.pe TLDSTFPCYPTVYKIDSKNAFTRYQIRGYIEDSODLEIYIRYNAKHETVNVPGT
48734426 TLDSTFPCYPTVYKIDSKNAFTRYQIRGYIEDSODLEIYIRYNAKHETVNVPGT
730 740 750 760 770 780

cryla-105.pe GSWPLSAQSPICNGENRCAHMLNEDLDCSDCKCAHSHHFLSDIDVGCTDIN
48734426 GSWPLSAQSPICNGENRCAHMLNEDLDCSDCKCAHSHHFLSDIDVGCTDIN
790 800 810 820 830 840

cryla-105.pe EDLGVWVIFKIKTODGHARLGNLEFLEELSEALAKKAEKKEDARKKLEHETIV
48734426 EDLGVWVIFKIKTODGHARLGNLEFLEELSEALAKKAEKKEDARKKLEHETIV
850 860 870 880 890 900

cryla-105.pe YKEAKESVDALFVNSQYDQLQADNTIAMIAADKRVHSIREAYTPELSVPGVMAAEP
48734426 YKEAKESVDALFVNSQYDQLQADNTIAMIAADKRVHSIREAYTPELSVPGVMAAEP
910 920 930 940 950 960

cryla-105.pe LEGRIETAFSLDARNVFKNGDFNGLSCWNVKGVHDVEEQNNQSRSVLVVPEWEAEVSQ
48734426 LEGRIETAFSLDARNVFKNGDFNGLSCWNVKGVHDVEEQNNQSRSVLVVPEWEAEVSQ
970 980 990 1000 1010 1020

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cryla-105.pe VVPCGGRYILRTAVKYGEGCVTHIEIENNTDELKSNVCVEEIPNNITVNDYTV 1030 1040 1050 1060 1070 1080
48734426 VVPCGGRYILRTAVKYGEGCVTHIEIENNTDELKSNVCVEEIPNNITVNDYTV 1000 1010 1020 1030 1040 1050

cryla-105.pe NQEEYGGAYTSRNRGYNIA----PSVPADYASVVEKSYTDGRNPNCFNRGRDYTPL 1090 1100 1110 1120 1130
48734426 TQEEYEGYTSRNRGVDGAVESNSVPADYASVEEYKAYTDGRNPNCPESNRGVDYTPL 1060 1070 1080 1090 1100 1110

cryla-105.pe PVGYTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE 1140 1150 1160 1170
48734426 PAGYVTELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE 1120 1130 1140 1150

cryla-105.pep
NRAA:56900936
56900936 source="GENBANK_PROT" CryIab [Bacillus thuringiensis]

SCORES Initl: 4673 Initn: 5126 Opt: 4687 z-score: 5319.6 E(): 0
>>NRAA:56900936
initn: 5126 initl: 4673 opt: 4687 z-score: 5319.6 expect(): 0
Smith-Waterman score: 6870; 88.5% identity in 1181 aa overlap
(1-1177.1-1155)

cryla-105.pe MNNPNINECTIPNCLSNREVEVLGGERIETGYTPIDISLSLTQFLSEFPVGGFVLGL 10 20 30 40 50 60
56900936 MNNPNINECTIPNCLSNREVEVLGGERIETGYTPIDISLSLTQFLSEFPVGGFVLGL 10 20 30 40 50 60

cryla-105.pe VDIWIGFQPSQMDAFLVQIEQLINQRIEFAFNQALSRLEGLSNLYQIYAESFREWEAD 70 80 90 100 110 120
56900936 VDIWIGFQPSQMDAFLVQIEQLINQRIEFAFNQALSRLEGLSNLYQIYAESFREWEAD 70 80 90 100 110 120

cryla-105.pe PTNPALREEMRIQFNDNMSALTATPLFAVQNYQVPLLSVYQAAHLNLSVLRDVSVFQ 130 140 150 160 170 180
56900936 PTNPALREEMRIQFNDNMSALTATPLFAVQNYQVPLLSVYQAAHLNLSVLRDVSVFQ 130 140 150 160 170 180

cryla-105.pe RMGFDAAITNSRYNDLTRILIGNYTHAVRWNTGLERVMGPOSROWIRYNGFRSLTLTV 190 200 210 220 230 240
56900936 RMGFDAAITNSRYNDLTRILIGNYTHAVRWNTGLERVMGPOSROWIRYNGFRSLTLTV 190 200 210 220 230 240

cryla-105.pe LDIVSLFPNYSRTYPIRTVSQLTREIYTNVPLENFGSPRGSAGQIGSIRSPHMDIL 250 260 270 280 290 300
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56900936 NSITITDHRGEYMSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVQALGQGVYR 310 320 330 340 350 360
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cryla-105.pe TISSLTLYRRPNIGINNQLSVLDGTEFAYCTSNLPSAVYRKSGTVSLDEIPQNNVV 310 320 330 340 350 360
56900936 TISSLTLYRRPNIGINNQLSVLDGTEFAYCTSNLPSAVYRKSGTVSLDEIPQNNVV 370 380 390 400 410 420

cryla-105.pe PPRQGFHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRAEFNNIIASDSITQIPLVKAH 430 440 450 460 470 480
56900936 PPRQGFHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRAEFNNIIASDSITQIPLVKAH 430 440 450 460 470 480

cryla-105.pe TIOSGTTVVRGPGFTGDIILRRISGPFAYTIVNINQLPQRYRARIYASTTNLRIYVT 490 500 510 520 530 540
56900936 NLGSGTSVVKGPGFTGDIILRRISGPFAYTIVNINQLPQRYRARIYASTTNLRIYVT 490 500 510 520 530 540

cryla-105.pe VAGERIFAGOFNKTMGTGDTPLTFQSFYATINTAFTFPMQSOSFTVGADTFSSGNEVYID 550 560 570 580 590 600
56900936 IDGRFINQNFSAIMSGSNLQSGSFRVGTFTTFNFSNGSSVFTLSAHVFNFSNGNEVYID 550 560 570 580 590 600

cryla-105.pe RFELIPVTATLEAEYNLEAQAQNALETSTNQLGKTNVTDYHIDQVSNLTVLSDEFC 610 620 630 640 650 660
56900936 RIEFVPAEVTAEAYDLERAQAQNALETSTNQLGKTNVTDYHIDQVSNLTVLSDEFC 610 620 630 640 650 660

cryla-105.pe LDEKRELSEKVKHAKLSIDERNLQDSNPKDINQRPQMGSGSTGITIGGDDVFKENYV 670 680 690 700 710 720
56900936 LDEKRELSEKVKHAKLSIDERNLQDSNPKDINQRPQMGSGSTGITIGGDDVFKENYV 670 680 690 700 710 720

cryla-105.pe TISGTFDECYPTLYQKIDESKLAFTYQLRGVIEDSDLEIYSTRYNKHEVNVPGT 730 740 750 760 770 780
56900936 TISGTFDECYPTLYQKIDESKLAFTYQLRGVIEDSDLEIYSTRYNKHEVNVPGT 730 740 750 760 770 780

cryla-105.pe GSWLPLSQSPSIGKCEPNRCAPHLEWNPDLDCRDEKCAHSHHSLDIDVGCTDLN 790 800 810 820 830 840
56900936 GSWLPLSQSPSIGKCEPNRCAPHLEWNPDLDCRDEKCAHSHHSLDIDVGCTDLN 790 800 810 820 830 840

cryla-105.pe EDLGVWVIFKIKTDGCHARLGNLEFLEKPLVGEALARKVRAEKWKDRKREKLEWETNIV 850 860 870 880 890 900
56900936 EDLGVWVIFKIKTDGCHARLGNLEFLEKPLVGEALARKVRAEKWKDRKREKLEWETNIV 850 860 870 880 890 900

cryla-105.pe YKEAKESVDALFVNSQVDLOQADTNIAHHAADKRVHSIREAVLPSELSVIGVNAALFEE 910 920 930 940 950 960
56900936 YKEAKESVDALFVNSQVDLOQADTNIAHHAADKRVHSIREAVLPSELSVIGVNAALFEE 910 920 930 940 950 960

cryla-105.pe LEGRIFTAFSLYDARNVYKNGDFNNGLSQVWVKGHVDVEEQNNRSLVLPWEAEVYSQE 970 980 990 1000 1010 1020
56900936 LEGRIFTAFSLYDARNVYKNGDFNNGLSQVWVKGHVDVEEQNNRSLVLPWEAEVYSQE 970 980 990 1000 1010 1020
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56900936
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56900936
cry1a-105.pep
SW:117543

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 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15880 15890 15900 15910 15920 15930 15940 15950 15960 15970 15980 15990 16000 16010 16020 16030 16040 16050 16060 16070 16080 16090 16100 16110 16120 16130 16140 16150 16160 16170 16180 16190 16200 16210 16220 16230 16240 16250 16260 16270 16280 16290 16300 16310 16320 16330 16340 16350 16360 16370 16380 16390 16400 16410 16420 16430 16440 16450 16460 16470 16480 16490 16500 16510 16520 16530 16540 16550 16560 16570 16580 16590 16600 16610 16620 16630 16640 16650 16660 16670 16680 16690 16700 16710 16720 16730 16740 16750 16760 16770 16780 16790 16800 16810 16820 16830 16840 16850 16860 16870 16880 16890 16900 16910 16920 16930 16940 16950 16960 16970 16980 16990 17000 17010 17020 17030 17040 17050 17060 17070 17080 17090 17100 17110 17120 17130 17140 17150 17160 17170 17180 17190 17200 17210 17220 17230 17240 17250 17260 17270 17280 17290 17300 17310 17320 17330 17340 17350 17360 17370 17380 17390 17400 17410 17420 17430 17440 17450 17460 17470 17480 17490 17500 17510 17520 17530 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19200 19210 19220 19230 19240 19250 19260 19270 19280 19290 19300 19310 19320 19330 19340 19350 19360 19370 19380 19390 19400 19410 19420 19430 19440 19450 19460 19470 19480 19490 19500 19510 19520 19530 19540 19550 19560 19570 19580 19590 19600 19610 19620 19630 19640 19650 19660 19670 19680 19690 19700 19710 19720 19730 19740 19750 19760 19770 19780 19790 19800 19810 19820 19830 19840 19850 19860 19870 19880 19890 19900 19910 19920 19930 19940 19950 19960 19970 19980 19990 20000 20010 20020 20030 20040 20050 20060 20070 20080 20090 20100 20110 20120 20130 20140 20150 20160 20170 20180 20190 20200 20210 20220 20230 20240 20250 20260 20270 20280 20290 20300 20310 20320 20330 20340 20350 20360 20370 20380 20390 20400 20410 20420 20430 20440 20450 20460 20470 20480 20490 20500 20510 20520 20530 20540 20550 20560 20570 20580 20590 20600 20610 20620 20630 20640 20650 20660 20670 20680 20690 20700 20710 20720 20730 20740 20750 20760 20770 20780 20790 20800 20810 20820 20830 20840 20850 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cry1a-105.pe LEGRIFTAFSLYDARNVKNKGNDFNGLSCWNVKGVHVDVEONNQRSLVVPWEAEVSOE
117543 LEGRIFTAFSLYDARNVKNKGNDFNGLSCWNVKGVHVDVEONNQRSLVVPWEAEVSOE
940 950 960 970 980 990

cry1a-105.pe VRVCPGRGILRVTAKEGEGECVTIHEIENNTDEKFSNCVVEEIIYNNVTVCNDYTV
117543 VRVCPGRGILRVTAKEGEGECVTIHEIENNTDEKFSNCVVEEIIYNNVTVCNDYTV
1000 1010 1020 1030 1040 1050

cry1a-105.pe NOEYGGVATSRNRYNEA----PSVPADYASVVEEKSYYTDGRENCFEFGYDYTPL
117543 TOEEVEGTYTSRNGYDCAVESNSVPADYASVVEEKSYYTDGRENCFEFGYDYTPL
1060 1070 1080 1090 1100 1110

cry1a-105.pe PGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
117543 PGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1120 1130 1140 1150

cry1a-105.pe
1140 1150 1160 1170
117543
1120 1130 1140 1150

cry1a-105.pep
NRAA:143099
143099 source="GENBANK_PROT" insecticidal protein

SCORES Init1: 4672 Initn: 5137 Opt: 4686 z-score: 5318.5 E(): 0
>>NRAA:143099
initn: 5137 init1: 4672 opt: 4686 z-score: 5318.5 expect(): 0
Smith-Waterman score: 6871; 88.6% identity in 1181 aa overlap
(1-1177:1-1155)

cry1a-105.pe MDNNPINECIPYNCLSNPEVEVLGERIETGYTPIDISLSLTOFLSEFVPGAGFVLGL
143099 MDNNPINECIPYNCLSNPEVEVLGERIETGYTPIDISLSLTOFLSEFVPGAGFVLGL
10 20 30 40 50 60

cry1a-105.pe VDIINGIFGSPQWDAFLVQIEQLINQRIEEFARNQASRLLEGSLNLYQIYAESFREWEAD
143099 VDIINGIFGSPQWDAFLVQIEQLINQRIEEFARNQASRLLEGSLNLYQIYAESFREWEAD
70 80 90 100 110 120

cry1a-105.pe PTNPALREEMRIQFNDMNSALTAIPLFAVQNYQVPLLSYVOAANHLHSLVRDVSFQ
143099 PTNPALREEMRIQFNDMNSALTAIPLFAVQNYQVPLLSYVOAANHLHSLVRDVSFQ
130 140 150 160 170 180

cry1a-105.pe RWGFDAAATINSRYNDLTRLIGNYTDHVRWYNTGLERWGPDSRWIRYNQFRRELTIV
143099 RWGFDAAATINSRYNDLTRLIGNYTDHVRWYNTGLERWGPDSRWIRYNQFRRELTIV
190 200 210 220 230 240

cry1a-105.pe LDIVSLFPNYSRTPYPIRTVSQLTREIYTNVPLENFGSPRGAQIGSIRSPHLMIL
143099 LDIVSLFPNYSRTPYPIRTVSQLTREIYTNVPLENFGSPRGAQIGSIRSPHLMIL
250 260 270 280 290 300
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cry1a-105.pe NSITIYTDARHGEYVWGHQIMASPVFGSGFEFTFPLKGTGMAAPQQRIVLAQLQGQVYR
143099 NSITIYTDARHGEYVWGHQIMASPVFGSGFEFTFPLKGTGMAAPQQRIVLAQLQGQVYR
310 320 330 340 350 360

cry1a-105.pe TLSSTLYRRPFGNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQVGVDSLDRIIPPQNNV
143099 TLSSTLYRRPFGNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQVGVDSLDRIIPPQNNV
370 380 390 400 410 420

cry1a-105.pe PPQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIRHSAEFNIIIASDSITQIPLVKAH
143099 PPQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIRHSAEFNIIIASDSITQIPLVKAH
430 440 450 460 470 480

cry1a-105.pe TLOSQTIVRGPGFTGGDILRRTSRGGFAYTIIVNINQLPQRYRARIYASTNRIYVT
143099 TLOSQTIVRGPGFTGGDILRRTSRGGFAYTIIVNINQLPQRYRARIYASTNRIYVT
490 500 510 520 530 540

cry1a-105.pe VAGERIFAGQFNKTMGTGDELTPQSFVSATINTAFTPMQSSFTVGDTSNGEVYID
143099 VAGERIFAGQFNKTMGTGDELTPQSFVSATINTAFTPMQSSFTVGDTSNGEVYID
550 560 570 580 590 600

cry1a-105.pe RELIPVTATLEAEYNLEAQAVALFTSNQGLKNTVDYHIDQVSNLVYLSDEF
143099 RELIPVTATLEAEYNLEAQAVALFTSNQGLKNTVDYHIDQVSNLVYLSDEF
610 620 630 640 650 660

cry1a-105.pe LDEKSELSEKVKHAKRLSDERNLLQDSNPKINQPERGWSGTGITOGGDDVFKENYV
143099 LDEKSELSEKVKHAKRLSDERNLLQDSNPKINQPERGWSGTGITOGGDDVFKENYV
670 680 690 700 710 720

cry1a-105.pe TLSGTFDECYPTLYQKIDESKLKAFTRYQVLRGVIEDSQDLEIYSIRYNAKHETVNPVT
143099 TLSGTFDECYPTLYQKIDESKLKAFTRYQVLRGVIEDSQDLEIYSIRYNAKHETVNPVT
730 740 750 760 770 780

cry1a-105.pe GSLMPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDVGCTDLN
143099 GSLMPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDVGCTDLN
790 800 810 820 830 840

cry1a-105.pe EDLGVWVIFKIKTODGHARLGNLEFLERKPLVGEALARYKRAEKKWRDKREKLEWETNIV
143099 EDLGVWVIFKIKTODGHARLGNLEFLERKPLVGEALARYKRAEKKWRDKREKLEWETNIV
850 860 870 880 890 900

cry1a-105.pe YKEAKESVDALFVNSQVDOQLADTNIAHIAADKRVHSIREAYLPGLSVIFGVNAAFEE
143099 YKEAKESVDALFVNSQVDOQLADTNIAHIAADKRVHSIREAYLPGLSVIFGVNAAFEE
910 920 930 940 950 960
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cryla-105.pe LEGRIFTSFYDARNVNGDFNGLSCWNVKGVDEVEQNRQNSVLVPEWEAEVSQE 970 980 990 1000 1010 1020
143099 LEGRIFTSFYDARNVNGDFNGLSCWNVKGVDEVEQNRQNSVLVPEWEAEVSQE 970 980 990 1000 1010 1020

cryla-105.pe VRVCGRGYILKTAKEGYGBQVTHIEENDELKFSNCVEEYIPNNVTVCNDYTV 1000 1010 1020 1030 1040 1050
143099 VRVCGRGYILKTAKEGYGBQVTHIEENDELKFSNCVEEYIPNNVTVCNDYTV 1000 1010 1020 1030 1040 1050

cryla-105.pe NOEYGGAYTSNRGYNEA---PSVDADYASGAKSYTDGRNPFENRGYRDYTPL 1090 1100 1110 1120 1130
143099 TOEEGYTTSNRGYDGAVESNSVPAVYASVEEYVTDREDNPFENRGYRDYTPL 1090 1100 1110 1120 1130

cryla-105.pe PVGYTKELYFPETDKVWEIETEGTGFIVDSVELLMEE 1140 1150 1160 1170 1180
143099 PVGYTKELYFPETDKVWEIETEGTGFIVDSVELLMEE 1140 1150 1160 1170 1180

cryla-105.pep
NRAA: 14190061

14190061 source="GENBANK_PROT" CryIab16 [Bacillus thuringiensis]

SCORES Initl: 4669 Initn: 5131 Opt: 4683 z-score: 5315.1 E(): 0
>>NRAA: 14190061
Initn: 5131 initl: 4669 opt: 4683 z-score: 5315.1 expect():
Smith-Waterman score: 6849; 88.1% identity in 1181 aa overlap
(1-1177.1-1155)

cryla-105.pe MDNNPINECIPNCLSNPEVEVLGGRIETGYTPIDISLSTQFLLEFVPGAGVLGL 10 20 30 40 50 60
14190061 MDNNPINECIPNCLSNPEVEVLGGRIETGYTPIDISLSTQFLLEFVPGAGVLGL 10 20 30 40 50 60

cryla-105.pe VDIWIGIFGSQWDAFLVOIEQLINORIEEFARNQATSRLEGSLNLYIYAESFREWAD 70 80 90 100 110 120
14190061 VDIWIGIFGSQWDAFLVOIEQLINORIEEFARNQATSRLEGSLNLYIYAESFREWAD 70 80 90 100 110 120

cryla-105.pe PTNPALREEMRIQFNDMNSALTTPAIPFVQNVYVLLSVYVQAAHLHLSVLRDVSVFGQ 130 140 150 160 170 180
14190061 PTNPALREEMRIQFNDMNSALTTPAIPFVQNVYVLLSVYVQAAHLHLSVLRDVSVFGQ 130 140 150 160 170 180

cryla-105.pe RWGFDATINSRNDLTRLIGNYTHAVRWNTGLERWGPDSRDWIRYNOFRETLTV 190 200 210 220 230 240
14190061 RWGFDATINSRNDLTRLIGNYTHAVRWNTGLERWGPDSRDWIRYNOFRETLTV 190 200 210 220 230 240

cryla-105.pe LDIVSLFPNDYRTYFIRTVSQTREIYTPVLENFDGSRGSAQIGESRSPHMDLIL 250 260 270 280 290 300
14190061 LDIVSLFPNDYRTYFIRTVSQTREIYTPVLENFDGSRGSAQIGESRSPHMDLIL 250 260 270 280 290 300

cryla-105.pe NSITIYTAHRGEYVNSGHOIMASPVGSGPEFTFPLYGTMGNAAPQORIVAOIQGVYR 310 320 330 340 350 360
14190061 NSITIYTAHRGEYVNSGHOIMASPVGSGPEFTFPLYGTMGNAAPQORIVAOIQGVYR 310 320 330 340 350 360

cryla-105.pe TLSSTLYRPFNIGINNQQSLVDLGTETAYGTSSNLPSAVYKRGTVDSLDEIPPONNV 370 380 390 400 410 420
14190061 TLSSTLYRPFNIGINNQQSLVDLGTETAYGTSSNLPSAVYKRGTVDSLDEIPPONNV 370 380 390 400 410 420

cryla-105.pe PPROQFSHRLSHVSMFSGFNSSSVIIIRAPMFSWIHRSAEFNNIIASDSITQPLVKAH 430 440 450 460 470 480
14190061 PPROQFSHRLSHVSMFSGFNSSSVIIIRAPMFSWIHRSAEFNNIIASDSITQPLVKAH 430 440 450 460 470 480

cryla-105.pe TLQSGTIVVRGPGFTGDIILRTSGGPAYTIIVNINGOLPORVYRARIYASTTNIRYVT 490 500 510 520 530 540
14190061 TLQSGTIVVRGPGFTGDIILRTSGGPAYTIIVNINGOLPORVYRARIYASTTNIRYVT 490 500 510 520 530 540

cryla-105.pe VAGERIFAGQNTMDGDLPTFQSFYATINTAFTPPMSQSFVAGATFSSGNEYVID 550 560 570 580 590 600
14190061 VAGERIFAGQNTMDGDLPTFQSFYATINTAFTPPMSQSFVAGATFSSGNEYVID 550 560 570 580 590 600

cryla-105.pe REELRYTATLEAENYLERAKAVNALTSINQLKNTVYHIDQVSNLVNLYLSDEFC 610 620 630 640 650 660
14190061 REELRYTATLEAENYLERAKAVNALTSINQLKNTVYHIDQVSNLVNLYLSDEFC 610 620 630 640 650 660

cryla-105.pe LDENKESKVKKAPSPERNLLQSNRGINQLDRGARGSTDTITIQGGDDVFKENYV 670 680 690 700 710 720
14190061 LDENKESKVKKAPSPERNLLQSNRGINQLDRGARGSTDTITIQGGDDVFKENYV 670 680 690 700 710 720

cryla-105.pe TLLSGTFDECYPTYNQKQESKLAFTYRQLRGYISQSLIYIRYNKAKHETVNVPGT 730 740 750 760 770 780
14190061 TLLSGTFDECYPTYNQKQESKLAFTYRQLRGYISQSLIYIRYNKAKHETVNVPGT 730 740 750 760 770 780

cryla-105.pe GSLWPLSAQSPICKCEPNRCAPHLEWNPFLDSCEDGKVAHSHHSLNIDVCTDLN 790 800 810 820 830 840
14190061 GSLWPLSAQSPICKCEPNRCAPHLEWNPFLDSCEDGKVAHSHHSLNIDVCTDLN 790 800 810 820 830 840

cryla-105.pe EDLGWVWIFKIKTDQGHARLGNLEFLEKPLVGEALARKRAEKKRDCKLEKLENN 850 860 870 880 890 900
14190061 EDLGWVWIFKIKTDQGHARLGNLEFLEKPLVGEALARKRAEKKRDCKLEKLENN 850 860 870 880 890 900

cryla-105.pe YKEAKESVDALFVNSQYDQLOADNTNIAHAAKRVHSIREAYLPESVIPGNAAFIEE 910 920 930 940 950 960
14190061 YKEAKESVDALFVNSQYDQLOADNTNIAHAAKRVHSIREAYLPESVIPGNAAFIEE 910 920 930 940 950 960

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cry1a-105.pe 970 980 990 1000 1010 1020
LEGRIFAFSLVDARNVKNQDFNGLSCNVKGVHVDVEEQNNQSRSLVVPWEAEVSQ
14190061
LEGRIFAFSLVDARNVKNQDFNGLSCNVKGVHVDVEEQNNQSRSLVVPWEAEVSQ
940 950 960 970 980 990
cry1a-105.pe 1030 1040 1050 1060 1070 1080
VRVCPGRGYILRVTAKEYGEGCVTHIEENNTDLKFSNCVVEEYVNNVTGNDYTV
14190061
VRVCPGRGYILRVTAKEYGEGCVTHIEENNTDLKFSNCVVEEYVNNVTGNDYTV
1000 1010 1020 1030 1040 1050
cry1a-105.pe 1090 1100 1110 1120 1130
NQEYGYATSRNRGYNEA---PSPADYASVYEKSYTDGRENCFENRGYRDYTP
14190061
TQEEYEGTVTSNRGYDGYESNSVPADYASAYEKKAYTDGRDNPFCESNRGYGYTFL
1060 1070 1080 1090 1100 1110
cry1a-105.pe 1140 1150 1160 1170
PVGVYTKELFEPEDTKVWIEIGETGTFIVDSVELLMEE
14190061
PAGIVTRELEYPEDTKVWIEIGETGTFIVDSVELLMEE
1120 1130 1140 1150
cry1a-105.pep
SW:117539

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

SCORES Initl: 4665 Initn: 5130 Opt: 4679 z-score: 5310.5 E(:) : 0
>>SW:117539
initn: 5130 initl: 4665 opt: 4679 z-score: 5310.5 expect(:) : 0
Smith-Waterman score: 6867; 88.4% identity in 1181 aa overlap
(1-1177:1-1155)

cry1a-105.pe MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTIDISLSLTQFLSEFPVPGAFVIGL 60
|||||
117539 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTIDISLSLTQFLSEFPVPGAFVIGL 60
10 20 30 40 50
cry1a-105.pe VDIWIFGFSQWDAFLVQIEQLINQRIEAFARNOAISRLGSLNLYQIYAESFREWAD 120
|||||
117539 VDIWIFGFSQWDAFLVQIEQLINQRIEAFARNOAISRLGSLNLYQIYAESFREWAD 120
70 80 90 100 110
cry1a-105.pe PTPNALREEMRIQFNDMNSALTTAIFLFAVQNYQVPLLSVYVQAANHLVSLRDSVVFQ 180
|||||
117539 PTPNALREEMRIQFNDMNSALTTAIFLFAVQNYQVPLLSVYVQAANHLVSLRDSVVFQ 180
130 140 150 160 170
cry1a-105.pe RWGFDAAATNSRYNDLRLGNVTDAVWYNTGLRWGPDSDWIRNQFRRELTIV 240
|||||
117539 RWGFDAAATNSRYNDLRLGNVTDAVWYNTGLRWGPDSDWIRNQFRRELTIV 240
190 200 210 220 230
cry1a-105.pe LDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENDFSGFRGSAQGIIEGSRSPHMLDIL 300
|||||
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117539
LDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENDFSGFRGSAQGIIEGSRSPHMLDIL
250 260 270 280 290 300
cry1a-105.pe NSITIYDARHGGEYVMSGHQIMASPVGSGPEFTFLYGTMGNAAPQORIVAOLGQGVYR 360
|||||
117539 NSITIYDARHGGEYVMSGHQIMASPVGSGPEFTFLYGTMGNAAPQORIVAOLGQGVYR 360
310 320 330 340 350 360
cry1a-105.pe TLSSTLYRRREFNIGINNQLSVLDGTETAYGTSNNLPSAVYRKSGTVDSLSDEIPPQNNV 420
|||||
117539 TLSSTLYRRREFNIGINNQLSVLDGTETAYGTSNNLPSAVYRKSGTVDSLSDEIPPQNNV 420
370 380 390 400 410 420
cry1a-105.pe PPROGFSHRLSHVSMFRSGFNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPLVKAH 480
|||||
117539 PPROGFSHRLSHVSMFRSGFNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPLVKAH 480
430 440 450 460 470 480
cry1a-105.pe TLOGSTTVVRGPGFTGCGDILARTSGGPFAYTVININGQLPQRYRIRYASTTNLRIVYT 540
|||||
117539 TLOGSTTVVRGPGFTGCGDILARTSGGPFAYTVININGQLPQRYRIRYASTTNLRIVYT 540
490 500 510 520 530 540
cry1a-105.pe VAGERIPAQCFKNTKMDTGDPLTTFQSFYSATINTAFTFPMSSQSFVGAADTFSSGNEVID 600
|||||
117539 VAGERIPAQCFKNTKMDTGDPLTTFQSFYSATINTAFTFPMSSQSFVGAADTFSSGNEVID 600
550 560 570 580 590 600
cry1a-105.pe RFELIPVTATLEAEVNLERAQKAVNALFTSTNQLGKTNVTDVHIDQVSNLYTSLDRPC 660
|||||
117539 RFELIPVTATLEAEVNLERAQKAVNALFTSTNQLGKTNVTDVHIDQVSNLYTSLDRPC 660
610 620 630 640 650 660
cry1a-105.pe LDEKRELSKVKHAKRLSDERNLQDSNFKDINRQPERGWSGSGTGIITIOGDDVFKENYV 720
|||||
117539 LDEKRELSKVKHAKRLSDERNLQDSNFKDINRQPERGWSGSGTGIITIOGDDVFKENYV 720
670 680 690 700 710 720
cry1a-105.pe TLOGSTTVVRGPGFTGCGDILARTSGGPFAYTVININGQLPQRYRIRYASTTNLRIVYT 780
|||||
117539 TLOGSTTVVRGPGFTGCGDILARTSGGPFAYTVININGQLPQRYRIRYASTTNLRIVYT 780
730 740 750 760 770 780
cry1a-105.pe TLLGTDECPYLYYQKIDESKLFKAFTRQLRGYIEDSQDLEIYSIRYNAKHETVNVPGT 840
|||||
117539 TLLGTDECPYLYYQKIDESKLFKAFTRQLRGYIEDSQDLEIYSIRYNAKHETVNVPGT 840
790 800 810 820 830 840
cry1a-105.pe EDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARKAEKKWRDKREKLEWETIV 900
|||||
117539 EDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARKAEKKWRDKREKLEWETIV 900
850 860 870 880 890 900
cry1a-105.pe YKEAKESVDALFVNSQYDQLOADNTNIAHAAADKRVHSIREAYLPDLSVPGVNAIFEE 960
|||||
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117539
YKEAKSVDAFLVNSQYDLQADNTNIAHAAKRVHSIREAYLPFLSVEFGVNAIFEE
840 890 900 910 920 930

cry1a-105.pe
LESEIVAFESLQANLKNQDNFNGLSNNAVGHVDVEEQNNORSVLVVPENAEVSQE
117539
LEGRIFFAFEDDANNVINDNENLSCNNAVGHVDVEEQNNORSVLVVPENAEVSQE
940 950 960 970 980 990

cry1a-105.pe
VRVCPGRGYILRVAYKCYSGGCVTSEIANTDELKFSACVFEIYPNNVTICNDYTV
117539
VRVCPGRGYILRVAYKCYSGGCVTSEIANTDELKFSACVFEIYPNNVTICNDYTV
1000 1010 1020 1030 1040 1050

cry1a-105.pe
NOEYGGAYTSRNRGYNEA---PSVPADYASVEENSYTGRRNCPENRGRTYTH
117539
TOEYGGTYTSRNRGYDGAYESNSVPADYASAYEAKVTDGRRDNPENRGRTYTH
1060 1070 1080 1090 1100 1110

cry1a-105.pe
PVGYVTELEVPETDKVWIEIGETEGTFIVDSVELLMEE
117539
PAGVYVTELEVPETDKVWIEIGETEGTFIVDSVELLMEE
1120 1130 1140 1150

cry1a-105.pep
NRAA:142886
142886 source="GENBANK_PROT" 5.3 class Delta endotoxin

SCORES Initl: 4665 Inltn: 5130 Opt: 4679 z-score: 5310.5 E(): 0
>>NRAA:142886
inltn: 5130 initl: 4665 opt: 4679 z-score: 5310.5 expect(): 0
Smith-Waterman score: 6867; 88.4% identity in 1161 aa overlap
(1-1177:1-1155)

cry1a-105.pe
MDNPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGFVLGL
142886
MDNPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGFVLGL
10 20 30 40 50 60

cry1a-105.pe
VDIINGIFGSQWDAFLVQIEQLINQRIEFPARNOAISRLGLSNLYQIYAESFREWAD
142886
VDIINGIFGSQWDAFLVQIEQLINQRIEFPARNOAISRLGLSNLYQIYAESFREWAD
70 80 90 100 110 120

cry1a-105.pe
PTNPALREEMRIQDNMSALTTATPLFAVQNVQVPLSVYVQAAHLHLSVLRDVSVFGQ
142886
PTNPALREEMRIQDNMSALTTATPLFAVQNVQVPLSVYVQAAHLHLSVLRDVSVFGQ
130 140 150 160 170 180

cry1a-105.pe
RWGFDATINSRYNDLTRILGNVTDHVAWRVNTGLEVMGCPDSRWIRYQFRELTLTV
142886
RWGFDATINSRYNDLTRILGNVTDHVAWRVNTGLEVMGCPDSRWIRYQFRELTLTV
190 200 210 220 230 240

cry1a-105.pe
LDIVSLFPNVDSRTVPIRTVSQLTREIYNPVLNFDGSRGSAQIGESIRSPHMLDIL
142886
LDIVSLFPNVDSRTVPIRTVSQLTREIYNPVLNFDGSRGSAQIGESIRSPHMLDIL
250 260 270 280 290 300

cry1a-105.pe
NSIIITYDAHRGEYWSGHQIMASPVGDFSGPEFTPLYGTMGNAAPORIVAOLOGGVYR
142886
NSIIITYDAHRGEYWSGHQIMASPVGDFSGPEFTPLYGTMGNAAPORIVAOLOGGVYR
310 320 330 340 350 360

cry1a-105.pe
TLSSTLVRRFPNIGINNQOLSVLDGTEFAYGTSNNLPASAVYRKSGTVDSLSDEIPPONNV
142886
TLSSTLVRRFPNIGINNQOLSVLDGTEFAYGTSNNLPASAVYRKSGTVDSLSDEIPPONNV
370 380 390 400 410 420

cry1a-105.pe
PPROGFSHRLSHVSMFRSGFSNSSVSIIRAPMFWSIHRSAENNIILASDSITOIPLVKAH
142886
PPROGFSHRLSHVSMFRSGFSNSSVSIIRAPMFWSIHRSAENNIILASDSITOIPLVKAH
430 440 450 460 470 480

cry1a-105.pe
TLQSGTIVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVT
142886
NLGSGTSVVKGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRIYVT
490 500 510 520 530 540

cry1a-105.pe
VGRSEIFAGQFNKMTDGTPLTFOSFSYATINTAFTFPMSSQSTTVGADTFSSGNEVIID
142886
IHGRPFAQSNFSAATMSSGSLQSGSRHLGFTTFPFNFSGSSVFTLSAHVFNSGNEVIID
550 560 570 580 590 600

cry1a-105.pe
RFEAATVTEAEVNLPEAKAVNALFTSTNGLKTNVTDYHLDQVSNLVTYLSDFEC
142886
RFEAATVTEAEVNLPEAKAVNALFTSTNGLKTNVTDYHLDQVSNLVTYLSDFEC
610 620 630 640 650 660

cry1a-105.pe
LDEKEELSEKVRKXELSDERDQDSNFKINRSPERGWSGSGTITIGGDDVFKENYV
142886
LDEKEELSEKVRKXELSDERDQDSNFKINRSPERGWSGSGTITIGGDDVFKENYV
670 680 690 700 710 720

cry1a-105.pe
TLSGTDFECYPTLYOKIDESKLRKAYTHYRGNTEDSQSEIYLIRYNASETVNPVGT
142886
TLSGTDFECYPTLYOKIDESKLRKAYTHYRGNTEDSQSEIYLIRYNASETVNPVGT
730 740 750 760 770 780

cry1a-105.pe
GSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSDRGKSHHSHHFSQVQVTDLN
142886
GSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSDRGKSHHSHHFSQVQVTDLN
790 800 810 820 830 840

cry1a-105.pe
EDLGVWVIFKIKTDGCHARLGNELEEKPLVGEALARKVRAEKKWRDKREKLEWETNIV
142886
EDLGVWVIFKIKTDGCHARLGNELEEKPLVGEALARKVRAEKKWRDKREKLEWETNIV
850 860 870 880 890 900

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cry1a-105.pe YKEAKESVDALFVNSQDQLQADTNIAHIAADKRVHSIREAYLPSELSVIPGVNAALFEE
142886 YKEAKESVDALFVNSQDQLQADTNIAHIAADKRVHSIREAYLPSELSVIPGVNAALFEE
880 890 900 910 920 930

cry1a-105.pe LEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDEEQNNQSRSLVLPWEAEVSQE
142886 LEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDEEQNNHRSVLVLPWEAEVSQE
940 950 960 970 980 990

cry1a-105.pe VRVCPGRGYTLRVTAKEGYGEGCVTHIEIENNTDELKESNCVEEIPNNVTCTNDYTV
142886 VRVCPGRGYTLRVTAKEGYGEGCVTHIEIENNTDELKESNCVEEIPNNVTCTNDYTV
1000 1010 1020 1030 1040 1050

cry1a-105.pe NOEYGGAYTSRNRGYNEA---PSPADYASVYEKSYTDGRRNCPCFNRGRVRYDTPL
142886 TOEYGGAYTSRNRGYDGAYESNSVSPADYASVYEKSYTDGRRNCPCFNRGRVRYDTPL
1060 1070 1080 1090 1100 1110

cry1a-105.pe PVGYVTELEYPFETDKVWIEIGETGTFIVDSVELLMEE
142886 PVGYVTELEYPFETDKVWIEIGETGTFIVDSVELLMEE
1120 1130 1140 1150

cry1a-105.pep
NRAA:40255

40255 source="GENBANK_PROT" unnamed protein product [Bacillus thuringiensis]

SCORES Initl: 4661 Initn: 5126 Opt: 4675 z-score: 5306.0 E(): 0
>NRAA:40255
Initn: 5126 Initl: 4661 Opt: 4675 z-score: 5306.0 expect(): 0
Smith-Waterman score: 6869; 88.6% identity in 1181 aa overlap
(1-1177;1-1155)

cry1a-105.pe MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLJSEFVPGAGFVLG
40255 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLJSEFVPGAGFVLG
10 20 30 40 50 60

cry1a-105.pe VDIWGFQPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGSLNLYQIYAESFREWAD
40255 VDIWGFQPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGSLNLYQIYAESFREWAD
70 80 90 100 110 120

cry1a-105.pe PTNPALEENRQFNDMNSALTTPILFAVQNYQVPLSVYQAAHLVLRDVSFVFG
40255 PTNPALEENRQFNDMNSALTTPILFAVQNYQVPLSVYQAAHLVLRDVSFVFG
130 140 150 160 170 180

cry1a-105.pe RWGFDAAATINSRNDLTRIGNYTHAVRWNTGLERWGPDSRDWIRYNQFRRETLTV
40255 RWGFDAAATINSRNDLTRIGNYTHAVRWNTGLERWGPDSRDWIRYNQFRRETLTV
190 200 210 220 230 240

cry1a-105.pe LDIVSLPNVDSRTYPIRVVSQLTREIYTNVPLENFDGSGFRSAQIEGSIIRSHPLMDIL
40255 LDIVSLPNVDSRTYPIRVVSQLTREIYTNVPLENFDGSGFRSAQIEGSIIRSHPLMDIL
250 260 270 280 290 300

cry1a-105.pe NSIITIYDAHRGEYMSHQIMASVPVGSFGEFTFFLYLGTMGNAAPQORIYAOLGQGVYR
40255 NSIITIYDAHRGEYMSHQIMASVPVGSFGEFTFFLYLGTMGNAAPQORIYAOLGQGVYR
310 320 330 340 350 360

cry1a-105.pe TLSSTLRRFPNIGINNQLSVLDGTEFAYGTSSNLPSSAVYKSGTVDLSDEIPPQNNV
40255 TLSSTLRRFPNIGINNQLSVLDGTEFAYGTSSNLPSSAVYKSGTVDLSDEIPPQNNV
370 380 390 400 410 420

cry1a-105.pe PPROGFSHRLSHVSMRSGFNSSVSIIIRAPMESWIHRSAEFNIIASDSITQIPLVKAH
40255 PPROGFSHRLSHVSMRSGFNSSVSIIIRAPMESWIHRSAEFNIIASDSITQIPLVKAH
430 440 450 460 470 480

cry1a-105.pe TLQSGTTVVRGPGFTGGDILRRTSGFPAYTIVNQQLPQRYRARIYASTTNLRIYVT
40255 TLQSGTTVVRGPGFTGGDILRRTSGFPAYTIVNQQLPQRYRARIYASTTNLRIYVT
490 500 510 520 530 540

cry1a-105.pe VAGERIFAGQFNKMTGDTLPQSFYATINTAFTFPMSSQSFVAGDTFSSGNEVYID
40255 VAGERIFAGQFNKMTGDTLPQSFYATINTAFTFPMSSQSFVAGDTFSSGNEVYID
550 560 570 580 590 600

cry1a-105.pe RPELIPVATLEAYNLEAOKAVNALFTSTNQLGKTNVTDYHIDQVSNLVTYLSDEEC
40255 RPELIPVATLEAYNLEAOKAVNALFTSTNQLGKTNVTDYHIDQVSNLVTYLSDEEC
610 620 630 640 650 660

cry1a-105.pe LDEKRELSKVKHAKELSDERNLLQDSNFKDINRQPERGWGSGTGTIQGGDDVFKENYV
40255 LDEKRELSKVKHAKELSDERNLLQDSNFKDINRQPERGWGSGTGTIQGGDDVFKENYV
670 680 690 700 710 720

cry1a-105.pe TILGTFDECYPTLVQKIDESKLKAFTRIQYOLRGYIEDSQDLEIYIRYNAKHETVNPQT
40255 TILGTFDECYPTLVQKIDESKLKAFTRIQYOLRGYIEDSQDLEIYIRYNAKHETVNPQT
730 740 750 760 770 780

cry1a-105.pe GSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSRDGEKCAHSHHFSFLDIDVGCTDLN
40255 GSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSRDGEKCAHSHHFSFLDIDVGCTDLN
790 800 810 820 830 840

cry1a-105.pe EDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARKAEEKKWRDKREKLEWETNIV
40255 EDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARKAEEKKWRDKREKLEWETNIV
850 860 870 880 890 900

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cr1a-105.pe YKEAKVNDALFVNSQYLOQADTNIAHIAADKRVHSIREAYLPGLSVIPGVNAAIFEE 960
40255 YKEAKESVIAKDFVNSQYDROQADTNIAHIAADKRVHSIREAYLPGLSVIPGVNAAIFEE 930
880 890 900 910 920 930
cr1a-105.pe LEGEIFAFESVDKRVNIRVNFNGLSCNNVCHVDVEQNNQSRVLPVPEAEVSOE 1020
40255 LEGRIFTAFSLTQARNWIKNGEDVNGSCWNVGNDVEQNNHRSVLPVPEAEVSOE 990
940 950 960 970 980 990
cr1a-105.pe VRVCPGRGYILRVTAKEGYGEGCVTHLENNILKTSNCVREIRVNNVTICNDYTV 1080
40255 VRVCPGRGYILRVTAKEGYGEGCVTHLENNILKTSNCVREIRVNNVTICNDYTV 1050
1000 1010 1020 1030 1040 1050 1060 1070 1080 1090
cr1a-105.pe NOEYGGAYTSRNRGNEA---PSVPADVASVEKSTDSRENPCFNNVRYDTTPA 1130
40255 TOEYEGTYTSRNRGYDGAYESVSPADVASVEKAYTDGNDNCEGRNGVGL 1100
1060 1070 1080 1090 1100 1110 1120 1130
cr1a-105.pe PVGYVTKELYFPETDKVWIEIGETGTFIVDSVELLWEE 1170
40255 PAGVYTKELYFPETDKVWIEIGETGTFIVDSVELLWEE 1150
1120 1130 1140 1150
cr1a-105.pap
NRAA:40278
40278 source="GENBANK_PROT" unnamed protein product [Bacillus thuringiensis]

SCORES Initl: 4657 Initn: 5122 Opt: 4671 z-score: 5301.4 E(): 0
>NRAA:40278
Initn: 5122 Initl: 4657 opt: 4671 Z-score: 5301.4 expect(): 0
Smith-Waterman score: 6865; 88.5% identity in 1181 aa overlap
(1-1177:1-1155)

cr1a-105.pe MDNPNINECIPVNCLSNPEVEVLGGERIETGTPIDISLSLTQFLSEFVPGAGFVLG 60
40278 MDNPNINECIPVNCLSNPEVEVLGGERIETGTPIDISLSLTQFLSEFVPGAGFVLG 60
10 20 30 40 50
cr1a-105.pe VDIITWIGFQSQWDAFLVQIEQLINQRIEFARNQAISLEGLSNLVQIAESFREWEAD 120
40278 VDIITWIGFQSQWDAFLVQIEQLINQRIEFARNQAISLEGLSNLVQIAESFREWEAD 120
70 80 90 100 110 120
cr1a-105.pe PTNPALREEWRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANHLVLRDVSVFQ 180
40278 PTNPALREEWRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANHLVLRDVSVFQ 180
130 140 150 160 170 180
cr1a-105.pe RWGFDATINSRVNDLTRLIGNYTDHAVRWNTGLERVPDSDRWIRYNOFRRELTIV 240
40278 RWGFDATINSRVNDLTRLIGNYTDHAVRWNTGLERVPDSDRWIRYNOFRRELTIV 240
190 200 210 220 230 240
```

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cr1a-105.pe LDIVSLPNPNDSTYPIRTVSQLTREIYTNVLENFDSFRGSAQIEGSIIRSPHLMIDL 300
40278 LDIVSLPNPNDSTYPIRTVSQLTREIYTNVLENFDSFRGSAQIEGSIIRSPHLMIDL 300
250 260 270 280 290 300
cr1a-105.pe NSIIYIDARHGYSYWSGHQIMASPVGFSGPETFPFLIGTGMNAAPQORIVAOLGGVYR 360
40278 NSIIYIDARHGYSYWSGHQIMASPVGFSGPETFPFLIGTGMNAAPQORIVAOLGGVYR 360
310 320 330 340 350 360
cr1a-105.pe TLSSTLVRRFPFNIGINNQLSVLDGTEFAYGTSSNLPASVYRKSGTVDLSLDEIPPNNV 420
40278 TLSSTLVRRFPFNIGINNQLSVLDGTEFAYGTSSNLPASVYRKSGTVDLSLDEIPPNNV 420
370 380 390 400 410 420
cr1a-105.pe PPROGFSHRLSHVSMFRSGFNSSVSIIRAPMFESWIHRSAEFNIIASDSITQIPLVKAH 480
40278 PPROGFSHRLSHVSMFRSGFNSSVSIIRAPMFESWIHRSAEFNIIASDSITQIPLVKAH 480
430 440 450 460 470 480
cr1a-105.pe TLQSGTIVVRGPGFTGGDILRLRTSGGPFAYTIIVNIGOLPORRARIYASTTNLRIYVT 540
40278 NLSGTSVVKGPGFTGGDILRLRTSGGPFAYTIIVNIGOLPORRARIYASTTNLRIYVT 540
490 500 510 520 530 540
cr1a-105.pe VAGERIFASQFNKMTMDTGPITFOSFYATINTAFTFPMSSSFTVGADTFSSGNEVYID 600
40278 IDGRINQGNSTANSSGNSQSGSFIVGFTTFFNFNSGNSGVFTLSAHRVFNSGNEVYID 600
550 560 570 580 590 600
cr1a-105.pe RFLPIPTALEAFVLERAKVANNALFTSTNGLKTNVDYHIDQVSNLVYLSDEF 660
40278 RIEPVPSTVFEASVDEPAQKAVNLFPSNQIGLKTVDYHIDQVSNLVLECLSEFC 660
610 620 630 640 650 660
cr1a-105.pe LDEKRELSEKVKHAKLSLERNLQDNFNDINROERNGSGSTGITIOGGDDVFKNV 720
40278 LDEKRELSEKVKHAKLSLERNLQDNFNDINROERNGSGSTGITIOGGDDVFKNV 720
670 680 690 700 710 720
cr1a-105.pe TLSGTFDECPTYLYOKIDESKLAFTYRGRGIEDSQIYISIRYNAMHETINVPT 780
40278 TLLGTFDECPTYLYOKIDESKLAFTYRGRGIEDSQIYISIRYNAMHETINVPT 780
730 740 750 760 770 780
cr1a-105.pe GSLMPLSNQSPICKCEPNRCAPHLEWNPDLDCSDCEKCAHSHNEFDIDV 840
40278 GSLMPLSNQSPICKCEPNRCAPHLEWNPDLDCSDCEKCAHSHNEFDIDV 840
790 800 810 820 830 840
cr1a-105.pe EDLGWVWIFKTKTQDGHARLGNLEFLEKPLVGEALARKAEKKWRDKREKLEWETIV 900
40278 EDLGWVWIFKTKTQDGHARLGNLEFLEKPLVGEALARKAEKKWRDKREKLEWETIV 900
850 860 870 880 890 900
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Information of Monsanto Company


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cyla-105.pe 910 920 930 940 950 960
YKEAKESVDALFVNSOYDQLOADTNIAHIAADKRVHSIREAYLPELSVIPGVNAALFEE
40278 YKEAKESVDALFVNSOYDQLOADTNIAHIAADKRVHSIREAYLPELSVIPGVNAALFEE
880 890 900 910 920 930 940 950 960

cyla-105.pe 970 980 990 1000 1010 1020
LEGRIFTAFSLYDARNVINKGDFNNGSLSCWNVKGVHDVEEQNNQRSLVLVPEWEAEVSQE
40278 LEGRIFTAFSLYDARNVINKGDFNNGSLSCWNVKGVHDVEEQNNQRSLVLVPEWEAEVSQE
940 950 960 970 980 990 1000 1010 1020

cyla-105.pe 1030 1040 1050 1060 1070 1080
VRVCPGRGYLLRVTAAYKEGEGCVTHIEIENNTDELKFSNCVBEIEYFNNTVTCNDIYV
40278 VRVCPGRGYLLRVTAAYKEGEGCVTHIEIENNTDELKFSNCVBEIEYFNNTVTCNDIYV
1000 1010 1020 1030 1040 1050 1060 1070 1080

cyla-105.pe 1090 1100 1110 1120 1130
NOEYGGAYTSRNRGYNEA---PSPADYASVYEKSYTDCGRNCFNCRGYRDTYPL
40278 TOEYEYCTYSRNRGYDGAYESNSVPADYASAYEKA YTDGRDNCFSNCRGYRDTYPL
1060 1070 1080 1090 1100 1110 1120 1130

cyla-105.pe 1140 1150 1160 1170
PVGVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
40278 PAGVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
1120 1130 1140 1150

cyla-105.pep
SW:117536

117536 description="130 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE
ENTOMOCIDAL PROTOXIN)." library="NA species="Bacillus thuringiensis serovar
aizawai" source="swiseprot_prot" version="NA type="PRT

SCORES Initl: 4657 Initn: 5122 Opt: 4671 z-score: 5301.4 E(): 0
>>SW:117536
Initn: 5122 initl: 4657 opt: 4671 z-score: 5301.4 expect(): 0
Smith-Waterman score: 5865; 88.5% identity in 1181 aa overlap
(1-1177:1-1155)

cyla-105.pe MDNPNINCEIPNCLSNPEVEVLGGERIETGTPIDISLSLTOFLLSSEVPVAGFVLGL
60
MDNPNINCEIPNCLSNPEVEVLGGERIETGTPIDISLSLTOFLLSSEVPVAGFVLGL
117536 MDNPNINCEIPNCLSNPEVEVLGGERIETGTPIDISLSLTOFLLSSEVPVAGFVLGL
10 20 30 40 50 60

cyla-105.pe VDIWIGFQSQWDAFLVQIEQLINQRIEFARNQAIISRLGSLNLIQIYASFREWAD
120
VDIWIGFQSQWDAFLVQIEQLINQRIEFARNQAIISRLGSLNLIQIYASFREWAD
117536 VDIWIGFQSQWDAFLVQIEQLINQRIEFARNQAIISRLGSLNLIQIYASFREWAD
70 80 90 100 110 120

cyla-105.pe PTPNALREEMRIQFNDMNSALTTPAFLFVQNVQVPLLSVVVQANLHLSVLDSVFGQ
180
PTPNALREEMRIQFNDMNSALTTPAFLFVQNVQVPLLSVVVQANLHLSVLDSVFGQ
117536 PTPNALREEMRIQFNDMNSALTTPAFLFVQNVQVPLLSVVVQANLHLSVLDSVFGQ
130 140 150 160 170 180

cyla-105.pe RWGFDAAATINSRYNDLTGLIGNYTHAVRWYNTGLERVWGPDSRDWIRYNOFRRELTIV
240
RWGFDAAATINSRYNDLTGLIGNYTHAVRWYNTGLERVWGPDSRDWIRYNOFRRELTIV
117536 RWGFDAAATINSRYNDLTGLIGNYTHAVRWYNTGLERVWGPDSRDWIRYNOFRRELTIV
190 200 210 220 230 240
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117536 RWGFDAAATINSRYNDLTGLIGNYTHAVRWYNTGLERVWGPDSRDWIRYNOFRRELTIV
190 200 210 220 230 240

cyla-105.pe LDIIVSLPNYDSRTYRTVTSQLTREIYTNVLENFDFGSRGSAQIEGSIIRSPHMLDIL
250 260 270 280 290 300
117536 LDIIVSLPNYDSRTYRTVTSQLTREIYTNVLENFDFGSRGSAQIEGSIIRSPHMLDIL
250 260 270 280 290 300

cyla-105.pe NSIITIYDHRGEYXWGHQIMASPVGFSPEFTFLYGTMGNAAPQORIVAOIQQGVIR
310 320 330 340 350 360
117536 NSIITIYDHRGEYXWGHQIMASPVGFSPEFTFLYGTMGNAAPQORIVAOIQQGVIR
310 320 330 340 350 360

cyla-105.pe TLLSSTLYRRFPFNIGINNQLSVLDGTFAFGTSSNLPASAVYRKSGTVDSLDEIPPNNVV
370 380 390 400 410 420
117536 TLLSSTLYRRFPFNIGINNQLSVLDGTFAFGTSSNLPASAVYRKSGTVDSLDEIPPNNVV
370 380 390 400 410 420

cyla-105.pe PPROGFSHRLSHVSMFPRSGFNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPLVKAH
430 440 450 460 470 480
117536 PPROGFSHRLSHVSMFPRSGFNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPLVKAH
430 440 450 460 470 480

cyla-105.pe TLOSGTTVVRGPGTGGDILRRTSGGPAYTIYINGOLPORVARIYASTTNLIYVT
490 500 510 520 530 540
117536 NLGSGTSSVVRGPGTGGDILRRTSGGPAYTIYINGOLPORVARIYASTTNLIYVT
490 500 510 520 530 540

cyla-105.pe VAGERIFAGQVKNMTDTPDTFQSFYATINTAFTFPMSOSSFTVGADTFSSGNEVYID
550 560 570 580 590 600
117536 IDGRIINOQNFSAATSSNQLSGSFRIVGFTFPNFNSGSSVFTLSAHVFNSENEVYID
550 560 570 580 590 600

cyla-105.pe RFELIPIVATLEAEVNLRAKAVNALFTSTNOLGKTNVTDYHIDQVSNLVTYLSDFEC
610 620 630 640 650 660
117536 RIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNLVECLDFEC
610 620 630 640 650 660

cyla-105.pe LDEKRELSKVKHAKRLSDERNLQDSNFKDINROPERSGMGSGTITIOGGDDVFKENVY
670 680 690 700 710 720
117536 LDEKRELSKVKHAKRLSDERNLQDSNFKDINROPERSGMGSGTITIOGGDDVFKENVY
670 680 690 700 710 720

cyla-105.pe TLLGTFCDECYPTLYQKIDESKXAFTRVQLRGYIEDSQDLEIYSIRYNAKHETVNPCT
730 740 750 760 770 780
117536 TLLGTFCDECYPTLYQKIDESKXAFTRVQLRGYIEDSQDLEIYSIRYNAKHETVNPCT
730 740 750 760 770 780

cyla-105.pe GSLWPLSASGPIKCGEENRCAPHLEWNPDLDCSRDGEKCAHSHHFLSLDIDVGCTDLN
790 800 810 820 830 840
117536 GSLWPLSASGPIKCGEENRCAPHLEWNPDLDCSRDGEKCAHSHHFLSLDIDVGCTDLN
790 800 810 820 830 840

cyla-105.pe EDLGVWVIFKIKTQDGHARLGNLFLEEKPLVGEALRVKSAEKKMEDKEKLEWETIV
850 860 870 880 890 900
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117536 EDGVVAKYIKITQCHARNLNEFLLEKPLGGEALRVKRAEKKKRKEKLEMTIV 840 850 860 870

cry1a-105.pe YKAKRSVDALFNSQDQLOADTNANHAADKRVHSIREAYLPELSIVPGVNAAFEE 910 920 930 940 950 960

117536 YKAKRSVDALFNSQDQLOADTNANHAADKRVHSIREAYLPELSIVPGVNAAFEE 880 890 900 910 920 930

cry1a-105.pe LEGRIETAFSLYDARNIKNGDPNNGSCMNVKCEYVEEQNHRSVLPPEWEAEVSQE 940 950 960 970 980 990

117536 LEGRIETAFSLYDARNIKNGDPNNGSCMNVKCEYVEEQNHRSVLPPEWEAEVSQE 940 950 960 970 980 990

cry1a-105.pe VRVCPGRGYILRVATYKGYGEGCVTIHEIENNDDEKFCVVEEYTPNNTVTNDYV 1030 1040 1050 1060 1070 1080

117536 VRVCPGRGYILRVATYKGYGEGCVTIHEIENNDDEKFCVVEEYTPNNTVTNDYV 1000 1010 1020 1030 1040 1050

cry1a-105.pe NQEEYCGATISNRNCYNEA---PSPVADYASVIEKSYTDGRENPCFNRXYDYTEL 1140 1150 1160 1170 1180 1190

117536 NQEEYCGATISNRNCYNEA---PSPVADYASVIEKSYTDGRENPCFNRXYDYTEL 1140 1150 1160 1170 1180 1190

cry1a-105.pe PVGYVTKLEVPFETDKVWIEIGETEGTIVDSVELLIMEE 1120 1130 1140 1150

117536 PVGYVTKLEVPFETDKVWIEIGETEGTIVDSVELLIMEE 1120 1130 1140 1150

cry1a-105.pap
NRAA:13173238

13173238 source="GENBANK PROT" insecticidal crystal protein BTRX24 [Bacillus thuringiensis serovar kunthalarX24]

SCORES Initl: 4599 Initn: 4599 Opt: 4613 z-score: 5235.7 E(): 0
>NPAA:13173238
initn: 4599 initl: 4599 opt: 4613 z-score: 5235.7 expect(): 0
Smith-Waterman score: 6228; 88.0% identity in 1075 aa overlap
(1-1075:1-1049)

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

13173238 MNNPINECPYVNCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFPVPGAGFVLG 70 80 90 100 110 120

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

13173238 VDIWIGIFGPSQWDAFLVQIQLINQRIEEFARNQASIRLEGLSNLYQIYAESPREWAD 70 80 90 100 110 120

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

13173238 PTNPALREEMRIQNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHSLVRDVSVFQ 130 140 150 160 170 180

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

13173238 RWGFDAAATNSRYNDLTRELIGNYTDHAVRYNTGLERVWGPDSRDWIRYNQFRRELTIV 190 200 210 220 230 240

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

13173238 LDIVSLFPYDSDRTYPIKTVSQTREIYNPVLENFDSFRGSAQIEGSIIRSPHMDIL 250 260 270 280 290 300

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

13173238 NSITITVDARHCEYVWSHQIMASPVGFSPEFTPELPGTGMNAAPOQRIVAOLOGGYR 310 320 330 340 350 360

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

13173238 TLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYKSGTVDSLDIPPQNNV 370 380 390 400 410 420

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

13173238 PPRQGFSEHLSHVSMFRSGFSNVSIIIRAPMFSWIRHSAEFNIIASDSITQIPLVKAH 430 440 450 460 470 480

cry1a-105.pe TLRGTYVVRGPGTGGDIILRTSGGPFAYTIVNIGOLQPVYRARIYASTNLIYVT 490 500 510 520 530 540

13173238 TLRGTYVVRGPGTGGDIILRTSGGPFAYTIVNIGOLQPVYRARIYASTNLIYVT 490 500 510 520 530 540

cry1a-105.pe RGERIETGYTPIDISLSLTQFLSEFPVPGAGFVLG 550 560 570 580 590 600

13173238 RGERIETGYTPIDISLSLTQFLSEFPVPGAGFVLG 550 560 570 580 590 600

cry1a-105.pe RPELIPVTATLEAEVNERAKVNNFTSTNGLSNYTDHIDQVSNLTVLSDEPC 610 620 630 640 650 660

13173238 RPELIPVTATLEAEVNERAKVNNFTSTNGLSNYTDHIDQVSNLTVLSDEPC 610 620 630 640 650 660

cry1a-105.pe LDEKLESEKVKHAKRLSDERNLQDSNFKRNPQPRQGGSTGTTTGGDQVFKENYV 670 680 690 700 710 720

13173238 LDEKLESEKVKHAKRLSDERNLQDSNFKRNPQPRQGGSTGTTTGGDQVFKENYV 670 680 690 700 710 720

cry1a-105.pe TLRGTYVVRGPGTGGDIILRTSGGPFAYTIVNIGOLQPVYRARIYASTNLIYVT 730 740 750 760 770 780

13173238 TLRGTYVVRGPGTGGDIILRTSGGPFAYTIVNIGOLQPVYRARIYASTNLIYVT 730 740 750 760 770 780

cry1a-105.pe GSLWPLSAOSPIGKCEPNRCAPLHEWNPDLDCSRGDEKCAHSHHSLDIDVGCTDLN 790 800 810 820 830 840

13173238 GSLWPLSAOSPIGKCEPNRCAPLHEWNPDLDCSRGDEKCAHSHHSLDIDVGCTDLN 790 800 810 820 830 840

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cry1a-105.pe 850 860 870 880 890 900
EDGVVVIKIKITODGHARLGNLEFLEKPLVGEALARKVRAEKKKWRDKREKLEWETNIV
13173238 EDGVVVIKIKITODGHARLGNLEFLEKPLVGEALARKVRAEKKKWRDKREKLEWETNIV
820 830 840 850 860 870

cry1a-105.pe 910 920 930 940 950 960
YKAKESVDALFVNSQYDQLQADNTIAMIHAAKRVHSIREAYLPESLVIPIGVNAAFEE
13173238 YKAKESVDALFVNSQYDQLQADNTIAMIHAAKRVHSIREAYLPESLVIPIGVNAAFEE
880 890 900 910 920 930

cry1a-105.pe 970 980 990 1000 1010 1020
LEGRIETAFSLYDAARNVKKNGDFNGLSCWNVKGVHDVVEEQNQRSVLVWPEAEVQSQE
13173238 LEGRIETAFSLYDAARNVKKNGDFNGLSCWNVKGVHDVVEEQNQRSVLVWPEAEVQSQE
940 950 960 970 980 990

cry1a-105.pe 1030 1040 1050 1060 1070 1080
VRVCPGRGVLRTAYKEGEGECVTHIEIENNTDELAFSCVVEEETPNNTVTGNDVTV
13173238 VRVCPGRGVLRTAYKEGEGECVTHIEIENNTDELAFSCVVEEETPNNTVTGNDVTV
1000 1010 1020 1030 1040 1050

cry1a-105.pe 1090 1100 1110 1120 1130 1140
NQEEYGGATSRNRYNEAPSVADYASVYEKSYTDGRRENPCFNRGRDYTPLVGY
13173238 LKKMRVRTLLVIEDMTEPMKAILLYQLIMHPMKKHQIMDEETILVNLITDMGITHY
1060 1070 1080 1090 1100 1110

cry1a-105.pap
NR0A:46409861

46409861 source="GENBANK_PROT" cry1a type crystal protein [Bacillus
thuringiensis serovar kenya]

SCORES Init1: 4586 Initn: 4586 Opt: 4605 z-score: 5228.9 E(): 0
>>NR0A:46409861
initn: 4586 init1: 4586 opt: 4605 z-score: 5228.9 expect(): 0
Smith-Waterman score: 4605; 87.8% identity in 792 aa overlap
(9-800.2-793)

cry1a-105.pe 10 20 30 40 50 60
MDNNPINECIPYCNLSNPEVEVLGGRIETGYTIDISLSLTOFLSEFVPGAGFVLGL
46409861 MQCVPYCNLSNPEVEVLGGRIETGYTIDISLSLTOFLSEFVPGAGFVLGL
10 20 30 40 50

cry1a-105.pe 70 80 90 100 110 120
VDIIWIGFQPSQWDAFLVQIQEQLINQRIEFAFNQAIISRLGSLNLYIYAESFREWAD
46409861 VDIIWIGFQPSQWDAFLVQIQEQLINQRIEFAFNQAIISRLGSLNLYIYAESFREWAD
60 70 80 90 100 110

cry1a-105.pe 130 140 150 160 170 180
PTNPALREEMRIQFNDNMNSALTITAIPLFAVQNVQVPLLSVVQVAAHLSVLRDVSFVGQ
46409861 PTNPALREEMRIQFNDNMNSALTITAIPLFAVQNVQVPLLSVVQVAAHLSVLRDVSFVGQ
120 130 140 150 160 170

cry1a-105.pe 190 200 210 220 230 240
RWGFDATINSRYNDLTGLIGNYTDHVRWYNTGLERVMGPDSDRMIRYNQFRRELITV
46409861 RWGFDATINSRYNDLTGLIGNYTDHVRWYNTGLERVMGPDSDRMIRYNQFRRELITV
190 200 210 220 230 240
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cry1a-105.pe 180 190 200 210 220 230
LDIVSLFPYDSRTYPTRTYSQLTREIYNPVLNFDGSPRGSAGIEGSIIRSPHMDIL
46409861 LDIVSLFPYDSRTYPTRTYSQLTREIYNPVLNFDGSPRGSAGIEGSIIRSPHMDIL
240 250 260 270 280 290

cry1a-105.pe 310 320 330 340 350 360
NSITITDARHGYWMSGHQIMASPVGFGSGPEFTPLPYGTMGNAAPQORIVAQLGQGVYR
46409861 NSITITDARHGYWMSGHQIMASPVGFGSGPEFTPLPYGTMGNAAPQORIVAQLGQGVYR
300 310 320 330 340 350

cry1a-105.pe 370 380 390 400 410 420
TLSTLYRPPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYKSGTVDSLDEIPPNNNV
46409861 TLSTLYRPPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYKSGTVDSLDEIPPNNNV
360 370 380 390 400 410

cry1a-105.pe 430 440 450 460 470 480
PPQGGSHRLSHVSMFRSGFSNVSIIIRAPMFSWIHPSAEFNNIIPSSQITQIPLKST
46409861 PPQGGSHRLSHVSMFRSGFSNVSIIIRAPMFSWIHPSAEFNNIIPSSQITQIPLKST
420 430 440 450 460 470

cry1a-105.pe 490 500 510 520 530 540
TLQSGTVVRGPGFTGGDILARTSGGPFAYTIVNINGQLPQRYRARIYASTTNRIYVT
46409861 TLQSGTVVRGPGFTGGDILARTSGGPFAYTIVNINGQLPQRYRARIYASTTNRIYVT
480 490 500 510 520 530

cry1a-105.pe 550 560 570 580 590 600
VAGERIPAGQFNKTMDDPLTQCSFYATINTATFPMSOSSFTVCAUTFFSGNEVYID
46409861 VAGERIPAGQFNKTMDDPLTQCSFYATINTATFPMSOSSFTVCAUTFFSGNEVYID
540 550 560 570 580 590

cry1a-105.pe 610 620 630 640 650 660
RFELIPVTATLAEYNERAKAVNALFTSNOLGLKTNVTDYHIDQVSNLVTYLSDFEC
46409861 RFELIPVTATLAEYNERAKAVNALFTSNOLGLKTNVTDYHIDQVSNLVTYLSDFEC
600 610 620 630 640 650

cry1a-105.pe 670 680 690 700 710 720
LDEKRELSKVKHAKRLSDENLQDSNFKDINRQPERGWSGTGITIQGDDVFKENYV
46409861 LDEKRELSKVKHAKRLSDENLQDSNFKDINRQPERGWSGTGITIQGDDVFKENYV
660 670 680 690 700 710

cry1a-105.pe 730 740 750 760 770 780
TLSGTDECPYLYQKIDESKUKATRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGT
46409861 TLSGTDECPYLYQKIDESKUKATRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGT
720 730 740 750 760 770

cry1a-105.pe 790 800 810 820 830 840
GSLWPLSAQSPKCGKEPNRCAPHLENNPDLDCSCRDCEKCAHHSHHFSLDIDVGCTDLN
46409861 GSLWPLSAQSPKCGKEPNRCAPHLENNPDLDCSCRDCEKCAHHSHHFSLDIDVGCTDLN
780 790 800 810 820 830

cry1a-105.pap
NR0A:27447986
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~~Product Characterization Center~~

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[illegible]

147986
YTPJFAGVTKLEYPETDKVWIEIGETGTIVDSVLLMEE
1130 1140 1150 1160

cryla-105.pep
NRAA:8469154

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MSL No. 20351
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SCORES      Init1: 3638      Initn: 5076      Opt: 4539      z-score: 5151.3 E(): 0
>>NRAA: 9469154
Init1: 5076      Init1: 3638      Opt: 4539      Z-score: 5151.3 expect(): 0
Smith-Waterman score: 5229;      68.1% identity in 1185 aa overlap
(1-1177;1-1169)

```

[illegible]

cryla-105.pe RMGFDATINSRYNDLTRLIGNYTHDVAVRWNTGLERVMGSPDSMDTIRYNQRFRELTIV
8469154 RMGLTQTNDLRYSLKNSIDYTNHCVRVNIGL---GNLNVIRPEYRQRFRELTISV

```
cryla-105.pe      310      320      330      340      350
NSIIITYDHRGEVYNSHQIWAIPVGFSFETPLPYGTWGNAAPOQRIVAQLQGQV--
:   :   :   :   :   :   :   :   :   :   :   :   :   :   :
NRLIITYGVRGIHGWAGHEVSSRGM--TNIRFLPYGTATAEPTFRITFTSTPGJLNL
```

```

420      430      440      450      460      470
NNNVPRQGFHRLSHVSMFRSGFNSVSIIRAPMFSWHRSAEFNNIIASDITQIPL
cry1a-105.pe
:::      |||||      CHVRFAOASLRNAEPLOYAPVMSFWHSRATPTNTIDPDVITQIPL
GFSITE--YSHRI-CHVRFAOASLRNAEPLOYAPVMSFWHSRATPTNTIDPDVITQIPL
4469154

```

	410	420	430	440	450	460
cr1a-105_pe	VKAHTLQSGTIVRGPFGTGGILRTISGSGPFAYITVINGLQQRVRAIRVASTNL	490	500	510	520	530
0460154	VYKPI WSGA TWVPGCFCTGCI PPTWAGNQGDMVNTAPI SQRVVIRVASTNLO					

[illegible]

```

720      730      740      750      760      770
cryla-105.pe ENYVTLSGTFDCYPTLYQKIDESKIKAFTRYOIRGVIEDSDLEIYIRNAKHEVNV
8469154 ENYVTLSGTFDCYPTLYQKIDESKIKAFTRYOIRGVIEDSDLEIYIRNAKHEVNV
710      720      730      740      750      760
8469154 ENYVTLSGTFDCYPTLYQKIDESKIKAFTRYOIRGVIEDSDLEIYIRNAKHEVNV
710      720      730      740      750      760

```

	840	850	860	870	880	890
CRY1a-105.pe	TDLNEDJGVWVFIKINTDGHARLGNLEFLEKPLVNGSALARVRAEKKWKDKRREKLEWE					
8459154	TDLNEDJGVWVFIKINTDGHARLGNLEFLEKPLVNGSALARVRAEKKWKDKRREKLELE					
	830	840	850	860	870	880

```
cryla-105.pe ifEELEGRIFTAFSLYDARNVKGDNFGNGLSCWNVKGHVDVEQNNQRSVLVPWEAE      960    970    980    990    1000    1010
ifEELEGRIFTASLSLDARNVKGDNFGNGLSCWNVKGHVDVEQNHNRSVLVPWEAE      8469154    8469155    8469156    8469157    8469158    8469159
```

```

1080      1090      1100      1110      1120      1130
cry1a-105.pe DTTVNQEEYGATYSNRGYNFA----PSPADYASVVEEKSYYTDGRRENPCFENGYRD
1086      1096      1106      1116      1126      1136
8469154 DYATQEEYEGTYSNRGYDGAYESNSVPADYASAEKAYTDGRDRNTCSNGYGD

```

```

1076      1150      1160      1170
cry_ia-105.pe YTPLPVGVTKELEYEPETDKVWIEIGTGTGTVDSVLLMEE
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
8469154 YTPLPAGVTKELEYEPETDKVWIEIGTGTGTVDSVLLMEE

```

cryla-105.pe
SW:8469154
8469154 description="PESICIDAL CRYSTAL PROTEIN CRYLGB (INSECTICIDAL DELTA-ENDOTOXIN CRYLO-BI) (CRYSTALLINE ENDOCRINAL PROTOXIN) (133 KDA CRYSTAL PROTEIN)." library="No Species" Baillus thuringiensis serovar wuhanensis" source="swissprot_prot" version="AA type=PRT

SCORES Initl: 3638 Initn: 5076 Opt: 533 z-score: 5151.3 E(): 0
>SW:8469154
initn: 5076 initl: 3638 opt: 4539 z-score: 5003 expected: 0
Smith-Waterman score: 5229; 68.1% identity in 1063 aa overlap
(1-1177:1-1169)

cryla-105.pe
8469154
MEIN-NQVCVYNNCLNPESELNVA-IFSEQVABHKTITILENFGAFAAGL
10 20 30 40 50 60
70 80 90 100 110 120
VDIINGIFGPDWDAFLVOELINQRIEERFARNOAISRLEGSLNLYQVYAESREWEAD
FDMIGIFNEQMSAFLRQVEELINQRIEERFARNOAISRLEGSLNLYQVYAESREWEAD
130 140 150 160 170 180
PTNPALREMRIFQNDMNSALTTAIFLAVQNYQVPLLSVYVQAANHLVLRDVSFVGQ
PDPASKERVTRFTDDALLTGVELMAIPGFEATLSVYVQAANHLVLRDVSFVGQ
120 130 140 150 160 170 180

cryla-105.pe
8469154
FDIINGIFNEQMSAFLRQVEELINQRIEERFARNOAISRLEGSLNLYQVYAESREWEAD
60 70 80 90 100 110 120
VDIINGIFGPDWDAFLVOELINQRIEERFARNOAISRLEGSLNLYQVYAESREWEAD
130 140 150 160 170 180
PTNPALREMRIFQNDMNSALTTAIFLAVQNYQVPLLSVYVQAANHLVLRDVSFVGQ
PDPASKERVTRFTDDALLTGVELMAIPGFEATLSVYVQAANHLVLRDVSFVGQ
120 130 140 150 160 170 180

cryla-105.pe
8469154
RWGLTQTNINDLYSLRKNISIRDTNCHVRFYNGIL---GNLNVIRPEYRQRELTISV
180 190 200 210 220 230
RWGLTQTNINDLYSLRKNISIRDTNCHVRFYNGIL---GNLNVIRPEYRQRELTISV
240 250 260 270 280 290 300
LDIVSLFPNDSRTVPIRTVSQLTREIYTNPVLENFDSFGSAQGEISRSPLMDIL
LDIVSLFPNDSRTVPIRTVSQLTREIYTNPVLENFDSFGSAQGEISRSPLMDIL
240 250 260 270 280 290 300

cryla-105.pe
8469154
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960 970 980 990 1000
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8330 8340 8350 8360 8370 8380
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
8390 8400 8410 8420 8430 8440
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
8450 8460 8470 8480 8490 8500
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
8510 8520 8530 8540 8550 8560
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
8570 8580 8590 8600 8610 8620
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
8630 8640 8650 8660 8670 8680
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
8690 8700 8710 8720 8730 8740
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
8750 8760 8770 8780 8790 8800
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
8810 8820 8830 8840 8850 8860
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
8870 8880 8890 8900 8910 8920
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
8930 8940 8950 8960 8970 8980
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
8990 9000 9010 9020 9030 9040
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
9050 9060 9070 9080 9090 9100
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
9110 9120 9130 9140 9150 9160
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
9170 9180 9190 9200 9210 9220
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
9230 9240 9250 9260 9270 9280
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
9290 9300 9310 9320 9330 9340
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
9350 9360 9370 9380 9390 9400
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
9410 9420 9430 9440 9450 9460
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
9470 9480 9490 9500 9510 9520
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
9530 9540 9550 9560 9570 9580
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
9590 9600 9610 9620 9630 9640
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
9650 9660 9670 9680 9690 9700
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
9710 9720 9730 9740 9750 9760
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
9770 9780 9790 9800 9810 9820
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
9830 9840 9850 9860 9870 9880
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
9890 9900 9910 9920 9930 9940
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
9950 9960 9970 9980 9990 10000
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
10010 10020 10030 10040 10050 10060
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
10070 10080 10090 10100 10110 10120
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
10130 10140 10150 10160 10170 10180
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
10190 10200 10210 10220 10230 10240
NSITIYDARHGYWYSHQIMASPVGSGPEFTPLPYGTMGNAPOQRIVAQLOQGV--
10250 102

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295862
PIEGTD--PFTGYSHRICHVGF⁴¹⁰FIASSPFI⁴²⁰SOYA--RAPIFSWTHRSATLNTIAPDVITQ⁴³⁰
440 450

```
cryla-105.pe    IPLVKAHTLQSGTIVVRGPGTGDIILRTSGGPAYTVINNGQLPQRYARIYAST
                    :|::||::||::||::||::||::||::||::||::||::||::||
IPLVKAFUHSAGATVKGPGGTGGDILIRTVGSFGDMRVNITAPLSQRYVRIYAST
```

```

540      550      560      570      580      590
cry1a-105.pe NRIYTVAGERIFAGQENKMTGDPLTFQSFVATINTAFIPMSQSFVTGADTFSS
295862      DLQFYININGTITINQFSSPTMSGDDLOQYGRVAGFTPTFSDANSTFETIGAGFSP

```

cr:yla-105.pe GNEVYIDRFELIPV'TATLEAEVNLERAOKNAALFTSTNOIGLKTNYTDYHIDCVSNI.VT

```
cryla-105.pe YLSDFCLEKSEKVKAKLSERNLLQDNFNKDINRQPERGWGGSGTITQQGDD
|||||
CLDSEFCLEKSEKVKAKLSERNLLQDNFNQINRQPDWGRSGTITQQGDD
295862
```

```
cry1a-105.pe      VFXENVVILSGTFDECPYTLVYQKIDESKLAFTRYQLRGVIEDSODLSIYSIRINAKHE      720    730    740    750    760    770
|||||            VFXENVVILPGTFDGCPTVLVYQKIDESKLKVTRYQLRGVIEDSODLSIYLIRINAKHE      700    710    720    730    740    750
```

cr1a-105.pe
TVNPGTSLMPLSAQSPICKGCEPNRCAPHLEWNPDLCSDRGKCAHSHHFSLDID
TVNPGTSLMPLSAQSPICKGCEPNRCAPHLEWNPDLCSDRGKCAHSHHFSLDID
TVNPGTSLMPLSAQSPICKGCEPNRCAPHLEWNPDLCSDRGKCAHSHHFSLDID
TVNPGTSLMPLSAQSPICKGCEPNRCAPHLEWNPDLCSDRGKCAHSHHFSLDID

```

crryla-105.pe  VGTDTNEDLGVWIFIKITQDGHARLGNLFEELKPLGEALARVTKRAEKKWDKREKL
|||||
VGTDTNEDLGVWIFIKITQDGHARLGNLFEELKPLGEALARVTKRAEKKWDKREKL
|||||
VGTDTNEDLGVWIFIKITQDGHARLGNLFEELKPLGEALARVTKRAEKKWDKREKL
|||||

```

900 910 920 930 940 950
 EWEINIVKEAKESVDALFVNSQYDQLQADTNIAIHADKRVHSIRAYLPFLSVIPGV
 ELETINIVKEAKESVDALFVNSQYDQLQADTNIAIHADKRVHSIRAYLPFLSVIPGV
 880 890 900 910 920 930 940 950
 EWEINIVKEAKESVDALFVNSQYDQLQADTNIAIHADKRVHSIRAYLPFLSVIPGV
 ELETINIVKEAKESVDALFVNSQYDQLQADTNIAIHADKRVHSIRAYLPFLSVIPGV

cry1a-105.pe NAAIFEELEGRIFAFSLYDARNVTKNGDFNGLSCNWKVGHVDVEEQNNORSVLLVYPEW
 960 970 980 990 1000 1010
 295862 NAAIFEELEGRIFAFSLYDARNVTKNGDFNGLSCNWKVGHVDVEEQNNHRSVLLVYPEW
 940 950 960 970 980 990

try1a-105.pe EAEVQEVRCPGGYLLRTAYKGYGEGCVTHETENNDELFSNCVEEETYPNNTV
EAEVQEVRCPGGYLLRTAYKGYGEGCVTHETENNDELFSNCVEEETYPNNTV
EAEVQEVRCPGGYLLRTAYKGYGEGCVTHETENNDELFSNCVEEETYPNNTV
EAEVQEVRCPGGYLLRTAYKGYGEGCVTHETENNDELFSNCVEEETYPNNTV

```

1080
1090
1100
1110
1120
ery/1a-105.pe TCNDTVNQVEYGAATSRNRGYNFA-----PSVPADYASVFEKSVTDGRNPCEFNRRG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

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294862 TCNDYTNQENKGNVTSNHNRYDEAYGNPNVPDYTPVVEKAYTDGRRNCPESNRG
1060 1070 1080 1090 1100 1110

cryla-105.pe VQVTPLEKGVYVLEVEVNDKVLIEIGETGTIVDSVELLIMEE
1130 1140 1150 1160 1170
295862 XGDIPLKAGVYVLEVEVNDKVLIEIGETGTIVDSVELLIMEE
1120 1130 1140 1150 1160

cryla-105.pep
SW:8469146

8469146 description="PESTICIDIAL CRYSTAL PROMOTER, CRYGIA (ANGELICIDAL
DELTA-ENDOTOXIN CRYGIA(A)) (CRYSTALLINE ENTOXOCIDAL PROTOXIN) 113 KDA CRYSTAL
PROTEIN." library="NA species="Bacillus thuringiensis" source="swisprot_prot"
version="NA type="PRT

SCORES Initl: 3732 Initn: 5058 Opt: 4435 z-score: 5033.2 E(1) 0
>SW:8469146
initn: 5058 opt: 3732 z-score: 5033.2 expect(1) 0
Smith-Waterman score: 5329; 69.9% identity in 1181 aa overlap
(8-1177:7-1166)

cryla-105.pe MDNPNINECIPNCLSNPEVEVLGERIETGYTPIDISLSITOPILLSFVPGAGNLS
10 20 30 40 50 60
8469146 MEISDQOQVTRFRLTDATVGTGLPTLAIENLVNLSVYTOAANLHLSLRDAVYGE
10 20 30 40 50

cryla-105.pe VDIWGFPSQWDAFLVQIEQLINQRIEFAFNOAISRLEGLSNLVOIIVAESFREWAD
60 70 80 90 100 110 120
8469146 FDIWLGALGVDSWLSFLQIEQLIRQIELEENRATALLGLSSNINVAELREWEND
60 70 80 90 100 110

cryla-105.pe PTNPALEENRQFNDMNSALTATPFAVQNVQVPLLSVYQVAAANLHLSLRDSVFGQ
130 140 150 160 170 180
8469146 PNPASQOQVTRFRLTDATVGTGLPTLAIENLVNLSVYTOAANLHLSLRDAVYGE
120 130 140 150 160 170

cryla-105.pe RWGFDAATINSRYNDLTRIGNYTDHAWVNTGLERYWGPDSFSDWIRYNOFRRELTIV
190 200 210 220 230 240
8469146 RWGLTQANIEDLYRLTSNIOEISDHCARYNOGLNEIGGI-SR---RYLDFORDLTISV
180 190 200 210 220 230

cryla-105.pe LDIVSFPNDSTYPIRTVSQLTREIYNPVLENDFSGFSGSAQIEGSIRSPHMDIL
250 260 270 280 290 300
8469146 LDIVLFPNDSTYPIRTVSQLTREIYNPVLENDFSGFSGSAQIEGSIRSPHMDIL
240 250 260 270 280 290

cryla-105.pe NSITIYDHRGEYVWSHQIMASPVGFS-GPEFTPIYGTMGNAAPQRI----VAQLG
310 320 330 340 350
8469146 DRIVITNSVRSTPYWAGIEVISRTQOQOQNEIRFPPLYGAANAEPVPIRTGFTDEQ
300 310 320 330 340 350

cryla-105.pe QGVRTLSTSLVRRPFNIGINNQLSVLDGTEFAFGTGSNLPASVYKES-G-TVLSLDEI
360 370 380 390 400 410
8469146 ROWRARSVSVFRS-----SGDPSLVDAVGFLIFSA---VSIYRNGFGNFTIDIEI
360 370 380 390 400 410

cryla-105.pe PPNNVPPRQGFSHLSVMSRSGFSSSVSIRAPMSEWHSRAEFNNIITASDITO
420 430 440 450 460 470
8469146 PIEGTD--PTGSHRLCHVGFCLASSPFISQYA--RAPFSNTHRSAILINTIAPDVITO
410 420 430 440 450

cryla-105.pe IPLVKAHTLOSQTIVVRGFGTGGDILRTSGGFAYTIVNINQLPQRYRARIYASTT
480 490 500 510 520 530
8469146 IPLVKAFTLHSGATIVKGFPGTGGDILRTNNGVSGFDMRVNITAPLSQRYRARIYASTT
460 470 480 490 500 510

cryla-105.pe MLRIYVTVAGERIFAGQFNKMTDGLPTTQSFSTATINTAFTPFMSQSSFTVGAUTFS
540 550 560 570 580 590
8469146 DLQFTYTNINGTTINIGNFSMDSGDDLOQYGRFVAGFTTPTFTSDANSTFTTIGAFGFSF
520 530 540 550 560 570

cryla-105.pe GNEVYIDRFELIPVTATLEAEVNLERAQKAVNALFTSTNOLGLXNTVTDYHIDQVSNLYT
600 610 620 630 640 650
8469146 NNEVYIDRFELIPVTATLEAEVNLERAQKAVNALFTSTNOLGLXNTVTDYHIDQVSNLYT
580 590 600 610 620 630

cryla-105.pe YLSEDFCLDEKRELSEKVKHAKRLSDERNLQDSNFKDINRQPERGSGSTGIIQGGDD
660 670 680 690 700 710
8469146 CLSEDFCLDEKRELSEKVKHAKRLSDERNLQDSNFKDINRQPERGSGSTGIIQGGDD
640 650 660 670 680 690

cryla-105.pe VFKEVYTSCTFDECYTYLYOKIDSKLAKFTYQYQYGVIEDSOILEYISRYNAKHE
720 730 740 750 760 770
8469146 VFKEVYTSCTFDECYTYLYOKIDSKLAKFTYQYQYGVIEDSOILEYISRYNAKHE
700 710 720 730 740 750

cryla-105.pe TVNPGTSLWPLSASQIGKCGENRCAFLHWNPDLDSCRDGKCAHSHHPSLDD
780 790 800 810 820 830
8469146 TVNPGTSLWPLSASQIGKCGENRCAFLHWNPDLDSCRDGKCAHSHHPSLDD
760 770 780 790 800 810

cryla-105.pe VGCTDLNEDLGVWYVSKNTODGHARYGNLFELEKDVWSEALARKRAEKKWRDKREL
840 850 860 870 880 890
8469146 VGCTDLNEDLGVWYVSKNTODGHARYGNLFELEKDVWSEALARKRAEKKWRDKREL
820 830 840 850 860 870

cryla-105.pe EWETNIVYKEAKESVDALFVNSQYDQLOQNTNINMIHAKLVHSIREAYVPELVICV
900 910 920 930 940 950
8469146 ELETNIVYKEAKESVDALFVNSQYDQLOQNTNINMIHAKLVHSIREAYVPELVICV
880 890 900 910 920 930

cryla-105.pe NAAIFELGRIFTAFSLYDARNYKNGDFNNGLSQNMVKGHVDSQVQNSVAVPEM
960 970 980 990 1000 1010
8469146 NAAIFELGRIFTAFSLYDARNYKNGDFNNGLSQNMVKGHVDSQVQNSVAVPEM
940 950 960 970 980 990

cryla-105.pe EAEVSQEVRCVCGRIILRVYAKEGYGGCVTTIHEINNTDELKFSNCVVEEYIPNNTV
1020 1030 1040 1050 1060 1070
8469146 EAEVSQEVRCVCGRIILRVYAKEGYGGCVTTIHEINNTDELKFSNCVVEEYIPNNTV
1000 1010 1020 1030 1040 1050

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[illegible]

```

cyla-105.pe NEVDFELIPVTLEAEYNLRAOKAVNALFTSTNQGLKTNVDYDIDOVSNLYT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
--VIDRIEVPVDATFEAGDYDLRRAOKAVNALFTSTNQRLGKTITDHYDIDOVSNLVEC
296087       590      610      620      630      640      650

```

```

cryla-105.pe LSDFDLKRELSKVKHARLSDGNLLQSNFINRQPERGWSGTITIQGDDV
                660 670 680 690 700 710
296087 LSDFDLKRELSKVKHARLSDGNLLQSNFINRQPERGWSGTITIQGDDV
                650 660 670 680 690 700

```

```

720      730      740      750      760      770
cyla-105.pe FKENYVLTSGTDECPYLYQKIDESKAFRQVLRGYIEDSQDLEIYSIRYNAKHET
296087 FKENYVLTSGTDECPYLYQKIDESKAFRQVLRGYIEDSQDLEIYSIRYNAKHET
710      720      730      740      750      760
cyla-105.pe FKENYVLTSGTDECPYLYQKIDESKAFRQVLRGYIEDSQDLEIYSIRYNAKHET
296087 FKENYVLTSGTDECPYLYQKIDESKAFRQVLRGYIEDSQDLEIYSIRYNAKHET

```

```

780      790      800      810      820      830
cry1a-105.pe VNVFGTGSIMPLASQSPITGKCGENRCAPHELNWPDLOCSCRDGEKCAKHHSHHFSLUIDIV
296087 VNVFGTGSIMPLASVENSIGPCGSENRCAPHLENNWPDLOCSCRDGEKCAKHHSHHFSLUIDIV
770      780      790      800      810      820

```

840 850 860 870 880 890
 CTDLNEDGVWVFKITQDGHARLGNLEFEEKPLVGEALARKKAKKWRDKKLE
 296087
 830 840 850 860 870 880
 GCTDLNEDGVWVFKITQDGHARLGNLEFEEKPLVGEALARKKAKKWRDKKLE

```

CRY1a-105.pe  WETIVYVEKAKESVDALFVNSQYDQLQADNTAMTHAAADKRVHIREAYPELISVTPGVN
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
FETIVYVEKAKESVDALFVNSQYDQLQADNTAMTHAAADKRVHIREAYPELISVTPGVN
296087         830    900    910    920    930    940    950

```

```

cyl=105.pe AATFEELGGITATSLYDARNVTKGDFNGLSQWNVKGVHDVEEONNORSVLVVPWE
296087 ADIFEELEGGITATSLYDARNVTKGDFNGLSQWNVKGVHDVEEQNNRSVLVVPWE
          960   970   980   990   1000   1010

```

060 1070

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CRYLA-105.pe AEVSQVRCVPCRGVILRTAYKEGYGEGCVTHIEENNTDELKFSNCVEEYIPNVTVT
296087
CRYLA-105.pe CNDVNVSEYGGVYVSEVRYNEA--KVPADVASVVEKSVTGGRENCEFRGY
296087
CRYLA-105.pe RDYTPLVGVVTKLEYFPEKDRWIEIGTEGTVDSVENLME
296087
CRYLA-105.pe RDYTPLVGVVTKLEYFPEKDRWIEIGTEGTVDSVENLME
CRYLA-105.pep
SW:8469148
8469148 description="PESTICIDIAL CRYSTAL PROTEIN CRYIHA (INSECTICIDAL
DELTA-ENDOTOXIN CRYIHA(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN (33 KDa CRYSTAL
PROTEIN)." library=NA species="Bacillus thuringiensis" source="Swissprot 1.0"
version=NA type=PRT
SCORES Initl: 3049 Initn: 4970 Opt: 4426 z-score: 5022.9 E(): 0
>>SW:8469148
Initn: 4970 Opt: 4426 z-score: 5022.9 expect():
Smith-Waterman score: 5232; 67.6% identity in 1187 aa overlap
(1-1177:1-1172)
CRYLA-105.pe MNNPINEGIPNCLSNPEVEVLGRIETGVP--IDISLSLTOFLSEFVPGAGFVL
8469148
CRYLA-105.pe GLVDIINGIFGSPQWDAFLVQIEQLINQRIEFAFNQAIISRLEGLNLYQIYAESPREWE
8469148
CRYLA-105.pe ASPNNEALQDQVRNRFNDNNSALTTATPLFAVQNYQVPLISVYVQANLHLSVLROVSFV
8469148
CRYLA-105.pe CQRMGFAAATNGRYNDLTLRLICNYTHAVRWNTGLERWVGPDSRWIRYNQPRRLTL
8469148
CRYLA-105.pe CQRMGLDVTVNNHYNRLNLTNTYSDHCAQWFRGLDNFGVSAR---YLDFOREVTI
CRYLA-105.pe TVLIDIVLFFNYDSRTYPIRTVSQLTREIYTNPVLENFQSGRGAQIESIRSPHLM
8469148
CRYLA-105.pe SVLDIVLFPNDIRTYPISTQSLTREIYTSVPAEP--GASLANLQNI---LREPHLMD
CRYLA-105.pe ILNSTITYTDHARGEYWSGHQIMASPVFGSGPEFTPLLYGTNGNAAQQQRIVAQLQGGV
CRYLA-105.pe ILNSTITYTDHARGEYWSGHQIMASPVFGSGPEFTPLLYGTNGNAAQQQRIVAQLQGGV

8469148 FLTLVITYGVOSGIYHWAGHEISSRTTGNLSNTOQFLPYGTAASADRAENMNIHSETI
CRYLA-105.pe YRTLSSTLYRPNIGINNQQLSVLDGTEFAYGTSSNLPFA--VYRKSQTVDSLDIEPPQ
8469148 YRTLSAIPYS--VSGISPNRTRVVEGRIARDNNLDSLPFLYRKEGTLDSFTLPE
CRYLA-105.pe NNNVPPQGFGRHLSHVSMFRSGFSNSVSIIIRAPMFWIHRSEFNIIASDSITQIPL
8469148 DESTPPYIGYSHRLCHARFAPSPVILEPSPFARLPVFWTHRSASPTNEVSPSRITQIPEW
CRYLA-105.pe VKAHTLOSQTTVVRGPGFTGGDILRRTS--GPFAYTIWINGOLPQRYRIRYASTTN
8469148 VKAHTLASGASVKGPGFTGGDITRNNINILGDLGLTVTVTGRLPQSYIRLRYASVAN
CRYLA-105.pe LRIYTVAGERIIFAGQFNKIMTGDPLTFQSFYATINTAFTFMSQSSFTVGDATFSSG
8469148 SSGVFRHLPPQSYGISFPRTMTDEPLTSRFSALTTLFTPTILTRAQEEFNL---TIPRG
CRYLA-105.pe NEVYIDREFELIPVATLEAEYNIISRAOKAVNALFTTNGLGKNTVTDYHIDOVSNLIVY
8469148 --WIDRIEFVDPATFEAGVDLERAOKAVNALFTTNGLGKNTVTDYHIDOVSNLIVY
CRYLA-105.pe LSDEFCDENESSEVVKHAKLSDERNLLQDSNFNDINRQPERGCGWGSGTITIQGDDV
8469148 LSNEELSSVAVNAKLSGDRNLLQDSNFISINGLLDGRMGSTDTITIQGDDV
CRYLA-105.pe FKENVILSGTFECVYLYKIDSENAKFAFRIQRIQRYIEDSODLEIYSIRYNAKHET
8469148 FKENVILSGTFECVYLYKIDSENAKFAFRIQRIQRYIEDSODLEIYSIRYNAKHET
CRYLA-105.pe VNVPTGSLMPLSAQSPICCCPNRCALFPPDLDCSTDEKCAHSHHSHFSLDIDV
8469148 VNVPTGSLMPLSVENISGFCGSEKCAHLEWNPJDCSCDGEKCAHSHHSHFSLDIDV
CRYLA-105.pe GCTDLNEDLGWVIFIKITQDGHARLGNLEFEEELV--EALARYRAEKWRDRKES
8469148 GCTDLNEDLGWVIFIKITQDGHARLGNLEFEEELV--EALARYRAEKWRDRKES
CRYLA-105.pe WETNIVYKEAKESVDALFVNSQYDQLOADNTNIAHIAADKRVHSREAYDELNIVGVN
8469148 FETNIVYKEAKESVDALFVNSQYDKLADNTNIAHIAADKRVHRIEAYDELNIVGVN
CRYLA-105.pe AALFELEGRIFTAFSLDARVNIKNGDFNGLSCWNVKGVHSDVEEQNNORSVLVPEWE
CRYLA-105.pe AALFELEGRIFTAFSLDARVNIKNGDFNGLSCWNVKGVHSDVEEQNNORSVLVPEWE

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```
8469148 ADIPELEGRIFTAYSLYDARNVIKNGDFNGLLWNKXGHVDVVEEQNHRSVLVWPEWE
950 960 970 980 990 1000

cry1a-105.pe AEVSGEVRCVPGRGYILRVITAYKEGEGGCVTITHEINNTDELAFSCVBEIEYIPWNTVT
1020 1030 1040 1050 1060 1070
8469148 AEVSGEVRCVPGRGYILRVITAYKEGEGGCVTITHEINNTDELAFSCVBEIEYIPWNTVT
1010 1020 1030 1040 1050 1060

cry1a-105.pe CNDVTNQEYGGAYTSRNRGYNEA---PSVPADVASVVEKSYTDGRRENPCENRGY
1080 1090 1100 1110 1120 1130
8469148 CNDVTNQEYGGAYTSRNRGYNEA---PSVPADVASVVEKSYTDGRRENPCENRGY
1070 1080 1090 1100 1110 1120

cry1a-105.pe RDTPLPGVVTKELEYFEETDKVWIEGTEGTFTVDSVLELLMEE
1140 1150 1160 1170
8469148 RDTPLPGVVTKELEYFEETDKVWIEGTEGTFTVDSVLELLMEE
1130 1140 1150 1160 1170

cry1a-105.pe RDTPLPGVVTKELEYFEETDKVWIEGTEGTFTVDSVLELLMEE
1130 1140 1150 1160 1170

cry1a-105.pep
NRAA:1669651
1669651 source="GENBANK_PROT" delta-endotoxin [Bacillus thuringiensis]

SCORES Initl: 2870 Initn: 4743 Opt: 4376 z-score: 4966.1 E(): 0
>NRAA:1669651
Initn: 4743 Initl: 2870 Opt: 4376 Z-score: 4966.1 expect(): 0
Smith-Waterman score: 5072; 67.6% identity in 1180 aa overlap
(8-1174.7-1164)

cry1a-105.pe MDNPNINECIPNCLSNPEVEVLGGERIETGYTPIDISLSITQFLSEFVPGAGVFLGL
10 20 30 40 50 60
1669651 MEISDONQYIPYNCLNPNSEIFNARNNFGVLS-QVSSGTRFLEAAVPEAGFALGL
10 20 30 40 50

cry1a-105.pe VDIWIGFGPSQWDAFLVOIEQLINORIEEFARNQAISSLEGSLNLYOIVAESFREWAD
70 80 90 100 110 120
1669651 FDIWIGALGVQWQSLFROIEQLINORIEEFARNQAISSLEGSLNLYOIVAESFREWAD
60 70 80 90 100 110

cry1a-105.pe PTNPALREEMRIQFNDMNSALTTAIPFVQNYQVPLLSVYQAAHLNLSVLRDVSFVG
130 140 150 160 170 180
1669651 PNPASQEVRTFRLTDDAIVTGLPTLATRNLEVNLSVYTOAANHLNLSLLRDVYFGE
120 130 140 150 160 170

cry1a-105.pe RWGFDATINSRNDLTRIGNYTHAVRWNTGLERWPGPSRWIRNGFRRELTIV
190 200 210 220 230 240
1669651 RWGLTQANIEDLYTRLTSNIQYSDHCARMYQGLNEIGGI-SR---RYLDFQRLDTISV
180 190 200 210 220 230

cry1a-105.pe LDIVSLF-PNVDSTYPIETVSQLTRELYNPVLENFDFSGRSAGQIEGSRSPHLMDOI
250 260 270 280 290
1669651 LDIVAPSPNDIRTYPIQSQLTRELYNPVLENFDFSGRSAGQIEGSRSPHLMDOI
240 250 260 270 280 290

cry1a-105.pe LNSITVITDAHRGEYWSGHQIMASPVG-FSGPEFTFFLYGTMGNAAPQQRIT----VAQL
300 310 320 330 340 350
```

```
1669651 IDRIIVITNSVRSTPWPWACHIEVISRRGTQOAGNEIRFPFLYGVAAAEPPVITIRPTGTDE
300 310 320 330 340 350

cry1a-105.pe CQGVITRLSTLRRRNFNIGINNQLSVLQGTGTFAYGTSNLPKSAVYRKS-G-TVDSLDE
360 370 380 390 400 410
1669651 CQGVITRLSTLRRRNFNIGINNQLSVLQGTGTFAYGTSNLPKSAVYRKS-G-TVDSLDE
360 370 380 390 400 410

cry1a-105.pe IPQNNNVPRQGFHRLSHVSMFSGFSNVSIIIRAPMFMSIHRSAEFNNIIASDSIT
420 430 440 450 460 470
1669651 IPQNNNVPRQGFHRLSHVSMFSGFSNVSIIIRAPMFMSIHRSAEFNNIIASDSIT
420 430 440 450 460 470

cry1a-105.pe QIPLVKAHTLQSGTIVVRGFTGDIILRRISGPFAYTIVNINQOLPQRYRARIYAST
480 490 500 510 520 530
1669651 QIPLVKAHTLQSGTIVVRGFTGDIILRRISGPFAYTIVNINQOLPQRYRARIYAST
480 490 500 510 520 530

cry1a-105.pe QIPLVKAHTLQSGTIVVRGFTGDIILRRISGPFAYTIVNINQOLPQRYRARIYAST
480 490 500 510 520 530
1669651 QIPLVKAHTLQSGTIVVRGFTGDIILRRISGPFAYTIVNINQOLPQRYRARIYAST
480 490 500 510 520 530

cry1a-105.pe TNLRIYVIVAGERIFAGQNKMTMDTGDPLTFQSFSTATINTAFTFMSQSSFTVGADTFS
540 550 560 570 580 590
1669651 TNLRIYVIVAGERIFAGQNKMTMDTGDPLTFQSFSTATINTAFTFMSQSSFTVGADTFS
540 550 560 570 580 590

cry1a-105.pe SG-NEVIDRFLIPVTATLEAENLRAQAKVNAFLTSTNOLGKTNVTDYHIDOVSNL
600 610 620 630 640 650
1669651 SG-NEVIDRFLIPVTATLEAENLRAQAKVNAFLTSTNOLGKTNVTDYHIDOVSNL
600 610 620 630 640 650

cry1a-105.pe PKLIEVIDRFLIPVTATLEAENLRAQAKVNAFLTSTNOLGKTNVTDYHIDOVSNL
580 590 600 610 620 630
1669651 PKLIEVIDRFLIPVTATLEAENLRAQAKVNAFLTSTNOLGKTNVTDYHIDOVSNL
580 590 600 610 620 630

cry1a-105.pe VTYLSDFCDEKRELSKVKHAKRLSDERNLQDSNFKDINRQPERGWSGTITQGG
660 670 680 690 700 710
1669651 VTYLSDFCDEKRELSKVKHAKRLSDERNLQDSNFKDINRQPERGWSGTITQGG
660 670 680 690 700 710

cry1a-105.pe DDVFKENYVTLSTGTFDECYPTLYOKIDESKLYKATRYOLRGYIEDSODLEIYLRINAK
720 730 740 750 760 770
1669651 DDVFKENYVTLSTGTFDECYPTLYOKIDESKLYKATRYOLRGYIEDSODLEIYLRINAK
720 730 740 750 760 770

cry1a-105.pe HETVNVPGTSLWPLSAQSPICKCGEPNRCAPHLENNPYLDCSCNGKKCAHSHHFSLD
780 790 800 810 820 830
1669651 HETVNVPGTSLWPLSAQSPICKCGEPNRCAPHLENNPYLDCSCNGKKCAHSHHFSLD
780 790 800 810 820 830

cry1a-105.pe IDVGCTDLNEDLGVWIFIKITQDGHARLGNLFELEKPLVGEALARKRAEKKWRDKRE
840 850 860 870 880 890
1669651 IDVGCTDLNEDLGVWIFIKITQDGHARLGNLFELEKPLVGEALARKRAEKKWRDKRE
840 850 860 870 880 890

cry1a-105.pe KLEMETNIVYKEAKESVDALFVNSQYDQGLQADTNIAHIAADKRVHSIREAYLPESVIP
900 910 920 930 940 950
1669651 KLEMETNIVYKEAKESVDALFVNSQYDQGLQADTNIAHIAADKRVHSIREAYLPESVIP
900 910 920 930 940 950

cry1a-105.pe GVNAAIPEELGRIPTAFSLYDARNVINKNGDFNGLSCWNKXGHVDVVEEQNHRSVLVVP
960 970 980 990 1000 1010
```

1669651 GVNAAFLPDELEGRITANSLYDARNVKNGLSCWVYKGVHVDVEVNSRLVLP
940 950 960 970 980 990
cry1a-105.pe ENKASQSVRCPCPSVILRVTVAKESGECVTHIEHNNTDLKFNCGVEEIIYFNN
1020 1030 1040 1050 1060 1070
1669651 ENKASQSVRCPCPSVILRVTVAKESGECVTHIEHNNTDLKFNCGVEEIIYFNN
1000 1010 1020 1030 1040 1050
cry1a-105.pe TVTCNDYTNQOEYGGATSNRGYNEA--ASVPADYTSVSEKSYDGRNCPCFN
1080 1090 1100 1110 1120
1669651 TVTCNDYTANQOEYKGYATSHNGYDQAYGNHRSYADYTPVYESKAYDGRDNPCESN
1060 1070 1080 1090 1100 1110
cry1a-105.pe RGYRDYTPLPAGYVSKLEYFPETDKWIEIGCTETGTVNVEVLLIMEE
1130 1140 1150 1160 1170
1669651 RGYRDYTPLPAGYVSKLEYFPETDKWIEIGCTETGTVNVEVLLIMEE
1120 1130 1140 1150 1160 1170
cry1a-105.pe
SW:8469141
8469141 description-"PESTICIDIAL CRYSTAL PROTEIN CRY1A (INSECTICIDAL
DELTA-ENDOTOXIN CRY1(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (137 KDA CRYSTAL
PROTEIN)." library=NA species="Bacillus thuringiensis serovar morrisoni"
source="swissprot_prot" version=NA type=PRT
SCORES Initl: 3021 Initn: 4044 Opt: 4338 z-score: 4922.6 E(): 0
>>SW-8469141
initn: 4044 initl: 3021 opt: 4338 z-score: 4922.6 expect(): 0
Smith-Waterman score: 4666; 62.7% identity in 1181 aa overlap
(34-1177:54-1215)
cry1a-105.pe NPINIECIPNCLSNPEVEVLGGRIETGVPIDISLSLTFLSEF-VPGAGFVLGLVD
10 20 30 40 50 60
8469141 SAQMDLSPDARIEDSLCVAEGNNIDPFVSASTVQTGISIAGRIILGLVLPFAGQLASFYS
30 40 50 60 70 80
cry1a-105.pe IIMGITGPS---QWDAFLVQIEQLI-NORIEEPARNQALSRLEGLSNLYOIVAESFREWE
70 80 90 100 110
8469141 FLUGELWPSGRDPWFIEFWEHVEQIVRQOQITDSVDRDIAIRLEGLGGRYSVQOALETWL
90 100 110 120 130 140
cry1a-105.pe ADPTNPAALREEMRIQFNDMNSALTAIPLFVQNVQVPLLSVYVQAAHLSLVRDVSVF
120 130 140 150 160 170
8469141 DNRDARSRIIRERYIALELDITAIPLFSIRNEVEVLLMVAQAANLHLLLRDASLF
150 160 170 180 190 200
cry1a-105.pe GQRGFGFAATNSRNDLTRIGNYTHAVRNTGLERVMGPPSGRWIRYNGFRRELTLL
180 190 200 210 220 230
8469141 GSEGMSSADVNQYQOEIRYETEEYSNHCYQWNTGLNRLRGTATWVRVYNGFRDLTL
210 220 230 240 250 260
cry1a-105.pe TVLDIVSLFNVDSTRYPIRTVSQLTREIYTNP--VLENFDGS-FRGSQO--GIEGSI-R
240 250 260 270 280 290
8469141 GVLDELVALFFSYDRTYPIPTTAQLTREYVTDPNGVVAGPNNSWFNGASFSALENAIR
280 290 300 310 320 330

cry1a-105.pe SPLMDILMSITTYD-AHRGEYY---WSGHOIMASPVGSGPEFTFPFLYIGTMGAPOQ
270 280 290 300 310 320 330 340
8469141 QPHLYDFLTNLTITRRSOGVTIMMLWAGHRTIFNRI--QGGSTSEMYGALTNPVSVS
330 340 350 360 370 380
cry1a-105.pe RIVAOQLGQVETLSST-----LYERPENIGINNQQLSVLDGTEFAYGTSSNL
350 360 370 380 390
8469141 DI-PFNRDVIKTVISLAGGSLSGTRYGLTVDMDIFRNHP-DIVTGLFYHPG-HAGI
390 400 410 420 430
cry1a-105.pe PSAYVRKSGTVDSLDEIPPNQNNVPPRQGFSHRSHVSMFRSGFSNVSIIIRAPMFSWI
400 410 420 430 440 450
8469141 ATQVK-----DSDTELPETTEQPNVRAFSHLLSHISM--GFTTQDVP----PVYSWT
440 450 460 470 480
cry1a-105.pe HRSAEFNIIADSITQIPLVKAHTLOSQTIVVRGPGFTGDIILRRTSGPPFAYTIVNIN
460 470 480 490 500 510
8469141 HQSADRINTINSRITQIPLVKAHTLOSQTIVVRGPGFTGDIILRRTSGPPFAYTIVNIN
490 500 510 520 530 540
cry1a-105.pe GOLPQBYRARIYASTTNLRITVTVAGERIFAGQFNKMTDGTDLTFQSFVATINTAFT
520 530 540 550 560 570
8469141 NLSQRIRARIYASTTNLRITVTVAGERIFAGQFNKMTDGTDLTFQSFVATINTAFT
550 560 570 580 590 600
cry1a-105.pe FPMQSQSSVYADTFSSGNEVYIDRFELIPVTATLEAEYNLERAKAVNALETSTNQLGL
580 590 600 610 620 630
8469141 FPMQSQSSVYADTFSSGNEVYIDRFELIPVTATLEAEYNLERAKAVNALETSTNQLGL
600 610 620 630 640 650 660
cry1a-105.pe KNNVYHIDQVSNYVLSDEKLVKRELSEKVKHAKRLSDERNLLODSNFKDINRQP
640 650 660 670 680 690
8469141 KTDVTDHIDQVSNYVLSDEKLVKRELSEKVKHAKRLSDERNLLODSNFKDINRQP
670 680 690 700 710 720
cry1a-105.pe ERMGSGSTGTTTGGDNFRKNVYVTSQAECEPTYNOKSDESKLKAFTRYQLRGYIE
700 710 720 730 740 750
8469141 DRMGISGTGISQGGDDIFKENVKURFSTVDKCTAYOKI--ASQSKSYTRYQLRGYIE
730 740 750 760 770 780
cry1a-105.pe DSQDLEYISIRYNKAKHETVNVPGTSGSLWPLSNPSPGKGGSPNRCAPKSNWPLDSCR
760 770 780 790 800 810
8469141 DSQDLEYISIRYNKAKHETVNVPGTSGSLWPLSNPSPGKGGSPNRCAPKSNWPLDSCR
790 800 810 820 830 840
cry1a-105.pe DCEKCAHSHHRSLLDIDVCVDNEDLGWVIFKIKTODTGDAKRGNLEKSPKPIAKL
820 830 840 850 860 870
8469141 YGEKCVHSHHRSLLDIDVCVDNEDLGWVIFKIKTODTGDAKRGNLEKSPKPIAKL
850 860 870 880 890 900
cry1a-105.pe ARVKRAEKKWRDREKLEWEINIVYKEAKESVDALFVNSQYDQLQADNTIAMHAARKRV
880 890 900 910 920 930
8469141 SRVKRAEKKWRDREKLEWEINIVYKEAKESVDALFVNSQYDQLQADNTIAMHAARKRV
910 920 930 940 950 960

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[illegible]

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SCORES      Initt: 3021      Initt: 4044      Opt: 4338      z-score: 4922.6 E( ): 0
>NRRA:8469141
      initt: 4044      initt: 3021      Opt: 4338      z-score: 4922.6 expect( ): 0
      Smith-Waterman score: 4666;      62.7% identity in 1181 aa overlap
      (34-1177:54-1215)

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cryia-105.pe	10	20	30	40	50	60
	NP	NINE	CIPY	NCSP	NEVVLG	ERTET
	Y	T	I	D	I	S
	L	T	O	L	L	S
	E	F	F	E	F	F
	V	P	G	A	G	V
	L	G	L	A	S	F
	8469141	30	40	50	60	70
	SAQMDLSP	DI	ED	SL	CV	AE
	NI	DP	FS	AV	Q	T
	IS	I	A	G	R	I
	L	G	V	L	P	P
	FA	Q	A	L	S	F
	Y	S				
	180	190	200	210	220	230
cryia-105.pe	70	80	90	100	110	
	I	I	G	F	G	P
	S					
	E	O	L	I		
	N	O	R	I		
	E	F	A	N	O	I
	S	L	E	G	L	S
	N	L	N	L	O	I
	Y	A	S	F	R	E
	8469141	30	40	50	60	70
	F	L	C	E	V	W
	P	S	R	D	P	H
	E	I	F	W	E	H
	E	V	E	I	Q	O
	I	T	S	V	R	A
	I	A	R	L	S	G
	L	G	R	G	Y	S
	Q	O	A	L	E	T
	W					
	120	130	140	150	160	170
cryia-105.pe	A	D	T	N	P	A
	L	E	E	R	N	R
	O	F	N	D	M	S
	A	L	T	T	A	I
	P	U	F	A	V	N
	Q	V	P	L	S	V
	Y	Q	A	N	I	H
	S	L	S	V	L	N
	D	S	V	F		
	8469141	120	130	140	150	160
	D	N	R	S	I	R
	E	I	R	E	A	L
	E	D	I	T	T	A
	I	P	L	S	I	R
	N	E	V	P	L	L
	M	V	Y	A	Q	A
	N	L	L	L	L	D
	A	S	L	F		
	180	190	200	210	220	230

cry1a-105.pe DGEKCAHSHHSLDNGVCTDNLNEDLGWVIFKIKTODGHARLGNLEFLKPKVLGAL
8469141 YGKSKHSHHSLDNGVCTDNLNEDLGWVIFKIKTODGHARLGNLEFLKPKVLGAL
850 860 870 880 890 900

cry1a-105.pe ARVSKHSHHSLDNGVCTDNLNEDLGWVIFKIKTODGHARLGNLEFLKPKVLGAL
8469141 SVRSEKSHHSLDNGVCTDNLNEDLGWVIFKIKTODGHARLGNLEFLKPKVLGAL
910 920 930 940 950 960

cry1a-105.pe HSIKREYLPVLSVFNAAFELEGRIFAFSNDARNVITGSDNGLSCWVKGHV
8469141 HRIKREYLPVLSVFNAAFELEGRIFAFSNDARNVITGSDNGLSCWVKGHV
970 980 990 1000 1010 1020

cry1a-105.pe DVSEQNQRSLVPEWEAEVSQEVRCVPGHILKNTAKREGTGECCVTHIENNPE
8469141 DVQ-QNHRSVLSEAEVSQEVRCVPGHILKNTAKREGTGECCVTHIENNPE
1030 1040 1050 1060 1070 1080

cry1a-105.pe LKFSNCEVEEIVPNNVTICNDYTVNQEYGG-AVTSNRGYNFA-----PAPADY
8469141 LKFSNCEVEEIVPNNVTICNDYTVNQEYGG-AVTSNRGYNFA-----PAPADY
1090 1100 1110 1120 1130 1140

cry1a-105.pe ASVVEKSYTDGRNCPENRGYDYLPLGVYTKLEVPFETDKVIEGETGTFI
8469141 TPVVEGMYTDQYNGHCVSDRGYRHTPLPAGYVTKLEVPFETDKVIEGETGTFI
1170 1180 1190 1200

cry1a-105.pe VDSVELLMEE
8469141 VGSVELLMEE
1210

cry1a-105.pep
NRAA.143227

143227 source="GENBANK_PROT" insecticidal endotoxin

SCORES Initl: 2559 Initn: 4966 Opt: 4319 Z-score: 4901.4 E(): 0
>NRAA:143227
initn: 4966 inltl: 2559 opt: 4319 Z-score: 4901.4 expect(): 0
Smith-Waterman score: 6513; 84.7% identity in 1186 aa overlap
(1-1177:1-1156)

cry1a-105.pe MDNPNINCPVNCLSNPEVEVLGGRIETGTPIDISLSLTQFLSEFVPGAGVLGL
143227 MDNPNINCPVNCLSNPEVEVLGGRIETGTPIDISLSLTQFLSEFVPGAGVLGL
10 20 30 40 50 60

cry1a-105.pe VDIWIGFPGSQWDAFLVQIEQLINQRIEFARNQALRLEGLNLYQIYVAESFREWAD
143227 VDIWIGFPGSQWDAFLVQIEQLINQRIEFARNQALRLEGLNLYQIYVAESFREWAD
70 80 90 100 110 120

cry1a-105.pe FTPALREEMRIQFNDMNSALTATPLFAVQNYQVPLLSVYQAAHLHSLVLRDVSVEGQ
143227 FTPALREEMRIQFNDMNSALTATPLFAVQNYQVPLLSVYQAAHLHSLVLRDVSVEGQ
130 140 150 160 170 180

cry1a-105.pe RWGFDAATINSRYNDLRELIGNYTDHNAVYNTGLERVGSDSDMIRYNQFRRELTIV
143227 RWGFDAATINSRYNDLRELIGNYTDHNAVYNTGLERVGSDSDMIRYNQFRRELTIV
190 200 210 220 230 240

cry1a-105.pe LDIVSLFPNVDRTYPIRTVSQLTREIYNPVLENFDFGSRGSAQIEGSIKSPHMDIL
143227 LDIVSLFPNVDRTYPIRTVSQLTREIYNPVLENFDFGSRGSAQIEGSIKSPHMDIL
250 260 270 280 290 300

cry1a-105.pe NSIITVTDHREYVWGHQIMASPVGSGPEFTPLLYGTMGNAAPQORIVAAQLGGVYR
143227 NSIITVTDHREYVWGHQIMASPVGSGPEFTPLLYGTMGNAAPQORIVAAQLGGVYR
310 320 330 340 350 360

cry1a-105.pe TLSTLTVRPPNIGINNQLSLDGTFAVGTSSNLPASVY-RKSGTVDSLDLPIPPQNN
143227 TLSTLTVRPPNIGINNQLSLDGTFAVGTSSNLPASVY-RKSGTVDSLDLPIPPQNN
370 380 390 400 410

cry1a-105.pe VPPQGSFHR-LSHVSMFRGFSNVSIIIRAPM-FSWIHESAEFNIIASDSITQILV
143227 VPPQGSFHR-LSHVSMFRGFSNVSIIIRAPM-FSWIHESAEFNIIASDSITQILV
420 430 440 450 460 470

cry1a-105.pe K--LDSNWNVVLFTTGGDLLELTG-QISTLRVNITAPLSQRYRIRYASTTNL
143227 K--LDSNWNVVLFTTGGDLLELTG-QISTLRVNITAPLSQRYRIRYASTTNL
480 490 500 510 520 530

cry1a-105.pe RIVYVAGERITACQNKIMDYGPYQSFYATINAFTPMSQSSFTVGADTFSSGN
143227 RIVYVAGERITACQNKIMDYGPYQSFYATINAFTPMSQSSFTVGADTFSSGN
540 550 560 570 580 590

cry1a-105.pe EVIDRFEIPVATLEAEYNLEFAQAAATSTNLSLTQFLSEFVPGAGVLGL
143227 EVIDRFEIPVATLEAEYNLEFAQAAATSTNLSLTQFLSEFVPGAGVLGL
600 610 620 630 640 650

cry1a-105.pe SDFCLDKRELSEKVKHAKLSDEKLNQSDNFQINROPEKSGTGITVQGNF
143227 SDFCLDKRELSEKVKHAKLSDEKLNQSDNFQINROPEKSGTGITVQGNF
660 670 680 690 700 710

cry1a-105.pe KENVITLSGTFFECPTLYQIDESKLAFRYQLRGVIEDSODLEIYIRYNAKHEV
143227 KENVITLSGTFFECPTLYQIDESKLAFRYQLRGVIEDSODLEIYIRYNAKHEV
720 730 740 750 760 770

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780      790      800      810      820      830
cry1a-105.pe NVPGTGSLWPLSAQSPIGKCEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHSFLDIDVG      830
143227      NVPGTGSLWPLSAQSPIGK-----HHSHHSFLDIDVG      800      810
780      790
840      850      860      870      880      890
cry1a-105.pe CTDLNEDLGVVWIFKIKTODGHARLGNLEFLEEKPLVGGALARKVAKKRWKREKLEW      890
143227      CTDLNEDLGVVWIFKIKTODGHARLGNLEFLEEKPLVGGALARKVAKKRWKREKLEW
820      830      840      850      860      870
900      910      920      930      940      950
cry1a-105.pe ETNIIVYKEAKESVDALFVNSQYDQLQADTNIAHHAADKRVHSIREAYLPELSVIPGVNA      950
143227      ETNIIVYKEAKESVDALFVNSQYDRLQADTNIAHHAADKRVHSIREAYLPELSVIPGVNA
880      890      900      910      920      930
960      970      980      990      1000      1010
cry1a-105.pe AFPEELGRIIFTAFSLYDARNVKNNGDNLSCMVNKGHVDVEEONNORSVLVVPWEWA      1010
143227      AFPEELGRIIFTAFSLYDARNVKNNGDNLSCMVNKGHVDVEEONNORSVLVVPWEWA
940      950      960      970      980      990
1020      1030      1040      1050      1060      1070
cry1a-105.pe EVSQEVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFCNCVEEEIYPNNTVTC      1070
143227      EVSQEVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFCNCVEEEIYPNNTVTC
1000      1010      1020      1030      1040      1050
1080      1090      1100      1110      1120      1130
cry1a-105.pe NDYATQEEVETGITSNRNGYDGAYESNSVPADYASAYEEKAYTDGRDNPCESRGGV      1130
143227      NDYATQEEVETGITSNRNGYDGAYESNSVPADYASAYEEKAYTDGRDNPCESRGGV
1060      1070      1080      1090      1100      1110
1140      1150      1160      1170
cry1a-105.pe DYTPLPGVYTKLEYFPETDKVWIEIGETGTFIVDSVELLMEE      1170
143227      DYTPLPGVYTKLEYFPETDKVWIEIGETGTFIVDSVELLMEE
1120      1130      1140      1150
cry1a-105.pep
SW:117542
117542 description="131 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE
ENTOMOCIDAL PROTOXIN)." library="NA species="Bacillus thuringiensis serovar
kurstaki" sources="swissprot_prot" version="NA type="PRT
SCORES      Init1: 2559      Initn: 4966      Opt: 4319      Z-score: 4901.4      E(): 0
>>SW:117542
Initn: 4966      Init1: 2559      opt: 4319      Z-score: 4901.4      expect(): 0
Smith-Waterman score: 6513;      84.7% identity in 1186 aa overlap
(1-1177:1-1156)
10      20      30      40      50      60
cry1a-105.pe MNNPNNECIPNCLSNPEVEVLGGERIETGVTPIIDISLSTQFLSEFVPGAGFVLGL      60
117542      MNNPNNECIPNCLSNPEVEVLGGERIETGVTPIIDISLSTQFLSEFVPGAGFVLGL
10      20      30      40      50      60
70      80      90      100      110      120
cry1a-105.pe VDIILWIFGFSQWDAFLVQIEQLINQRIEERFARNQAIISRLGLESLNLYQIYAESFREWEAD      120
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117542      VDIILWIFGFSQWDAFLVQIEQLINQRIEERFARNQAIISRLGLESLNLYQIYAESFREWEAD
70      80      90      100      110      120
130      140      150      160      170      180
cry1a-105.pe PTNPALREERIOFNDMNSALITTAIPFAVONTQVPLLSVYVOAANLHLSVLDRVSVFGQ      180
117542      PTNPALREERIOFNDMNSALITTAIPFAVONTQVPLLSVYVOAANLHLSVLDRVSVFGQ
130      140      150      160      170      180
190      200      210      220      230      240
cry1a-105.pe RWGFDATINSRVNDLTRILIGNYTDHVRWNTGLERVWGPDSRDWIRYNOFRRELTIV      240
117542      RWGFDATINSRVNDLTRILIGNYTDHVRWNTGLERVWGPDSRDWIRYNOFRRELTIV
190      200      210      220      230      240
250      260      270      280      290      300
cry1a-105.pe LDIVSLFPNTDSRTYPIRTVSQLTREIYTNPVLNFDGSRGSAQIEGSIIRSPHMDIL      300
117542      LDIVSLFPNTDSRTYPIRTVSQLTREIYTNPVLNFDGSRGSAQIEGSIIRSPHMDIL
250      260      270      280      290      300
310      320      330      340      350      360
cry1a-105.pe NSITIIYDARGEYWSGHQIMASPVGSGPEPTFFLYGTMGNAAPQORIVAQLGQGVYR      360
117542      NSITIIYDARGEYWSGHQIMASPVGSGPEPTFFLYGTMGNAAPQORIVAQLGQGVYR
310      320      330      340      350      360
370      380      390      400      410
cry1a-105.pe TLSSTLYRRFPNIGINNQLSVLDGTEFAYGTSNLPASVY-RKSGTVDLSDEIIPPONNN      410
117542      TLSSTLYRRFPNIGINNQLSVLDGTEFAYGTSNLPASVY-RKSGTVDLSDEIIPPONNN
370      380      390      400      410      420
420      430      440      450      460      470
cry1a-105.pe VPPRQGSFHR-LSHVMFSGFSNSSVSIIRAPM-FSWIHRGAEFNNIIASDSITQIPLV      470
117542      VPPRQGSFHR-LSHVMFSGFSNSSVSIIRAPM-FSWIHRGAEFNNIIASDSITQIPLV
430      440      450      460      470      480
480      490      500      510      520      530
cry1a-105.pe KAHTLQSG--TTVVRGPGFTGGDILLRTSGGPFAYTIVNINQQLPQRYRARIYASTTNL      530
117542      K---LQSWLWNSVVKGLGFTGGDILLELTG-QISTLRVNITAPLSQRIYRIRIYASTTNL
490      500      510      520      530      540
540      550      560      570      580      590
cry1a-105.pe RIYVTAGERIFAGQNKMTDGPDLTFQSFVATINTAFTFPMQSGSFTVGADTFSSGN      590
117542      OPHSIDGRPINQGNFSAIMSSGSLQSGSFRTVGFTTFPFNFSGSSVFTLSRAHFNNGN
540      550      560      570      580      590
600      610      620      630      640      650
cry1a-105.pe EYIDRDELPTATLAEYENDERAQAVALNFTISNQLGKINVTYHIDQVSNLVTYL      650
117542      EYIDRIEFVPAVTFEAEYDLERAQAVALNELFTSSNQIGLKTVDYHIDQVSNLVECL
600      610      620      630      640      650
660      670      680      690      700      710
cry1a-105.pe SDEFLCKELSEKVKHAKRLSDERNLLQDPNFRGINQLDRGWRGNTDITIQGHDVDF      710
117542      SDEFLCKELSEKVKHAKRLSDERNLLQDPNFRGINQLDRGWRGNTDITIQGHDVDF
660      670      680      690      700      710
720      730      740      750      760      770
cry1a-105.pe KENYVTLGTFDECYPTIYLYQIDESLKAFTRYQLRGVIEDSODLETYSIRYNAKHETV      770
```

117542 KENYVLLGTFTFECSTYLYOKIDESKLKAYTRYQYRGVIEDSQDLSEIYIRNAKHETV
720 730 740 750 760 770
cry1a-105.pe NVYTGSDAPLSPSPIGKCEPNKCAPHLEWNPDLDCSDGKCEKAAHHSHFSLDVG
780 790 800 810 820 830
117542 NVYTGSDAPLSPSPIGKCEPNKCAPHLEWNPDLDCSDGKCEKAAHHSHFSLDVG
780 790 800 810 820 830
cry1a-105.pe CTDLNEDLGVMVIFKTKODGHANLQKAFLEKPLGKARVRAKRWKREKLEW
840 850 860 870 880 890
117542 CTDLNEDLGVMVIFKTKODGHANLQKAFLEKPLGKARVRAKRWKREKLEW
840 850 860 870 880 890
cry1a-105.pe ETNIVYKEAKESVDALFVNSOYDOLADTNRHAAKSVLPSREAYLPESVSGVNA
900 910 920 930 940 950
117542 ETNIVYKEAKESVDALFVNSOYDOLADTNRHAAKSVLPSREAYLPESVSGVNA
900 910 920 930 940 950
cry1a-105.pe ALFEELEGRIFTAFSLYDARNVKNKGNFNGLSQVNVKGVHVDVEQNNHSHVLEWEP
960 970 980 990 1000 1010
117542 ALFEELEGRIFTAFSLYDARNVKNKGNFNGLSQVNVKGVHVDVEQNNHSHVLEWEP
960 970 980 990 1000 1010
cry1a-105.pe EVSQEVRCVPGRGYILRVYAYKEGEGCVTHIEINNTDELKFCNVEEIEIPNVTVC
1020 1030 1040 1050 1060 1070
117542 EVSQEVRCVPGRGYILRVYAYKEGEGCVTHIEINNTDELKFCNVEEIEIPNVTVC
1020 1030 1040 1050 1060 1070
cry1a-105.pe NDYTVNOEEYGGAYTSNRNGYNEA---PSVPADYASVVEEKSYSYDGRNPFCEFRGVR
1080 1090 1100 1110 1120 1130
117542 NDYTVNOEEYGGAYTSNRNGYNEA---PSVPADYASVVEEKSYSYDGRNPFCEFRGVR
1080 1090 1100 1110 1120 1130
cry1a-105.pe DYTLPLPGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLIMEE
1140 1150 1160 1170
117542 DYTLPLPGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLIMEE
1140 1150 1160 1170
cry1a-105.pep
NRAA:45387401
45387401 source="GENBANK_PROT" crystal protein [Bacillus thuringiensis serovar
kurstaki]
SCORES Initl: 2468 Initn: 4316 Opt: 4247 z-score: 4819.5 E(): 0
>>NRAA:45387401
Initn: 4316 Initl: 2468 Opt: 4247 z-score: 4819.5 expect(): 0
Smith-Waterman score: 5007; 65.4% identity in 1188 aa overlap
(1-1177:1-1170)
cry1a-105.pe MDNPNINECIPYCNLSNPEVEVLGGERIETGYTP--IDISLSLQTLFSLFVFGAGFVL
10 20 30 40 50
45387401 MDNPNINECIPYCNLSNPEVEVLGGERIETGYTP--IDISLSLQTLFSLFVFGAGFVL
10 20 30 40 50
60 70 80 90 100 110

cry1a-105.pe GLVDIIWGIFGSPQMDAFVIOEQLINQRIEERFARNQAIISLEGSLNLYQIYAESFEWE
70 80 90 100 110 120
45387401 GLVDIIWGIFGSPQMDAFVIOEQLINQRIEERFARNQAIISLEGSLNLYQIYAESFEWE
70 80 90 100 110 120
cry1a-105.pe ADPTNPALREMIQFNDMNSALTTAIPFAVONVQVPLLSVYQAAANLHLSVLRDVSVF
120 130 140 150 160 170
45387401 ADPTNPALREMIQFNDMNSALTTAIPFAVONVQVPLLSVYQAAANLHLSVLRDVSVF
120 130 140 150 160 170
cry1a-105.pe GQRMGFDAATINSRYNDLRLIGNYTHAVRWYNTGLERVMPGDSRDMIRYNQFRRLTL
180 190 200 210 220 230
45387401 GQRMGFDAATINSRYNDLRLIGNYTHAVRWYNTGLERVMPGDSRDMIRYNQFRRLTL
180 190 200 210 220 230
cry1a-105.pe GERMGLTOINVDDLRYRLNIRKYSYDHCARWNEGLDNIISGLS---RSINFOREVTI
190 200 210 220 230
45387401 GERMGLTOINVDDLRYRLNIRKYSYDHCARWNEGLDNIISGLS---RSINFOREVTI
190 200 210 220 230
cry1a-105.pe TVLDIVSLFPNYSRTPYRTVTSQLTREIYTNVLENFDSGFRSAQIGSIRSPLMD
240 250 260 270 280 290
45387401 TVLDIVSLFPNYSRTPYRTVTSQLTREIYTNVLENFDSGFRSAQIGSIRSPLMD
240 250 260 270 280 290
cry1a-105.pe ILNSTITVTAHGEYVMSGHQIWAISPVGSGPEFTFPLYGTMGNAAPQORIVAQLQGV
300 310 320 330 340 350
45387401 ILNSTITVTAHGEYVMSGHQIWAISPVGSGPEFTFPLYGTMGNAAPQORIVAQLQGV
300 310 320 330 340 350
cry1a-105.pe YRLASSTLYRRPNIGINQQQLSVLDGTEFAYGTSNLPSA-VYKSGTVDSLDEIPPN
360 370 380 390 400 410
45387401 YRLASSTLYRRPNIGINQQQLSVLDGTEFAYGTSNLPSA-VYKSGTVDSLDEIPPN
360 370 380 390 400 410
cry1a-105.pe NNWDRKQCHRLSHSMRSGFNSNSVSIIRAPMESWHRSAEFNNIISDSITQIPLV
420 430 440 450 460 470
45387401 NNWDRKQCHRLSHSMRSGFNSNSVSIIRAPMESWHRSAEFNNIISDSITQIPLV
420 430 440 450 460 470
cry1a-105.pe KAHTLQSGTVVAGPGFPGSDTARTSGGFAY--YVINGQLFQ---RYEARIRYASIT
480 490 500 510 520 530
45387401 KAHTLQSGTVVAGPGFPGSDTARTSGGFAY--YVINGQLFQ---RYEARIRYASIT
480 490 500 510 520 530
cry1a-105.pe KASSLRN-STVVSQGFVGGDIVAKGWHQIYATDSMMNR-PSVALSRYLRLRYACRG
470 480 490 500 510 520
45387401 KASSLRN-STVVSQGFVGGDIVAKGWHQIYATDSMMNR-PSVALSRYLRLRYACRG
470 480 490 500 510 520
cry1a-105.pe NURIYVTVAGERIPAGCFWKTMDYEDPSTFQSPSYTNTTATFPACSGSTVGCADTFSS
540 550 560 570 580 590
45387401 NURIYVTVAGERIPAGCFWKTMDYEDPSTFQSPSYTNTTATFPACSGSTVGCADTFSS
540 550 560 570 580 590
cry1a-105.pe GNEVVDREFFELIPVATLEAEVNLERAKAVNALFTSTNGKNTNVDLHJDMNSLVI
600 610 620 630 640 650
45387401 GNEVVDREFFELIPVATLEAEVNLERAKAVNALFTSTNGKNTNVDLHJDMNSLVI
600 610 620 630 640 650
cry1a-105.pe YLSDEFCLDEKRELSKXKAKRLSDERNLQDSNRPGRGWSGTGITIQGSD
660 670 680 690 700 710
45387401 YLSDEFCLDEKRELSKXKAKRLSDERNLQDSNRPGRGWSGTGITIQGSD
660 670 680 690 700 710
cry1a-105.pe CLSDDEFCLDEKRELSKXKAKRLSDERNLQDSNRPGRGWSGTGITIQGSD
650 660 670 680 690 700
45387401 CLSDDEFCLDEKRELSKXKAKRLSDERNLQDSNRPGRGWSGTGITIQGSD
650 660 670 680 690 700

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cry1a-105.pe VFKENYVLTSGTDFECYPTLYQKIDESKLMKAFTRYQRLGYIEDSQDLSEIYSIRYNAKHE
45387401 VFKENYVLTGTFDECYPTLYQKIDESKLMKAFTRYQRLGYIEDSQDLSEIYSIRYNAKHE
710 720 730 740 750 760

cry1a-105.pe TVNVFGTSLMPLSAQSPCKGCEPNRCAPHEWNPDLDCSCRDGEGKCAHSHHFSIDID
45387401 TVNVFGTSLMPLSAQSPCKGCEPNRCAPHEWNPDLDCSCRDGEGKCAHSHHFSIDID
770 780 790 800 810 820

cry1a-105.pe VECTDLNEDLGWVIFKIKTQDGHARLGNLEFLEKPLVCEALARKVKAEEKWRDKREKL
45387401 VECTDLNEDLGWVIFKIKTQDGHARLGNLEFLEKPLVCEALARKVKAEEKWRDKREKL
830 840 850 860 870 880

cry1a-105.pe EWEINIVYKEAKESVDALFVNSQYQLQADTNIAIMHAADKR VHSIREAYLPFLSVIPGV
45387401 EWEINIVYKEAKESVDALFVNSQYQLQADTNIAIMHAADKR VHSIREAYLPFLSVIPGV
900 910 920 930 940 950

cry1a-105.pe NNAITFEELEGRIFTAFSLYDARNVINGDFNGLSCWNVKGHVVDVEEQNQRSVLVVPFW
45387401 NNAITFEELEGRIFTAFSLYDARNVINGDFNGLSCWNVKGHVVDVEEQNQRSVLVVPFW
960 970 980 990 1000 1010

cry1a-105.pe EAEVSOEVRCPGRGYILRVAYKEGYEGCVTHIEJENNTDLKXSCNVEEYIPNNTV
45387401 EAEVSOEVRCPGRGYILRVAYKEGYEGCVTHIEJENNTDLKXSCNVEEYIPNNTV
1020 1030 1040 1050 1060 1070

cry1a-105.pe KTEVSOEVRCPGRGYILRVAYKEGYEGCVTHIEJENNTDLKXSCNVEEYIPNNTV
45387401 KTEVSOEVRCPGRGYILRVAYKEGYEGCVTHIEJENNTDLKXSCNVEEYIPNNTV
1080 1090 1100 1110 1120 1130

cry1a-105.pe YRDYTPLEVGVTKELEYFPEPKVWIEIGETGTFVDSVLLMEE
45387401 YRDYTPLEVGVTKELEYFPEPKVWIEIGETGTFVDSVLLMEE
1130 1140 1150 1160 1170 1180

cry1a-105.pep
SW:8469135
8469135 description="PESTICIDIAL CRYSTAL PROTEIN CRY1AF (INSECTICIDAL
DELTA-ENDOTOXIN CRY1AF) (CRYSTALLINE ENTOMOCIDAL PROTOXIN)." library=NA
species="Bacillus thuringiensis" source="swissprot_prot" version=NA type=PRT
INIT: 2986 Initn: 4785 Opt: 4198 z-score: 4765.4 E(): 0
>>SW:8469135
initn: 4785 initn: 2986 opt: 4198 z-score: 4765.4 expect(): 0
Smith-Waterman score: 4919, 81.6% identity in 942 aa overlap
(1-942:1-911)

cry1a-105.pe MONNPNINECIPYNCLSNPEVLOGGRIETGYTPIDISLSTQFLLSFVPGAGFVLGL
8469135 MONNPNINECIPYNCLSNPEVLOGGRIETGYTPIDISLSTQFLLSFVPGAGFVLGL
10 20 30 40 50 60
```

```
cry1a-105.pe VDIWNGIEGPSQMDAFLVQTEQLINORIEEFARNQATISLEGSLNLYQIYAESFREWAD
8469135 VDIWNGIEGPSQMDAFLVQTEQLINORIEEFARNQATISLEGSLNLYQIYAESFREWAD
70 80 90 100 110 120

cry1a-105.pe PTNPALREEMRIQFNDMNSALITTAIPFAVQNYQVPLLSVYQAANLHSLVRDVSFVGQ
8469135 PTNPALREEMRIQFNDMNSALITTAIPFAVQNYQVPLLSVYQAANLHSLVRDVSFVGQ
130 140 150 160 170 180

cry1a-105.pe PTNPALREEMRIQFNDMNSALITTAIPFAVQNYQVPLLSVYVCNYI---ISSESVMCGQ
8469135 PTNPALREEMRIQFNDMNSALITTAIPFAVQNYQVPLLSVYVCNYI---ISSESVMCGQ
130 140 150 160 170 180

cry1a-105.pe RMGFAATINRYNDLTRILIGNYTHAVRWNTGLERVWGPDSRDWIRYNQFRELTLTV
8469135 RMGFAATINRYNDLTRILIGNYTHAVRWNTGLERVWGPDSRDWIRYNQFRELTLTV
180 190 200 210 220 230

cry1a-105.pe LDIIVSLFENYDSRTYPIRTVVSQLTREIYTNVPLENFDGSRGSAQIEGSIKPSHLMIDL
8469135 LDIIVSLFENYDSRTYPIRTVVSQLTREIYTNVPLENFDGSRGSAQIEGSIKPSHLMIDL
250 260 270 280 290 300

cry1a-105.pe NSITTYTDAHRGEYVWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAGLQGGVYR
8469135 NSITTYTDAHRGEYVWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAGLQGGVYR
310 320 330 340 350 360

cry1a-105.pe TSSSTLYRRPNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSDLEIPQNNNV
8469135 TSSSTLYRRPNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSDLEIPQNNNV
370 380 390 400 410 420

cry1a-105.pe PPRQGFHRLSHVSMFSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPLVKAH
8469135 PPRQGFHRLSHVSMFSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPLVKAH
430 440 450 460 470 480

cry1a-105.pe TLQSGTTVVRGPGFTGGDILRRTSQGFAYTIVNINQQLPQRYRARIYASTNLIYVT
8469135 TLQSGTTVVRGPGFTGGDILRRTSQGFAYTIVNINQQLPQRYRARIYASTNLIYVT
490 500 510 520 530 540

cry1a-105.pe NLGSGTSSVVKGPGFTGGDILRRTSQGFAYTIVNINQQLPQRYRARIYASTNLIYVT
8469135 NLGSGTSSVVKGPGFTGGDILRRTSQGFAYTIVNINQQLPQRYRARIYASTNLIYVT
480 490 500 510 520 530

cry1a-105.pe VAGEIIPAGQNKMTDGDILRRTSQGFAYTIVNINQQLPQRYRARIYASTNLIYVT
8469135 VAGEIIPAGQNKMTDGDILRRTSQGFAYTIVNINQQLPQRYRARIYASTNLIYVT
550 560 570 580 590 600

cry1a-105.pe RPELIPVATLAEAYNLERAQKAVNALFTSTNQLGLKNTVTDVHIDVSNLTVLSDEFC
8469135 RPELIPVATLAEAYNLERAQKAVNALFTSTNQLGLKNTVTDVHIDVSNLTVLSDEFC
610 620 630 640 650 660

cry1a-105.pe LDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGSGTGTITQGGDDVFNKYY
8469135 LDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGSGTGTITQGGDDVFNKYY
670 680 690 700 710 720
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cry1a-105.pe 680 690 700 710
720 730 740 750 760 770 780
790 800 810 820 830 840
850 860 870 880 890 900
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
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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
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2230 2240 2250 2260 2270 2280
2290 2300 2310 2320 2330 2340
2350 2360 2370 2380 2390 2400
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3070 3080 3090 3100 3110 3120
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3550 3560 3570 3580 3590 3600
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4150 4160 4170 4180 4190 4200
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4270 4280 4290 4300 4310 4320
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4810 4820 4830 4840 4850 4860
4870 4880 4890 4900 4910 4920
4930 4940 4950 4960 4970 4980
4990 5000 5010 5020 5030 5040
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9610 9620 9630 9640 9650 9660
9670 9680 9690 9700 9710 9720
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9790 9800 9810 9820 9830 9840
9850 9860 9870 9880 9890 9900
9910 9920 9930 9940 9950 9960
9970 9980 9990 10000
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cry1a-105.pe 680 690 700 710
720 730 740 750 760 770 780
790 800 810 820 830 840
850 860 870 880 890 900
810 820 830 840 850 860
870 880 890 900 910 920
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1810 1820 1830 1840 1850 1860
1870 1880 1890 1900 1910 1920
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2710 2720 2730 2740 2750 2760
2770 2780 2790 2800 2810 2820
2830 2840 2850 2860 2870 2880
2890 2900 2910 2920 2930 2940
2950 2960 2970 2980 2990 3000
3010 3020 3030 3040 3050 3060
3070 3080 3090 3100 3110 3120
3130 3140 3150 3160 3170 3180
3190 3200 3210 3220 3230 3240
3250 3260 3270 3280 3290 3300
3310 3320 3330 3340 3350 3360
3370 3380 3390 3400 3410 3420
3430 3440 3450 3460 3470 3480
3490 3500 3510 3520 3530 3540
3550 3560 3570 3580 3590 3600
3610 3620 3630 3640 3650 3660
3670 3680 3690 3700 3710 3720
3730 3740 3750 3760 3770 3780
3790 3800 3810 3820 3830 3840
3850 3860 3870 3880 3890 3900
3910 3920 3930 3940 3950 3960
3970 3980 3990 4000 4010 4020
4030 4040 4050 4060 4070 4080
4090 4100 4110 4120 4130 4140
4150 4160 4170 4180 4190 4200
4210 4220 4230 4240 4250 4260
4270 4280 4290 4300 4310 4320
4330 4340 4350 4360 4370 4380
4390 4400 4410 4420 4430 4440
4450 4460 4470 4480 4490 4500
4510 4520 4530 4540 4550 4560
4570 4580 4590 4600 4610 4620
4630 4640 4650 4660 4670 4680
4690 4700 4710 4720 4730 4740
4750 4760 4770 4780 4790 4800
4810 4820 4830 4840 4850 4860
4870 4880 4890 4900 4910 4920
4930 4940 4950 4960 4970 4980
4990 5000 5010 5020 5030 5040
5050 5060 5070 5080 5090 5100
5110 5120 5130 5140 5150 5160
5170 5180 5190 5200 5210 5220
5230 5240 5250 5260 5270 5280
5290 5300 5310 5320 5330 5340
5350 5360 5370 5380 5390 5400
5410 5420 5430 5440 5450 5460
5470 5480 5490 5500 5510 5520
5530 5540 5550 5560 5570 5580
5590 5600 5610 5620 5630 5640
5650 5660 5670 5680 5690 5700
5710 5720 5730 5740 5750 5760
5770 5780 5790 5800 5810 5820
5830 5840 5850 5860 5870 5880
5890 5900 5910 5920 5930 5940
5950 5960 5970 5980 5990 6000
6010 6020 6030 6040 6050 6060
6070 6080 6090 6100 6110 6120
6130 6140 6150 6160 6170 6180
6190 6200 6210 6220 6230 6240
6250 6260 6270 6280 6290 6300
6310 6320 6330 6340 6350 6360
6370 6380 6390 6400 6410 6420
6430 6440 6450 6460 6470 6480
6490 6500 6510 6520 6530 6540
6550 6560 6570 6580 6590 6600
6610 6620 6630 6640 6650 6660
6670 6680 6690 6700 6710 6720
6730 6740 6750 6760 6770 6780
6790 6800 6810 6820 6830 6840
6850 6860 6870 6880 6890 6900
6910 6920 6930 6940 6950 6960
6970 6980 6990 7000 7010 7020
7030 7040 7050 7060 7070 7080
7090 7100 7110 7120 7130 7140
7150 7160 7170 7180 7190 7200
7210 7220 7230 7240 7250 7260
7270 7280 7290 7300 7310 7320
7330 7340 7350 7360 7370 7380
7390 7400 7410 7420 7430 7440
7450 7460 7470 7480 7490 7500
7510 7520 7530 7540 7550 7560
7570 7580 7590 7600 7610 7620
7630 7640 7650 7660 7670 7680
7690 7700 7710 7720 7730 7740
7750 7760 7770 7780 7790 7800
7810 7820 7830 7840 7850 7860
7870 7880 7890 7900 7910 7920
7930 7940 7950 7960 7970 7980
7990 8000 8010 8020 8030 8040
8050 8060 8070 8080 8090 8100
8110 8120 8130 8140 8150 8160
8170 8180 8190 8200 8210 8220
8230 8240 8250 8260 8270 8280
8290 8300 8310 8320 8330 8340
8350 8360 8370 8380 8390 8400
8410 8420 8430 8440 8450 8460
8470 8480 8490 8500 8510 8520
8530 8540 8550 8560 8570 8580
8590 8600 8610 8620 8630 8640
8650 8660 8670 8680 8690 8700
8710 8720 8730 8740 8750 8760
8770 8780 8790 8800 8810 8820
8830 8840 8850 8860 8870 8880
8890 8900 8910 8920 8930 8940
8950 8960 8970 8980 8990 9000
9010 9020 9030 9040 9050 9060
9070 9080 9090 9100 9110 9120
9130 9140 9150 9160 9170 9180
9190 9200 9210 9220 9230 9240
9250 9260 9270 9280 9290 9300
9310 9320 9330 9340 9350 9360
9370 9380 9390 9400 9410 9420
9430 9440 9450 9460 9470 9480
9490 9500 9510 9520 9530 9540
9550 9560 9570 9580 9590 9600
9610 9620 9630 9640 9650 9660
9670 9680 9690 9700 9710 9720
9730 9740 9750 9760 9770 9780
9790 9800 9810 9820 9830 9840
9850 9860 9870 9880 9890 9900
9910 9920 9930 9940 9950 9960
9970 9980 9990 10000

1850365 RSGDAATINSRYNDLTRIGNYTHAVRWNTGLERWGPDSRDMIRYNQFRRLTLV
180 190 200 210 220 230
cry1a-105.pe 250 260 270 280 290 300
LDIVSLPNDSTRTYRTVTSQTLREIYTNVPLENFDGSRGSAQIEGSRSPHLMIL
1850365 LDIVSLPNDSTRTYRTVTSQTLREIYTNVPLENFDGSRGSAQIEGSRSPHLMIL
240 250 260 270 280 290
cry1a-105.pe 310 320 330 340 350 360
NSITITDARHGEYVWSGQIMASPVGSGPEFTFLYGTMGNAPOQRIVAQLGQGVYR
1850365 NSITITDARHGEYVWSGQIMASPVGSGPEFTFLYGTMGNAPOQRIVAQLGQGVYR
300 310 320 330 340 350
cry1a-105.pe 370 380 390 400 410 420
TLSSITLRRPNTGIGNNOQLSVLDGTEFAYGTSSNLPSSAVYKSGTVDSLEIPQNNV
1850365 TLSSITLRRPNTGIGNNOQLSVLDGTEFAYGTSSNLPSSAVYKSGTVDSLEIPQNNV
360 370 380 390 400 410
cry1a-105.pe 430 440 450 460 470 480
PPROQFSHRLSHVSMFSGFSNSVSIIRAPMFWSIHRSAEFNNIISDSTQIPLVKAH
1850365 PPROQFSHRLSHVSMFSGFSNSVSIIRAPMFWSIHRSAEFNNIISDSTQIPLVKAH
420 430 440 450 460 470
cry1a-105.pe 490 500 510 520 530 540
TLSSITLRRPNTGIGNNOQLSVLDGTEFAYGTSSNLPSSAVYKSGTVDSLEIPQNNV
1850365 TLSSITLRRPNTGIGNNOQLSVLDGTEFAYGTSSNLPSSAVYKSGTVDSLEIPQNNV
480 490 500 510 520 530
cry1a-105.pe 550 560 570 580 590 600
VAGERIFAGNNDGMDGLTFQSFVSATINTAFTFMSQSSFTVGADTFSSGNEYID
1850365 VAGERIFAGNNDGMDGLTFQSFVSATINTAFTFMSQSSFTVGADTFSSGNEYID
540 550 560 570 580 590
cry1a-105.pe 610 620 630 640 650 660
REELPVPATLEKSWERAKAVALLSTNQLGKINVTYHIDVSNLVTYLSDEFC
1850365 REELPVPATLEKSWERAKAVALLSTNQLGKINVTYHIDVSNLVTYLSDEFC
600 610 620 630 640 650
cry1a-105.pe 670 680 690 700 710 720
LDEKSELSEKVKHAKRLSDERNLDQSNLDIOPERGSGSGITIOGGDDVFKENY
1850365 LDEKSELSEKVKHAKRLSDERNLDQSNLDIOPERGSGSGITIOGGDDVFKENY
660 670 680 690 700 710
cry1a-105.pe 730 740 750 760 770 780
TLSSITLRRPNTGIGNNOQLSVLDGTEFAYGTSSNLPSSAVYKSGTVDSLEIPQNNV
1850365 TLSSITLRRPNTGIGNNOQLSVLDGTEFAYGTSSNLPSSAVYKSGTVDSLEIPQNNV
720 730 740 750 760 770
cry1a-105.pe 790 800 810 820 830 840
GSLWPLSAQSPKCKCEPNRCAPYLEMNPDDCSRDSEKCAHSHHFSLDIDVGCTDLN
1850365 GSLWPLSAQSPKCKCEPNRCAPYLEMNPDDCSRDSEKCAHSHHFSLDIDVGCTDLN
780 790 800 810 820 830
cry1a-105.pe 850 860 870 880 890 900
EDLGWVIFKIKTODGHARLGNLEFLEKPLVSEARARVAKKWRDRKRELEWETIV
1850365 EDLGWVIFKIKTODGHARLGNLEFLEKPLVSEARARVAKKWRDRKRELEWETIV
840 850 860 870 880 890
cry1a-105.pe 910 920 930 940 950 960
YKEAKESVDALFVNSQVDLOADTNIAHAAKRVHSIREAIPLSVIRGNAFEE
1850365 YKEAKESVDALFVNSQVDLOADTNIAHAAKRVHSIREAIPLSVIRGNAFEE
870 880 890 900 910 920
cry1a-105.pe 970 980 990 1000 1010 1020
LEGRIFTAFSLYDARNVIKNGDFNNGLSNMVKGHVDEEQNNQSRVLPWEAEVSQE
1850365 LEGRIFTAFSLYDARNVIKNGDFNNGLSNMVKGHVDEEQNNQSRVLPWEAEVSQE
970 980 990 1000 1010 1020
cry1a-105.pe 1030 1040 1050 1060 1070 1080
MONNPINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTFQLLSEFVPGAGFVLG
1850365 MONNPINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTFQLLSEFVPGAGFVLG
10 20 30 40 50 60
cry1a-105.pe 110 120 130 140 150 160
VDIINGIFCPQWDALFVIOELINORIEEFARNOAISRLGSLNLYQIYAESFWEAD
1850365 VDIINGIFCPQWDALFVIOELINORIEEFARNOAISRLGSLNLYQIYAESFWEAD
70 80 90 100 110 120
cry1a-105.pe 130 140 150 160 170 180
PTNPALREEMRIQFNDMNSALTITTAIPFAVQNYQVPLLSVYVQAAHLHSLVLRDVSFVGQ
1850365 PTNPALREEMRIQFNDMNSALTITTAIPFAVQNYQVPLLSVYVQAAHLHSLVLRDVSFVGQ
130 140 150 160 170 180
cry1a-105.pe 190 200 210 220 230 240
RWGFDATINSRYNDLTRIGNYTHAVRWNTGLERWGPDSRDMIRYNQFRRLTLV
1850365 RWGFDATINSRYNDLTRIGNYTHAVRWNTGLERWGPDSRDMIRYNQFRRLTLV
190 200 210 220 230 240

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1850365      EDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKAARKKWRDKEKLEWETNIV
            810      820      830      840      850      860

cry1a-105.pe YKEAKESVDALFWNSQDQLQADTNIAHIAADKRVHISIRAYLPQLSVIPGVNAAIFEE
            910      920      930      940      950      960
1850365      YKEAKESVDALFWNSQDQLQADTNIAHIAADKRVHISIRAYLPQLSVIPGVNAAIFEE
            870      880      890      900      910
cry1a-105.pe LEGRIPTAFSLYDARNVIKNGDFNGLSCWNKVGHVDEEQNQRSVLVVPVEAEVQSE
            970      980      990      1000      1010      1020
cry1a-105.pe
NRAA:46409857

46409857 source="GENBANK_PROT" cry1a type crystal protein [Bacillus
thuringiensis serovar kurstaki]

SCORES      Initl: 3342      Initn: 3342      Opt: 4135      Z-score: 4694.7      E(): 0
>NRAA:46409857
      Initn: 3342      Initl: 3342      Opt: 4135      Z-score: 4694.7      expect(): 0
Smith-Waterman score: 4135;      79.5% identity in 799 aa overlap
(9-800:2-793)

cry1a-105.pe MDNPNINECIPYCNLSNPEVEVLGGERIETGTPIDISLSLTLFLLSEFVPGAGFVLGL
            10      20      30      40      50      60
46409857      MQCVPNCLSNPEVEVLGGERIETGTPIDISLSLTLFLLSEFVPGAGFVLGL
            60      70      80      90      100      110
cry1a-105.pe VDIIWIFGPSQWDAFLVQIEQLINQRIEFARNQAIRLGLSLNLQIYIAESFREWEAD
            120      130      140      150      160      170
46409857      VDIIWIFGPSQWDAFLVQIEQLINQRIEFARNQAIRLGLSLNLQIYIAESFREWEAD
            120      130      140      150      160      170
cry1a-105.pe PTFNPALEENRIQFNDMNSALTTPAIFAVQNYQVPLLSVYVQAAHLVSLRDVSVFQ
            180      190      200      210      220      230
46409857      PTFNPALEENRIQFNDMNSALTTPAIFAVQNYQVPLLSVYVQAAHLVSLRDVSVFQ
            180      190      200      210      220      230
cry1a-105.pe RWGFDAAATINSRYNDLTGLIGNYTDHAWRYNTGLERVMGPDSDRWYRNQFRRELTIV
            240      250      260      270      280      290
46409857      RWGFDAAATINSRYNDLTGLIGNYTDHAWRYNTGLERVMGPDSDRWYRNQFRRELTIV
            240      250      260      270      280      290
cry1a-105.pe LDIVSLFPAYDSETPYIETVSQLTREIYTNPVLENFDSFGSGAQEGSIRSPHMDIL
            300      310      320      330      340      350
46409857      LDIVSLFPAYDSETPYIETVSQLTREIYTNPVLENFDSFGSGAQEGSIRSPHMDIL
            300      310      320      330      340      350
cry1a-105.pe NSITITDHRGEYWSGHQIMASPVGSGPFEPTPELYGTMGNAAPQORIVAGLGGVYR
            360      370      380      390      400      410
46409857      NSITITDHRGEYWSGHQIMASPVGSGPFEPTPELYGTMGNAAPQORIVAGLGGVYR
            360      370      380      390      400      410
cry1a-105.pe TLSSTLYRRP-FNIGINNQQLSVLDTGTEFAYGT--SSNLPFSAVYRKSGTVDLSDEIPPNQ
            420      430      440      450      460      470
46409857      TLSSTLYRRP-FNIGINNQQLSVLDTGTEFAYGT--SSNLPFSAVYRKSGTVDLSDEIPPNQ
            420      430      440      450      460      470
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cry1a-105.pe NVPRPGFSHRLSHVSMRSPFNSSVSIIRAPMESWIHRSAAEFNNIIASDSITQIPLVK
            420      430      440      450      460      470
46409857      SVPRPGFSHRLSHVSMRSPFNSSVSIIRAPMESWIHRSAAEFNNIIASDSITQIPLVK
            420      430      440      450      460      470
cry1a-105.pe AHTLQSGTIVRPGFTGDDLRLRTSGGPFAYT--IVNINQGLPQ---RYRARIRYASTT
            480      490      500      510      520      530
46409857      GNFLNGS-VISGPGFTGDLVRLNSSGNNIQNRGYIEVPIHFSTSTRYRVRVYASVT
            480      490      500      510      520      530
cry1a-105.pe NLRYYTVAGERIFAGQFNKTMGTGDDPLTFQSFYSATINTAFTPFMSQSFVVGADTFSS
            540      550      560      570      580      590
46409857      PIHLNVMGNSSIFNSTVPATATSLDNLQSSDFGYFESANFTSSLGN--IVGVNFSG
            540      550      560      570      580      590
cry1a-105.pe GNEVYIDRELPVPTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDVHIDQVSNLVT
            600      610      620      630      640      650
46409857      TAGVILDRFEFIPVATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDVHIDQVSNLVT
            600      610      620      630      640      650
cry1a-105.pe YLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGMGSGTGTIIQGGDD
            660      670      680      690      700      710
46409857      CLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGMGSGTGTIIQGGDD
            660      670      680      690      700      710
cry1a-105.pe VFKEYNYVLSGTDFDCYTYLYQKIDSKLKAFTRIQURGYIEDSQBLEIYSIRYNKXHE
            720      730      740      750      760      770
46409857      VFKEYNYVLSGTDFDCYTYLYQKIDSKLKAFTRIQURGYIEDSQBLEIYSIRYNKXHE
            720      730      740      750      760      770
cry1a-105.pe TVNVPGTGLWPLSAQSGPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHHSHHFSLDID
            780      790      800      810      820      830
46409857      TLNVPGTGLWPLSAQSGPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHHSHHFSLDID
            780      790      800      810      820      830
cry1a-105.pe
NRAA:13173240

13173240 source="GENBANK_PROT" insecticidal crystal protein BTRX28 [Bacillus
thuringiensis serovar kunthalarX28]

SCORES      Initl: 4088      Initn: 4088      Opt: 4105      Z-score: 4658.4      E(): 0
>NRAA:13173240
      Initn: 4088      Initl: 4088      Opt: 4105      Z-score: 4658.4      expect(): 0
Smith-Waterman score: 5720;      82.3% identity in 1079 aa overlap
(1-1075:1-1049)

cry1a-105.pe MDNPNINECIPYCNLSNPEVEVLGGERIETGTPIDISLSLTLFLLSEFVPGAGFVLGL
            10      20      30      40      50      60
13173240      MDNPNINECIPYCNLSNPEVEVLGGERIETGTPIDISLSLTLFLLSEFVPGAGFVLGL
            10      20      30      40      50      60
cry1a-105.pe VDIIWIFGPSQWDAFLVQIEQLINQRIEFARNQAIRLGLSLNLQIYIAESFREWEAD
            70      80      90      100      110      120
46409857      VDIIWIFGPSQWDAFLVQIEQLINQRIEFARNQAIRLGLSLNLQIYIAESFREWEAD
            70      80      90      100      110      120
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13173240 VDIITWIFGSPQNDALFVNSQVDRLOADNTIAMIHAADKRVHSIREAYLPESLPGVNA
720 730 740 750 760 770
cry1a-105.pe VPGTGSILWPLSLAQSPTGKCGEPNRCAPHLEWNPDLDCSCROGEKCAHSHHFLSLDIDVGC
780 790 800 810 820 830
13173240 VPGTGSILWPLSLAQSPTGKCGEPNRCAPHLEWNPDLDCSCROGEKCAHSHHFLSLDIDVGC
780 790 800 810 820 830
cry1a-105.pe TDLNEDLGWVWIFKIKTODGHARLGNLEFLEEKPLVGEALARKVRAEKKWRDKREKLEWE
840 850 860 870 880 890
13173240 TDLNEDLGWVWIFKIKTODGHARLGNLEFLEEKPLVGEALARKVRAEKKWRDKREKLEWE
840 850 860 870 880 890
cry1a-105.pe TINIYKEAKESVDALFVNSQVDRLOADNTIAMIHAADKRVHSIREAYLPESLPGVNA
900 910 920 930 940 950
13173240 TINIYKEAKESVDALFVNSQVDRLOADNTIAMIHAADKRVHSIREAYLPESLPGVNA
900 910 920 930 940 950
cry1a-105.pe IFEELEGRIFTAFSLDARNVIKNGDFNGLSCWNVKGVHDVEEQNNQSVLVVPEWEAE
960 970 980 990 1000 1010
13173240 IFEELEGRIFTAFSLDARNVIKNGDFNGLSCWNVKGVHDVEEQNNQSVLVVPEWEAE
960 970 980 990 1000 1010
cry1a-105.pe VSGEVRCPCGRIYLLVAYKGEYGEVCVTHIEINNTDELKFSNCVEEIEYFNNTVTGN
1020 1030 1040 1050 1060 1070
13173240 VSGEVRCPCGRIYLLVAYKGEYGEVCVTHIEINNTDELKFSNCVEEIEYFNNTVTGN
1020 1030 1040 1050 1060 1070
cry1a-105.pe DITNVEYCGATFSGRGHNEARVADVASVEKSYTIGRRENCFCFNRGVDYTP
1080 1090 1100 1110 1120 1130
13173240 DITNVEYCGATFSGRGHNEARVADVASVEKSYTIGRRENCFCFNRGVDYTP
1080 1090 1100 1110 1120 1130
cry1a-105.pe NRAA:5052774
5052774 source="GENBANK_PROT" insect: Bacillus [Bacillus
thuringiensis]
SCORES Initl: 3591 Initn: 3591 Opt: 4088 Z-score: 4641.9 E(1): 0
>>NRAA:5052774
Initn: 3591 Initl: 3591 Opt: 4088 Z-score: 4641.9 E(1): 0
Smith-Waterman score: 4088; 86.7% identity in 228 aa overlap
(1-723:1-723)
cry1a-105.pe MDNPNNECIPNCLSNPEVEVLGGRIETGTPIDISLSTPLSEFVPLGKGL
10 20 30 40 50 60
5052774 MDNPNNECIPNCLSNPEVEVLGGRIETGTPIDISLSTPLSEFVPLGKGL
10 20 30 40 50 60
cry1a-105.pe VDIITWIFGSPQNDALFVNSQVDRLOADNTIAMIHAADKRVHSIREAYLPESLPGVNA
70 80 90 100 110 120
5052774 VDIITWIFGSPQNDALFVNSQVDRLOADNTIAMIHAADKRVHSIREAYLPESLPGVNA
70 80 90 100 110 120

13173240 VDIITWIFGSPQNDALFVNSQVDRLOADNTIAMIHAADKRVHSIREAYLPESLPGVNA
720 730 740 750 760 770
cry1a-105.pe VPGTGSILWPLSLAQSPTGKCGEPNRCAPHLEWNPDLDCSCROGEKCAHSHHFLSLDIDVGC
780 790 800 810 820 830
13173240 VPGTGSILWPLSLAQSPTGKCGEPNRCAPHLEWNPDLDCSCROGEKCAHSHHFLSLDIDVGC
780 790 800 810 820 830
cry1a-105.pe TDLNEDLGWVWIFKIKTODGHARLGNLEFLEEKPLVGEALARKVRAEKKWRDKREKLEWE
840 850 860 870 880 890
13173240 TDLNEDLGWVWIFKIKTODGHARLGNLEFLEEKPLVGEALARKVRAEKKWRDKREKLEWE
840 850 860 870 880 890
cry1a-105.pe TINIYKEAKESVDALFVNSQVDRLOADNTIAMIHAADKRVHSIREAYLPESLPGVNA
900 910 920 930 940 950
13173240 TINIYKEAKESVDALFVNSQVDRLOADNTIAMIHAADKRVHSIREAYLPESLPGVNA
900 910 920 930 940 950
cry1a-105.pe IFEELEGRIFTAFSLDARNVIKNGDFNGLSCWNVKGVHDVEEQNNQSVLVVPEWEAE
960 970 980 990 1000 1010
13173240 IFEELEGRIFTAFSLDARNVIKNGDFNGLSCWNVKGVHDVEEQNNQSVLVVPEWEAE
960 970 980 990 1000 1010
cry1a-105.pe VSGEVRCPCGRIYLLVAYKGEYGEVCVTHIEINNTDELKFSNCVEEIEYFNNTVTGN
1020 1030 1040 1050 1060 1070
13173240 VSGEVRCPCGRIYLLVAYKGEYGEVCVTHIEINNTDELKFSNCVEEIEYFNNTVTGN
1020 1030 1040 1050 1060 1070
cry1a-105.pe DITNVEYCGATFSGRGHNEARVADVASVEKSYTIGRRENCFCFNRGVDYTP
1080 1090 1100 1110 1120 1130
13173240 DITNVEYCGATFSGRGHNEARVADVASVEKSYTIGRRENCFCFNRGVDYTP
1080 1090 1100 1110 1120 1130
cry1a-105.pe NRAA:5052774
5052774 source="GENBANK_PROT" insect: Bacillus [Bacillus
thuringiensis]
SCORES Initl: 3591 Initn: 3591 Opt: 4088 Z-score: 4641.9 E(1): 0
>>NRAA:5052774
Initn: 3591 Initl: 3591 Opt: 4088 Z-score: 4641.9 E(1): 0
Smith-Waterman score: 4088; 86.7% identity in 228 aa overlap
(1-723:1-723)
cry1a-105.pe MDNPNNECIPNCLSNPEVEVLGGRIETGTPIDISLSTPLSEFVPLGKGL
10 20 30 40 50 60
5052774 MDNPNNECIPNCLSNPEVEVLGGRIETGTPIDISLSTPLSEFVPLGKGL
10 20 30 40 50 60
cry1a-105.pe VDIITWIFGSPQNDALFVNSQVDRLOADNTIAMIHAADKRVHSIREAYLPESLPGVNA
70 80 90 100 110 120
5052774 VDIITWIFGSPQNDALFVNSQVDRLOADNTIAMIHAADKRVHSIREAYLPESLPGVNA
70 80 90 100 110 120

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[illegible]

8469143 YTLPLAGYETKLEVFETDTVWPRNRYSD
1130 1140 1150

cry1a-105.pep
SW:8469143

8469143 description="PESTICIDAL CRYSTAL PROTEIN CRYIIB (INSECTICIDAL DELTA-ENDOTOXIN CRYII(B)) (CRYSTALLINE ENTOMOCIDAL PROTEIN) (131 KDA CRYSTALL PROTEIN)." library="NA species="Bacillus thuringiensis serovar morrisoni" source="swissprot_prot" version="NA type="PRT

SCORES Initl: 3030 Initn: 5096 Opt: 4083 z-score: 4633.2 E(): 0
>>SW:8469143
initn: 5096 initl: 3030 opt: 4083 z-score: 4633.2 expect(): 0
Smith-Waterman score: 5110; 67.0% identity in 1156 aa overlap
(8-1155:7-1147)

cry1a-105.pe MDNNPNINICIPNCLSPVEVVGERTETGTP--IDISLSLTOFLISEVPAGVFL
10 20 30 40 50
>>SW:8469143
initn: 5096 initl: 3030 opt: 4083 z-score: 4633.2 expect(): 0
Smith-Waterman score: 5110; 67.0% identity in 1156 aa overlap
(8-1155:7-1147)

8469143 MEVNHQNECVFNPCKNPKTEMLDIEGSSRSRQVAAEISLGLTRFLLESLLPAGSGFG
10 20 30 40 50
>>SW:8469143
initn: 5096 initl: 3030 opt: 4083 z-score: 4633.2 expect(): 0
Smith-Waterman score: 5110; 67.0% identity in 1156 aa overlap
(8-1155:7-1147)

cry1a-105.pe GLVDIIWGIFGSQWDAFLVQIOLINQRIEFAFNQAISSLEGLSNLVQIAVESFREWE
60 70 80 90 100 110
>>SW:8469143
initn: 5096 initl: 3030 opt: 4083 z-score: 4633.2 expect(): 0
Smith-Waterman score: 5110; 67.0% identity in 1156 aa overlap
(8-1155:7-1147)

8469143 GLFDIIWGIVGQDSFLTEIQTLDQIRAEHVRNQAISLEGLSGSEVHIESLREWE
60 70 80 90 100 110
>>SW:8469143
initn: 5096 initl: 3030 opt: 4083 z-score: 4633.2 expect(): 0
Smith-Waterman score: 5110; 67.0% identity in 1156 aa overlap
(8-1155:7-1147)

cry1a-105.pe ADPTWALNEEMRIQFNDMNSALTTAIPFAVQNYQVPLSVYQAAHLHLSVLRDVSVF
120 130 140 150 160 170
>>SW:8469143
initn: 5096 initl: 3030 opt: 4083 z-score: 4633.2 expect(): 0
Smith-Waterman score: 5110; 67.0% identity in 1156 aa overlap
(8-1155:7-1147)

8469143 ASPNNSLGQVNEFNSNDNALITAIPILRGQGEIFELLTVYQAAHLHLSLLRDVVF
120 130 140 150 160 170
>>SW:8469143
initn: 5096 initl: 3030 opt: 4083 z-score: 4633.2 expect(): 0
Smith-Waterman score: 5110; 67.0% identity in 1156 aa overlap
(8-1155:7-1147)

cry1a-105.pe GQNGEDFATINSRVWLTGAINQTHDAVRMYNTGLERVGVDSRDMIRYQFRRLLT
180 190 200 210 220 230
>>SW:8469143
initn: 5096 initl: 3030 opt: 4083 z-score: 4633.2 expect(): 0
Smith-Waterman score: 5110; 67.0% identity in 1156 aa overlap
(8-1155:7-1147)

8469143 GQRGLLSATVNNALNLTINLTNDHQRQWNRGLDN-FGVVT---ARYLDFOREVTI
180 190 200 210 220 230
>>SW:8469143
initn: 5096 initl: 3030 opt: 4083 z-score: 4633.2 expect(): 0
Smith-Waterman score: 5110; 67.0% identity in 1156 aa overlap
(8-1155:7-1147)

cry1a-105.pe TVLDIVSLFPNVDSTIPIRVSQLAEIYTPVPSNPDGSGRGAQIEGSIKPSPLMD
240 250 260 270 280 290
>>SW:8469143
initn: 5096 initl: 3030 opt: 4083 z-score: 4633.2 expect(): 0
Smith-Waterman score: 5110; 67.0% identity in 1156 aa overlap
(8-1155:7-1147)

8469143 SVLDIVALFPNVDSTIPIRVSQLAEIYTPVPSNPDGSGRGAQIEGSIKPSPLMD
240 250 260 270 280 290
>>SW:8469143
initn: 5096 initl: 3030 opt: 4083 z-score: 4633.2 expect(): 0
Smith-Waterman score: 5110; 67.0% identity in 1156 aa overlap
(8-1155:7-1147)

cry1a-105.pe ILNSITVITDAHGRGYVWSGHQIMASPVGSGRTTFPPGVMGNAPOQVTVQLOGGV
300 310 320 330 340 350
>>SW:8469143
initn: 5096 initl: 3030 opt: 4083 z-score: 4633.2 expect(): 0
Smith-Waterman score: 5110; 67.0% identity in 1156 aa overlap
(8-1155:7-1147)

8469143 FLTFIVITGVGGIYHWAGHIESSRTTGNLSNPOFAYGTSANRPPNLAHISEN
300 310 320 330 340 350
>>SW:8469143
initn: 5096 initl: 3030 opt: 4083 z-score: 4633.2 expect(): 0
Smith-Waterman score: 5110; 67.0% identity in 1156 aa overlap
(8-1155:7-1147)

cry1a-105.pe YRTLSLTLYRRFPNIGINNQOLSVDLTGFAYGTSNLPSSA--YRTSSVDSNLSLPP
360 370 380 390 400 410
>>SW:8469143
initn: 5096 initl: 3030 opt: 4083 z-score: 4633.2 expect(): 0
Smith-Waterman score: 5110; 67.0% identity in 1156 aa overlap
(8-1155:7-1147)

8469143 YRTLSAPIYS--VSGSIGPNTRAVEGRFLTARDNNLSLPLFLYRKEGSLSSVLPPE
360 370 380 390 400 410
>>SW:8469143
initn: 5096 initl: 3030 opt: 4083 z-score: 4633.2 expect(): 0
Smith-Waterman score: 5110; 67.0% identity in 1156 aa overlap
(8-1155:7-1147)

cry1a-105.pe NNVPYPPQGSKRLSHVSMFRSGNSVSLINAPMFSWIRHSAEFNNIIASDSTQIPL
420 430 440 450 460 470
>>SW:8469143
initn: 5096 initl: 3030 opt: 4083 z-score: 4633.2 expect(): 0
Smith-Waterman score: 5110; 67.0% identity in 1156 aa overlap
(8-1155:7-1147)

8469143 DENEPPYIGYHRLCHAFBSVSLPEPNFARIPVFSWTHRSAGPTNVEVSSRITQIPW
410 420 430 440 450 460
>>SW:8469143
initn: 5096 initl: 3030 opt: 4083 z-score: 4633.2 expect(): 0
Smith-Waterman score: 5110; 67.0% identity in 1156 aa overlap
(8-1155:7-1147)

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cry1a-105.pe 480 490 500 510 520 530
VKAHTLOSQTIVRGPGTGGDILRTSGGPFAYIVINQOLQORVARIRVASTNLR
8469143 470 480 490 500 510 520
VKAHTLOSQAFVKGPGTGGDILRTNLTGLTAURVLTGOLQPTNIRIARISANG
cry1a-105.pe 540 550 560 570 580 590
IYVTVAGERIFACQNKMTGDLTPQSPSVATINTAFTPMQSSFTVGADTFSSGNE
8469143 530 540 550 560 570 580
GTLIFQSPSYGLTPKMTDIDELTSPARTLFTITQQAELNL--TIOQG--
cry1a-105.pe 600 610 620 630 640 650
VYIDRFELIPVATLEAEYNLERAKAVNALFTSNQGLKTNVTDYHIDQVSNLVYLS
8469143 590 600 610 620 630 640
VYIDRIEIPVATFEAEYDLERAQEAVALFTSSNQLGKTDTIDYHIDQVSNLVDCLS
cry1a-105.pe 660 670 680 690 700 710
DEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKOINRQPERCGSGSTIGTIOGGDVFK
8469143 650 660 670 680 690 700
DEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKOINRQPERCGSGSTIGTIOGGDVFK
cry1a-105.pe 720 730 740 750 760 770
ENYVTLSGTDECYPTYLYQKIDESKLKAFTRYQLRGYIEDSQLEIYSIRYNAKHETVN
8469143 710 720 730 740 750 760
ENYVTLPGTDECYPTYLYQKIDESKLKAYTRYQLRGYIEDSQLEIYLIRYNAKHETVN
cry1a-105.pe 780 790 800 810 820 830
VPGTSLWLPUSAGSPIGKCGEPNRCAPHELEWNPDLDCSCRDGKCAHSHHFLSDIDVGC
8469143 770 780 790 800 810 820
VPGTSLWLPUSVESPIGKCGEPNRCVPLEWNSNLDSCSCRDGKCAHSHHFLSDIDVGC
cry1a-105.pe 840 850 860 870 880 890
TDLNEDGVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARKVRAEKKWRDKRELEWE
8469143 830 840 850 860 870 880
TDLNEDGVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARKVRAEKKWRDKRELTQLE
cry1a-105.pe 900 910 920 930 940 950
TNIVYKEAKESVDALFVNSQDQLQADTNIAITHAADKRVHSIREAYLPELSIPGVNAA
8469143 890 900 910 920 930 940
TNIVYKEAKESVDALFANSQYNRLQADTNIAITHAADKRVHIREAYLPELSIPGVNAG
cry1a-105.pe 960 970 980 990 1000 1010
IFELEGRIFTAFSLYDARNVITKNGDFNGLSCWYKGVHVEYENONRSVLYVPEWEAE
8469143 950 960 970 980 990 1000
IFELEGRIFTAFSLYDARNVITKNSDFNGLSCWYKGVHVEYENONRSVLYVPEWEAE
cry1a-105.pe 1020 1030 1040 1050 1060 1070
VSQEVVPCPGRGVILRVAYKEGYGEGCVTIHEIENNTDELKFCNVEEIRYNNVTVCN
8469143 1010 1020 1030 1040 1050 1060
VSQEVVPCPGRGVILRVAYKEGYGEGCVTIHEIENNTDELKFCNVEEIRYNNVTVCN
cry1a-105.pe 1080 1090 1100 1110 1120 1130
DYTNQBEYGGAYTSNRNGYNEA----PSVPADYASVYEKSYYTDGRNCPCFNRGFRD
8469143 1070 1080 1090 1100 1110 1120
AYPADQEGYEGACTSRNRYDEVICNTPLPADYADYIYENAYIDGRNCPFNRGFRD

cry1a-105.pe 1140 1150 1160 1170
YTPLPVGYVTKLEYPPPTDVKWIEICEGTEGTFIVDSVELLIMEE
8469143 1130 1140 1150 1160
YTPLPAGYETKELEYPPPTDVKWIEICEGTEGTFIVDSVELLIMEE
cry1a-105.pep
NRAA:546641
546641 source="GENBANK_PROT" insecticidal protein Cry I A (c) product [toxic
domain] [Bacillus thuringiensis, ssp. kurstaki HD-1, peptide, 723 aa]
SCORES Init1: 3561 Initn: 3561 Opt: 4070 z-score: 4621.4 E(): 0
>>NRAA:546641
Initn: 3561 init1: 3561 opt: 4070 z-score: 4621.4 expect(): 0
Smith-Waterman score: 4070; 86.7% identity in 728 aa overlap
(1-723.1-723)
cry1a-105.pe 10 MNPNINCEIPNCLSNPEVEVLGGERIETGYTPTIDISLSLTOFLSEFVPGAGFVLGL
546641 10 MNPNINCEIPNCLSNPEVEVLGGERIETGYTPTIDISLSLTOFLSEFVPGAGFVLGL
cry1a-105.pe 70 80 90 100 110 120
VDIILWIGFQPSQMDAFLVQIQEQLINQRIEFARNOAISRLGSLNLYCIYVAESFREWAD
546641 70 80 90 100 110 120
VDIILWIGFQPSQMDAFLVQIQEQLINQRIEFARNOAISRLGSLNLYCIYVAESFREWAD
cry1a-105.pe 130 140 150 160 170 180
PTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLSVYQAANLHLSVLRDVSFVQ
546641 130 140 150 160 170 180
PTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLSVYQAANLHLSVLRDVSFVQ
cry1a-105.pe 190 200 210 220 230 240
EWGDAATINSRYNDLTALIGNYTHAVRWYNTGLERWVGSDRDRWRYNQFRRELTIV
546641 190 200 210 220 230 240
EWGDAATINSRYNDLTALIGNYTHAVRWYNTGLERWVGSDRDRWRYNQFRRELTIV
cry1a-105.pe 250 260 270 280 290 300
LDIVSLFPNYSRTYPIRTVQSLTQREIYTNVPLENFDGSGFRGSAQIEGSIIRSPHMDIL
546641 250 260 270 280 290 300
LDIVSLFPNYSRTYPIRTVQSLTQREIYTNVPLENFDGSGFRGSAQIEGSIIRSPHMDIL
cry1a-105.pe 310 320 330 340 350 360
NSITITYDAHRGYWYSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAGLGGGVYR
546641 310 320 330 340 350 360
NSITITYDAHRGYWYSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAGLGGGVYR
cry1a-105.pe 370 380 390 400 410 420
TLSSTLVRFPNIGINNQLSVLDGTEFAFGTSNLPASVYVKSGTWDSDLEIPPNVNV
546641 370 380 390 400 410 420
TLSSTLVRFPNIGINNQLSVLDGTEFAFGTSNLPASVYVKSGTWDSDLEIPPNVNV
cry1a-105.pe 430 440 450 460 470 480
PPROGFSHRHSVHSMFSPGNSVSIIRAFMFHSIHRSAEFNNIIASDSITQIPLVKAH
8469143 430 440 450 460 470 480
PPROGFSHRHSVHSMFSPGNSVSIIRAFMFHSIHRSAEFNNIIASDSITQIPLVKAH

546641 PPRQGFSLRLSNVMSRG-SSSSVSIIRAPMFSMIHRSAEFNNIIASDSITQIPAVKGN
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
cry1a-105.pe TLSSGTTVGGPAGGGLRLKSGEP---FAYIVNIN-GQPPQRYRARIYASTNL
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
546641 FLNCS-VISGPGTASD-WELNSGNTQNGRYIEVPIHFSSTSTRYRVRYSVTPI
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
cry1a-105.pe RIVYTVAGERIFAGENNIMDTGSP-GRSFSVATINAPAFPMSSQSFVVGADTFSSGN
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
546641 HRVNWGNSIESNTVPATNS-ENLQSSIEGYFSNAFTSLGN---IVGVNFSGTA
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
cry1a-105.pe EVIDRFELIPVTATLEAEYNLERAKAVNALFTSTNQLGLTQVYDHYHDSNVTYL
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
546641 GVVIDRFELIPVTATLEAEYNLERAKAVNALFTSTNQLGLTQVYDHYHDSNVTYL
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
cry1a-105.pe SDFCLDKRELSKVKHAKRLSDERNLQDSNFKDINRQPERGSSGITIQGDDVF
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
546641 SDFCLDKRELSKVKHAKRLSDERNLQDSNFKDINRQPERGSSGITIQGDDVF
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
cry1a-105.pe KENVVTLGSGTFDECYPTLYVQKIDESKLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
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
546641 KENVVTLGSGTFDECYPTLYVQKIDESKLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
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
cry1a-105.pep
NRAA:13173242
13173242 source="GENBANK PROT" insecticidal crystal protein BTRX27 [Bacillus
thuringiensis serovar kunthalarx27]
SCORES Init1: 3616 Initn: 5362 Opt: 4008 Z-score: 4548.1 E(): 0
>NRAA:13173242
Initn: 5362 Init1: 3616 Opt: 4008 Z-score: 4548.1 expect(): 0
Smith-Waterman score: 5623; 81.3% identity in 1079 aa overlap
(1-1075:1-1049)
cry1a-105.pe MDNPNNECIPYNCILSNPEVEVLGGERIETGTPIDISLSLTQFLLSEVPVPGAGFVLGL
10 20 30 40 50 60
13173242 MDNPNNECIPYNCILSNPEVEVLGGERIETGTPIDISLSLTQFLLSEVPVPGAGFVLGL
10 20 30 40 50 60
cry1a-105.pe VDIWIGFGSQWDAFLVQIEQLINQRIEFPARNOAISRLGSLNLYQIYAESFREWEAD
70 80 90 100 110 120
13173242 VDIWIGFGSQWDAFLVQIEQLINQRIEFPARNOAISRLGSLNLYQIYAESFREWEAD
70 80 90 100 110 120
cry1a-105.pe PTFNPALEENRIQFNDMNSALTITAIPLFVQNYOVPLLSVYQVQANLHLSVLR--DVSVF
130 140 150 160 170
13173242 PTFNPALEENRIQFNDMNSALTITAIPLFVQNYOVPLLSVYQVQANLHLSVLR--DVSVF
130 140 150 160 170
180 190 200 210 220 230

cry1a-105.pe GQRMGFEAATINSRYNDLIRIGNYTHAVRWYNTGLERVMGPDSDRMIRYNQFRRELT
180 190 200 210 220 230
13173242 SSR--FNALNLAHWTTLIRIGNYTHAVRWYNTGLERVMGPDSDRMIRYNQFRRELT
180 190 200 210 220 230
cry1a-105.pe TVLDIVSLFPNDSTYPIRTVSQLTIREIYTPVLENDFGSRGSAQIEGSRPHLMD
240 250 260 270 280 290
13173242 TVLDIVSLFPNDSTYPIRTVSQLTIREIYTPVLENDFGSRGSAQIEGSRPHLMD
240 250 260 270 280 290
cry1a-105.pe ILNSITTYDAHRGEYVWSGHIWASPVGSGPEFTFPLYGTMGNAAPQORIVAOLGQGV
300 310 320 330 340 350
13173242 ILNSITTYDAHRGEYVWSGHIWASPVGSGPEFTFPLYGTMGNAAPQORIVAOLGQGV
300 310 320 330 340 350
cry1a-105.pe YRTLSSTLYRRFPNIGINNQLSVLDCTEFAYGTSSNLPFSVAYRKSGTVDLSDEIPQNN
360 370 380 390 400 410
13173242 YRTLSSTLYRRFPNIGINNQLSVLDCTEFAYGTSSNLPFSVAYRKSGTVDLSDEIPQNN
360 370 380 390 400 410
cry1a-105.pe NVPPRQGFSLRLSNVMSRG-SSSSVSIIRAPMFSMIHRSAEFNNIIASDSITQIPAVK
420 430 440 450 460 470
13173242 NVPPRQGFSLRLSNVMSRG-SSSSVSIIRAPMFSMIHRSAEFNNIIASDSITQIPAVK
420 430 440 450 460 470
cry1a-105.pe SHLSSGTTVGGPAGGGLRLKSGEP---FAYIVNIN-GQPPQRYRARIYASTNLRIY
480 490 500 510 520 530
13173242 SHLSSGTTVGGPAGGGLRLKSGEP---FAYIVNIN-GQPPQRYRARIYASTNLRIY
480 490 500 510 520 530
cry1a-105.pe IDRELIPVTATLEAEYNLERAKAVNALFTSTNQLGLTQVYDHYHDSNVTYLSD
600 610 620 630 640 650
13173242 IDRELIPVTATLEAEYNLERAKAVNALFTSTNQLGLTQVYDHYHDSNVTYLSD
600 610 620 630 640 650
cry1a-105.pe FCLDEKRELSKVKHAKRLSDERNLQDSNFKDINRQPERGSSGITIQGDDVFKEN
660 670 680 690 700 710
13173242 FCLDEKRELSKVKHAKRLSDERNLQDSNFKDINRQPERGSSGITIQGDDVFKEN
660 670 680 690 700 710
cry1a-105.pe VYTLGTFDECYPTLYVQKIDESKLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
720 730 740 750 760 770
13173242 VYTLGTFDECYPTLYVQKIDESKLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
720 730 740 750 760 770
cry1a-105.pe VPGTGSMLPWSAOSPIGKGENRCAPHLEWNPDLDCSDCEKCAHHSHFSLDADVC
780 790 800 810 820 830
13173242 VPGTGSMLPWSAOSPIGKGENRCAPHLEWNPDLDCSDCEKCAHHSHFSLDADVC
780 790 800 810 820 830
cry1a-105.pe VPGTGSMLPWSAOSPIGKGENRCAPHLEWNPDLDCSDCEKCAHHSHFSLDADVC
780 790 800 810 820 830
13173242 VPGTGSMLPWSAOSPIGKGENRCAPHLEWNPDLDCSDCEKCAHHSHFSLDADVC
780 790 800 810 820 830


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cry1a-105.pe TDLNEDLGWVIFKIKITQDCHARLGNLEFLEEKPLVGEALARKRAEKKWRDREKLEWE
13173242 TDLNEDLGWVIFKIKITQDCHARLGNLEFLEEKPLVGEALARKRAEKKWRDREKLEWE
900 910 920 930 940 950
cry1a-105.pe TNIVYKEAKESVDALFVNSQYDQLQADTNIAHAAADKRVRHSIREAYLPFELSVIPGVNAA
13173242 TNIVYKEAKESVDALFVNSQYDQLQADTNIAHAAADKRVRHSIREAYLPFELSVIPGVNAA
960 970 980 990 1000 1010
cry1a-105.pe IFEELGEGIFTAFSLDARNVINKNGDFNGLSCWNVKGVHDVEEQNQRORSVLVPEWEAE
13173242 IFEELGEGIFTAFSLDARNVINKNGDFNGLSCWNVKGVHDVEEQNQRORSVLVPEWEAE
1020 1030 1040 1050 1060 1070
cry1a-105.pe VSQEVRCPCGIVLRVTAYKEGYGEGCVTHIEENNTDELKFSNCVVEEYIPNNTVTGN
13173242 VSQEVRCPCGIVLRVTAYKEGYGEGCVTHIEENNTDELKFSNCVVEEYIPNNTVTGN
1080 1090 1100 1110 1120 1130
cry1a-105.pe DVTVQEEYGGAYTSRNRGNEAPSPADYASVYEKSYDGRRENCFENRGYRDVTPL
13173242 IILRLKNNMVRVTLVIEDMTFPMKAILLYQLIMHQPMKKKHQMDDEETILVNLTEDMGI
1060 1070 1080 1090 1100 1110
cry1a-105.pep
NR04:40280
40280 source="GENBANK_PROT" unnamed protein product [Bacillus
thuringiensis]gi|117529|sp|P19415|CribDA_BACTA_Pesticidal crystal protein cry1Da
(Insecticidal delta-endotoxin Cry1D(a)) (Crystalline entomocidal protoxin) (132
kDa crystal protein)
SCORES Init1: 3102 Initn: 5514 Opt: 3954 z-score: 4486.5 E(): 0
>>NR04:40280
initn: 5514 init1: 3102 opt: 3954 z-score: 4486.5 expect(): 0
Smith-Waterman score: 5542; 71.8% identity in 1186 aa overlap
(1-1177:1-1165)
cry1a-105.pe MDNNPINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLQFLLSEFVPGAGVLGL
40280 MEIN-NQOCVPYCNLSNPKETILGELTGTNTVADISLGLINFLYNSFVPGGFIIVGL
10 20 30 40 50
cry1a-105.pe VDIWIFGSPQWDALVQIEQLINQRIEFAFNQALISRLGSLNLYQIYAESPREWEAD
40280 DELIWFIFGSPQWDIFLAQIEQLISQRIEFAFNQALISRLGSLNLYQIYAFSDWEKD
60 70 80 90 100 110
cry1a-105.pe PTNPALREEMRIQFNDMNSALTAIPLEFAVONXOVPLSVYQANLHSLVLRDVSFVGQ
40280 PTNPALREEMRIQFNDMNSALTAIPLEFAVONXOVPLSVYQANLHSLVLRDVSFVGQ
120 130 140 150 160 170
cry1a-105.pe RWGFDAAITNSRYNDLTRILGNYTTHAVRWYNTGLERWVGPDSDROWINRYNFRBELTIV
40280 RWGFDAAITNSRYNDLTRILGNYTTHAVRWYNTGLERWVGPDSDROWINRYNFRBELTIV
180 190 200 210 220 230 240
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40280 RMGYDTATINRRYSDLTSLHYVTNHCYDVTNQCRLREGLRFLSDWIVNRFREQLTISV
180 190 200 210 220 230
cry1a-105.pe LDIVSLFPNDSDRTPIRTVSQLTREIYTN-PVL-ENFD--GSFRGSAQIEGSIIRSPHL
40280 LDIVAFFNFDYDRTPIRTVSQLTREIYTN-PVL-ENFD--GSFRGSAQIEGSIIRSPHL
240 250 260 270 280 290
cry1a-105.pe MDLANSITIVTDARHCEYWSGHQIMASPVGSGPEFTPELYCTMNAAPQORIVAQIQ
40280 VDFLNSFTIYDLSLARYAWGHLVNSPRTGTTINLIRSPLYRGEGNTERPVTITASPSV
300 310 320 330 340 350
cry1a-105.pe GYVRTLSLTLYRRPFIINNOQ-LSVLDTGTEFAYGTSSNLPSAVYKSGTVDLSLDEIPP
40280 PIFRTLS-----YITGLDNPVAGIEGVEF---QNTISRSIYKSGPIDSFSELPP
360 370 380 390 400
cry1a-105.pe QNNVPPRQGSFHRLSHVSMFRSGFSNSVSIIRAPMFWIHRSAEFNNIIASDSITQIP
40280 QDASVSPAIGYSHLCHAT-FLERISGPRIA---GTVFSWTHRSASPTNEVSPRITQIP
410 420 430 440 450 460
cry1a-105.pe LVKAHTLQSGTIVVRGPGFTGGDILRRTSGGPAVTIVNINGOLPORVYRARIYASTNL
40280 WYKAHTLASGASVILKPGFTGGDILRRTSGGPAVTIVNINGOLPORVYRARIYASTNL
470 480 490 500 510 520
cry1a-105.pe RIYTVAGERIFAQGNKMTGDELTQPSFSYATINTAFTPFMSQSSFTVGADTFSSGN
40280 SGTFYRQSPSYGIFSPKTMADAGEPLTSRFAHTLTFTPTTISRACEFDL---YIQSG-
530 540 550 560 570 580
cry1a-105.pe EYVIDRFLIPVTAITAEYNLERAKAVNALFTSTNQLGLKTNVTDHIDQVSNLVTYL
40280 -YVIDRFLIPVTAITAEYNLERAKAVNALFTSTNQLGLKTNVTDHIDQVSNLVTYL
590 600 610 620 630 640 650
cry1a-105.pe SDFECLDEKRELSEKVHAKRLSDERNLLQDSNFKDINROPERGWSGTGTTIOGGDDVF
40280 SDFECLDEKRELSEKVHAKRLSDERNLLQDSNFKDINROPERGWSGTGTTIOGGDDVF
660 670 680 690 700 710
cry1a-105.pe KENYVTLSGTDECPYLYQKIDSKLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
40280 KENYVTLSGTDECPYLYQKIDSKLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
720 730 740 750 760 770
cry1a-105.pe NVPGTGLSWPLSPASGPIKCGENSCAPHEWNEDLDCSCRDGEKCAHSHHFSLDIDVG
40280 NVPGTGLSWPLSPASGPIKCGENSCAPHEWNEDLDCSCRDGEKCAHSHHFSLDIDVG
780 790 800 810 820 830
cry1a-105.pe CTDLNLDELGVWVIFKIKITQDCHARLGNLEFLEEKPLVGEALARKRAEKKWRDREKLEW
40280 CTDLNLDELGVWVIFKIKITQDCHARLGNLEFLEEKPLVGEALARKRAEKKWRDREKLEW
840 850 860 870 880 890
```

40280 CTDLNEDLVGWNIFKTKQGHARLGNLEFLERKPLGELARVKRAEKKWRDKRETLQL
820 930 940 850 860 870

cryla-105.pe ETNIVYKESKALFVNSQDQADNTAMIAHADKRVHSIRAYLPELSVIPGNA
900 910 920 930 940 950
40280 ETINYSKAKESVDAFVNSQDRLQDNTAMIAHADKRVHSIRAYLPELSVIPGNA
880 890 900 910 920 930

cryla-105.pe AIFEELEGRITAFSLDARNVINGKNGLSNWNKNGNDVEEONQORSVLVPPWEA
960 970 980 990 1000 1010
40280 AIFEELEERIFTAFSLDARNVINGKNGLSNWNKNGNDVEEONQORSVLVPPWEA
940 950 960 970 980 990

cryla-105.pe EYSQEVRCPCRGYLLAVTAYKEGEGCTHRIENTDELKPSNVCVEEAXPNVTC
1020 1030 1040 1050 1060 1070
40280 EYSQEVRCPCRGYLLAVTAYKEGEGCTHRIENTDELKPSNVCVEEAXPNVTC
1000 1010 1020 1030 1040 1050

cryla-105.pe NDTYNQOEYGGAYTSNRGYNEA---PSVPADYASVYEKSYTGRNPPCENRGY
1080 1090 1100 1110 1120 1130
40280 INVTATQEEYEGTYSNRGYDEAYGNPSPADYASVYEKSYTGRNPPCENRGY
1060 1070 1080 1090 1100 1110

cryla-105.pe DYTLPVGVYKVEYEPEDTKVWIEIGETGTGTVDSVLLIMEE
1140 1150 1160 1170
40280 DYTLPVGVYKVEYEPEDTKVWIEIGETGTGTVDSVLLIMEE
1120 1130 1140 1150 1160

cryla-105.pe

SW:117529

117529 description="PESTICIDIAL CRYSTAL PROTEIN CRYIDA (INSECTICIDAL
DELTA-ENDOTOXIN CRYID(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (132 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar aizawai"
source="swissprot_prot" version="NA type="PRT

SCORES Initl: 3102 Initn: 5514 Opt: 3954 z-score: 4486.5 E(): 0
>>SW:117529
Initn: 5514 initl: 3102 opt: 3954 z-score: 4486.5 expect(): 0
Smith-Waterman score: 5542; 71.8% identity in 1186 aa overlap
(1-1177:1-1165)

cryla-105.pe MNNNINIECPYNCNLSNPEVVGGERIETGYTPIDISLSLQFLSLFVPGAGVIGL
10 20 30 40 50 60
117529 MEIN-NQOCVPYNCNLSNPEVVGGERIETGYTPIDISLSLQFLSLFVPGAGVIGL
10 20 30 40 50

cryla-105.pe VDIINGIGPQWDIAFLVQIEQLINORIEEFARNQASIRLEGLSNLYQIAESFREWAD
70 80 90 100 110 120
117529 LELINGFIGPQWDIAFLVQIEQLINORIEEFARNQASIRLEGLSNLYQIAESFREWAD
60 70 80 90 100 110

cryla-105.pe PTNPALREEMRIQFNDMNSALITTAIPFAVQNYOVPLLSVYVQAAHLVLSDVDFVGO
130 140 150 160 170 180
117529 PTNPALREEMRIQFNDMNSALITTAIPFAVQNYOVPLLSVYVQAAHLVLSDVDFVGO
120 130 140 150 160 170

cryla-105.pe RMGFDAATINSRNDLRLIGNYTHAVRWYNTGLERVMGPDSDRMIRYNOFRRELTLY
190 200 210 220 230 240
117529 RMGYDTATINRYSDLTSLIHYVNTNHCVDYTNQGLRLERFLSDWIVYVNRFRQLTISV
180 190 200 210 220 230

cryla-105.pe LDVLSLEPNYSRTYRTVSOLTSREIYTN-PVL-ENFD--GSFRGSAQIEGSIKSPHL
250 260 270 280 290
117529 LDVLAFFNYDIRTYPIQTATQUTREVYLDLPFINENLSPAASPTTFSAAESALIRSPHL
240 250 260 270 280 290

cryla-105.pe MDILANSITTYTDARHGEYVMSGHQIMASPVGSGPEFTFPLYGTMGNAPOQORIVAOLGQ
300 310 320 330 340 350
117529 VDFLNSFTIYDLSLARVAYMGHLYVNSFTGTITNLIRSLPYLREGNTERPVTITASPSV
300 310 320 330 340 350

cryla-105.pe GVTIRLSLTYRRPFNIGINNQ--LSVLDGTFEYAGTSSNLPASVYKSGTVDLDEIPP
360 370 380 390 400 410
117529 PIFRITLS-----YITGLDNPVAGIEGVF---QNTISIRYKSGPIDFSFSLPP
360 370 380 390 400

cryla-105.pe QNNVPPRQGSFHSRLSHVSMFRSGFSNVSIIIRAPMFSWIHSAFENNIIASDSITQIP
420 430 440 450 460 470
117529 QDASVSPAIGYSHRLCHAT-FLERISGPRIA---GTVFSWTHRSASPINEVSPRITQIP
420 430 440 450 460

cryla-105.pe LKANKLALSGTVVVRGFGTGGDILRTSGGPFAYTIVNINGQLPQRYEARIRYASTTNL
480 490 500 510 520 530
117529 WKAKHTLASASVAKGPGTGGDILRTSGGPFAYTIVNINGQLPQRYEARIRYASTTNL
480 490 500 510 520

cryla-105.pe RIVTVVERIFACVTKTQDLSLTQFSYATINTATFPMSQSSFTVGADTFSSGN
540 550 560 570 580 590
117529 SGTNYRSPPSYQSFPTWDAGFNSTNSFAHTLFTPIIFRAQEEFDL---YIOSG-
530 540 550 560 570 580

cryla-105.pe EVVIDRFELIPVTALPEYVNLKRAVIALETSSNOLKNTVTDVHIDOVSNLVYL
600 610 620 630 640 650
117529 -VVIDRIFELIPVTALPEYVNLKRAVIALETSSNOLKNTVTDVHIDOVSNLVACL
590 600 610 620 630

cryla-105.pe SDEFCLDEKRELSEKVKHAKRLSDERNLSDSKNDINQERGMGSGTGTIGQDDVF
660 670 680 690 700 710
117529 SDEFCLDEKRELSEKVKHAKRLSDERNLSDSKNDINQERGMGSGTGTIGQDDVF
640 650 660 670 680 690

cryla-105.pe KENYVTLSTGTFDECPYLYLQKIDESKLKATRYQLRGYIEDSQLEIYSIRYKAEVY
720 730 740 750 760 770
117529 KENYVTLSTGTFDECPYLYLQKIDESKLKATRYQLRGYIEDSQLEIYSIRYKAEVY
700 710 720 730 740 750

cryla-105.pe NVPGTGSLLWPLSASPIGCKGECNRCAPHEWNPDLCSCDGEKCAHSHHFSLDIDVG
780 790 800 810 820 830
117529 NVPGTGSLLWPLSASPIGCKGECNRCAPHEWNPDLCSCDGEKCAHSHHFSLDIDVG
760 770 780 790 800 810

```
cryla-105.pe CTDLNEDLGWVWIFKIKTODGHARLGNLEFLEKPKVGGALARVRAEKWKREKLEW      840 850 860 870 880 890
117529 CTDLNEDLGWVWIFKIKTODGHARLGNLEFLEKPKVGGALARVRAEKWKREKLEW      820 830 840 850 860 870 880 890

cryla-105.pe ETNIVYKEAKESVDALFVNSQYDQLQADTNIAHIAADKRVHSIREAYLPESLIPGVNA      900 910 920 930 940 950
117529 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAHIAADKRVHSIREAYLPESLIPGVNA      880 890 900 910 920 930

cryla-105.pe AFBELEGRIFTAFSLYDARNVKNKGDFNNGLSCHWNVKGVHDVVEQNNQORSVLVPEWEA      960 970 980 990 1000 1010
117529 AFBELEGRIFTAFSLYDARNVKNKGDFNNGLSCHWNVKGVHDVVEQNNQORSVLVPEWEA      940 950 960 970 980 990

cryla-105.pe EYSQVRVPCRGVYLLRVTAKEGYGEGCVTHIEIENNTDELKFCNVEEIEYFNNTVTC      1020 1030 1040 1050 1060 1070
117529 EYSQVRVPCRGVYLLRVTAKEGYGEGCVTHIEIENNTDELKFCNVEEIEYFNNTVTC      1000 1010 1020 1030 1040 1050

cryla-105.pe DYTPLPAGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLIMEE      1140 1150 1160 1170
117529 DYTPLPAGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLIMEE      1120 1130 1140 1150 1160

cryla-105.pep
SW:8469147
8469147 description="PESTICIDIAL CRYSTAL PROTEIN CRYIDB (INSECTICIDAL
DELTA-ENDOTOXIN CRYID(B)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (131 KDA CRYSTAL
PROTEIN) " library=NA species="Bacillus thuringiensis" source="swissprot_prot"
version=NA type=prt
SCORES Initl: 3058 Initn: 5383 Opt: 3868 z-score: 4388.8 E(): 0
>>SW:8469147
initn: 5383 initl: 3058 opt: 3868 z-score: 4388.8 expect(): 0
Smith-Waterman score: 5417; 70.6% identity in 1185 aa overlap
(1-1177:1-1160)

cryla-105.pe MDNNPINECIPYNCISNPEVEVLGGERIEGTPTDLSLSLQTLFELFEVPGAGVLGL      10 20 30 40 50 60
8469147 MDINHQ-NQCTIPYNCISNPDAILLDAERLETGNTVADISIGLINFLYNFNFGGFIIVGL      10 20 30 40 50
cryla-105.pe VDIINGIFPSQWDAPFLVOIEQLINORIEEFARNQALSRLEGLSNLYOIAESFREWAD      70 80 90 100 110 120
8469147 VDIINGIFPSQWDAPFLVOIEQLINORIEEFARNQALSRLEGLSNLYOIAESFREWAD      60 70 80 90 100 110 120
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cryla-105.pe PTNFALREEMRIQFNDMNSALTAIPLFAVQNYQVFLLSVYQAAANLHLSVLKRVSVFGQ
8469147 PSNPALREEMRTQFNMNSALTAIPLLRVNVEVALLSVYQAAANLHLSVLKRVSVYQ
120 130 140 150 160 170

cryla-105.pe RKGFDATINSRINDLTRILIGNYTHAVRWNTGLERVWGPSRSDRWIRYNOFRRLTLTV
8469147 RKGFDATINSRINDLTRILIGNYTHAVRWNTGLERVWGPSRSDRWIRYNOFRRLTLTV
180 190 200 210 220 230

cryla-105.pe LDIVSLPENYDSRTYPIRTVSQLTREIYTN-P-VLENFD--GSFRGSAQGIIEGSIKSPHL
8469147 LDIVSLPENYDSRTYPIRTVSQLTREIYTN-P-VLENFD--GSFRGSAQGIIEGSIKSPHL
240 250 260 270 280 290

cryla-105.pe MDILNSITTYIDAHARGEYVMSGHQIMASPVGSGPEFTFLYGTMTGNAAPOQRIVAQLGQ
8469147 MDILNSITTYIDAHARGEYVMSGHQIMASPVGSGPEFTFLYGTMTGNAAPOQRIVAQLGQ
300 310 320 330 340 350

cryla-105.pe GYVRLSTLYRRFNGINNGQLSVLDGTEPAVGTSSNLPNAVYKSGYVDSLDLIPRO
8469147 GYVRLSTLYRRFNGINNGQLSVLDGTEPAVGTSSNLPNAVYKSGYVDSLDLIPRO
360 370 380 390 400 410

cryla-105.pe NNNVPPROGFSHRLSHVMSFRGFSNNSVIRAPMFSWIRHSAEFNNIIASDITQIPL
8469147 NNNVPPROGFSHRLSHVMSFRGFSNNSVIRAPMFSWIRHSAEFNNIIASDITQIPL
420 430 440 450 460 470

cryla-105.pe VKAHTLGQITVVRGFGFTGGDILRTRTGGPFAYTIIVNNGQLPORVIRARIRYASTTNLR
8469147 VKAHTLGQITVVRGFGFTGGDILRTRTGGPFAYTIIVNNGQLPORVIRARIRYASTTNLR
480 490 500 510 520 530

cryla-105.pe IVTVVAGERIFAGQFNKTMTDGDLTTFOSFSYATINTATFFPMSSOSFTVGADTFSSGNE
8469147 IVTVVAGERIFAGQFNKTMTDGDLTTFOSFSYATINTATFFPMSSOSFTVGADTFSSGNE
540 550 560 570 580 590

cryla-105.pe VVIDREFELIPVTATLEAEYNLERAKAVNALFTSTNQLGKTNVDYHIDQVSNLVTYLS
8469147 VVIDREFELIPVTATLEAEYNLERAKAVNALFTSTNQLGKTNVDYHIDQVSNLVTYLS
600 610 620 630 640 650

cryla-105.pe DEFCFLDKRELSSEKVKHAKLSDERNLLQDSNFKDINRQPERGWGSGTGTIQGGDDVFK
8469147 DEFCFLDKRELSSEKVKHAKLSDERNLLQDSNFKDINRQPERGWGSGTGTIQGGDDVFK
660 670 680 690 700 710

cryla-105.pe ENVVLTSGTEFCYPTVLYOKIDESKLAFTRYOLRGYIEDSODLEIYSIRYNAKHETVN
8469147 ENVVLTSGTEFCYPTVLYOKIDESKLAFTRYOLRGYIEDSODLEIYSIRYNAKHETVN
720 730 740 750 760 770

cryla-105.pe ENVVLTGTFDECPYTVLYOKIDESKLAFTRYOLRGYIEDSODLEIYSIRYNAKHETVN
8469147 ENVVLTGTFDECPYTVLYOKIDESKLAFTRYOLRGYIEDSODLEIYSIRYNAKHETVN
780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990
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CRY1A-105.pe VPTGSLWPLSLQSNLKKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDVGC
8469147 VPTGSLWPLSLQSNLKKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDVGC
CRY1A-105.pe TDNLNEDLWVTKKQDQCHARGLEFDEKPKLVGEGALARKVRAEKKWRKREKLEWE
8469147 TDNLNEDLWVTKKQDQCHARGLEFDEKPKLVGEGALARKVRAEKKWRKREKLEWE
CRY1A-105.pe TNIVYKEAKESVDALFVNSQVDDQADTNIMHADRVRHSREAYLPSELSVIFGVNAA
8469147 TNIVYKEAKESVDALFVNSQVDDQADTNIMHADRVRHSREAYLPSELSVIFGVNAA
CRY1A-105.pe IPELEGRIFTAFSLYDARNVKNQGNLSCWNGKNDVBEQNNORVLPVPEWLE
8469147 IPELEGRIFTAFSLYDARNVKNQGNLSCWNGKNDVBEQNNORVLPVPEWLE
CRY1A-105.pe VSOEVRVCGRGVILRVYAYKEGEGCVTIHEIENNTDEKFKSCVEEYKPMVITCN
8469147 VSOEVRVCGRGVILRVYAYKEGEGCVTIHEIENNTDEKFKSCVEEYKPMVITCN
CRY1A-105.pe DYTNQOEYGYATSRNRGYNEA---PSVPADYASVYEEKSYTDGRENCPENRGRYRD
8469147 DY--NKNHGANACSSNRGYDESYESSIPADYAPVYEEAYTDGQGNPCPEFNRGH--
CRY1A-105.pe YTLPLGVYVTKLEYFPETDKVWIEIGETEGFIVDSVELLMEE
8469147 -TLPAGYVTALEYFPETDVTWVEIGETEGFIVDSVELLMEE
CRY1A-105.pep
NRAA:295864
295864 source="GENBANK PROT" crystal protein [Bacillus
thuringiensis]gi|8469147|sp|Q45747|C1DB BACTU Pesticidal crystal protein
cryIb (insecticidal delta-endotoxin CryIb) (Crystalline entomocidal protoxin)
(131 kDa crystal protein)
SCORES Initl: 3058 Initn: 5383 Opt: 3868 Z-score: 4388.8 E(): 0
>>NRAA:295864
initn: 5383 initl: 3058 opt: 3868 Z-score: 4388.8 expect(): 0
Smith-Waterman score: 5417; 70.6% identity in 1185 aa overlap
(1-1177;1-1160)
CRY1A-105.pe MDNPNINECPYCNLSNPEVEVLGGERIETGTPIDISLSLTOPLSEVPAGVVLG
295864 MDINHQ--NQCIPYCNLSNPEVDAILLDAERLETGNTVADISGLINFLYSNFPVGGGIVGL
CRY1A-105.pe VDIITWIFGSGQWDAFLVQVIEQLINORIEFARNQAIISRLGLSNYIEYVYETTFRAWEKD
295864

295864 LELINGFVGPQWEIFLAQIEQLISQRIEFARNQAIISRLGLSNYIEYVYETTFRAWEKD
CRY1A-105.pe PTPALREEMRIQFNDMNSALTITAIPLFAVQNYQVPLLSVYQAAHLHSLVLRDVSVEGQ
295864 PTPALREEMRIQFNDMNSALTITAIPLFAVQNYQVPLLSVYQAAHLHSLVLRDVSVEGQ
CRY1A-105.pe RWGFDATINSYNDLIRLIGNVTDHAVRYNTGLRWGCPDSDMIRYNQERRELTIV
295864 RWGFDATINSYNDLIRLIGNVTDHAVRYNTGLRWGCPDSDMIRYNQERRELTIV
CRY1A-105.pe LDIVLPPNVDSTRTPIRTVSQLTREIYN-P-VLENFD--GSPRGAQIEGSIIRSPHL
295864 LDIVLPPNVDSTRTPIRTVSQLTREIYN-P-VLENFD--GSPRGAQIEGSIIRSPHL
CRY1A-105.pe MDILNSITTYTDAHRGEYNGHQINASVPVSGSGPEFTPLPYGTMGNAAPQORIVAOLGQ
295864 MDILNSITTYTDAHRGEYNGHQINASVPVSGSGPEFTPLPYGTMGNAAPQORIVAOLGQ
CRY1A-105.pe GVHTLSLTYLRPPNIGINQQQLSVLDGTAYGTSSNLPSAVYKSGTVDSLEIDPQ
295864 GVHTLSLTYLRPPNIGINQQQLSVLDGTAYGTSSNLPSAVYKSGTVDSLEIDPQ
CRY1A-105.pe NNVPVPGQSHRLSHVSMFRSGFSSSVSIIRAPMFWIHRSAEFNNIADSITQIPL
295864 NNVPVPGQSHRLSHVSMFRSGFSSSVSIIRAPMFWIHRSAEFNNIADSITQIPL
CRY1A-105.pe VKAHTLASGVKAGPGFQGNIRNSMGSGARVFTTGLPQSYIIFRYASVANS
295864 VKAHTLASGVKAGPGFQGNIRNSMGSGARVFTTGLPQSYIIFRYASVANS
CRY1A-105.pe VYIDRFELIETATLEAEVNLERAQKAVNALFTSNQSLKINVTIYHIDQVSNLYVLS
295864 VYIDRFELIETATLEAEVNLERAQKAVNALFTSNQSLKINVTIYHIDQVSNLYVLS
CRY1A-105.pe DEFLDKRELSEKVKHAKRSLDERNLLQSNFDINQPROPERGGSGTGIGQSDVPRK
295864 DEFLDKRELSEKVKHAKRSLDERNLLQSNFDINQPROPERGGSGTGIGQSDVPRK
CRY1A-105.pe ENYVTLSTDECYPTLYVOKYIDSKLKATRYOLRGVIEQSDLETYSIRYNAKHETVN
295864 ENYVTLSTDECYPTLYVOKYIDSKLKATRYOLRGVIEQSDLETYSIRYNAKHETVN

Monsanto Company
Final Report
Product Characterization Center

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295864  ENYVLTGTGTCYTYLYQIDESKLKAYTRYQLRGYIEDSQDLEIYLIRYNAKHEIVN
      710      720      730      740      750      760
      780      790      800      810      820      830
cry1a-105.pe  VGTGSLPLSAQSPICKGCEPNRCAPHLEWNPDLDCSCDGGKCAHHSHSLDIDVGC
      770      780      790      800      810      820
295864  VPTGSLPLSPVQSPICKGCEPNRCAPHLEWNPDLDCSCDDEEKAHHSHSLDIDVGC
      770      780      790      800      810      820
cry1a-105.pe  TDINEDLGWVWIFKIKTODGHARLGNLFLEKPLVGEALARKRAEKWRDKREKLEWE
      840      850      860      870      880      890
295864  TDINEDLGWVWIFKIKTODGHARLGNLFLEKPLVGEALARKRAEKWRDKREKLEWE
      840      850      860      870      880      890
cry1a-105.pe  TNIVYKEAKESVDALFVNSQYDQLQADTNIAHAAKRVHSIREAYLPSELVPGVNA
      900      910      920      930      940      950
295864  TNIVYKEAKESVDALFVNSQYDQLQADTNIAHAAKRVHSIREAYLPSELVPGVNA
      900      910      920      930      940      950
cry1a-105.pe  IFELEGRIFTAFSLYDARNVIRKNGDFNNGLSQWVKGHVDDVEEQNNQBSVLVWPEWAE
      960      970      980      990      1000      1010
295864  IFELEGRIFTAFSLYDARNVIRKNGDFNNGLSQWVKGHVDDVEEQNNQBSVLVWPEWAE
      960      970      980      990      1000      1010
cry1a-105.pe  VSOEVRCVCGRYILRVTAKEGEGGCVTTHEIENNTDELKFSNCVEEIIYPPNVTTCN
      1020      1030      1040      1050      1060      1070
295864  VSOEVRCVCGRYILRVTAKEGEGGCVTTHEIENNTDELKFSNCVEEIIYPPNVTTCN
      1020      1030      1040      1050      1060      1070
cry1a-105.pe  DYVNGVEEGVGYSTRNRGNEA---PSVPADYASVTEEKSITDGRNCPCEFNRRFD
      1080      1090      1100      1110      1120      1130
295864  DY--NKNHGACSSRRNGYDESYESNSIPADYAPVVEEEAYTDQGRNCPCEFNRRH-
      1070      1080      1090      1100      1110      1120
cry1a-105.pe  YTPLPVGYVTKLEVFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1140      1150      1160      1170
295864  -TLPAGVYTALEVFPETDTVAVEIGETEGTFIVDSVELLLMEE
      1120      1130      1140      1150      1160
cry1a-105.pep
NRAA:13899010
13899010 source="GENBANK_PROT" insecticidal crystal protein [Bacillus
thuringiensis]
SCORES  Init1: 3058  Initn: 5369  Opt: 3854  z-score: 4372.9  E(): 0
>>NRAA:13899010
Initn: 5369  Init1: 3058  Opt: 3854  z-score: 4372.9  expect(): 0
Smith-Waterman score: 5403; 70.5% identity in 1185 aa overlap
(1-1177:1-1160)
cry1a-105.pe  MDNPNINECTPYNCLSNPEVLGGERIETGYTIDISLTFQILLSRPGAGFVLGL
      10      20      30      40      50      60
13899010  MDINHQ--NQCIPYNCLSNPAILLDAERLETNTGVADISLGLINFLNFSVPFGGFGIVGL
      10      20      30      40      50
      70      80      90      100      110      120
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cry1a-105.pe  VDIINGIFGQSDAFVLVQIEQLINQRIEERFARQAIISRLEGLSNLYQIYAESFWEAD
      60      70      80      90      100      110
13899010  LELINGFVGPOWEIFLAQIEQLISRIEERFARQAIISRLEGLSNLYQIYETTFWEKD
      60      70      80      90      100      110
cry1a-105.pe  PTNPALREEMRIQNDWNSALTTAIPLFAVQNYQVPLLSVYQAAHLHSLVLRDVSVPQG
      130      140      150      160      170      180
13899010  PNPALREEMRIQNDWNSALTAAIPLFAVQNYQVPLLSVYQAAHLHSLVLRDVSVPQG
      130      140      150      160      170      180
cry1a-105.pe  RWGFDAAATINSRYNDLTRLIGNVTDHAVWVYNTGLERVWGPDSRDWIRYNQFRRLTLTV
      190      200      210      220      230      240
13899010  RWGFDPAIVNSRYSDLTRLHVYTDHCVTDYNDGLKNLEGRSLSDWVYVNRFRRLTLTV
      190      200      210      220      230      240
cry1a-105.pe  LDIVSLFPNYSRTYPIRTVTSQLTREIYTN-P-VLENFD--GSFRGAQIGESIRSPHL
      250      260      270      280      290
13899010  LDIIAFPNYDTEAYPIQTASQLTREVLDLPVNETLSPPASVPTFSAESAIRSPHL
      240      250      260      270      280      290
cry1a-105.pe  MDILNSITIIDARGEYVNSHQINMASPVGSGPEFTFFLYGTMGNDAPQQRIVQAQLGQ
      300      310      320      330      340      350
13899010  VDFLSFTIYDLSASVAYWGHVNSFRITGTTNLRSPLYGREGTERPVTISASPSV
      300      310      320      330      340      350
cry1a-105.pe  GVVRTLSLTLRRPNIGINNQLSVLDGTEFAYGTSSNLPASVARKSGTVDSLEIPPO
      360      370      380      390      400      410
13899010  PIFRTLS---VETGLN--NNNPVAGIEGVF---QNTLSRSIYKSGPIDSFSELPPQ
      360      370      380      390      400
cry1a-105.pe  NNNVPPRQFSRSLSHVSMFRSGFSNVSIIIRAPMFSWIRHSAEFNIIASDITQIPL
      420      430      440      450      460      470
13899010  DVSVSPAIGYSHRLCHAT-FLEIRISGPRIA--GTVFSWTHRSASPINEVSPSRITQIPW
      410      420      430      440      450      460
cry1a-105.pe  VKAHTLQSGTTVVRGPGFTGDIILRRTSGPFPAYTIYVINGQLPQRYRARIYASTNLR
      480      490      500      510      520      530
13899010  VKAHTLASGASVIRKPGFTGDIILRRTSGMDLGLARVFTTGRLPQSYIRFRYASVNR
      470      480      490      500      510      520
cry1a-105.pe  IYTVVAGERIFAGQFNKIMTDGDLTFQSFVSATINTAFTFPMQSSFTVGADTFSSGNE
      540      550      560      570      580      590
13899010  GTERYSQPSYGISFPKMDAGEALTSRFAHTLTFPIFSRAQBEFDL---YIOSG--
      530      540      550      560      570      580
cry1a-105.pe  VYIDREFLIPVTALEAFYNLERAQKAVNALETSTNQLGKTNVTDYHIDQVSNLVYLS
      600      610      620      630      640      650
13899010  VYIDREFIPVDTAFESIEINLERAQKAVNALETSTNQLGKTDVTDYHIDQVSNLVECLS
      590      600      610      620      630      640
cry1a-105.pe  DECLDEKELSEKVKHAKSLDERNLQDSNFKINQPERGMSGSTGITOGGDDVFK
      660      670      680      690      700      710
13899010  DEFCLDEKELSEKVKHAKSLDERNLQDPNFRGINQPPQDRGMRGSTDITTIQGGDDVFK
      650      660      670      680      690      700
      720      730      740      750      760      770
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TSINRQLDRGWSIDITIQQGNDVFKE

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cry1a-105.pe 650 660 670 680 690 700
720 730 740 750 760 770
NYVTLSCYDFECYTYLYOKIDESKLKAFTRYQYRGVIEDSOILEYSTRYNAKHETVNV
8469144 NVYLPGFDECYTYDIQIDESKLKATRYELRGVIEDSQLEVLIRYNAKHETVNV
710 720 730 740 750 760

cry1a-105.pe 780 790 800 810 820 830
PGTGSILWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHSFLDIDVGCT
8469144 PGTGSILWPLSVESPIGRCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHSFLDIDVGCT
770 780 790 800 810 820

cry1a-105.pe 840 850 860 870 880 890
DUNEDLGWVWIFIKITQDGHARGNLEFLEKPLVGEALARVRAEKWRDKREKLEMET
8469144 DUNEDLGWVWIFIKITQDGHARGNLEFLEKPLVGEALARVRAEKWRDKREKLEMET
830 840 850 860 870 880

cry1a-105.pe 900 910 920 930 940 950
NIVYKEAKESVDALFVNSQVDOIQADTNIMIHADKRVHSIREAYLPELSVIPGVNAAI
8469144 NIVYKEAKESVDALFVNSQVDOIQADTNIMIHADKRVHSIREAYLPELSVIPGVNAAI
890 900 910 920 930 940

cry1a-105.pe 960 970 980 990 1000 1010
FEELEGRIPTAFSLYDARNYKNGDFNGLSCMNKGVHDVDEQNNQORSLVAVPEWEAEV
8469144 FEELEGRIPTAFSLYDARNYKNGDFNGLSCMNKGVHDVDEQNNQORSLVAVPEWEAEV
950 960 970 980 990 1000

cry1a-105.pe 1020 1030 1040 1050 1060 1070
SQEVRVCPGRGYILRVYAYKEGEGECVTIHEIENNTDELKFNVCVEEIIYNNVTVCND
8469144 SQEVRVCPGRGYILRVYAYKEGEGECVTIHEIENNTDELKFNVCVEEIIYNNVTVCND
1010 1020 1030 1040 1050 1060

cry1a-105.pe 1080 1090 1100 1110 1120 1130
YTVNQEEYG-GAYTSNRGVNEA---PSVPADYASVYEEKSVYTGRENPCFENRGYR
8469144 YTVNQEEYG-GAYTSNRGVNEA---PSVPADYASVYEEKSVYTGRENPCFENRGYR
1070 1080 1090 1100 1110 1120

cry1a-105.pe 1140 1150 1160 1170
DYTPLEPGVYVKELEYFPETDKYVIEIGETGTFIVDSVELLMEE
8469144 DYTPLEPGVYVKELEYFPETDKYVIEIGETGTFIVDSVELLMEE
1130 1140 1150 1160

cry1a-105.pep
SW:8469144

8469144 description="PESTICIDIAL CRYSTAL PROTEIN CRY1AJA (INSECTICIDAL
DELTA-ENDOTOXIN CRY1J(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (133 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis" source="swissprot_prot"
version="NA type="PRT

SCORES Initl: 2454 Initn: 4384 Opt: 3795 z-score: 4305.8 E(): 0
>>SW:8469144
initn: 4384 initl: 2454 opt: 3795 z-score: 4305.8 expect(): 0
Smith-Waterman score: 5215; 67.5% identity in 1186 aa overlap
(1-1177:1-1167)
```

```
cry1a-105.pe 10 20 30 40 50
MONNNINNECIYPNCLNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVGAGFVLGL
8469144 MEIN-NQKQCIYPNCLNPEVEVLGGERIETGYTPIDISLSLTQFLLNPFVGGGFIISGL
10 20 30 40 50

cry1a-105.pe 70 80 90 100 110 120
VDIIGIFGPSQWDAFLVQIEQLINQRIEFARNOAISRLSEGLSNLYQIYAESFREWAD
8469144 VDKINGALRPSEWDLFLAQERLIDQRIEATVRAKATELEGGRNYQIYAEAFKEMESD
60 70 80 90 100 110

cry1a-105.pe 130 140 150 160 170
PTNPALREEMRIQDNMSALTTAIPLEAVONYOVPLLSVYQAAHLHSLVLRDVSFVGQ
8469144 PDNEAANGRVDRFRIIDGLITEANIPFRIGFEVPLLSVYQAAHLHALLRDLVSIFGE
120 130 140 150 160 170

cry1a-105.pe 190 200 210 220 230 240
RWGFGDAATINSRYNDLRLIGNYTHAVRYNTGLERWGVGPDSDRWIRYNQFRRELTIV
8469144 RWGLTKNVNDIYNRQIREIHEYSNHCVDYNTLELERGFESIAQWRIYNQFRRELTIV
180 190 200 210 220 230

cry1a-105.pe 250 260 270 280 290
LDIVLFPNYSRTYPIRTVSQTLREIYNPVLENFDGSPR-GSAQG--IEGSIKSPHLM
8469144 LDIVLFPNYSRLYPIQTSQTLREIYVSPSEFYGVINSNGNIIGTLTEQOIRRHLM
240 250 260 270 280 290

cry1a-105.pe 300 310 320 330 340 350
DIILNSITVDAHRGEYVAGHQIMASPVGSGPEFTFELYGTMGNAAPQQRIVAQLOGG
8469144 DFNSIMITSDNRREHYVAGLEMTAYFTGPAGACVSPFLVGRGESAPLTV-KRSVNDG
300 310 320 330 340 350

cry1a-105.pe 360 370 380 390 400 410
VYRTLSSTLYRRPFGNIGNQQLSVLDGTEFAYGTSNLPASVAVKSGTVDSLDIIPPQN
8469144 IYRILSAPFYSAPF-LGTIVLIG-SRGEKFDALNNISPPSTIVRHGTVDSLSVIPQD
360 370 380 390 400 410

cry1a-105.pe 420 430 440 450 460 470
NNVPPRQGFSHLSHVSFMRSGFSNVSIIIRAPMFSWIHRSAEFNNIITASDIQIPLV
8469144 NSVPPHRGSSHLSHVSMTAS-----SPIFHWTHRSATTTNTINPNAIQIPLV
420 430 440 450 460 470

cry1a-105.pe 480 490 500 510 520 530
KARTLOSQTVTVRGPGFTGGDILRRTSGGPFAYTVININGOLPORVRIYASTTNLRI
8469144 KAPNLASGATVVRGPGFTGGDILRRTSGGPFAYTVININGOLPORVRIYASTTNLRI
470 480 490 500 510 520

cry1a-105.pe 540 550 560 570 580 590
YVTVAGERIFAGQFNKMTGDEPLTFQSFYSYATINTAFTFMSQSFYVADTFSSGNEV
8469144 FTRINGTSVNQCNFQRTWNRNDNLNESCNGFRTAGFSTPFPSFSAQSTFTLGTQAFSN-QEV
530 540 550 560 570 580

cry1a-105.pe 600 610 620 630 640 650
YIDRFELIPVATLAEAYENLERAQKAVNALFTSTNQLGKTNVTDHIDOVSNLTYLSD
8469144 YIDRIEFVPAFTFEESDLERAQKAVNALFTSTNQLGKTNVTDHIDOVSNLTYLSD
590 600 610 620 630 640
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00100456789010110213014015016017018019020021022023024025026027028029030031032033034035036037038039040041042043044045046047048049050051052053054055056057058059060061062063064065066067068069070071072073074075076077078079080081082083084085086087088089090091092093094095096097098099010001010102010301040105010601070108010901100111011201130114011501160117011801190120012101220123012401250126012701280129013001310132013301340135013601370138013901400141014201430144014501460147014801490150015101520153015401550156015701580159016001610162016301640165016601670168016901700171017201730174017501760177017801790180018101820183018401850186018701880189019001910192019301940195019601970198019902000201020202030204020502060207020802090210021102120213021402150216021702180219022002210222022302240225022602270228022902300231023202330234023502360237023802390240024102420243024402450246024702480249025002510252025302540255025602570258025902600261026202630264026502660267026802690270027102720273027402750276027702780279028002810282028302840285028602870288028902900291029202930294029502960297029802990300030103020303030403050306030703080309031003110312031303140315031603170318031903200321032203230324032503260327032803290330033103320333033403350336033703380339034003410342034303440345034603470348034903500351035203530354035503560357035803590360036103620363036403650366036703680369037003710372037303740375037603770378037903800381038203830384038503860387038803890390039103920393039403950396039703980399040004010402040304040405040604070408040904100411041204130414041504160417041804190420042104220423042404250426042704280429043004310432043304340435043604370438043904400441044204430444044504460447044804490450045104520453045404550456045704580459046004610462046304640465046604670468046904700471047204730474047504760477047804790480048104820483048404850486048704880489049004910492049304940495049604970498049905000501050205030504050505060507050805090510051105120513051405150516051705180519052005210522052305240525052605270528052905300531053205330534053505360537053805390540054105420543054405450546054705480549055005510552055305540555055605570558055905600561056205630564056505660567056805690570057105720573057405750576057705780579058005810582058305840585058605870588058905900591059205930594059505960597059805990600060106020603060406050606060706080609061006110612061306140615061606170618061906200621062206230624062506260627062806290630063106320633063406350636063706380639064006410642064306440645064606470648064906500651065206530654065506560657065806590660066106620663066406650666066706680669067006710672067306740675067606770678067906800681068206830684068506860687068806890690069106920693069406950696069706980699070007010702070307040705070607070708070907100711071207130714071507160717071807190720072107220723072407250726072707280729073007310732073307340735073607370738073907400741074207430744074507460747074807490750075107520753075407550756075707580759076007610762076307640765076607670768076907700771077207730774077507760777077807790780078107820783078407850786078707880789079007910792079307940795079607970798079908000801080208030804080508060807080808090810081108120813081408150816081708180819082008210822082308240825082608270828082908300831083208330834083508360837083808390840084108420843084408450846084708480849085008510852085308540855085608570858085908600861086208630864086508660867086808690870087108720873087408750876087708780879088008810882088308840885088608870888088908900891089208930894089508960897089808990900090109020903090409050906090709080909091009110912091309140915091609170918091909200921092209230924092509260927092809290930093109320933093409350936093709380939094009410942094309440945094609470948094909500951095209530954095509560957095809590960096109620963096409650966096709680969097009710972097309740975097609770978097909800981098209830984098509860987098809890990099109920993099409950996099709980999010000100101002010030100401005010060100701008010090101001011010120101301014010150101601017010180101901020010210102201023010240102501026010270102801029010300103101032010330103401035010360103701038010390104001041010420104301044010450104601047010480104901050010510105201053010540105501056010570105801059010600106101062010630106401065010660106701068010690107001071010720107301074010750107601077010780107901080010810108201083010840108501086010870108801089010900109101092010930109401095010960109701098010990110001101011020110301104011050110601107011080110901110011110111201113011140111501116011170111801119011200112101122011230112401125011260112701128011290113001131011320113301134011350113601137011380113901140011410114201143011440114501146011470114801149011500115101152011530115401155011560115701158011590116001161011620116301164011650116601167011680116901170011710117201173011740117501176011770117801179011800118101182011830118401185011860118701188011890119001191011920119301194011950119601197011980119901200012010120201203012040120501206012070120801209012100121101212012130121401215012160121701218012190122001221012220122301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SW:61252386

61252386 description="Pesticidal crystal protein cryIaC (Insecticidal delta-endotoxin CryIC(a)) (Crystalline entomocidal protoxin) (134 kDa crystal protein)." library=NA species=Bacillus thuringiensis serovar entomocidus source="swissprot_prot" version=NA type=PRT

SCORES      Initl: 3103   Inittn: 5072   Opt: 3784   Z-score: 4293.1 E(): 0
>>SW:61252386
Initn: 5072   Inittl: 3103   opt: 3784   Z-score: 4293.1 expect(): 0
Smith-Waterman score: 5389;    68.9% identity in 1206 aa overlap
(1-1177:1-1189)

cryIa-105.pe  MNPNPNEICNPYCLNSPEVLEVLGGRIETGYTPIDISLSLQFLSEFVPAGFVLGL
        10      20      30      40      50
61252386     MEEN-NQNOCIPNCLNSPREVLLDGERISTGSSIDISLSLVQLVSNFVPGSGFLVGL
        10      20      30      40      50

cryIa-105.pe  VDIINGIFGSQWDAFLVQIEOLINQRIEGFARNQAISKLEGSLNLYQIAESFRWEAD
        70      80      90      100     110     120
61252386     IDFWGVIGVSQWDAFLVQIEOLINERIAEFARNAAIANLEGNGNFNYVEAFKEWEED
        70      80      90      100     110     120

cryIa-105.pe  PTNPALREEMRPIQFNDMNSALTATPTAFAVONTVOPLSVYVQAANHLHSLVRDVSVFGQ
        130     140     150     160     170     180
61252386     PNNPTRIVRIDRIDGGLDERDPSPRISGFEVPLSVYAQAANHLHALRLDRSDVFGE
        130     140     150     160     170     180

cryIa-105.pe  RWGFDAAITINSRYNDLTRILGNYTGHAVNTGLERVGPDSRDWRYNQOFRELTLTV
        190     200     210     220     230     240
61252386     RWGLTTINNVENYNRLIRHIDEYADHCANTNLRGLNNLPKSTYQDWITYNLRRDLTLTV
        190     200     210     220     230     240

cryIa-105.pe  LDIVSLFPNDSTRYPTRIVSQLTREIYTNPVLENTDFGRSGAG-----IGES-IRSP
        250     260     270     280     290
61252386     LDIAAFFENDNRRIPIQVGOLTREVYTDPLI-NFNPOLQSVAQLPTFNVMESSRIRNP
        250     260     270     280     290

cryIa-105.pe  HLMWDIANSITTYDADR-GE-YWGSHGIINASVPVSGPEFTFLVYGTMGAAPQORIVA
        300     310     320     330     340     350
61252386     HLFIDLNLNLITDFWSVGRNVPPGWGHVKSISLLIG--GGNITSPIYGREANQEPDPSRFI-
        300     310     320     330     340     350

cryIa-105.pe  QLCQGCVKRTLSTSLYR---RPNFIGNNQQLSLVDGTGEAYGTSNLPASVYRKSGTVDS
        360     370     380     390     400
61252386     -ENGPFVFTLSNPTRLQLQPWPAPPFN--LRGVEGVDFS--TPTN--SFTRYRGRTGVDS
        360     370     380     390     400

cryIa-105.pe  LDEIPPQNPNVPRQGSFHRLSHVSMF-RSGFSNSSVSIIRAMPFSWIHRSAEENNIIAS
        410     420     430     440     450     460
61252386     LTLELPDENSVPPREGYSFHRCLKHATFVQRSTGPLTATGVV----FSWTDRSATLTNTIDP
        410     420     430     440     450     460

cryIa-105.pe  DSITQIPLVKAHTLQSGTTYVWPGTGCDILRRTSGGFPAVTININGQLPQPYRARIR
        470     480     490     500     510     520
61252386     ERINOIPLVKGFVRWGMGTSVITPGFTGCDILRRNTDPEDVSLQVNINSITQYRURFR

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cry1a-105.pe 530 470 480 490 500 510 520 580
FASTNLRITVAVGERINAGQ-----FNKMTDGTDLTTFOSFYATINTATTFMSQ
61252386 YASSTDAVVIVGAAVGVGGQVNNLQKWEIGENTSTRTFRYDFNSFPFRANP
540 550 560 570 580
cry1a-105.pe 590 600 610 620 630
GUTPSGNEVAVRPELIPVTANRANLRAKAVNALFTSTNOLG
61252386 DIIGSEQPLFGAGSISG-EAYIKNLTIIATFAESDLERAKAVNALFTSSNOIG
590 600 610 620 630
cry1a-105.pe 640 650 660 670 680 690
LKTNTVDYHIDOVSNLVYLSDEFCLDKRSEKVNAAKRDERNLLQSNKDLNRQ
61252386 LKTDYDHYDQVSNLVDCLSDEFCLDKRELSKYNANLSDERNLLQSNKDLNRQ
650 660 670 680 690 700
cry1a-105.pe 700 710 720 730 740 750 760
PERGSGSTGTTIQGGDDVFKENYVTLSTGDECPYLYQKTSKAKFTNQASVYI
61252386 PORGRSGSTTITIQGGDDVFKENYVTLSTGDECPYLYQKTSKAKFTNQASVYI
710 720 730 740 750 760
cry1a-105.pe 760 770 780 790 800 810 820
EDSQLEIYIRYNAKHETVNVPGTGLWPLSAQSPGCKGEPNRCAPHLEWFDLQCC
61252386 EDQLEIYIRYNAKHETVNVPGTGLWPLSAQSPGCKGEPNRCAPHLEWFDLQCC
770 780 790 800 810 820
cry1a-105.pe 820 830 840 850 860 870
RQGECAHSHHFLDIDVCGTDLNEGLVWIFKIKTQDGHARLGNLEFLEKPLVGEA
61252386 RQGECAHSHHFLDIDVCGTDLNEGLVWIFKIKTQDGHARLGNLEFLEKPLVGEA
830 840 850 860 870 880
cry1a-105.pe 880 890 900 910 920 930
LARVKRAEKKWRDKREKLEWEINIVYKEAKESVDALFVNSQYDQLQADNTIAMIHAADKR
61252386 LARVKRAEKKWRDKREKLEWEINIVYKEAKESVDALFVNSQYDQLQADNTIAMIHAADKR
890 900 910 920 930
cry1a-105.pe 940 950 960 970 980 990
VHSIREAVLPESVIPGVNAAIFEELEGRIETAFSLYDARNVKNCGFNNGLSCWNVKGH
61252386 VHSIREAVLPESVIPGVNAAIFEELEGRIETAFSLYDARNVKNCGFNNGLSCWNVKGH
950 960 970 980 990
cry1a-105.pe 1000 1010 1020 1030 1040 1050
VQVEQNQRSLVLPWEAEVSQEVRCPCRGYILRVATYKGEYGEVGTIHEIENNTD
61252386 VQVEQNQRSLVLPWEAEVSQEVRCPCRGYILRVATYKGEYGEVGTIHEIENNTD
1010 1020 1030 1040 1050 1060
cry1a-105.pe 1060 1070 1080 1090 1100 1110
ELKFSNCVVEEIPYNNVTCTNDYTNQVEYGGATSNRNYNEA----PSPVADYASVYE
61252386 ELKFSNCVVEEIPYNNVTCTNDYTNQVEYGGATSNRNYNEA----PSPVADYASVYE
1070 1080 1090 1100 1110 1120
cry1a-105.pe 1120 1130 1140 1150 1160 1170
EKSYTDGRRENPCFNEGSDYTPLVGVVTKLEYFPETDKWIIEIGTEGTIVDSVE
61252386 EKSYTDGRRENPCFNEGSDYTPLVGVVTKLEYFPETDKWIIEIGTEGTIVDSVE
1170 1180 1190 1200 1210 1220

cry1a-105.pe 1130 1140 1150 1160 1170 1180
LLIMEE
61252386 LLIMEE
cry1a-105.pe
NRAA:18913153
18913153 source="GENBANK PROT" delta-endotoxin [Bacillus
thuringiensis]gi|19880135|gb|AA00264.1| insecticidal protein Cry1Ca [Bacillus
thuringiensis]
SCORES Initl: 3103 Initn: 5089 Opt: 3783 Z-score: 4292.0 E(): 0
>NRAA:18913153 (1189 aa)
Initn: 5089 Initl: 3103 Opt: 3783 Z-score: 4292.0 expect(): 0
Smith-Waterman score: 5406; 69.1% identity in 1206 aa overlap
(1-1177:1-1189)
cry1a-105.pe 10 20 30 40 50 60
MDNNPNNEICIPYNCLSNPEVEVLGGERIETGTPIDISLSTQFLSEFVPGAGFVLGL
18913153 MEEN-NQOCIPYNCLSNPEVEVLGGERIETGTPIDISLSTQFLSEFVPGAGFVLGL
10 20 30 40 50
cry1a-105.pe 60 70 80 90 100 110 120
IDFVNSITVPSQMDAFVQLVQIEQLINRIEETAFARNAQISRLGSLNLYIYAESFREWEAD
18913153 IDFVNSITVPSQMDAFVQLVQIEQLINRIEETAFARNAQISRLGSLNLYIYAESFREWEAD
60 70 80 90 100 110
cry1a-105.pe 120 130 140 150 160 170 180
PNNDAITRVIDREFLDGDLERDAPRISGFEVPLLSVYQAANLHLAILRDSVIFGE
18913153 PNNDAITRVIDREFLDGDLERDAPRISGFEVPLLSVYQAANLHLAILRDSVIFGE
120 130 140 150 160 170
cry1a-105.pe 180 190 200 210 220 230 240
RMGFDAATINSTRNDLRLTGATYDHAVRMNTGSERVWGPDSRDWRYNQFRRELTLTV
18913153 RMGFDAATINSTRNDLRLTGATYDHAVRMNTGSERVWGPDSRDWRYNQFRRELTLTV
180 190 200 210 220 230
cry1a-105.pe 250 260 270 280 290
LDIVSLFNYSRTPYRTVQSLTNTYNNVLENVQSPGSAQ-----IEGS-IRSP
18913153 LDIVSLFNYSRTPYRTVQSLTNTYNNVLENVQSPGSAQ-----IEGS-IRSP
240 250 260 270 280 290
cry1a-105.pe 300 310 320 330 340 350
HLMJLILNSITITDAHR-GE-VYWSGHOIMASPVGFSPESTFAYGTMDAIPORIVA
18913153 HLMJLILNSITITDAHR-GE-VYWSGHOIMASPVGFSPESTFAYGTMDAIPORIVA
300 310 320 330 340 350
cry1a-105.pe 360 370 380 390 400
QLGQGVYRTLSSTLYR---RPFNIGINNQLQSLVDLGTFFAYGTSSNLPSAVRSCVDS
18913153 QLGQGVYRTLSSTLYR---RPFNIGINNQLQSLVDLGTFFAYGTSSNLPSAVRSCVDS
360 370 380 390 400
cry1a-105.pe 410 420 430 440 450 460
-FNGPVFTLSNPTLRLQLQWPAPPFN--LRGVEGVFEFS--TPTN--SFTYRGEGTVDS
18913153 -FNGPVFTLSNPTLRLQLQWPAPPFN--LRGVEGVFEFS--TPTN--SFTYRGEGTVDS
410 420 430 440 450 460

```
cry1a-105.pe LDEIPPNVPPROGFSHRLSHVSMF-RSCFSNSVSIRAPMFSWIHRAEFNNIIAS
18913153 ILELPEDNSVPPREGYSHRLCHAFVQVSGTPLITGVV-----FSWTHRSATLNTIDP
410 420 430 440 450 460

cry1a-105.pe DSITQPLVKAHTLQSGTIVRGPGFTGGDILRRTSGGPAYTIVNNGQLPQRYRARIR
18913153 ERINGIPLVKGFVRWGTSVITGPGFTGGDILRRTSGGPAYTIVNNGQLPQRYRARIR
470 480 490 500 510 520

cry1a-105.pe YASTNLRIVV-TVAGERIPAGQ-----FNKTMDCDPLTFQTSYATINTAFTFPMQ
18913153 YASSRDARVILTGAASTGVGGQVSNMPLQKTEIGENLTSTFRYTDFSNPFSPRNP
530 540 550 560 570 580

cry1a-105.pe SSFTV-----GADTFSSGNEVDIRFELIPVTATLEAYNLERAKAVNALFTSTNQLG
18913153 DIIGISEQPLFGAGTSSG-ELYIDKIELLADATFEAESDLERAKAVNALFTSSNOIG
590 600 610 620 630 640

cry1a-105.pe LKTNVDYHIDQVSNLVYLSDEFCLDEKRELSKVHAKRUSDERNLQDSNFKDINRQ
18913153 LKTDVTDYHIDQVSNLVYLSDEFCLDEKRELSKVHAKRUSDERNLQDSNFKDINRQ
640 650 660 670 680 690 700

cry1a-105.pe PERGGSGTITIGGDDVFNENYVTLSTGDECPYLYOKIDESKLAFTRYCLRGYI
18913153 PGRWRSITITIGGDDVFNENYVTLSTGDECPYLYOKIDESKLAFTRYCLRGYI
710 720 730 740 750 760

cry1a-105.pe EDSQLEIYSIRYNAKHEIVNVFGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC
18913153 EDSQLEIYSIRYNAKHEIVNVFGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC
770 780 790 800 810 820

cry1a-105.pe RDEKCAHSHHFSIDIDVCGTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEA
18913153 RDEKCAHSHHFTLIDVCGTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEA
820 830 840 850 860 870 880

cry1a-105.pe LARVRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSOYDQLOADNTNIAMTHADKR
18913153 LARVRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSOYDQLOADNTNIAMTHADKR
880 890 900 910 920 930

cry1a-105.pe VHSIREAYLPESVPGVNAAFEELEGRIFTFASLYDARNVTKNGDFNGLSNVKGH
18913153 VHSIREAYLPESVPGVNAAFEELEGRIFTFASLYDARNVTKNGDFNGLSNVKGH
940 950 960 970 980 990 1000

cry1a-105.pe VDVEQNORSVLPVPEWEAEVSQEVRCFGRGYLLRYATKGGYGGCVTHIEENNTD
18913153 VDVEQNORSVLPVPEWEAEVSQEVRCFGRGYLLRYATKGGYGGCVTHIEENNTD
1000 1010 1020 1030 1040 1050

cry1a-105.pe VDVEQNHRSLVLPVPEWEAEVSQEVRCFGRGYLLRYATKGGYGGCVTHIEEDNTD
18913153 VDVEQNHRSLVLPVPEWEAEVSQEVRCFGRGYLLRYATKGGYGGCVTHIEEDNTD
1010 1020 1030 1040 1050 1060

cry1a-105.pe VDVEQNHRSLVLPVPEWEAEVSQEVRCFGRGYLLRYATKGGYGGCVTHIEEDNTD
18913153 VDVEQNHRSLVLPVPEWEAEVSQEVRCFGRGYLLRYATKGGYGGCVTHIEEDNTD
1060 1070 1080 1090 1100 1110
```

```
cry1a-105.pe ELKFSNCVEEIEYPNNVTICNDYTVNOEYGGAYTSRNGYNEA-----PSVPADYASVYE
18913153 ELKFSNCVEEIEYPNNVTICNNYTCGTQOEYEGTYSRNGQYDEAYGNPNPSVPADYASVYE
1070 1080 1090 1100 1110 1120

cry1a-105.pe EKSYYDGRRENPECFNRRGRDVTPLPGVYIVKLEFPEPKDKWIEIGETEGTIVDSVE
18913153 EKSYYDGRRENPECFNRRGRDVTPLPGVYIVKLEFPEPKDKWIEIGETEGTIVDSVE
1120 1130 1140 1150 1160 1170 1180

cry1a-105.pe LLLMEE
18913153 LLLMEE

cry1a-105.pe
SW:8488968

8488968 description="PESTICIDIAL CRYSTAL PROTEIN CRYICA (INSECTICIDIAL
DELTA-ENDOTOXIN CRYIC(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (I34 KDA CRYSTAL
PROTEIN)." library="NA Species="Bacillus thuringiensis serovar aizawai"
source="swissprot_prot" version="NA type="PRI

SCORES Init1: 3103 Initn: 5089 Opt: 3783 z-score: 4292.0 E(): 0
>>SW:8488968
initn: 5089 init1: 3103 opt: 3783 z-score: 4292.0 expect(): 0
Smith-Waterman score: 5406; 69.1% identity in 1206 aa overlap
(1-1177:1-1189)

cry1a-105.pe MDNNPINECPYNCNLSNPEVEVLGGERIETGYTPIDISLSLTFQLLSEFVFCAGFVLGL
8488968 MEEN-NQOCTPYNCNLSNPEVEVLGGERISTGSSIDISLSLQVFLVSNFVPGGFLVGL
10 20 30 40 50 60

cry1a-105.pe VDIIMGIFQPSQWDAFLVQIEQLINORIEEFARNOAISRLGLSNLYQIYAESFREMEAD
8488968 IDEVWGIYQPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKENEED
70 80 90 100 110 120

cry1a-105.pe PTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYQAAHLNLSLRDVSFQG
8488968 PNPATRTVIDRFRIIDGLERDIPSFRIISGFEVPLLSVYQAAHLNLSLRDVSFQ
130 140 150 160 170 180

cry1a-105.pe RWCFDAIINRSYNDLTRLGNVTDAVFWNTGLERWGWGSDSDMIRYNQFRRLITV
8488968 RWGLTITINVNENRLRIHIDEADHCANTYRNLGNLNPDKSTYQDWTITNRRLDLITV
190 200 210 220 230 240

cry1a-105.pe LDIVSFNPNRSRTVPRTVTSQLTREIYTNPVLENFDCSFRGSAQG-----IEGS-IRSP
8488968 LDIAAFNPNDRNRYFPQVQQLTREYTDPLI-NFNPLQSVQAQLPTFNVMESAIRNP
250 260 270 280 290 300

cry1a-105.pe HLMIDLINSTITYDAHR-GE-YWWSGHIAMASVFGSPFTFPLTYGTMGNAAPQORIVA
18913153 HLMIDLINSTITYDAHR-GE-YWWSGHIAMASVFGSPFTFPLTYGTMGNAAPQORIVA
310 320 330 340 350
```

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8488968 HLFDLNLNLTIDNESVGRFYWGHRVLISSLLG--GGNITSPYIGREANQPPRSFT-
300 310 320 330 340 350
cryla-105.pe QISGVYRKSSTVYR---RPNIGIINNOQLSVLDGTEFAYGTSSNPSAVYKSGTIDS
360 370 380 390 400
8488968 -PNSGVENTSNPILVLLDQPPAPPN--LRGVEGVFES--TPTN--SFTYRGRGTIDS
360 370 380 390 400
cryla-105.pe LDETPQNNVPQGFSEHLSHVM--SGFSSNSVGLIRPMSVHRSAPENNLIAS
410 420 430 440 450 460
8488968 LTELPPEDNSVPPREGYSRHCATFVORSSTPPLTTGVV--FSWTHRSATLINTIDP
410 420 430 440 450 460
cryla-105.pe DSITQIPLVKAHTLQSGTTVVRGPGFTGCDLRLATSGGPFATVYNNINGQDLPYRARR
470 480 490 500 510 520
8488968 ERINOIPLVGFVWGTSVITGPGFTGCDLRLATSGGPFATVYNNINGQDLPYRARR
470 480 490 500 510 520
cryla-105.pe YASTNLRIVY-TVAGERIFAGQ-----FNKMTDGDPLTFQSTVATNTAFVPMGQ
530 540 550 560 570 580
8488968 YASSRDARVILVTCGAAGTGGVGVQSVNMPLOKMTWEGENLTSTRTYDFSNPMSFRANP
530 540 550 560 570 580
cryla-105.pe SSFTV-----GATFSSGNEVYIDRFELIPVATLAEVNLERAKAVNALFTSTNOLG
590 600 610 620 630
8488968 DIIGISEQPLFGAGSSSG-ELYIDKIEIILADATFPAESDULERAKAVNALFTSSNOIG
590 600 610 620 630
cryla-105.pe LKNTVDYHIDQVSNLVTLSDEFCLDEKRELSKVHAKRLSDERNLLQDSNFKDINRQ
640 650 660 670 680 690
8488968 LKNTVDYHIDQVSNLVTLSDEFCLDEKRELSKVHAKRLSDERNLLQDSNFKDINRQ
640 650 660 670 680 690
cryla-105.pe PERGWGSGTITIQGGDDVFKENYVTLSTGTECYPTLYQKIDESKUKATRYQLRGYI
700 710 720 730 740 750
8488968 PDGRWGSSTITIQGGDDVFKENYVTLSTGTECYPTLYQKIDESKUKATRYQLRGYI
700 710 720 730 740 750
cryla-105.pe EDSQLETYSRYNAKHETVNVPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC
760 770 780 790 800 810
8488968 EDSQLEIYLIRNAKHEIVNVPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSC
760 770 780 790 800 810
cryla-105.pe RDGEKCAHSHHSFLDIDVGCTDLNEDLGWVIFPKIQDGHARLGNLEFLEEXPLVGEA
820 830 840 850 860 870
8488968 RDGEKCAHSHHSFLDIDVGCTDLNEDLGWVIFPKIQDGHARLGNLEFLEEXPLVGEA
820 830 840 850 860 870
cryla-105.pe LARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQADNTNAMIHAADKR
880 890 900 910 920 930
8488968 LARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQADNTNAMIHAADKR
880 890 900 910 920 930
cryla-105.pe VHSIREAVLPESVPGVNAAIPEELGRIFTAYSIDYARNVTKNGDFNGLLCWNVKGH
940 950 960 970 980 990

8488968 VHSIREAVLPESVPGVNAAIPEELGRIFTAYSIDYARNVTKNGDFNGLLCWNVKGH
950 960 970 980 990
cryla-105.pe VDFEQNNQSRSLVLPWEPWAEVSEVGRVCFGRGYILLRTAYKEGYGGCVTIHEINNTD
1000 1010 1020 1030 1040 1050
8488968 VDFEQNNHRSVLVLPWEPWAEVSEVGRVCFGRGYILLRTAYKEGYGGCVTIHEINNTD
1010 1020 1030 1040 1050 1060
cryla-105.pe ELKSNVCVEEIVPNNVTTCNDYTVNQEYGGAYTSRNGYNEA----PSVPADYASVYE
1060 1070 1080 1090 1100 1110
8488968 ELKSNVCVEEIVPNNVTTCNDYTVNQEYGGAYTSRNGYNEA----PSVPADYASVYE
1070 1080 1090 1100 1110 1120
cryla-105.pe EKSXTDGRRENPCFNRGYRDTPLPGVYTKLEYFPETDKVWIEIGETEGTFIVDSVE
1120 1130 1140 1150 1160 1170
8488968 EKSXTDGRRENPCFNRGYRDTPLPGVYTKLEYFPETDKVWIEIGETEGTFIVDSVE
1130 1140 1150 1160 1170 1180
cryla-105.pe LLMEE
1190
8488968 LLMEE
1190
cryla-105.pe LLMEE
1190
7141141 Source="GENBANK_PROT" toxin CrylCa6 [Bacillus thuringiensis]
Scores Initl: 3100 Initl: 5080 Opt: 3776 z-score: 4284.0 E(): 0
>NBA:7141141
Initl: 5080 Initl: 3776 z-score: 4284.0 expect(): 0
Smith-Waterman score: 3397; 68.8% identity in 1206 aa overlap
(1-1177:1-189)
cryla-105.pe MDNNPNECPYNCSSQPSVVLGGENETVTPIDISLSTQFLSEFVPGAGFVLGL
10 20 30 40 50 60
7141141 MEEN-NOQCIPNCSNPEVLPDPSISTGSGSISLSLVQFLVSNFVPGGFLVGL
10 20 30 40 50
cryla-105.pe VDIWIGFSPQMDALVOLEKINSLRLEENKQASRLGEGNLSLQIYAESFREWED
60 70 80 90 100 110 120
7141141 IDFWVGIVGPSQMDALVQLQELINERDESRNAAQVCEVGNFNFTYTPAFKEWED
60 70 80 90 100 110 120
cryla-105.pe PTNPALREEMRIQFNDMNSALATAPLFAVQVQVPLSVYQAANLHISQSDVSPQ
130 140 150 160 170 180
7141141 PNPATRTVIDRFRILDLGLDERDIPSPRISGFEVPLLSVYQALHIALILQVPLIGE
120 130 140 150 160 170 180
cryla-105.pe RNFQDAATINSRNDLTRILGNVTHVAVRWINTGLERWGPSPRWIKINGFRELDTV
190 200 210 220 230 240
7141141 RNFQDAATINSRNDLTRILGNVTHVAVRWINTGLERWGPSPRWIKINGFRELDTV
180 190 200 210 220 230
cryla-105.pe LDIVSLFNFYDSRTYPIRTVSQLTREITVNPVLENFDGSPRGSAGQ-----IRSP
250 260 270 280 290

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[illegible]

[illegible]

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```
60 70 80 90 100 110
cryla-105.pe PTPALREEMRIQFNWNSALATTAIPLEAVONVQVPLLSVYQOANLHLVLRDVSVEGO 180
61252387 PNPATRIYRVIDRFDRIIDGLLEERDIPSPRISGFVEVLVSVAQOANLHLALRDSVIFGE 170
120 130 140 150 160 170
cryla-105.pe RWGFDAAATINRNDLTRIGNYTDHVRWYNTGLERVMQPSRDMIRYNFRRELTIV 240
61252387 RGLTITINVENYNNLRIHIDEVADHCANTYNRGLNLPKSTYQDMITYNLRDLTLTV 230
180 190 200 210 220 230
cryla-105.pe LDIVSLFNYDSRTYPIRTVSQLTRIEITYNPNVLENFNGSPRGAQ-----IEGS-IRSP 290
61252387 LDIAAFFNYDNRRYPIQVPVQLTREVYTDLI-NFNPOQSVAQLFTFNWMESSAIRNP 280
240 250 260 270 280 290
cryla-105.pe HLMIDILNSITITDAHR-GE-YWGSCHOIMASPVGFGSPEFTPEPLVGTMGNAAPQOQIVIA 350
61252387 HLFIDILNLLITFDWFSVGRNFWGHRVIVSSLLIG--GNITSPYIGREANQOEPFRSFT- 340
300 310 320 330 340 350
cryla-105.pe QLGQGVYRTLSTLYR---RPFNIGINNQQLSVLDGTGTEFAYGTSNLPSAVYRKSQTVDS 400
61252387 FNGVFRTLSNPTLRLLQOPWAPPFN--LRGVEGVES--TPTN--SFTYRGRGTVDS 390
360 370 380 390 400
cryla-105.pe LDEIPQNNVPPRQGSFRLSHVSMF-RSGFNSSVSIIRAPMFWHRSFENFIAS 460
61252387 LTLPPEPNSVPPREGYSHLCHATFVORSGTFLTTGVV---FSWTHRSATLITDIP 450
410 420 430 440 450 460
cryla-105.pe DSTOIPLVKAHTLOSQTIVVRGPGFTGGDILRRTSGGPFAYTIVNINQOLPQRYRIR 520
61252387 ERINOLPLVKGFRVWGTSVITGPGFTGGDILRRTSGGPFAYTIVNINQOLPQRYRIR 510
470 480 490 500 510 520
cryla-105.pe YASTNLRIVY-TVAGERIFAG-----FNKTMGTGDLPTFOSFYATINTAFPMQ 580
61252387 YASSRDARVILVTGAATSTGVGGQSVNMFLOKMEIGENLTSRTFRYTDSPNPFSSFRANP 570
530 540 550 560 570 580
cryla-105.pe SFTV-----GADTFSSGNEVYDFELIPVATLEAEYNLERAKAVNALFTSNOLG 630
61252387 DIIGISEQLFGAGSISG-ELYIDKIEILLADATFEAESDRLERAKAVNALFTSSNOIG 620
590 600 610 620 630
cryla-105.pe LKNTVDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLQDSNFQDINRQ 690
61252387 LKTDVDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLQDSNFQDINRQ 680
640 650 660 670 680 690
cryla-105.pe PERGWGSGTIGQGGDDVFKENYVTLSTGTFDECYPTLYQKIDESKLAFRYQLRGIYI 750
61252387 PDRGWRGSGTIDITIQGGDDVFKENYVTLPGTVDECYPTLYQKIDESKLAFRYQLRGIYI 740
700 710 720 730 740 750
```

```
760 770 780 790 800 810
cryla-105.pe EDSQLEIYSIRYNKXHEITVNVPGTGSLLWPLSAQSPIGKGPENRCAPHLEWNPDLDCSC 810
61252387 EDSQLEIYLIRYNKXHEITVNVPGTGSLLWPLSAQSPIGKGPENRCAPHLEWNPDLDCSC 820
770 780 790 800 810 820
cryla-105.pe RDGEKCAHSHHSLDIDVGCCTDLNEDLGVWVIFKIKTQGHARLGNLEFLEKPLVGEA 870
61252387 RDGEKCAHSHHFTLDIDVGCCTDLNEDLGLWVIFKIKTQGHARLGNLEFLEKPLVGEA 880
830 840 850 860 870 880
cryla-105.pe LARVYRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSOYDQLOADNTIAMIAADKR 930
61252387 LARVYRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSOYDQLOADNTIAMIAADKR 940
890 900 910 920 930 940
cryla-105.pe VHSIREAVLPESLVPICVNAAIPEELEGRIFTATSLYDARNVKNKGFNNGLSWNVKGH 990
61252387 VHSIREAVLPESLVPICVNAAIPEELEGRIFTATSLYDARNVKNKGFNNGLSWNVKGH 1000
950 960 970 980 990 1000
cryla-105.pe VDVEQNQRSLVLPVEAEVSQEVVRVCPGRGYILRVTAKEGYGEGCVTHIEINNTD 1050
61252387 VDVEQNQRSLVLPVEAEVSQEVVRVCPGRGYILRVTAKEGYGEGCVTHIEINNTD 1060
1010 1020 1030 1040 1050 1060
cryla-105.pe ELKFSNCVVEEIVYNNVTNDYVNOEYGGAYTSNRGNEA---PSVPADYASVYE 1110
61252387 ELKFSNCVVEEIVYNNVTNDYVNOEYGGAYTSNRGNEA---PSVPADYASVYE 1120
1070 1080 1090 1100 1110 1120
cryla-105.pe EKSYTDGRRENPCENRGYDYTPLPVGVYTKLEYFPETDKVWIEIGETGTFIVDSVE 1170
61252387 EKSYTDGRRENPCENRGYDYTPLPVGVYTKLEYFPETDKVWIEIGETGTFIVDSVE 1180
1130 1140 1150 1160 1170 1180
cryla-105.pe LLMEE 1190
61252387 LLMEE 1180
cryla-105.pe LLMEE 1190
61252387 LLMEE 1180
61252387 description="Pesticidal crystal protein crylCa (Insecticidal
delta-endotoxin CryIC(a)) (Crystalline entomocidal protoxin) (134 kDa crystal
protein)." library="NA species="Bacillus thuringiensis serovar aizawai"
source="swissprot_prot" version="NA type="PRT
SCORES Initl: 3085 Initn: 5071 Opt: 3765 Z-score: 4271.5 E(): 0
>>SW.61252387
Initn: 5071 initl: 3085 opt: 3765 Z-score: 4271.5 expect(): 0
Smith-Waterman score: 5388; 68.8% identity in 1206 aa overlap
(1-1177:1-1189)
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cry1a-105.pe MDNPNVNCSPYCNLSREVEVLGGERITGYTPIDLSLSLQFLLSBVEFGAGVLGIG
61252387 MEEN-RONGQVYCNLSREVEVLGGERITGSSSIDLSLQFLVSNFVPGGGFLVGL
cry1a-105.pe VDIWCHGSGSOWDAPFQIQLINORIEFANNOAISRLGSLNLYIYASFREWHEAD
61252387 IDFWMGIVGSGSDANLUVQIEQUMERTAEFFARMALNLEGNGNNVYVAFKWEEMED
cry1a-105.pe PTPPALREEMRIQFNDMSALTAIILFAVONQALSLVSVQVNLKSLVRDVSFVGQ
61252387 PNNPATRTVAIDRFILDLGLERDISLSEFEVPEL SVVQANLHLKILLRDSVIGE
cry1a-105.pe RWGFDAATINSRYNDLTLRIGNYTDHAYVNTGLRWGSDGSRDWTYNOFRETLLTV
61252387 RWGLTTINVENYNELRIHDEYADHCAHYNRYGLNNLPKSTYQDNTYNNRLKDLTV
cry1a-105.pe LDIVSLFPNYDSRTYPIRTYSQLTREIYNPVLNFDGSRGSAQ-----TSGS-RSP
61252387 LQIAAFPNYDNRRIPIQVQGLTRVEYTDPLI-NFNPOLQSVLAQLPTFRNVMSAIPNP
cry1a-105.pe HLMDLINSITIVTDAAHR-GE-YVMSGHQIMAGSPVGSFGEPTFLYLYTGMNAAPQIRVA
61252387 HLFDLNLNLTITDFWFSYGRNFWYGHRRVLSLIG--GNNLTSPYIGREANOEPREST-
cry1a-105.pe QLOGGYRTLSLTLYR--RPFNIGNNQOLSVDLTGEFAYGTSSNLPASVYKSGTVDS
61252387 -FNGVPFRTLSNPTLLRQFPWAPPFN--LRGVEGVFVS--TPTN--SFTYRGRGTVD
cry1a-105.pe LDEIIPQNNVNPPOGFSHRLSHVSMF-RSGSNSSVSIIIPAMFSWIRSHSEFNIIIAS
61252387 LTELPPEDNSVPPREGYSHRLCHAFVQSGRTPLTTGV----FSWTHRSATLNTIDP
cry1a-105.pe DSITQIPLVKAHTLOSGTIVVRGPGTGGDILRRTSGGPFAYTIVNINQOLPORVARIR
61252387 ERINQIPLVKGRFVWGGSVITPGTGTDILRRNTFGDVSLOVNNINSPIQRYELAFRR
cry1a-105.pe YASTWNLRIYV-TVAGERIFAQ-----FNKMTDGDPLTFSFYSATINTAFTPFMSQ
61252387 YASRDARVILVTGAASTGVGGVGSVNNMPLQKMTWIEGNLTSTRFTYDFSNPFPSFRANP
cry1a-105.pe SSTTV-----GADTFSSGNEVIDRFELIPVATLEAYNLRQAQVNNALFTTINQOL
61252387 DIGISEQPLFGAGSISGG-ELYIDKIEILADATFEASDLERQAQVNNALFTTINQOL

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cyla-105.pe LKNTVDYHIDQVSNLVTYLSDFCLDEKRELSEVKHAKSLDERNLQDNFQINR 650 660 670 680 690
61252387 LKTDVTDYHIDQVSNLVDCLSDFCLEKRELSEVKHAKSLDERNLQDNFQINR 650 660 670 680 690 700

cyla-105.pe PERGGSTGIIQGGDDVFKENVTLSGTDFECPTTYLYOKIDSKLAFTRYOLRY 700 710 720 730 740 750
61252387 PDWRGSGTDIIQGGDDVFKENVTLPOTVDECPTTYLYOKIDSKLAFTRYOLRY 710 720 730 740 750 760

cyla-105.pe EDSODLEIYSRYNAKHETNVPGTSLWPLSAQSPICKGCPNRCAPHLENNPDLDCS 760 770 780 790 800 810
61252387 EDSODLEIYIRYNAKHETNVPGTSLWPLSAQSPICKGCPNRCAPHLENNPDLDCS 770 780 790 800 810 820

cyla-105.pe RDGEKCAHSHHFSLDIDVGCTDNLNEDGLVWIFIKTDQGHARLGNLEFBEKPLVGEA 820 830 840 850 860 870
61252387 RDGEKCAHSHHFTLIDVGCTDNLNEDGLVWIFIKTDQGHARLGNLEFBEKPLVGEA 830 840 850 860 870 880

cyla-105.pe LARVKRAEKWRDKREKLEWTETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHAADR 880 890 900 910 920 930
61252387 LARVKRAEKWRDKREKLEWTETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHAADR 890 900 910 920 930 940

cyla-105.pe VHRIRKALPELSVIPGYNVAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLLCNVKXGH 940 950 960 970 980 990
61252387 VHRIRKALPELSVIPGYNVAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLLCNVKXGH 950 960 970 980 990 1000

cyla-105.pe YDVEEQVQSVLVVYPENAFINVOYRVCPRGYILRTVAYKEGYGECVTTIETENNMT 1000 1010 1020 1030 1040 1050
61252387 YDVEEQVQSVLVVYPENAFINVOYRVCPRGYILRTVAYKEGYGECVTTIETENNMT 1010 1020 1030 1040 1050 1060

cyla-105.pe ELKFSNCVEEVPNNPTTCNNYGTGTPGPRYTSYRGEAYGNNSVPADVASVE 1060 1070 1080 1090 1100 1110
61252387 ELKFSNCVEEVPNNPTTCNNYGTGTPGPRYTSYRGEAYGNNSVPADVASVE 1070 1080 1090 1100 1110 1120

cyla-105.pe EKSVTGGRNCPENRGYRDYPLPGVYKELESPWVWIEFTKSTFTVDSVE 1120 1130 1140 1150 1160 1170
61252387 EKSVTGGRNCPENRGYRDYPLPGVYKELESPWVWIEFTKSTFTVDSVE 1130 1140 1150 1160 1170 1180

cyla-105.pe LLMEE 1180
61252387 LLMEE 1180

cyla-105.pep 42717976 source="GENBANK PROT" cy1aACAT modified toxin (synthetic construct)
NRRA:42717976

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SCORES Initl: 3130 Initn: 3741 Opt: 3752 z-score: 4260.5 E(): 0
>>NRAA:42717976
Initn: 3741 initl: 3130 opt: 3752 z-score: 4260.5 expect(): 0
Smith-Waterman score: 3752; 85.6% identity in 679 aa overlap
(1-674:1-675)

cryla-105.pe MDNPNINICIPYCNLSNPEVEVLGGERTGTPTIDISLSLTQFLLSFVPGAGVLGL 60
42717976 MDNPNINICIPYCNLSNPEVEVLGGERTGTPTIDISLSLTQFLLSFVPGAGVLGL 60
70 80 90 100 110 120
cryla-105.pe VDIIWGIFGQSDAFLVQIEQLINQRIEFARNQAIKRLGSLNLYQIYAESFREWAD 120
42717976 VDIIWGIFGQSDAFLVQIEQLINQRIEFARNQAIKRLGSLNLYQIYAESFREWAD 120
70 80 90 100 110 120
cryla-105.pe PTNPALREEMRIQFNDMNSALTTAIPLFVQYQVPLSVYQAAHLHSLVLRDVSFQ 180
42717976 PTNPALREEMRIQFNDMNSALTTAIPLFVQYQVPLSVYQAAHLHSLVLRDVSFQ 180
130 140 150 160 170 180
cryla-105.pe RWGFDAAATINSRNDLTRIGNYTDHVRWYNTGLERWVGPDSDRWYRQFRELTLTV 240
42717976 RWGFDAAATINSRNDLTRIGNYTDHVRWYNTGLERWVGPDSDRWYRQFRELTLTV 240
190 200 210 220 230 240
cryla-105.pe LDIIVSLFPNDSTRTYPIRTVSQLTREIYTNPVLENDFSGSAGGERSIRSPHMDIL 300
42717976 LDIIVSLFPNDSTRTYPIRTVSQLTREIYTNPVLENDFSGSAGGERSIRSPHMDIL 300
250 260 270 280 290 300
cryla-105.pe NSITIIDAHRGYYWMSGHQMASPVGFGSGPEFTPLGYTMGNAAPQORIVAGLGQGVYR 360
42717976 NSITIIDAHRGYYWMSGHQMASPVGFGSGPEFTPLGYTMGNAAPQORIVAGLGQGVYR 360
310 320 330 340 350 360
cryla-105.pe TLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSNLPASVYKSGTVDLSDEIPQNNV 420
42717976 TLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSNLPASVYKSGTVDLSDEIPQNNV 420
370 380 390 400 410 420
cryla-105.pe PPROGFSHRLSHVMSFRSGFNSSVSIIRAPMFSWHRSAEENIILASDSTIOLPLVKAH 480
42717976 PPROGFSHRLSHVMSFRSGFNSSVSIIRAPMFSWHRSAEENIILASDSTIOLPLVKAH 480
430 440 450 460 470 480
cryla-105.pe TLQSGTIVVRGPGFTGGDILRLRTSGGPFVAT--IVNINGQLPQ---RYRARIYASTML 530
42717976 FLFNGS-VISGPGFTGGDILRLVRLNNGNNIONRGVIEVPHTFSTSTRYRVRVRYASTPI 530
490 500 510 520 530
cryla-105.pe RIYTVAGERIFAGQFNKMTDGLPTQFSFATINTAFTPMQSSFTVGADITSSGN 590
42717976 HLNVNMGNSIFSNFTVPATATSLDNLQSSDFGFESANAFSTSLGN---IVGVNFSGTA 590
540 550 560 570 580 590
```

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cryla-105.pe EVIDRFELIPVTATLEAEYNLRAAKAVNALFTSTNQLGKTNVDYHIDQVSNLVTYL 600
42717976 GVILDRFELIPVTATLEAEYNLRAAKAVNALFTSTNQLGKTNVDYHIDQVSNLVTYL 600
610 620 630 640 650
cryla-105.pe SDFECLDEKRELSKVKHAKRLSDERNLQDSNFKDINRQPERGWGSGTITIQGDDVVF 710
42717976 SDFECLDEKRELSKVKHAKRLSDERNLQDSNFKDINRQPERGWGSGTITIQGDDVVF 710
660 670 680 690 700 710
cryla-105.pep
NRAA:208155
208155 source="GENBANK_PROT" cryIA(a)

SCORES Initl: 3622 Initn: 3622 Opt: 3622 z-score: 4113.3 E(): 0
>>NRAA:208155
Initn: 3622 initl: 3622 opt: 3622 z-score: 4113.3 expect(): 0
Smith-Waterman score: 3622; 88.9% identity in 615 aa overlap
(1-615:1-615)

cryla-105.pe MDNPNINICIPYCNLSNPEVEVLGGERTGTPTIDISLSLTQFLLSFVPGAGVLGL 60
208155 MDNPNINICIPYCNLSNPEVEVLGGERTGTPTIDISLSLTQFLLSFVPGAGVLGL 60
10 20 30 40 50 60
cryla-105.pe VDIIWGIFGQSDAFLVQIEQLINQRIEFARNQAIKRLGSLNLYQIYAESFREWAD 120
208155 VDIIWGIFGQSDAFLVQIEQLINQRIEFARNQAIKRLGSLNLYQIYAESFREWAD 120
70 80 90 100 110 120
cryla-105.pe PTNPALREEMRIQFNDMNSALTTAIPLFVQYQVPLSVYQAAHLHSLVLRDVSFQ 180
208155 PTNPALREEMRIQFNDMNSALTTAIPLFVQYQVPLSVYQAAHLHSLVLRDVSFQ 180
130 140 150 160 170 180
cryla-105.pe RWGFDAAATINSRNDLTRIGNYTDHVRWYNTGLERWVGPDSDRWYRQFRELTLTV 240
208155 RWGFDAAATINSRNDLTRIGNYTDHVRWYNTGLERWVGPDSDRWYRQFRELTLTV 240
190 200 210 220 230 240
cryla-105.pe LDIIVSLFPNDSTRTYPIRTVSQLTREIYTNPVLENDFSGSAGGERSIRSPHMDIL 300
208155 LDIIVSLFPNDSTRTYPIRTVSQLTREIYTNPVLENDFSGSAGGERSIRSPHMDIL 300
250 260 270 280 290 300
cryla-105.pe NSITIIDAHRGYYWMSGHQMASPVGFGSGPEFTPLGYTMGNAAPQORIVAGLGQGVYR 360
208155 NSITIIDAHRGYYWMSGHQMASPVGFGSGPEFTPLGYTMGNAAPQORIVAGLGQGVYR 360
310 320 330 340 350 360
cryla-105.pe TLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSNLPASVYKSGTVDLSDEIPQNNV 420
208155 TLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSNLPASVYKSGTVDLSDEIPQNNV 420
370 380 390 400 410 420
```

370 380 390 400 410 420
cry1a-105.pe PPRQGFSHRLSHVSVFSGFNSVSIIRAPMFSWIHSAEFNNIIASDSITQIPLVKAH
208155 PPRQGFSHRLSHVSVFSGFNSVSIIRAPMFSWIHSAEFNNIIASDSITQIPLVKAH
208155 PPRQGFSHRLSHVSVFSGFNSVSIIRAPMFSWIHSAEFNNIIASDSITQIPLVKAH
cry1a-105.pe TLOGSTVVRGPGFTGGDILRRYGGPFAYTVNNGQLPQRYRIRYASTINRIYVT
208155 TLOGSTVVRGPGFTGGDILRRYGGPFAYTVNNGQLPQRYRIRYASTINRIYVT
208155 TLOGSTVVRGPGFTGGDILRRYGGPFAYTVNNGQLPQRYRIRYASTINRIYVT
cry1a-105.pe VAGERIFAGQFNKMTDGDPLTFQSFYATINTAFTPMSSQSFYAGADTFSSGNEVID
208155 VAGERIFAGQFNKMTDGDPLTFQSFYATINTAFTPMSSQSFYAGADTFSSGNEVID
208155 VAGERIFAGQFNKMTDGDPLTFQSFYATINTAFTPMSSQSFYAGADTFSSGNEVID
cry1a-105.pe RFLPILVTALEAEYNLERAKAVNALFTSTNQLGLKTNVTDHIDQVSNLYTSLDEFC
208155 RFLPILVTALEAEYNLERAKAVNALFTSTNQLGLKTNVTDHIDQVSNLYTSLDEFC
208155 RFLPILVTALEAEYNLERAKAVNALFTSTNQLGLKTNVTDHIDQVSNLYTSLDEFC
cry1a-105.pe
NRAA:36244769
36244769 source="GENBANK_PROT" Cry1Ab1 [synthetic construct]
SCORES Init1: 3607 Initn: 3607 Opt: 3619 z-score: 4109.9 E(): 0
>NRAA:36244769
initn: 3607 init1: 3607 opt: 3619 z-score: 4109.9 expect(): 0
Smith-Waterman score: 3619; 88.7% identity in 617 aa overlap
(1-617:1-617)
cry1a-105.pe MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSFVFGAGFVLGL
36244769 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSFVFGAGFVLGL
36244769 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSFVFGAGFVLGL
cry1a-105.pe VDIIMGIFGSPQMDAFLVQIEQLINQRIEFAFARQAISRLEGSLNLYQIYAESFREWAD
36244769 VDIIMGIFGSPQMDAFLVQIEQLINQRIEFAFARQAISRLEGSLNLYQIYAESFREWAD
36244769 VDIIMGIFGSPQMDAFLVQIEQLINQRIEFAFARQAISRLEGSLNLYQIYAESFREWAD
cry1a-105.pe PTNPALREEMRIQFNDMNSALITTAIPFAVQNYQVPLLSVVOAANLHLSVLVDVSVFGQ
36244769 PTNPALREEMRIQFNDMNSALITTAIPFAVQNYQVPLLSVVOAANLHLSVLVDVSVFGQ
36244769 PTNPALREEMRIQFNDMNSALITTAIPFAVQNYQVPLLSVVOAANLHLSVLVDVSVFGQ
cry1a-105.pe RMGFDAAATINSRYNDLTRLIQNYTHAVRWYNTGLERWVGPDSDRWIRYQNFRELTIV
36244769 RMGFDAAATINSRYNDLTRLIQNYTHAVRWYNTGLERWVGPDSDRWIRYQNFRELTIV
36244769 RMGFDAAATINSRYNDLTRLIQNYTHAVRWYNTGLERWVGPDSDRWIRYQNFRELTIV
cry1a-105.pe LDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDFGSRGSAQGTGEGSIRSPHMDIL
LDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDFGSRGSAQGTGEGSIRSPHMDIL

36244769 LDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDFGSRGSAQGTGEGSIRSPHMDIL
250 260 270 280 290 300
cry1a-105.pe NSITITDARHGEYWSHQIMASPVGFGPEFTPLTGTGNGNAAPQORIVLAQLGGVYR
36244769 NSITITDARHGEYWSHQIMASPVGFGPEFTPLTGTGNGNAAPQORIVLAQLGGVYR
36244769 NSITITDARHGEYWSHQIMASPVGFGPEFTPLTGTGNGNAAPQORIVLAQLGGVYR
cry1a-105.pe TLOGSTVVRGPGFTGGDILRRYGGPFAYTVNNGQLPQRYRIRYASTINRIYVT
36244769 TLOGSTVVRGPGFTGGDILRRYGGPFAYTVNNGQLPQRYRIRYASTINRIYVT
36244769 TLOGSTVVRGPGFTGGDILRRYGGPFAYTVNNGQLPQRYRIRYASTINRIYVT
cry1a-105.pe PPRQGFSHRLSHVSVFSGFNSVSIIRAPMFSWIHSAEFNNIIASDSITQIPLVKAH
36244769 PPRQGFSHRLSHVSVFSGFNSVSIIRAPMFSWIHSAEFNNIIASDSITQIPLVKAH
36244769 PPRQGFSHRLSHVSVFSGFNSVSIIRAPMFSWIHSAEFNNIIASDSITQIPLVKAH
cry1a-105.pe TLOGSTVVRGPGFTGGDILRRYGGPFAYTVNNGQLPQRYRIRYASTINRIYVT
36244769 TLOGSTVVRGPGFTGGDILRRYGGPFAYTVNNGQLPQRYRIRYASTINRIYVT
36244769 TLOGSTVVRGPGFTGGDILRRYGGPFAYTVNNGQLPQRYRIRYASTINRIYVT
cry1a-105.pe VAGERIFAGQFNKMTDGDPLTFQSFYATINTAFTPMSSQSFYAGADTFSSGNEVID
36244769 VAGERIFAGQFNKMTDGDPLTFQSFYATINTAFTPMSSQSFYAGADTFSSGNEVID
36244769 VAGERIFAGQFNKMTDGDPLTFQSFYATINTAFTPMSSQSFYAGADTFSSGNEVID
cry1a-105.pe RFLPILVTALEAEYNLERAKAVNALFTSTNQLGLKTNVTDHIDQVSNLYTSLDEFC
36244769 RFLPILVTALEAEYNLERAKAVNALFTSTNQLGLKTNVTDHIDQVSNLYTSLDEFC
36244769 RFLPILVTALEAEYNLERAKAVNALFTSTNQLGLKTNVTDHIDQVSNLYTSLDEFC
cry1a-105.pe
NRAA:60308967
60308967 source="GENBANK_PROT" translated Cry1Ac [Bacillus thuringiensis serovar
kenyae]
SCORES Init1: 3107 Initn: 3107 Opt: 3567 z-score: 4050.4 E(): 0
>NRAA:60308967
initn: 3107 init1: 3107 opt: 3567 z-score: 4050.4 expect(): 0
Smith-Waterman score: 3567; 84.0% identity in 662 aa overlap
(1-657:1-657)
cry1a-105.pe MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSFVFGAGFVLGL
60308967 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSFVFGAGFVLGL
60308967 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSFVFGAGFVLGL
cry1a-105.pe VDIIMGIFGSPQMDAFLVQIEQLINQRIEFAFARQAISRLEGSLNLYQIYAESFREWAD
60308967 VDIIMGIFGSPQMDAFLVQIEQLINQRIEFAFARQAISRLEGSLNLYQIYAESFREWAD
60308967 VDIIMGIFGSPQMDAFLVQIEQLINQRIEFAFARQAISRLEGSLNLYQIYAESFREWAD

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cry1a-105.pe PTPALREEMRIQFNDMSALTTAIPLEAVQNYQVPLLSVYVQAANHLHSLVLRDVSFVGQ
 60308967 PTPALREEMRIQFNDMSALTTAIPLEAVQNYQVPLLSVYVQAANHLHSLVLRDVSFVGQ
 130 140 150 160 170 180
 cry1a-105.pe RWGFDATINSRYNDLTRIGNYTHAVRWYNTGLERWVGSDSRDWYRNOFRRELTIV
 190 200 210 220 230 240
 60308967 RWGFDATINSRYNDLTRIGNYTHAVRWYNTGLERWVGSDSRDWYRNOFRRELTIV
 190 200 210 220 230 240
 cry1a-105.pe LDIIVSLFPNDYDSTPIRTVSQLTREIYINPVLENFDSFRGSGAGIEGSIIRSPHMDIL
 250 260 270 280 290 300
 60308967 LDIIVSLFPNDYDSTPIRTVSQLTREIYINPVLENFDSFRGSGAGIEGSIIRSPHMDIL
 250 260 270 280 290 300
 cry1a-105.pe NSITIYDAHRGEYVWSGHOIMASPVGSGPEFTPELYGTMGNAAPQORIVAGLQGVYR
 310 320 330 340 350 360
 60308967 NSITIYDAHRGEYVWSGHOIMASPVGSGPEFTPELYGTMGNAAPQORIVAGLQGVYR
 310 320 330 340 350 360
 cry1a-105.pe TLSSTLYRRFPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSGTVDLSDEIPQNNV
 370 380 390 400 410 420
 60308967 TLSSTLYRRFPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSGTVDLSDEIPQNNV
 370 380 390 400 410 420
 cry1a-105.pe PPROGFSHRLSHVSMRPSGFSNNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPLVKAH
 430 440 450 460 470 480
 60308967 PPROGFSHRLSHVSMRPSGFSNNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPLVKAH
 430 440 450 460 470 480
 cry1a-105.pe TLQSGTIVVRPGFTGTDILRRTSQGFAYT--IVNINQLPOR---YRAIRYASFTNL
 490 500 510 520 530
 60308967 FLFNGS-VISGPGFTGTDILRRTSQGFAYT--IVNINQLPOR---YRAIRYASFTNL
 480 490 500 510 520 530
 cry1a-105.pe RIYVTVAGERIFAGQFNKMTDGTDLTFQSFYSATINFTAFPMSSQSFVVGADTFSSGN
 540 550 560 570 580 590
 60308967 HLNVMNGNSIFSNITVPKAGSLDNQSSDFGYPESANFTSLGN--MVGVRNFSGTA
 540 550 560 570 580 590
 cry1a-105.pe EYVIDRELPVATLEAEVNLERAQKAVNALFTSNOLGLKNTVDYHDVSNLVYL
 600 610 620 630 640 650
 60308967 GVIIIDREFIPVATLEAEVNLERAQKAVNALFTSNOLGLKNTVDYHDVSNLVYL
 600 610 620 630 640 650
 cry1a-105.pe SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKQINRQPERGWGSGTITIQGGDDVF
 660 670 680 690 700 710
 60308967 SD
 660 670 680 690 700 710

cry1a-105.pep
 NRAA:8469142

8469142 source: "GENBANK PROT" Pesticidal crystal protein cry1Jb (Insecticidal
 delta-endotoxin Cry1J(b)) (Crystalline entomocidal protoxin) (134 kDa crystal
 protein)

SCORES Initl: 2622 Initn: 4047 Opt: 3490 Z-score: 3959.1 E(): 3.1e-212
 >NRAA:8469142 (1170 aa)
 Initn: 4047 Initl: 2622 Opt: 3490 Z-score: 3959.1 expect(): 3.1e-212
 Smith-Waterman score: 4915; 64.4% identity in 1191 aa overlap
 (1-1177:1-1170)
 cry1a-105.pe MDNPNINECIPNCLSNPEVEVLGGERIETGYTIPIDISLSLTQFLSEFVPGAGFVLGL
 10 20 30 40 50 60
 8469142 MEIN-NQNCIPNCLSNPEVEVLGGERIETGYTIPIDISLSLTQFLSEFVPGAGFVLGL
 10 20 30 40 50 60
 cry1a-105.pe VDIWIFGSPQMDAPLVQIQLINQRIEFARNQIARLEGLSNLYQIYAESFREWAD
 70 80 90 100 110 120
 8469142 FDKWGLALRESDWELFLAQIQELIDRIEATVRAKAIAELEGLGRSQFQYAEKWEET
 70 80 90 100 110 120
 cry1a-105.pe PTPALREEMRIQFNDMSALTTAIPLEAVQNYQVPLLSVYVQAANHLHSLVLRDVSFVGQ
 130 140 150 160 170 180
 8469142 PTPALREEMRIQFNDMSALTTAIPLEAVQNYQVPLLSVYVQAANHLHSLVLRDVSFVGQ
 130 140 150 160 170 180
 cry1a-105.pe RWGFDATINSRYNDLTRIGNYTHAVRWYNTGLERWVGSDSRDWYRNOFRRELTIV
 190 200 210 220 230 240
 8469142 RWGFDATINSRYNDLTRIGNYTHAVRWYNTGLERWVGSDSRDWYRNOFRRELTIV
 190 200 210 220 230 240
 cry1a-105.pe VLDIVSLFPNDYDSTPIRTVSQLTREIYINPVLENFDSFRGSGAGIEGSIIRSPHMDIL
 240 250 260 270 280 290
 8469142 VLDIVSLFPNDYDSTPIRTVSQLTREIYINPVLENFDSFRGSGAGIEGSIIRSPHMDIL
 240 250 260 270 280 290
 cry1a-105.pe MDILNSITIVTDAHRGEYVWSGHOIMASPVGSGPEFTPELYGTMGNAAPQORIVAGLQGVYR
 300 310 320 330 340 350
 8469142 MDILNSITIVTDAHRGEYVWSGHOIMASPVGSGPEFTPELYGTMGNAAPQORIVAGLQGVYR
 300 310 320 330 340 350
 cry1a-105.pe GYRTLSLTSLYRRFPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSGTVDLSDEIPQNNV
 360 370 380 390 400 410
 8469142 GYRTLSLTSLYRRFPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSGTVDLSDEIPQNNV
 360 370 380 390 400 410
 cry1a-105.pe IPPQNNVPPRQFSHRLSHVSMRPSGFSNNSVSIIRAPMFSWIHRSAEFNIIASDSIT
 420 430 440 450 460 470
 8469142 IPPQNNVPPRQFSHRLSHVSMRPSGFSNNSVSIIRAPMFSWIHRSAEFNIIASDSIT
 420 430 440 450 460 470
 cry1a-105.pe QIPLVKAHTLOSQTIVVRPGFTGTDILRRTSQGFAYTINFTAFPMSSQSFVVGADTFSSGN
 480 490 500 510 520 530
 8469142 QIPLVKAHTLOSQTIVVRPGFTGTDILRRTSQGFAYTINFTAFPMSSQSFVVGADTFSSGN
 480 490 500 510 520 530
 cry1a-105.pe TNLRIYTVVAGERIFAGQFNKMTDGTDLTFQSFYSATINFTAFPMSSQSFVVGADTFSSGN
 540 550 560 570 580 590
 8469142 TNLRIYTVVAGERIFAGQFNKMTDGTDLTFQSFYSATINFTAFPMSSQSFVVGADTFSSGN
 540 550 560 570 580 590
 cry1a-105.pe SNFYFVVRGRNLGVNGREIMKMTGSTGEELKSASFVLGEFTTTPNFNFENQVPLQIEIOSLS
 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

8469142 description="PESTICIDIAL CRYSTAL PROTEIN CRY10B (INSECTICIDAL DELTA-ENDOTOXIN CRY10B) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (134 KDA CRYSTAL PROTEIN)." library="NA species="Bacillus thuringiensis" source="swissprot_prot" version="NA type="PRT

SCORES Initl: 2622 Initn: 4047 Opt: 3490 Z-score: 3959.1 E(): 3.1e-212
>>SW:8469142
Initn: 4047 initl: 2622 opt: 3490 Z-score: 3959.1 expect(): 3.1e-212
Smith-Waterman score: 4915; 64.4% identity in 1191 aa overlap
(1-1177:1-1170)

cry1a-105.pe MDNPNINCEIPNCLSNPEVEVLGGRIETGTPIDISLSTQFLISEFVPGAGFVLGL
8469142 MEIN-NQNCIPNCLSNPEVEVLGGRIETGTPIDISLSTQFLISEFVPGAGFVLGL
cry1a-105.pe VDIINGIFGSQMDAFVQIEQLINQRIEFARNQAIISLEGLSNLYQIYAEFREWED
8469142 FDKWALRPSDWELFLAQIEQLIDQRIETATVRAKAIAELEGISFOLYVEAFKEWEET
cry1a-105.pe PTNPALREEMRIQFNDMSALTATPFAVQNVQVPLLSVYVQANHLVLRDVSFVGQ
8469142 PONTAARSRTVTEAFRIIDIAQIEANIPSPRIPGFEVLLSVYAAQANHLALLRDSVIFGE
cry1a-105.pe RQCFDAITNSRYNDTRIIGNYTHAVRWNTGLERVMGPDSSR-DMIRYNQFRELTLT
8469142 RGLTINVDNINRYNQVKIEHSEYSDHCVDYKYLEERL-GFTSRAQWKIYNQFRELTLT
cry1a-105.pe VDIIVS-PNDSRTPTSTVQLTREIYNPVLNFDGSRGSAQ-GI--EGSIRSPHL
8469142 VDIIVS-PNDSRTPTSTVQLTREIYNPVLNFDGSRGSAQ-GI--EGSIRSPHL
cry1a-105.pe MDILNITIVTARSEVYVAGSIOIAPSPGFCRETEPIYGTMGNAPOORIVAGLQ
8469142 MDFFNTMTYTSNRENTWGLEMTA--PFAQVQSPFLAGTRGDAAPFN-VRSVND
cry1a-105.pe GYVRLTSLYRPPFNIGNNQLSVL--STEFATST--NLPSAVRISGTVDSLDE
8469142 GYVRLTSLYRPPFNIGNNQLSVL--STEFATST--NLPSAVRISGTVDSLDE
cry1a-105.pe IPPQNNVPFQGFQSHRLSHVSMFRSGFSSSVIIRAPMFSNHRSEFNNSGATIT
8469142 IPPQNNVPFQGFQSHRLSHVSMFRSGFSSSVIIRAPMFSNHRSEFNNSGATIT
cry1a-105.pe QIPVAKHTLSQGTTVVRGPGTGGDILRLTSGGFAITVINGOLPQVRARIRVAST
8469142 QIPVAKHTLSQGTTVVRGPGTGGDILRLTSGGFAITVINGOLPQVRARIRVAST

cry1a-105.pe SGNEVYIDFELIPVTATTAENLERAQAVNALETSTNOLGLKTNVTDYHIDQVSNLV
8469142 SGNEVYIDFELIPVTATTAENLERAQAVNALETSTNOLGLKTNVTDYHIDQVSNLV
cry1a-105.pe TYLSDEFCLDENSELSEKVKHAKVLSERNLLOSPNINQPERGGSGTGITIQGGD
8469142 TYLSDEFCLDENSELSEKVKHAKVLSERNLLOSPNINQPERGGSGTGITIQGGD
cry1a-105.pe DVFKENVYTLSTGTFDECYPTLYOKIKLSKAKFTVARGNEDSODSLEYRYNAKH
8469142 DVFKENVYTLSTGTFDECYPTLYOKIKLSKAKFTVARGNEDSODSLEYRYNAKH
cry1a-105.pe ETVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSSRQCKCAHSHHSDII
8469142 ETVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSSRQCKCAHSHHSDII
cry1a-105.pe DVGCTDLNEDLGVMVIFKIKTODGHARLGNLEFLEKPLVGBALARVRAKKWRDKRK
8469142 DVGCTDLNEDLGVMVIFKIKTODGHARLGNLEFLEKPLVGBALARVRAKKWRDKRK
cry1a-105.pe LEWENTVYKAEKESVDALFVNSVDLOADTNAMTHAADKRVHSIEAVLPESLWPG
8469142 LEWENTVYKAEKESVDALFVNSVDLOADTNAMTHAADKRVHSIEAVLPESLWPG
cry1a-105.pe VNAALFEELEGRIPTAFSLYDARNVINKGDFNGLSCWNVKGVHDVEEQNNQSVLWPE
8469142 VNAALFEELEGRIPTAFSLYDARNVINKGDFNGLSCWNVKGVHDVEEQNNQSVLWPE
cry1a-105.pe WEAEVSQKRVCFGRGYILRVTAKEGEGCVTIHIEINNTDELFKSNVCEEIEYFNPT
8469142 WEAEVSQKRVCFGRGYILRVTAKEGEGCVTIHIEINNTDELFKSNVCEEIEYFNPT
cry1a-105.pe VTCNDYTVNOEEYGGAYT--SRNRYNEA----PSVPADYASVVEKSYTDGRENPCPEF
8469142 VTCNDYTVNOEEYGGAYT--SRNRYNEA----PSVPADYASVVEKSYTDGRENPCPEF
cry1a-105.pe NRGYRDYTPFVGVVTKLEYLFFETDKVWIEIGETGTFVDSVLLMEE
8469142 NRGYRDYTPFVGVVTKLEYLFFETDKVWIEIGETGTFVDSVLLMEE
cry1a-105.pe DRGVNVPPLPAGVTVKLEYLFFETDKVWIEIGETGTFVDSVLLMEE
8469142 DRGVNVPPLPAGVTVKLEYLFFETDKVWIEIGETGTFVDSVLLMEE

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cry1a-105.pe TNLRIVTVAGRIIPAGQFNKMTDGDPLTFQSFYATINTATFFPMQSSSTVGRDTFS 540 550 560 570 580 590
8469142 SNFYFVRGNLGVNGREIMKMTSTGEELKSASFVLGEFIPFNFFENOVPLQIEQLSLS 530 540 550 560 570 580
cry1a-105.pe SGNEVYDFELIPVATLEAEYNLERAKAVNALFTSTNQLGKTNVTDYHIDQVSNLV 600 610 620 630 640 650
8469142 PGGEVYDLKIEIPADITFEAEYDLERAKAVNALFTSTNQLGKTNVTDYHIDQVSNLV 590 600 610 620 630 640
cry1a-105.pe TYLSDFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGSGSTGIIQGGD 660 670 680 690 700 710
8469142 ECLSDFFCLDEKRELSKVKHAKRLSDERNLLQDPNFTSINGQLDRGWRGSDITIQGNN 650 660 670 680 690 700
cry1a-105.pe DVFKENYVLTSTGTFDECYPTLYLQKIDESKLFKAFTRYQIRGYIEDSODLEIYISRYNAKH 720 730 740 750 760 770
8469142 DVFKENYVLTSTGTFDECYPTLYLQKIDESKLFKAFTRYQIRGYIEDSODLEIYISRYNAKH 710 720 730 740 750 760
cry1a-105.pe ETNVNPGTGLWPLSAQSPIGKCGEPRNCAPHLEWNPDLDCSCRDGKCAHSHHFSLDI 780 790 800 810 820 830
8469142 ETNLNPGTGLWPLSAQSPIGKCGEPRNCAPHLEWNPDLDCSCRDGKCAHSHHFSLDI 770 780 790 800 810 820
cry1a-105.pe DVGCTDLNEDLGVWIFKIKTDQGHARLGNLFLEBEKPLVGEALARVKRAEKKWRDKREK 840 850 860 870 880 890
8469142 DVGCTDLQEDLGVWVVFVKIKTDQGHARLGNLFLEBEKPLVGEALARVKRAEKKWRDKREK 830 840 850 860 870 880
cry1a-105.pe LEWETNIVYKEAKESVDALFVNSOYDQLOQADTNIAHIAADKRVHSIREAYLPELSVIPG 900 910 920 930 940 950
8469142 LELETKEVYTEAKEAVDALFVDSQYDQLQADTNIGMTHAADKLVHRICEYILPELPFFPG 890 900 910 920 930 940
cry1a-105.pe VNAAIFEELEGRIFTAFSLYDARNVINKGDFNNGLSKWNKGVHDVDEEQNNQSVLWVPE 960 970 980 990 1000 1010
8469142 INALIFEELENRISTAFLEYEARNVINNGDFNNGLTGNVKGHDVQ-QSHHRSVLVIPE 950 960 970 980 990 1000
cry1a-105.pe WEAEVSGEVVRCFGRGYILRVTAIYKEGYEGCVTHIEENTNDELKFSNCVEEYIPNNT 1020 1030 1040 1050 1060 1070
8469142 WEAEVSGKVRVCFGRGYILRVTAIYKEGYEGCVTHIEEDNTDELKFRNCEEEDYSNDT 1000 1010 1020 1030 1040 1050
cry1a-105.pe VTQNDYTVNQEEYGGAYT--SRNRYNEA---PSVPADYASVVEEKSYYTDGRNPECF 1080 1090 1100 1110 1120
8469142 GTCNYPASOGAGACADVCSNRNRYGDAYEYNTSASVNYKTYEEETIYDVEDNHCEY 1060 1070 1080 1090 1100 1110
cry1a-105.pe NRGYRDYTLPGVYVTKLEYFPETDKVWIEIGETEGTIVDSVELLIMEE 1130 1140 1150 1160 1170
8469142 DRGVNYPPLPAGYVTKLEYFPETDKVWIEIGETEGTIVDSVELLIMEE 1120 1130 1140 1150 1160 1170

cry1a-105.pep
NRAA:2414156
2414156 source="GENBANK_PROT" delta-endotoxin [Bacillus thuringiensis]
SCORES Init1: 3203 Initn: 3464 Opt: 3475 z-score: 3946.2 E(): 1.6e-211
>NRAA:2414156
initn: 3464 init1: 3203 opt: 3475 z-score: 3946.2 expect(): 1.6e-211
Smith-Waterman score: 3475; 86.0% identity in 622 aa overlap
(1-617:1-618)
cry1a-105.pe MDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLQTLSEFVPGAGFVLGL 10 20 30 40 50 60
2414156 MDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLQTLSEFVPGAGFVLGL 10 20 30 40 50 60
cry1a-105.pe VDIWGIFGSPQWDAFLVQIQLINQRIEFARNQAIISRLGSLNLYIYAESFREWEAD 70 80 90 100 110 120
2414156 VDIWGIFGSPQWDAFLVQIQLINQRIEFARNQAIISRLGSLNLYIYAESFREWEAD 70 80 90 100 110 120
cry1a-105.pe PTPNPALEEMRIQFNDMNSALTATPLFAVQNVQVPLLSVYVQAANHLVLRDVSFQ 130 140 150 160 170 180
2414156 PTPNPALEEMRIQFNDMNSALTATPLFAVQNVQVPLLSVYVQAANHLVLRDVSFQ 130 140 150 160 170 180
cry1a-105.pe RWGFDAAATINSRYNDLTGLIGNYTDHAWMYNTGLERVMGPDSDRWIRYNQPRELTLTV 190 200 210 220 230 240
2414156 RWGFDAAATINSRYNDLTGLIGNYTDHAWMYNTGLERVMGPDSDRWIRYNQPRELTLTV 190 200 210 220 230 240
cry1a-105.pe LDIVSLFPNVDSTPIRTVSQLTREIYNPVLNFDGSGFRGSAQGIEGSIRSPHMLDL 250 260 270 280 290 300
2414156 LDIVSLFPNVDSTPIRTVSQLTREIYNPVLNFDGSGFRGSAQGIEGSIRSPHMLDL 250 260 270 280 290 300
cry1a-105.pe NSITIYTDHARGEYVWSGHQIMASPVGSGPEFTPLGYTMGNAAPQORIVAQLGGVYR 310 320 330 340 350 360
2414156 NSITIYTDHARGEYVWSGHQIMASPVGSGPEFTPLGYTMGNAAPQORIVAQLGGVYR 310 320 330 340 350 360
cry1a-105.pe TLSSTLYRRPFNIGINNOQLSVLDGTEFAYGTSSNLPNAVYRKSGTVDSLOEIPPNNNV 370 380 390 400 410 420
2414156 TLSSTLYRRPFNIGINNOQLSVLDGTEFAYGTSSNLPNAVYRKSGTVDSLOEIPPNNNV 370 380 390 400 410 420
cry1a-105.pe PPROGFSHRLSHVSMFRGSGFNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPLVKXAH 430 440 450 460 470 480
2414156 PPROGFSHRLSHVSMFRGSGFNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPLVKXAH 430 440 450 460 470 480
cry1a-105.pe TLQSGTTVVRGPGTGGDILARTSGGPFAYT--IVNINGQLPQ--RYRARIYASTNL 490 500 510 520 530
2414156 FLFNGS-VISGPGTGGDILVRLNSSGNNIGNRGYIEVPIHPFSTSTRYRVRYASVTPI 490 500 510 520 530


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cryla-105.pe      PTPALREEMRIQFNDWNSSALTITAIPLFAVQNYQVPLLSVYVQAANLHLSVLVDVSVFVGQ
4090435          130   140   150   160   170   180
|||||
cryla-105.pe      RWGFDAAATINSRYNDLRLIGNYTDHAVRWYNTGLERVMGPDSDRMIYRQNFRRELTITV
4090435          130   140   150   160   170   180
|||||
cryla-105.pe      RWGFDAAATINSRYNDLRLIGNYTDHAVRWYNTGLERVMGPDSDRMIYRQNFRRELTITV
4090435          130   140   150   160   170   180
|||||
cryla-105.pe      LDIVSLFPNYDSRTVPIRTVSQTLTRIYTNPVLENDFGSRFGSAQGIKESIRSPHMLDIL
4090435          250   260   270   280   290   300
|||||
cryla-105.pe      NSITIVTDHARGEYVWSGHQIMASPVGFSGFPEFTPLVGTMGNAAPQORIVAQLOGGVYR
4090435          310   320   330   340   350   360
|||||
cryla-105.pe      TLSSTLYRRPFNIGINNOQLSVLDGTEFAVGTSSNLPSAVYRKSGTVDSIDEIIPPQNNVV
4090435          370   380   390   400   410   420
|||||
cryla-105.pe      PPROGFSHRLLSHVMSFRSGFNSSVSIIRAPMFSMIHRSAEFNIIASDSITQIPLVRKAH
4090435          430   440   450   460   470   480
|||||
cryla-105.pe      TLQSGTTVVRVGPFGTGGDILARTSGGPFAYT--IVNINGQLPQ---RYRARIRYASTNML
4090435          490   500   510   520   530
|||||
cryla-105.pe      FLFNGS-VTSGPCFTGGDLVRLNSGNNIGNRGYIEVPIHFEPSTSTRYRVRYASVTPI
4090435          490   500   510   520   530
|||||
cryla-105.pe      RIYVTVAGERIFAGQNKMTDGTPLTFQSFSTATINTAFTFPMQSSFTVGADTFSSGN
4090435          540   550   560   570   580   590
|||||
cryla-105.pe      EYVIDREFLIPVTAILEAYNLERAKAVNALFTSNQLGLKTNVTDVHIDQVSNLVTYL
4090435          600   610   620   630   640   650
|||||
cryla-105.pe      GVVIDRFEPIPVATILE
4090435          600   610
|||||
cryla-105.pe
NR001:40275
40275 source="GENBANK_PROT" unnamed protein product [Bacillus thuringiensis]

SCORES      Initl: 2909      Inltn: 2909      Opt: 3406      Z-score: 3867.8      E(): 3.8e-207
>>NR001:40275
Initl: 2909      Inltn: 2909      Opt: 3406      Z-score: 3867.8      expect(): 3.8e-207
Smith-Waterman score: 3406;      84.4% identity in 623 aa overlap
(1-618:1-618)

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cryla-105.pe
40275
MONNPNINECIPYNCLSNPEVEVLGERIETGYTPIDISLSLTOFLSEFVPGAGFVLGL
MONNPNINECIPYNCLSNPEVEVLGERIETGYTPIDISLSLTOFLSEFVPGAGFVLGL
cryla-105.pe
40275
VDIINGIFGSPQMDAFVQLQINORIEEFARNQAIISRLGSLNLYQIYAESFREWEAD
VDIINGIFGSPQMDAFVQLQINORIEEFARNQAIISRLGSLNLYQIYAESFREWEAD
cryla-105.pe
40275
PTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLSVVQAAHLHLSVLRDVSFVGQ
PTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLSVVQAAHLHLSVLRDVSFVGQ
cryla-105.pe
40275
RMGFDAATINSRYNDLTRILGNVTHAVRWNTGLERWVGPDSRDWRINQFRRELTLTV
RMGFDAATINSRYNDLTRILGNVTHAVRWNTGLERWVGPDSRDWRINQFRRELTLTV
cryla-105.pe
40275
LDIVSLFNYDSRTYPIRTVSQLTRITVFNVLNFGSPGSAQIGSIRSPLHMDIL
LDIVSLFNYDSRTYPIRTVSQLTRITVFNVLNFGSPGSAQIGSIRSPLHMDIL
cryla-105.pe
40275
NSITITDAHRGEYWGSHQIMASPVGSGPEFTFPYIGTMGNAAPQQRIVQAQCGQYVR
NSITITDAHRGEYWGSHQIMASPVGSGPEFTFPYIGTMGNAAPQQRIVQAQCGQYVR
cryla-105.pe
40275
TLSSITFYRPPNIGINNQQSLVDLGTETAYGTSSNLPSAVYRKSQGVDSLDEIPQNNV
TLSSITFYRPPNIGINNQQSLVDLGTETAYGTSSNLPSAVYRKSQGVDSLDEIPQNNV
cryla-105.pe
40275
PPROGFSHRLSHVSMFSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPLVKAH
PPROGFSHRLSHVSMFSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPLVKAH
cryla-105.pe
40275
FLVNGS-VISGPGFTGGDLRLNSGNNIQNGYIEVPIHFPSTIRTRVRVRSVTPPI
FLVNGS-VISGPGFTGGDLRLNSGNNIQNGYIEVPIHFPSTIRTRVRVRSVTPPI
cryla-105.pe
40275
RIYVTVAGERIFAGQFNKIMDTGDLPTFQSFYSYATINTAFTFPMSSQSFVGAADTFSSGN
RIYVTVAGERIFAGQFNKIMDTGDLPTFQSFYSYATINTAFTFPMSSQSFVGAADTFSSGN
cryla-105.pe
40275
HLNVNKGSSIFSNVTPATATSLDNLQSSDRCYFESANATSSIGN--IVGVNFSGTA
HLNVNKGSSIFSNVTPATATSLDNLQSSDRCYFESANATSSIGN--IVGVNFSGTA
cryla-105.pe
40275
EVIDRFFELIPVTATLEAENYLERAKAVNALFTSTNQLGLKNTVDYHIDQVSNLVLYL
EVIDRFFELIPVTATLEAENYLERAKAVNALFTSTNQLGLKNTVDYHIDQVSNLVLYL
GVVIDRFFELIPVTATLEAENYLERAKAVNALFTSTNQLGLKNTVDYHIDQVSNLVLYL

cryla-105.pe
NRAA: 37993013
37993013 source="GENBANK_PROT" hybrid CryIAB-CryIa protein [synthetic construct]
SCORES Init1: 3321 Initn: 3430 Opt: 3376 Z-score: 3833.5 E(): 3.1e-205
>NRAA: 37993013
initn: 3430 init1: 3321 opt: 3376 Z-score: 3833.5 expect(): 3.1e-205
Smith-Waterman score: 3500; 83.9% identity in 641 aa overlap
(1-628:1-640)
cryla-105.pe
37993013
MONNPNINECIPYNCLSNPEVEVLGERIETGYTPIDISLSLTOFLSEFVPGAGFVLGL
MONNPNINECIPYNCLSNPEVEVLGERIETGYTPIDISLSLTOFLSEFVPGAGFVLGL
cryla-105.pe
37993013
VDIINGIFGSPQMDAFVQLQINORIEEFARNQAIISRLGSLNLYQIYAESFREWEAD
VDIINGIFGSPQMDAFVQLQINORIEEFARNQAIISRLGSLNLYQIYAESFREWEAD
cryla-105.pe
37993013
PTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLSVVQAAHLHLSVLRDVSFVGQ
PTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLSVVQAAHLHLSVLRDVSFVGQ
cryla-105.pe
37993013
RMGFDAATINSRYNDLTRILGNVTHAVRWNTGLERWVGPDSRDWRINQFRRELTLTV
RMGFDAATINSRYNDLTRILGNVTHAVRWNTGLERWVGPDSRDWRINQFRRELTLTV
cryla-105.pe
37993013
TLSSITFYRPPNIGINNQQSLVDLGTETAYGTSSNLPSAVYRKSQGVDSLDEIPQNNV
TLSSITFYRPPNIGINNQQSLVDLGTETAYGTSSNLPSAVYRKSQGVDSLDEIPQNNV
cryla-105.pe
37993013
PPROGFSHRLSHVSMFSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPLVKAH
PPROGFSHRLSHVSMFSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPLVKAH
cryla-105.pe
37993013
FLVNGS-VISGPGFTGGDLRLNSGNNIQNGYIEVPIHFPSTIRTRVRVRSVTPPI
FLVNGS-VISGPGFTGGDLRLNSGNNIQNGYIEVPIHFPSTIRTRVRVRSVTPPI
cryla-105.pe
37993013
RIYVTVAGERIFAGQFNKIMDTGDLPTFQSFYSYATINTAFTFPMSSQSFVGAADTFSSGN
RIYVTVAGERIFAGQFNKIMDTGDLPTFQSFYSYATINTAFTFPMSSQSFVGAADTFSSGN
cryla-105.pe
37993013
HLNVNKGSSIFSNVTPATATSLDNLQSSDRCYFESANATSSIGN--IVGVNFSGTA
HLNVNKGSSIFSNVTPATATSLDNLQSSDRCYFESANATSSIGN--IVGVNFSGTA
cryla-105.pe
37993013
EVIDRFFELIPVTATLEAENYLERAKAVNALFTSTNQLGLKNTVDYHIDQVSNLVLYL
EVIDRFFELIPVTATLEAENYLERAKAVNALFTSTNQLGLKNTVDYHIDQVSNLVLYL
GVVIDRFFELIPVTATLEAENYLERAKAVNALFTSTNQLGLKNTVDYHIDQVSNLVLYL

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490      500      510      520      530      540
540      550      560      570      580
cry1a-105.pe TVAGERIFAGQ-----FNKTMGTGDELTFQSFYSATINTAFTPMSSQSFV-----G
37993013 TGAASTGVGGVSNVNNPQKQMEIGENLTSTRTPTFTDFSNPFRANPDIIGISEQPLFG
550      560      570      580      590      600
590      600      610      620      630      640
cry1a-105.pe ADTSSGNEVYDRPELIPVTATLEAEYNLERAKQAVNALFTSTNQLGKTNVTDYHIDQ
37993013 AGSISGG-ELYIDKIEILLADATFEAESDLEAKQAVNAL
610      620      630      640
650      660      670      680      690      700
cry1a-105.pe VSNLVTVLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWSGTGIT
cry1a-105.pep
NRAA:62548840
62548840 source="GENBANK_PROT" delta-endotoxin CryI-A32 [Bacillus
thuringiensis]
10      20      30      40      50      60
cry1a-105.pe MDNNPNINECIPYCNLSNPEVEVLGGRIETGYTPIDISLTQFLSEFVPGAGFVLGL
62548840 PEVEVLGGRIETGYTPIDISLTQFLSEFVPGAGFVLGL
10      20      30      40      50      60
cry1a-105.pe VDIINGIFGSDMAFLVQIEQLINQRIEEFARNQAIISRLGSLNLYQIYAESFREWAD
62548840 VDIINGIFGSDMAFLVQIEQLINQRIEEFARNQAIISRLGSLNLYQIYAESFREWAD
50      60      70      80      90      100
130      140      150      160      170      180
cry1a-105.pe PTNPALREEMRIQFNDMNSALTTAIPFAVQVQVPLLSVYVQAAHLNLSVLKRVDSVFGQ
62548840 PTNPALREEMRIQFNDMNSALTTAIPFAVQVQVPLLSVYVQAAHLNLSVLKRVDSVFGQ
110      120      130      140      150      160
190      200      210      220      230
cry1a-105.pe RNFQDAATINRNDLTRILIGNYTHAVRWYNTGLERWVGPDS--RWIYNGFRBELT
62548840 RNFQDAATINRNDLTRILIGNYTHAVRWYNTGLERWVGPDS--RWIYNGFRBELT
170      180      190      200      210      220
240      250      260      270      280      290
cry1a-105.pe LTVLDIVSLFNDVDSRTYPIRTVSQLTSTREIYTNVLENFDPGSPRGSAGIIGS-IRSPHL
62548840 LTVLDIVSLFNDVDSRTYPIRTVSQLTSTREIYTNVLENFDPGSPRGSAGIIGS-IRSPHL
230      240      250      260      270      280
300      310      320      330      340      350
cry1a-105.pe MDILANSITITDARHGEYWMGSHQIMASVFGSPFETFFLYGTGMGNAPQORIVAQGG
62548840 MDPLANLITDILIRGVHGWAGHRTVSHFTG-SSQVITTPQYGITANAPERTIAPSTFP
290      300      310      320      330
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360      370      380      390      400      410
cry1a-105.pe GV---YTLSSLYRPPNIGINNQQLSVLDTGTERAYGTSNLPASVAVYKSGTVDLSLEI
62548840 GNLFYTLGNPPFRSENITPTGLGNVVGQVGFQIPNNAEV---LYRSGVTVDLSNEL
340      350      360      370      380      390
420      430      440      450      460      470
cry1a-105.pe PPQNNVPPRQGFHSRLSHVSNFRSGFSNVSIIIRAPMFSIHRSAEFNIIASDSITQ
62548840 PIDGEN--SLVGSVHSLSHVTLTSLYNTNITSLSL---PTFVWTHHSATNTINPDIITQ
400      410      420      430      440      450
480      490      500      510      520      530
cry1a-105.pe IPLVKAHTLOSQTGVVRGPGFTGGDILARTSGGPFAYTIVNINGQLPQRYEARIRYAST
62548840 IPLVAGFRLGSGTSTVTKGPGFTGGDILARTTIGEFVSLQVNINSPIQRVRLFRYASSR
460      470      480      490      500      510
540      550      560      570      580      590
cry1a-105.pe NLRIVTVAGERIFAGQFNKTMGTGDLTTFOSFSYATINTAFTPMSSQSFVAGDTFSS
62548840 DARITVAGQIRVDMTLEKTMWEIGESLTSRTSYTNFNSPFSFRANPDIIRIAEELPIR
520      530      540      550      560      570
600      610      620      630      640      650
cry1a-105.pe GNEVIIDRFELIPVTATLEAEYNLERAKQAVNALFTSTNQLGKTNVTDYHIDQVSNLVT
62548840 CGELYIDKIEILLADATFEAEYDLERAKQAVNALFTSTNQLGKTNVTDYHIDQVSNLVE
580      590      600      610      620      630
660      670      680      690      700      710
cry1a-105.pe YLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWSGTGIIQGGDD
62548840 CLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWSGTGIIQGGDD
640      650      660      670      680      690
720      730      740      750      760      770
cry1a-105.pe VFKENYVLTSGTDFECVPTLYQKIDESKLFKAFTRVQLRGYIEDSQDLEIYSIRYNAKHE
62548840 VFKENYVLTSGTDFECVPTLYQKIDESKLFKAFTRVQLRGYIEDSQDLEIYSIRYNAKHE
700      710      720      730      740      750
780      790      800      810      820      830
cry1a-105.pe TVNVFPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDSCRDGKCAHSHHFSLDID
62548840 TVNVFPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDSCRDGKCAHSHHFSLDID
760
cry1a-105.pep
NRAA:2555147
2555147 source="GENBANK_PROT" CryIA(c) [synthetic construct]
SCORES      Init1: 3101      Initn: 3331      Opt: 3355      z-score: 3809.9      E(): 6.4e-204
>>NRAA:2555147
initn: 3331      init1: 3101      opt: 3355      z-score: 3809.9      expect(): 6.4e-204
Smith-Waterman score: 3355;      84.2% identity in 613 aa overlap
(5-612:6-614)
10      20      30      40      50
cry1a-105.pe MDNNPNINECIPYCNLSNPEVEVLGGRIETGYTPIDISLTQFLSEFVPGAGFVLG
2555147 MAMITPSLHACIPYCNLSNPEVEVLGGRIETGYTPIDISLTQFLSEFVPGAGFVLG
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cryla-105.pe VDIIMGIFGSPQMDAFLVQIEQLINORIEEFARNQAIISRLGLESLNLYOIAESFREWEA 60 70 80 90 100 110 120
2555147 VDIIMGIFGSPQMDAFLVQIEQLINORIEEFARNQAIISRLGLESLNLYOIAESFREWEA 130 140 150 160 170 180 190
cryla-105.pe DFTNPALREEMRIQFNDMSALTTPALFVQNVQVPLLSVYVQAAHLHLSVLDRVSFG 120 130 140 150 160 170 180
2555147 DFTNPALREEMRIQFNDMSALTTPALFVQNVQVPLLSVYVQAAHLHLSVLDRVSFG 190 200 210 220 230 240 250
cryla-105.pe QWGFDAATINSRYNDLTRELIGNYTDHVRWNTGLVWQPSRDMIRVNOFRELTIT 180 190 200 210 220 230 240
2555147 QWGFDAATINSRYNDLTRELIGNYTDHVRWNTGLVWQPSRDMIRVNOFRELTIT 250 260 270 280 290 300 310
cryla-105.pe VLDIVSLFPNYSRTYPIRTVSQLTREIYNPVLNFDGFRGSAQGIERSIRSPHMDIL 240 250 260 270 280 290 300
2555147 VLDIVSLFPNYSRTYPIRTVSQLTREIYNPVLNFDGFRGSAQGIERSIRSPHMDIL 310 320 330 340 350 360 370
cryla-105.pe LNSITITDHRGEYVWSGHQIMASPVGFGSPFETPLVGTGMNAAPORIVAGLQGVY 360 370 380 390 400 410 420
2555147 LNSITITDHRGEYVWSGHQIMASPVGFGSPFETPLVGTGMNAAPORIVAGLQGVY 430 440 450 460 470 480 490
cryla-105.pe HTLSSTLYRRPFNIGINNOQLSVLDGTEFAYGTSSNLPASVYKSGTVDLSDEIPPONNN 420 430 440 450 460 470 480
2555147 HTLSSTLYRRPFNIGINNOQLSVLDGTEFAYGTSSNLPASVYKSGTVDLSDEIPPONNN 490 500 510 520 530 540 550
cryla-105.pe VPPROGFSHRLSHVSMFRSGFNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPLVKA 540 550 560 570 580 590 600
2555147 VPPROGFSHRLSHVSMFRSGFNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPLVKA 610 620 630 640 650 660 670
cryla-105.pe NLFNGS-VISGFGFTGGDLVRLNSSGNNIQNRGYIEVHPFSTSTRVRYASVTP 680 690 700 710 720 730 740
2555147 NLFNGS-VISGFGFTGGDLVRLNSSGNNIQNRGYIEVHPFSTSTRVRYASVTP 750 760 770 780 790 800 810
cryla-105.pe LRIYVTVAGERIFAGQFNKMTDGLTFQSFYSATINTAFTFPMSSQSFVTGADTFSSG 820 830 840 850 860 870 880
2555147 LRIYVTVAGERIFAGQFNKMTDGLTFQSFYSATINTAFTFPMSSQSFVTGADTFSSG 890 900 910 920 930 940 950
cryla-105.pe NEVYIDRELPITVATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDVHIDQVSNLTV 960 970 980 990 1000 1010 1020
2555147 NEVYIDRELPITVATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDVHIDQVSNLTV 1030 1040 1050 1060 1070 1080 1090
cryla-105.pe AGVYIDREFEIPVATLEPP 600 610 620 630 640 650 660
2555147 AGVYIDREFEIPVATLEPP 670 680 690 700 710 720 730
cryla-105.pe NRAA:1171235 540 550 560 570 580 590 600
2555147 NRAA:1171235 610 620 630 640 650 660 670

1171235 source="GENBANK_PROT" CryIA(C)
SCORES Initl: 2906 Initn: 3047 Opt: 3343 z-score: 3796.3 E(): 3.7e-203
>NRAA:1171235
Initn: 3047 Opt: 3343 z-score: 3796.3 expect(): 3.7e-203
Smith-Waterman score: 3343; 84.2% identity in 612 aa overlap
(1-607:1-607)
cryla-105.pe MDNPNINECIPNCLSNPEVEVLGGERIETGTPIDISLSTQFLLSEFVPGAGVLGL 10 20 30 40 50 60
1171235 MDNPNINECIPNCLSNPEVEVLGGERIETGTPIDISLSTQFLLSEFVPGAGVLGL 60 70 80 90 100 110 120
cryla-105.pe VDIIMGIFGSPQMDAFLVQIEQLINORIEEFARNQAIISRLGLESLNLYOIAESFREWEA 130 140 150 160 170 180
1171235 VDIIMGIFGSPQMDAFLVQIEQLINORIEEFARNQAIISRLGLESLNLYOIAESFREWEA 180 190 200 210 220 230 240
cryla-105.pe PTNPALREEMRIQFNDMSALTTPALFVQNVQVPLLSVYVQAAHLHLSVLDRVSFG 240 250 260 270 280 290 300
1171235 PTNPALREEMRIQFNDMSALTTPALFVQNVQVPLLSVYVQAAHLHLSVLDRVSFG 300 310 320 330 340 350 360
cryla-105.pe LNSITITDHRGEYVWSGHQIMASPVGFGSPFETPLVGTGMNAAPORIVAGLQGVY 360 370 380 390 400 410 420
1171235 LNSITITDHRGEYVWSGHQIMASPVGFGSPFETPLVGTGMNAAPORIVAGLQGVY 420 430 440 450 460 470 480
cryla-105.pe HTLSSTLYRRPFNIGINNOQLSVLDGTEFAYGTSSNLPASVYKSGTVDLSDEIPPONNN 480 490 500 510 520 530 540
1171235 HTLSSTLYRRPFNIGINNOQLSVLDGTEFAYGTSSNLPASVYKSGTVDLSDEIPPONNN 540 550 560 570 580 590 600
cryla-105.pe VPPROGFSHRLSHVSMFRSGFNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPLVKA 600 610 620 630 640 650 660
1171235 VPPROGFSHRLSHVSMFRSGFNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPLVKA 660 670 680 690 700 710 720
cryla-105.pe NLFNGS-VISGFGFTGGDLVRLNSSGNNIQNRGYIEVHPFSTSTRVRYASVTP 720 730 740 750 760 770 780
1171235 NLFNGS-VISGFGFTGGDLVRLNSSGNNIQNRGYIEVHPFSTSTRVRYASVTP 780 790 800 810 820 830 840
cryla-105.pe LRIYVTVAGERIFAGQFNKMTDGLTFQSFYSATINTAFTFPMSSQSFVTGADTFSSG 840 850 860 870 880 890 900
1171235 LRIYVTVAGERIFAGQFNKMTDGLTFQSFYSATINTAFTFPMSSQSFVTGADTFSSG 900 910 920 930 940 950 960
cryla-105.pe NRAA:1171235 540 550 560 570 580 590 600
2555147 NRAA:1171235 610 620 630 640 650 660 670

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1171235 HLNVMGNSIFSNTPATATSLDNLOSDFGYFESANFTSSLGN---IVGVNFSGTA
540 550 560 570 580 590
cry1a-105.pe EYIDRFEIPVTATLEAEYNLERAKAVNALFTSTNQLGKTNVTDYHIDQVSNLVTYL
600 610 620 630 640 650
1171235 GVIIDREFEIPVTATLE
600
cry1a-105.pep
NRAA:5916230
5916230 source="GENBANK_PROT" Cry Iac insecticidal toxin [synthetic construct]

SCORES Initl: 2951 Inltn: 3181 Opt: 3192 z-score: 3624.9 E(): 1.3e-193
>NRAA:5916230
Inltn: 3181 Initl: 2951 Opt: 3192 Z-score: 3624.9 expect(): 1.3e-193
Smith-Waterman score: 3192; 84.0% identity in 589 aa overlap
(29-612:3-587)

cry1a-105.pe MDNNPINECIPNCLSNPEVEVLGGRIETGYTPIDISLSLTQFLSEFVPGAGFVLGL
10 20 30 40 50 60
5916230 MAIETGYTPIDISLSLTQFLSEFVPGAGFVLGL
10 20 30

cry1a-105.pe VDIIWGIFGSQWDAFLVOIEQLINQRIEFARNQAIISRLGSLNLYQIYAESFREWEAD
70 80 90 100 110 120
5916230 VDIIWGIFGSQWDAFLVOIEQLINQRIEFARNQAIISRLGSLNLYQIYAESFREWEAD
40 50 60 70 80 90

cry1a-105.pe PTNPALREEMRIQFNDMNSALTTAIPFVQNYQVPLLSVYQAAANLHLSVLRDVSVFQ
130 140 150 160 170 180
5916230 PTNPALREEMRIQFNDMNSALTTAIPFVQNYQVPLLSVYQAAANLHLSVLRDVSVFQ
100 110 120 130 140 150

cry1a-105.pe RWGFDAAATINSRYNDLTRLIGNYTDHVRVNTGLERVAGPDSRDWRVYNOFRRELTIV
190 200 210 220 230 240
5916230 RWGFDAAATINSRYNDLTRLIGNYTDHVRVNTGLERVAGPDSRDWRVYNOFRRELTIV
160 170 180 190 200 210

cry1a-105.pe LDIIVLSPFNDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIGSIRSPHLMIDL
250 260 270 280 290 300
5916230 LDIIVLSPFNDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIGSIRSPHLMIDL
220 230 240 250 260 270

cry1a-105.pe NSIITYDARGYYYSGHQINAVSPVGSPEFTFFLYGTMGNAAPQORIYAQLQGQVVR
310 320 330 340 350 360
5916230 NSIITYDARGYYYSGHQINAVSPVGSPEFTFFLYGTMGNAAPQORIYAQLQGQVVR
280 290 300 310 320 330

cry1a-105.pe TLISSLTVDARGYYYSGHQINAVSPVGSPEFTFFLYGTMGNAAPQORIYAQLQGQVVR
370 380 390 400 410 420
5916230 TLISSLTVDARGYYYSGHQINAVSPVGSPEFTFFLYGTMGNAAPQORIYAQLQGQVVR
340 350 360 370 380 390

cry1a-105.pe PPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPVKAH
430 440 450 460 470 480
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5916230 PPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPVKAH
400 410 420 430 440 450
cry1a-105.pe TLOSGITVVRGPGFTGGDLRLRTSGGPFAYT--IVNINGQLPQ---EYRARIYASTNLL
490 500 510 520 530
5916230 FLFNGS-VISGPGFTGGDLRLRLSSNGNIONRGYIEVPIHPFSTSTRYRVRIASVTPI
460 470 480 490 500 510

cry1a-105.pe RIYVTVAGERIFAGQFNKMTDGTGDLTQFSVATINTAFTFPMQSSTFGVADTFSSGN
540 550 560 570 580 590
5916230 HLNVMGNSIFSNTPATATSLDNLOSDFGYFESANFTSSLGN---IVGVNFSGTA
520 530 540 550 560 570

cry1a-105.pe EYIDRFEIPVTATLEAEYNLERAKAVNALFTSTNQLGKTNVTDYHIDQVSNLVTYL
600 610 620 630 640 650
5916230 GVIIDREFEIPVTATLE
580

cry1a-105.pep
NRAA:1171233
1171233 source="GENBANK_PROT" CryIA(a)

SCORES Initl: 2251 Inltn: 3103 Opt: 3192 z-score: 3624.6 E(): 1.4e-193
>NRAA:1171233
Inltn: 3103 Initl: 2251 Opt: 3192 Z-score: 3624.6 expect(): 1.4e-193
Smith-Waterman score: 3192; 78.0% identity in 623 aa overlap
(1-621:1-620)

cry1a-105.pe MDNNPINECIPNCLSNPEVEVLGGRIETGYTPIDISLSLTQFLSEFVPGAGFVLGL
10 20 30 40 50 60
1171233 MDNNPINECIPNCLSNPEVEVLGGRIETGYTPIDISLSLTQFLSEFVPGAGFVLGL
10 20 30 40 50 60

cry1a-105.pe VDIIWGIFGSQWDAFLVOIEQLINQRIEFARNQAIISRLGSLNLYQIYAESFREWEAD
70 80 90 100 110 120
1171233 VDIIWGIFGSQWDAFLVOIEQLINQRIEFARNQAIISRLGSLNLYQIYAESFREWEAD
70 80 90 100 110 120

cry1a-105.pe PTNPALREEMRIQFNDMNSALTTAIPFVQNYQVPLLSVYQAAANLHLSVLRDVSVFQ
130 140 150 160 170 180
1171233 PTNPALREEMRIQFNDMNSALTTAIPFVQNYQVPLLSVYQAAANLHLSVLRDVSVFQ
130 140 150 160 170 180

cry1a-105.pe RWGFDAAATINSRYNDLTRLIGNYTDHVRVNTGLERVAGPDSRDWRVYNOFRRELTIV
190 200 210 220 230 240
1171233 RWGFDAAATINSRYNDLTRLIGNYTDHVRVNTGLERVAGPDSRDWRVYNOFRRELTIV
190 200 210 220 230 240

cry1a-105.pe LDIIVLSPFNDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIGSIRSPHLMIDL
250 260 270 280 290 300
1171233 LDIIVLSPFNDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIGSIRSPHLMIDL
250 260 270 280 290 300

cry1a-105.pe PPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPVKAH
310 320 330 340 350 360
```

cryla-105.pe NSITIVDAHREYVMSGHQIMASVFGSGPETFFLYCTMGNAAPQORIVAQOGVVR
1171233 NSITIVDAHREYVMSGHQIMASVFGSGPETFFLYCTMGNAAPQORIVAQOGVVR
310 320 330 340 350
cryla-105.pe TLSSSLVLRP-FHIGLMMQSLVLDGFEFAGT-SSNLPSAVRKSGTVDSLDIIPPQNN
1171233 TLSSSLVLRP-FHIGLMMQSLVLDGFEFAGT-SSNLPSAVRKSGTVDSLDIIPPQNN
360 370 380 390 400 410
cryla-105.pe NVPPRQGFHRLSHVMSFSGFSNVSIIICAPMSWIHRSFNNIIASDITQIPLVK
1171233 NVPPRQGFHRLSHVMSFSGFSNVSIIICAPMSWIHRSFNNIIASDITQIPLVK
420 430 440 450 460 470
cryla-105.pe SVPPRAGFHSRLSHVMTLSQ--AAQAVTAPAPKSWOAHSAEFNNIAPSQITQIPLVK
1171233 SVPPRAGFHSRLSHVMTLSQ--AAQAVTAPAPKSWOAHSAEFNNIAPSQITQIPLVK
480 490 500 510 520 530
cryla-105.pe AHTLOSQTIVRGEGFTGGDILRTSGGPFAYTIVNSQLPORVARIIPASTTNRIY
1171233 AHTLOSQTIVRGEGFTGGDILRTSGGPFAYTIVNSQLPORVARIIPASTTNRIY
540 550 560 570 580 590
cryla-105.pe VTVAGERIFAGQFNKMTDGDPLTFQSFYATINTATFPMSOGFTVGANTFSGNEVI
1171233 VTVAGERIFAGQFNKMTDGDPLTFQSFYATINTATFPMSOGFTVGANTFSGNEVI
600 610 620 630 640 650
cryla-105.pe IDRFELIPVATLEAEYNLERAKAVNALFTSTNQLGLKTNVDYHIDOVSNLVYLSDE
1171233 IDRFELIPVATLEAEYNLERAKAVNALFTSTNQLGLKTNVDYHIDOVSNLVYLSDE
660 670 680 690 700 710
cryla-105.pe IDRIEFVPAEYTFEAYDLERAO
1171233 IDRIEFVPAEYTFEAYDLERAO
720 730 740 750 760 770
cryla-105.pep
NRAA:13173244
13173244 source="GENBANK PROT" insecticidal crystal protein BTRX3 (Bacillus
thuringiensis serovar kunthalanags3)
SCORES Init1: 2134 Initn: 4262 Opt: 3035 z-score: 3442.1 E(): 2e-183
>>NRAA:13173244
Initn: 4262 Init1: 2134 Opt: 3035 Z-score: 3442.1 expect(): 2e-183
Smith-Waterman score: 4176; 61.9% identity in 1168 aa overlap
(1-1148:1-1120)
cryla-105.pe MDNNINIECIPYNCLSNPEVEVLGGERIETGYTPIDISLQTLFLLSEFVPGAGFVLGL
13173244 MDNNINIECIPYNCLSNPEVEVLGGERIETGYTPIDISLQTLFLLSEFVPGAGFVLGL
70 80 90 100 110 120
cryla-105.pe VDIINGIFGQSDWAFVLQIEQLINORIENSLGKTFDWDKAKQSLSNLRRI---FREW
13173244 VDIINGIFGQSDWAFVLQIEQLINORIENSLGKTFDWDKAKQSLSNLRRI---FREW
120 130 140 150 160 170
cryla-105.pe EADPTNPALREEMRIQFNDMNSALTTAIPLEFAVQNYQVPLLSVVOAANLSVLRLDVSV
13173244 EADPTNPALREEMRIQFNDMNSALTTAIPLEFAVQNYQVPLLSVVOAANLSVLRLDVSV
120 130 140 150 160 170

180 190 200 210 220 230
cryla-105.pe FQKQWGDAAITNSRNDLUTRIGNYDTHAVRWNTGLERVWGPDSRDWIRYQFREL
13173244 FQKQWGDAAITNSRNDLUTRIGNYDTHAVRWNTGLERVWGPDSRDWIRYQFREL
240 250 260 270 280 290
cryla-105.pe LTVLIDIVSLF---PNYDSRTYPIR--TVSQLTREIYTNVPLENDFSGFRSAQIEGSI
13173244 LTVLIDIVSLF---PNYDSRTYPIR--TVSQLTREIYTNVPLENDFSGFRSAQIEGSI
300 310 320 330 340 350
cryla-105.pe RSPHLMIDILANSITITDARHGEYVMSGHQIMASVFGSGPETFFLYCTMGNAAPQORIV
13173244 RSPHLMIDILANSITITDARHGEYVMSGHQIMASVFGSGPETFFLYCTMGNAAPQORIV
360 370 380 390 400 410
cryla-105.pe AOLGQGVIRTLISSTLYRRPF-NIGINNQOOLSVLDCGTEFAYGTTSSNLPSAVRKSGTVDSL
13173244 AOLGQGVIRTLISSTLYRRPF-NIGINNQOOLSVLDCGTEFAYGTTSSNLPSAVRKSGTVDSL
420 430 440 450 460 470
cryla-105.pe DEIPQNNVPPRQGFHRLSHVMSFSGFSNVSIIICAPMSWIHRSFNNIIASDS
13173244 DEIPQNNVPPRQGFHRLSHVMSFSGFSNVSIIICAPMSWIHRSFNNIIASDS
480 490 500 510 520 530
cryla-105.pe ITQIPLVATLEAEYNLERAKAVNALFTSTNQLGLKTNVDYHIDOVSN
13173244 ITQIPLVATLEAEYNLERAKAVNALFTSTNQLGLKTNVDYHIDOVSN
540 550 560 570 580 590
cryla-105.pe STNLRIVVAGHETPACQNNKMDTGDPITFQSFYATINTATFPMSOGFTVGADT
13173244 STNLRIVVAGHETPACQNNKMDTGDPITFQSFYATINTATFPMSOGFTVGADT
600 610 620 630 640 650
cryla-105.pe FSSGNEVIDRFEFLPVATLEAEYNLERAKAVNALFTSTNQLGLKTNVDYHIDOVSN
13173244 FSSGNEVIDRFEFLPVATLEAEYNLERAKAVNALFTSTNQLGLKTNVDYHIDOVSN
660 670 680 690 700 710
cryla-105.pe LVTVLSDFCLDEKRELSEKVKHAKELSDENLQDSNKKQNRPERGWSGCTITIQ
13173244 LVTVLSDFCLDEKRELSEKVKHAKELSDENLQDSNKKQNRPERGWSGCTITIQ
720 730 740 750 760 770
cryla-105.pe GDDVFKENYVTLSGTDECYPTVLYOKIDESKLAFTYRCYKDSQLELISLQNN
13173244 GDDVFKENYVTLSGTDECYPTVLYOKIDESKLAFTYRCYKDSQLELISLQNN
780 790 800 810 820 830
cryla-105.pe KHEVTNVPCTGSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSDGKCAHHSHFSL
13173244 KHEVTNVPCTGSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSDGKCAHHSHFSL
840 850 860 870 880 890
cryla-105.pe ESESVD-----APRME--SDLRFLGSDGKCMCPFPFSL
13173244 ESESVD-----APRME--SDLRFLGSDGKCMCPFPFSL
900 910 920 930 940 950

Monsanto Company
Final Report
Product Characterization Center

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1942525 PTFNPALEEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVTVQAAHLHSLVLRDVSVFQ
100 110 120 130 140 150
190 200 210 220 230 240
cry1a-105.pe RWGFDATNSRVNDLTGLIGNYTDHAWRYNTGLERWGPDSRDWRYNQFRELTLTV
1942525 RWGFDATNSRVNDLTGLIGNYTDHAWRYNTGLERWGPDSRDWRYNQFRELTLTV
160 170 180 190 200 210
250 260 270 280 290 300
cry1a-105.pe LDIVSLFPNYDRTYPIRTVSQLTREIYTNPVLENFDSFRGSAQIGESIRSEPHLMDIL
1942525 LDIVSLFPNYDRTYPIRTVSQLTREIYTNPVLENFDSFRGSAQIGESIRSEPHLMDIL
160 170 180 190 200 210
250 260 270 280 290 300
cry1a-105.pe NSITIIYDHRGEYWSGHQIMASPVGFSQPEFTFLYGTMTGNAAPOQRIVAQLGQVYR
1942525 NSITIIYDHRGEYWSGHQIMASPVGFSQPEFTFLYGTMTGNAAPOQRIVAQLGQVYR
280 290 300 310 320 330
370 380 390 400 410
cry1a-105.pe TILSSTLYRRP-FNIGINNQOQLVLDGTEFYAGT-SSNLPASAVYRKSGTVDLSDEIIPPQNN
1942525 TILSSTLYRRP-FNIGINNQOQLVLDGTEFYAGT-SSNLPASAVYRKSGTVDLSDEIIPPQNN
340 350 360 370 380 390
420 430 440 450 460 470
cry1a-105.pe NVPPRQGFHRSVHSMFRSGFSNVSIIIRAPMFSWIHRAEFNNIIASDSITQIPLVK
1942525 NVPPRQGFHRSVHSMFRSGFSNVSIIIRAPMFSWIHRAEFNNIIASDSITQIPLVK
400 410 420 430 440
540 550 560 570 580 590
cry1a-105.pe VTVAGERIFAGQNKMTDGPDPFQSFVSATINTAFTPPMSQSFTVGADTFSSGNEVY
1942525 VTVAGERIFAGQNKMTDGPDPFQSFVSATINTAFTPPMSQSFTVGADTFSSGNEVY
510 520 530 540 550 560
600 610 620 630 640 650
cry1a-105.pe IDREFLIPVTALAEYNNILRAQAKVALFTSNQLGLKNTVTDYHIDQVSNLVTYLSDE
1942525 IDREFLIPVTALAEYNNILRAQAKVALFTSNQLGLKNTVTDYHIDQVSNLVTYLSDE
570 580 590
6196667 source="GENBANK_PROT" insecticidal crystal protein CryIc [Bacillus
thuringiensis]
cry1a-105.pe
NRAA:61696667
6196667 source="GENBANK_PROT" insecticidal crystal protein CryIc [Bacillus
thuringiensis]
SCORES Initl: 2723 Initn: 4225 Opt: 2923 z-score: 3315.4 E(): 2.2e-176
>NRAA:61696667
Initn: 4225 initl: 2723 opt: 2923 z-score: 3315.4 expect(): 2.2e-176
Smith-Waterman score: 4546; 66.4% identity in 1061 aa overlap
(1-1036:1-1044)
```

```
1942525 PTFNPALEEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVTVQAAHLHSLVLRDVSVFQ
100 110 120 130 140 150
190 200 210 220 230 240
cry1a-105.pe RWGFDATNSRVNDLTGLIGNYTDHAWRYNTGLERWGPDSRDWRYNQFRELTLTV
1942525 RWGFDATNSRVNDLTGLIGNYTDHAWRYNTGLERWGPDSRDWRYNQFRELTLTV
160 170 180 190 200 210
250 260 270 280 290 300
cry1a-105.pe LDIVSLFPNYDRTYPIRTVSQLTREIYTNPVLENFDSFRGSAQIGESIRSEPHLMDIL
1942525 LDIVSLFPNYDRTYPIRTVSQLTREIYTNPVLENFDSFRGSAQIGESIRSEPHLMDIL
160 170 180 190 200 210
250 260 270 280 290 300
cry1a-105.pe NSITIIYDHRGEYWSGHQIMASPVGFSQPEFTFLYGTMTGNAAPOQRIVAQLGQVYR
1942525 NSITIIYDHRGEYWSGHQIMASPVGFSQPEFTFLYGTMTGNAAPOQRIVAQLGQVYR
280 290 300 310 320 330
370 380 390 400 410
cry1a-105.pe TILSSTLYRRP-FNIGINNQOQLVLDGTEFYAGT-SSNLPASAVYRKSGTVDLSDEIIPPQNN
1942525 TILSSTLYRRP-FNIGINNQOQLVLDGTEFYAGT-SSNLPASAVYRKSGTVDLSDEIIPPQNN
340 350 360 370 380 390
420 430 440 450 460 470
cry1a-105.pe NVPPRQGFHRSVHSMFRSGFSNVSIIIRAPMFSWIHRAEFNNIIASDSITQIPLVK
1942525 NVPPRQGFHRSVHSMFRSGFSNVSIIIRAPMFSWIHRAEFNNIIASDSITQIPLVK
400 410 420 430 440
540 550 560 570 580 590
cry1a-105.pe VTVAGERIFAGQNKMTDGPDPFQSFVSATINTAFTPPMSQSFTVGADTFSSGNEVY
1942525 VTVAGERIFAGQNKMTDGPDPFQSFVSATINTAFTPPMSQSFTVGADTFSSGNEVY
510 520 530 540 550 560
600 610 620 630 640 650
cry1a-105.pe IDREFLIPVTALAEYNNILRAQAKVALFTSNQLGLKNTVTDYHIDQVSNLVTYLSDE
1942525 IDREFLIPVTALAEYNNILRAQAKVALFTSNQLGLKNTVTDYHIDQVSNLVTYLSDE
570 580 590
6196667 source="GENBANK_PROT" insecticidal crystal protein CryIc [Bacillus
thuringiensis]
cry1a-105.pe
NRAA:61696667
6196667 source="GENBANK_PROT" insecticidal crystal protein CryIc [Bacillus
thuringiensis]
SCORES Initl: 2723 Initn: 4225 Opt: 2923 z-score: 3315.4 E(): 2.2e-176
>NRAA:61696667
Initn: 4225 initl: 2723 opt: 2923 z-score: 3315.4 expect(): 2.2e-176
Smith-Waterman score: 4546; 66.4% identity in 1061 aa overlap
(1-1036:1-1044)
```

```
1942525 PTFNPALEEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVTVQAAHLHSLVLRDVSVFQ
100 110 120 130 140 150
190 200 210 220 230 240
cry1a-105.pe RWGFDATNSRVNDLTGLIGNYTDHAWRYNTGLERWGPDSRDWRYNQFRELTLTV
1942525 RWGFDATNSRVNDLTGLIGNYTDHAWRYNTGLERWGPDSRDWRYNQFRELTLTV
160 170 180 190 200 210
250 260 270 280 290 300
cry1a-105.pe LDIVSLFPNYDRTYPIRTVSQLTREIYTNPVLENFDSFRGSAQIGESIRSEPHLMDIL
1942525 LDIVSLFPNYDRTYPIRTVSQLTREIYTNPVLENFDSFRGSAQIGESIRSEPHLMDIL
160 170 180 190 200 210
250 260 270 280 290 300
cry1a-105.pe NSITIIYDHRGEYWSGHQIMASPVGFSQPEFTFLYGTMTGNAAPOQRIVAQLGQVYR
1942525 NSITIIYDHRGEYWSGHQIMASPVGFSQPEFTFLYGTMTGNAAPOQRIVAQLGQVYR
280 290 300 310 320 330
370 380 390 400 410
cry1a-105.pe TILSSTLYRRP-FNIGINNQOQLVLDGTEFYAGT-SSNLPASAVYRKSGTVDLSDEIIPPQNN
1942525 TILSSTLYRRP-FNIGINNQOQLVLDGTEFYAGT-SSNLPASAVYRKSGTVDLSDEIIPPQNN
340 350 360 370 380 390
420 430 440 450 460 470
cry1a-105.pe NVPPRQGFHRSVHSMFRSGFSNVSIIIRAPMFSWIHRAEFNNIIASDSITQIPLVK
1942525 NVPPRQGFHRSVHSMFRSGFSNVSIIIRAPMFSWIHRAEFNNIIASDSITQIPLVK
400 410 420 430 440
540 550 560 570 580 590
cry1a-105.pe VTVAGERIFAGQNKMTDGPDPFQSFVSATINTAFTPPMSQSFTVGADTFSSGNEVY
1942525 VTVAGERIFAGQNKMTDGPDPFQSFVSATINTAFTPPMSQSFTVGADTFSSGNEVY
510 520 530 540 550 560
600 610 620 630 640 650
cry1a-105.pe IDREFLIPVTALAEYNNILRAQAKVALFTSNQLGLKNTVTDYHIDQVSNLVTYLSDE
1942525 IDREFLIPVTALAEYNNILRAQAKVALFTSNQLGLKNTVTDYHIDQVSNLVTYLSDE
570 580 590
6196667 source="GENBANK_PROT" insecticidal crystal protein CryIc [Bacillus
thuringiensis]
cry1a-105.pe
NRAA:61696667
6196667 source="GENBANK_PROT" insecticidal crystal protein CryIc [Bacillus
thuringiensis]
SCORES Initl: 2048 Initn: 2888 Opt: 2977 z-score: 3380.5 E(): 5.3e-180
>NRAA:1942525
Initn: 2888 initl: 2048 opt: 2977 z-score: 3380.5 expect(): 5.3e-180
Smith-Waterman score: 2977; 76.9% identity in 593 aa overlap
(29-619:1-590)
```

```
1942525 PTFNPALEEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVTVQAAHLHSLVLRDVSVFQ
100 110 120 130 140 150
190 200 210 220 230 240
cry1a-105.pe RWGFDATNSRVNDLTGLIGNYTDHAWRYNTGLERWGPDSRDWRYNQFRELTLTV
1942525 RWGFDATNSRVNDLTGLIGNYTDHAWRYNTGLERWGPDSRDWRYNQFRELTLTV
160 170 180 190 200 210
250 260 270 280 290 300
cry1a-105.pe LDIVSLFPNYDRTYPIRTVSQLTREIYTNPVLENFDSFRGSAQIGESIRSEPHLMDIL
1942525 LDIVSLFPNYDRTYPIRTVSQLTREIYTNPVLENFDSFRGSAQIGESIRSEPHLMDIL
160 170 180 190 200 210
250 260 270 280 290 300
cry1a-105.pe NSITIIYDHRGEYWSGHQIMASPVGFSQPEFTFLYGTMTGNAAPOQRIVAQLGQVYR
1942525 NSITIIYDHRGEYWSGHQIMASPVGFSQPEFTFLYGTMTGNAAPOQRIVAQLGQVYR
280 290 300 310 320 330
370 380 390 400 410
cry1a-105.pe TILSSTLYRRP-FNIGINNQOQLVLDGTEFYAGT-SSNLPASAVYRKSGTVDLSDEIIPPQNN
1942525 TILSSTLYRRP-FNIGINNQOQLVLDGTEFYAGT-SSNLPASAVYRKSGTVDLSDEIIPPQNN
340 350 360 370 380 390
420 430 440 450 460 470
cry1a-105.pe NVPPRQGFHRSVHSMFRSGFSNVSIIIRAPMFSWIHRAEFNNIIASDSITQIPLVK
1942525 NVPPRQGFHRSVHSMFRSGFSNVSIIIRAPMFSWIHRAEFNNIIASDSITQIPLVK
400 410 420 430 440
540 550 560 570 580 590
cry1a-105.pe VTVAGERIFAGQNKMTDGPDPFQSFVSATINTAFTPPMSQSFTVGADTFSSGNEVY
1942525 VTVAGERIFAGQNKMTDGPDPFQSFVSATINTAFTPPMSQSFTVGADTFSSGNEVY
510 520 530 540 550 560
600 610 620 630 640 650
cry1a-105.pe IDREFLIPVTALAEYNNILRAQAKVALFTSNQLGLKNTVTDYHIDQVSNLVTYLSDE
1942525 IDREFLIPVTALAEYNNILRAQAKVALFTSNQLGLKNTVTDYHIDQVSNLVTYLSDE
570 580 590
6196667 source="GENBANK_PROT" insecticidal crystal protein CryIc [Bacillus
thuringiensis]
cry1a-105.pe
NRAA:1942525
1942525 source="GENBANK_PROT" insecticidal Toxin: Structure And Channel
Formation
SCORES Initl: 2048 Initn: 2888 Opt: 2977 z-score: 3380.5 E(): 5.3e-180
>NRAA:1942525
Initn: 2888 initl: 2048 opt: 2977 z-score: 3380.5 expect(): 5.3e-180
Smith-Waterman score: 2977; 76.9% identity in 593 aa overlap
(29-619:1-590)
```

cryla-105.pe MDNPNNECHVNSLSNPEVEVLGGERIETGYTPIDISLSLQFLSLLFVPGAGFVLGL
61696667 MEENASQCTIPNCSNPEVILGGERISTGSSIDISLSLQFLVNSVPGGFLVGL
cryla-105.pe VDIWGLRGPSONDAVDFEQLINQLEFARNQASRLGLESLNLYIAESFREHEAD
61696667 IDFWGVIGVSCNDALFVSEQLERIAEARNANALGLEGNFNFNIVYEAPEKEEED
cryla-105.pe PTNPALREEMRIQFNDMNSALTAIPLEAVNVOPLLSVYQALHLVLRLDVSFVGO
61696667 PNPATREVIDRFLDGLLEDPSPRISGFPELITIVYQAANHLNLRDSVIFGE
cryla-105.pe RMGFDAAATNSRYNDLRLIGNYTHAVRWNTGSRVGPDSRDMIRYNFRRELNTV
61696667 RNLGATINNVNENYRLIRHIDEYADHCANTYNRGLNLPASTTSGOWITYNFRRLNTV
cryla-105.pe LDIVSLFENYSRTYPIRTYSOLTRIEYTNVLENFQSPRGAOG----LEAS-IRST
61696667 LDIAAFFPNYDNRRIPIQPVQGLTREVIDELI--NFNPQVQSAQLPTFNWESS-IRND
cryla-105.pe HLMDLINSITITVDAHR--GE--YWSGHQIMASPVGFSGPFTPLPYLGTGNAAPQORIVA
61696667 HLFIDLNLITFTDFWVSGRNFVWGHVRSLLIG--GNNITSPVIGREANQEPFRSFT-
cryla-105.pe QLGQGVYITLSSTLYR---RPNIGINNCQLSVLDGTETAYGTSSMLSPVRSKGTVD
61696667 -FNGVFRLLSNPTLRLLOQPMAPPFN--LRGVEGYEFS--TPTN--SFTYRGRTVDS
cryla-105.pe LDEIPPNVPPROGFSHRLSHVSNF-RSGFSNVSIIIRAPMFSWIRHSAFNIIAS
61696667 LTELPEDNSVPPREGYSHRLCHATFVQVSGTPELTIGVV---FSWTHRSATITNIDP
cryla-105.pe DSITQIPLVKAHTLQSGTIVRGPGFTGDLIRLRTSGPPAYTIVNINQQLPQRYARIR
61696667 ERINQIPLVKFRVWGTSVITPGFTGDLIRLRTSGDPSVLSQVNNINSPIQRYLRFR
cryla-105.pe YASTNLRIYV-TVAGERIFAQO-----FNKMTDGTDLTFCQSFYATINTATFPMSQ
61696667 YASSRDARVILVTAAGTGVGGQVSVNMPLOKMTWEIGENITJSFTFRYDFDPSNPSFRANP
cryla-105.pe GADTFSSNGEVNIDRFELIPVTATLEAEYNLERAKAVNALFTSTNOLG
61696667 DIIGSEQLPGAGSISG-ELYIDKIELLADATFEASDLERAKAVNALFTSSNOIG

cryla-105.pe LKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSEKVHAKRLSDERNLLQDSNFKDINRQ
61696667 LKTDVTDYHIDQVSNLVDCDEFCLDEKRELSEKVHAKRLSDERNLLQDPNFRGINRQ
cryla-105.pe PERGSGSTGITQGGDVFKNYVITLSGTDECYPIYLYOKIDESKLFKATRYQLRGYI
61696667 PDRGSGSTGITQGGDVFKNYVITLSGTDECYPIYLYOKIDESKLFKATRYVELRGYI
cryla-105.pe EDSQLEIYSTRYNAKHETVNPVPGTGSLLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC
61696667 EDSQLEIYLRYNKHEIVNPVPGTGSLLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC
cryla-105.pe EDGECASHHSHFSLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEA
61696667 EDGECASHHSHFSLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEA
cryla-105.pe LARVRAEKKWRDKREKLEMEINIVYKEAKESVDALFVNSQYDQLQADNTIAMTHAADKR
61696667 LARVRAEKKWRDKREKLEMEINIVYKEAKESVDALFVNSQYDQLQADNTIAMTHAADKR
cryla-105.pe VHSIEAYLPESVPGVNAAFEELEGRIFTAFSLYDARNVKNKGNGLSCWNVKGH
61696667 VHSIEAYLPESVPGVNAAFEELEGRIFTAFSLYDARNVKNKGNGLSCWNVKGH
cryla-105.pe VDVEANRHSVLVPEWSEVQVRCVPCGRGYILRVTAIRKGYEGEGCVTIHEINNTD
61696667 VDVEANRHSVLVPEWSEVQVRCVPCGRGYILRVTAIRKGYEGEGCVTIHEINNTD
cryla-105.pe ELKFSNCVREELFNNTVGMNTVNOBEYSGANTSRNGYNEAPSPADVASVEEKS
61696667 ELKFSNCVREELFNNTVGMNTVNOBEYSGANTSRNGYNEAPSPADVASVEEKS
cryla-105.pe
SW: 9087134
9087134 description="PESTICIDIAL CRYSTAL PROTEIN CRY7AB (INSECTICIDIAL
DELTA-ENDOTOXIN CRYVIA (B)) (CRYSTALLINE ENTOMOLOGICAL CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar dakota"
source="swissprot_prot" version="NA type="PRT
SCORES Initl: 671 Initn: 2624 Opt: 2690 Z-score: 3050.1 (1) 14e-164
>>SW: 9087134
initn: 2624 initl: 671 opt: 2690 Z-score: 3050.1 expect (1) 14e-164
Smith-Waterman score: 2778; 41.1% identity in 1196 aa overlap
(4-1177:29-1136)
cryla-105.pe MDNPNNECHVNSLSNPEVEVLGGERIETGYTPIDISLSLQFLSLLFVPGAGFVLGL
9087134 MDNPNNECHVNSLSNPEVEVLGGERIETGYTPIDISLSLQFLSLLFVPGAGFVLGL

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[illegible]

Smith-Waterman score: 2716; 41.1% identity in 1196 aa overlap
(4-1179-29-1136)

cr1yla-105.pe
MUNNLGVEDSRN...
10 20 30
NNNNNINECTPYNCLSPNEVEVLGGERLECYTP
100 110 120 130 140 150
NNNNNINECTPYNCLSPNEVEVLGGERLECYTP
100 110 120 130 140 150
cr1yla-105.pe
IDISLSITQFLLSE...
40 50 60 70 80 90
IDISLSITQFLLSE...
100 110 120 130 140 150
cr1yla-105.pe
ARNOAISRLGSLNLYOIAESFREWEAD...
100 110 120 130 140 150
ARNOAISRLGSLNLYOIAESFREWEAD...
100 110 120 130 140 150
cr1yla-105.pe
NYQVPLSVVQVORANLHLSVLDVS...
160 170 180 190 200 210 220 230 240
NYQVPLSVVQVORANLHLSVLDVS...
160 170 180 190 200 210 220 230 240
cr1yla-105.pe
NTGLERVWGPDSRDMIRYQFRRELT...
220 230 240 250 260 270 280 290 300
NTGLERVWGPDSRDMIRYQFRRELT...
220 230 240 250 260 270 280 290 300
cr1yla-105.pe
VLENFDSFRGSAQIEGS...
280 290 300 310 320 330 340 350
VLENFDSFRGSAQIEGS...
280 290 300 310 320 330 340 350
cr1yla-105.pe
MASPVGFSGPFTPLPYGTMGNAAP...
330 340 350 360 370 380
MASPVGFSGPFTPLPYGTMGNAAP...
330 340 350 360 370 380
cr1yla-105.pe
SVIDTGFAYTSTNLSAVYRKSG...
390 400 410 420 430
SVIDTGFAYTSTNLSAVYRKSG...
390 400 410 420 430
cr1yla-105.pe
FNSSVSIRAPMFSWHRSAFENNI...
440 450 460 470 480 490
FNSSVSIRAPMFSWHRSAFENNI...
440 450 460 470 480 490
cr1yla-105.pe
LERTSGGPATYVINGQLPQRYRARI...
500 510 520 530 540 550
LERTSGGPATYVINGQLPQRYRARI...
500 510 520 530 540 550
cr1yla-105.pe
GDFTFQSFYATINTAFTFPMSSQSF...
560 570 580 590 600 610
GDFTFQSFYATINTAFTFPMSSQSF...
560 570 580 590 600 610

9087134
EKGDLTVSGFYIEYETTIOFFNEHPK...
590 600 610 620 630 640
EKGDLTVSGFYIEYETTIOFFNEHPK...
590 600 610 620 630 640
cr1yla-105.pe
LERAKAVNALFTSTNQLGKTKNTVD...
620 630 640 650 660 670
LERAKAVNALFTSTNQLGKTKNTVD...
620 630 640 650 660 670
9087134
LEKAKAVNTLFTEGN-ALQKYVTDYK...
650 660 670 680 690 700
LEKAKAVNTLFTEGN-ALQKYVTDYK...
650 660 670 680 690 700
cr1yla-105.pe
LSDENLQDSNFKDINRQPERGMSGT...
680 690 700 710 720 730
LSDENLQDSNFKDINRQPERGMSGT...
680 690 700 710 720 730
9087134
LSYSNLLDPTFDSINSSEENGWYGS...
710 720 730 740 750 760
LSYSNLLDPTFDSINSSEENGWYGS...
710 720 730 740 750 760
cr1yla-105.pe
KIDESKLNKAFTRQLRGYIEDSDLEI...
740 750 760 770 780 790
KIDESKLNKAFTRQLRGYIEDSDLEI...
740 750 760 770 780 790
9087134
KIDESKLSRYKLGFISSQDLAEYIRY...
770 780 790 800 810 820
KIDESKLSRYKLGFISSQDLAEYIRY...
770 780 790 800 810 820
cr1yla-105.pe
ENRCA--PHLEWNPDLDCSC-RDGEK...
800 810 820 830 840 850
ENRCA--PHLEWNPDLDCSC-RDGEK...
800 810 820 830 840 850
9087134
ENRCAQOVLNDENPSSSESSWQDG--...
830 840 850 860 870 880
ENRCAQOVLNDENPSSSESSWQDG--...
830 840 850 860 870 880
cr1yla-105.pe
QDGHARLGNLEFEEKPLVGEALARK...
860 870 880 890 900 910
QDGHARLGNLEFEEKPLVGEALARK...
860 870 880 890 900 910
9087134
LEKAKAVNTLFTEGN-ALQKYVTDYK...
880 890 900 910 920 930
LEKAKAVNTLFTEGN-ALQKYVTDYK...
880 890 900 910 920 930
cr1yla-105.pe
NSQVPLSVVQVORANLHLSVLDVS...
920 930 940 950 960 970
NSQVPLSVVQVORANLHLSVLDVS...
920 930 940 950 960 970
9087134
LEKAKAVNTLFTEGN-ALQKYVTDYK...
940 950 960 970 980 990
LEKAKAVNTLFTEGN-ALQKYVTDYK...
940 950 960 970 980 990
cr1yla-105.pe
ARNKIKKDFNNLSQVAKGHVDSQV...
980 990 1000 1010 1020 1030
ARNKIKKDFNNLSQVAKGHVDSQV...
980 990 1000 1010 1020 1030
9087134
VRNVVRNGLFCLSDM--SANYVOEEN...
1000 1010 1020 1030 1040 1050
VRNVVRNGLFCLSDM--SANYVOEEN...
1000 1010 1020 1030 1040 1050
cr1yla-105.pe
TAKGEGGCVITLHEENLTKRPSQV...
1040 1050 1060 1070 1080 1090
TAKGEGGCVITLHEENLTKRPSQV...
1040 1050 1060 1070 1080 1090
9087134
TARKIGEGYITLDEEGHTDQNFYTC--...
1060 1070 1080 1090 1100 1110
TARKIGEGYITLDEEGHTDQNFYTC--...
1060 1070 1080 1090 1100 1110
cr1yla-105.pe
RGNEAPSVPADYASVVEEKSXTDGR...
1100 1110 1120 1130 1140 1150
RGNEAPSVPADYASVVEEKSXTDGR...
1100 1110 1120 1130 1140 1150
9087134
VWIEIGETEGTFFIVDSVELLMEE
1160 1170
VWIEIGETEGTFFIVDSVELLMEE
1160 1170
9087134
VWIEIGETEGTFFIVDSVELLMEE
1180 1190
VWIEIGETEGTFFIVDSVELLMEE
1180 1190
cr1yla-105.pe
VWIEIGETEGTFFIVDSVELLMEE
1200 1210
VWIEIGETEGTFFIVDSVELLMEE
1200 1210
NRAA:9087135

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[illegible]

```
cryla-105.pe -GDPILTQTSFSYATINTAFTPMQCQSFTVGADTFSSNGEVIYDRFLIIVTALEAYN  
          ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
9087135 EGKLTGSGFYEVSTTIQPFDKPXKITLJHLSDDSNSSSYFVDSIEFIPIVDWYDEKEK  
        560      570      580      590      600      610
```

```
cryla-105.pe LERAKAVNALFTSTNQGLKTNVTYDHYIQOVSNLVTLSDEFCLDEKRELSEKVHAKR
820      830      840      850      860      870
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
LEKAQKAVNLTFTGRN-ALQKDVTYDKVDQSILVDCISGDLYPNEKRELQNLVKYAKR
9087135
```

```

580      590      600      710      720      730
cryla-1.05.pe  JSDERNLLQDSNFKDINRQPERGMSGTITIOGGDDVFKENIVYLTGSDTCYPYLYQ
9087135      LSYERNLLDPTFDSINSEENGWAGXNGIVGDFPKGNLYIFSGTNDTQYPLYQ
710      720      740      750      760

```

```

cryla-105.pe KIDESKATRYRQVLRGYEJESQLEIYSTRVNAKHETVNVPGTGSWLPISAQSPCKGK
              740      750      760      770      780      790
9087135      KIDESKKEVTRYKLGKFJESQLEIYSTRVNAKHETLDV--SDNLLP--DILPENTCG
              770      780      790      800      810      820

```

```

cryla-105.pe  ENRCA--PHLEWNPDLDCSC-ROGECAHSHSHSLDIDVGCTDLNEDLGVWVFKFT
               800    810    820    830    840    850
9087135      ENRCAQOVLDPNPSGCSQMDG--ILDSHFSFTNIDTSGINHNHNSGJWLVFKST
               830    840    850    860    870

```

```
cryla-105.pe ODCHARLGNLEFLEEEXPLVGEALARVKRAEKKKDRKXLEWNIYVYKEAKESVDALVF  
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  
LEGYAFONLEVIEDPVTGEGEALARVKRQETTKWNKLQAOLTTTQTATYTARKAOLDNLFPA
```

```

cryla-105.pe  NSQYDQLCAQTNMTAMTHAADKEVHSIREAYLPSELYPCWAAAFEELEGRITAFSLVD
                |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
                NAQDSHLKIDVTTAAETAAKARKVQISREAYMSWLSVVPQWNPFTLSSEVQRAFQLVDYD
09087135      090  090  090  090  090  090  090  090  090  090  090  090  090  090  090

```

```

cryla-105.pe  ARN1KNGCDFNNGISOWNVKGHVDVECONNQRSVLIVVPENAEVISOEVRVCPGRGILYIV
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
VENVYVNRGRFNGLSDWIIVTSDVKVQEEENG-NVLYNNWDAQVLQNKVLQYQGRGILYIV
9087135      1000 1010 1020 1030 1040 1050

```

```

cryla-105.pe  TAYKRGEGCVIHEIENNDELKFSNCVEEYIYNNVTCTNDYVNOEYGGATSRN
               ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
9087135      TARKIGEGVINTTDEEGHTVOLRFTAC--EVIDASN-----AFIS-
               ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
               1040 1050 1060 1070 1080 1090

```

```
cry'la-105.pe  RGYNAPSVPADVASVEEKSSTDORRENCPENRGYDTPLPVGYTWKELSYFFETOK
1100      1110      1120      1130      1140      1150
9087135        -----GYITKELEFFFFDTTEK-----
1160      1170
```


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[illegible]

[illegible]

CRY1A-185, PE DARWVNGSFFNGSLGKNGVGHVYDEEQNNQSRVSVVVPWEAEVQVCPGRIYLLR
8469158 DWRVVRNRSFNGS, SDWITVSQVRKQDEENG - NVYLNNNDAAVLQNVKLLQVDRGYLLH

cry1a-105 ^{pe}	VTAKGCGCGVCTHELENTDPEAFSCVFEEETPNNTVTGNDYTVNQEEYGATYS	1048	1050	1060	1070	1080	1090
8469158	VTARKIGIGEVITVDSGHTDQKRCGEEIDAN	1048	1050	1060	1070	1080	1090

```

cryla-105.pe  NRGYNAPSVPADYASVVEEKSITDSRRBNPCFNRGYNVTPLPVGVNTELEFPETD
1100          1110          1120          1130          1140          1150
-----
8469158      -----GYTKNELFFPDOTE

```

```
cryla-105.pe KVHIEIGETGTFIVDSVELLMEE      1160    1170  
|| || || || || || || || || || || || || || || ||  
8469158 KVHIEIGETGIFVPSIELFLMEELC        1120    1130
```

cryla-105.pap
SW: 8469158

8469158 description="PESTICIDIAL CRYSTAL PROTEIN CRY7AA (INSECTICIDAL DELTA-ENDOTOXIN CRYVIIA)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (129 KDA CRYSTAL PROTEIN)." library=NA species="Bacillus thuringiensis" source="swissprot_prot" version=NA type=PRT

SCORES In11: 635 In1n: 2653 Opt: 2684 z-score: 3043.2 E(): 3.2e-161
>SW:8469158
In1n: 2653 In11: 635 opt: 2684 z-score: 3043.2 expect(): 3.2e-161
Smith-Waterman score: 2772; 41.4% identity in 1197 aa overlap
(4-1177:39-1136)

cryla-105.pe MDNNPINECIPYCNLSNPEVEVLGGRIETGYTP
 : : : : : : : : : : : :
8469158 MNLNLGVEDSNRLTNNSLNYPTQKALSPSLKNMNVQDFLSITERE--QPCLASGNNTA
 10 20 30

```
cryla-105.pe IDISLSTOFLISEE-VPGAGVLGVLDIIMGIPQSO--WDAFVLAQEQLINORITEE  
: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
INTVSVTGATLSALGVGSFTNYFYLVKIALGPENKGKIWEPTFEALIDOKIEEY  
8469158          70      80      90      100      110
```

[illegible]

```
cryla-1.05.pe      160          170          180          190          200          210
NYOPLSLTVYAQANHLHLSVLRSVDSPGPGWGFDAATINSYNDLITGLCNVTDHYRWY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
GYEIPLLTYAQAANHLHLSLVSTLYGDKWGFTQNNTTEENYNRQKRISYSZDCTKWY
180              190              200              210
```

860	870	880	890	900	910
-----	-----	-----	-----	-----	-----

860	870	880	890	900	910
-----	-----	-----	-----	-----	-----

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```
>>SW:8469145
initn: 3419 initl: 1824 opt: 2667 z-score: 3023.4 expect(1): 4.1e-160
Smith-Waterman score: 4431; 59.5% identity in 1174 aa overlap
(51-1177:72-1229)

cry1a-105.pe EVLGGERTGYTIDISLSLQFLSEFVPGAGFVLGLVDDIINGIFGFS---QWDAPL
8469145 AEVNNIDPFVSASTVQTGINTAGRIAGLVGVPFAGQASFYSLVGLMPSGRDPEWFLP
(51-1177:72-1229)

cry1a-105.pe VEVLGGERTGYTIDISLSLQFLSEFVPGAGFVLGLVDDIINGIFGFS---QWDAPL
8469145 AEVNNIDPFVSASTVQTGINTAGRIAGLVGVPFAGQASFYSLVGLMPSGRDPEWFLP
(51-1177:72-1229)

cry1a-105.pe VQEQILINRIEFPARNQAIISRLGLSNLYQIVAESFREWADPTNPALREEMRIQFNDM
8469145 EHEVQILRQVTEINTRTAIALEGIGRGYSYQQALETWLDNENDARSISILLERYVAL
(51-1177:72-1229)

cry1a-105.pe NSALTATPAIFAVQNYQVPLLSVYQAAHLHLSVLDSVFGQWGFDAATINRSYNDLT
8469145 ELDTTATPAIFRIREEVPLLMVYQAAHLHLLRLDASLFGSEWGNASDVNQYQEQI
(51-1177:72-1229)

cry1a-105.pe RLIGNYTDHARVWNTGLERVWGPDSMDIRYNQFRELITVLDIVSLFNPVDSSTYPI
8469145 RYTEESVNHCVQWYNTGLNLRGNAESRLYNQFRELITVLDIVSLFNPVDSSTYPI
(51-1177:72-1229)

cry1a-105.pe RTVSQLTREIYNPVLN-----FDGS--FRGSA--QIGESGI-RSPHLMILNSITTY
8469145 NTSQAQLTREIYDPIGRNAGSGFASFTNNFNNAAPSAFAEALFRPPHLLDPPEQLITY
(51-1177:72-1229)

cry1a-105.pe TDAHGRGY-----YMSGQIWAISVPGSGPEFTFLYGTMGNAAPQQRIVAGQGQVYRT
8469145 SASRSWSTQHMNYWGHRLNFRPIGOT---LNTSTQGLTNTSINFTVLTQFTSRDYRT
(51-1177:72-1229)

cry1a-105.pe LSST---LVRRPFNIGINQQLSLVDGTEFAVGTSSNLPASVYKSGT--VDSLDEIPP
8469145 ESNAGTNILFTTPVN-GVPMARFNFINPQNI-YERGATYISQPIQGVGIOLFDSSETLPP
(51-1177:72-1229)

cry1a-105.pe QNNVPPRGFGRHLSHVSMPRSGFSNSVSIIRAPMFWSHRSFAENNIASDSITQIP
8469145 ETTERPNYESYGRHLSHIGLI---IGNT---LRAPVSWTHRSADRTNIGPNRITQIP
(51-1177:72-1229)

cry1a-105.pe LVKRAHTLQSGTIWRPGPFTGDLIRRTSGGPFATYIIVNINGQLPQRYRARIYSTNL
8469145 LVKALNHSQGVTVWGGPFTGDLIRRTSGGPFATYIIVNINGQLPQRYRARIYSTNL
(51-1177:72-1229)

cry1a-105.pe RIYVTVAGEIRFAGPNKMTDGTPLTFQSFVATINTAFTFPMSSQSFVAGDPTSSGN
8469145 QFFTRINGTIVTIGNFNRIMRGONLEIRSFRTAGTFFPLFNAQSFIFLGAQSFNSN-Q
(51-1177:72-1229)
```

SCORES Initl: 1824 Initn: 3419 Opt: 2667 z-score: 3023.4 E(1): 4.1e-160

cryla-105.pep
NRAA: 8469145

8469145 source="GENBANK PROT" Pesticidal crystal protein crylBb (Insecticidal delta-endotoxin CryIb(b)) (Crystaline entomocidal protoxin) (140 kDa crystal protein)[gi|474894|gb|AAA2344.1| crystal protein

SCORES Initl: 1824 Initn: 3419 Opt: 2667 Z-score: 3023.4 E(): 4.1e-160
>NRAA: 8469145
Initn: 3419 Initl: 1824 opt: 2667 Z-score: 3023.4 expect(): 4.1e-160
Smith-Waterman score: 4431; 59.5% identity in 1174 aa overlap
(51-1177:72-1229)

cryla-105.pe VEVLGGERIETGVTPIIDISLSLTQFLISEFVPGAGFVLGLVDIIWIGIFGPS--QMDAFL
8469145 AEVNNIDPFVSASTVGTGINIAGRIILGVLPAGQGLASFYSFLVGLWPSGRDPWEIFL
8469145 30 40 50 60 70 80 90 100
cryla-105.pe VOIEQLNRIEFANQAIISLEGLSNLYQIYAEFRWEADPTNPALREEMRIQNDM
8469145 ERVEQLRQVTTENTATIAARLEGISGRYSQOALETMDNRNDARSILERYVAL
8469145 110 120 130 140 150 160
cryla-105.pe NSALTATPLFAVONYOVLLSVYQVAAHLHLSVLRDVSFGORWGFDAATINSRYNDLT
8469145 EDITATPLFRIRNEVEVLVYAAANLHLLLDASLFGSEWGMASSDVNGYVQEQI
8469145 170 180 190 200 210 220
cryla-105.pe RLIGNYTHARVWNTGLERVGPDSRWIRNQFRRLTLVLDIVSLFENYDSRTYPI
8469145 RYTESNHCYVYNGLANLGTNAESMLRYNFRDLTLGLVDLVALFPSTYTRTYPI
8469145 230 240 250 260 270 280
cryla-105.pe RVSLTRETINRPN-----FDGS--FRGSA--OGIEGSI-RSPHMDILNSITY
8469145 NTSAQDTESSTDTPEKNAFGFASTNNFNAPSFSAIEAAIFRPPLLDFPEQLITY
8469145 290 300 310 320 330 340
cryla-105.pe TDAHGEY-----YWSHOMASPVNPSGRTFTPLVSTWCAAPQORIVAQLGQGVYRT
8469145 SASSRSSTOHMYVWGHRLNRPICGT--NTSVGLTNNTSIRVTLQFTSRDYRT
8469145 350 360 370 380 390 400
cryla-105.pe LST-----LYRPPNIGINQQQLSVLDGTEPAKCHSNLPSAVYKST--VNSLRIIPP
8469145 ESNAGTNILFTPVN-GVPMARFNFINQNI-YERGAITTSOPYQAGTQVQDSSETPP
8469145 410 420 430 440 450 460 470 480 490 500 510 520 530
cryla-105.pe QNNVPPRQGSFRLSLVSNFRSGFNSVSIILIPAMFWSIHESAFNIIASDSYVQI
8469145 ETTERPNYESYHSLSHIGLI-----IGNT-----LRAPVYTHRSADRTNIGNRNPOIP
8469145 480 490 500 510 520 530
cryla-105.pe LVKAHTLQSGTIVVVRGPGFTGGDIILRTSGGPFAYTIVNINGQLPQRYRARIYASTNLL
8469145 LVKALNLHSGTVVVGPGFTGGDILLRTNTGTGFDILRLININVLPSQRYRVRIRVASTTDL

cryla-105.pe EYVYDRFELIPVQNLAEYNLERAKVAVNALFTSTNQGLKTNVTDYHIDQVSNLVTVL
8469145 EYVYDRFELIPVQNLAEYNLERAKVAVNALFTSTNQGLKTNVTDYHIDQVSNLVTVL
8469145 640 650 660 670 680 690
cryla-105.pe SDECLDKKLELSKAKAKLSLDERNLND-----SNFKDINRQPE
8469145 SDECLDKKLELSKAKAKLSLDERNLND-----SNFKDINRQPE
8469145 700 710 720 730 740 750
cryla-105.pe RGWGGSTGIITQGGDDVFENYVLSGTFCYPTLYQYKIDESKAKAFTRYQLRGYIED
8469145 RGWGGSTGIITQGGDDVFENYVLSGTFCYPTLYQYKIDESKAKAFTRYQLRGYIED
8469145 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930
cryla-105.pe SODELIVSYRYNAKHETVNPVGTGSLWPLSAQPKCEPAPRCAPHLEWPDJDCSRD
8469145 SODELIVSYRYNAKHETVNPVGTGSLWPLSAQPKCEPAPRCAPHLEWPDJDCSRD
8469145 940 950 960 970 980 990
cryla-105.pe GEKCAHSHHESLIDVGGCTDLNEDLGVWVIFKIKTQDGHARGLNLEFLKPKANGALM
8469145 GEKCAHSHHESLIDVGGCTDLNEDLGVWVIFKIKTQDGHARGLNLEFLKPKANGALM
8469145 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170
cryla-105.pe RYKRAEKWRDKREKLEWETINIVYKEAKESVDALFVNSQVDQLOADTNIAHHAADKRVH
8469145 RYKRAEKWRDKREKLEWETINIVYKEAKESVDALFVNSQVDQLOADTNIAHHAADKRVH
8469145 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320 1330 1340 1350
cryla-105.pe STREAYLPESLVIPGVNNAIFEELEGRIPTAFSLYDARNVKNNGDNGLSCWNVKGVHD
8469145 STREAYLPESLVIPGVNNAIFEELEGRIPTAFSLYDARNVKNNGDNGLSCWNVKGVHD
8469145 1360 1370 1380 1390 1400 1410 1420 1430 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530
cryla-105.pe VEEQNNQSVLVPPEWAEVSOEVRVCPGRGYILRVYAYKEGYGECGVTHIEINNTDEL
8469145 VEEQNNQSVLVPPEWAEVSOEVRVCPGRGYILRVYAYKEGYGECGVTHIEINNTDEL
8469145 1540 1550 1560 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690 1700 1710 1720
cryla-105.pe KFSNCVVEEIPPNVTCTNDYVNOEEYGGAYTSRNGYNAPSVA-----DIASVYEKK
8469145 KFSNCVVEEIPPNVTCTNDYVNOEEYGGAYTSRNGYNAPSVA-----DIASVYEKK
8469145 1730 1740 1750 1760 1770 1780 1790 1800 1810 1820 1830 1840 1850 1860 1870 1880 1890 1900 1910
cryla-105.pe SYTDGRENPCENRGGYDYTPLPVGYVTKLEYFPETDKVWIEGTEGTFIVDSVELL
8469145 SYTDGRENPCENRGGYDYTPLPVGYVTKLEYFPETDKVWIEGTEGTFIVDSVELL
8469145 1920 1930 1940 1950 1960 1970 1980 1990 2000 2010 2020 2030 2040 2050 2060 2070 2080 2090 2100
cryla-105.pe TYTDVRNHCEDRGVNPVPPVPGAYVTKLEYFPETDKVWIEGTEGTFIVDSVELL
8469145 TYTDVRNHCEDRGVNPVPPVPGAYVTKLEYFPETDKVWIEGTEGTFIVDSVELL
8469145 2110 2120 2130 2140 2150 2160 2170 2180 2190 2200 2210 2220 2230 2240 2250 2260 2270 2280 2290
cryla-105.pe LMEE
8469145 LMEE

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cry1a-105.pe LMBE
8469145 LMBE

cry1a-105.pep
NR001:14486714

14486714 source="GENBANK_PROT" Cry1Ba [Bacillus thuringiensis]

SCORES Init1: 1835 Initn: 2981 Opt: 2661 z-score: 3016.6 E(): 9.9e-160
>>NR001:14486714
Initn: 2981 Init1: 1835 Opt: 2661 Z-score: 3016.6 expect(): 9.9e-160
Smith-Waterman score: 4330; 58.9% identity in 1177 aa overlap
(51-1177:67-1228)

cry1a-105.pe VEVLGGERIETGYTIDISLSTQFLSEFVPGAG----FVLGLVLDIWMIGFPGSQWDAF
30 40 50 60 70 80 90
14486714 AEGNNIDPFVSASTVQTGINIAGRILGLVGPVAGQLASFSYFVLGELWP-KGRQWEIF
40 50 60 70 80 90

cry1a-105.pe LVQIEQLINQIEFARNQAIRSGLSNLVQIYAESFWEADPTPALREEMRIQFND
80 90 100 110 120 130
14486714 LEHVEQLINQOITENANTALARLOGLGDSFRAYQOSLEDLNRDDARTSRVLYTQVIA
100 110 120 130 140 150

cry1a-105.pe MNSALTTAIPLFAVQYQVPLSVYQAAHLHLSVLRDVSFVGORGWGFDAATINSRYNDL
140 150 160 170 180 190
14486714 LEIDFLNAMPALRINQVPLLMVYQAQANLHLLLRDASIFGSEFGLTSQBIQRYERQ
160 170 180 190 200 210

cry1a-105.pe TRILIGNYDHAIRVNTGLERVMGDPDSMDIRYNQFRRLTLVLVDIVSLFNPYDSRTYP
200 210 220 230 240 250
14486714 VETRDYSYCVENYNTGLNSLRGTNAASWRYNQFRRLTLVLVDLVALFYSYDRTYP
220 230 240 250 260 270

cry1a-105.pe IRVVSQLTREIYTPVLE-----NPDGFSFGSAQIEGS-IRSPHMLDIINSITIYT
260 270 280 290 300
14486714 INTSAQLTREYVYDIAIGATGVNMMYNNAPSFSAIEAAARSPHLLDLEQTIFTS
280 290 300 310 320 330

cry1a-105.pe DARRGE-----YVWSGHQIMASPVGFSPEFTPLPYGTGMGAAQQRIVALQCGGVRTL
310 320 330 340 350 360
14486714 ASRWENRTHMYTWRGTIOQSPRIG--GGLNTHGATWTSINPWTLPFAS--RDVYTE
340 350 360 370 380 390

cry1a-105.pe SST-----LYRRFPNIGINNQLQSLVDGTAFAYGTSNNLPAYVRKSGT--VDLSLEIP
370 380 390 400 410
14486714 SYAGVLLGWILEPIH-GVPTVRNFNTPNQISDRGTANY-SQPYESPGQLQKDSLELP
400 410 420 430 440

cry1a-105.pe PQNNVPPRPGFSHRLSHVSNFSGSSVSVIIRAPMFWSHRSAGFNIIIASDSITQI
420 430 440 450 460 470

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14486714 PETTERPNYSVSHRLSHIGIILQ-----SRVNV---PVYSWTHRSADRTNTIGNRITOI
450 460 470 480 490 500
cryla-105.pe PNVKADITSGTAVVVRGPGFAGDMLARTSGSPFAVTVININGOLPORARIRKRVASTIN
480 490 500 510 520 530
14486714 PNVKASEPGQTVVVGKFTGGLDINRINNGGFGPIRVTVNGPITQRYIRIGFYASTVD
540 550 560 570 580 590
cryla-105.pe LRIYVTVAGERIFACQFKMTDSDPQSFYSVANTFTFPMSSQSFVTVGADTFSSG
540 550 560 570 580 590
14486714 FDFVSRGGTTVNNFRFLKMSQDELKYQFVRAPFTTPTFTQDIIIRTSIQGLSGN
570 580 590 600 610 620
cryla-105.pe PNVYIDREFELIPVATLEAEVNLERAQANNAFTSTNQLGKPNVTYDHYQOQNLVTV
600 610 620 630 640 650
14486714 GEVYIDKIEIIPVATFATFEAYDLERAQAVNALFTNFRRLKTDVTDYDNOQVSNVAC
630 640 650 660 670 680
cryla-105.pe LSEDFCLDEKSEKVKHAKLSDERNLLQDSNFKDINRQP-----
660 670 680 690 700 710
14486714 LSEDFCLDEKSEKVKHAKLSDERNLLQDSNFKDINRQP-----
690 700 710 720 730 740
cryla-105.pe ERGWGSGTIIOGGDDVFKENYVTLSTGTFDECYPTLVYOKIDESKLPATRYOLRYIE
700 710 720 730 740 750
14486714 EHGWMGSENIITIOGNDVFKENYVTLPGTFNECYPTLVYOKIGESLKYTRYGLRGYIE
750 760 770 780 790 800
cryla-105.pe DSODLEIYSIRYNAKHETVNVPGTGLMPLSAQSPICKGCEPNRCAHLEWNPDLDCSCR
760 770 780 790 800 810
14486714 DSDOLEIYLIRYNAKHETVNVPGTGLMPLSAQSPICKGCEPNRCAHLEWNPDLDCSCR
810 820 830 840 850 860
cryla-105.pe DGEKCAHSHHFLSDIDVGCTDINEDLGWVVFIRKIKTDGCHARLGNLEFLKPLVGEAL
820 830 840 850 860 870
14486714 DGEKCAHSHHFLSDIDVGCTDINEDLGWVVFIRKIKTDGCHARLGNLEFLKPLVGEAL
870 880 890 900 910 920
cryla-105.pe ARVKAERKWKDEKLEKLEMETNIVYKEAKESVDALFVNSQYDQLOADNTNIAHAAKRV
880 890 900 910 920 930
14486714 SRVKAERKWKDEKLEKLEMETNIVYKEAKESVDALFVNSQYDQLOADNTNIAHAAKRV
930 940 950 960 970 980
cryla-105.pe HSIRAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARVVIKNGDFNNGLSCHWVKGHV
940 950 960 970 980 990
14486714 HSIRAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARVVIKNGDFNNGLSCHWVKGHV
990 1000 1010 1020 1030 1040
cryla-105.pe DVEEQNNRSVLVYVPEWEAEVSOEVRVCPGRGYILRVYAYKEGEGCVYTHEIENNTDE
1000 1010 1020 1030 1040 1050
14486714 DVQ-QSHRSDLVPEWEAEVSOEVRVCPGRGYILRVYAYKEGEGCVYTHEIENNTDE
1050 1060 1070 1080 1090 1100
cryla-105.pe LKFSNCVBEIEIPNNVTVCNDIYVNGQEEYG--GATSRNGYNEARVPA-----DYASVY
1060 1070 1080 1090 1100 1110

14486714 LKFNREEEVEYPTDTGTCDNTAHQGTAGCADCNSRNAGYEDAYEVDVTASVNYKPTY
1110 1120 1130 1140 1150 1160
cryla-105.pe EKSXTDGRNCEPCENRGRDYRTPVGVYTKLEVPFETDKWIEIGETEGFIVDSV
1120 1130 1140 1150 1160 1170
14486714 EETVTDVRDNHCEVDRCGVVYVPPVAGVYVTELEVFPETDTVWIEIGETEGFIVDSV
1170 1180 1190 1200 1210 1220
cryla-105.pe ELLLMEE
1170 1180 1190 1200 1210 1220
14486714 ELLLMEE
1170 1180 1190 1200 1210 1220
cryla-105.pe
1170 1180 1190 1200 1210 1220
SW:1345842
1345842 description="PESTICIDIAL CRYSTAL PROTEIN CRYIBA (INSECTICIDAL
DELTA-ENDOTOXIN CRYIB (A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (140 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar entomocidus"
source="swissprot_prot" version="NA type="PRT
SCOPES Initl: 1835 Initn: 3007 Opt: 2661 z-score: 3016.6 E(): 9.9e-160
(1228 aa)
initl: 3007 opt: 1835 opt: 2661 z-score: 3016.6 expect(): 9.9e-160
Smith-Waterman score: 4340; 59.0% identity in 1177 aa overlap
(521177-67-1228)
cryla-105.pe VEVLGEGEIEGTPTIDISLSTQFLSEFVPGAG----FVLGLVDIIGWIFGFSQWDAF
30 40 50 60 70 80 90
14486714 AEGNIDFPNAAVQVGINIAGRIILGVLPVFPAGLASFYFLVGLWLP-RGRDOWEIF
40 50 60 70 80 90
cryla-105.pe LVCISQLNQRIEERANONISREGLSNLYIAESFREWEADPTNPALEEMRIQFND
80 90 100 110 120 130
1345842 LEHNSQDNOQIKSNATLALRGLSSFRAYQOQSLDLEWLENRDDARTSRVLYQYIA
100 110 120 130 140 150
cryla-105.pe MSAITTAIPFAONTGVPPLSMKTAANHLHLSWLRDVSFGQWGFDAATINSRYNDL
140 150 160 170 180 190
1345842 LEIDFLNAMPFAIRNQEVDLENLVAAQAEHLLADASFOSEFGLTSOEIOYPERQ
160 170 180 190 200 210
cryla-105.pe TRILIGNYTHAVRYNTGLERWVGPDSDMLRISQFERRLTJTLVLDIVSLPNNDSRTYP
200 210 220 230 240 250
1345842 VERTEDYSDYCVWYNTGLNLRGTMAASWVRVYQFENDTLGLVNLVAFPSYDRTYP
220 230 240 250 260 270
cryla-105.pe IRTVSQITREYITNPVLE-----NFDGFRSAGIIEGS-INSPHMDLNSQIT
260 270 280 290 300 310
1345842 INTSAQLTREYITDAIGATGVNNAWNNYNNAPSFSAIEAAAIRSPHLDLPFISQITIF
280 290 300 310 320 330
cryla-105.pe DAHRGE-----YVMSGHOIMASVPVGFSPFTFELYTMGNAAPOQRIVAOLGQGVRTD
310 320 330 340 350 360
1345842 ASSRSNTHMTYWRGHTIQSRDIG--GGLNTSTHGATNTSINPVTLPFAS--RDVYTE
340 350 360 370 380 390

cry1a-105.pe	370	380	390	400	410
1345842	SVAGVLGGIYLEIH-GVPTVRFTNPQNISDRGTANY-SOPYESPOLQKDSETELP	400	410	420	430
cry1a-105.pe	420	430	440	450	460
1345842	PQNNVPRQGFHSHLSVMSFSGSNSSVSIIRAPMFSWIHRSSEFNFIASDSITOI	460	470	480	490
cry1a-105.pe	480	490	500	510	520
1345842	PLVKAHTLQSGTVVRGPGFTGDIILRTSGGPFAYTIIVNINGQLPQRYRARIYSTTN	520	530	540	550
cry1a-105.pe	560	570	580	590	600
1345842	PWKASELPQGTIVVRGPGFTGDIILRTNTGGPGIRVTGNGPLTORVRIGRFVASTVD	600	610	620	630
cry1a-105.pe	640	650	660	670	680
1345842	NEVYIDRRELIPVATLEAEVNLERAQKAVNALFTSTNOLGLKTNVTDVHIDQVSNLVTY	680	690	700	710
cry1a-105.pe	720	730	740	750	760
1345842	GEVYIDKTEIIPVATPEAEYDLERAQEAVALFTNTNPRLLKTDVTDVHIDQVSNLVAC	760	770	780	790
cry1a-105.pe	800	810	820	830	840
1345842	LSDEFCLDEKRELEKVKHAKRLSDERNLLQSNFKNRQNP-----	840	850	860	870
cry1a-105.pe	880	890	900	910	920
1345842	ERGWGSGTITIGGDDVKNVYVTLSGTFDCYPTLYLYKIDESKLKAFTRVQLRGVIE	920	930	940	950
cry1a-105.pe	960	970	980	990	1000
1345842	DSQDLRIYSIRYNAKHETVNVPGTGLMPLSAQSPIGKCGEPNRCAPIHLEWNPDLDCSCR	1000	1010	1020	1030
cry1a-105.pe	1040	1050	1060	1070	1080
1345842	DSQDLRIYLRINAKHETLDVPGTESLWPLSVESPIGRGCGEPNRCAPIHLEWNPDLDCSCR	1080	1090	1100	1110
cry1a-105.pe	1120	1130	1140	1150	1160
1345842	DGKCAHSHHFLSDIDVGCCTDLNEDLGWVWIFPKITQDGHARLGNLEFLFEKPLVGEAL	1160	1170	1180	1190
cry1a-105.pe	1200	1210	1220	1230	1240
1345842	DGKCAHSHHFLSDIDVGCCTDLNEDLGWVWVFKITQDGHARLGNLEFLFEKPLVGEAL	1240	1250	1260	1270
cry1a-105.pe	1280	1290	1300	1310	1320
1345842	ARVUKRAEKWRDKREKLEWETNIVVYKAEKESVDALFVNSQVDLOQADTNIMTHADKEV	1320	1330	1340	1350
cry1a-105.pe	1360	1370	1380	1390	1400
1345842	SRVUKRAEKWRDKREKLEWETNIVVYKAEKESVDALFVNSQVDLOQADTNIMTHADKEV	1400	1410	1420	1430
cry1a-105.pe	1440	1450	1460	1470	1480
1345842	HSIREAYLPESLPIGVNAAIFEELEGRIFTAFSLYDARNVKNKGDFNGLSCWNYKGVH	1480	1490	1500	1510
cry1a-105.pe	1520	1530	1540	1550	1560
1345842	HRIREAYLSELPIGVNAAIFEELEGRIFTAFSLYDARNVKNKGDFNGLSCWNYKGVH	1560	1570	1580	1590

cry1a-105.pe	1000	1010	1020	1030	1040	1050
1345842	DVEEQNNORSILVVPWEAEVSOEVRVCGPGGYILRVITAYKCGYGGCVTTHIEENNTDE	1060	1070	1080	1090	1100
cry1a-105.pe	1110	1120	1130	1140	1150	1160
1345842	LKFSNCVVEEIIYPNNTVTNDYTVNQEEVG--GAYTSRNRGYNEAESPVA---DIASVY	1170	1180	1190	1200	1210
cry1a-105.pe	1220	1230	1240	1250	1260	1270
1345842	LKFKKEEVEEYPTDCTGNDYTAHQGTAGCADACNSRNAGYEDAVEVDVTASVNYKPTY	1280	1290	1300	1310	1320
cry1a-105.pe	1330	1340	1350	1360	1370	1380
1345842	EKSXYTDERRNCPCEFRGRGYRDTPLPGVYVTKLEYFPETDKWIEIGETEGTIFVDSV	1390	1400	1410	1420	1430
cry1a-105.pe	1440	1450	1460	1470	1480	1490
1345842	EETVYTDVRDNHCEYDRGVNYPVPAGYVTKLEYFPETDTVWIEIGETEGKFIIVDSV	1500	1510	1520	1530	1540
cry1a-105.pe	1550	1560	1570	1580	1590	1600
1345842	ELLMLLEE	1610	1620	1630	1640	1650

61252383 description="Pesticidal crystal protein cry1Ba (Insecticidal delta-endotoxin Cry1B(a)) (Crystalline entomocidal protoxin) (140 kDa crystal protein)." library="NA species="Bacillus thuringiensis serovar entomocidus" source="swissprot_prot" version="NA type="PRT

SCORES Initl: 1835 Initn: 3008 Opt: 2661 z-score: 3016.6 E(): 9.9e-160
>>SW:61252383
initn: 3008 initl: 1835 opt: 2661 z-score: 3016.6 expect(): 9.9e-160
Smith-Waterman score: 4341; 59.0% identity in 1177 aa overlap
(51-1177:67-1228)

cry1a-105.pe	30	40	50	60	70
61252383	VEVLGGERIETGYTIDISLSLTQFLSSEFVPCAG----FVLGSLVDIINGIFGPSQNDAF	80	90	100	110
cry1a-105.pe	120	130	140	150	160
61252383	AEGNNIDPFVSASTVQTGINTAGRIILGVLPFAGQLASFSYFLVGLWELP-RGRDQWEIF	170	180	190	200
cry1a-105.pe	210	220	230	240	250
61252383	LVOIEQLINORIEEFARNQAIISRLGLSNLYQIYAEISPREWEADPTNPALREEMRIQFND	260	270	280	290
cry1a-105.pe	300	310	320	330	340
61252383	LEHVEQLINQQTENARNTALRLQGLSDSFAYQOQSLDLENRDDARTSRVLTQYIA	350	360	370	380
cry1a-105.pe	390	400	410	420	430
61252383	MNSALTAIPLFAVQNYQVPLLSVYQAAHLHLSVLRDVSFVGQRWFDATINGSYNDL	440	450	460	470
cry1a-105.pe	480	490	500	510	520
61252383	LELDFLNAPLFAIRNQEVPLLMVYQAANLHLLLRDASLFGSEFGLTSEIQRVYEQ	530	540	550	560
cry1a-105.pe	570	580	590	600	610
61252383	TRLGNTDHAIRVWNTGLERWCPDSRWIRXNQFRBELTLVLDIVSLFPNYSRTYP	620	630	640	650
cry1a-105.pe	660	670	680	690	700
61252383	VERTRDYSYCVYENYNTGLNSIRGTNAASVRYNQFRKDLTLGLDLVLPFFSIDRTYP	710	720	730	740
cry1a-105.pe	750	760	770	780	790
61252383	260	270	280	290	300

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61221651 LEIDFENAMPLFAIRNQEVPLIMVYQAANLHLLLRDASLFGSEFGLTSQRIQYRERQ
160 170 180 190 200 210

cry1a-105.pe TRILIGNYTHAVRWNTGLERVGPDSDWIRYNOFRRELTTLVLOIVSLFFNYSRTYP
200 210 220 230 240 250
61221651 VETRDYSDYCVWNTGLNSLGTNAASWRYNOFRDLTLGLVLOLVALFSLYDTRTP
220 230 240 250 260 270

cry1a-105.pe IRIVSOLTREITNPVLE-----NFDGSPRGSAQOIEGS-IRSPHMLDLNLSITTYT
260 270 280 290 300
61221651 INTSAQLTREVYTDIGAATGVNMAWMNYYNNAPFSIAEAAIRSPHLLDFLEQLTIFS
280 290 300 310 320 330

cry1a-105.pe DAHRGE-----YWSGHOIMASPVGSGPEFTPLVYGTMGNAAPQORIVAQLGQGVRTL
310 320 330 340 350 360
61221651 ASRWNTRHMTYWRGHTIQSRPIG--GGINTSTGCAINTSINPVLRFAS--RDVYRTE
340 350 360 370 380 390

cry1a-105.pe SST-----LYRPFNIGINNQQSLVDGTGTFAYGTSNLPASVYRKSQT--VDSLDEIP
370 380 390 400 410
61221651 SYAGVLLWGLYLEPIH-GVPTVRFNFTNPQNISDRGTANY--SQPYESFGLQMDSETLP
400 410 420 430 440

cry1a-105.pe PONNNPPQGGSHRLSHVSMFRSGFSNVSITIRAPMFSHTHSAEFNNIILASDISITQI
420 430 440 450 460 470
61221651 PETERPNVESYHRLSHIGIILQ-----SRVNV-----PYSWTHSADRNTIGPNWITQI
450 460 470 480 490 500

cry1a-105.pe PLVKAHTLQSGTIVVRGPGFTGGDILRTSGGPFAYTIVNINGOLPORYARIRVASTTN
480 490 500 510 520 530
61221651 PMVKASELPQGITVVRGPGFTGGDILRTSGGPFAYTIVNINGOLPORYARIRVASTVD
510 520 530 540 550 560

cry1a-105.pe LRIYTVVAGERIPAGQFNKMTMDTGLPTFOSFSYATINTAFTFMSQSSFTVGADTFSSG
540 550 560 570 580 590
61221651 FDFVFSRGGTVNNFRFLRTMNSGDELKYGNFVRRAFITPFTTQIQDIIRTSIQSLGN
570 580 590 600 610 620

cry1a-105.pe NEVVIDRFELIPVTALAEAYNLERAOKAVNALFTSTNLGLKNTVTDYHIDOVSNLVTY
600 610 620 630 640 650
61221651 GEVIDKIEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDOVSNLVAC
630 640 650 660 670 680

cry1a-105.pe LSDFFCLDEKRELSKVKHAKLSDERNLQDSNFQDNRPQ-----
660 670 680 690
61221651 LSDFFCLDEKRELSKVKHAKLSDERNLQDSNFQDNRPQ-----
690 700 710 720 730 740

cry1a-105.pe ERGGGSGTITIGGDDVFKENYVLTSGTDECPYLYLQKIDESKLAFTRLQRLGYIE
700 710 720 730 740 750
61221651 BHGWGSGENITIQEGNDVFKENYVLTSGTDECPYLYLQKIDESKLAFTRLQRLGYIE
750 760 770 780 790 800

cry1a-105.pe DSODLEYLIRYNAKHETVDPGCTSLWPLSAQSPGKGCENRCAPHEMNPDLDCSCR
760 770 780 790 800
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61221651 DSODLEYLIRYNAKHETVDPGCTSLWPLSAQSPGKGCENRCAPHEMNPDLDCSCR
810 820 830 840 850 860

cry1a-105.pe DGKCAHHSHFSLDIDVGCTDLNEDLGVWVIFKIKTODGHARLGNLEFLEKPLVGEAL
820 830 840 850 860 870
61221651 DGKCAHHSHFSLDIDVGCTDLNEDLGVWVIFKIKTODGHARLGNLEFLEKPLVGEAL
870 880 890 900 910 920

cry1a-105.pe ARVKRAEKKWRDKREKLEWETNIVYKEAESVDALFVNSQYDQLQADTNIAHAAKRV
880 890 900 910 920 930
61221651 SRVKRAEKKWRDKREKLEWETNIVYKEAESVDALFVNSQYDQLQADTNIAHAAKRV
930 940 950 960 970 980

cry1a-105.pe HSIREAYLPESLVIQGVNAAIFEELEGRIFTAFSLYDARNVKNKNGDFNGLSCWNVKGVH
940 950 960 970 980 990
61221651 HRIREAYLPESLVIQGVNAAIFEELEGRIFTAFSLYDARNVKNKNGDFNGLSCWNVKGVH
990 1000 1010 1020 1030 1040

cry1a-105.pe DVEQNNORSVLVWFENAEVSQEVRCGRGIVLRVTAYKEGYGEGCVTHIEINNTDE
1000 1010 1020 1030 1040 1050
61221651 DVQ-QSHRSDLVIFPEWAEVSQEVRCGRGIVLRVTAYKEGYGEGCVTHIEINNTDE
1050 1060 1070 1080 1090 1100

cry1a-105.pe LKFSNCVEEIEVPNNVTVCNDYTVNQEVG--GAVTSRNRGYNAPSVA---DYASVY
1060 1070 1080 1090 1100 1110
61221651 LKFSNCVEEIEVPNNVTVCNDYTVNQEVG--GAVTSRNRGYNAPSVA---DYASVY
1110 1120 1130 1140 1150 1160

cry1a-105.pe BEKSYTDGRRNCPBNFGNYRDTPLPGVYVKELEYFPETDKVWIEIGETGTFIVDSV
1120 1130 1140 1150 1160 1170
61221651 BEETVTVRRDNHCYDGVYVPPVPGVYVKELEYFPETDKVWIEIGETGTFIVDSV
1170 1180 1190 1200 1210 1220

cry1a-105.pe ELLLMEE
61221651 ELLLMEE

cry1a-105.pep
NRAA:1200002
1200002 source="GENBANK PROT" cry1Ba2 [Bacillus
thuringiensis gi|13959051|gb|AAK51084.1| delta-endotoxin Cry1Ba2 [Bacillus
thuringiensis serovar entomocidus gi|61252383|sp|P0A374|Cry1Ba BACTE Pesticidal
crystal protein cry1Ba (insecticidal delta-endotoxin Cry1B(a)) (Crystalline
entomocidal protoxin) (140 kDa crystal protein)

SCORES Initl: 1835 Initn: 3008 Opt: 2661 z-score: 3016.6 E(): 9.9e-160
>NRAA:1200002
Initn: 3008 Initl: 1835 Opt: 2661 Z-score: 3016.6 expect(): 9.9e-160
Smith-Waterman score: 4341; 59.0% identity in 1177 aa overlap
(51-1177:67-1228)

cry1a-105.pe VEVLGGERIETGYTIDISLSLTQFLSEFVPGAG---FVLGLVDIITWIGFSGQMDAF
30 40 50 60 70
1200002 AEGNNIDPFVSASTVQTGINIAGRIILGLVGLVFPFAGQLASFYSLVGLWLP-RGRDQWEIF
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SCORES Initl: 1835 Initn: 3007 Opt: 2661 Z-score: 3016.6 E(): 9.9e-160
>>NDAA:580949
initn: 3007 initl: 1835 opt: 2661 Z-score: 3016.6 expect(): 9.9e-160
Smith-Waterman score: 4340; 59.0% identity in 1177 aa overlap
(51-1177:67-1228)

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cryla-105.pe VEVLGERLEGTYPIDISLSLQFLSEFVPGAG---FVLGVIIWIGFSPQWDAF
580949 AEGNIDPFVSASTVQTGINIAGILGVLPFAQQLASFSVLGELWP-RGRDQWEIF

cryla-105.pe LVQIEQLNQRIEFARNQAIISRLGLSLYQIAESFREWADPNPALREEMRIQFND
580949 LEHVEQLINQITENARTALARLQGLGDSFRAYQSLSDWLENRODARTRSVLVYQVIA

cryla-105.pe MNSALTAIPFAVONYOVPLLSVYQAAHLHLSVRDVSFQGRWGFDAATINSRYNDL
580949 LEDDFLAMPFAIRNQEVFLMVYQAANLHLLDASLFSSEGLTSQBIQRYERQ

cryla-105.pe TRILIGNYTHAVRNTGLERWGPDSRDWIRYNOFRRLTLVLDIVSLFNPYSRTYP
580949 VETRDYSYCVENYTNGLSLRGTNAAWVAYNQFRDLTLGVLDLVALFSPYDTRYP

cryla-105.pe IRTVSQLTREIYNPVL-----NFDGSRGSAQIEGS-IRSPHMLDILNSITIYT
580949 INTSAQLTREVTDAIGATGVNMAWNNYNNAPSFSAIEAAIRSPHLLDLEQLTIFS

cryla-105.pe DARGE-----YWSGHQIMASPVGSGPEFTFPLYGTMGNAPOQRIVAQLQGQVYTL
580949 ASSRWNTRHMTYWRGHTIQSRPIG--GGINTSTGATNTSINPVLTRFAS--RDVYRIE

cryla-105.pe SST-----LYRPPNIGINNQLSVLDGTGTFAYGTSNNLPSAVYRKSQT--VDSLDEIP
580949 SYAGVLLMGILYLEPIH-CVPTVRNFNTPNQISDRGTANY-SQPYESPLQLKDSLETLP

cryla-105.pe PQNNVPPPGGSHRLSHVSMFRSGFSNSVSLIRAPMFSWIRHSAEFNNIITASDITOI
580949 PETTERPNYESHRLSHIGILQ----SRVNV--PVSYTHRSADRNTIGPNRITOI

cryla-105.pe PLVKAHTLOSGLTVVRGPGFTGGDILRRTSGGPFAYTIVNGLPORVEARIRVASTIN
580949 PMWKASELPGTIVVRGPGFTGGDILRRTSGGPFAYTIVNGLPORVEARIRVASTIN

cryla-105.pe LRIYTVAGERIFAQFNKMTMDTGLPTFQSFYATINFTAFPMSSQSFVAGDFSSG
580949 FDFVSGGTIVNFRFLRTWNSGDELKYNFVRRAFTTPTFTIQDIIIRTISQIGLSGN

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cryla-105.pe NEWYIDRELTPVTATLEAYNLESAQKAVNALSTNQGLKNTVTDVHDIDVSNLVTY
580949 GEYIDKLEIIPVTATLEAYNLESAQKAVNALSTNQGLKNTVTDVHDIDVSNLVTY

cryla-105.pe LSEFCLDEKSELSEKVKHAKRLSDERNLLQDSNFKDINRQP-----
580949 LSEFCLDEKSELSEKVKHAKRLSDERNLLQDSNFKDINRQP-----

cryla-105.pe ERGWSGTITIGQGDVFKENVTLSGTTFDECYPTLYKIDESKKAFTYQLRGVIE
580949 EHGWMGSENITIQGNVFKENVTLSGTTFDECYPTLYKIDESKKAFTYQLRGVIE

cryla-105.pe 760 770 780 790 800
580949 760 770 780 790 800

cryla-105.pe 820 830 840 850 860 870
580949 820 830 840 850 860 870

cryla-105.pe 880 890 900 910 920 930
580949 880 890 900 910 920 930

cryla-105.pe 940 950 960 970 980 990
580949 940 950 960 970 980 990

cryla-105.pe 1000 1010 1020 1030 1040 1050
580949 1000 1010 1020 1030 1040 1050

cryla-105.pe 1060 1070 1080 1090 1100 1110
580949 1060 1070 1080 1090 1100 1110

cryla-105.pe 1120 1130 1140 1150 1160 1170
580949 1120 1130 1140 1150 1160 1170

cryla-105.pe ELLMEE
580949 ELLMEE

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8469153 cry1a-105.pep
NRAA:8469153
8469153 source: GENBANK "PST" Pesticial crystal protein cry1Bd (Insecticidal
delta-endotoxin Cry1B(d)) Metastable entomocidal protoxin (140 kDa crystal
protein) gi|409787|gb|AF010792.1| insecticidal crystal protein Cry1I [Bacillus
thuringiensis serovar thuringiensis]
SCORES Init1: 1809 Initn: 3145 Opt: 524 z-score: 3006.4 E(): 3.7e-159
>>NRAA:8469153
initn: 3175 initl: 1809 opt: 2652 z-score: 3006.4 expect: 3.7e-159
Smith-Waterman score: 4261; 56.7% identity to 1218 aa velleap
(10-1177:40-1231)
cry1a-105.pe
8469153 EINALSIPAVSNHSAQMQLSLDARIEDSLCIAEGNNINPNDP---SAGSVQVY---INIA
10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180
40 50 60 70 80 90 100 110 120 130 140 150 160 170 180
cry1a-105.pe AGFVLGLVDIIWIGFSPQWDAFLVQIISOLINRILIFARNQMS
8469153 GRILGVLPFAGQQLASFYSLVUGELWPS-GRDPWEFLFLEHVQLIRQVTEKFNKIA
70 80 90 100 110 120 130 140 150 160 170 180
100 110 120 130 140 150 160 170 180 190 200 210
cry1a-105.pe SVYQAAHLHLSVLRDVSFVGQWGFDAATINSRYNDLTGLICNYTDHAWRYNTGLERV
8469153 MYTAQSNLHLLLRDASLFGSEWGNASSDVNQYQIQIRYETYSNHCVMQYNTGLNL
190 200 210 220 230 240
220 230 240 250 260 270 280 290 300
cry1a-105.pe WGPDSRDWIRYNQPRRELTITLVDIVSLFPNYDRTYPIRTVSQLTREIYNPVLN---
8469153 RGTNAESLRYNQPRDLTLGLVDLVALFPSSYDRTYPIINTSAQLTREIYDTPIGRTNAP
250 260 270 280 290 300
cry1a-105.pe --FDGS--FRGSA--OGIEGSI-RSPHMLDLNLSIITYDAIRGY-----YSGHQIM
8469153 SGFATSTNPNFNNAPSFSAIEAFLFPPLDLPPELTITYSASSRWSSTOHMNYWVGHRLN
310 320 330 340 350 360
cry1a-105.pe ASPVGFSGPEFTFLYTCMGNAAPQORIVAOLOGOVVRLTSSST---LYRRFPNIGINNQ
8469153 FRPIGT---LNTSTQGLTNTSINPVLQFTSRDVRTESNAGTILITPYN-GYPWA
370 380 390 400 410
380 390 400 410 420 430
cry1a-105.pe QLSVLGDTGFAYGTSNNLPSAVYRKSGT--VDSLDEIPPNQNNVPPROGFSHRLSHVSMF
8469153 RFNFIPQNI-YERGATTYSQPYQGVGIQLFDSETLPPETPTPTTPNVEYSYSHRISHGLI
420 430 440 450 460 470
cry1a-105.pe RSGFNSNVSVIIRAFMFSWIRHSAEFNNIIASDSITQIPLVKATHLQSTTVVRGPGFTG
440 450 460 470 480 490

8469153 cry1a-105.pe
480 490 500 510 520 530 540 550
---ICNT---LRAPVYSWTHRSADRTNTIGPNITQIPAVKGRFLFNGS-VISGPGFTG
cry1a-105.pe GDLA--RTSGGPEAVTVINNGOLPQ---RYRARIRYASTTNLRYVTVAGERIFAGQF
8469153 GUVLRLNNGNIGNRGYEVFIQFTSTSTRYRVRYASVTSIELNVLNGLNSSIFNTIL
530 540 550 560 570 580
cry1a-105.pe NKMTMTGDLPTFOSFYATINTAFTFPMSSQSFVTGADTFSSGNEVYIDREFELIPVTATL
8469153 PATAASLDNLQSGDFGVETNNFT---SATGNIVGARNFSAEVIIDREFEIPVTATL
590 600 610 620 630 640
cry1a-105.pe EAEYNLEAQAQVNAALFTSNGLTKNTVTDYHIDQVSNLVTYLSDEFCLDEKELSEKV
8469153 EAEYDLERAQAQVNAALFTSNPRRLKTDVTDYHIDQVSNVNAACLSDEFCLDEKELFEKV
650 660 670 680 690 700
cry1a-105.pe KXAKRLSDERNLLOD-----SNFKDINRQPERGWSGTITIQGGDD
8469153 KXAKRLSDERNLLODPNFTFISGOLSFASIDQSNFTSINELSEHGWSGSENVIOEGND
710 720 730 740 750 760
cry1a-105.pe KXENYVLTSGTDFECYTYVQKIDSKLAFTRYOLRGYIEDSQDLLEYISIRYNAKHE
8469153 VPEENWLTPTNECYPNVLYQKIGESLKAATRYOLRGYIEDSQDLLEYILIRYNAKHE
770 780 790 800 810 820
cry1a-105.pe TVWVTSLSLAPSLAPSGKCGKPCNRCAPHEWNPDLDCSCRDGKCAHSHHFLDID
8469153 TLDPGSLPFLSVKSLGKCGKPCNRCAPHEWNPDLDCSCRDGKCAHSHHFLDID
830 840 850 860 870 880
cry1a-105.pe VGTDSNEDLVVYTVKIQDGHARDNLPLEEKELVGEALRVKRAEKKWDRKREKL
8469153 VGTDLHENLGSWTVVKIKTQRYKAGNLFESEKSLIGELASRVKRAEKKWDRKREKL
890 900 910 920 930 940
cry1a-105.pe ERETNIYVKEKESVDALFVNGQYDGLQNDINIAADKRHSREAYLPELSVIRGV
8469153 QLETKRVYTEAKETVDALFVDHSHNLDQDIGNINNAQRIVHRHENDYDELFPPIPGI
950 960 970 980 990
cry1a-105.pe NAAIPEELEGRIFTAFSLYDARNVKNNGDFNNGSLCNVICHVDVDSQVNSVLVYFVW
8469153 NAVIFEELNRISTAFSLYDARNVKNNGDFNNGSLCNVICHVDVDSQVNSVLVYFVW
1010 1020 1030 1040 1050 1060
cry1a-105.pe EAEVSGEVRVCPGGLYLRVYAYKEGYGCGVTTHEINNTDELKXNCVEEYTPANTV
8469153 EAEVSGAVRVCPCGGLYLRVYAYKEGYGCGVTTHEINNTDELKXNCVEEYTPANTV
1070 1080 1090 1100 1110 1120
cry1a-105.pe TCNDYTVNGEEVGGAYTSRRNGYNEAPSV----PADYASVYEKSYTDGRRENPCFNRG
1080 1090 1100 1110 1120

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[illegible]

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222213658
 NTDELFNSCREEENPNNTVTCDNYNQEEYGGVTSRNGYNEAPSPVA---DYAS
 1110 1120 1130 1140 1150 1160
 NTDELPNICEEEVYEDTCDNYTAHQGT--AACNSRAGYEDAYEDVTTSVKNPK
 1110 1120 1130 1140 1150 1160

~~cryia-105.pe vWEGSYGRRNENFNGYGYDYSLPVQVKELEYEPDFTKWNIEIGTEGTFLVD
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
TYEEETVFRDNHCEYKGGYVFPVPAGNVTKLEJVEYPDFTKWNIEIGTEGTFLVD~~

1170
cryla-105.pe SVELLMEEE
|||||
22213635 SVELLMEEE
1230

cry1a-105.pep
SW:8469153

8469153 description="PESTICIDIAL CRYSTAL PROTEIN CRYBID (INSECTICIDAL DELTA-ENDOTOXIN CRYBID) (CRYSTALLINE ENTOMOTOXIN PROTOXIN) (40 KDa CRYSTAL PROTEIN)." library="NA species="Bacillus thuringiensis serovar. wuhanensis" source="swissprot prot" version="NA type="PRT

SCORES Inl1: 1809 Inltn: 3175 Opt: 2652 z-score: 3006.4 E(): 3.7e-159
 --SSW:8469153
 inltn: 3175 inl1: 1809 opt: 2652 z-score: 3006.4 expect(): 3.7e-159
 Smith-Waterman score: 4261; 56.7% identity in 1218 aa overlap
 (10-1177;40-1231)

```

cyla-1.05.pe
8469153      EIINALSIPAVNSHAQMDLSLARDIEDSLCAEKNINPLV---SASTVQIG--INIA
              10    20    30    40    50    60
              MNPNFNIENICPNCLSNPEVGLGRIETGYTPIDIS
              10    20    30

```

40 50 60 70 80 90
 cryla-105.pe LSLTQFLSSEFVPG-AGEVGLGLVDIIWGIFGPSQWDALFVQIEQLINQRLEEFARNQAI
 8469153 GRILGVGVPPACQLASFSYSLVGLWPS-GRDPWEIFLEHVQEIQRQVTTENTRTAIA

[illegible][illegible]

```

220      230      240      250      260      270
cyy1a-105.pe WGPDSRRIRYNQFRRELTLLVILSVLPNTYDSRTYRTVSQLTREIYTPVLEN---
8469153      RGTNAESWLRYNQFRRDITGLGDLVALPFSYDTTYTINTSAQLTREIYTOPIGRTNAP

```

```
cryla-105.pe --FDGS--FRGSA--QGIEGSI-RSPHLMILNSTITYTDARGEY-----YWGGHQIM
```

8469153 SGFASTWFWNNWWSFSAIEAALFRPPLHDPFQOLIIYISASSRWSSTCHNNYVWGHRLN
310 320 330 340 350 360

cr1a-105.pe ASPVSGSEFTEFPYGMGMAAPQIRVAQGGQVRLTSS---LYRPPFNGINNO
330 340 350 360 370

8469153 FRPIGTT---LNTSTOGLTNTSINPVTIQTFSRDVARTESNAGTNILFTFVN-GVPMFA
370 380 390 400 410

cr1a-105.pe QLSVLDTGFAYGTSSNLPSAVYRKSGT--VDSLDEIPPONNVPPROGFSHRHSVSMF
420 430 440 450 460 470

8469153 RFNFIPQNI-YERGATTYQGVGIGLQFDESELPETTPETPRNYSYSHRSLSHGLI
480 490 500 510 520

cr1a-105.pe RSGFSNWSYIIRAPMSWTHRSAREFNWIIASDSTOIPVKAHTLOSCTTVRPGPFTG
530 540 550 560 570 580

8469153 ---LGN---LRAPVSWTHRSADKINIIQNRITQIPAVKGRFLFNGS-VISGPFGTG
590 600 610 620 630

cr1a-105.pe GDILR-RTSGGPFAYTIVNINGLOPQ---RYRARIRYASTNLRIVYVAGERIFAGOF
640 650 660 670 680 690 700

8469153 GDVULNRNNGNIQNRGVIEVPIQFTSTIRYRVARYASVTSIELNVNLGSSIFTNLT
710 720 730 740 750 760

cr1a-105.pe NKTMDTGDPILTQSFYSATINMTAFTPMQSGSFTVGADITSSNGEVIIDRPELIPVTAIL
770 780 790 800 810 820 830

8469153 PATAASLDNLQSDGFGYVEINNAFT---SATNIGVARNFSANAEVIIDRPELIPVTATF
840 850 860 870 880 890 900

cr1a-105.pe EAEVYLERAKXVWALFTSTNOLGLKNTVDYHIDQVSNLVTVLSDPEFLCDEKRELESEKV
910 920 930 940 950

8469153 EADIDELERKAVNAFTSTNPRKKTIDVIDHIDQVSNWVACLSDEFLCDEKRELESEKV
960 970 980 990

cr1a-105.pe KXARLSRERNLND-----SNFKINRQPERGGSGTITQTGGDD
1000 1010 1020 1030 1040 1050

8469153 KYAKRLSDNLDQPNP---LQGLSFASDQSGSFTSINELSEHGWSGSENVITQEGND
1060 1070 1080 1090 1100

cr1a-105.pe VKENYVTLGTFDECYPTNLYKIDBSKAPVYQLRGTESDDEIYSIRNAKHE
1110 1120 1130 1140 1150 1160 1170

8469153 VKENYVTLGTFDECYPTNLYKIDBSKAPVYQLRGTESDDEIYSIRNAKHE
1180 1190 1200 1210 1220 1230 1240

cr1a-105.pe TVNYPGTGSLWPLSQAOSPIGKCEPNCAPHEPNDPDCSCDGGKCAHSHHSLDND
1250 1260 1270 1280 1290 1300 1310 1320

8469153 TLDVPGDTSLWPLSVKSPIGRCGEPNCAPHEPNDPDCSCDGGKCAHSHHSLDND
1330 1340 1350 1360 1370 1380 1390 1400

cr1a-105.pe VGCTDLNEDLGVMVFKIKTODGHARLGNLEFLSEKPLVGALARKVRAKWKVQRRKK
1410 1420 1430 1440 1450 1460 1470 1480

8469153 VGCTDLNHLGVMVFKIKTODGHARLGNLEFLSEKPLVGALARKVRAKWKVQRRKK
1490 1500 1510 1520 1530 1540 1550 1560

cr1a-105.pe EMETNIVYKEAKESVDALFVNSQYDQLQADTNIAHDAADKRVHSIREAYLPDLSVPGV
1570 1580 1590 1600 1610 1620 1630 1640

```

cryla-105.pe 260 270 280 290 300
RTVSQLTREIYNPVLEN-----FDGS--FRGA---QGIEGSI-RSPHMLDILNLSITYY
NTSAQLTREIYTDPIGTNAPSGFASFTWNNPNNAPSSAIEAAIFRPPHLLDFPEQIITY
290 300 310 320 330 340
310 320 330 340 350 360
TDARR-----GEYWSGHQIMASPVQFSQPEFTPLIGTWMGAAPQORIVAQLGGQVYRT
SASRSWSSTOHMYWVGRHLNFRPIGIGT---LNTSTQGLNNTSINPVLTKQTSRDVYRT
350 360 370 380 390
cryla-105.pe 370 380 390 400 410
LSST---LVRRPFNIGINNQSLVDLGTPEYAGTSSNLPASVVRKSG--TWDSLDEIPP
ESNAGTNILFTTPVN-GVPWARFNFINPQNI-YERGATTYSQPVQGVIGOLFDSSETLPP
400 410 420 430 440 450
cryla-105.pe 420 430 440 450 460 470
QNNVPPRGFGSHLSHVSMRSGFSNSVSIIIRAPMSWIHRSAEFNNIIASDSITOIP
ETTERPNYSVSHRLSHGIGI---IGNT---LRAPVYSWTHRSADRTNITGNRITOIP
460 470 480 490 500
cryla-105.pe 480 490 500 510 520 530
LVKXHTLQSGTTVVRGPGFTGGDILRTSGGPFATYIVNNGQLPQRYARIRYASTTNL
LVKALNLSHGVTVWGPGFTGGDILRTTGTGDIRINVPQSRKYRIRYASTTDL
510 520 530 540 550 560
cryla-105.pe 540 550 560 570 580 590
RIVYVAGERIFAGFNKMTDGLPTFOSFSYATINTAFFPMSOSSFTVCAGDTFSGN
OFFTRINGTVNIGNSFTWNRGDNLEYSFRTAGSTFPNFLNAQSTTTLGAQSFN-Q
570 580 590 600 610 620
cryla-105.pe 600 610 620 630 640 650
EVIDRFEIPIVATLEAYNLERAKAVNALFTSTNQLGKTNVTDYHIDQVSNLVTYL
EVIDRVEFPVAEVTFEAYDLERAKAVNALFTSTNPRRLKTDVTDYHIDQVSNVACL
630 640 650 660 670 680
cryla-105.pe 660 670 680 690
SDFCLDEKRELSEKXKAKLSERNLIQD-----SNFKDINROPE
SDFCLDEKRELFEXKYAKLSERNLIQDPNFTTISGULSFASIDGOSNPPSINELSE
690 700 710 720 730 740
cryla-105.pe 700 710 720 730 740 750
RGWGSGTITIOGGDVFKENYVTLSGTDFCEVPTLYQKIDESLKAFTRVQLRGYIED
HGWGNSNVTIQEGDNVFKENYVTLPTTFNECYPNLYQKIGESELKXATRYQLRGYIEN
750 760 770 780 790 800
cryla-105.pe 760 770 780 790 800 810
SQDLIEYIRYNAKHETVNPFGTCSLWPLSAQSPICKGCEPNRCAHPLEWNPDLDCSQRD
SQDLIEYLIRYNAKHEANVPGTESIWSISAESITGKTEPNRCAPHYENWNPDLDCSQRD
810 820 830 840 850 860
cryla-105.pe 820 830 840 850 860 870
GEKCAHSHRHSIDIVDGTDLNEDLGWVIFKIKTDQGHARLGNLFELEKPLVGEALIA
GEKCAHSHRHSITDIVDGTDLNHLGNLWIFKIKTDQGHARLGNLEYLEKPLVGEALR
870 880 890 900 910 920

```

```

SCORES      Init1: 1760      Initn: 3383      Opt: 2550      z-score: 2890.4      E(): 1.1e-152
>>NRRA:565394
Initn: 3383      Init1: 1760      Opt: 2550      z-score: 2890.4      expect(): 1.1e-152
Smith-Waterman score: 4314;      58.7% identity in 1176 aa overlap
(51-1177:72-1233)

```

```
cryla-105.pe VEVILGGRIETGVTPIDISLSLTQFLSEFVPCAGVLGLVDIIWIFGPS---OWDAFL  
      30      40      50      60      70  
565394 AEVNNDIPFYASTVQTGINIAGRIILGVLGVPFQAQLASFYSFLVGELWPSPGRDWEJFL  
      50      60      70      80      90      100  
  
cryla-105.pe VOIEQLINORIEBFARNOAISRLSGLSNLYOIAYESFREWEADPTPALREMRIOQNMD  
      80      90      100      110      120      130  
565394 EHVQLIRQOVYNTENTAIARLEGIGRGVSYQAALSTLWDNDRASRSLIERVAL  
      110      120      130      140      150      160  
  
cryla-105.pe NSALTATPILPAVONYOYPLISVVYQAAHLLSVLRDSVFQRGWGFDAATINSRYNDLT  
      140      150      160      170      180      190  
565394 ELDTITAPLPIFRNEEYPLLWYAQAANLHLLLRDASLFGSEMGWASSDVNYQQEQI  
      170      180      190      200      210      220  
  
cryla-105.pe RUIGNYTHAVRYNTGLERWGPDSRDTRYNQPRRELTITLVIVSYFPNYDSRTYPI  
      200      210      220      230      240      250  
565394 RYTEYSNHCVQWYNGLNNLRGTNAESLYRNQPRDITGLVLDLVAIFPSYDTRTYPI  
      230      240      250      260      270
```


cry1a-105.pe SODELEYSIRYNAKHETVNPVGTGSLWPLSAQSPIGKGPENRCAPHLWNPDLDCSCRD
8469150 SODELEYSIRYNAKHETVNPVGTGSLWPLSAQSPIGKGPENRCAPHLWNPDLDCSCRD
810 820 830 840 850 860
cry1a-105.pe GEKCAHSHHESLDIDVGCTDLNEDLGVWVIFKIKTQDGHARGNLEFEEKPLVGEALA
8469150 GEKCAHSHHESLDIDVGCTDLNEDLGVWVIFKIKTQDGHARGNLEFEEKPLVGEALA
870 880 890 900 910 920
cry1a-105.pe RVKRAEKKWRKREKLEWETNIVYKEAKESVDALFVNSOYDLOQADNTAMTHAADKEVH
8469150 RVKRAEKKWRKREKLEWETNIVYKEAKESVDALFVNSOYDLOQADNTAMTHAADKEVH
930 940 950 960 970 980 990
cry1a-105.pe SIREAYLPELSVIPGVNAALFEELEGRIETAFSLYDARNVKNKGDFNGLSCWNVKGHVD
8469150 SIREAYLPELSVIPGVNAALFEELEGRIETAFSLYDARNVKNKGDFNGLSCWNVKGHVD
990 1000 1010 1020 1030 1040
cry1a-105.pe VEQNNQRSLVVPWEAREVSQEVRCVGRGVLRTVAYKEGEGCVTHIEHNNTDEL
8469150 VEQNNQRSLVVPWEAREVSQEVRCVGRGVLRTVAYKEGEGCVTHIEHNNTDEL
1050 1060 1070 1080 1090 1100
cry1a-105.pe KFSNCVEEIEVNNVTICNDYVNO--EEYGAVTSNRGNAPSVA---DVASVE
8469150 KFSNCVEEIEVNNVTICNDYVNO--EEYGAVTSNRGNAPSVA---DVASVE
1110 1120 1130 1140 1150 1160
cry1a-105.pe ESKYTDGRNCPENRGYDYTPLPVGVYTKLEYFPEDTKVMIEIGTEGTFIVDSVE
8469150 ESKYTDGRNCPENRGYDYTPLPVGVYTKLEYFPEDTKVMIEIGTEGTFIVDSVE
1170 1180 1190 1200 1210 1220
cry1a-105.pe LLLMEE
8469150 LLLMEE
1230
cry1a-105.pep
NRAA:62288329
62288329 source="GENBANK_PROT" crystal protein Cry9Ed1 [Bacillus thuringiensis]
SCORES Initl: 507 Initn: 1561 Opt: 2175 Z-score: 2464.6 E(): 5.5e-129
>>NRAA:62288329
Initn: 1561 Initl: 507 Opt: 2175 Z-score: 2464.6 expect(): 5.5e-129
Smith-Waterman score: 2299; 37.8% identity in 1196 aa overlap
(16-1177:57-1154)

cry1a-105.pe LLESEFVPAG---FVLGLVDITWIGIFGPSQWDAFLVQIEQLINQRI--EEFARNOAISRL
62288329 LG---VPFAGQVTFYTFLLNQLPPTNNNAWFAQVEELIDQRISSDOVVRN-ALDDL
50 60 70 80 90 100 110 120 130
cry1a-105.pe EGLSNLYQAYAESFREWEADPTNPALREMRIQ-FNDNSALTITAIPLFAV---QNVQV
62288329 TGLHDYNEYLAALAEELDRP-NGA-RANLAFQRFENLHTAFVTRMPSFGTGFSGQSDAV
140 150 160 170 180 190
cry1a-105.pe PLISVYVQAAHLHLSVLRDVSVSGQWGFDAATINSRYN--DLTRLIGNYTDHVRWYN
62288329 ALLTVYQAANLHLLKDAEITYGARWGQQSQQLNFYNAQQDQRTIRI---YTNHCVAIYN
200 210 220 230 240 250
cry1a-105.pe TGLERVWGSDSRMIRVYNQFRRELITLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYNPV
62288329 RGLLEDLKGNTIESWVYHQFRREMTLMDLVALFPYVYVQYVNGANPQLTREIYIDPV
260 270 280 290 300 310
cry1a-105.pe LENP---DGSFR--GSA-----QGIEGS-IRSPHLMIDLSITIIYDHAHGEY-----Y
62288329 VFNPANQGLCRWGNPNYMTFSGLENAFIRPHLFDRLANSLTI--NSHRFPISSNFMDY
320 330 340 350 360 370
cry1a-105.pe WSGHQMASPVGSGPEFTPLVXTGMGNAAPQORIVAGLQGVVRLTSLVYRRFPNIGI
62288329 WAGHTLRYSYMNNSAVQ-----EDSYGALTPTRVITNPGVNGTNHISTEAVDFRSLVGI
380 390 400 410 420 430
cry1a-105.pe NN-QQLSVLDGTGFAYGTSNLPASAVYKSGTVDSLDLDEIPQNNVPPRQGFSHRLSHVS
62288329 YGVHRASFVPGGLFN-GTIS--PANAGCRN-LHDTRDVLPLEENNGSP---SHRLSHVT
430 440 450 460 470
cry1a-105.pe M--FRSGFNSVSIIRAPMPSWHRSAEFNNIIASDSITQIPLVKAHTLQSGTTVVRGP
62288329 FLSFQTNQAGSLANGSGVPLVYVWARQDIDFNNTITANRITQLPLVKAFAIAAGTTIVKGP
480 490 500 510 520 530
cry1a-105.pe GFTGGILARTSGGPFVAVTINVGOLPORYRIRYRIVASTTNLRIVYTVAGERIFAGOFN
62288329 GFTGGILARTSGGPFVAVTINVGOLPORYRIRYRIVASTTNLRIVYTVAGERIFAGOFN
540 550 560 570 580 590
cry1a-105.pe KTMDDTGLTQSFYATINTAFTPMSSQSFVAGADTFSSGNEVYIDRFELIPVATILE
62288329 RTMSRQESRYSVSEFTPTFTTQSDFIQTSIGLSGNGEVYIDRIEILIPVNPARE
600 610 620 630 640 650
cry1a-105.pe AEYNLEAKAVNALFTSTNGLKXNVTDYHIDQVSNLVTLSDFCLDEKKEELSEKVK
62288329 AEEDLEAAKAVASLFTTRD-GLQNVNVDYDQAAANLVSCLSDEQYHDKRMLEAVR
660 670 680 690 700 710

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Product Characterization Center

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cry1a-105.pe 680 690 700 710 720 730
HAKLSQKRLQDQNFQINQPERGCGSTGTTIQGDDVFKENTVTLSGTFDECPYPT
62288329 720 730 740 750 760 770
HAKLSQKRLQDQNFQINQPERGCGSTGTTIQGDDVFKENTVTLSGTFDECPYPT
cry1a-105.pe 740 750 760 770 780 790
YLYKQIESKAPKATLEBWEEDSODILIRYNKAKHETVNVFGTGLWPLSAQSI
62288329 780 790 800 810 820 830
YLYKQIESKAPKATLEBWEEDSODILIRYNKAKHETVNVFGTGLWPLSAQSI
cry1a-105.pe 800 810 820 830 840 850
GKCEPNRCAHLEWNPOLDCCSDCKC-AHCEPFLSIDIDVGTDMEDLGVWVIFKI
62288329 840 850 860 870 880 890
GKCEPNRCAHLEWNPOLDCCSDCKC-AHCEPFLSIDIDVGTDMEDLGVWVIFKI
cry1a-105.pe 860 870 880 890 900 910
KTQGHARLGNLEFEELVGEALARVKAEEKMDNERLEWETNLYKESVDAL
62288329 900 910 920 930 940 950
KTQGHARLGNLEFEELVGEALARVKAEEKMDNERLEWETNLYKESVDAL
cry1a-105.pe 920 930 940 950 960 970
FVNSOYDQLOADNTAMTHAADKSVHSIREAYLPSELVTPGVNRAIFELEGHETESL
62288329 960 970 980 990 1000 1010
FVNSOYDQLOADNTAMTHAADKSVHSIREAYLPSELVTPGVNRAIFELEGHETESL
cry1a-105.pe 980 990 1000 1010 1020 1030
YDARNVKNQDGNGLSVNWKGVHDVEEQNNQSVLVVPEWEAEVQVCPGSGYIL
62288329 1020 1030 1040 1050 1060 1070
YDARNVKNQDGNGLSVNWKGVHDVEEQNNQSVLVVPEWEAEVQVCPGSGYIL
cry1a-105.pe 1040 1050 1060 1070 1080 1090
RVYAYKEGEGCVTIHEIENNTDELKFSNCVEEELYPNNVTGNDYVNOEQYGGAYS
62288329 1080 1090 1100 1110 1120 1130
RVYAYKEGEGCVTIHEIENNTDELKFSNCVEEELYPNNVTGNDYVNOEQYGGAYS
cry1a-105.pe 1100 1110 1120 1130 1140 1150
ENRGVNEAPSPVADYASVVEKSYDGRRENPCFNRGYRDTPLPVGYVTKLEYFPEP
62288329 1140 1150 1160 1170 1180 1190
ENRGVNEAPSPVADYASVVEKSYDGRRENPCFNRGYRDTPLPVGYVTKLEYFPEP
cry1a-105.pe 1160 1170
DKWVIEIGETEGTFIVDSVELLMEE
62288329 1170 1180 1190 1200 1210 1220
DKWVIEIGETEGTFIVDSVELLMEE
cry1a-105.pe 1180 1190 1200 1210 1220 1230
EHTWVESEGAFYDSDIELIETQE
62288329 1220 1230 1240 1250 1260 1270
EHTWVESEGAFYDSDIELIETQE
cry1a-105.pe 1220 1230 1240 1250 1260 1270
EHTWVESEGAFYDSDIELIETQE
62288329 1260 1270 1280 1290 1300 1310
EHTWVESEGAFYDSDIELIETQE
```

45593719 source="GENBANK PROT" insecticidal protein Cry9Ec (Bacillus thuringiensis serovar galleriae)

SCORES Initl: 527 Initn: 1822 Opt: 2173 z-score: 2462.4 E(): 7.3e-129
>NRAA:45593719
Initn: 1822 Initl: 527 Opt: 2173 z-score: 2462.4 expect(): 7.3e-129
Smith-Waterman score: 2295; 37.7% identity in 1195 aa overlap

```
(16-1177:57-1154)
cry1a-105.pe 10 20 30 40
MDNPNINECIPYCNLSNPEVVLGGERIETGYTIDISLSIQF
45593719 30 40 50 60 70 80
YPLTDDENAGLQNMVKEYLQYDGYDGTSLNPNLSINTRDVLQGTG---INIVGRVLGF
cry1a-105.pe 50 60 70 80 90 100
LLSEFVPGAG---FVLGLVDLIWIGIFGPGSOWDAFLVQIEQLINQRI-EFAPNQAISRL
45593719 90 100 110 120 130
LG---VEFAGOLVTFYTLNLQMLPTNNNAWAEAFMAQIEELIDORISEQVVERN-ALDAL
cry1a-105.pe 110 120 130 140 150
EGLSNLYIYAESFREWEADPTNPALEEMRIQ-FNDMNSALTTAIFLFAV---QNYQV
45593719 140 150 160 170 180 190
TGIHDYNEYLALEEWLERP-NGA-RANLAFORFENLHQLFVQMPSPFGSGPGRSDAV
cry1a-105.pe 160 170 180 190 200 210
PLLSVYVQAANLHLSVLRDVSFQGRWGFDAAATINSRYNDLTRLIGNYTDHVRWYNTGL
45593719 200 210 220 230 240 250
ALLTVYQAANLHLLKLDAGIYGARWGLNQGINLYFNAQDRTQIYTNHCVAITYNRL
cry1a-105.pe 220 230 240 250 260 270
ERVWGPDSRDWIRYNOFRRELTTLVDIVSLFVNDSTRTYPIRVUSQLTREIYTNVLEN
45593719 260 270 280 290 300 310
ENLRGTNTIESWYVHQFRRELTTLVDIVSLFVNDSTRTYPIRVUSQLTREIYTNVLEN
cry1a-105.pe 280 290 300 310 320 330
PDGSG---OGEGS---IRSPHLMIDLNSITIVTAHGEY-----YWSG
45593719 320 330 340 350 360 370
PPAPVLCREKRNANPWFSELENTFRPPHLEFRLNSLTI--NSHFFPSSNFMQYVAG
cry1a-105.pe 340 350 360 370 380 390
PSIIVAGPVGSGPPEPPLVYGTGNNAPQOIRIVAGLQ-OGVYRTLSLTYRRPFNIGINN
45593719 380 390 400 410 420 430
HTLRRSNNNSAVOESG-YG---ATSTRTNTINTGVNGTNRISTEAVDFRSGLLGVYG
cry1a-105.pe 400 410 420 430 440 450
QQLSVLDGTEFAYGTSNLSNVAITKSGSDSLDEIPQNNVPPRQGFSLHLSVSMF
45593719 430 440 450 460 470 480
VHRASFVPGSLFN-GTIS--PAAQGRN-LHMTDDEPLEENN-SP---SHRLSHVT-F
cry1a-105.pe 440 450 460 470 480 490
RSGFSNNSVETIIRA---PMFSWIRHSAEFNNIASITQIPLVKAMTOSGVTVVGP
45593719 480 490 500 510 520 530
LSFLTDQAGSIRNSGAVLYVWARQDIDLANTITANKTQIPLVKAMTOSGVTVVGP
cry1a-105.pe 500 510 520 530 540 550
FTGGDILRRSTGQPFAYTVININGQLPQRYRARIYASTNIRIYVTVAGSIFPAQK
45593719 540 550 560 570 580 590
FTGGDILRRSTGQPFAYTVININGQLPQRYRARIYASTNIRIYVTVAGSIFPAQK
cry1a-105.pe 560 570 580 590 600 610
TMDTGCDPLTFQSFYSYATINTAFTPMSSQSTFTVAGTDFSSGNEYVDFRFLPVATLEA
45593719 600 610 620 630 640 650
TMSQESRSEVTVREFTSFNFQIQDTRLRLVQSFSSGQGVYVDKRIELIIPVNTFREA
```

8928043 description="PESTICIDIAL CRYSTAL PROTEIN CRY9EA (INSECTICIDAL DELTA-ENDOTOXIN CRYIXE(A)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (130 KDA CRYSTAL PROTEIN)." library="NA species="Bacillus thuringiensis serovar aizawai" source="swissprot_prot" version="NA type="PRT"

SCORES Initl: 434 Initn: 1436 Opt: 2084 z-score: 2361.2 E(): 3.1e-123
>SW:8928043

initn: 1436 initl: 434 opt: 2084 z-score: 2361.2 expect(): 3.1e-123

Smith-Waterman score: 2219; 36.4% identity in 1195 aa overlap
(16-1177:57-1150)

cry1a-105.pe MDNNPINECIPYNCISNPVEVLGGERIETGYTIDISLSTOF 10 20 30 40

8928043 YPLASDPNAAFOQMNYKEYLOTGYDGTGSLINPLNSINPRDVLQTG---INIVGRILGF 30 40 50 60 70 80

cry1a-105.pe LLSEFVPGAG---FVLGLVDIIMGIFGSPQMDAFLVQIEQLINQRIE-EFARNQASRL 50 60 70 80 90 100

8928043 LG---VPFASOLVTFTFLNQLWPTNDNAWEAFMAQIEELIDQKISAQVWRN-ALDDL 90 100 110 120 130

cry1a-105.pe EGLNLGYIAESFREWEADPTNPALREMRIOFNDMNSALTITPLFAV---QNYQVP 110 120 130 140 150

8928043 TGLHDYEEYLAALAEWLERP-NGARANLVTOQFENLHTAFVTRMPSPGTGPGSQORDAVA 140 150 160 170 180 190

cry1a-105.pe LLSVYQAAHLHSLVLRDVSFGQWGFDAATINSRYNDLTGLIGNYTDHAVRWYNTGLE 160 170 180 190 200 210

8928043 LHTVQAARAHLLHLLKDAIEYIGRWGLQGGQINLYFNAQQRFTIYNHCVEYRGL 200 210 220 230 240 250

cry1a-105.pe RVWGPDRDIRYNQFRRELTITVLIDVSLFPNYDSRTYPTRTVSQLTREIYNPVLN- 220 230 240 250 260 270

8928043 DVRGNTESLNVHRREREMTUMADLVLPFYVVRQYPNGANPQLTREIYTDPIVYNP 260 270 280 290 300 310

cry1a-105.pe -----FDGFRGSAQIEGS-IRSPHLMILNSITII-----YTDARGEY--YMSGH 280 290 300 310

8928043 PANQICRRGNPNYTFSELENAFIRPPLFERLARLTISNRNPTAPTNSFLDYMSGH 320 330 340 350 360 370

cry1a-105.pe QIMASPGVSPGPEFTPLVGTMGNAAPQQRIVAGLQGVVRLTSLTYRRPF-NIGINNQ 320 330 340 350 360 370

8928043 TLQSQHA--NNPTTYTSIGQITSNT---RLFNITNGA--RAIDSRA--RNFGLNLY 380 390 400 410 420

cry1a-105.pe QLSVLDTGTFAYGTSSNLPSAVYKSGTVDSLDIEIPPQNNNPPRQGSRLSHSVMSFRS 380 390 400 410 420 430

8928043 GVSSLNI--PFTGVMSIEITNAANTCRQDLTTTELPLENNF-----NLLSHVTLRF 430 440 450 460 470 480

cry1a-105.pe GFSSNS--VSIIRAPMFWHRSAPFNIIASDITQIPLVKAHTLQSGTTVVRGPGFTG 440 450 460 470 480 490

8928043 NITQGGPLATLGFVPTVMTREDVDFTNITADIRITQLPWVKASEIGGTTVVRGPGFTG 490 500 510 520 530 540

cry1a-105.pe EYNLEAQAVNALFTSNQGLKTNVTDYHIDQVSNLVTVLSDFECLDEKRELSEKVKH 620 630 640 650 660

45593719 EEDLEAKKAVANLFTHRD-GLQNVTVQYDQAAANVLSCLSDSEQSHDKKMLLEAVRA 670 680 690 700 710

cry1a-105.pe AKLSERNLLODSNFKDINQPERGWSGTITIGQDDVFKENYVTLSTGTDECPYTY 680 690 700 710 720 730

45593719 AKLSRERNLQDPDFNEINTIEENGWKSANGVTISEGPPFKGRALQLASA-RENNPTY 720 730 740 750 760 770

cry1a-105.pe LYQKIDESKLAFYQLRGYIEDSQLEIYSIRYNAKHETVNPVPGTGSWLPLSAQSPIG 740 750 760 770 780 790

45593719 IYQKVDASVLKPYTRYRLDGFVASSQDLDLIHQKHVKNVFDNL---VSDSYSYG 780 790 800 810 820 830

cry1a-105.pe KCGFPNRCAPHLNPDLDSCRDGKRC-AHSHSHFSLDIDVGCTDNLGLVWVIFKIK 800 810 820 830 840 850

45593719 SCSGINRCEQHVLVDMLQDAEHPMDCCAAETHFESSYIDTGLDNLSPVQGIWVKVR 840 850 860 870 880 890

cry1a-105.pe TODGHARLGNLEFLEKPLVGEALARKRAEKWKRDKREKLEWETNIVYKEAKESVDALF 860 870 880 890 900 910

45593719 TTDGYATLGNLELVEVGPLSGESLEREQKDNKAKNAELGRKEAETDRVYQAAQAINHLF 900 910 920 930 940 950

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

45593719 VDYDQQLNPEIGLAEMNEASNLLESIPGVYSDTVLQIPGVNIEYITELSNRQQASLYF 960 970 980 990 1000 1010

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

45593719 MSRAVQNGDFNGLSDSNWATTDATVQ-QDGTWHFLVLSHWDQVQSRLRVPQNCXYLR 1020 1030 1040 1050 1060 1070

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

45593719 VTARKVGGDGYVTIODGAHQETLTFNAC-----DYDWN-----GTVND 1080 1090 1100 1110

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

45593719 NT-----YITKEVVFYFETK 1120

cry1a-105.pe KWIIEIGTEGTFLVDSVELLME 1160 1170

45593719 HWMIEVSEGAFYIDSIEFIEIQ 1130 1140 1150

cry1a-105.pe 8928043

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cry1a-105.pe 500 510 520 530 540 550
GDIIRYGGFFAKTWINQOLQVRARIRYASTNIRIVTVAGERIFAG-QFNKTM
8928043 560 570 580 590
GDIIRYGGFFAKTWINQOLQVRARIRYASTNIRIVTVAGERIFAG-QFNKTM

cry1a-105.pe 560 570 580 590 600 610
DTGDLPEQESYANINAFPMSSQSVVADTFSS--GNEVIDRFELIPVATLEA
8928043 620 630 640 650
AONGSLTYESFN--NEVTHIRYSQDTILRLNIPISGQGVYVDKLEIVPINPREA

cry1a-105.pe 620 630 640 650 660 670
EYNLERAKAVNALFTSTNOLKKNVDYHITQVNLVYLSDFCC-DEKRELSKVKH
8928043 680 690 700 710
EDLEDAKAVASLFTRED-GLQVNDIVQDAKAVYSQSDQYQDKRLLEAVRA

cry1a-105.pe 680 690 700 710 720 730
AKRSERNLQDSNFKDINRQPERGGSTGITIQGDDQKKNYVLSQTEDECPYV
8928043 740 750 760 770
AKRSERNLQDPDFNEINSTEENGKASNGVITSEGGPFYGRALQASAREGKY

cry1a-105.pe 740 750 760 770 780 790
LYOKIDESKLKATRYQLRGYIEDSODLEIYSIRYNAKHETVNVPTGSLWPSAQPIG
8928043 800 810 820 830
LYOKIDESKLKATRYQLRGYIEDSODLEIYSIRYNAKHETVNVPTGSLWPSAQPIG

cry1a-105.pe 800 810 820 830 840 850
KCGENRCAPHEMLDPCSDRGEKC-AHSHHFSLDIDVGCTDLNEDLGWVIFPKIK
8928043 860 870 880 890
SCSGINRCEQHQVDQDAEDHPDKCEAAQTHEFSSVIHTGDLNAGVDQGIWVILQVR

cry1a-105.pe 860 870 880 890 900 910
TODGHARLGNLEFLEKPLVGEALARVGAEKWDRKREKLEWETNIVYKAKESVDALF
8928043 920 930 940 950
ITDGYATLGNLELVEGVLPSGESLEREQDRNAKNWEVEVKRAEIDRIYQDAKQAINHLF

cry1a-105.pe 920 930 940 950 960 970
VNSQVDQLQADTNIAHAAKRVHSIREAYLPESLPIGVNAAIFEELEGRIFTAFSLY
8928043 980 990 1000 1010
VDYQDQLSPEVGMADIIDAQNLIASISDVSDAVLQIPGINVEMYTSLNRLQQAQSYLY

cry1a-105.pe 980 990 1000 1010 1020 1030
DARNVKNQDNGNLSQWNVKGVHVDVEEQNNQSRSLVVPWEAEVSEVQVCPQGVILR
8928043 1040 1050 1060 1070
TSRNVYQNGDFNSGLDSWNAITDQVQDQGNMH-FLVLSHWDAQVSOQFVQPNCKYLR

cry1a-105.pe 1040 1050 1060 1070 1080 1090
VTAYKEGEGECVTHIENNTDELKFSNCVEEIIYNNVTICNDVYNQEEYGAYSR
8928043 1100 1110 1120 1130
VTAKVVGNDGCVTVIQDGAHRETLTFNAC-----DDVN-----GTHVND

cry1a-105.pe 1100 1110 1120 1130 1140 1150
NRGYNEAPSVADYASVYEKSYTDGRENCFENRGYRDTPLPVGYVTKELVYFPETD
8928043 1160 1170 1180 1190
N-----SYITKELVYFPKTE 1120

cry1a-105.pe 1160 1170
KWIIEIGETEGTIVDSVELLIMEE
8928043 1180 1190
HMWVEVSETEGTIVDSIEFIEIQE

cry1a-105.pe 1180 1190
NRAA:27413810

27413810 source="GENBANK_PROT" crystal endotoxin Cry9Ea [Bacillus
thuringiensis]gi|8928043|sp|Q9ZNL9|CR9EA BACTA Pesticidal crystal protein
cry9Ea (insecticidal delta-endotoxin CryIXE(a)) (Crystalline entomocidal
protoxin) (130 kDa crystal protein)gi|3986086|db|BAA34908.1| Cry9 like protein
[Bacillus thuringiensis serovar aizawai]

SCORES Initl: 434 Initn: 1436 Opt: 2084 z-score: 2361.2 E(): 3.1e-123
>>NRAA:27413810
Initn: 1436 Initl: 434 opt: 2084 Z-score: 2361.2 expect(): 3.1e-123
Smith-Waterman score: 2219; 36.4% identity in 1195 aa overlap
(16-1177:57-1150)

cry1a-105.pe 10 20 30 40
MDNNPNINECIPYNCILSNPEVEVLGGERIETGYTIDISLSLTQF
27413810 YPLASDPNAAFQNNYKEYLQYDGYDGTGSLINPILSNIPROVLQIG--INIVGRILGF
30 40 50 60 70 80

cry1a-105.pe 50 60 70 80 90 100
LSEFVPGAG----FVLGVDIWIIGFQSDWAFVLQIEQLINORIE-EFARNQAISRL
27413810 LG--VPPAGQGVTFYTLINQLQWPTNDNAWFAFMAQIEELIDOKISAVVRN-ALDDL
90 100 110 120 130

cry1a-105.pe 110 120 130 140 150
EGSNVYQVQESFEMADPTNPALREEMRIQFNDMNSALTTPAIFAV---QNYQVP
27413810 TQHDYIEVILAMSEWLEP--NCRANLVQRFENLHTAFVTRMPSFGTGTGSGQSDAVA
140 150 160 170 180 190

cry1a-105.pe 160 170 180 190 200 210
LLSVYVQVNLN-SVLRSYV--VQRMGPD-ATINSRYNLDLTLIGNYTDHVRVYNTGLE
27413810 LLTVYQAANLHLLLEDAEIVCAET--QQGQINNVFNQAQERTRIYTNHCVETYNRGL
200 210 220 230 240 250

cry1a-105.pe 220 230 240 250 260 270
RWGDPDSWIRNQRFRELTIVADILSLFPFDEIRYPIRTVQLREIYTNPVLEN-
27413810 DVRGNTESLWNRHFRREMTLMMDLVAFPPVNVRO--GKANGPOLTRERYTPEIVYNP
260 270 280 290 300 310

cry1a-105.pe 280 290 300 310 320 330
FDGSPRGSAGQIEGS-IRSPHLMIDTINSIT--VTDARGFVYWSGF
27413810 PANQICIRGWNQNTYTFSELENAFIRPPLHFLNELNLTSNRKTRATNSFLATYSH
320 330 340 350 360 370

cry1a-105.pe 320 330 340 350 360 370
QIMASPVFGSPETFPFLYGTGMGNAAPQORIVAQVGQVYRTLSLTYRPF-NGINNO
27413810 TLQSQHA--NNPTTYETSYQITSNIT---RLFNITNGA--RAIDSGA--RNFGNLYANDY
380 390 400 410 420 430

cry1a-105.pe QLSVLDTGTEAYGTSSNLPASVAVKSGTVDLSDEIPQNNVPPRQGFSHRLSHVSMFRS
27413810 GYSSLNI--PPTGMSSEINANTCRQDLITTEELPLENNF-----NLLSHVIFLRF
430 440 450 460 470 480 490
cry1a-105.pe GFSNSS--VSIIRAPMFSMIHRSAEFNIIASDSITOPLVKAHTLQSGTTVVRGPFTG
27413810 NTTQGGPLATLGFVPTVWTRDVFNTITADRIQTOLPWKASEIGGTTTVVRGPFTG
490 500 510 520 530 540 550
cry1a-105.pe GDLIRRTSGGFATVINGQLPQRYARIRYASTTNLRIRYTVAGERIFAG-QFNKTM
27413810 GDLIRRTDGGAVGTIRANVNAPLTOQYRIRLYASTTTSFVNLFVNNSA--AGFTLPSFM
550 560 570 580 590
cry1a-105.pe DTGDLPTFQSFYSATINTAFTFMSQSSFTVGADTFSS--GNEVYIDRFELIPVATLAE
27413810 AQNGSLTYESN--TLEVHTTRFSQSDTLRLNIPFSISGQEVYVDKLEIVLPINPREA
600 610 620 630 640 650 660
cry1a-105.pe EYNLERAKAVNALFTSTNQLGKTNVTDYHIDQVSNLVLYLSDEFCLDEKREUSEKVXH
27413810 EEDLEDAKAVASLFTRTD--GLQVNVTDYQVDAQANLVCLSDQEQYHDKMLLEAVRA
660 670 680 690 700 710
cry1a-105.pe AKELSDERNLLQDSNFYDINRQPERGKSGTGITIQGGDDVFKNVYVLTSGTTFDECPTY
27413810 AKRLSRERNLQDDPFNEINSTEENGWKRASNGVTIISGGPFFKGRALQJASA--RENPTY
720 730 740 750 760 770
cry1a-105.pe LYOKIDESKLAFTRYQYLRGYIEDSODLEIYSIRYNAKHETVNVPGTGLSMLPSAQSPIG
27413810 IYOKYDASTLKEPYTRYKLDGFVQSSODLEIDLJHHKHVHLVKNVPNL-----VSDTYSDG
780 790 800 810 820 830
cry1a-105.pe KCGEPNRCAPHLEWNPDLDCSRDGEK--AHSHHPSLDIDVCGTDLNEDLGVWVIFKIK
27413810 SCSGINRCEEQHQVDVQDAEDHPKDCCEAAQTHEFSSYIHTGDLNASVDQGIWVVLQVR
840 850 860 870 880 890
cry1a-105.pe TDGCHARLGNLEFLEKPLVGEALASVKAEEKWDRKLEWETNIVYVKEAKESVDALF
27413810 TTDGYATLGNLEFVEGFLSGESLREQRDNKAKWNEFGVKRAETDRIYQDAKQALNHLF
900 910 920 930 940 950
cry1a-105.pe VNSQYDQLQADNTAMIHAADKRVHSIREAYLPESLVIPGVNAAIFEELEGRIFTAFSLY
27413810 VDQDQQLSPGVGMADIIIDAQNLIASISDVSDAVLQIPLGYNEMVETLSNRLQQAQSVLY
960 970 980 990 1000 1010
cry1a-105.pe DARVTKNGDFNNGUSCMWKGHVDDVEEQNNORSVLVVPFEWAEVSGEVRVCPGKGIILR
27413810 TSRNVVQNGDFNNGUSCMWKGHVDDVEEQNNORSVLVVPFEWAEVSGEVRVCPGKGIILR
1020 1030 1040 1050 1060 1070 1080 1090

cry1a-105.pe VTAYKEGYGCGCVTHIEIENNTDELKFSNCVBEIEYPPNNVTCNDYTVNQEEYGGATSR
27413810 VTAKVNGGCGYVTIQDGAHREITLTFNAC-----DYDVN-----GTHVND
1070 1080 1090 1100 1110 1120
cry1a-105.pe NRGYNAPSPADYASVYEKSYTGRRNCFENRGYRDYPLPGVYVTKLEYFPETD
27413810 N-----SYITRELFFYFKTE
1130 1140 1150 1160 1170
cry1a-105.pe KVMIEIGETEGIFIVDSVLLMEE
27413810 HMWVEVSETEGTFYIDSIEPIETQE
1130 1140 1150
cry1a-105.pep
NRAA:1234884
1234884 source="GENBANK_prot" delta-endotoxin [Bacillus thuringiensis]
SCORES Initl: 1104 Initn: 2337 Opt: 1851 z-score: 2099.2 E(): 1.2e-108
>NRAA:1234884
initn: 2337 initl: 1104 opt: 1851 z-score: 2099.2 expect(): 1.2e-108
Smith-Waterman score: 2658; 55.8% identity in 773 aa overlap
(1-748:1-756)
cry1a-105.pe MONNPNINECTPNCLNPEVILGGERETGYTPIDISLSLTQFLSFEVPGAGFVLGL
1234884 MEEN-NQWQICIPNCLNPEVILGGERETGYTPIDISLSLTQFLSFEVPGAGFVLGL
10 20 30 40 50
cry1a-105.pe VDIIMGIFGSPQWDAFLVQIEQLINORIEEFARNQAISRLEGLSNLYQIYAESPREWAD
1234884 IDFMGIVGSPQWDAFLVQIEQLINERIAEFARNQAISRLEGLSNLYQIYAESPREWAD
60 70 80 90 100 110
cry1a-105.pe PTPNALREEMRIQFNDMNSALTATPLFAVQNYQVPLLSVYVQAANLHLSVLDRVSPGQ
1234884 PNNPATRTRIVDRFRILDGLERDIPFRISGFEVPLLSVYVQAANLHLSVLDRVSPGQ
120 130 140 150 160 170
cry1a-105.pe RMGFDAAATNSRYNDLTRLGNVTDHAWVNTGLERWVGPDSDRWIRYVQFRRLTLTV
1234884 RMGLTININVENYNELIRHIDEADHCANTYNGNLNLPKSTYQDMITYNLRLRLTLTV
180 190 200 210 220 230
cry1a-105.pe LDIVSLFPNYSRTPRTVTSQLTREIYNPVLENFDFSGFRSAQ-----GIEGS-IRSP
1234884 LDIAAFPPNVDNERYPQPVQGLTRREVTDPLI-NFNPLQSLVAQLFTFNVMESSAIRNP
240 250 260 270 280 290
cry1a-105.pe HLMIDLNSITITDAHR-GE-YWWSGHQIMASVPGSPFETFLVGTWGNAAPOQRIVA
1234884 HLFEDILNLTITFDWFSVGRNFWGGRVSISSLIIG--CGNLTISITYGREANQEPFRSFT-
300 310 320 330 340 350

SCORES Init1: 1104 Initn: 1736 Opt: 1823 z-score: 2068.3 E(): 6.5e-107
>>NRAA:11277639 (655 aa)
Initn: 1736 Init1: 1104 Opt: 1823 z-score: 2068.3 expect(): 6.5e-107
Smith-Waterman score: 2057; 50.7% identity in 671 aa overlap
(1-646:1-654)

cry1a-105.pe 10 20 30 40 50 60
MDNNPINECTPYNCLSNPEVEVLGGERIETGYTPIDISLSLQFLLSEFVPGAGFVLGL
11277639 MEEN-NQOCIPYNCLSNPEEVLGGERISTGNSIDISLSLQFLLSEFVPGAGFVLGL
10 20 30 40 50

cry1a-105.pe 70 80 90 100 110 120
VDIIMGIFGSDQDAFLVQIEQLINQRIEFAFNAQAIISRLGSLNLYQIYAESFREWAD
11277639 IDFWGIVGSDQDAFLVQIEQLINQRIEFAFNAQAIISRLGSLNLYQIYAESFREWAD
60 70 80 90 100 110

cry1a-105.pe 130 140 150 160 170 180
PTNPALREEMRIQFNDMNSALTTPAIPFAYQNYQVPLSVYQAAHLVLRDVSFVGQ
11277639 PNPATRTVDRFRIDGLERDIPSFRIISGFEVPLSVYQAAHLVLRDVSFVGQ
120 130 140 150 160 170

cry1a-105.pe 190 200 210 220 230 240
RMGFDATINSRYNDLRLIGNYTDHVAWYNTGLERVMGPDGRDWRVQFRRLTLTV
11277639 RMGLTIINVENYRLRHIDEVADHCANTYNGNLNPKSTYQDWTYTLRLRLTLTV
180 190 200 210 220 230

cry1a-105.pe 250 260 270 280 290
LDIVSLFPNDYRTYPIRTVSQLTREIYNPVLENFDSGRSAQG-----IEGS-IRSP
11277639 LDIAAFPNYDNRYPYQVQGLTREVYTDPLI-NFNPLQSVQALFTFNVMESAIRNP
240 250 260 270 280 290

cry1a-105.pe 300 310 320 330 340 350
HMDILNLSITVTDHR-GE-YWWSGHOIMASPVCFSGPFTPELYGTWGNAPQORIVA
11277639 HLPDILNLSITVTDHR-GE-YWWSGHOIMASPVCFSGPFTPELYGTWGNAPQORIVA
300 310 320 330 340 350

cry1a-105.pe 360 370 380 390 400
QLGQGVYRTLSST---LYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASVYKSGTVDS
11277639 -FNGPVFRTLSNPTLRLIQPWPAPPFN--LAGVGVFEFS--IPTN--SFTYRGRGTDS
360 370 380 390 400

cry1a-105.pe 410 420 430 440 450 460
LDIPIPNNNVPPRGFSHRLSHVSMF-RSGFSNDSVSIIRKAPMFSIRHSAEFNNIAT
11277639 LTELPPEDNSVPREGYSHRLCHATFVQSGTFPFLITGW----FSWTHRSATLNTIDP
410 420 430 440 450 460

cry1a-105.pe 470 480 490 500 510 520
DSITQIPYKANTLOSQTTVRGEGTGGDILRRSTSGGPFAYTIVNIGLQOLPYRABIR
11277639 ERINQIPYKANTLOSQTTVRGEGTGGDILRRSTSGGPFAYTIVNIGLQOLPYRABIR
470 480 490 500 510 520

cry1a-105.pe 530 540 550 560 570 580
YASTTNLRIVV-TVAGERIFAGQ-----FNKTMIDTGDPLATFQFSYATINTAFTFPMQ
11277639 YASRDARVILTGAASTGVGGQVSVNMPLOKMEIGENLSRTFRYTDPSNPFSPRNP
530 540 550 560 570 580

cry1a-105.pe 590 600 610 620 630
GATFSSGNEVYDRFELIIVTATLEAVENLERACKAVNALFTSTNOLG
11277639 DIIGISEQPLFGAGSISG-ELYDKRIEIIILADATPEASDLERACKAVNALFTSSNQIG
590 600 610 620 630

cry1a-105.pe 640 650 660 670 680 690
LKTNTVDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQ
11277639 LKTDVTDYHIDP
640 650 660 670 680 690

cry1a-105.pep
NRAA:38231198
38231198 source="GENBANK_PROT" Cry1C [Chloroplast transformation vector
PN-1C101]

SCORES Init1: 1104 Initn: 1770 Opt: 1823 z-score: 2068.2 E(): 6.6e-107
>>NRAA:38231198 (661 aa)
Initn: 1770 Init1: 1104 Opt: 1823 z-score: 2068.2 expect(): 6.6e-107
Smith-Waterman score: 2091; 51.1% identity in 677 aa overlap
(1-652:1-660)

cry1a-105.pe 10 20 30 40 50
MDNNPINECTPYNCLSNPEVEVLGGERIETGYTPIDISLSLQFLLSEFVPGAGFVLGL
38231198 MEEN-NQOCIPYNCLSNPEEVLGGERISTGNSIDISLSLQFLLSEFVPGAGFVLGL
10 20 30 40 50

cry1a-105.pe 70 80 90 100 110 120
VDIIMGIFGSDQDAFLVQIEQLINQRIEFAFNAQAIISRLGSLNLYQIYAESFREWAD
38231198 IDFWGIVGSDQDAFLVQIEQLINQRIEFAFNAQAIISRLGSLNLYQIYAESFREWAD
60 70 80 90 100 110

cry1a-105.pe 130 140 150 160 170 180
PTNPALREEMRIQFNDMNSALTTPAIPFAYQNYQVPLSVYQAAHLVLRDVSFVGQ
38231198 PNPATRTVDRFRIDGLERDIPSFRIISGFEVPLSVYQAAHLVLRDVSFVGQ
120 130 140 150 160 170

cry1a-105.pe 190 200 210 220 230 240
RMGFDATINSRYNDLRLIGNYTDHVAWYNTGLERVMGPDGRDWRVQFRRLTLTV
38231198 RMGLTIINVENYRLRHIDEVADHCANTYNGNLNPKSTYQDWTYTLRLRLTLTV
180 190 200 210 220 230

cry1a-105.pe 250 260 270 280 290
LDIVSLFPNDYRTYPIRTVSQLTREIYNPVLENFDSGRSAQ-----GIEGS-IRSP
38231198 LDIAAFPNYDNRYPYQVQGLTREVYTDPLI-NFNPLQSVQALFTFNVMESAIRNP
240 250 260 270 280 290

cry1a-105.pe 300 310 320 330 340 350
HMDILNLSITVTDHR-GE-YWWSGHOIMASPVCFSGPFTPELYGTWGNAPQORIVA
38231198 HLPDILNLSITVTDHR-GE-YWWSGHOIMASPVCFSGPFTPELYGTWGNAPQORIVA
300 310 320 330 340 350

cry1a-105.pe 360 370 380 390 400
QLGQGVYRTLSST---LYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASVYKSGTVDS

38231198
-FNGPFTLSNPLRLAQDPAPPEN--LRGVGVFFS--TPTN--SFTYVRGRGTVDS
380 390 400
cry1a-105.pe
LDETPQNNVPPVPSHRLSHVSNP--RGFSNSVSLIRAPMFSWIRSAEFNNIIAS
420 430 440 450 460
38231198
LTELPPQNSVPPGSGSHYASHAFVORSCTFLTTGVW---FSWTHRSATLNTIDP
410 420 430 440 450 460
cry1a-105.pe
DSITQPLVKAHTLOSCTVREGPGFSGEDARTSGGPRAYATVNNINGOLPVRARIR
470 480 490 500 510 520
38231198
ERINQPLVKGFRVGGTISVNSCPGGDILPEAFDFVSLQNNISPIORVELRFR
470 480 490 500 510 520
cry1a-105.pe
YASTTNLRIVV-TVAGERIFAGQ-----FNRINDQPPVQFQSFYATNTAFETPMQ
530 540 550 560 570 580
38231198
YASRDARVILVTGAASTGVGGQVSNMPLQKTMETGHNLSRTFRVQSFMSFRAMP
530 540 550 560 570 580
cry1a-105.pe
SSFTV-----GADTFSSGNEVYIDRFELIPVTATLEAEYNLRAQAKNVAETSTNUG
590 600 610 620 630 640
38231198
DIIGISQPLFGAGSISG-ELYIDKIEIILADATFEASDLRAQAKNVALTSNIG
590 600 610 620 630 640
cry1a-105.pe
LKTVDYDHIDQVSNLVTLSDEFCLDEKSELSEKVKHAKRLSDERNLLODSNFKDINRQ
640 650 660 670 680 690
38231198
LKTVDYDHIDQVSNLVE
650 660
cry1a-105.pe
NRAA:1334252
1334252 source="GENBANK_prot" delta-endotoxin [Bacillus thuringiensis]
SCORES Initl: 533 Initn: 2179 Opt: 1773 z-score: 2007.8 E(): 1.5e-103
>>NRAA:1334252
Initn: 2179 Initl: 533 opt: 1773 Z-score: 2007.8 expect(): 1.5e-103
Smith-Waterman score: 2300; 36.8% identity in 1198 aa overlap
(26-1177:29-1144)
cry1a-105.pe
MDNNPINECIPYNCISNPEVEVLGGERIETGTPIDISLSL--TOFLSEFVFGA--
10 20 30 40 50
1334252
VFELKTCIWHAFFLTKLSSYKDYLMSEGVDYDSYINPNQVNRGTGLQTGIDIVAVVVGALG
10 20 30 40 50 60
cry1a-105.pe
GFLVGLVDIINGIFGSO-----WDAFLVQLQELINQRIEERFARNQALISRLGLSNL
60 70 80 90 100
1334252
GPVGGILTGLSTLFGFLWPSNDQVWEAFTEQMEELIEQIRISDQVWRTALDDLTIGINY
70 80 90 100 110 120
cry1a-105.pe
YQIYAESFREHEADPTNPALREEMRIO--FNDMSALTALPLFAV---QNYQVPLISVY
110 120 130 140 150 160
1334252
YNOYLIALKEWEERPNQ--VRANVLQRFELHALFVSSNPFSGQSGQRFQQLLVY
130 140 150 160 170
170 180 190 200 210 220

cry1a-105.pe
VOAANLHLSVLSDVSVFQORMGDAATI--NSRYNDLTLLIGNYTDHAVRWYNTGLRVRWG
180 190 200 210 220 230
1334252
AQAAHLHLLADAEEKYGARGLRFESQIGNLYFNELOTRFRTDYNHCVNAYNGLAGLRG
180 190 200 210 220 230
cry1a-105.pe
PDSRDWIRNQRRELITVLIVDSFPYDSRTPISTVSQLTREIYNPV--LENFDGS
230 240 250 260 270
1334252
TSAESMLKHQFRREATIAMDILIAFFPYNTIRRYPIAVNPQLTREVITDPLGVFSESS
240 250 260 270 280 290
cry1a-105.pe
F-----RGSA-----QGEGSI--RSPHMDILNSIITYTDA---HRGEY--WSGH
280 290 300 310
1334252
LFPELRLCRLWQETSAMTFSNLENAIISSPHLPDTNNLMIVTGSFVHLTNOLIEGWIGH
300 310 320 330 340 350
cry1a-105.pe
QIMASPVGSGPEFTPLVGTMGNAPOQRIVAQLOGGVYITLSLTLYRPFNIGINNOQ
320 330 340 350 360 370
1334252
SVTSSLLA--SGP--TTVLRNRYGTTISVNYFSFNDRDVYQINT---RSHTGLGFQNPAP
360 370 380 390 400 410
cry1a-105.pe
LSVLDDGTEF--AYCTSSNLPASVYKSGTVDSEIIPPQNNNVPPRGQFSHRLSHV--SMFR
380 390 400 410 420 430
1334252
LFGITRAQFPVGGTISVTQNALICEQVNSIDELPSLDPNEPISRSYSYHRLSHITSYLH
420 430 440 450 460 470
cry1a-105.pe
SGFSSSVSIIIRA--PMFSWIRSAEFNNIIASDSITQPLVKAHTLOSCTTVVRGPGFT
440 450 460 470 480 490
1334252
RVLTIDGNIYSGNLPVYVWTHRDVLTNTITADRTQPLVKSFEIPAGTIVVRGPGFT
480 490 500 510 520 530
cry1a-105.pe
GSDLRKRGPPATVNNINGOLPVRARIRYASTTNLRIVTVAGERIFAGQFNKTM
540 550 560 570 580 590
1334252
GGTLRRITGVGTGIRVIRVTPDQYRIIRFRFASTTNLFIGIRVGDQVNYDFDGRIM
540 550 560 570 580 590
cry1a-105.pe
DTGDPITFQSFSTATTINAF--PMSQSSFT--WGLTFSSGNEVYIDRFELIPVTATLEAEY
560 570 580 590 600 610
1334252
NKGDELRYESFATRET--DENFRQGLKLVAFNANASQSEVYDFRLEIIPVNPAREAKE
600 610 620 630 640 650
cry1a-105.pe
NLERAQKAVNALITSTNQLGKLTNDYNDQVSNLVTVISDFPCNERSELSEKVKHAK
620 630 640 650 660 670
1334252
DLEAAKAVASLFTFRTRD--GLQVNVKDYQVQVQVSNLVSDQYGYDKKMLLENVRAAK
660 670 680 690 700 710
cry1a-105.pe
RLSDERNLLODSNFKDINRQPPGNGSGTGITIQGGDVPEKNNVTLSGDEAFPTIYLY
680 690 700 710 720 730
1334252
RLSRERNLLODPDPNTINTEENGWASNGVITISEGGPYKGRALSLAS--RENAPFTIYLY
720 730 740 750 760 770
cry1a-105.pe
QKIDSKLKAFTYQRLRGVIEDSODLEIYSIRVNAKHETVNVPGT--GSLWPLSASAPIC
740 750 760 770 780 790
1334252
QKVDASELKPYTRYSDRGVSKSQDLEIDLTHHKKVHLKVNYPDNLVSDTYDPPDDSCSGIN
770 780 790 800 810 820 830 840 850

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```
670      680      690      700      710      720
670      680      690      700      710      720
cry1a-105.pe LSEKVKHAKRLSDERNLLODSNPKDINQPERGCGSTGTTGGDDVFKENYVTLSCGF
62288327 LMEAVRAAKRLSRERNLLODPFNEINSTEENGWAKSNGIILISEGGPFKGRVQLQASA-
730      740      750      760      770      780
cry1a-105.pe DECYPTLYIQKIDSKLAFYQLRGVIEDSQLEIYSRYNAKHETVNVPGTGSWLPL
62288327 RENYPTIYQKVDAVLKPYTRYLDGFKVKSSELEIDLHVKHVLKVNVPDNL---V
730      740      750      760      770      780
cry1a-105.pe SAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGEKC-AHHHHHSLDIDVGCTDNLGLV
62288327 SDTPDGSCRGVNRCDQHQVDVQIDTEHHPMDCCCAAQTHEFSSYINTGLNSVDPQGI
850      860      870      880      890      900
cry1a-105.pe WIFKTKTODGHARLGNLFLFEKPLVGEALARYKRAEKKWRDKREKLEWETNIVYKEAK
62288327 WVLKVRADGATLGNLFLVEVGFSLGESLEREQDNKNAELGREGRAETDRVYLAAK
910      920      930      940      950      960
cry1a-105.pe ESDVALFVNSQYDQLOADTNIAHIAADKRVHSIREAYLPESLVIQVNAALFEELEGRI
62288327 QAINHLFVDYDQDQQLNPEIGLAEINEASNLVESITGVYSDTVLIQIPGISYEIYELSDRL
970      980      990      1000      1010      1020
cry1a-105.pe FTAFSLYDARNVINKGDFNGLSCMNKGVGHVDEEQNNQSRVLLVPEWAEVSGEVRCVP
62288327 QOASLYTSRNAVQNGDFDGLSDMNATDASVOQDGNMH-FLVLSHWDAQVTOQLRVNP
1030      1040      1050      1060      1070      1080
cry1a-105.pe GRGYILRVYAKGEGYGGCVTTHEIENNDELKFSNCEVEEIVPNNTVTCNDYTVNQEEY
62288327 NCKYVLRVYAKGEGYGGCVTTHDGAHRETLTFNAC-----DYDYN---
1090      1100      1110      1120      1130      1140
cry1a-105.pe GGAYTSRNRGYNEAPSVADYASVVEKSYTDGRRENPCFNRGREDYTPLPVGVYTKEL
62288327 -GTYNQNT-----YITKEV
1150      1160      1170
cry1a-105.pe EYEPETDKWJEIGETGTEIVDSVLLIMEE
62288327 VFYPHEHWVEVSESEGAIFYDIELIETQE
1140      1150      1160
cry1a-105.pep
SW:8469140
```

```
SCORES      Init1: 895      Initn: 1625      Opt: 1716      z-score: 1946.1      E(): 4.2e-100
>>SW:8469140
initn: 1625      init1: 895      opt: 1716      z-score: 1946.1      expect(): 4.2e-100
Smith-Waterman score: 1728;      44.0% identity in 663 aa overlap
(S1-683:76-719)

cry1a-105.pe VEVLGGERIETGTPIDISLSTQFLLSEFVPGAGFVLGLVDIIMGIFGP---SQWDAFL
8469140      SEHESIDPFVSASTIQTGIGIAGKILGTLPVFPFAGQIASLYSIFILGELMPKSGKSWEIFM
50      60      70      80      90      100
cry1a-105.pe VQIEQLINQRIEERFARNOALISLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDM
8469140      EHVEEINOKILTARYNAKLSLDLGLGDLALAVYHESLESWENNRNTRARSVVKNOXIAL
110      120      130      140      150      160
cry1a-105.pe NSALTTAIPLFAVQNYQVPLLSVYQAAANLHLSVLDRVSVFGQRMGFOAATINSRYNDLT
8469140      ELMFQKLPSPFAVSGEEVPLPIYQAAANLHLLLRDASIFGKESGLSASELSTFYNRQV
170      180      190      200      210      220
cry1a-105.pe RLIGNYTHAVRWNTGLERVMGPDSDRWIRYNOFRRELTTLVDIVSLFPNYSRTYPI
8469140      ERTROYSDHCIKWNTGLNLRGTNAKSVRYNQFRKDMTLMVLVDLVALFSPYDTLVYPI
230      240      250      260      270      280
cry1a-105.pe RTVSQLTREITNPNVL-----ENFDGS--FRGSA---QGLEGS-IESPHLMDILNSITII
290      300      310      320      330      340
cry1a-105.pe TDAHR---GEY--YWSGHQIMASPVGFGSPFTFLYGTMGNAAPQQRIVAQLGQGVRT
8469140      SLLSRWSNTQYMNWVGHRLESPIG-----GAL-NTSTGTSNTSINPVTLOF
310      320      330      340      350      360
cry1a-105.pe LSTLIRFPFNIGIN---NOQLSVLDGTEFAYG-----TSSNLPASVYRKSGT--VDLSL
8469140      TSRDYRTESLAGLNLELTPQVNGVPRVDHMKFTFLPIASDNFYILGYAGVGTQLQDSE
400      410      420      430      440      450
cry1a-105.pe DEIPQNNVPPROGFSHRLSHVSMFSGFSNSSVSIIRAPMFESWHRSAEFNNLIASDS
8469140      NELPETTGQPNYESYSHRLSHIGLI-----SASHVKALVSWHRSADRTNTIEPNS
460      470      480      490      500
cry1a-105.pe ITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIIVNINGQLPQRYRARIYA
8469140      ITOIPLVKAFLNLSGAAVVRGPGFTGGDILRRRTNTGTFGDIRVNIINPPFAQRYRVIRYA
510      520      530      540      550      560
cry1a-105.pe STNLRIYVAVGERIFAGQNFNTMTDPLTFQSFYSATINTAFTFPMSSQSFVVGADT
8469140      STTDLOFHTSINGKAINQGNFSAIATMNRGDELDTYFTFTGFTTFFPSFSDVQSTFTIGAWN
570      580      590      600      610      620
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[illegible]

140 150 160 170 180 190
cry1a-105.pe NSALTITAFVAVQYQVLLSVVOAANLHLSVLVDVSGFWDGDAATINSYNDLT
8469140 ELMFVKLPSFAVSGSEVPLPIYAQAANLHLLLRDASIFGKWLSSASEISFYNRQV
170 180 190 200 210 220
cry1a-105.pe RLIGNYTDHAWNTGLERWGPDSRDWIRYNQFRRELITLVLDIVSFPNYSRTYPI
8469140 ERTDYSRDKIKWNTGLNLRGTNAKSWRVNQFRKDMTLMVLDLVALFPSPYDLVYPI
230 240 250 260 270 280
cry1a-105.pe RTVSQLTREIYNPVL-----ENFDGS--FRGSA---QGIEGS-IRSPHLMILNSITIY
8469140 KITSQLTREVYTDAGTVHPNQAFSTTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIY
290 300 310 320 330 340
cry1a-105.pe TDAHR---GEY--YMSGHQIMASVPVGFSGPEFTFLYGTMGNAAPQORIVAGLGGVYRT
8469140 SILSRWSNTQYNNWGHRLSESPIG-----GAL-NTSQGSTNTSINPVLQF
350 360 370 380 390
cry1a-105.pe LSSTLYRRFRFNIGIN---NQLSVLDTGFAYG-----TSSNLPASAVRKSGT--VDSL
8469140 TSRDVYRTESLAGNLFLTQPVNGVRVDVFWKFTPLFIASDNFYLYGAVGTQLQDSE
400 410 420 430 440 450
cry1a-105.pe DEITPQNNVPPRQGFSHRSHVSMFRSGFNSVSIIRAPMPSWHRSAEFNIIAGDS
8469140 NELPPTQCPNYESYHRJSHIGLI-----SASHVKALVYSWTHRSADRTNIEPS
460 470 480 490 500
cry1a-105.pe ITOIPLVKAHTLOSQTTVVRGPGFTGDLRLRTSGGPAYTVINNGOLPORARIRYA
8469140 ITOIPLVKAFLNLSGCAVVRGPGFTGDLRLRTSGGPAYTVINNGOLPORARIRYA
510 520 530 540 550 560
cry1a-105.pe STNLIYTVVAGERIFAGQFNKIMDTGDLPLTFQSFYATINTAFTFPMQSQSFVAGDT
8469140 STTDLOFTSINGKAINQGNFSATMRGDLDTKFTTIGFTTFFSFSVQSTFTIGAWN
570 580 590 600 610 620
cry1a-105.pe FSSGNEVYIDREFLIPYATLEAYNLRAOKAVNALFTSNQGLKNTVTDYHIDQVSN
8469140 FSSGNEVYIDREFLIPYATLEAYNLRAOKAVNALFTSNQGLKNTVTDYHIDQVSN
630 640 650 660 670 680
cry1a-105.pe LVTVLDFECLDEKRELSEKVKHAKLSDERNLLQDSNFKDINRQPERGCGSGTGITQIG
8469140 LVESLSDEFYLDKEKELFEIVKVAQIHERNM
690 700 710
cry1a-105.pe GDDVFKENTVLTSGTTFDECYPTLYXQKIDESKLKAFTRQYLRGVIEDSQDLFIYSIRNA
720 730 740 750 760 770
cry1a-105.pe

NRAA:21665941
21665941 source="GENBANK_PROT" Cry [Bacillus thuringiensis]
>NRAA:21665941
initn: 1595 initl: 888 Initn: 1595 Opt: 1716 z-score: 1946.1 E(): 4.2e-100
Smith-Waterman score: 1732; 42.7% identity in 705 aa overlap
(4-683:36-719)
cry1a-105.pe MDNNPINECIPYNCLSNPEVEVLGGERIETGY
21665941 PDHQSFSSNAKVDKISTDLKNETIQLONINHEDECLKISEVENPEPVFV-SASTIQTG-
10 20 30 40 50 60
cry1a-105.pe TPIDISLSTQFLSEFVPGAGFVLGLVDIIWGIFGP---SQMDAFLVQIEQLINQRIEE
21665941 ----ISIA-GKILGLTGLVPAGQVASYLSYFLLGELWPKGNOMEIFWEHVEELINQKIST
70 80 90 100 110
cry1a-105.pe FARNQAIISLEGLSNLQIYAESFREWEADPTNPALREEMRIQFNDMNSALTATPLFAV
21665941 YARNKALTDLKGLGDALAVHESLESWGVNRNTRARSVKSQVIALELMFVKQLPSFAV
120 130 140 150 160 170
cry1a-105.pe QNYQVPLLSVYVOAANLHLSVLVDVSGFQWRGFDATINSRYNDLTRLIGNYTHAVRW
21665941 SGSEVPLPIYAQAANLHLLLRDASIFGKWLSSASEISFYNRQVRGAGYSDHCYKW
180 190 200 210 220 230
cry1a-105.pe YNTGLERWGPDSRDWIRYNQFRRELITLVLDIVSFPNYSRTYPIRTVSQLTREIYN
21665941 YSTGLNLAGTNAESWVRVYQFRKDMTLMVLDLVALFPSPYDLVYPIKTSQLTREVYTD
240 250 260 270 280 290
cry1a-105.pe PV-LENFDGSFRGSA-----QGIEGS-IRSPHLMILNSITIYDAHRGEYVWSGH
21665941 AIGTVHPNASFASITWYNNNAPSFAIESAVVRNPHLLDFLEQVITYLSLSR----WSNT
300 310 320 330 340 350
cry1a-105.pe QIMASVPVGSPEFTFLYGTMGNAAPQORIVAGLGGVYRTLSSTLYRRFPNIGIN---
21665941 QYNNM---WGHRLFEFTIGOMLNTSQGSTNTSINPVLFTSRDVTESLAGNLFL
360 370 380 390 400 410
cry1a-105.pe NQQLSLDGTGFAYG-----TSSNLPASAVRKSGT--DSLDEIPQNNVPPRQGFSH
21665941 TOPVNGVPRVDVPHKVFVTHPTIASDNFYYPYAGICTLOQDSNELPPTTQGPNYESYSH
420 430 440 450 460 470
cry1a-105.pe RLSHVSMFRSGFNSVSIIRAPMPSWHRSAEFNIIASDITQIPLVKAHTLOSQTTV
21665941 RLSHIGLI-----SASHVKALVYSWTHRSADRTNIEPSITQIPLVKAFLNLSGAAV
480 490 500 510 520
cry1a-105.pe

[illegible]

CRYIA-105.p
SW: 8469157

8469157 description="PESTICIDIAL CRYSTAL PROTEIN CRY9DA (INSECTICIDAL DELTA-ENDOTOXIN CRYIXD(A)) (CRYSTALLIN ENTOMOCIDAL PROTOXIN) (132 KDA CRYSTALLIN PROTEIN)" library="NA species="Bacillus thuringiensis serovar japonensis" source="swissprot prot.version=NA type=PRT

SCORES In1L: 756 In1tn: 2154 Opt: 1715 z-score: 1941.8 E(): 7.3e-100
>SW:8469157 In1tn: 2154 In1ti: 756 Opt: 1715 z-score: 1941.8 expect(): 7.3e-100
Smith-Waterman score: 2285; 36.0% identity in 1197 aa overlap
(16-1177:57-1169)

cty1a-105.pe
 MDNNPNI¹⁰EC²⁰IPY³⁰NCS⁴⁰VEVLG⁵⁰GE⁶⁰IE⁷⁰GY⁸⁰TP⁹⁰DIS¹⁰⁰LS¹¹⁰L¹²⁰TQ¹³⁰
 YPI¹⁴⁰TDD¹⁵⁰NAG¹⁶⁰INMY¹⁷⁰KEV¹⁸⁰LT¹⁹⁰YGG²⁰⁰PY²¹⁰TD²²⁰IP²³⁰LN²⁴⁰PL²⁵⁰SV²⁶⁰SG²⁷⁰KD²⁸⁰IV²⁹⁰GI³⁰⁰NG³¹⁰VR³²⁰IL³³⁰SG³⁴⁰IF³⁵⁰PF³⁶⁰GE

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cryla-105.pe  --LLSEFVPGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRLEEFARNQAIISLEGLS
               : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
8469157       PFSSQWTVTVTYLL---NSLWPPDENSVDAMFMERVEELIDQKISEAVKGRALDDLTGLQ

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110      120      130      140      150      160
cyla-105.pe NLYQVAFSEFRWEADPTPALREEMRIQDNMSALTALPLF---AVNQVPLLIV
110      120      130      140      150      160
8469157 YNLYVEALDEWLNRP-NGARASLYSORENLTLDLFTQFWPFGSGGSONYATILPLV

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cryla-105.pe YVQAAHLHLSVLSDVSFGQWGFDAATINSRYNDLTKLIGNYTDHAVRWYNGLERVMG      170   180   190   200   210   220
:|||||:|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
YAQAANLHLLLLKDAIDYIGARWGILNQTQIDFHSRQSLSLTQTYNHCVTAAYNDGLAEURG      230   240   250

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8469157	TTAESFKNQVVRDMTLTAMDVLVALFPYNNLRQVPDGTNPQLTRVYDTPADFPDELOQ	270	280	290	300	310	320
cryla-105.pe	-----FDGSPRG--SAQGLEGS-IRSPHLMDSINTIIVTAHREYVWSG----	280	290	300	310	320	
8469157	TTQLGRSWINPAFENHNFSLVLENSLIRPPLPERLSNQLVNVYOTNGSAMRGSRVRY	330	340	350	360	370	380
cryla-105.pe	320	330	340	350	360	370	
8469157	HYLHSSIIQKSYGLSDPGVAMINQVNDIIYQIISQVSN--FASPVGSSYSVMDTNFYLS	390	400	410	420	430	440
cryla-105.pe	380	390	400	410	420	430	
8469157	SGQVSGISGY-----TOOGIPAVCLAQRNSTDLPSELNPEGDII---RNYSHRLSHITQY	450	460	470	480	490	
cryla-105.pe	440	450	460	470	480	490	
8469157	RFOATGSGSPSVTSANLPTCVWTHRDVLDNTITANQITQLPLVKAYELSSCATYKVGPG	500	510	520	530	540	550
cryla-105.pe	500	510	520	530	540	550	
8469157	FTGQDILRRTSGFPAYTIVNINGOLPORYARIRIYASTNLRIYTVVAGERIFAGQFNK	560	570	580	590	600	610
cryla-105.pe	560	570	580	590	600	610	
8469157	TMDGDELTPGSPYATINTAFTFPMQSQSFVGTADTFSSGNEVIYIDRELIPVTAILEA	620	630	640	650	660	670
cryla-105.pe	620	630	640	650	660	670	
8469157	EEDLEAKAKAKANLFTIRBZLQVNVTVQVQAPAAVLNLSCLSDQYGHDKMLLEAVR	680	690	700	710	720	730
cryla-105.pe	680	690	700	710	720	730	
8469157	AAKLSRERNLLQDPDFNTINSTBNGKASNGVITSBGGPFPGKRALQASA-RENYPT	740	750	760	770	780	790
cryla-105.pe	740	750	760	770	780	790	
8469157	YIYQKVDASVLKPYTRYTRJELDGFKVKSQDLIELIHYHKLWLVNVSVDNL	800	810	820	830	840	850
cryla-105.pe	800	810	820	830	840	850	
8469157	GSCSGMNRCEQOQVNAQLETHEHPHMDCCEAQOATHESSVINTGDLNASVDOGVNWK	860	870	880	890	900	910
cryla-105.pe	860	870	880	890	900	910	

8469157 VRTDGYATLGNLELVGFLSGESLEREQDQNAKNAEALGRKRAEIDRVLYAAKQAINH
910 920 930 940 950 960

cry1a-105.pe LFWNQYQDLQADNIAHIAADKRVHSIREAYLPFLSVIPGVNNAIFEELEGRIFTAFS
920 930 940 950 960 970
8469157 LFDVYQDQLNPEIGLAEINEASNLVESISGVSDTLQLQIPGPIEYIELSDRLQOASY
970 980 990 1000 1010 1020

cry1a-105.pe LYDARNVLKNGDFNGLSCWNVKGVHDVVEEQNNORSVLVVPWEAEVSEVRCVPGGYI
980 990 1000 1010 1020 1030
8469157 LVTSRNAVQNGDFNSGLDSWNTTDSVQDQGNMH-FLVLSHWDQVSOQLRVNPNCKYV
1030 1040 1050 1060 1070 1080

cry1a-105.pe LRVTAKEGEGEGCVTHIEIENNTELKFSNCVEEIEYPNNTVTCNDYVNOEEYGGAYT
1040 1050 1060 1070 1080 1090
8469157 LRVTAKEGEGEGCVTHIEIENNTELKFSNCVEEIEYPNNTVTCNDYVNOEEYGGAYT
1090 1100 1110 1120 1130 1140

cry1a-105.pe SRRNGVNEAPVPADYASVVEEKSYYDGRNCPENRGYDYPLPGVYVTKLEYFPE
1100 1110 1120 1130 1140 1150
8469157 NDN-----SYITEEVVFPE
1130 1140

cry1a-105.pe TDKVWIEIGETEGTFFIVDSVELLMEE
1160 1170
8469157 TKHMVVESESEGSFYIDSIEFETQE
1150 1160

cry1a-105.pep
NRAA:8469157

8469157 source="GENBANK_PROT" Pesticial crystal protein cry9Da (Insecticidal
delta-endotoxin CryIXD(a)) (Crystalline entomocidal protoxin) (132 kDa crystal
protein)|gi|2102642|dbj|BAAL19948.1| cry9Da1 [Bacillus thuringiensis]

SCORES Init1: 756 Initn: 2154 Opt: 1715 Z-score: 1941.8 E(): 7.3e-100
>>NRAA:8469157
Initn: 2154 Init1: 756 opt: 1715 Z-score: 1941.8 expect(): 7.3e-100
Smith-Waterman score: 2285; 36.0% identity in 1197 aa overlap
(16-1177:57-1169)

cry1a-105.pe MDNPNNEICFPYNCLSNPEVIGLGERIETGYTIDISLSLTFQF
10 20 30 40
8469157 YPLTDDPNAGLQNNYKEYLQTYGGDYTDPLINPNLVSQKDVQLQGINVIGLLSLTFGF
30 40 50 60 70 80

cry1a-105.pe LLSEFVPGAGVLGLVDIIWIGIFGSQWDAFLVQIEQLNQRIEFARNQAISLEGLS
50 60 70 80 90 100
8469157 PFSQWVTVYVLL---NSLWPDNDNSVMDAMEVEELIDQKISEAVKGRALDLSLQ
90 100 110 120 130 140

cry1a-105.pe NLQYIAESFRWEADPTNPALREMRIOFNDMNALTAIPF---AVQYQVPLLSV
110 120 130 140 150 160
8469157 YNLYVEALDEWLRNP-NGARASLVYSQRFNILDSLFTQFMPSFGSPSQNYATLLPV
150 160 170 180 190 200

cry1a-105.pe YVOANLHLSVLRDVSVFGQWGFDAATINSGRYNDLIRLIGNYTHAVRWYNTGLERVWG
170 180 190 200 210 220
8469157 YAOANLHLLLLKADDIYGNRWGLNQTQIDQFHSROSLTQYTHCVTAINDGLAELRG
210 220 230 240 250 260

cry1a-105.pe PDSRMIRYNQFRELTLVDIVLSFNYSRTYPIRTVSQLTREIYNPV---LEN-
230 240 250 260 270
8469157 TTAESWFKYQVREEMTLTAMDILVALFYNLQVDPGTNPQLTREVYTDPIAFDPLEQF
270 280 290 300 310 320

cry1a-105.pe -----FDGSPRG---SAQIGES-IRSPHMDILNSITIYDHAHGEYVWSG-----
280 290 300 310
8469157 TTQCRSWINPAPFRNLNFSVLENSLIRPPLHFERLSNQLVNVYQTSNGSAWRGSRVRY
330 340 350 360 370 380

cry1a-105.pe HQIMASPVGFGSPGFEFTPLXYGTMGNAAPQ--RIVAQLQGQGVRTLSLTYRPFENIGIN
320 330 340 350 360 370
8469157 HYLHSSIIQEKSYGLLSDPVGANINQVNDIYQIISOVSN-FASPVGSSYSVWMDTNFYLS
390 400 410 420 430 440

cry1a-105.pe NQQLSVLDCTEFAYGTSNLSNPASVYKSGTVDSLDETPPONNNVPPRQGFSLHSHVSMF
380 390 400 410 420 430
8469157 SGQVSGISGY-----TOQGIPAVLCQQRNSTDELPSLNPEGDI---RNYSHLSHTQY
450 460 470 480 490

cry1a-105.pe R-SGFSNSSVSLIRA--PMFSWIRSAFNIIASDSITQIPLVKAHTLQSGTTVVRGPG
440 450 460 470 480 490
8469157 RFOATQSGSPSVSANLPTCWTHRDVLDLNTITANQITQLPLVKAYELSSGATVVKQPG
500 510 520 530 540 550

cry1a-105.pe FTGCDILARTSGGPFATYIVNNGQVQRYRARIYASTTNLRIYVTVAGERIFAGQFNK
500 510 520 530 540 550
8469157 FTGGLDVIRTNITGGFGAIRVSVGTPLTQRYRIRFRYASTIDFDFVTRGGTTINNFRFR
560 570 580 590 600 610

cry1a-105.pe TMDTGDLPLTFQSFYATINTAFTFPMSSQSFVVGADTFSSGNEVYIDRFELIPVATLEA
560 570 580 590 600 610
8469157 TMRGQESRYEYRTVEFTTFFNFPTQSDIIRTSIQGLSGNGEYLDRIEILIPVNPAREA
620 630 640 650 660 670

cry1a-105.pe EYLVLEAKQAV-NALFTSTNOLGKTNVTDYHIDQVSNLYTSLSDEFCLDEKRELSKVK
620 630 640 650 660 670
8469157 EEDLEAKAKAQNLFETRD-GLQVNVTDYQVDAANLYSCLSDQYGHDKKMLLEAVR
680 690 700 710 720 730

cry1a-105.pe HAKRLSDERNLQDSNFKDINRQFERGWSGTGITIQGGDDVFKENYVTLSTGTFDECYPT
680 690 700 710 720 730
8469157 AAKRLSRENLQDDPFTINSTENGWKAANGVTISEGGPFKFGKALQALASA-RENYPT
740 750 760 770 780 790

cry1a-105.pe YLQKIDESKLKAFTRQLRGYEDSDQDLEIYISRYNAKHETVNVFQTSNLWPLSAQSPI
740 750 760 770 780 790
8469157 YIYQKVDASLVKPYTRVLRGDFVKSSQDLEIDLIIHYHKVHLVKNVPDNL-----VSDTYSD
800 810 820 830 840

CRYIA-105.pe KGCCEPNCAPHSTNFDLDCSRGKCAHSHHPSLDLDVGCDDIADNEDJGWWIFPK
8469157 GSCGMRZCQOMVNAOETPHHPMDCEAAQTHEFSYINTGDLNASVDQGINWLK
CRYIA-105.pe KTDQWARKCNAPFEEAAGEALAKVKKWDRKRELEWENIVYKAKESVDA
8469157 VRTIDGATIGLNEVEGFLSPESLFEQDNDKNNELGRAEIDRVLAKQAINH
CRYIA-105.pe LFVNSQVDOLOQADNITAMTHAKKNSIREKXVLSVPGVMAIKFELEGRIFTAFS
8469157 LFVDYQDQQLNPEIGLAEINEASNIVSLSVYSDALLOIINGINVEIYELSLRLOQASY
CRYIA-105.pe LYDARNVTKGDFNGLSCWNVKGVHVDVEEQNORSVUVVWEAEKOEYVUCPGRGN
8469157 LYTSRNVQNGDFNSGLDSWNTTIDASVQDGNHFLVLSHNDASNSQQLNPNPKYV
CRYIA-105.pe LRVAYKEGYGEGCVTHIEIENNTDELAFSCVVEEETPNVTTCNDVTNOSYQAVT
8469157 LRVYARKVGGDGVVIRGAAHQTILFNAC
CRYIA-105.pe SENRNGNEAPSVADYASVYEKSYTDGRENPCFNRGYDYTPLPYVYKLEYFPE
8469157 NDN
CRYIA-105.pe TKVWIEGEGTEGTFIVDSVELLMEE
8469157 TKHMMVEVSESGFYIDSIEFETOE
CRYIA-105.pep
SW:8469149
8469149 description="PESTICIDIAL CRYSTAL PROTEIN CRYIIA (INSECTICIDAL
DELTA-ENDOTOXIN CRYII(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (81 KDA CRYSTAL
PROTEIN)." library=NA species="Bacillus thuringiensis serovar kurstaki"
source="swissprot_prot" version=NA type=PRT
SCORES Init1: 896 Initn: 1603 Opt: 1712 z-score: 1941.5 E(): 7.5e-100
>>SW:8469149
Initn: 1603 Init1: 896 Opt: 1712 z-score: 1941.5 expect(): 7.5e-100
Smith-Waterman score: 1728; 42.7% identity in 705 aa overlap
(4-683:36-719)
CRYIA-105.pe MDNPNINECIPYCNLSNPEVEVLGGRIETGY
8469149 QDKHQSFSNAKVDKISTDSLKNETDIELQNHNECLKMWSENVPPV-SASTIQIG-
CRYIA-105.pe TPIDISLSITOFLLSEFVPGAGFVLGLVDIINGIFGP---SQWDAFLVQIEQLINQRIEE

8469149 --IGIA---GKILGUGVPFGQVASYLSYILGELWPKQKQWEIFMEHVEEIIQNKIST
CRYIA-105.pe FARNQAIISRLGSLNLYQIYAESFREWEADFTNPALREEMRIQFNMDNSALITTAIFLFAV
8469149 YARNKALTDLKGLDALAYVHDSLESWGNRNTRARSVVKSOYLALELMFVQKLPSFAV
CRYIA-105.pe QNYQVPLLSVYQAAHLHUSVLURDVSVFGQWGFDAATINSRYNDLRLKLGNYTDHVRW
8469149 SGEEVPLLPITYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDSDHCVKM
CRYIA-105.pe YNTGLERWGPDSRDIRYNQFRRELTTLVLDIVSLFPNVDSTRTYPIRTVSQLTREIYTN
8469149 YSTGLNNLRGTNAESWVRNQFRDMTLMVLLDLVALFPDYDTOMYPIKTTAQLTREYTD
CRYIA-105.pe PV-----LENFDGS--FRGSA--QGIEGSI--RSPHLMILNSIITYTDAHREYVWSGH
8469149 AIGTVHPHPSTSTWYNNNAPSFSAIEAAVVRNPHLLDFLEQVTIYLSLR-----WSNT
CRYIA-105.pe QMASPVGSCSPETFLVGTWGNAPQORIVAGLQGVYRTLSLTYRRFFNIGIN---
8469149 QNNN--WGCHKLEFRTIGGTLNISTOGSNTSINPVLFTSDRDYRTESLAGLNLFL
CRYIA-105.pe NOGLAVLDGTEAYG-----TSSNLPASVYRKSGTV--DSLDEIPPNQNNVPPRQGFSH
8469149 TOPVNSGPRVDFHWKFWHPHPSADNFYVPGYAGIGTLODSENELPPEATGPVYESYSH
CRYIA-105.pe RLSHVSMRSPGFSNSSVSIIRAPMFSWHRSEFNIIASDSITQIPLVKAHTLOSCTTV
8469149 RLSHIGLI-----SASHVYKAVVWTHRSRSTNIEPNSITQIPLVKAFNLSSGAAV
CRYIA-105.pe VQPGFTGDDILRSTSGCPNATLNINGQPAVAYRIRYASTTRIRYIVTVAGERIFA
8469149 VQPGFTGDDILRSTSGCPNATLNINGQPAVAYRIRYASTTRIRYIVTVAGERIFA
CRYIA-105.pe GQFNMTGDTPLTFQSFVSATINTAFTFPMQSSFNIGASTFSSQVMEYRPELANT
8469149 GNFSATMRGEDLDYKTRVGTGFTTFFSFLVDVQSTFTTIGAWNSSNEVYINGEPVPEVE
CRYIA-105.pe ATLEAFYNLEAKAVNALFTSNQGLKTNVTYHIDQVSNLVTVLSDEPCDERBELS
8469149 VTVEAYDFEKAQKVATLFTSNPRGLTKVDKYHIDQVSNLVESLSDEFYLDKESLFL
CRYIA-105.pe EKVYKAKLSDERNLLQDSNFKDINFQPERGNGSGTGITIQGGDDYFKENYVTLSGITFDE

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8469149  ||:|:|:| |||:
          EIVYAKQLHIERNM
          710

cryla-105.pep
NRAA:32709126

32709126 source="GENBANK PROT" CryII [Bacillus
thuringiensis]gi|8469149|sp|O45752|CryIIA.BACTX Pesticidal crystal protein
cryIIa (insecticidal delta-endotoxin CryII(a)) (Crystalline entomocidal protoxin)
(81 kDa crystal protein)gi|142768|gb|AA22354.1| insecticidal protein

SCORES   Initl: 896   Initn: 1603   Opt: 1712   z-score: 1941.5   E(): 7.5e-100
>>NRAA:32709126
initn: 1603   initl: 896   opt: 1712   z-score: 1941.5   expect(): 7.5e-100
Smith-Waterman score: 1728;   42.7% identity in 705 aa overlap
(4-683:36-719)

cryla-105.pe
          10      20      30
          MDNPNINECIPYNCLSNPEVEVLGGERISTGY
32709126  QDKHQSFSNAKVDKISTDLSKNETDIELQNHEDCLKXSEYENVEPVFV-SASTIQTG-
          10      20      30      40      50      60
          100      110      120      130      140      150
cryla-105.pe  TPIDISLSLTOFLSEFVPGAGFVLGLVDIIWGFPG---SOWDAFLVQIQLINQRIEE
          40      50      60      70      80      90
          100      110      120      130      140      150
32709126  --IGIA---GKILGTGLVFPAGQVASYLSFILGELWPKGNOWEIFMEHVEEIIINQKIST
          70      80      90      100      110

cryla-105.pe  FARNQAISRLEGSLNLYQIYASFREWEADPTNPALREEMRIQFNDMSALTTPAIFLFAV
          100      110      120      130      140      150
32709126  YARNKALDGLGDLAVYHDSLESWVGNRNTRASRVVKSQYIALEIMFVQKLPSFAV
          120      130      140      150      160      170

cryla-105.pe  QNYQVPLLSVYVQAANHLHSLVLRDVSFVGQWGFDAATINSRVNDLTGLIGNYTDHAVRW
          160      170      180      190      200      210
32709126  SGEVPLLPYIAQAANHLHLLRDASIFGKENGSLSSSEISTFNQOVERAGDYSIDHCVKW
          180      190      200      210      220      230

cryla-105.pe  YNTGLRVWGPSRDMIRYNQFRRELTITVDIVSLFPNYDSRTPIRTVSQLREIYTN
          220      230      240      250      260      270
32709126  YSTGLNLRGTNAESWVRYNQFRDMTLMWLDLVALFPSTYDQWYPIKTKQLTFREYVD
          240      250      260      270      280      290

cryla-105.pe  FV-----LENFGS--FRGSA---QIEGSI-RSPHMLDLINSIIYDARGHYWWSGH
          280      290      300      310
32709126  ALGVHPHPSFTSTWTNNNAFSAIEAAVVRNPHLLDFLEQVITYISLLSR---WSNT
          300      310      320      330      340      350

cryla-105.pe  QJMASPVGFSPEFTPELGTMGNAAPQIRIVAGLGQGVYRTLSSTLYRRFPNIGIN---
          320      330      340      350      360      370
32709126  QYMMN---WGHKLEFRTIGTILNISTGCTNTSINPVLPFTSRDVRTESLAGLWLF
          360      370      380      390      400      410

cryla-105.pe  NQOLSVLDTGTFAYG-----TSSNLPASAVYRKSGTV--DSLDEIPQNNVPPRQGFSH
          380      390      400      410      420
32709126  TQVNGVPRVDFHWKFVTHPIASDNFYVPGVAGIGTQLQDSNELPPEATQPNYESYSH
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33326396 SGEVPLLPYVQAANLHLLLRDASIFGKEWGLSSSEISFYNRQVERAGDYSCHVKW
180 190 200 210 220 230
cry1a-105.pe TMTGLERWGPDRWIRYNRRELTLTLDIVSLFNFYDSRTYPIRTYSQLTREIYN
240 250 260 270
33326396 YSTGLNLRGTINAEWVRVNOFRDNTLMDLVALFFSDYDTOMYPIKTTAQLTREYTD
240 250 260 270 280 290
cry1a-105.pe PV-----LENFDS--FRGSA--CGEGSI-RSPHMDILNSITIIDAHREYVWSGH
280 290 300 310
33326396 AIGTVHPHPSTFTTWNNAFSAIEAAVVRNPHLLDFSQVATYLSLSR----WSNT
300 310 320 330 340 350
cry1a-105.pe QIMASPVGFSPEFTPLPYGTMGNAAPQQRVIAQLGGVYKPSSTLYRRRNIGIN---
320 330 340 350 360 370 380 390
33326396 QYMMN---WGHKLEPRTIGTGLNISTQGSTNITSINPNTLPFTSDVYFSLAGNLLF
360 370 380 390 400 410
cry1a-105.pe TSSNLPSAVYRKSQTV--DLSDEPFPNNVPRGQPEH
380 390 400 410
33326396 TOPVNGVRVDFHWKVFVTHPIASDNFYVPGYAGIGTQLQDSENELEPPSPQNYESYSH
420 430 440 450 460 470 480
cry1a-105.pe RUSHVMSFRSGFNSVSIIRAPMFSWIHRSAPENLLIASDSITQIPLVKATILQSGTV
430 440 450 460 470 480
33326396 RLSHIGLI-----SASHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSGAAV
480 490 500 510 520
cry1a-105.pe VRGPGFTGGDILRTSGGPFATVINGOLPQRYRIRYASTNLRIYVAGERIFA
490 500 510 520 530 540
33326396 VRGPGFTGGDILRTTGTGFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQ
530 540 550 560 570 580
cry1a-105.pe GQFNKMTDGLTFLQSFYSYATINTAFTFPMSSQSSFTVGADTFSSGNEVYIDREFLIPVT
550 560 570 580 590 600
33326396 GNFSATMNRGEDLDYKTFRTVGTFTFPFSFLDVQSTFTTGAMWFFSSGNEVYIDREFLIPVE
590 600 610 620 630 640
cry1a-105.pe ATLEAYNLERAQKAVNALPSTNQGLKTVNTDYHTIDQVSNLYVLSDFECDEKBELS
610 620 630 640 650 660
33326396 VTYEAYDFEKAQEKVYALTSTNTRGLKTDVDDYHIDQVSNLVSLSDFEYLDKERELF
650 660 670 680 690 700
cry1a-105.pe EVKHAKLSDERNLLQDSNFKDINRQPERGWSGTGTTIQGGDDVFKENVYTLSTGTFDE
670 680 690 700 710 720
33326396 EIVKAKQLHIERNMP
710 720
cry1a-105.pep
NRAA:33325407
33325407 source="GENBANK_PROT" Cry1a (Bacillus thuringiensis)

initn: 1603 initl: 896 opt: 1712 Z-score: 1941.3 expect(): 7.8e-100
Smith-Waterman score: 1726; 42.7% identity in 705 aa overlap
(4-683:36-719)

33325407 QDKHQSFSNAKVDKISTSLKNETDIELQNHEDCLMKSEYENVEFPV-SASTIQTG-
10 20 30 40 50 60
cry1a-105.pe MDMNPINECIPYACLNSPEVVLGGERIETGY
10 20 30
33325407 QDKHQSFSNAKVDKISTSLKNETDIELQNHEDCLMKSEYENVEFPV-SASTIQTG-
10 20 30 40 50 60
cry1a-105.pe TPIDISLSLTOFLLEFVPGAGFVLGLVDIINGIFOP---SQMDAFLVQIEQLINQRIEE
40 50 60 70 80 90
33325407 --IGIA--GKILGTILGVFPAGQVASLYSFLGELMPKGNQWELFMHVEEIIQKIST
70 80 90 100 110
cry1a-105.pe FARNOAISRLGLESLNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALITTAIFLFAV
100 110 120 130 140 150
33325407 YARNKALITDLKGLGDALAYHDSLESWGNRNTRARSVVKSOYIALELMFVQKLPFAV
120 130 140 150 160 170
cry1a-105.pe QNYQVPLLSYVQAANLHLSVLDRVSVFGQWGFDAATINSYNDLRLIGNYTDHAVRW
160 170 180 190 200 210 220 230
33325407 SGEVPLLPYVQAANLHLLLRDASIFGKEWGLSSSEISFYNRQVERAGDYSCHVKW
180 190 200 210 220 230
cry1a-105.pe YSTGLNLRGTINAEWVRVNOFRDNTLMDLVALFFSDYDTOMYPIKTTAQLTREYTD
240 250 260 270 280 290
33325407 AIGTVHPHPSTFTTWNNAFSAIEAAVVRNPHLLDFSQVATYLSLSR----WSNT
300 310 320 330 340 350
cry1a-105.pe PV-----LENFDS--FRGSA--CGEGSI-RSPHMDILNSITIIDAHREYVWSGH
380 390 400 410 420
33325407 TOPVNGVRVDFHWKVFVTHPIASDNFYVPGYAGIGTQLQDSENELEPPSPQNYESYSH
420 430 440 450 460 470
cry1a-105.pe RUSHVMSFRSGFNSVSIIRAPMFSWIHRSAPENLLIASDSITQIPLVKATILQSGTV
430 440 450 460 470 480
33325407 RLSHIGLI-----SASHVKALVYSWTHRSADRTNTEIPNSITQIPLVKAFNLSGAAV
480 490 500 510 520 530 540
cry1a-105.pe VRGPGFTGGDILRTSGGPFATVINGOLPQRYRIRYASTNLRIYVAGERIFA
490 500 510 520 530 540
33325407 VRGPGFTGGDILRTTGTGFGDIRVNIINPPFAQRYRIRYASTTDLQFHTSINGKAINQ
530 540 550 560 570 580
cry1a-105.pe GQFNKMTDGLTFLQSFYSYATINTAFTFPMSSQSSFTVGADTFSSGNEVYIDREFLIPVT
550 560 570 580 590 600
33325407 GNFSATMNRGEDLDYKTFRTVGTFTFPFSFLDVQSTFTTGAMWFFSSGNEVYIDREFLIPVE
590 600 610 620 630 640
cry1a-105.pe ATLEAYNLERAQKAVNALPSTNQGLKTVNTDYHTIDQVSNLYVLSDFECDEKBELS
610 620 630 640 650 660
33325407 VTYEAYDFEKAQEKVYALTSTNTRGLKTDVDDYHIDQVSNLVSLSDFEYLDKERELF
650 660 670 680 690 700
cry1a-105.pe EVKHAKLSDERNLLQDSNFKDINRQPERGWSGTGTTIQGGDDVFKENVYTLSTGTFDE
670 680 690 700 710 720
33325407 EIVKAKQLHIERNMP
710 720
cry1a-105.pep
NRAA:33325407
33325407 source="GENBANK_PROT" Cry1a (Bacillus thuringiensis)

SCORES Initl: 896 Initn: 1603 Opt: 1712 Z-score: 1941.3 E(): 7.8e-100
>>NFAA:33325407

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cryla-1.05.pe QIMASPVGSGPEFFTEPLGYTMGNAAPOQRIVAOLGCGVYRTSSLTLYRPENTGIN-
1261624 QYMMH---WGCHKLEFRFRTIGTGLNIISQGSTWTSINPVTLPFTRSDVYRTESLAGLNLF
360 370 380 390 400 410
cryla-1.05.pe NQQLSVLDGTETFAIG-----TSSNL--PSAVYKSGTVDSLEDEIPQNNVPPRQGFESH
420 430 440 450 460 470
1261624 TOPVNGVRDVFHWKFTVTHPIASDNIFFYGYIGTQLQDSENELEPPEATGQPNVYKSH
420 430 440 450 460 470
cryla-1.05.pe RLSHVSWMFSGFSGNSVSIIRAPMFWSHRSAPFNNIITASDITQPLVKAHTLQSGTV
480 490 500 510 520 530
1261624 RLSHIGLI-----SASHVKALVYSWTHRSADRTNIEPNSITQPLVKAFNLSGAAV
480 490 500 510 520
cryla-1.05.pe VRGPGFTGGDILRRTSGGPFAYTIVNQLQRYRARIYVASTNIRIYTVVAGERIFA
540 550 560 570 580 590
1261624 VRGPGFTGGDILRRTNIGTFGDIRVNIPPPFAQRVRVIRYVASTDLQHTSINGKALNQ
540 550 560 570 580 590

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cryla-105.pe  ATLEAEVNEPBAOKAVNALPFTSTNOLGKTNVDYHDIVDSNLYVLSDEFCILDEKREL
1261624      VTVEAEYDFEKAQEKVTLFTSTNPRGLKTDVKDYLQDVSNVAESLSEDFYLDKREL
              650   660   670   680   690   700

cryla-105.pe  EVKVKHRLSDLSNLLQDSNFKDINRQPERGMGSGTGITIQGGDDVFNENYVLSGTFDE
1261624      EIVKYAKQLHIERNM
              710

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cryla-105.pep
NRAA:1621216

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

SCORES      Initl: 889      Initn: 1600      Opt: 1709      z-score: 1938.1      E(): 1.2e-99
>>NRAA:1621216
      initn: 1600      initl: 889      opt: 1709      z-score: 1938.1      expect(): 1.2e-99
      Smith-Waterman score: 1725:      42.7%      identity in 705 aa overlap

```

```

(4-665:36-7197)
cryIa-105.pe
1621216 QDKHQSFSSNAKVDKISTLSKNETDIQLONIHNEHCLMKSEYNEVPFV-SASTIQTG-
10 20 30 40 50 60
MDNNPNINECPYCNLCNPEVVLGGERIETGY
30

```

```
cryla-105.pe TPBISLSLTQFLLSEVFVGAGVGLVDVIINGIFQP---SQWDAFLVQEQLINQRIBEE  
| | : : | | | | : : | | : : | | : : | | : : | | : :  
--IGIA---GKILGTGVFPAGOVASLYSFI L GELMFKPKQNWEI FMEHVEEII N Q K I S T
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cryla-105.pep
NRAA:14537812
14537812 source="GENBANK_PROT" CryIIa [Bacillus thuringiensis]
SCORES Initl: 896 Initn: 1603 Opt: 1707 z-score: 1935.8 E(): 1.6e-99
>NRAA:14537812
Initn: 1603 initl: 895 opt: 1707 z-score: 1935.8 expect(): 1.6e-99
Smith-Waterman score: 1723; 42.7% identity in 705 aa overlap
(4-683:36-719)
cryla-105.pe
MDNPNINECIPYCNLSNPEVEVLGGERIETGY
14537812 QDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECKMSEVENVEPFV-SASTIQIG-
10 20 30 40 50 60
cryla-105.pe TPIDISLSLTFLLSEFVPGAGFVLGVDIINGIFGP--SQWDAFLVQIEQLINORIEE
40 50 60 70 80 90
14537812 --IGIA---GKILGTILGVFFAGQVASYLSIFELGELMPKGNQWEIFMEHVEEIIINQIKIST
70 80 90 100 110
cryla-105.pe FARNQAIISRLGSLNLYQIYAESFREWEDPTNPALREEMRIQFNDMNSALTITAIPLFAV
100 110 120 130 140 150
14537812 YARNKALITDILKGLGDALAVYHDSLESWGNRRNTRARSVVKSOYIALELMFVQKLPSFAV
130 140 150 160 170
cryla-105.pe QNYGVPLSVYVQAANHLHSILRVSVFGQWGFDAATINSRYNDLRLIGNYTDHAVRW
160 170 180 190 200 210
14537812 SGEVPLLPYIQAANHLHLLRDASIFGKEMGLSSSEISTFYNNQVERAGDYSDHCVKW
180 190 200 210 220 230
cryla-105.pe YNTGLRVGPDSDRWIRYNGPREFLTULQSFYVDSRNPRTVTSOLTREIYTN
220 230 240 250 260 270
1621216 YSTGLNLRGTNAESWVRINQFRDMDIYVLDVALNSYITQWYPIKTAQLTREVIYD
240 250 260 270 280 290
cryla-105.pe PV-----LENFDGS--FRGSA---QGIEGSI-RSPHNDIANSITIYDAHGEYVWSGH
280 290 300 310 320 330 340 350 360 370 380 390 400 410 420
1621216 AIGTVHPHPSTSTTWNNAPFSIAEAAVWRPHLLDFLEQVTSLSLSR---WSNT
300 310 320 330 340 350 360 370 380 390 400 410 420
cryla-105.pe QMASPVGSGPEFTFPPLGYTMGNAAPQQRIVAQCGVYRTLSLTYRRPFGN---
320 330 340 350 360 370 380 390 400 410 420
1621216 QYMMN---WGCHKLEFRTIGTGLNISTQSTNTSINPVLPTPSRDVYTESLAGNEL
360 370 380 390 400 410 420
cryla-105.pe NOQLSVLDGTGEFAYG-----TSSNLPASVVRKSGTV--DSLDELPQNNVPPRGFSGH
380 390 400 410 420
1621216 TQPVNGVRVDFHFKVETHPIASDNFYVYGVAGIGYIGLODSENELPEATQPNYESYSH
420 430 440 450 460 470 480
cryla-105.pe RLSHVSMFRGFSNSSVSIIRAPMFSWTHRSADFNNIIASDSITQIPLVKAHTLQSGTVV
430 440 450 460 470 480
1621216 RLSHIGLI-----SASHVKALVYSWTHRSADRTNTEFPNSITQIPLVKAFLNLSGAAV
480 490 500 510 520
cryla-105.pe VRGPGFTGGDLRLRTWIGTIGDIRVINPFPQRYRIRYASTIDLOFHTSINGKAIQ
500 510 520 530 540 550 560 570 580
1621216 VRGPGFTGGDLRLRTWIGTIGDIRVINPFPQRYRIRYASTIDLOFHTSINGKAIQ
530 540 550 560 570 580
cryla-105.pe QGFNKTMDTGPITFQSFYATINTAFTFPMQSSFTVAGDTFSSGNEVYIDRFELIPVT
550 560 570 580 590 600
1621216 GNFSATWRGEDLDYKTFRTVGTFTFPSFLDVOSTFTIGAMWFFSSGNEVYIDRFELIPVE
590 600 610 620 630 640
cryla-105.pe ATLEAEYNLRQAKVNAALFTSTNQLGKINVTYDHYDQVSNLVTYLSDEFCLDEKRELS
610 620 630 640 650 660
1621216 VTYEAYDFEKAQKVYALFTSTNPRGLKTDVQKDYDQVSNLVSLSDEFCLDEKRELF
650 660 670 680 690 700
cryla-105.pe EKVYKAKLSERNLLQDSNFKDKINQPERGCGSGTITIQGDDVFXENVYTLISGTFDE
670 680 690 700 710
1621216 EIVKYANELHIERNM
710

cryla-105.pep
NRAA:14537812
14537812 source="GENBANK_PROT" CryIIa [Bacillus thuringiensis]
SCORES Initl: 896 Initn: 1603 Opt: 1707 z-score: 1935.8 E(): 1.6e-99
>NRAA:14537812
Initn: 1603 initl: 895 opt: 1707 z-score: 1935.8 expect(): 1.6e-99
Smith-Waterman score: 1723; 42.7% identity in 705 aa overlap
(4-683:36-719)
cryla-105.pe
MDNPNINECIPYCNLSNPEVEVLGGERIETGY
14537812 QDKHQSFSSNAKVDKISTDSLKNETDIELQINHEDECKMSEVENVEPFV-SASTIQIG-
10 20 30 40 50 60
cryla-105.pe TPIDISLSLTFLLSEFVPGAGFVLGVDIINGIFGP--SQWDAFLVQIEQLINORIEE
40 50 60 70 80 90
14537812 --IGIA---GKILGTILGVFFAGQVASYLSIFELGELMPKGNQWEIFMEHVEEIIINQIKIST
70 80 90 100 110
cryla-105.pe FARNQAIISRLGSLNLYQIYAESFREWEDPTNPALREEMRIQFNDMNSALTITAIPLFAV
100 110 120 130 140 150
14537812 YARNKALITDILKGLGDALAVYHDSLESWGNRRNTRARSVVKSOYIALELMFVQKLPSFAV
130 140 150 160 170
cryla-105.pe QNYGVPLSVYVQAANHLHSILRVSVFGQWGFDAATINSRYNDLRLIGNYTDHAVRW
160 170 180 190 200 210
14537812 SGEVPLLPYIQAANHLHLLRDASIFGKEMGLSSSEISTFYNNQVERAGDYSDHCVKW
180 190 200 210 220 230
cryla-105.pe YNTGLRVGPDSDRWIRYNGPREFLTULQSFYVDSRNPRTVTSOLTREIYTN
220 230 240 250 260 270
14537812 YSTGLNLRGTNAESWVRINQFRDMDIYVLDVALNSYITQWYPIKTAQLTREVIYD
240 250 260 270 280 290
cryla-105.pe PV-----LENFDGS--FRGSA---QGIEGSI-RSPHNDIANSITIYDAHGEYVWSGH
280 290 300 310 320 330 340 350 360 370 380 390 400 410 420
14537812 AIGTVHPHPSTSTTWNNAPFSIAEAAVWRPHLLDFLEQVTSLSLSR---WSNT
300 310 320 330 340 350 360 370 380 390 400 410 420
cryla-105.pe QMASPVGSGPEFTFPPLGYTMGNAAPQQRIVAQCGVYRTLSLTYRRPFGN---
320 330 340 350 360 370 380 390 400 410 420
14537812 QYMMN---WGCHKLEFRTIGTGLNISTQSTNTSINPVLPTPSRDVYTESLAGNEL
360 370 380 390 400 410 420
cryla-105.pe NOQLSVLDGTGEFAYG-----TSSNLPASVVRKSGTV--DSLDELPQNNVPPRGFSGH
380 390 400 410 420
14537812 TQPVNGVRVDFHFKVETHPIASDNFYVYGVAGIGYIGLODSENELPEATQPNYESYSH
420 430 440 450 460 470 480
cryla-105.pe RLSHVSMFRGFSNSSVSIIRAPMFSWTHRSADFNNIIASDSITQIPLVKAHTLQSGTVV
430 440 450 460 470 480
14537812 RLSHIGLI-----SASHVKALVYSWTHRSADRTNTEFPNSITQIPLVKAFLNLSGAAV
480 490 500 510 520
cryla-105.pe VRGPGFTGGDLRLRTWIGTIGDIRVINPFPQRYRIRYASTIDLOFHTSINGKAIQ
500 510 520 530 540 550 560 570 580
14537812 VRGPGFTGGDLRLRTWIGTIGDIRVINPFPQRYRIRYASTIDLOFHTSINGKAIQ
530 540 550 560 570 580
cryla-105.pe QGFNKTMDTGPITFQSFYATINTAFTFPMQSSFTVAGDTFSSGNEVYIDRFELIPVT
550 560 570 580 590 600
14537812 GNFSATWRGEDLDYKTFRTVGTFTFPSFLDVOSTFTIGAMWFFSSGNEVYIDRFELIPVE
590 600 610 620 630 640
cryla-105.pe ATLEAEYNLRQAKVNAALFTSTNQLGKINVTYDHYDQVSNLVTYLSDEFCLDEKRELS
610 620 630 640 650 660
14537812 VTYEAYDFEKAQKVYALFTSTNPRGLKTDVQKDYDQVSNLVSLSDEFCLDEKRELF
650 660 670 680 690 700
cryla-105.pe EKVYKAKLSERNLLQDSNFKDKINQPERGCGSGTITIQGDDVFXENVYTLISGTFDE
670 680 690 700 710
14537812 EIVKYANELHIERNM
710


```
3329593      YSTGLNLRGTAESWVRYNQPRDMTLMVLDLVALFPSTYDQMYPIKTTAQTREVTYD
                240   250   260   270   280   290
cryla-105.pe  PV-----LEFDSG--FRSGA---QGIEGSI-RSPHMLDILMSITIIYDAERGEYWSGH
                :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
3329593      AITGVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSR----WSNT
                300   310   320   330   340   350
cryla-105.pe  QIMASPVGFSGPEFTPLVGTMGNAAPQORIVLAQLGGVVRTLSLTYRRPFNIGIN--
                320   330   340   350   360   370
3329593      QIMNM---WGHKLEPRTIGTLINISIQSGTNSINPVTLPFTSRDVTETESLAGNLFL
                360   370   380   390   400   410
cryla-105.pe  NOQLSVLDGTEFAYG-----TSSNLPSAVYRKSGTV--DSLDEIPQNNVPPRQGFSH
                380   390   400   410   420
3329593      TQPVNGVPRVDFHMKVTHPIASDNFYYPGVAGIGTQLQDSENELPPEATQOPNYESYSH
                420   430   440   450   460   470
cryla-105.pe  RLSHVSMFRSGFNSSVSIIRAPMFSWIHRSABENNIASDSITQIPLVKAHTLQSGTIV
                430   440   450   460   470   480
3329593      RLSHIGLI-----SASHVKALVSVWTHRSADRTNTEFNSITQIPLVKAFNLSSGAIV
                480   490   500   510   520
cryla-105.pe  VRGPGFTGDIILRTSGGPFATVININGOLPQRYRARIYASTTNLIYIVVAGERIFA
                490   500   510   520   530   540
3329593      VRGPGFTGDIILRTSGGPFATVININGOLPQRYRARIYASTTNLIYIVVAGERIFA
                530   540   550   560   570   580
cryla-105.pe  GQFNKIMTDGDLTFFOSFYATINTAFTFPMSSQSFVAGADTFSSGNEVYIDREFELIPVT
                550   560   570   580   590   600
3329593      GNFSATMRGDDLDYKTFRTVGTFTPFSLDVQSTFTIGAMWFFSSGNEVYIDREFVPE
                590   600   610   620   630   640
cryla-105.pe  ATLEAEYNLEAQAVALFTSTNQLGKTNVTDYHIDQVSNLYTVLSDERFCLDEKRELS
                610   620   630   640   650   660
3329593      VTYEAYDFEKAQEKVTAFTSTNPRGLKTDVXDYHIDQVSNLVSLSDEFLDEKRELF
                650   660   670   680   690   700
cryla-105.pe  EVKVKAKLSLDERNLQDSNFKDINRQPERGWSGTGTTIQGGDDVFKENYVTLSTGTFDE
                670   680   690   700   710
3329593      EIVKYAKQLHIERNM
                710
cryla-105.pep
NRAA:3329593
33260894 source="GENBANK_PROT" delta-endotoxin [Bacillus thuringiensis serovar
kurstaki]

SCORES      Initl: 889      Initn: 1596      Opt: 1705      z-score: 1933.6      E(): 2.1e-99
>>NRAA:33260894
Initn: 1596      Initl: 889      Opt: 1705      z-score: 1933.6      expect(): 2.1e-99
Smith-Waterman score: 1721;      42.6% identity in 705 aa overlap
(4-683:36-719)

cryla-105.pe  MDNPNINEICLPYNCLSNPEVEVLGGERIETGY
                10   20   30
3329593      QDKHQSFSNNAKVDKISTDSLNKNETDIELQINHEDCLKMSYENVEFPV--SASTIQTG-
                10   20   30   40   50   60
cryla-105.pe  TPIDISLSLTQFLSEFPVPGAGFVLGLVDIIGWIFGP---SOWDAFLVQISLINQRIEE
                40   50   60   70   80   90
3329593      --IGIA---GKILGTLGVFPAGQVASYLSFILGELMPKGNOWEIFMHEVZEILNQIST
                70   80   90   100   110
cryla-105.pe  FARNQAIISRLGSLNLYQIYAESFREWEADPTNPALREENRIQFNDMSALTTPILPFAV
                110   120   130   140   150
3329593      YARNKALTDLKGLDALAVYHDSLESVWGNRNTRARSVVKSYQYTALEIMFVQKLPSFAV
                120   130   140   150   160   170
cryla-105.pe  QNYQVPLSVTVQAAHLHLSVLVDVSGQWGFDAATINSRVDNLTGLNYTDHVRW
                160   170   180   190   200   210
3329593      SGEVFLPLPIYQAANUHLLLRLDASIFGKEWGLSSSEISITFFNROVERAGSDHCVKW
                180   190   200   210   220   230
cryla-105.pe  YNTGLERVWGPDSRDWIRYNQFRRELTITVLIDVSLFPNYSRTYPIRTVSQLTREIYN
                220   230   240   250   260   270
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3329593      YSTGLNLRGTAESWVRYNQPRDMTLMVLDLVALFPSTYDQMYPIKTTAQTREVTYD
                240   250   260   270   280   290
cryla-105.pe  PV-----LEFDSG--FRSGA---QGIEGSI-RSPHMLDILMSITIIYDAERGEYWSGH
                :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
3329593      AITGVHPHPSFTSTTWNNAAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSR----WSNT
                300   310   320   330   340   350
cryla-105.pe  QIMASPVGFSGPEFTPLVGTMGNAAPQORIVLAQLGGVVRTLSLTYRRPFNIGIN--
                320   330   340   350   360   370
3329593      QIMNM---WGHKLEPRTIGTLINISIQSGTNSINPVTLPFTSRDVTETESLAGNLFL
                360   370   380   390   400   410
cryla-105.pe  NOQLSVLDGTEFAYG-----TSSNLPSAVYRKSGTV--DSLDEIPQNNVPPRQGFSH
                380   390   400   410   420
3329593      TQPVNGVPRVDFHMKVTHPIASDNFYYPGVAGIGTQLQDSENELPPEATQOPNYESYSH
                420   430   440   450   460   470
cryla-105.pe  RLSHVSMFRSGFNSSVSIIRAPMFSWIHRSABENNIASDSITQIPLVKAHTLQSGTIV
                430   440   450   460   470   480
3329593      RLSHIGLI-----SASHVKALVSVWTHRSADRTNTEFNSITQIPLVKAFNLSSGAIV
                480   490   500   510   520
cryla-105.pe  VRGPGFTGDIILRTSGGPFATVININGOLPQRYRARIYASTTNLIYIVVAGERIFA
                490   500   510   520   530   540
3329593      VRGPGFTGDIILRTSGGPFATVININGOLPQRYRARIYASTTNLIYIVVAGERIFA
                530   540   550   560   570   580
cryla-105.pe  GQFNKIMTDGDLTFFOSFYATINTAFTFPMSSQSFVAGADTFSSGNEVYIDREFELIPVT
                550   560   570   580   590   600
3329593      GNFSATMRGDDLDYKTFRTVGTFTPFSLDVQSTFTIGAMWFFSSGNEVYIDREFVPE
                590   600   610   620   630   640
cryla-105.pe  ATLEAEYNLEAQAVALFTSTNQLGKTNVTDYHIDQVSNLYTVLSDERFCLDEKRELS
                610   620   630   640   650   660
3329593      VTYEAYDFEKAQEKVTAFTSTNPRGLKTDVXDYHIDQVSNLVSLSDEFLDEKRELF
                650   660   670   680   690   700
cryla-105.pe  EVKVKAKLSLDERNLQDSNFKDINRQPERGWSGTGTTIQGGDDVFKENYVTLSTGTFDE
                670   680   690   700   710
3329593      EIVKYAKQLHIERNM
                710
cryla-105.pep
NRAA:33260894
33260894 source="GENBANK_PROT" delta-endotoxin [Bacillus thuringiensis serovar
kurstaki]

SCORES      Initl: 889      Initn: 1596      Opt: 1705      z-score: 1933.6      E(): 2.1e-99
>>NRAA:33260894
Initn: 1596      Initl: 889      Opt: 1705      z-score: 1933.6      expect(): 2.1e-99
Smith-Waterman score: 1721;      42.6% identity in 705 aa overlap
(4-683:36-719)
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cryla-105.pe MDNPNINECPYNCNLSNPEVEVLGGRIETGY
32260894 ODKHS--SWAKVDKSTDS--KNETDIELQININHECLKMSYEVNEPPTV--SASTIQTG--
cryla-105.pe TPIDSLSTQFLSFGAGFVLSGNDKNGIFGP---SNDALVELIOLINORIEE
32260894 --IGIA--SKITLTVAGAGOSLVSFIDELNPRGNQWEIIFMEHVEEIIQNKIST
cryla-105.pe FARNQAIISLEGLSNLYQITNAESREWEALPTNPALEEMRIQFNNSGALTAIPFAV
32260894 YARNKALTDLGLGDAVAVHDSLEWNNNNNTAKRSKSOVIALDLNMYOKLPSFAV
cryla-105.pe QNYQVPLSVVQVAAHLVLSVLRDVSFGQWRGFPNATNSRINDLTRIGNYTHAKRW
32260894 SGEVPLPIYAQAANLHLLLRDASIFGKEWGLSSLSISFNRQVRAQYDHPQKW
cryla-105.pe YNTGLERVAGPSDRMRYNQFRRELTATVILVSLPNDYDSRTYPIRTYVLSOLREIYN
32260894 YSTGLNLRGNTAESWVRNQFRDMVILVLOLVALPFSYDTQYPIKTAQLIRSVYD
cryla-105.pe PV-----LENFPGS---FRGSA---QIEGSI--RSPHMDILNISTYIYDAHREYVWSGH
32260894 AIGTVHPHPSFTSTTWNYNAPSFSAIEAAVVRNPHLDLFEQVITYLSLSR-----WSNT
cryla-105.pe QIVASPVGSGPEFTFPYMGNAAPQRIYVAGQGVYRTLSSTLYRPNNGIN---
32260894 QYMN---WGGHKLFEFTIGTGLNISTGNTSINPVTLPTSDRYTESLAGNLFL
cryla-105.pe NQQLSVLDGTEFAYG-----TSSNLPASVYRKSGTV--DSLDEIPPONNVPPRQGFESH
32260894 TOPVNGVPRVDHFWKFTVHPIASDNFYPCYAGIGTQLODSENELPPEATGQPNYESYSH
cryla-105.pe RLSHVSMFSGFSNSVSIIRAPMFSWIHRSAEFNIIASDITQIPLVKAHFLQSGTIV
32260894 RLSHIGLI-----SASHVRLVYSWTHRSADRNTIEPNSITQIPLVKAFLNLSGAAV
cryla-105.pe VRGPGFTGGDILRRSTGGPFAYTVINWGOLPORVRRIRYASTTNLRIVYTVAGERIFA
32260894 VRGPGFTGGDILRRNTGTGFDIRWNPFPQRYRVRIRYASTITQPHISINGKAIQ
cryla-105.pe GQFNKTMWDGDLTTFQSFYSYATINTAFTFPMSQSSFTYAGADTFSSGNEVIDRIFELIPVT
32260894 GNFSAWNRGEDLDYKTFRTVGFTTFPSFLDVQSTFTLIGANNFSGNEVIDRIFEPVPE

cryla-105.pe ATLEAEVNLERAQAVNALFTSTNQLGKTNVTDYHIDQVSNLVTYLSDFECLDEKRELS
32260894 VTYEAYDFEKAQEKVLTALFTSTNPRGLTKVDYHIDQVSNLVSLSDFEFLDEKRELF
cryla-105.pe EKVKHAKLSDERNLLQDSNFKDINQPERGWSGSGTIGTIQGGDDVFKENYVTLSGTFDE
32260894 EIVKYANELHIERNM
cryla-105.pep
NRAA:48880
48880 source="GENBANK_PROT" crystal protein [Bacillus thuringiensis]
SCORES Init1: 457 Initn: 1720 Opt: 1706 Z-score: 1931.6 E(): 2.7e-99
>>NRAA:48880
Initn: 1720 Init1: 457 Opt: 1706 Z-score: 1931.6 expect(): 2.7e-99
Smith-Waterman score: 1991; 34.0% identity in 1222 aa overlap
(1-1172:26-1151)
cryla-105.pe MDNPN-----NINECIPYNCNLSNPEVEVLGGRIE
48880 MNQNHGIIIGASNCGCCASDDVAKYPLANNPYSSALNLSNCSQNSILN--WINIIGDAAKE
cryla-105.pe TGTPDPSLSLTQFLSEFVPG-AGFVGLVVD-IIMGIFGQWDALFVQIEQLINORI
48880 A-----VSGTIVSLIITAPSITGLISIVYDLIGKVLGSSGQSISLSDICDLISIDLRV
cryla-105.pe TEFARNAQISRLEGISNLYQITNAESREWEALPTNPALEEMRIQFNNSGALTAIPFAV
48880 SSVLNDGDIADFNRYRNYDPAESWKNKP-NSASAEELRFRFIADSEFDRLITRG
cryla-105.pe --TAIPLFAVQVQVLSVAVAAASHLSVLSUSFGQWRG-FDAATINSRYNDLTR
48880 SLTNGSLARQNAOILNAPSASAPFCDLQDTRTGTNGLYNATPEINYSQSLVEL
cryla-105.pe IGNTDHAWRVNTGLE--RVWGPDSRWNTQPFRTDVLVDIVSFPNDSRTYPI
48880 IELYDYCVHRYNRGFEELRQRTSATAMLEPRYRSEMTLMVLDITATYSSSITINPPI
cryla-105.pe RTVSQLTREIYNPVLNENFNGSFRGSA-----OGIEGSRSHLMKAVYVYV
48880 ETDQLSRVIYDPTGTFVHRSLSRGESWFSFVNANFSDLENALPNPNSWNLNNA
cryla-105.pe DA-----HRGEYVWSGHQIMASVFGSGPEFTFPYLYGTMGNAAPQRIYVAGQGV
48880 GSLTLPVSPSTDRARV-WYGRDRISP---ANSQFTTELISQHTTATQ---TILGRNI

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cry1a-105.pe 360 370 380 390 400 410
YATLSSTLYRPPENIGNNQSLVLDGTFAYGTSSNLPASVVRKSGT---VDSLDE-I
48880 410 420 430 440 450 460
PVDQACNLNDITYGVN-RAVYHDAE---GQSRVVEGYIRITGIDNPRVQNTYL
420 430 440 450 460

cry1a-105.pe 420 430 440 450 460
PPQNNVPPFGQSHSLVSMFRSGF---SSNSVSIIRAPMFSMIRSHAFNIIASD
48880 470 480 490 500 510
PGENSDIPTEDYTHILSTTINLTGLQVANSRRSLV---MYGWTSHKLARNNTINPD
470 480 490 500 510

cry1a-105.pe 470 480 490 500 510 520
SITQIPLVKHTLOSQTIVVRGPGTGGDILRTSGGPFAYTIVNINQLPQRVARIY
48880 520 530 540 550 560 570
RITQIPLVKHTLOSQTIVVRGPGTGGDILRTSGGPFAYTIVNINQLPQRVARIY
520 530 540 550 560 570

cry1a-105.pe 530 540 550 560 570 580
ASTTNLRIVTVAGERIFAGQFNKMTDGLTFQSFYATINTAFIPMSQSSFTVGAD
48880 580 590 600 610 620 630
ASTTNLRIVTVAGERIFAGQFNKMTDGLTFQSFYATINTAFIPMSQSSFTVGAD
580 590 600 610 620 630

cry1a-105.pe 590 600 610 620 630 640
TFSSNGEYIDRFELIPVTAILEAEYNLERAKAVNALFTSTNQLGKTNVTDYHIDQVS
48880 640 650 660 670 680 690
PSFIRQEVYVDRIEFIPNPTREAKEDLEAAKAVASLFTTRTD-GLQVNVKDYQVDAQA
640 650 660 670 680 690

cry1a-105.pe 650 660 670 680 690 700
NAVTVLSPDFCLDEKRELSEKVKHAKELSDERNLLQDSNFKDINRPERGCGSGTITIQ
48880 700 710 720 730 740 750
NLVSLDSDEQYQDKWMLLEAVRAAKRLSRERNLLQDPDNTINSTEENGKASGVNIIIS
700 710 720 730 740 750

cry1a-105.pe 710 720 730 740 750 760
GGDDVFKENYVTLSTGTCYPTLYQKIDESKLKATRYQLRGYIESQDLIYSIRYN
48880 760 770 780 790 800 810
EGGPFYKGRATQLASA-RENYPTIYQKVDASLKPVTYRVLGDFVKSSQDLIDLIIHH
760 770 780 790 800 810

cry1a-105.pe 770 780 790 800 810 820
AKHETVNPVT--GSLWPLSAQSPICKGCEFNRCAPHLEW--NPDLDSCRDGKCAHHS
48880 820 830 840 850 860 870
KVLKVNVPDLVSDTYFDSCSGINRCQEQMNAQLETEHHPMDC-CE-----AAQT
820 830 840 850 860 870

cry1a-105.pe 830 840 850 860 870 880
HFFSLDIDVGCTDNLNEDLGVWVIFKIKTDGHDHGLNLEFLEKPLVGLAARVKAEEK
48880 880 890 900 910 920 930
HFFSSYIDTGLNSVDQGIWAFKVRTTDCGYATLGNLELVEVGPLSGESLEQRDNTK
880 890 900 910 920 930

cry1a-105.pe 890 900 910 920 930 940
WRDKREKLEWETNIVYKEAKESVDALFVNSQYDQQLQADTNIAHAAKRVHSIREAYLP
48880 940 950 960 970 980 990
WSAELGRKRAETDRVYQDAKQSLNHLFVDYDQQLNPEIGMADIMDAQNLVASISDVYSD
940 950 960 970 980 990

cry1a-105.pe 950 960 970 980 990 1000
EUSVIPGVNAIIFEELEGRIPTAFSLYDARNVKNQFNGLSCWKNVGHVDEVEQNNQR
48880 1000 1010 1020 1030 1040 1050
AVLQIPGINYEITYELSNRLQQAQSLYLTSRNAVQNGDFNGLDLSMNATAGASVQDQGNTH
990 1000 1010 1020 1030 1040 1050
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cry1a-105.pe 1010 1020 1030 1040 1050 1060
SVLVVPEAEVSEVRVCPGRGYILRVTAKEGYGEGCVTTHIEINNTDELKFSNVVEE
48880 1050 1060 1070 1080 1090 1100
FLVLSHDAQVSOQFVQPCNKYILRVTAKEGYGEGCVTTHIEINNTDELKFSNVVEE
1050 1060 1070 1080 1090 1100

cry1a-105.pe 1070 1080 1090 1100 1110 1120
EYIPNNVTNCDYTVNQEEYGGAYTSRRNGYNEAPSVADYASVVEEKSYTDGRNPECE
48880 1110 1120 1130 1140 1150 1160
DYDIN---GTYYTDNT-----
1110 1120 1130 1140 1150 1160

cry1a-105.pe 1130 1140 1150 1160 1170 1180
FNRGARDYPLPGVYTKELFPPETDKVWIEIGETEGTFFIVDSVELLLMEE
48880 1170 1180 1190 1200 1210 1220
YLTKEVVFHPETQHMWVVEVNETEGAFHDSIEF
1170 1180 1190 1200 1210 1220

cry1a-105.pe
SW:8469164
8469164 description="PESTICIDIAL CRYSTAL PROTEIN CRY9AA PRECURSOR (INSECTICIDIAL
DELTA-ENDOTOXIN CRYIXA(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (130 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar Galleriae"
sources="swissprot_prot" version="NA type="PRT

SCORES Init1: 457 Initn: 1750 Opt: 1706 z-score: 1931.6 E(): 2.7e-99
>>SW:8469164
initn: 1750 init: 457 opt: 1706 z-score: 1931.6 expect(): 2.7e-99
Smith-Waterman score: 1995; 33.9% identity in 1227 aa overlap
(1-1177:26-1156)

cry1a-105.pe MDNNP-----NINECIPYCNLSNEVEVLGGERIE 10 20 30
8469164 MNKHGIGASNGCGASDDVAKYPLANNPYSSALNLSNCSNLSN--WINIIGDAAKE 10 20 30 40 50
cry1a-105.pe TGYTPIDISLITQFLSEFVPG-AGFVLGLVD-IIWGIFGSPQWDAFLVQIEOLINORI 40 50 60 70 80
8469164 A-----VSIQTTIVSLITAPSLTGLISIVVDLIGKVLGSSGQSISDLSCDLSLIDLRV 60 70 80 90 100 110
cry1a-105.pe 90 100 110 120 130 140
EEFARNQAISRLGSLNLYQIYAESFREWADPTNPALREEMRIQF---NDMNSALT--
8469164 SQSLNDGLADFGNSGVLLYRNLYLEALDSNNKNP-NSASAEELRTRFIADSEFDRLTRG 120 130 140 150 160 170
cry1a-105.pe 150 160 170 180 190
--TAPLFAVQNYQVPLLSVYQAAHLVLRVDSVFGQWNG-FDAATINRYNDLTRL
8469164 SLTNGSLARQNAQILLPSFASAFPHLLLRDATRYGTNGLYNATPFINYSKLVEL 180 190 200 210 220 230
cry1a-105.pe 200 210 220 230 240 250
IGNYTDHARVWYNTGLE--RWGPDSDRWIRYNOFRRELTLTLDIVSLFPNYSRTYPI
8469164 IEIYDVCVHWYNGFNLQRTQSATWLEFHYRREMLMVLVDIVASFSSLDITNYPY 240 250 260 270 280 290
cry1a-105.pe 260 270 280 290 300
RTVSQUTREIYTNVLENFDGSPFGSA-----QGIEGSIKSPHLMILNLSITTYT 260 270 280 290 300
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8469164 ETDFOLSPNYTDPGFGFCHSSLRGSWFNFVRANFSDLENAIPNPRSPWFLNMIIST
300 310 320 330 340 350
cry1a-105.pe DA-----HREYVSGHQMAGPVSFCPETFFLGTGMNAPQRIVAOLGQGV
360 370 380 390 400 410
8469164 GSUTLPVSGSTPRARVWASRISP--ANSSITELISGQHTTATO---TILGRNI
360 370 380 390 400 410
cry1a-105.pe YRLSTLVRFPFNGINNOCLSVLDGCEAVATGSSNPSAVYAKSG---TVDSLDE-I
360 370 380 390 400 410
8469164 FRVDSACNLNDITTYGVN-RAVNHASE--SGRSGYGYIRNGINPRVQINITYL
410 420 430 440 450 460
cry1a-105.pe PPQNNVPPROGFSHRLSHVSMFRSGF---SNCSVSLIRAPKSWHRSASFNNIASD
420 430 440 450 460 470
8469164 PGNSDIPPTDYTHLSTTINLTGILRQVASNRRSSN--WYGTWTHSARNTINPD
470 480 490 500 510 520
cry1a-105.pe SITQILVKAHTLSSGTVVRGCGFGGDIARTSGSPFATVINGSLRQVYRARI
470 480 490 500 510 520
8469164 RITQILTVKVDTRGVGVNDPGFVGALLQRIQDHGSLVLRVQFFLHRQVIRIRY
520 530 540 550 560 570
cry1a-105.pe ASITNLRIVTVVAGERIPAGOFNKMTDGLPTFQSFYATINTAFTFPMSSSTVGAD
530 540 550 560 570 580
8469164 ASITNLRVNGVSFGTL--SONLPSTNRLGDLRYGSFAIREFNISIRPTASPDQIRLTIE
580 590 600 610 620 630
cry1a-105.pe TFSGNEVYIDFELIPVTAILEAYNLEAKVNAALFTSTNGLKTNVTDYHIDQVS
590 600 610 620 630 640
8469164 PSFIRQEVYVDRIEFIPVNPTRAEKDLAAKAVASLFTTRD--GLQNVKXDQYVDQAA
640 650 660 670 680 690
cry1a-105.pe NLVTYLSDFCLDEKRELSEKVKHAKLSDERNLLODGNFKDINRQPERGMWGSGTGITIQ
650 660 670 680 690 700
8469164 NLVSCLSDEQYGYDKMLLEAVRAAKLSRENLLODQPDFTNTNSTEENGWASNGVTIS
700 710 720 730 740 750
cry1a-105.pe GGDDVFKNYVTLSTGTFDECYPTLYQKIDESKLAFTYRLQRYIEDSQDLKYSIRYN
710 720 730 740 750 760
8469164 EGGPFYKRAIQLASA--RENYPTVIYOKVDASELPYTRYRLDGFVKSSQDLIDLIHHH
760 770 780 790 800 810
cry1a-105.pe AKHTTNVPGT--GSLWPLSAQSPDGKCEPNRCAHLEW--NPDLCSCDEQEKHHHS
770 780 790 800 810 820
8469164 KVHLVRNPNLVSDTYPDDSCGINRCQQQMVNNAQUETEHHHPMDC--CE-----AAQT
820 830 840 850 860 870
cry1a-105.pe HFFSLDIDVGCGLDNLDELGVWVIFKTIQDCHARLGNLEFLEKPLVGEALAAVKAEEK
830 840 850 860 870 880
8469164 HEFFSYIDTGLNNSVDQGIWAIKPVRTTIDGYATLGNLELVENGLSGESLREQDNTK
870 880 890 900 910 920
cry1a-105.pe WRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADNTIAMTHAADKRVHSIREAYLP
890 900 910 920 930 940

8469164 WSAELGRKAETDRVYQDAKQSNHILFVDYQDQQLNLMADIMDAQNLAASISDVYSD
930 940 950 960 970 980 990
cry1a-105.pe ELSVIPGVNAATFEELSGRIFTAFSLYDARNVKNNGFNGLSCNVNKGHVDEBONNOR
950 960 970 980 990 1000
8469164 AVLQIFGNVIELSNRLQQASLYLTSRNAVQNGFNNGLDSWATAGASVQODGNTH
990 1000 1010 1020 1030 1040
cry1a-105.pe SLVLPVPEAEVSQVRVRCGRGYILRVYAKGYGCGCVTHIEENNTDELKFSNVCEE
1010 1020 1030 1040 1050 1060
8469164 -FLVLSHMDAQVSQQFRVQNCXYVLRVTAEXVGGDGYVTRDDAHTETILTFNAC---
1050 1060 1070 1080 1090 1100
cry1a-105.pe EIYFNNVTTCNDITVNGEEYGGATSRNGYNEAPSDVADYASVYEKSYTGRRENPCF
1070 1080 1090 1100 1110 1120
8469164 -----DYDIN-----GTVYTDNT-----
1110
cry1a-105.pe FNRGYRDTPLPVGVTVTKLEYPEETDKVMIEIGETGCTFIVDSVELLMEE
1130 1140 1150 1160 1170
8469164 -----YLTXEVVFPETQHWVVEVNETEGAFHDSIEFVETEX
1120 1130 1140 1150
cry1a-105.pe "GENBANK PROT" delta-endotoxin CryIG protoxin [Bacillus
40271] gi|18469164|sp|Q99031|CR9AA BACTG Pesticidal crystal protein
this gene is a precursor (insecticidal delta-endotoxin CryIXA(a)) (Crystalline
entotoxin) (130 kDa crystal protein) gi|228273|prf|1802272a delta
endotoxin
SCORES Initl: 457 Initn: 1700 Opt: 1706 z-score: 1931.6 E(): 2.7e-99
>NR001:40271
initn: 1750 initl: 157 opt: 1706 z-score: 1931.6 expect(): 2.7e-99
Smith-Waterman score: 9957
(1-1177:26-1156)
cry1a-105.pe MDNNECVRNLSNPEVEVLGGERIE
40271 MNQKHGIIAGSNCCGASDDVAKYFANNSSYSANLSSONSSIN--MINIIGDAAKE
10 20 30 40 50
cry1a-105.pe TGYTPIDISLSTOFLSEFPVG-AGFVLGLVD--LWNGRFGPSQWDAVLVMEOLNORI
40 50 60 70 80
40271 A---VSGITTVISLITAPSLTGLISIVYDLGLKVGSSSSQSLSLICLLSLNDLRY
60 70 80 90 100
cry1a-105.pe EEFARNOAISRLGLESLNLYQIYAESFREMEADPTNPALEMRIOF---NNNSALY---
90 100 110 120 130 140
40271 SOSVINDGIADFNFGSVLLYRNKLEALDSMNKNP-NSASAEELRFRFRIADSEFDRNLTFS
120 130 140 150 160 170
cry1a-105.pe --TAIPLFVQNVQVPLSVVTVQAAHLHLSVLVDVSVFGQWGF--FDAATINSRYNDLTFL
150 160 170 180 190

40271 SLTNGSIAQRQAIIILLPSFASAFHLLLRDARTYGTNMGVLYNATPFYINQSKLVEL
180 190 200 210 220 230
cryla-105.pe IGNYTDHAWYNTGLE--RWGPDSDRWYNOQFRELTLVLVDIVLSFNDSTRTYPI
200 210 220 230 240 250
40271 IELXTDYCVHWYNRGNEQLRQGTSAWLEFHYRENTLMVLVDIVASFSSLDITNYPI
240 250 260 270 280 290
cryla-105.pe RTVSLTRELYTPVLENFDGSGFSA-----QIEGSIKPSHLMIDILNSITVT
260 270 280 290 300
40271 EIDFQLGRVIYIDPFGVHRSLSRGSFVWRANFSOLENAIPNRPSPFLNMIIST
300 310 320 330 340 350
cryla-105.pe DA-----HRGEYWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAQLQGQV
310 320 330 340 350
40271 GSLTVPSPSTDRARY-WYGSRRDISP---ANSQFTELISGHTTAQ---TILGRNI
360 370 380 390 400
cryla-105.pe YKTSSTLYRRPFGINNOQLSVLDGTEFAIGTSSNLPSAVYRKS-----TVDSLDE-I
360 370 380 390 400 410
40271 FRVDSQACNLNDITYGN-RAVFYHDAEE--GSQSRVSGEYRTTGDINDPRVQNTIYL
410 420 430 440 450 460
cryla-105.pe PPONNVPPRQGSFHLSSHVSMFRSGF---SNSVSIIRAPMFWIHRSEFNIIASD
420 430 440 450 460
40271 PGNSDIPTEDYTHILSTTINLTGIRQVANSRSLV---MYGWHKSLARNINP
470 480 490 500 510
cryla-105.pe SITQIPLVKAKTLOSQTIVVRGFTGGDILRTSGPFAITVINGQLPQRYARIY
470 480 490 500 510 520
40271 RTQIPLTKYVDTRGTGVSYNDPGFPGALLQRTDHSGLGVLRVQFPLHLRQQYRIVRY
520 530 540 550 560 570
cryla-105.pe ASTTNRLIYTVAGERIFAGQFNKMTDGDPLTFQSFYSATINTAFTPMQSSSFTVGAD
530 540 550 560 570 580
40271 ASTNIRLSVNGSGFTI--SQNLPSMTLGEDLRYGSPAIREFNTSIRPTASPDQIRLTIE
580 590 600 610 620 630
cryla-105.pe TFGSSGVEYIDRFELIPVATLEAEYNLERAKAVNALFTSTNQLGLNTVTDYHIDQVS
590 600 610 620 630 640
40271 PSFIRQEVYVDRIEFIPVNPRTPEAKEDLEAKKAVASLFTTRD-GLQVNVKDYQVDDAA
640 650 660 670 680 690
cryla-105.pe NLVTYLSDFCLBCKELSEKVKHAKRLSDERNLQSNPKDINQPERGWSGTITIQ
650 660 670 680 690 700
40271 NLVSCLSDEQGYDKKMLLEAVRAAKRLSERNLQDPDFNTINSTENGWKSNGVTIS
700 710 720 730 740 750
cryla-105.pe GDDVFKENYVTLSGTFDECYTYLYOKIDESKLAKFYQLRGVIEDSOLEIYSRYN
710 720 730 740 750 760
40271 EGGPYKRAIQLASA-RENYPTIYQKVDASELKPYTRLDGPFVKSSQLELDLHHH
760 770 780 790 800 810
cryla-105.pe AKHETVNVPGT--GSLWPLSAQSPGKCGEPNRCAPHLEW--NPDLDCSRRDGEKCAHHS
770 780 790 800 810 820

40271 KVHLKXNVPDLVSDTYPDSDSGINRCQSQMVNAQLETEHHPMD-CE-----AAQT
820 830 840 850 860
cryla-105.pe HFFSLDIDVGCCTDLNEDLGVVWIFPKITQDGHARLGNLEFLEEKPLGEALARKVRAEKK
830 840 850 860 870 880
40271 HEFSSYIDTDGLNSSVDQGIWAFKVRTDGTATLGNLELVEVGPLSGESLEQRDNTK
870 880 890 900 910 920
cryla-105.pe WEDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHADKRVHSIREAYLP
890 900 910 920 930 940
40271 WSAELGRKRAEIDRVTDKAKSINHLPFVDYDQQLNPEIGMADINDAONLVASISDYSD
930 940 950 960 970 980
cryla-105.pe ELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVKNKNGDFNNGLSCWNVKGVHVDVEEQNNQR
950 960 970 980 990 1000
40271 AVLQIPGINTVEIVTLESNRLOQASVLYTSRNAVQNGDFNNGLSWNAAGASVQDQGNTH
990 1000 1010 1020 1030 1040
cryla-105.pe SVLVVPEWEAEVGEVVRVCPGRGYILRVYAKSGYEGCVTHIENNTDELAFSNCVEE
1010 1020 1030 1040 1050 1060
40271 -FLVLSHMDAQVSOQFRVQPNCKYVLRVTAEKVGGDGYVTRDDAHTTETLTFNAC---
1050 1060 1070 1080 1090 1100
cryla-105.pe EIYPNNVTVCNDTVMOEYGGAYTSNRNGVNEAPSVPADYASVVEEKSYTDGRRENPC
1070 1080 1090 1100 1110 1120
40271 -----DYDIN-----GYVTDT-----
1110
cryla-105.pe FNRGYRDYPLPGVYTKLEYFPETDKWIEIGETGTFIVDSVELLMEE
1130 1140 1150 1160 1170
40271 -----YLTKEVVFHPETQHMVVEVNETEGAFHIDSIEFVETEK
1120 1130 1140 1150
cryla-105.pep
NRAA:40290
40290 source="GENBANK_PROT" delta-endotoxin [Bacillus thuringiensis]
SCORES Init1: 896 Initn: 1592 Opt: 1701 z-score: 1929.0 E(): 3.7e-99
>>NRAA:40290
Initn: 1592 Init1: 896 Opt: 1701 z-score: 1929.0 expect(): 3.7e-99
Smith-Waterman score: 1717; 42.6% identity in 705 aa overlap
(4-683:56-719)
cryla-105.pe MDNNPNINECIPNCLSNPEVEVLGSGRIETGY
10 20 30 40 50 60 70 80 90
40290 QDKHQSFSSNAKVKIDSTSLDKNETDIELQNHEDCLAKMSEVENVEPVFV-SASTIQTG-
10 20 30 40 50 60 70 80 90 100 110
cryla-105.pe TPDIDISLTOFLLSFVPGAGFVLGVDIITWIGFPG---SQWDAFLVQIELINORIEE
40 50 60 70 80 90 100 110
40290 --IGIA---GKILGTGLVPGAGVASLYSFLIGELWPKGNONEIFMEHVEEIIINQKIST
70 80 90 100 110
cryla-105.pe FARNQAIISRLSGLSNLYQIVAESFREWEDPTNPALEENRQFNDMNSALTTPAIFAV
100 110 120 130 140 150

40290 VARNKALPDKGLGDAVWHDLSWGNRRNTRARSVOYIALELMPVKLPFSFV
120 130 140 150 160 170
cryla-105.pe QNVPLSVIVICADHLSVLRDVPORWGFDAATINSRYNDLITGLIGNYTHAVRW
160 170 180 190 200 210
40290 SGEVPLPSTYVORAKLLELLDASIFGNSGSSSEISTFYNQVERAGERSYHCVM
180 190 200 210 220 230
cryla-105.pe YNTGLERVWGPDSRWIRNORRELTATLIDVSLFPNPGRRNPPIRTVSOLTRITYN
220 230 240 250 260 270
40290 YSTGLNLRGTNAESWVRNQPRDMLWILDEPESVDIOMYHKLTAOLTREYVID
240 250 260 270 280 290
cryla-105.pe PV-----LENFDGS--FRGSA--QGIEGSI-RSPHMDLNTIYTDHARGVWNSH
280 290 300 310 320 330
40290 AIGTVHPHPTSTTWYNNNAPSFAIEAAWRNPHLDFLQVITVSLAR---WSNT
300 310 320 330 340 350
cryla-105.pe QMASPVCFSGPEFTPLVGTWGNAPQORIVAOLGQVRYLTSLTRPRNIGIN--
320 330 340 350 360 370
40290 QYMMN---WGHKLEFTTIGTTLNISTOGSTNTSINPVLPFTSRDVRTESLGLNPL
360 370 380 390 400 410
cryla-105.pe NOOLSVLDGTEFAYG-----TSSNLPSAVYRKSGTV--DSLDEIPQNNVPPROGFSH
380 390 400 410 420 430
40290 TOPVNGPRVDHMKVTHPIASDNFYYPGVAGIGTQLODSENELPPEATQPNVYESYSH
420 430 440 450 460 470
cryla-105.pe RLSHVSMRSGFNSVSIIRAPMFESWIHRSAEFNIIASDSITQIPLVKAHTLQSGTTV
430 440 450 460 470 480
40290 RLSHIGLI-----SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGGAUV
480 490 500 510 520 530
cryla-105.pe VGRPGFTGCDILARTSGGPAYTIVININGQLPORVRIARYASTTNLRIYTVAGERIPA
500 510 520 530 540 550
40290 VGRPGFTGCDILARTSGGPAYTIVININGQLPORVRIARYASTTNLRIYTVAGERIPA
530 540 550 560 570 580
cryla-105.pe GGFNKTMDTGPIITFOSFYATINTAFTFPMSSQSFVAGADTFSSGNEVYIDREFLIPVT
550 560 570 580 590 600
40290 GNFSATMNRGEDLDYKTFRTVGTTPFSLVQSTFTTIGAWNFSSGNEVYIDREFLIPVE
590 600 610 620 630 640
cryla-105.pe ATLEAYNLEPAQAVNALFTSTNQLGKTWVTHYDQVSNLVYVLSDEFLCKLEKELS
610 620 630 640 650 660
40290 VTYEAYDFEKAQCKVTAFTSTNPRGLKTDVYHDQVSNLVSLGDFYLDKRELF
650 660 670 680 690 700
cryla-105.pe EKVKHAKLSERNLLQDSNFKDINRQPERGWSGSGTIGTIGQGGDDVFNENYVTLSGTDE
670 680 690 700 710 720
40290 EIVKVAQKHIERNN
710 720
cryla-105.pep

SW-8927997
8927997 description="PESTICIDIAL CRYSTAL PROTEIN CRYIID (INSECTICIDAL
DELTA-ENDOTOXIN CRYII (D)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (81 KDA CRYSTAL
PROTEIN)" library=NA species="Bacillus thuringiensis" source="swissprot_prot"
version=NA type=PRI
SCORES Initl: 888 Initn: 1589 Opt: 1695 z-score: 1922.2 E(): 9e-99
>>SW:8927997
Initn: 1589 Initl: 888 Opt: 1695 z-score: 1922.2 expect(): 9e-99
Smith-Waterman score: 1711; 43.2% identity in 696 aa overlap
(14-683:41-719)
cryla-105.pe MNNNPINECIPYNCILSNPEVE-VLGGRIETGYTIDISLSL
10 20 30 40
8927997 SFSSNATVDSKFTDPLEHNTNMLQNSHEDCLMKSEYSEVPFVSVSTIQTGIGIA---
20 30 40 50 60
cryla-105.pe TOFLSEFVPGAGFVLGLVDIIWIGIF--GPSQWDAFLVQIEQLINQRIIEEFARNOAISR
50 60 70 80 90
8927997 GKILGNLGVFPAGQVAVSLYSFILGELMPKGSOWEIFMEHVEELINQIKISTYARNKALAD
70 80 90 100 110 120
cryla-105.pe LEGLSNLYQIVAESFREWADPTNPALREEMRIQFDMNSALTTPILPFAVQNYQVPLLS
100 110 120 130 140 150
8927997 LKGLDALAVVHESLESLEWENNTNRVSVKQYIALELMFVQKLPFSFVSGEVEPLP
130 140 150 160 170 180
cryla-105.pe GQSRQWIRYNQFRRTATVLLVSVLSPNYDSRTYPIRTVSQLTREIYTNPV-LENFDG
190 200 210 220 230 240
8927997 GTNAESWRYNQFRDMMVADLVALRSYDTEMYPITPSAQLTREYVYTDAGTGHNA
250 260 270 280 290 300
cryla-105.pe SFRGSA-----QSGSI-RSPHMDLNTIYTDHARGVWNSH
280 290 300 310 320 330
8927997 SFASITWYNNNAPSFTIEAAWRNPHLDFLQVITVSLAR---WSNTQYMMN--W
310 320 330 340 350 360
cryla-105.pe SGPEFTFLYGTMGNAPOQRIVAOLGQVRYLTSLTRPRNIGIN--NOOLSVLDG
330 340 350 360 370 380
8927997 GGHKLEFTTIGTTLNISTOGSTNTSINPVLPFTSRDVRTESLGLNPL
370 380 390 400 410 420
cryla-105.pe TEFAYG-----TSSNLPSAVYRKSGTV--DSLDEIPQNNVPPROGFSH
390 400 410 420 430 440
8927997 VDFHMKVTHPIASDNFYYPGVAGIGTQLODSENELPPEATQPNVYESYSH
430 440 450 460 470 480
cryla-105.pe SGFSNSVSIIRAPMFESWIHRSAEFNIIASDSITQIPLVKAHTLQSGTTVVRGPGFTG
440 450 460 470 480 490
8927997 -----SASHVKALVYSWTHRSADRTNIEPNSITQIPLVKAFNLSGGAUVVRGPGFTG
490 500 510 520 530 540

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cryla-105.pe      500    510    520    530    540    550
DILRTSGGFATVINGLOPORYEARIRXASTNLRIVTAGERIFACQFNKMTDI
| | | : : : | | | : | | | | | | | : | | | : | | | :
8927997          540    550    560    570    580    590
DILORTITGFDIRVNINPPFAORYELRIRVASTNLFEHTSINGKAINQCNGFATMNR
540    550    560    570    580    590

cryla-105.pe      560    570    580    590    600    610
GDPLTFOSFYATINTARTFPMSSOSSFTVCADTFSGSNEVIDRFELIPWTLEAEYNL
| | | : : : | | | : | | | | | | | : | | | : | | | :
8927997          600    610    620    630    640    650
GEDLDYKAFRTVGTFPTFSFNAOSTITGANFNLSIGNEVIDRIEFVPVEVTYEAYDL
600    610    620    630    640    650

cryla-105.pe      620    630    640    650    660    670
EKAQKANVALFTSTINGOLGIKNVTDYHDQSNVLTVYSDFCLDKRELSUKVHXAKRL
| | | : : : | | | | | | | | | | | : | | | : | | | :
8927997          660    670    680    690    700    710
KKAODEITAMFTSTNLRRLKNTVDCHIDQSNLVLSDESFYLDEKKRELFEIVIAKQL
660    670    680    690    700    710

cryla-105.pe      680    690    700    710    720
SDERNLLQDSNFNDINROPEGWGSGTGITIQGGDDVFKENVTLTSGTDECPTYLYQK
: | | |
8927997          NIERNM

```

cryla-105.pap
NRRA: 8927997

8927997 source="GENBANK_PROT" pesticidal crystal protein cryiid (Insecticidal delta-endotoxin CryII(d)) (Crystalline entomocidal protoxin) (81 kDa crystal protein)gi|5531642|gb|AD44366.1| insecticidal crystal protein [Bacillus thuringiensis]

```

SCORES      Initl: 888      Initn: 1589 Opt: 1695 z-score: 1922.2 E(): 9e-99
>>NRAR: 8927997
      Initl: 1589 Initn: 888 Opt: 1695 z-score: 1922.2 expect(): 9e-99
Smith-Waterman score: 1711; 43.2% identity in 696 aa overlap
      (14-683; 41-719)

```

```

cryla-105.pe      10      20      30      40
MNNPNINECIPYNCISNPEVE-VLGGERTETGYTIDISLSL
                :::  |  |  |  |  |  |  |  |  |
SFSSNATYKDSFTDPLEHTNMELONSHEDCKLKXSESVESPVSTTIGIA---
8927997

```

```

cry1a-105.pe  TOFLLSFVPFCAGVLVDIIWGIF--GPSOWDAFLVQTEQLINORIEEFARNQALSR
              50    50    60    70    80    90
8927997       GKILGNLGVFPFAGQASVLSYFILGELPKGSKQWEIEMHEVELINQKISTYARNKALAD
              80    90    100    110    120

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cryla-105.pe LEGLSNLYQIYA5FREWEDTTPALREMR IQFDNNNSALT TTAIFLFAVQYQVPLIS
100 110 120 130 140 150
9827997 LAGLCDAI AAVYHESI FSWTFENNDNTVP SVUUKAVGTAT FLAFMVKLI SFEVAVSFEETVFLD

```
cryla-105.pe VVQAA NHLSVLDSVSFGWGFDAATNSRYNDLFLGNTYDHAHWYNTGLRW
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
8927997 IYAQAANHLLLRDASIPKXEWGLSESESTFYNQSSQTQGEVDYCSEWYNTGLNLR
160 170 180 190 200 210
```

[illegible]

540282 source="GENBANK_PROT" insecticidal proteingi|2119864|pir||I39814
insecticidal protein cryv1 - Bacillus thuringiensis

```

SCORES Init1: 889 Initn: 1585 Opt: 1694 Z-score: 1921.1 E(): 1e-98
>>NPAA540282
Initn: 1585 Init1: 889 opt: 1694 Z-score: 1921.1 expect(): 1e-98
Smith-Waterman score: 1710; 42.4% identity in 705 aa overlap

```

[illegible][illegible][illegible]

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[illegible]

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cry1a-105.pe NLLQDSNFKDINRPERGCGSGTIGITIOGGDDVFKENVYVTLSTGTFDECYPTLYLXKIDES
547556 NLLQDDPFTNINSTENGKASNGVTIISBGGFFKGRALQASA-RENYPTIYIQKVDAS
740 750 760 770 780
cry1a-105.pe KLAFTYRLRGYVIEDSDQLEIYSIRYNAKHETVNPVGTGSLWPLSLAQSGIKGCGEPNRC
750 760 770 780 790 800
547556 VLKPYTRYRLDGVFKVSSODLEIDLIIHHKVLVKNVNDL---VSDTSDGSCGINRC
790 800 810 820 830 840
cry1a-105.pe APHLEWNPDLDCSRDGEKC-AHSHHFSLDIDVGTDLNBDLGVWVIFIKITQDGHARL
810 820 830 840 850 860
547556 DEQHQVMDQLDAEHHPMDCCCEAAQTHEFFSSYINTGDLNASVDQGIWVLKVRTDGYATL
850 860 870 880 890 900
cry1a-105.pe GNLEFLEKPLVGEALARKVKAEEKMEDKELEWETWIVYKEAKESVDALFVNSQYDL
870 880 890 900 910 920
547556 GNLEFLEKPLVGEALARKVKAEEKMEDKELEWETWIVYKEAKESVDALFVNSQYDL
910 920 930 940 950 960
cry1a-105.pe QADTNIAHIAADKRVHSIREAYLPESLVIPGVNAAIPEELEGRIFTAFSLYDARNVIQN
930 940 950 960 970 980
547556 NPEIGLAEINEASNLVESISGVYSDDLQIPRGINYEIYELSDRLQOASLYTSRNVQCN
970 980 990 1000 1010 1020
cry1a-105.pe GDFNGLSCMNKGVHVDVEEQNNORSVLVWPEWAEVQEVVCPGKYLRLVTAYKEGY
990 1000 1010 1020 1030 1040
547556 GDFNGLSDNMTMDASVQDGNMH-FLVLSHWDQVQSQQLRVNPNCKYVLRVTARKVGG
1030 1040 1050 1060 1070 1080
cry1a-105.pe GEGCVTHEENNTDELAFNCVEEIIYPNNTVTCNDYTVNOEYVGAYTSRNGVNEAP
1050 1060 1070 1080 1090 1100
547556 GDGYVIRDAHQHQTILFNAC-----DIDVN-----GTIVNDN-----
1090 1100 1110
cry1a-105.pe SVPADVASVEEKSYTDGRENPCFENRGYRDTPLVGYVTKLEYFPETDKWIEIGE
1110 1120 1130 1140 1150 1160
547556 -----SYITEEVVFPETKHMVEYSE
1120 1130 1140
cry1a-105.pe TEGTFIVDSVALLMEE
1170
547556 SEGTFIVDSVALLMEE
1150
cry1a-105.pe
SW:8927981
8927981 description="PESTICIDIAL CRYSTAL PROTEIN CRY1C (INSECTICIDIAL
DELTA-ENDOTOXIN CRYII(C)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (81 KDA CRYSTAL
PROTEIN)." library="NA" species="Bacillus thuringiensis" source="swissprot_prot"
version="NA" type="PRT
SCORES Initl: 862 Initn: 1515 Opt: 1604 Z-score: 1818.8 E(): 5.2e-93
-->SW:8927981
initn: 1515 initl: 862 opt: 1604 Z-score: 1818.8 expect(): 5.2e-93
```

```
Smith-Waterman score: 1610; 41.9% identity in 663 aa overlap
(51-683:76-719)
cry1a-105.pe VEVLGGERIETGTPIDISLSLTQFLISEFPCAGFVLGVLDIIWIGFGP---SOWDAFL
30 40 50 60 70
8927981 SEHESIDPFSASTOTGTIGIAGKILGTGLVPPGQIASLSYFILGELWPKGKSOWEIFM
50 60 70 80 90 100
cry1a-105.pe VQIEQLNQRIEERFARNQAIKRLGSLNLYQIYASFWREADPTNPALREEMRIQFNDM
80 90 100 110 120 130
8927981 EHVAAIINRKISTYARNKALTDLKGDLAVYHESLESWGVNENNRTRARSVVKNOYIAL
110 120 130 140 150 160
cry1a-105.pe NSALTITAIPLFAVQNVQVPLSVVQAANIHLVLDVSVFGQWGFDAATINSRYNDLT
140 150 160 170 180 190
8927981 ELMFVQKLPSFAVSGEEVPLPIYAQAANLHLLLDASIFEKNGGLSASEISTFYNRQV
170 180 190 200 210 220
cry1a-105.pe RLIGNYTDHARVWYNTGLERVMGDSRDMIRYNQFRRELTITLVDIVSLFPNYSRTYPI
200 210 220 230 240 250
8927981 ERTDYSYHCVKWNTGLNLRATNGQSVVYNQFRKDIELMWLDLVRVFPVSYDTLVYPI
230 240 250 260 270 280
cry1a-105.pe RIVSOLTREIYNPV-LENFQSGPRGSA-----QCIEGS-IRSPHMDILNSITY
260 270 280 290 300
8927981 KITSQITREYDDAIGTVDNQALRSTWTNNNAPSFAIEAAVIRSPHLLDEKVTIY
290 300 310 320 330 340
cry1a-105.pe TDAHR---GEYV--WSGHOIMASVPVSGSGPEFTFLYLTGMGAAPQRIVAOLGQGVVHT
310 320 330 340 350 360
8927981 SLLSRWNTQYMMWGGHRLSRDIG-----GAL-NTSQSTWTSINPVTLQF
350 360 370 380 390
cry1a-105.pe LSSTLYRRFPNIGIN---NQQLSVLDGTGFAYG-----TSSNLPASAVYKSGT--VDSL
370 380 390 400 410
8927981 TSDFVATESWAGLNLFTQPVNGVPRVDFHMKFPTLPASDNFYILGYAGVGTQLQDSE
400 410 420 430 440 450
cry1a-105.pe DEIPQNNVPRQGFSHRLSHVSMFSGFSNNSVSIIRAPMFSWIHRSAEFNIIASDS
420 430 440 450 460 470
8927981 NELPPTTGQPNYESYSHRLSHIGLI-SG-----SHVKALVYVSWTHRSADRTNIETNS
460 470 480 490 500
cry1a-105.pe ITQIPLVKARTLQSGTIVVRGPGFTGDIILRTSGSPFAYTIVNINQLPQRYARIRYA
480 490 500 510 520 530
8927981 ITQIPLVKAFNLSGAAVVRGPGFTGDIILRTSGTGHILRTKSGTGHIRVNIINPPFAQRYVEMSYA
510 520 530 540 550 560
cry1a-105.pe STTNLRIVYVAGERIFAGQFNKMTMGDPLTFQSFYSATINTAFTPMQSSFTVGADT
540 550 560 570 580 590
8927981 STTDLPQHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGTFTPTFSFSDVQSTFTIGAWN
570 580 590 600 610 620
cry1a-105.pe ESSGNEVYIDRELEIPVATATLAEYNLERAKQAVNALTSTNQGLKATNTVDYHIDQSN
600 610 620 630 640 650
```

8927981
TSRDFYRTESWAGNLFITOPVNGVPRVDFHWKFTFLPIASDNFYFYLGYAGVGTVQDQSE
400 410 420 430 440 450
cryla-105.pe DEIPPNVPPROGFGSHRLSHVMSFRSGFNSSVSIIRAPMFSWHRGAENNIASDS
420 430 440 450 460 470
8927981 NEUPPETGQPNYESYSHRLSHGLI-SG-----SHVKALVSWTHRSADRTNIEPNS
460 470 480 490 500
cryla-105.pe ITQIPLVKAFNLSSGAAVVRGPGFTGCHILRRKTSCTFCHIRVNINPPFAQRYVRMSYA
480 490 500 510 520 530 540 550 560
8927981 ITQIPLVKAFNLSSGAAVVRGPGFTGCHILRRKTSCTFCHIRVNINPPFAQRYVRMSYA
510 520 530 540 550 560
cryla-105.pe STTNLRIVTVAGERIFAGOFNKMTDMGDFLTFQSFVSATINTAFTFPMSSQSFVVGADT
540 550 560 570 580 590
8927981 STTNLRIVTVAGERIFAGOFNKMTDMGDFLTFQSFVSATINTAFTFPMSSQSFVVGADT
570 580 590 600 610 620
cryla-105.pe FSSGNEVYIDRFELIPVATILEAEYNLERAKAVNALFTSNQLKXNTVTDYHIDQVSN
600 610 620 630 640 650
8927981 FSSGNEVYIDRFELIPVATILEAEYNLERAKAVNALFTSNQLKXNTVTDYHIDQVSN
630 640 650 660 670 680
cryla-105.pe LVSLSDELVDKELFEIVKYAKQIHIERNN
690 700 710
cryla-105.pe GDDVFNKVVTLGGTFCPCYTYLYQKIDESKLKAFTRQYLRGVIEDSQLEIYSIRYNA
720 730 740 750 760 770
cryla-105.pe
NRAA:54112021
54112021 source="GENBANK PROT" (Bacillus thuringiensis
serovar japonensis)
SCORES Initl: 425 Initn: 1433 Opt: 1565 z-score: 1794.0 E(): 1.2e-91
>NRAA:54112021
Initn: 1833 Initl: 425 Opt: 1585 z-score: 1794.0 E(): 1.2e-91
Smith-Waterman score: 2199; 34.7% identity in 1188 aa overlap
(1-1177:29-1163)
cryla-105.pe
54112021
cryla-105.pe
54112021
cryla-105.pe
54112021
cryla-105.pe

8927981
FSSGNEVYIDRFELIPVATILEAEYNLERAKAVNALFTSNQLKXNTVTDYHIDQVSN
630 640 650 660 670 680 690 700 710
cryla-105.pe LVSLSDELVDKELFEIVKYAKQIHIERNN
690 700 710
8927981 LVSLSDELVDKELFEIVKYAKQIHIERNN
710 720 730 740 750 760 770
cryla-105.pe GDDVFNKVVTLGGTFCPCYTYLYQKIDESKLKAFTRQYLRGVIEDSQLEIYSIRYNA
720 730 740 750 760 770
cryla-105.pe
NRAA:54112021
54112021 source="GENBANK PROT" Pesticidal crystal protein (CryIIc)
delta-endotoxin CryII(c) (Crystalline entomocidal protein) (81 kDa crystal
protein) [3702807] [gb|AAC62933.1] crystal protein toxin (Bacillus
thuringiensis)

8927981
TSRDFYRTESWAGNLFITOPVNGVPRVDFHWKFTFLPIASDNFYFYLGYAGVGTVQDQSE
400 410 420 430 440 450
cryla-105.pe DEIPPNVPPROGFGSHRLSHVMSFRSGFNSSVSIIRAPMFSWHRGAENNIASDS
420 430 440 450 460 470
8927981 NEUPPETGQPNYESYSHRLSHGLI-SG-----SHVKALVSWTHRSADRTNIEPNS
460 470 480 490 500
cryla-105.pe ITQIPLVKAFNLSSGAAVVRGPGFTGCHILRRKTSCTFCHIRVNINPPFAQRYVRMSYA
480 490 500 510 520 530 540 550 560
8927981 ITQIPLVKAFNLSSGAAVVRGPGFTGCHILRRKTSCTFCHIRVNINPPFAQRYVRMSYA
510 520 530 540 550 560
cryla-105.pe STTNLRIVTVAGERIFAGOFNKMTDMGDFLTFQSFVSATINTAFTFPMSSQSFVVGADT
540 550 560 570 580 590
8927981 STTNLRIVTVAGERIFAGOFNKMTDMGDFLTFQSFVSATINTAFTFPMSSQSFVVGADT
570 580 590 600 610 620
cryla-105.pe FSSGNEVYIDRFELIPVATILEAEYNLERAKAVNALFTSNQLKXNTVTDYHIDQVSN
600 610 620 630 640 650
8927981 FSSGNEVYIDRFELIPVATILEAEYNLERAKAVNALFTSNQLKXNTVTDYHIDQVSN
630 640 650 660 670 680
cryla-105.pe LVSLSDELVDKELFEIVKYAKQIHIERNN
690 700 710
cryla-105.pe GDDVFNKVVTLGGTFCPCYTYLYQKIDESKLKAFTRQYLRGVIEDSQLEIYSIRYNA
720 730 740 750 760 770
cryla-105.pe
NRAA:54112021
54112021 source="GENBANK PROT" (Bacillus thuringiensis
serovar japonensis)
SCORES Initl: 425 Initn: 1433 Opt: 1565 z-score: 1794.0 E(): 1.2e-91
>NRAA:54112021
Initn: 1833 Initl: 425 Opt: 1585 z-score: 1794.0 E(): 1.2e-91
Smith-Waterman score: 2199; 34.7% identity in 1188 aa overlap
(1-1177:29-1163)
cryla-105.pe
54112021
cryla-105.pe
54112021
cryla-105.pe
54112021
cryla-105.pe

8927981
TSRDFYRTESWAGNLFITOPVNGVPRVDFHWKFTFLPIASDNFYFYLGYAGVGTVQDQSE
400 410 420 430 440 450
cryla-105.pe DEIPPNVPPROGFGSHRLSHVMSFRSGFNSSVSIIRAPMFSWHRGAENNIASDS
420 430 440 450 460 470
8927981 NEUPPETGQPNYESYSHRLSHGLI-SG-----SHVKALVSWTHRSADRTNIEPNS
460 470 480 490 500
cryla-105.pe ITQIPLVKAFNLSSGAAVVRGPGFTGCHILRRKTSCTFCHIRVNINPPFAQRYVRMSYA
480 490 500 510 520 530 540 550 560
8927981 ITQIPLVKAFNLSSGAAVVRGPGFTGCHILRRKTSCTFCHIRVNINPPFAQRYVRMSYA
510 520 530 540 550 560
cryla-105.pe STTNLRIVTVAGERIFAGOFNKMTDMGDFLTFQSFVSATINTAFTFPMSSQSFVVGADT
540 550 560 570 580 590
8927981 STTNLRIVTVAGERIFAGOFNKMTDMGDFLTFQSFVSATINTAFTFPMSSQSFVVGADT
570 580 590 600 610 620
cryla-105.pe FSSGNEVYIDRFELIPVATILEAEYNLERAKAVNALFTSNQLKXNTVTDYHIDQVSN
600 610 620 630 640 650
8927981 FSSGNEVYIDRFELIPVATILEAEYNLERAKAVNALFTSNQLKXNTVTDYHIDQVSN
630 640 650 660 670 680
cryla-105.pe LVSLSDELVDKELFEIVKYAKQIHIERNN
690 700 710
cryla-105.pe GDDVFNKVVTLGGTFCPCYTYLYQKIDESKLKAFTRQYLRGVIEDSQLEIYSIRYNA
720 730 740 750 760 770
cryla-105.pe
NRAA:54112021
54112021 source="GENBANK PROT" (Bacillus thuringiensis
serovar japonensis)
SCORES Initl: 425 Initn: 1433 Opt: 1565 z-score: 1794.0 E(): 1.2e-91
>NRAA:54112021
Initn: 1833 Initl: 425 Opt: 1585 z-score: 1794.0 E(): 1.2e-91
Smith-Waterman score: 2199; 34.7% identity in 1188 aa overlap
(1-1177:29-1163)
cryla-105.pe
54112021
cryla-105.pe
54112021
cryla-105.pe
54112021
cryla-105.pe

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54112021      SEGQFFKRALQLASA--RENYPTIYQKVDSSMLKPYTRYKLDGFFVQSSQDLEILHII
              770      780      790      800      810      820
cryla-105.pe NAKHETVNVPGTSLWPLSASGPIKGCPNRCAPHEWNPDLDCSCROGKC-AHHSSH
              770      780      790      800      810      820
54112021      HKVHLVKNVPDNLV-----DYFDGSGNGINRCCEQWVNSQSLTEHHPMDCCEASQTHE
              830      840      850      860      870
cryla-105.pe FSLDIDVGCTDNLNEDLGVWVIFKIKTDQGHASLGNLEFLEKPLVGEALRAVKRAEKKWR
              830      840      850      860      870      880
54112021      FSSVIHTGLDNASVDOGIVWVYKIRTTDSATLGNLELVGVPLSGESLERECRONAKWN
              880      890      900      910      920      930
cryla-105.pe DKREKLEWETNVIYKEAESVDALFVNSQVDQLQADTNIMIHAAKRVHSTREAYLPEL
              890      900      910      920      930      940
54112021      AELGKRKAEDRVYQGAQQAINHFLVDYQDQQLNPEVGLAEISEARNLIESIDVYCDVA
              940      950      960      970      980      990
cryla-105.pe SVIPGVNAALIFELEGRIFTAFSLDYARNVKNKGDFNGLSCMVVKGHVDVEEQNNQRSV
              950      960      970      980      990      1000
54112021      LRIFGINVWYVTELSNRLQQAAYLYTSRAVONGDFNSGLDSWATTTDATVQDGMVY-F
              1000      1010      1020      1030      1040      1050
cryla-105.pe LVVPWEAEVSGEVRVCPGRGYILLRTAYKEGEGCVTHIEINNTDELKFSNCVBEI
              1010      1020      1030      1040      1050      1060
54112021      LVLSHMDAQVSOQFRVQPNCKYVLRTAKVGVNGDGYVTIOGGAHRETLTFNAC-----
              1060      1070      1080      1090      1100      1110
cryla-105.pe YPNNTVTCNDYTNQEEYGGATYSNNGYNEAPSVADYASVYEKSYTDGRENPCFEF
              1070      1080      1090      1100      1110      1120
54112021      -----DYDWN-----GHWNDN-----
              1120
cryla-105.pe RGYRDTPLPVGVVTKELVEYPTDQVWIEIGETGTTIVDSVELLMEE
              1130      1140      1150      1160      1170
54112021      -----SVITKELEFPKTEHWMVEVSETSGTIVDISIELTQE
              1130      1140      1150      1160
cryla-105.pep
NRAA:58700647
58700647 source="GENEBANK_PROT" Cry8 [Bacillus thuringiensis]

SCORES      Initl: 489      Inltn: 1080      Opt: 1565      Z-score: 1774.3      E(: 1.6e-9)
>NRAA:58700647
Inltn: 1080      Inl1: 489      opt: 1565      Z-score: 1774.3      expect(: 1.6e-90)
Smith-Waterman score: 1610;      38.9% identity in 785 aa overlap
(403-1174:20-736)

cryla-105.pe IGINNQLSVLDGTEFAYGTSSNLPASVAVFKSGTVDSDLEIIPQNN--NVP-PRQ-GFSSH
              380      390      400      410      420
58700647      GSANSAHTLIFSDSTCGRLSESITKNSAEILPPTSESIDTPQNPQVTYSH
              10      20      30      40
cryla-105.pe RLSHVSFRSGFSGNSVSIIIRAPMFSWIHRKSFNNFIASDSITQIPLVKA--HTLQSGT
              430      440      450      460      470      480

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58700647 RLDYATIRANKSGNPLGTHSRDNRNTIYPNKIQIPAVKAFSYTESFNV
50 80 90 100
cry1a-105.pe TNRGCEFGDILERTSGPFATVUNGOLPORVYRIRYASTINRIVTVAGERI
400 500 520 530 540
cry1a-105.pe NVIAGPSTGSDILERTSGPFATVUNGOLPORVYRIRYASTINRIVTVAGERI
110 120 130 140 150 160
58700647 QSDREFQTSNENENLNFENFQVVEARNIFSDADENHOVSTONQNGFVIDRIEF
170 180 190 200 210 220
cry1a-105.pe IPVTATLEAFYNLERAKAVNALFTSTNGLTNRNNDYHIDVSNLTVLSDEPCLDK
610 620 630 640 650
58700647 IPVNAITYEAFQDLDSAKXAVNTFTNTKD-GURPGVTSEVNOANLVEGSDULYPNEK
230 240 250 260 270 280
cry1a-105.pe RELCEKVKHAKRLSDERNLLODSNFKDINRQPERGWSGTGTTIQGGDVFKNYVLSG
670 680 690 700 710 720
58700647 RLLDFAKAKRLSEARNLLODPDFQFIN--GENGWASTGLEVEGDALFKRYLAPG
230 300 310 320 330 340
cry1a-105.pe TFD---ECPTLYYQKIDESKKAFTRYQLRGVIEDSQLEIYSIRYNAKHETVNPVGG-
730 740 750 760 770 780
58700647 AREMDTETPTLYYQKVEGVLPKPTRYRLRGVFGSSQGLEISTIRHQTNRIVKNVPDDL
350 360 370 380 390 400
cry1a-105.pe -GSLWPLSAQSPGKCGEPNRCAPHEWNPDLDCSCRDGKCAHSHHSLDIDVGCCTDL
790 800 810 820 830 840
58700647 LPDVPVNGRINRCSEKYNVNSRLEGERGLPNGRSAE-----AHEFLPIDIGELDY
410 420 430 440 450
cry1a-105.pe NEDLGWVWIFKIKTODGHARLGNLEFLEKPLVGEALARKVRAEKAKKRDREKLEWETNI
840 850 860 870 880 890
58700647 NENAGIWWGFKITDPEGATLGNLELVEEGPLSGDALERLQREEQWKLQWTKRREETDR
460 470 480 490 500 510
cry1a-105.pe VYKAKESVDALFVNSQYDQLQADNTAMTHAADKRVHSIRAYLPELSVIPGVNAAIFE
900 910 920 930 940 950
58700647 KYTAARQVRLYADYQDQQLNPNFVEITDITAAQNLIQISIPVYNEMFPEIQGNVTKYT
520 530 540 550 560 570
cry1a-105.pe ELEGRITFATSLVDARNVKNKGDFNGLSCWNVKGVHDVVEEQNORSVLVVPWEAEVQS
960 970 980 990 1000 1010
58700647 ELTNELQAGWGLYDQRNAIPNGDFNLSNWNNTSGVNVQQLNNT-SVLVWPNWDSQVSQ
580 590 600 610 620 630
cry1a-105.pe EVRVCPGRGVLRTAYKEGEGCVTIHEIENNTDELKFSNCVEEETPNNTVTCNDYT
1020 1030 1040 1050 1060 1070
58700647 QFTVPQNRVYLVARTAKEGVGNGVSVIRDGNGQNTETLTFSA-----SDVN
640 650 660 670 680
cry1a-105.pe VQNEEYGGATYSNRNGYNAPSVPADYASVYKESYTDGRRENPCFNRGYRDTPLPVG
1080 1090 1100 1110 1120 1130

58700647 TDSV-INTQVSNINGLYNEQ-----TG
690 700
cry1a-105.pe YVTKELVFPETDKVWIEIGETGETFIVDSVELLMEE
1140 1150 1160 1170
58700647 YTKVTFIPYTDQVWIEIEMSETGCMFVIESVELIVDE
710 720 730
cry1a-105.pep
NRAA:62126062
62126062 source="GENBANK_PROT" crystal endotoxin [Bacillus thuringiensis]
SCORES Initl: 1541 Initn: 1541 Opt: 1550 z-score: 1764.5 E(): 5.5e-90
>NRRA:62126062
Initn: 1541 Initl: 1541 Opt: 1550 z-score: 1764.5 expect(): 5.5e-90
Smith-Waterman score: 1550; 92.6% identity in 244 aa overlap
(707-950:1-244)
cry1a-105.pe LSDERNLLODSNFKDINRQPERGWSGTGTTIQGGDVFKNYVLSGTFDECYPTLYQ
680 690 700 710 720 730
62126062 TIQGGDVFKNYVLSGTFDECYPTLYQ
10 20 30
cry1a-105.pe KIDSKKATRIQLRGVIESQLEIYSIRYNAKHETVNPVGGSLWPLSAQSPGKCG
740 750 760 770 780 790
62126062 KIDSKKATRIQLRGVIESQLEIYSIRYNAKHETVNPVGGSLWPLSAQSPGKCG
740 750 760 770 780 790
cry1a-105.pe EPNECAHLENNPDLDCSCRDGKCAHSHHSLDIDVGCCTDLNEDLGWVWIFKIKTODG
800 810 820 830 840 850
62126062 EPNECAHLENNPDLDCSCRDGKCAHSHHSLDIDVGCCTDLNEDLGWVWIFKIKTODG
800 810 820 830 840 850
cry1a-105.pe HARLGNLEFLEKPLVGEALARKVRAEKAKKRDREKLEWETNIYVYKAKESVDALFVNSQ
860 870 880 890 900 910
62126062 HARLGNLEFLEKPLVGEALARKVRAEKAKKRDREKLEWETNIYVYKAKESVDALFVNSQ
860 870 880 890 900 910
cry1a-105.pe YDQLQADNTAMTHAADKRVHSIRAYLPELSVIPGVNAAIFEELSGRNTAFSLYDAEN
920 930 940 950 960 970
62126062 YDQLQADNTAMTHAADKRVHSIRAYLPELSVIPGVNAAIFEELSGRNTAFSLYDAEN
920 930 940 950 960 970
cry1a-105.pe VIKNGDFNGLSCWNVKGVHDVVEEQNORSVLVVPWEAEVNSQSVRVCPGRGVLRTAY
980 990 1000 1010 1020 1030
cry1a-105.pep
NRAA:8469159
8469159 source="GENBANK_PROT" Pesticidal crystal protein cry8a (Insecticidal
delta-endotoxin CryVIII(a)) (Crystalline entomocidal protoxin) (130 kDa crystal
protein)gi|532524|gb|AAA21119.1| CryIII delta-endotoxingi|1096647|prf|2152230A
delta-endotoxin

Monsanto Company

Final Report

Product Characterization Center

Study No. 06-01-62-04
MSL No. 20351
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SCORES Initl: 503 Initn: 1400 Opt: 1542 Z-score: 1745.2 E(): 6.5e-89
>>NRAA.8469159
initn: 1400 initl: 503 opt: 1542 Z-score: 1745.2 expect(): 6.5e-89
Smith-Waterman score: 2142; 34.8% identity in 1200 aa overlap
(18-1177:59-1160)

```
cry1a-105.pe      10      20      30      40
MDNPNNEICIPYCNLSNEVEVLGGRIETGYTPDLSLSLTQFL
8469159      40      50      60      70      80
LANDQNTLQNNYKDYLNKTESTNAELSRNPGTFISAQAVGTG---IDIVSTIISLG
(18-1177:59-1160)

cry1a-105.pe      50      60      70      80      90      100
SEFVPGAGFVLGLVDIIWGIFGSPQ---WDAFLVQIEQLINQRIEFAFARNOAISRLGL
8469159      90      100      110      120      130      140
---IPVLGEVFSILGSLIGLWPSNNENWQIFMNRVEELIDQKILDSVRSRAIADLANS

cry1a-105.pe      110      120      130      140      150      160
SNLYQIYAESFREAEPTNPALREEMRIQNDMSALTATPLFAVQYQVPLLSVYVQ
8469159      150      160      170      180      190      200
RIAVEYQNALEDWRKPHSTRSAALVKERFGNAEAILRLNMGFSQSTNYETPLPYAQ

cry1a-105.pe      170      180      190      200      210      220
AAMLHLVLRDVSVFGQWGFDAATINSRYNDLTRIGNYTDHAVYNTGLERVWGPDS
8469159      210      220      230      240      250      260
AASLHLWMDVQIYKEMGYPQNDIDLFYKEQVSYARYSDHCQWYVYAGLNKLRGTGA

cry1a-105.pe      230      240      250      260      270      280
RWIRYNQFRELTLVDIVSLFNYDSRTYPIRTVSQLTREIYNVLENFDSFR--
8469159      270      280      290      300      310      320
KQWVDYNRFRMMVMDLVALFPYDARIYPLETNAELTRIFDTPGVSVYTCQSSTL

cry1a-105.pe      290      300      310      320
GSAQGLEGSIRSPHLMILANSITITYTDHRG---EY--YNSGHQIAPSP
8469159      330      340      350      360      370      380
ISWYDIPALPFSFTLENLRKPFDFLLQELIRYITSFQNGTITIEYNYWGGQLTISY

cry1a-105.pe      330      340      350      360      370      380
VFGSGPEFTFLYGTMGNAAPQORIVAQLGQG-VYRTLSSTLYRRPFNI--GINNQQLSVL
8469159      390      400      410      420      430      440
IYGS----SPNKYS--GVLAGEDIIP-VGQNDIYRVVWTVYIGRYTNSLLGNVPYTFYS

cry1a-105.pe      390      400      410      420      430      440
DGTFAYGTSNLSFAYRKSQVTSLSDEIPQNNVPFPQGFSSHLSHVSMFRGFSNS
8469159      440      450      460      470      480      490
NNTQKTYKPKQFAGGK---TIDSGEELIYEN----YQSYSHRVSYITSFEIKSTGG

cry1a-105.pe      450      460      470      480      490      500
SVSIIIRAPMFWIHRSAEFNNIIASDITQIPLVKAHTLQSGTIVVRGPG-FTGGDILRR
8469159      490      500      510      520      530      540
TVLGV-VPIFGWTHSSASRNFIYATKISQIPINKASTSGGAVWNPQELNGGVPNKL

cry1a-105.pe      510      520      530      540      550
TSGGPFAYTI-VNINGQ-LPQRYRARIRYASTNLRIRVTVAGERIFAQ-----FNKTM
8469159      550      560      570      580      590      600
SGSGSQVINLRVATDAGASQRYRIRIRYASDRACKFTIISRSPENPATYSIAIYNTM
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cry1a-105.pe      560      570      580      590      600      610
DTGDLPTFOSFYAT---INTATFPMSSQSFYADTFFSGNEVYDFRFLIPVTATLE
8469159      610      620      630      640      650      660
STNASLTYSTFAYAESFINGIS--GSSRTFDISITKEAGAAANLYIDRIEIPVNTLFE

cry1a-105.pe      620      630      640      650      660      670
AEYNLERACKAVNALFTSTNOLGKTNVTDVHIDOVSNLVTYLSDEFCLDEKSELSEKVK
8469159      670      680      690      700      710      720
AEDLVAKAVNGLVFNKEND-ALQTSYDYQVNOANLANLECLSDLEYFNKRMLEMDAVK

cry1a-105.pe      680      690      700      710      720
HAKRLSDERNLIQDSNFKDINRQPERGMGSGSTGIITQGGDDVFKENYVTLSTGTFD---EC
8469159      730      740      750      760      770      780
EAKRLVQARNLLQDTGNRIN--GENGTGSGTIGIEVVEGDLVFKDRSLSLTSAREIDTET

cry1a-105.pe      730      740      750      760      770      780
YPTLYLQKIDSKKATRYQLRGYIEDQDLIYSIRYNAKHETVNVFGTGLWPLSAQ
8469159      790      800      810      820      830      840
YPTLYLQKIDSKKATRYQLRGYIEDQDLIYSIRYNAKHETVNVFGTGLWPLSAQ

cry1a-105.pe      850      860      870      880      890      900
SPIGKGEPRNCA--PHLEWNPDLDCSRDGEKCAHSHHFLSIDIVGCTDLNEDLVWV
8469159      910      920      930      940      950      960
RPVNSCGGVDCGSEQVYVDANLALENNNGENGMSSD-SHAFSPHIDTGEIDLNENTGIWI

cry1a-105.pe      910      920      930      940      950      960
IFKIKTQDGHARLGNLFLEKPLVGEALARYKAEKKWRDKREKLEWETNIVYKEAKES
8469159      970      980      990      1000      1010      1020
VFRIPTNGNATLGNLFEEGELSGTLEWAQQOEQQQODKMKARAAASEKTYVAAKQA

cry1a-105.pe      970      980      990      1000      1010      1020
VDALFVNSQYDQLQADTNMIAMIAADKRVHSIREAYLPFELSVIPGVNAAIFEELEGRIPT
8469159      1030      1040      1050      1060      1070      1080
IDRLFADYQDQKLGSGVMSDLAAQNLVQSIPIYVYNDALPEIPGMNYTSFTLTNRLOQ

cry1a-105.pe      1030      1040      1050      1060      1070      1080
AFSLYDARNVKNKGDFNNGLSVWVKGHVDVEEQNNORSVLVVPWEAEVSVQEVRCPR
8469159      1090      1100      1110      1120      1130      1140
AWNLQDLQNAIPNGDFNGLSNNATSDVWVQ-QLSDTSVLVTPNNWSQVSOQFTVQPNY

cry1a-105.pe      1090      1100      1110      1120      1130      1140
GYILRVATYKGYGEGCVTTHEIENNTDELKFSNCVBEETYPNNVTCTNDYTNQOEYGG
8469159      1150      1160      1170      1180      1190      1200
RYVLRYTARKEGVGDGVIIIRDGANQETLTFFN-----ICDDDT-----G

cry1a-105.pe      1090      1100      1110      1120      1130      1140
AYTSRNRGNEAPSVPADYASVVEEKSYYTDGRNFCFNRGYRDYTPLPVGVYVKELEY
8469159      1150      1160      1170      1180      1190      1200
VLST-----DQYS-----YITKTVFV
(18-1177:59-1160)

cry1a-105.pe      1150      1160      1170
FPETDKVWIEIGETEGTFIVDSVELLIMEE
8469159      1150      1160      1170
TPSTEQVWIDMSETGVFNIESVELLEEE
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cryla-105.pep
NR04.41056817
41056817 source: "GENBANK" PROT: "HBP-1" CxvIII delta-endotoxin [Bacillus
thuringiensis]

SCORES Initl: 503 Initl: 1398 Opt: 1542 Z-score: 1745.2 E(): 6.5e-89
>>NR04.41056817
Initl: 1398 Initl: 503 Opt: 1542 Z-score: 1745.2 E(): 6.5e-89
Smith-Waterman score: 2142; 34.8% identity in 1208 aa overlap
(18-1177:59-1160)

cryla-105.pe
41056817 LANDOTWTLONMNYKDYLMYTESTNAELSRNPTFSAODAVG---IDIVSTISG
10 20 30 40
MNNPNIIECIPYNSRVEVVGGERFGYTPINISLTLQFLL

cryla-105.pe SEFVPGAGFVLGLVDIIMGIFGSPQ---WDAFLVQIEQLINSRIFARNOKIFLAGS
41056817 ---IPVLGEVFSILGSLGLLWPSNNVWQIFMNVREVLIDOKILDSNSRIADLAF
90 100 110 120 130 140 150 160 170 180 190 200

cryla-105.pe SNLYQIYAESFREADPTNPALREEMRIQFNDMSALTALPLPAQNVQVLLSVYQ
41056817 RIAYEYONALEDMRNPHSTRSAALVKERFGNAELFTNNGFSQNTYETPLLPYAQ
110 120 130 140 150 160 170 180 190 200

cryla-105.pe AANLHSLVRDVSFGQWGFDAATINSRYNDLTRLIGNYTDHVAWNTGLERWGPDS
41056817 AASLHLLVMDVQIYKQWGPONDIDL FYKEQVSTARYSDHCVOVWYAGLKLGTGA
170 180 190 200 210 220

cryla-105.pe RDWIRYQFRELTLVLDIVSLFNYDSRTYPIRTVSQTLTYREITNPVLENFDGSGFR--
41056817 KQWVDYARFRRENNVMDLVALFPNDARYPLETNAELTREFITDPVGSYVTGQSSTL
230 240 250 260 270 280 290 300 310 320

cryla-105.pe -----GSAQIGESIRSPHLMILNSITITDAHRC---EY--YWSGHIWASP
41056817 ISWDMIPALPFSFTLENLRLKPKDPFTLLQELRMVTSFRONGTTEIYTNWGGGRTLSY
290 300 310 320

cryla-105.pe VGFSGPEFTPLVGTMGNAAPQORIVAQLGQ--VYRTLSSTLYRFPFNI--GINNQSLVL
41056817 IYGS-----SNKYS--GVLAGEADIIP--VGQNDIYRVWVTYIGRYTNSLLGVNPFYFS
330 340 350 360 370 380

cryla-105.pe DQTEFAGTSSNLPASVYRKSGTVDSDLEIPQNNVPFRQFSLHLSHVNFRSGFNS
41056817 NNTQTKYSKPKQAGGIK---TIDSGEELTYEN-----YQSYSHRVSYITSPFIKSTGG
390 400 410 420 430 440 450 460 470 480

cryla-105.pe SVSITRAMFSWHSRSENNIADSDITQIPLVKAHTLQSGCTTVRGPG--FTGGLILR
41056817 TVLGV--VPIFGTHSSASRNNFIYAIKISQIPINKASRTSGGAVNFGELNGSPWKL
450 460 470 480 490 500

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MSL No. 20351
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cryla-105.pe DTEPAGTSSNLPSAVKSVKSTVDLSDEIPQNNVPPROGFSHLSHYMFRSGFSNS
8469159 NNTQKTSKPKQFAGIK---TDSGEELTYEN-----YQSHRVSYSITSFKSTGGS
440 450 460 470 480 490 500

cryla-105.pe SVSIIAPMFWSHRAEFNIIASDSITQIPLVKAHTLOSQTIVVRGPG-FTGCDILRR
8469159 TVLGV-VPIFGWTHSSASRNFIVATKISQIPINKASRTSGGAVNFOGLYNGGPPWKL
490 500 510 520 530 540 550

cryla-105.pe TSGGPFAYTI-VNINQO-LPORYRARIYASTNLRYYVAGERIFAGQ-----FNKTM
8469159 SSGSQVINLRVATDAKASQYRIRIRYASDRAGFTISSRSPENPATYASAIAYNTNM
550 560 570 580 590 600 610

cryla-105.pe DTGDLPLFOFSVAT---INTAFTPMQSSQFTVGADTFSSGNEVYIDRFELIPVATLE
8469159 STNASTYTFVAESGPNLGIS---GSSRTFDISITKEAGANLYIDRIEFILPNTLFE
610 620 630 640 650 660 670

cryla-105.pe AEYNIERAKAVNALFTSNOLGKTNVTDYHIDQVSNLVTLVSDFCLDEKRELSKVK
8469159 AEEDLDVAKAVNGLTNEKD-ALOTSTVDYVQVQAANLIECLSDLYPNEKRLWDVAK
670 680 690 700 710 720 730

cryla-105.pe HAKRUSDERNLQDSNFKDKINQPERGMSGTITIGGDDVFKENYVTLSTGTFD---EC
8469159 EAKRLVQARNLODTGFNRIN--GENGTGSTEIVGSDVFLFKDSRLRLTSAREIDTET
730 740 750 760 770 780 790

cryla-105.pe YPTLYOKIDESKLKFTVQLRQYVIEDSQLEIYIRYNAKHETVNVPGTGSJLWPLSAQ
8469159 YPTLYQOIDEKLLKPYTRYKLGKFGIGSSQDLKILIRHRANQIVNVNPD--NLLP--DV
790 800 810 820 830 840 850

cryla-105.pe SPIGKCGEPNKA--PHLEWNPDLDCRDCGKCAHSHHFLSDIDVGTCTDNLNEDLGWV
8469159 RPNVSCGVDRCSGOQYVDANLALNNGENGNMSSD-SHAFSFHIDTGEIDNENTGIWI
840 850 860 870 880 890 900

cryla-105.pe IPKRTQDCHARIGNLEFEEKPLVGEALARKVKAERKDRKLEWETNIVYKEAKES
8469159 VFKPTINGNATIGNLEFEEKPLVGEALARKVKAERKDRKLEWETNIVYKEAKES
900 910 920 930 940 950 960

cryla-105.pe VDALFVNSQYDQLOADTNLAMIHAADKEVHSIRIYAYLPELSVPGVNAIIEELEGRI
8469159 IDRLFADYQDQKLNKGVMSDDLAQNLVQSPFYVYNDALEIPGPNVYTSFTLTNRLQ
960 970 980 990 1000 1010 1020

cryla-105.pe AFSLYDAENVIKNGDFNNGKSVNKGHVDVEEQNNQSVLVVPEWEAEVQVRVCPGR
8469159 ANNLVQLQNALPNDGFENGLSNWATSDVNVQ-OLSDTSVLVTPNWNQVQOFTVQPNY
1020 1030 1040 1050 1060 1070 1080

cryla-105.pe PFETDKWIEIGTEGTFIVDSVELLMEE
41056817 TPSTEQWIDMSETEGVFNIESVELVEEE
1140 1150 1160 1170 1180 1190 1200

cryla-105.pep
SW:8469159

8469159 description="PESTICIDIAL CRYSTAL PROTEIN CRY8CA (INSECTICIDAL
DELTA-ENDOTOXIN CRYIIIC(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (130 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar japonensis"
source="swissprot_prot" version="NA type="PRT

SCORES Initl: 503 Initn: 1400 Opt: 1542 z-score: 1745.2 E(): 6.5e-89
>>SW:8469159
Initn: 1400 Initl: 503 Opt: 1542 z-score: 1745.2 expect(): 6.5e-89
Smith-Waterman score: 2142; 34.8% identity in 1200 aa overlap
(18-1177:59-1160)

cryla-105.pe MDNPNINECIPYNCLSNPEVVLGERIETGTVIDISLSLTOFL
8469159 LANDQTNLONMYKDYLNKTESTNAELSRNPGTFISAQDVGTTG---IDIVSTIISGLG
30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200

cryla-105.pe SEFVPGAGFVLGDIWIGFGSQ---WDAFLVQLEQLINQRIEFPARNQALSRLEG
8469159 ---IPVGEVFSILGLLGLPNNENVMQIPFNREILIDQKILDSVRSEALADLANS
90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260

cryla-105.pe SNLVQIVAESFREWEADPTNPALREEMRIQFNDMSALITAPLFAVONQVPLSVYQ
8469159 RAVEYQNALEDNRNPNHSTRSAALVKERFGNAELLRNMGSFSQNYETPLPYAQ
150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500

cryla-105.pe AANLHSLVLRDVSFGQWGFDAATINSRYNDLFRIGNVTDHVRVNTYNTGLERVWGPD
8469159 AASLHLLVMDVQLYKGWGYFQNDIDLKYEQVSYTARYSDHCQVWYNAGLNKLRGTGA
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

cryla-105.pe RWRVYNGFRRELTIVLDIVLSPFNYSRTYPIRTVQSLTRETINYPNLENFSGFR--
8469159 KQWDYNFRFREMVMVLDLVALFPYDARIYPLETNAELTREITFDVGSYVTGQSSTL
270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500

cryla-105.pe -----GSAQGIEGSIRSPHMDILNSITIIDAHRG---EY--YNSGHIQWASP
8469159 ISWDMIPALPSPSTLENLLRPDPFFILQEIWMYSFRQNTIEYNYMGGRLLSY
330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500

cryla-105.pe VGFSGPEFTFLYTMGNAAPQIVVAOLGQ--VYRTLSSTLYRRFPNI-GINNQQLSVL
8469159 IYGS-----SFNKYS--GVLGAGEDIIP-VGQNDIYRVWVYIGRYTNSLGLNVPVTFYS
330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500

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8928019 cry1a-105.pe GYLAVTVEGYSCTHEIENNTDELAFSCVVEEYIPNNTVCNDVTVAQEEYGG
8469159 NVLRVARKKADGQVINSIDONTOITLTFN
cry1a-105.pe AVTSNRNNDNPSVAAASAEKSYTDCRRNPCEFNRGYRDTPLPVGVTKELEY
8469159 VLST
cry1a-105.pe FPEOKWIEIGETEGTIVDSVLLMEE
8469159 TPSTEQWIDMSSETGVNIESVELVLEE
cry1a-105.pep
NRAA:8928019
8928019 source="GENBANK_PROT" Pesticidal crystal protein cryIa (Pesticidal
delta-endotoxin cryIIIB(a)) (Crystalline entomocidal protoxin, 134 kDa)
protein|gi|436835|gb|AA21118.1| CryIII delta-endotoxin
SCORES Init1: 801 Initn: 2006 Opt: 1542 z-score: 1745.1 E(): 6.5e-89
>NRAA:8928019
Initn: 2006 Init1: 801 opt: 1542 z-score: 1745.1 expect(): 6.5e-89
Smith-Waterman score: 2454; 39.1% identity in 1190 aa overlap
(18-1174:59-1166)
cry1a-105.pe
8928019
cry1a-105.pe SEFV-PCAGFVLGVLDIIGIFGFSQWDAPLQVIEQLINORIEEFARNOAIRLEGLGNL
8928019 VPFVGVISLYTQIDILWPSKQKQSQWEIFMEQVEELINQKIAEYAEKALSELGLGN
cry1a-105.pe YQIYAESFREWADPTNP-ALREEMRIQFNDMNSALTATPLFAVQNYQVPLSVVQAA
8928019 YQLVLTALBEWKENPNSRALRD-VNRNFELDSLTQYMPSPFRVTNFVFPFVLTMAA
cry1a-105.pe NLHSLVRDVSFGQWGFDAATINSYNDLFLIGNVTDHAWYNTGLERVWGDSDRD
8928019 NLHLLRDASIFGEWGLSTSTINNYNRQMKLTAEYSDHCVRWYETGLAKLGSAAQ
cry1a-105.pe WIRYNOFRRELTIVLDIVSLFPNVDSRTPIRTVSOLTRELYNPV-LENFQSGPR
8928019 WIDNQFRRELTIVLDIVSLFVSNYDRTYPLATTAQLTREYVDLGAVDVFN1-GSWY
cry1a-105.pe GSAQGI-EGSIRSPHLMILANSITYTD-AHRGEYVSGHQMVASPVFSGPE

8928019 DKAPFSIEKAIIRPHVFDYITGLTVTKRSTSDRYMRWAGHOISYKHIGTSST-
cry1a-105.pe FTFFPLVGTMGNAAPQORIVAQLGQGVYRTLSSTL-
8928019 FT-QHYGTQNLQSTNF-DFNYDIYKTLNGAVGLDIIVPGYTYTF-FGMPETEFTMV
cry1a-105.pe DGEFAYGTSSNLPSAVYKRSKGTVDLSDEIPQNNVPPRQGSFHSLSHVMSFRGFSNS
8928019 NOLNTRKTLTKPKASXDIIDRTROSELELPETSGQPNYESYSHLGHITFI-YSSS
cry1a-105.pe SVSIRAPMFSWIRHSEFNIIASDSITQIPLVKATLQSGTTVVRGPGFTGDLRLRT
8928019 TSTYV-PVFSWTRHSADLTNTVKSGETIQIPGKSTIGRTNIYIKRGYTGDLVALT
cry1a-105.pe SG-GPEAYTIVNINGQLPQRYRARIYASTNLIYVTVAG-ERIFAGQFNKMTDGD--
8928019 DRIGSCFOMIFPESQ--RFRIRIYAS--NETSYISLYGLNQSGTLKFNQYTSKNEN
cry1a-105.pe PLTFQSFSTAINATFPPMSQS--SFTVGADTFSSGNEVYIDRFELIPIVATLEAYNL
8928019 SLTNDPKYIEYPRVISVSNNSIQLSIGIQT--NTNLFILDRIFIPVDTEYAEIDL
cry1a-105.pe ERQKAVNLSISNOLGKLTNTVDYHDOVSNLVLSDEFCLDEKRELSKVKHAKRL
8928019 EAKKAVNLSISNOLGKLTNTVDYHDOVSNLVLSDEFCLDEKRELSKVKHAKRL
cry1a-105.pe SERNLLQNDQFQIN--GENVSTGIEVTEGSAVFKGRYLPLPCAREIDITYPTYL
8928019 SEARNLLQNDQFQIN--GENVSTGIEVTEGSAVFKGRYLPLPCAREIDITYPTYL
cry1a-105.pe YOKIDESKLAKTATQIRGTEUSODLES--RWAKHETVSTGSLWPLSAQSPGK
8928019 YQKVEEGVLPVTRVLRGFGVSGSGLESYTRHNTNINYNKVPD--DLSP--DVPPVNN
cry1a-105.pe CGEENRCAPHELNWPLDSCRCDEKCAHSHFS--ADINGCTDNLPLCWVIFKTKO
8928019 DGRINRCSEKYVNSLEVENRSGE-----AHEFSIPIDTSELNENAGWYKRTIDP
cry1a-105.pe DGHARLGNLEEFKPLVGEALARKAEKKWADKREKLEWETIVIVKEAESVLTAVN
8928019 EGYATLGNLEVEGFGSLGDALERLOKEQOQKIQWTRRETDYRYMASKQAVDNYAS
cry1a-105.pe SQYQLOADNTNIAHIAADKRVHSIRAYLPELSVTPGVNVAIFELEGRIFTAFSLDYA

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8928019 YDQQLNPNVEITDLTAAQDLIOSIPYVYENFPEIPGMNYTFKTELDRLOQAWGLYDQ
960 970 980 990 1000 1010
cry1a-105.pe RNVKNGDFNGLSCWVKGHVDVEEQNNQSRVLLVPEWEAEVQSVRVCPRGVLRAVT
980 990 1000 1010 1020 1030
8928019 RNAIPNGDYRNELSNWNTTSGVNVQ-QIHNTSLVLPWNNEQVSKFTQPNQVRVLRVT
1020 1030 1040 1050 1060 1070
cry1a-105.pe AYKEGEGECVTIHEIENNTDELKFCNCVEEIIYNNVTNCNDYTVNQEEYGGAYTSNR
1040 1050 1060 1070 1080 1090
8928019 ARKEGVNGYVSIIRDGNQSEITLTFSA-----SYDITNGM-YDTQASNTN-
1080 1090 1100 1110
cry1a-105.pe GYNEAPSVDYASVYEKSYTDGRENCFENRGYDYLPLVGVTKELEYFFETDKV
1100 1110 1120 1130 1140 1150
8928019 GYNTN-----SYMIK-----PA-ISRTVDISSV---Y-----NQM
1120 1130 1140
cry1a-105.pe WIEIGETGTFIVDSVELLMEE
1160 1170
8928019 WIEISETGTFVIESVELVDVE
1150 1160
cry1a-105.pep
SW:8928019
8928019 description="PESTICIDIAL CRYSTAL PROTEIN CRY8BA (INSECTICIDIAL
DELTA-ENDOTOXIN CRYIIIB(A)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (134 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar kumamotoensis"
source="swissprot_prot" version="NA type="PRT
SCORES Initl: 801 Initn: 2006 Opt: 1542 z-score: 1745.1 E(): 6.5e-89
>>SW:8928019
initn: 2006 initl: 801 opt: 1542 z-score: 1745.1 expect(): 6.5e-89
Smith-Waterman score: 2454; 39.1% identity in 1190 aa overlap
(18-1174:59-1166)
cry1a-105.pe MDNNPINECIPYNCISNPEVEVLGGERIFGTPTDIDISLSITQFL
10 20 30 40
8928019 FANEPTNALQMDYKDYLMKAGNVEYFGSPVEFLSEQDAVAAA---IDIVGKLLTGLG
30 40 50 60 70 80
cry1a-105.pe SEFV-PGAGFVLGVDIIMIGIFGSPQWDALVQIEQLINRIEFAFNQAISRLGLSNL
50 60 70 80 90 100
8928019 VPFVGPIVSLYQIDILMPFSQKQSQWEIFMEQVEELINGKIAEVARNAKALSELEGLNN
90 100 110 120 130 140
cry1a-105.pe YQIYAESEFWEADPTNP-ALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYQAA
110 120 130 140 150 160
8928019 YQYLTLAEWEKENPNGSRALRD-VRNRFELDSLFTQYMPFSRVNTVEVFLTVYTMAA
150 160 170 180 190 200
cry1a-105.pe NHHLSVLRDVSFGQWGFDAATINSRYNDLTRLIGNYTHAVRWNTGLERVGPSRD
170 180 190 200 210 220
8928019 NHHLLLRDASIFGEENGWLGSTSTINNYNRQMKLTAEYSDHCVKVYETGLAKGSSAKQ
210 220 230 240 250 260
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cry1a-105.pe WIRYNOFRRELTTLVDIVSLFNPYDSRTYPIRTVSQLTREITNPV---LENDFGSGFR
230 240 250 260 270 280
8928019 WIDYNOFRREMTLVLDVVALFNSYRTYPLATTAQLTREVTDELGAVDVFNIT-GSWY
270 280 290 300 310 320
cry1a-105.pe GSAQGI-----EGSIRSHLMILNISIITYD-----AHRGEYWSGHQIMASPVGFGSGPE
290 300 310 320 330
8928019 DKAPSEIEKAARPPHVFEDYITGLTVTKRSFTSDRYMRWAGHQISYKHIGTST-
330 340 350 360 370 380
cry1a-105.pe FTPLXGTMGNAAPQQRIVAQLGQGYRTLSSTL-----YRRFNGIGNQOLSVL
340 350 360 370 380
8928019 FT-QMIGTGNQLQSTSNF-DFTNYDIYKTLNSGAVLDDIVVPGYTYTF-FGMPETEFTFMV
390 400 410 420 430
cry1a-105.pe DGTEFAYGTSSNLPSAVVRKSGTVDSLDEIIPPONNVPPRQGFSHLSHVMSRSGFSNS
390 400 410 420 430 440
8928019 NQLNNRTKTLTYKPAKSDIIDRTDSELELPETSGQPNYESYSHRLGHITFI---YSSS
440 450 460 470 480 490
cry1a-105.pe SVSIIRAPMFSWIHRSAEFNIIASDSITQIPLKAHTLQSGTTVVVRGPGFTGGDILRRT
450 460 470 480 490 500
8928019 TSTYV--PVFSWTHRSADLTNTVKSGEITQIPGKKSSTIGRTNYIIGRGYTGGDLVALT
500 510 520 530 540 550
cry1a-105.pe SG-GFPAIVYINGQLPQRYRARIRYASTNLIYITVAG-ERIFAGQFNKMTDGD--
510 520 530 540 550
8928019 DRIGSCFQMIFFESQ---RFRIRIRYAS--NETSYISLYGLNQSGTLKFNQTVSNKNEN
560 570 580 590 600
cry1a-105.pe PLTFQSFYATINTAFTFPMQS--SFTVGADTFSSGNEVYIDRFELIPIVATLAEVNL
560 570 580 590 600 610
8928019 DLTYNDFYIEYPRVISVNASSNIQRLSIGIQT--NTNLFILDRIFIEFIPVDETAEATDL
610 620 630 640 650 660
cry1a-105.pe ERAKAVNALFTSNQGLKNTVTDHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRL
620 630 640 650 660 670
8928019 EAAKAVNALFTNTKD-GLOPGVTDYEVNQANLVECLSDDLYPNEKRLLLFADVREAKRL
670 680 690 700 710 720
cry1a-105.pe SDERNLQDSNFKDINRQPERGWSGTGITOGGDDVFKENYVTLSTGTFD---ECYTYL
680 690 700 710 720 730
8928019 SEARNLLQDPDFQFIN--GENGWASTGIEVIEGDVAFKGRYLRLPGAREIDTETPTYL
730 740 750 760 770 780
cry1a-105.pe YOKIDESKLAFTYQLRGYIEDSDOLIEYSIRYNNAKHETVNVPGTGLWPLLSAQSPIGK
740 750 760 770 780 790
8928019 YQKVSEGLVKPYTRYLRGFGVSSQGLIEYITRHTNRIVKNVFD--DLLP--DVPPVNN
790 800 810 820 830 840
cry1a-105.pe CCEPNRCAPHLEWNPDDCSCDGEKCAHHSHHFDLDIVGCTDLMEDLVGVWVIFKIKTQ
800 810 820 830 840 850
8928019 DGRINRCSEQYVNSRLVENRSGE-----AHEEFSIPIDTGELDYNENAGIWWGVFKITDP
850 860 870 880 890
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