

Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-04
MSL No. 20351
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46409859  SODLEIYLIRYNAKHETLDVPGTSESVMVSLVESPIGRGEPNR
            810   820   830   840
cry1a-105.pe  GEKCAHSHHFSLDIDVGCITDNLNEDLGWVIFIKIKTQDGHARLGNLFLEKPLVGEALA
            820   830   840   850   860   870
cry1a-105.pep
NRAA:40356
40356 source="GENBANK_PROT" unnamed protein product [Bacillus thuringiensis]

SCORES   Init1: 1300   Initn: 2802   Opt: 1489   z-score: 1687.2 E(): 1.1e-85
>>NRAA:40356
Initn: 2802   init1: 1300   opt: 1489   z-score: 1687.2   expect(): 1.1e-85
Smith-Waterman score: 3115;   58.6% identity in 838 aa overlap
(1-815:1-823)

cry1a-105.pe  MDNPNINCEIPVCLSNPEVEVLGGERIETGYTIDISLTOFLSEFVPGAGFVLGL
            10    20    30    40    50
40356  MEEN-NQNCIPIYCNLSNPEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGFLVGL
            10    20    30    40    50

cry1a-105.pe  VDIWIFGPSQMDAFLVQIEQLINQRIEFAFARNOAISRLGLSNLVQIYAESFREWAD
            70    80    90    100   110   120
40356  IDFWGIVGPSQMDAFLVQIEQLINQRIEFAFARNOAISRLGLSNLVQIYAESFREWAD
            60    70    80    90    100   110

cry1a-105.pe  PTPALREEMRIQFNDMSALTTAIPFAVQNYQVPLLSVYQAAHLNVLRSVFGQ
            130   140   150   160   170   180
40356  PNPATRIKVIDRFLDGLDERIDFSPRISGEFVPLLSVYQAAHLNVLRSVFGQ
            120   130   140   150   160   170

cry1a-105.pe  RWGFOAATINSKRYNDLTRLIGNYTDHAYVNTGLERWGPDSRDWIRNQPRRLITLV
            190   200   210   220   230   240
40356  RWGLTTINVENYNRLIRHIDEYADHCANTYRGLNLPKSTYQDMITNRLRDLTLV
            180   190   200   210   220   230

cry1a-105.pe  LDIVSLFPNYSRTPIRTVSQLTREIXYNVLENFDGSPRGSQAQ-----GIEGS-IRSP
            250   260   270   280
40356  LDIAAFFNYDNRRYPIQPVGQLTREVYTDPLI-NFNPQLQSVAQLPTFNWESSALRNP
            240   250   260   270   280   290

cry1a-105.pe  HLMDLNLSITITYDAHR-GE-VYWSGHQIMASPVGSGPEFTFPFLYMGNAAPQQRIVA
            300   310   320   330   340   350
40356  HLFDLNLLITFDWFSVGRNFWGGRHVISLIG--GNNITSPYIGREANQEPFRSFT-
            300   310   320   330   340   350

cry1a-105.pe  QLGQGVYRVLTS-STLYRRPFGNIGNNQLSVLDCGTEFAYGTSNLPSPAYVYKSTVDSLD
            360   370   380   390   400   410
40356  -FNGVPFRLISITPL--RLIQPCORHFNLRGGEGVEFSTPTN--SFTYRGRGTVDLSLT
            360   370   380   390   400   410

cry1a-105.pe  EIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNGSVSIIRAPMFSWIFHSAEFNNIATSDS
            420   430   440   450   460   470
40356  ELPPEDNSVPPREGYSHRLCHATFVQRSGTPTLTGVV---FSWTHRSALITNTIDPFR
            420   430   440   450   460
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cry1a-105.pe  ITQIPLVKAHTLOSQTTVVRGPGFTGGDILRRTSQGPFFAYTIUNINGQLPQRARIRYA
            480   490   500   510   520   530
40356  INQIPLVKGFRVWGTSITGPGFTGGDILRRNTFGFVSQVNSINSPITQRYRLFRFYA
            470   480   490   500   510   520

cry1a-105.pe  STTNLRIVV-TVAGERIFAGQ-----FNKMTDGTDLPTFOSFVSATINTAFTFPMSSQS
            540   550   560   570   580
40356  SSRDARVILVTGAAGTGVGGVSVNMPLQKTMEIGENLTSTRTYTFDFSNPFSFRANPDI
            530   540   550   560   570   580

cry1a-105.pe  FTV-----GATFSSGNEVYIDRFELIPVTATLEAEYNLEAQAQVNAALFTSTNQLGLK
            590   600   610   620   630
40356  IGISEQPLFGAGISSG-ELYIDKIEIILADATFEAESDLERAQAQVNAALFTSSNQIGLK
            590   600   610   620   630   640

cry1a-105.pe  TNVTDVHIQVSNLVLYLSDFCLDEKRELSKVKHAKLSDERNLILODSNFXDINRQPE
            640   650   660   670   680   690
40356  TDVTDVHIQVSNLVLYLSDFCLDEKRELSKVKHAKLSDERNLILODSNFXDINRQPD
            650   660   670   680   690   700

cry1a-105.pe  RGWGGSTIGTIQGGDDVFKNYVYTLSTGTFDECYTYLYQKIDESKLAFTRYQLRGYIED
            700   710   720   730   740   750
40356  RGWRGSTDITIQGGDDVFKNYVYTLPGTVDECYTYLYQKIDESKLAFTRYQLRGYIED
            710   720   730   740   750   760

cry1a-105.pe  SQLEIYSIRYNAKHETVNVPGTSLWPLSAQSPIGKGFENRCAPHEWNPDLDCSCD
            760   770   780   790   800   810
40356  SQLEIYLITAYNAKHEIVNVPGTSLWPLSAQSPIGKGFENRCAPHEWNPDLDCSC
            770   780   790   800   810   820

cry1a-105.pe  GEKCAHSHHFSLDIDVGCITDNLNEDLGWVWIFIKIKTQDGHARLGNLFLEKPLVGEALA
            820   830   840   850   860   870
cry1a-105.pep
SW:8928040

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

SCORES   Init1: 519   Initn: 1580   Opt: 1478   z-score: 1672.7 E(): 7e-85
>>SW:8928040
Initn: 1580   init1: 519   opt: 1478   z-score: 1672.7   expect(): 7e-85
Smith-Waterman score: 1884;   34.3% identity in 1204 aa overlap
(18-117:23-1109)

cry1a-105.pe  MDNPNINCEIPVCLSNPEVEVLGGERIETGYTIDISLTOFLSEFV-PGA
            10    20    30    40    50
8928040  MAQTYIKIGVQSTVENSEISIFNFPEVDSDDTVAVVSAGIVV-VGTLITAF--ASFVNPVG
            10    20    30    40    50

cry1a-105.pe  GFV-IG-LVDIIMGI--FGPSQ-WDAFLVQIEQLINQRIEFAFARNOAISRLGLSNLYQI
            60    70    80    90   100
8928040  VLISFGTLAPLWPDPEEDPKKISQFMKHGEDLLNQITISTAVKEIALAHNGFDVLTY
            60    70    80    90   100
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cryla-105.pe	110	120	130	140	150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560	1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680	1690	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800	1810	1820	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920	1930	1940	1950	1960	1970	1980	1990	2000	2010	2020	2030	2040	2050	2060	2070	2080	2090	2100	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200	2210	2220	2230	2240	2250	2260	2270	2280	2290	2300	2310	2320	2330	2340	2350	2360	2370	2380	2390	2400	2410	2420	2430	2440	2450	2460	2470	2480	2490	2500	2510	2520	2530	2540	2550	2560	2570	2580	2590	2600	2610	2620	2630	2640	2650	2660	2670	2680	2690	2700	2710	2720	2730	2740	2750	2760	2770	2780	2790	2800	2810	2820	2830	2840	2850	2860	2870	2880	2890	2900	2910	2920	2930	2940	2950	2960	2970	2980	2990	3000	3010	3020	3030	3040	3050	3060	3070	3080	3090	3100	3110	3120	3130	3140	3150	3160	3170	3180	3190	3200	3210	3220	3230	3240	3250	3260	3270	3280	3290	3300	3310	3320	3330	3340	3350	3360	3370	3380	3390	3400	3410	3420	3430	3440	3450	3460	3470	3480	3490	3500	3510	3520	3530	3540	3550	3560	3570	3580	3590	3600	3610	3620	3630	3640	3650	3660	3670	3680	3690	3700	3710	3720	3730	3740	3750	3760	3770	3780	3790	3800	3810	3820	3830	3840	3850	3860	3870	3880	3890	3900	3910	3920	3930	3940	3950	3960	3970	3980	3990	4000	4010	4020	4030	4040	4050	4060	4070	4080	4090	4100	4110	4120	4130	4140	4150	4160	4170	4180	4190	4200	4210	4220	4230	4240	4250	4260	4270	4280	4290	4300	4310	4320	4330	4340	4350	4360	4370	4380	4390	4400	4410	4420	4430	4440	4450	4460	4470	4480	4490	4500	4510	4520	4530	4540	4550	4560	4570	4580	4590	4600	4610	4620	4630	4640	4650	4660	4670	4680	4690	4700	4710	4720	4730
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CRYIA-105.pe KAFTRQLRGYIEDSQDLEYISIRYNAKHETVNVPGTSGIMPLSAQSPIGK-----
8928040 KPTRYQLRGFYVESQDLDFVRGATDIVNNVPG--DLEILSYASAPINCPCEIEITRLD
740 750 760 770 780 790

CRYIA-105.pe ---GENRCAPHLEWFDLDCSCRGECAHHSHRSLOIDVGCTDMEDLGWWVFIFIK
8928040 TTGCALDRCKQSNNVNSAADR---PDQNGDPHAFSFHDITGDNNRNLIWIIFKLA
800 810 820 830 840

CRYIA-105.pe TQDGHARLGNLFEEELPVGELAVRVRAEKKW-RDKREKLEMETIVVYKEAKESVDAL
8928040 TPQGYATFNGLIELFLPSLGEALAQVORKEOKWKNTTKKE-EAAKLVAARAAQTIIINOL
850 860 870 880 890 900 910

CRYIA-105.pe FVNSQVDQLQADTNMIHAADKR VHSIREAYPELSVIPGVNAAIFEELGRIFTAFSL
8928040 FADSOGTKLRDETFENLSADKLVIKIRDYSEVLSPGLNYDLFWELNLRIQNAILD
910 920 930 940 950 960

CRYIA-105.pe YDARNVKINGDFNNGLSKNVKGHVDEEQNNORSVLVPVEAEVSQEVPCVCGRYILL
8928040 YARNVTIVNGEFRGLANWNASSTEVF-QIQAHPCWSYLGNAQAQVALNKVPKHGGYVL
940 960 980 990 1000 1010 1020 1030

CRYIA-105.pe RVTAKEKNGESCYYTHEENNTDELKFNCVVEEIYPNNVTCTDNVQEEYGAVTS
8928040 RVTAKAGIGNGGTTLDGANHIDLTFSSC-----D-----SGFTTS
1030 1040 1050 -----D-----SGFTTS
1060

CRYIA-105.pe RRGNEHPSPVDADYVAVFEERS-TDSRENPCFNRGYRDYTLPLVGYVTKELSYFFET
8928040 SN-----ELAN-----VVTKLRFIPDT
1070 -----VVTKLRFIPDT
1080

CRYIA-105.pe DKVWEIGETEGTFIVDSVELLMEE
8928040 DOIRIEIGETRSTFYVESVDLLMRED
1090 -----
1100

CRYIA-105.pep
NR001:4574730
source="GENBANK PROT" Cry28Aa delta-endotoxin [Bacillus thuringiensis]
serovar finitimus[gi|8928040|sp|Q9X682|C28AA BATCF Pestinidal crystal protein]
ry28Aa [Insecticidal delta-endotoxin CryXXVIII(a)] (Crystalline entomoxanthase
protoxin) (126 kDa crystal protein)

SCORES Initl: 519 Initn: 1580 Opt: 1478 Z-score: 1672.7 E(): 7e-85
->NR001:4574730
initn: 1580 initl: 519 opt: 1478 Z-score: 1672.7 expect(): 7e-85
Smith-Waterman score: 1884; 34.3% identity in 1204 aa overlap
(18-1177:23-1109)

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cryIIa-105.psep
 NRRAA:4574730
 4574730 source="GENBANK PROT" Cry282aa delta-endotoxin [Bacillus thuringiensis
 serovar finitimus]gi|8928040|sp|09X682|C28AA BACTF Pesticidal crystal protein
 Cry282Aa (insecticidal delta-endotoxin CryXXVIIIa(a) (Crystalline entomotoxin
 protoxin) (126 kDa crystal protein)
 SCORES Init1: 519 Initn: 1580 Opt: 1478 z-score: 1672.7 E(): 7e-85
 >NRRAA.4574730
 initn: 1580 init1: 519 opt: 1478 Z-score: 1672.7 expect(): 7e-85
 Smith-Waterman score: 1884; 34.3% identity in 1204 aa overlap
 (18-1177:23-1109)

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cry1a-105.pe MDNPNINECIPNCLSNPEVEVLGGERIETGYTIDISLSLTOLLSFPV-PGA 10 20 30 40 50
4574730 MAQTYKIGVQSTEVNSESIFNFPEVSDTVAVVSGIIV-VGITLTAF--ASFVNPV 10 20 30 40 50

cry1a-105.pe GFV-LG-LVDIWI--FGPSQ-WDAFLVQIEQLINRIEFAFARNAQISRLGLSNLYQI 60 70 80 90 100
4574730 VLISFGTLAPVLPDPPEDFPKIWSQFMKGEDLLNQTISTAKEALAHNGFDVITY 60 70 80 90 100

cry1a-105.pe YAESFREWADPTNPALREEMRIQDNMSALTATPLFAVQNYQVPLSYVQAAHL 110 120 130 140 150 160
4574730 YERAFNDKRNPSANTARL-VSORFENAHFNFSNMPQLQPTDYDTLLSCYTEAAHL 110 120 130 140 150 160

cry1a-105.pe SVLRDVSFVGORGFDA-----ATINSRYNDLTRLIGNYTDHVRWNTGLRWGPDFS 170 180 190 200 210 220
4574730 NLLHQGVQFADWADQPHSPMLKSSGYDELLVIERKIYNYCTKYHKGLNHLKESEK 170 180 190 200 210 220

cry1a-105.pe EDWIRYQFRELTLVLDIVSLFENYDSRTYPIRTVSQTSQREIYTNFVLENFDGSRGS 230 240 250 260 270 280
4574730 ITWDAYTYREMTLIVLDVATFPDIRRFRGVELELTREVYTS--LDHLT----- 230 240 250 260 270 280

cry1a-105.pe AQGIEGSRPHMLDILMSITIIYTD--HRGEYWSGHQIMASPGVFGSGPFTPLYGTMG 290 300 310 320 330 340
4574730 -----RPPGLFTWLSDELIESVAEGDYL-SG--IRESKY-YTGNOF-FTMKNYIG 290 300 310 320 330

cry1a-105.pe NAAPQQRIVAQLQGQGYRTLSSTLYRRPFN--IGINNQOLSVLGDTFAFGTSSNLPNAV 350 360 370 380 390 400
4574730 NTNRLSKQITLPLPGEFMTLSI--NRPFQTIAGIN-KLYSLIOKIYFTTFKNDNE---- 340 350 360 370 380

cry1a-105.pe YRKSQTVDSLDLIPQNNVPPROG-----FSHRLSHVSMF--RSFGSSSVIIRAPM 410 420 430 440 450
4574730 YQXNFVNQNE-POEITNYPNDYGGNSQKPKHNLHFPLIIHKLEFAEYFHSIF---A 390 400 410 420 430 440

cry1a-105.pe FSMIHRSAEFNNIIASDSITQIPLVKAHTLQSGTIVVGRGFTGGDLIRRTSGGPFAYTI 460 470 480 490 500 510
4574730 LGWTHSVNSQNLISESVTQIPLVKAHEV-TNNSVIRKPGFTGGDLIELDKCSIKCKA 450 460 470 480 490 500

cry1a-105.pe VNINGQLPQVRARIRYASTNRIYTV---AG---ERIFAGQFNKMTDGTDLFTQS 520 530 540 550 560
4574730 SSL-----KKVAISLFYAANNAIVSIDVGSAGVLLQPTFRKGNNTTQD--LNYKD 510 520 530 540 550

cry1a-105.pe FSVATINTAFTPMSQSFT--VGADTFSSGNEVIDRFLIPVTATLEAEYNLERACKA 570 580 590 600 610
4574730 FQHTLLVDIEPESESIHILKREDDVEEGVILLIDKLEFKPIDENYTNENWLEKAKKA 560 570 580 590 600 610

cry1a-105.pe VNALFTSTNQLGKLTNTVDYHIDQVSNLVTVLSDEFCLDEKRELSEKVKHAKRUSDERNL 630 640 650 660 670 680
4574730 VNVLFINATN-ALAKMDVTDYHIDQVANLVCEISDDLYAKKEIKFTFCIKFAKQLSOARNL 620 630 640 650 660 670

cry1a-105.pe LQDSNFKDINRQPERGSGSTGITIQGGDDVFKENYVTLSTGTCDECYPTLYOKIDESKL 690 700 710 720 730 740
4574730 LSDPNFNNLN--AENSNTANTGVITIEGDPYKGRATQLSAAEDENFTPLYOKIDESLL 680 690 700 710 720 730

cry1a-105.pe KAPTXYOLRGVIEDSQDLEYIRYNAKHTVNVPGTGLWPLSAGSPIGKC----- 750 760 770 780 790
4574730 KPYTRYQLRGVEGSDLELDLYRYGATDIVMNVPG--DLEILSYSAFINPCEETRLD 740 750 760 770 780 790

cry1a-105.pe ---GEPNRCAPHLEWNPDLDCSRDEKCAHSHHESLDIDVCTDMLDGLVWVIFKIK 800 810 820 830 840 850
4574730 TTCGALDRCKGNSVNSAADVR---PDQVNGDHPAFSFDITGTTDNNRNLGIWIFKIA 800 810 820 830 840 850

cry1a-105.pe TODGHARLNLEFLEEKPLVGALARKAEKKW-RDKREKLEWETNIVYKEAKESVDAL 860 870 880 890 900 910
4574730 TPDGYATFGNLELLELGLSGEALAQVORKEQKGNKNTTOKEE-EAAKLVAAYAKQTINQL 850 860 870 880 890 900

cry1a-105.pe FVNSQYDQLQADNTIAMTHAADKRVHSIREAYLPESVIPGVNAAIFEELEGRIFTAFSL 920 930 940 950 960 970
4574730 FADSGQTKLRFDFEFSNLISADKLVIKYIRDVSEVLSVPLGNYDLFMELENRIQNAIDL 910 920 930 940 950 960

cry1a-105.pe YDARNVTKNGDNFNGLSVNVKGVHDVVECONNORSVLVVPWEAEVQEVRCPCGYIL 980 990 1000 1010 1020 1030
4574730 YDARNVTVNGEFRNGLANWMASSNTEVR-QIOAHFCWYSLGWAQVAQSLNVKPDHGYVL 970 980 990 1000 1010 1020

cry1a-105.pe RVTRAYEGYEGECVTIHEIENNTDELKFSNCVVEEIIYFNNTVTCNDYVNOEEYGAITS 1040 1050 1060 1070 1080 1090
4574730 RVTAKEGIGNGYVITLDCANHIDTLTFSSC-----D-----SGFTTS 1030 1040 1050 1060 1070 1080

cry1a-105.pe RNRGYNEAFVPADYASVYEKSYTGRENCFENRGIRDYTPLPVGVYVTKLEYFPET 1100 1110 1120 1130 1140 1150
4574730 SN-----ELAA-----YVTKLEIFPDT 1090 1100 1110 1120 1130 1140 1150

cry1a-105.pe DKVWIEIGETGTFIVDSVEILLMEE 1160 1170
4574730 DQIRIEIGETSTRFTFVSVDLIRMED 1090 1100 1110

cry1a-105.pep
NRAA:61661422

61661422 source="GENBANK_PROT" Cry7 delta-endotoxin [Bacillus thuringiensis]

SCORES Init1: 621 Initn: 1569 Opt: 1472 z-score: 1671.3 E(): 8.5e-85
 >NRAA: 81667422
 Initn: 1569 Init1: 621 Opt: 1472 z-score: 1671.3 expect(): 8.5e-85
 1673 1757
 50.0% identity in 558 aa overlap

61561422
 600 610 620 630 640 650
 cryla-105.pe SGNEVYIDRFLIPUTATLEKEYNLAQAQAVNALPSTNOGLKINVTVDYHIDQVSNLV
 61561422
 600 610 620 630 640 650
 cryla-105.pe SGNEVYIDRFLIPUTATLEKEYNLAQAQAVNALPSTNOGLKINVTVDYHIDQVSNLV

cryla-105.pe TYLSDEFCLDEKRELSEKVKHAKRLSDERNILLODSNKDZARQPERGNGSGTIGTIOGGD

6161641422

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780      790      800      810      820
pe ETUWPGTGSUWPLUSASPGKCGPNRCAP--HLEWNPDLDCS-RDGEKCAHSHRPS
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
ETFDV--SNMLLP--DISPVNACGPNRCVAVOYLDENPRUCSSVQDG--ILSDSHGFS
150      160      170      180      190      200

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ccryla-105.pe LDIDVGCTLDNEDLGWVWLFKIKTODGCHARGLNLEFLEEPLVGBALARYKRAEKKWRDK  
|::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|  
LNINTGSDFNESVGIIWLVFKISTEGYAKFGNLVENIENGPGVIGBALARYKRQETKWRNQ
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890      900      910      920      930      940
REKLEWEINIVYKEAVESVDALFVNSQVDQADNTNAMIHAARXRVHSREAYLPESV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
L7QLTETQAIYTRAKOALDNLFANAQDSHLKTTGTTFAIYAAKRVQSVREAYSWLSV
270      280      290      300      310      320

```

[illegible]

```

1010      1020      1030      1040      1050      1060
ryla-105.pe vPEAEVSEVRCFGRGYILRTAKEGYGGCVTHEIENNTDELFSNCVSEETYP
11661422      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
LSNRDAQVLOCLKYDRGYILRTAKEGYGGCVYTHDEGNTDOLTFGAC--EEDA
390      400      410      420      430      440

```

```

1070
1080
1090
1100
1110
1120
rryla-105.pe NNTVTCNDYTVNQEEGAYTSRRNGYNAPSVPADYASVVEKSYTDGRNPCEFRNG
: | |
SN-----AFIS-----
1661422
-----

```

```

1130      YRDYTPGVXVTKLEFFPPTDKWIVBIGETEGTVDSVELLMEE       1140
1131      ryia-105.pe |::|::|::|::|::|::|::|::|::|::|::|::|::|   1160
1132      -----TCGYITKELEFPFDPTEKRVIBIGETEGTVQVESVFLMMEELC    1170
1133      11661422          450      470      480

```

cry1a-105.pap
 NR044:62433238
 62433238 source="GENBANK_PROT" Cryhmel [Paenibacillus popilliae]
 SCORES Init1: 624 Initn: 1761 Opt: 1433 z-score: 1620.4 E(): 5.8e-82
 >NR044:62433238
 initn: 1761 init1: 624 opt: 1433 z-score: 1620.4 expect(): 5.8e-82
 Smith-Waterman score: 2124; 34.8% identity in 1332 aa overlap
 (4-1177:42-1340)

```

cry1a-105.pe      MDNPN-INICYPNCLSNPEVLGERI-ET      10 20 30
62433238          SYQHGNEMOIIQSSNSLLSPKYPATDPNVIAGRSNNWLDTCVGVGDGTSRSP      20 30 40 50 60 70

```

62433238
DAVAVGRISHTIFRLG--VPYSAGEQLSFLLDTLW-LEGNTQWELMRHAEALINE
cryia-105.pe GYTPIDISLSITQF-LLSEFYP---GAGFVLGLVDIIWGIFGPSOWDAFLVQIEQLNQ

~~CYLA-005-06 RIEFARNQAIISREGLSNLYQIYAESFREWEADPTNPALREEMRQFNMDNSALTATP
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
QPDVYRTKALAELTDLGNINLNYTAAFEDWKNRPSSQEVTRTVDRFNILDGLFEAYLP~~

6243238 SFAYQVFPPLSLSYAVANINHLVLDRDSSIHGLDUGLSFSTVDNNYNNRQNSATYAIH
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
LFVAQNQYQPSLSPYYQAOANHLHSVLDRDSVFQGRGFFDAATINSRYNDLTRILGNYYTH

ccryla-105.pe AWTNYGLREVCPYBRAWIRYNOFRELTLVLDVSLFPNVDSTYPIRVLSQLTRE
219 220 230 240 250 260
CTTWYGLVNOQSSDSWAWYNFRFRTLVLDICALFSDYDVSYPIORIGELVIRG

cryla-105.pe IYTPVLENFDFSGSNQ-----IIS-SIPHLMDINSITIYDA---HRGEYYW
|||:::||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
IYTDPVFSTGTSYSLWSQAPSPSEINTEINTAIFPSFTFANYANTTCGLYLELSKNDWF

[illegible]

```

380      390      400      410      420      430      440      450
cryla-105.pe INQQLSVLDGTE-FAYGTSSNLVSAYRKSGTVSLDLEIPQNWNPPQQSFHSAWV
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
ISTSEFWSLGVARYQNSPOFAASITR-----QLGEVNSAVPSALDRSHLSYAI
380      400      420      440      460      470

```

```

SMRSGFNSVSVIIRAPMFSWHRSAFNFIASDSITQIPLKAHTLOSQTTVRGPG
      :|||:         :|||:         :|||:         :|||:         :|||:
T----AFARSVGTIL--VHEWTSTTVSRNNRIEDPKITQIPAKVSHITINCOVWSGTF

```


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```

cry1a-105.pe 500 490 500 510 520 530
|||||FTGGDILRTSGGPAYTUNINGQLPQRYRARIYSTNNLRIYVYAGERIYFAGQFNK
62433238 540 550 560 570 580 590
|||||FTGGNWLPSDNGSFRLLTITSSSQ---SYRIRIRYASATFFYLDIRIGDTSNTFAVTPT

cry1a-105.pe 560 570 580 590 600 610
|||||TMDTGDP-LTFQSFVSATINTAFTPFMSQSFVTGADTFSSGN-EVVIDREELIPVATL
62433238 590 600 610 620 630 640
|||||TLSSGSQTPVYSEFGFINIPYFTFTAPTESRYTFDFMFYSIGSANVLIDRIEFVPIEGSL

cry1a-105.pe 620 630 640 650 660
|||||---EAEYNLEAKAVNALFTSTNGLKTNVTDYHIDQVSNLTVLTSDEFCLDEKRELS
62433238 650 660 670 680 690 700
|||||FEYETKQOLEKARKAVNHLFDGSKALKEDTIDYEIDQAAVWDCISDE-CGHEKMILL

cry1a-105.pe 670 680 690 700 710 720
|||||EVKHAKELSDERNLLQDSNFKDINRQPER--GNGSGTITIQGGDDVFKENYVLTSGTF
62433238 710 720 730 740 750 760
|||||DEVKVAQLSQARNLLNGNFDLLPALERENPKTSPNVTIRRDNP:IFKGYLSWAGAN

cry1a-105.pe 730 740 750 760 770 780
|||||D-----ECPTYLYQKIDESKLAFTRYQLRGLYEDSODLEIYSIRYNKHETV-NVPGT
62433238 770 780 790 800 810 820
|||||DIEATNDFTTYVYQKIDEAKLPYTRYKYRGVFGSSKALELLVTRNVEVDALLDPDN

cry1a-105.pe 790 800 810 820 830 840
|||||GSLMPLSAQSPICKGCEPNRCAPHL-----EWNPDL-----DCSC-----
62433238 830 840 850 860 870 880
|||||---LP---HAPIVCGEFDRCCKPYSPYPLLPCECNPEFINQMOPSCSHHTQMVDYNNMNS

cry1a-105.pe 820 830 840 850 860 870
|||||TSTTMNPTLTPEIASSQSFGFKHRKC-HQAQHFEDHDTGIDLVEDLGLWVIFKICAT
62433238 890 900 910 920 930 940
|||||-----RDGEKCAHSHHSFSLDIDVGCTDLNEDLGVWVIFKIKTO

cry1a-105.pe 860 870 880 890 900 910
|||||DGHARLGNLEFTEEKPLVGEALARVKAERKFKREKLEWETNIVYKEAKESVDALFVN
62433238 950 960 970 980 990 1000
|||||DGYASLDLLEVEEGALGVEALELVKKREKKWRHQHCQOTKHKKYDAAKHAWALFTN

cry1a-105.pe 920 930 940 950 960 970
|||||SOYDQLQADNTIAMIHAAKKEVHSIREAYLPGLSVIPGVNAAFEELEGRIFTAFSLYDA
62433238 1010 1020 1030 1040 1050 1060
|||||TRVEKLKFTTISNLYADHLVQSPYVYNKYVPVPGMNYELYSSELNTLVQNAFYLDQ

cry1a-105.pe 980 990 1000 1010 1020 1030
|||||RNVTIKNGDFNNGISCMWVKGHVDEEONQORSVLVPEWEAEVSEQEVRCVPGHYLRVT
62433238 1070 1080 1090 1100 1110 1120
|||||RNLIKKGRESNGLMTWQAAPARVE-QEFKESVLVLPMDVANSQDLCEHNRGNYLRVT

cry1a-105.pe 1040 1050 1060 1070 1080 1090
|||||AYKEGYGEGCVTIHEIENNTDELKFSNC-VEEEIYP-----NNTVTGNDY-----TVNOEE
62433238 1070 1080 1090 1100 1110 1120
|||||ARKEDPGAGNVTFSDCNHVDKLSFTSCDIATNAVPGAQANDPAAGVAGCQGCQIDRVP
```

```

cry1a-105.pe 1120 1130 1140 1150 1160 1170
|||||cry1a-105.pe YG-----GAVTS-----RNRGY-----NEAPSVP-----ADYAS
62433238 1180 1190 1200 1210 1220 1230
|||||YGQSGYRADGVAVYEQSGHRDGVYRQSGYGTGDTGYEQSGHRADMPYQSGYGRADGVA

cry1a-105.pe 1110 1120 1130
|||||cry1a-105.pe VVEEKSY-----TDG-----RRENPCFNRG-YRDYTPLP-----
62433238 1240 1250 1260 1270 1280 1290
|||||YEQSGHREADGVYQSGYGTGDTGYDQSANQTKVHGCHTIDGLPHPHGCGCYPDVRSDG

cry1a-105.pe 1140 1150 1160 1170
|||||cry1a-105.pe --VGVTKELEYPEPTDKYWEIGETGTFIVDSVELLMEE
62433238 1300 1310 1320 1330 1340
|||||QQLAVTKSIDLPFDIDKVRIDIGETGNFRVSVELICWEX

cry1a-105.pe 1300 1310 1320 1330 1340
|||||cry1a-105.pe pep
NRAA:46409863
46409863 source="GENBANK_PROT" cry1 type crystal protein (Bacillus thuringiensis
serovar kenya)

SCORES Initl: 1143 Initn: 2719 Opt: 1429 z-score: 1619.3 E(): 6.7e-82
>NRAA:46409863
Initn: 2719 Initl: 1143 Opt: 1429 z-score: 1619.3 expect(): 6.7e-82
Smith-Waterman score: 2814; 56.8% identity in 805 aa overlap
(9-800:2-782)

cry1a-105.pe 10 20 30 40 50 60
|||||MDNNPNINECIPYCNLSNPEVEVLGGERITGTTPIDISLSTQFLSEFPVPGAGVGL
62433238 10 20 30 40 50 60
|||||MQCVPYCNLSNPEVEVLGGERITGTTPIDISLSTQFLSEFPVPGAGVGL

cry1a-105.pe 70 80 90 100 110 120
|||||VDIIWIGIFGSPQWDAFLVQIEQLINQRIEFAFNOAISRLGSLNLYQIYAESFREWEAD
62433238 70 80 90 100 110 120
|||||LDKIWALRFSMDWELFLEQLIDRIERTVPAKAIAELEGLGRSTQLYGEAFKEWKT

cry1a-105.pe 130 140 150 160 170 180
|||||PTNPALREENRIQFNDMNSALTTPILFAVQNYQVPLLSVYVQANHLVLRDVSFQO
62433238 130 140 150 160 170 180
|||||PDNTAARSRTVERFRIDAQIEANIPSRVSGFEVPLLVYVQANHLVLRDVSFQO

cry1a-105.pe 190 200 210 220 230 240
|||||RWGFDATINSRVNDLTLLIGNYTDHVRVNTGLERVWGPDSRDWIRYNQFRRELTIV
62433238 190 200 210 220 230 240
|||||RWGTTTINVDIYNQVNRIGKYSKHCVDITYTELERLGRFSIAQWIRYNQFRRELTIV

cry1a-105.pe 250 260 270 280 290
|||||LDIVSLFPNVDSRTPIPTISQLTREIYNTPVLENFDGSPRGS---AQGIESIRSPLHM
62433238 250 260 270 280 290
|||||LDIVAVFPNVDSRLPIPTISQLTREIYNTPVLENFDGSPRGS---AQGIESIRSPLHM

cry1a-105.pe 300 310 320 330 340 350
|||||DILNSITITDAHRGEYVWGHQIMASPVGFSGPFTFPLYGTMGNAAPQQRIVLAQLGGQ
```

46409863 DFNSIMSDNRHRYNGLENTAINT--EGHQRSPFLAGTIGNSAPVTVRN--GEG 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350

cry1a-105.pe VYALSTLYRPPNIGLNNQSLVAD--GTEFAY--CTSSNLPASVYRKSQTVDLSDEI 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400

46409863 IYRILSDYRSPF--L--SVLGSRGSEPPASNTTISLPSTIYRNRGTVDLSLVI 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400

cry1a-105.pe PPQNNVPPROGFSRHSLSYMSRSGFSNVAIRAPMFNINRSGAENNIASDSITQ 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460

46409863 PPQDYSVPHPRGYSHLSHVTM--DNSS--DFHWTNRKATPNTIDPSITQ 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450

cry1a-105.pe IPLVK-AHTLOSITTVRGCGFTGGLRLRTSGSPFATVINGQQLPQRYRATYAST 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520

46409863 IPAVKGAIFNS--PVITPGHTGGDIIRFNPNTQNNNT--PHSNVAVORAIRMYAAE 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500

cry1a-105.pe TNLRI-----YVTVAGERIFAGQFNKMTDGTGPTFQSFVATINTAFEPNSQSFVNG 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580

46409863 ADCILSGNVIYTGAGVTERPIKATMTGSPGLTYYSFOYADNLINLTAPIRANFASI 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560

cry1a-105.pe ADTFSSGNEVIIDRFELIPVATILEAEYNLERAQAVNALFTSNQGLKTNVTDYHIDQ 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630

46409863 RRNSQPGN--LYDRIEFIPIDIREAEHDLERAEQAVNALFTSNQGLKTNVTDYHIDQ 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620

cry1a-105.pe VSMVTLSDGFCIDKEKRELSEKVKHAKLSDERNLQDSNFKDINQROPGMGSGTGT 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690

46409863 VSNLVACLSDFCLDEKRELSEKVKHAKLSDERNLQDSNFKDINQROPGMGSGTGT 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670

cry1a-105.pe IOGGDDVFKENTVTLSTGTFDECYPTLYQKIDESKLKAFTRYQLRGYIEDSDLEIYSIR 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750

46409863 IOGGNDVFKENTVTLSTGTFDECYPTLYQKIDESKLKAFTRYQLRGYIEDSDLEIYSIR 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730

cry1a-105.pe YNAKHETVNVPTGSLAPLSAQSPICKGCGERNRCAPHLEWNPDLDCSDRGKCAHSHH 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810

46409863 YNAKHETVNVPTGSLAPLSAQSPICKGCGERNRCAPHLEWNPDLDCSDRGKCAHSHH 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790

cry1a-105.pe FSLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARYKRAEKWR 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870

cry1a-105.pep NPAA:46359600

46359600 source="GENBANK_PROT" parasporal crystal protein [Paenibacillus lentimorbus]

SCORES Initl: 630 Initn: 1713 Opt: 1395 Z-score: 1577.1 E(): 1.5e-79
>NRAA:46359600
initn: 1713 initl: 630 opt: 1395 Z-score: 1577.1 expect(): 1.5e-79

Smith-Waterman score: 2086; 34.1% identity in 1312 aa overlap
(25-1177:65-1344)

cry1a-105.pe MDNNPNINICIPYNCLSNPEVEVLGGERIETGYTPIIDISLSLTOF--LLSEFVP-- 10 20 30 40 50

46359600 NKYPYATDNVTAEGRSYKWLDMCVGEGDGRSLEATAVAVGVRISHIFRLLG--VPY 40 50 60 70 80 90

cry1a-105.pe ---GAGFVGLVDIIWIGIFGSPQNDAPLVQIEQLINQRIEFAFNQAIISRLGLESLYQI 60 70 80 90 100

46359600 SAQGEQLFSFLDITLW--LEGNTOWEELMRHABELINEQVDPYVTRKALAEITDLGNLNL 100 110 120 130 140 150

cry1a-105.pe 110 120 130 140 150 160

46359600 YIAAFEDMKRNPSSQOEVTRVDRFNLGLFEALVPSFAPGVGYEVLPLSVYANVNIHL 160 170 180 190 200 210

cry1a-105.pe 170 180 190 200 210 220

46359600 LVLRDSIYGLDWGLSSTVDNNYNQQRNSATYANHCTTWYQIGLQRLQSGDASSWVNY 220 230 240 250 260 270

cry1a-105.pe 230 240 250 260 270 280

46359600 NEFSEITLIVLDICAFPSYDVRSYPIQLRGELTRGIYTDPAVYSGTSGYSWLQAPSF 280 290 300 310 320 330

cry1a-105.pe ---LEG-SIRSHLNLNLSITIVTDA---HRGEVYWSGHQIMASPVGSGPEFTPLYG 290 300 310 320 330

46359600 AEIERCA--REPNFNTASARVITGTILEVLSKNDPFWSKSHMYNTETN--SGILIOGPIYG 340 350 360 370 380 390

cry1a-105.pe 340 350 360 370 380 390

46359600 MTGTGTRIRTESYMOEYISVREAFMAHAGAGAPF--LGISTSEFFWSLGVRRYQNGRSPQF 400 410 420 430 440

cry1a-105.pe 400 410 420 430 440 450

46359600 ASQIITR-----QLPGVNSAVP--LDELSHSLTIT--APFVAVSGTIL--VHEMT 450 460 470 480 490

cry1a-105.pe 460 470 480 490 500

46359600 STTVSRNNRIEDKITQIPAKVSKTL--SNQVVSCTGTCTNNRPSDNGSRRLNITSFS 500 510 520 530 540 550

cry1a-105.pe 520 530 540 550 560 570

46359600 SQ---SYRIRIHYSATFFYLDITDGTNTFAVPTTFLSSGSGTVPYFSFGFINQYTH 560 570 580 590 600 610

cry1a-105.pe 580 590 600 610 620 630

46359600 TFPMSSSTFVCGADTFSSGN--EYIDREFLIPVATL---EAEYNLERQAKVNALFTST 620 630 640 650 660 670

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46359600 TTAPTESRYTFDFMFYSIGSANVLIDRIEIVPIGVLPFEYETKQOLEKARKAVNHLFTDG
620 630 640 650 660 670
cry1a-105.pe NQLGLKTNVTDVHIDQVSNLYTSLDFECLDEKRELSKVHAKRLSDERNLQDSNFKD
640 650 660 670 680 690
46359600 SKKALKEDTIDYDIOANVDCISDE-CGHDKMLLDDEVYAKQLSQANLLNENFD
680 690 700 710 720 730
cry1a-105.pe INR--QPERGWGSGTITIQGGDDVFKENYVTLSTGFD-----ECYPTLYOKIDESKLK
700 710 720 730 740
46359600 LYSALEKENPWTSPNVTIRODNPIFKGHVLSWAGANDIEATNTFTYVYKIDKALIK
740 750 760 770 780 790
cry1a-105.pe AFTRYQLRGVIEDSDQLEIYSIRYNAKHETV-NVPGTGLWPLSAQSPIGKCGEPNRCAP
750 760 770 780 790 800
46359600 PYTRYKVRGVFGSSKALELLVTRYNEEDAILDVPDN---IP-HAFTPV--CGEFDCKP
800 810 820 830 840
cry1a-105.pe HL-----ENPDL-----DCSC-----
810
46359600 YSYPPILLPECNVEFINQMPSSCHHNMQVDYNNMTSTSTTNMFSMNPPLTPEIASQSG
850 860 870 880 890 900
cry1a-105.pe --RDGKCAHSHHFSLDIDVGTDLNEOLGVWVIFKIKIQDCHARLGNLEFLEKPLVG
820 830 840 850 860 870
46359600 FGRKHAKC-HQAQPEPHIDGTDLVDELGIWVIFKICADGTGASLDLLEIEGALGV
910 920 930 940 950 960
cry1a-105.pe EALARYKRAKKWRKREKLEWETNIVYKEAESVDFVNSQDQLOQADTNIAHHAAD
880 890 900 910 920 930
46359600 EALELVKKREKKWRHQHCQSTKHYDAAKHAYMALFTNKRYEKLKFTTISILYAD
970 980 990 1000 1010 1020
cry1a-105.pe KRVSIREAYLPESLVPVGNAAIFEELEGRIPTAFSLYDARNVINGDFNNGLSCHWVK
940 950 960 970 980 990
46359600 HLVSQIPYVYKVPVPCWNYELXSELNTLYONAFVLYDORNLIKNGRFSGLMHWQAT
1030 1040 1050 1060 1070 1080
cry1a-105.pe GHVDVEEQNQSLLVLPWEAEVSQEVRCVGRGYILRVTAKEGEGCVTIHEIENN
1000 1010 1020 1030 1040 1050
46359600 PHARVE-QEYKESLVLPFNWDANVSQDLCEIHNRGYVLRVTKRKEPDGAGNVTFSDCENH
1090 1100 1110 1120 1130 1140
cry1a-105.pe TDELKFSNC-VEEETYP-----NNVTICNDY-----TVNQBEYG-----GAY
1060 1070 1080
46359600 VDKLSTSCDITATNAVGAQADPAAGVAYGQCGQIDRVYPYQSGYGRADGVAYEQSGHR
1150 1160 1170 1180 1190 1200
cry1a-105.pe TS-----RNRGY-----NEAPSVP-----ADYASV-----VEEKSY-
1090 1100 1110
46359600 TDGVYPYQSGYGTGVTYEQSGHRADGVYPYQSGYGRADGVAYEQSGHRADGVYPYQSGY
1210 1220 1230 1240 1250 1260
cry1a-105.pe TDG-----RRENPCFNRG-YRDTPLP-----VGYTKLEYFPETDKWV
1120 1130 1140 1150

46359600 TDGVTYDQSANQTRKYVHGCHTDGLPHPEHGCCYPDRVSDGQQLAYVTKSIDLPFDTKVR
1270 1280 1290 1300 1310 1320
cry1a-105.pe HEIGETEGTPIVDSVELLMEE
1160 1170
46359600 IDIGETEGNFRVESVELICMEK
1330 1340
cry1a-105.pe
NRAA:908825
908825 source="GENBANK_PROT" delta-endotoxin (AA 429-726) [Bacillus
thuringiensis]
SCORES Init1: 1355 Initn: 1355 Opt: 1355 Z-score: 1541.5 8(): 1.4e-77
>NRAA:908825
Initn: 1355 init1: 1355 opt: 1355 Z-score: 1541.5 expect(): 1.4e-77
Smith-Waterman score: 1355; 71.7% identity in 297 aa overlap
(429-725:1-297)
cry1a-105.pe AVYRKSTVDSLDEIPPNQNNVPPRQGRHLSHVMFSGSNSSVSIIRAPMFSWIHR
400 410 420 430 440 450
908825 RLSHVSMFSGSNSSVSIIRAPMFSWIHR
460 470 480 490 500 510
cry1a-105.pe SAEFNIIASDITQIPLVKAHTLQSGTTVVRGPGFTGDLRRTSGPPAYTIVNNGQ
460 470 480 490 500 510
908825 SAEFNIISSQITQIPLTSTKSLGSGTSVVRGPGFTGDLRRTSGPQISTLRVNITAP
40 50 60 70 80 90
cry1a-105.pe LPORYRARIRYASTNLRIYVTVAGREIFAGQFNKMTDGTPLTFQSFYATINTAFTFP
520 530 540 550 560 570
908825 LSQRYVRIRYASTNLRIYVTVAGREIFAGQFNKMTDGTPLTFQSFYATINTAFTFP
100 110 120 130 140 150
cry1a-105.pe MSQSSFTVGADTFSSGNEVYIDRFELIPVTATLEAFYNLEAQAQVNAFLTSTNQLGKT
580 590 600 610 620 630
908825 NGSSVFTLSAHVFNSEVYIDRIEFVPAEVTFAEYDLERAQAQVNAFLTSTNQLGKT
160 170 180 190 200 210
cry1a-105.pe NVTDYHIDQVSNLYTSLDFECLDEKRELSKVHAKRLSDERNLQDSNFKDINRQPER
640 650 660 670 680 690
908825 DVTDYHIDQVSNLYTSLDFECLDEKRELSKVHAKRLSDERNLQDSNFKDINRQPER
220 230 240 250 260 270
cry1a-105.pe GWGSGTITIQGGDDVFKENYVTLSTGFDCEYPTLYOKIDESKLKAFTRYQLRGVIEDS
700 710 720 730 740 750
908825 GWRGSDTITIQGGDDVFKENYVTLSTGFDCEYPTLYOKIDESKLKAFTRYQLRGVIEDS
280 290
cry1a-105.pe
NRAA:39653329
39653329 source="GENBANK_PROT" Cry1a [Bacillus thuringiensis]

SCORES Initl: 1279 Initn: 1279 Opt: 1279 z-score: 1457.9 E(): 6.5e-73
>>NRAA:46359602
Initn: 1732 Initl: 660 Opt: 1261 z-score: 1424.9 expect(): 4.5e-71
Smith-Waterman score: 2167; 35.2% identity in 1344 aa overlap
(4-1177:23-1332)

cryla-105.pe WYNTGLKRGKRSR... 210 240 250 260
39653329 VLDIVAPNYDSRRYPIRTVSQLTREIYT
20 30

cryla-105.pe NPVLENFDSFRGSAAGIEGIRSRPHMDLNS... 270 280 290 300 310 320
39653329 NPVLENFDSFRGSAAGIEGIRSRPHMDLNS... 330 340 350 360 370 380 390 400
40 50 60 70 80 90

cryla-105.pe GPEFTPLGTWGNAAPOORIVAOLGQGVYRTLSL... 330 340 350 360 370 380 390 400
39653329 GPEFTPLGTWGNAAPOORIVAOLGQGVYRTLSL... 410 420 430 440 450 460 470 480 490 500
100 110 120 130 140 150

cryla-105.pe YGTSNLPANVYKSGTVDLDEIPPNVPPROGFSHRLSHVSMFRSGFSNS... 390 400 410 420 430 440 450
39653329 YGTSNLPANVYKSGTVDLDEIPPNVPPROGFSHRLSHVSMFRSGFSNS... 460 470 480 490 500
160 170 180 190

cryla-105.pe APMFWSIHRSAEFNNIADSIQIPLVKAHTLQSGT... 450 460 470 480 490 500
NRAA:46359602

46359602 source="GENBANK_PROT" parasporal crystal protein [Paenibacillus
lenticimorbus]

SCORES Initl: 660 Initn: 1732 Opt: 1261 z-score: 1424.9 E(): 4.5e-71
>>NRAA:46359602
Initn: 1732 Initl: 660 Opt: 1261 z-score: 1424.9 expect(): 4.5e-71
Smith-Waterman score: 2167; 35.2% identity in 1344 aa overlap
(4-1177:23-1332)

cryla-105.pe MNPNP-INCEIPYCNLSNPEVEVLGGERTYETYPIDISL 10 20 30 40
46359602 MQIIPSSNALLSPKPYATDPNVIAEGRSYNNWLLT... 10 20 30 40 50 60
10 20 30 40 50 60

cryla-105.pe SLTQFLSEFFVPGAGVLG-LVDIITWIGFGP--SOWDAFLVQI... 50 60 70 80 90
46359602 GLSIDILAIYILGFIAPLRSALAGOLFSSGDTLMQHLIEQLINOKIAEYARNA 70 80 90 100 110 120
100 110 120 130 140 150 160 170 180

cryla-105.pe ISRLGLSNLYQIAESFRWEADPTNPALREMIQFNDDNSALT... 100 110 120 130 140 150 160 170 180
46359602 LAEFQGLGRQGLYLEALEDEQNLRSOPHKERVQTRILDSFTSSIPSAVRYEVP 130 140 150 160 170 180

cryla-105.pe LLSVYVQAANHLISLVLRDVSVFQORMGFDAATINSRYNDL... 220 230 240 250 260 270
46359602 LLSVYVQAANHLISLVLRDVSVFQORMGFDAATINSRYNDL... 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990

cryla-105.pe RVMGDSRDMIRYNFRRELTAVLDIVLFFNYDSRTYPIRTVSQLTREIYTNPVLEN- 220 230 240 250 260 270
46359602 RLOQTRATDMIRYNFRRELTAVLDIVLFFNYDSRTYPIRTVSQLTREIYTNPVLEN- 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990

cryla-105.pe FDGSGFRG--SAQIEG-SIRSPHMDLNSITVYTDHR---GEY----YWSHQIMA 280 290 300 310 320
46359602 WLOSTPGLISFSSLENVVVRAPHLFTWJSRVITDITGILSTVIGGQYNNNNNRWTHYOTL 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990

cryla-105.pe SPVGFSGPEFTPLGTWGNAAPOORIVAOLGQGVYRTLSLTYRRFPNIGINNQLSVL 330 340 350 360 370 380
46359602 RTTG--GTSFQSPYGS--TAPPIORTNLTITSGDVIIESSVVTSSLYGANSVAFTCT 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990

cryla-105.pe DCTEFAYGTSNLPANVYKSGTVDLDEIPPNVPPROGFSHRLSHVSMFRSGFSNS 390 400 410 420 430 440
46359602 TGRSL-YENPTVYPPA--OKL-----IHLPFGVDSGRNATNYSRHSLSYISGFSGLGPS 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990

cryla-105.pe SUSTIRAPMFSIHRSA-EFNNIADSIQIPLVKAHTLQSGT... 450 460 470 480 490 500
46359602 GTGLV--KWTSTATRENNITLDRIVQLPAVKASLNN-CQVVKGTGFTGGDWLKP 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990

cryla-105.pe TSGGFAITNNQAPONVRARIYASTNLIYTVVAGERIFAGQFNKMTDGDPLT 500 510 520 530 540 550 560
46359602 NNSTFSMTSAFRSAVT--YHFRVYASSASFVISEEYGR-FPTTVPLLSTMSPLP 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

cryla-105.pe ---FOSFSATNTATFTF... 570 580 590 600 610
46359602 QNTPFAPKIVDLPSTVITRTSAS... 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

cryla-105.pe EAYNLERAKAVNALFTSNQGLDNNVDYHIDVSNATVLSRCDCKRELSEKV 620 630 640 650 660 670
46359602 ETQOOLEKARKAVNHLFTDGSKKALKEDTTVELSQANVDCSDE-CHKMKMLDEV 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

cryla-105.pe KHAKRLSDERNLQDSNPKDINRQPER--GWGGSTGHTIQGDDFKENYVLSFTD-- 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
46359602 KYAKQLSQANLLINGNFDLLYPALERENPMKTSNVTIQRDNPINFGHMSWACANV 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

cryla-105.pe ---ECPTVLYOKIDESKKAFTYQYOLRGYIEDSODLEIYSINAKHETV-NVPSQSD 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
46359602 ATWDTFTVYVOKIDEAKLPYTRYKVRGFGVGSODLELLVYRNEEDAILDVPD--- 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990

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cry1a-105.pe WPLSAQSPGKCGEPRNCAPHL-----EWNPD-----DCSC-----
IP-HAPTEV--CGEFDRCCKPSYPLPECNPEFFINQMPQSSCHNMVDYNNMTSST
820      830      840      850      860      870      880      890      900      910      920      930

cry1a-105.pe -----RDGEKCAHSHHFSFSDIDVGCTDLNEDLGWVIFKIKT
820      830      840      850      860      870      880      890      900      910      920      930

TMPSWNPPLTPEIASSQSGFRKHKC-HOAHQEFHIDTGTIDLVDELGIWVIFKICA
880      890      900      910      920      930

cry1a-105.pe ODGHARLGNLEFLEKPLVGEALARKAEKKWRDKREKLEWETNIVYKEAESVDALFV
860      870      880      890      900      910      920      930

TDGYASLDLVEIEGALGVAELELVKREKKWRHQKQHCQSKTKHYDAKHAVALFT
940      950      960      970      980      990

cry1a-105.pe NSQVDQLQADTNIAHIAADKRVHSI---REAYLPESLVIPIGVNAAIFEELEGRIPTAFS
920      930      940      950      960      970      980      990

NTRYELKFKETTISDILYADHLVQSIPVYVKNYVEVS---GMNYELYELATLVQNAFY
1000     1010     1020     1030     1040

cry1a-105.pe LYDARNVINGDFNNGLSGNVKGHVDEEQNNQSRSLVLPVEAEVQSEVRCFGRGI
980      990      1000     1010     1020     1030     1040

LYDQRLNLIKGRFSNGLMYOATPHARVE-QEYDRSLVLPNMDANVSQQLGCIENRGYV
1050     1060     1070     1080     1090     1100

cry1a-105.pe LRVYAYKEGEGCVTHIEIENNTDELKFSNC-VEEETYP-----NNTVTCNDY-----TV
1040     1050     1060     1070     1080     1090     1100     1110     1120     1130     1140     1150     1160

LRYTARKEDPGAGNVFTSDCANHVDKLSCTSDIATNAVGAQANDPAAGVAYGQGGQCI
1110     1120     1130     1140     1150     1160

cry1a-105.pe NQEEVG-----GAYTS-----RNRGY-----NEAPSPADYASVYEKSYT
1090     1100     1110     1120     1130     1140     1150     1160     1170     1180     1190     1200     1210     1220

DRVPYFGSGRADGVAYEQSGHRTDGVPRQSGRADGVADHDPGVGRADGVA-YEQSGYR
1170     1180     1190     1200     1210     1220

cry1a-105.pe -----DGRRENPCFNR-GY-----RDYPLP-----
1120     1130     1140     1150     1160     1170     1180     1190     1200     1210     1220

ADGVAYEQSGRADGVPGYQSGYGTGVYDQSAKQTRKYHGCHTDGLPHPEHGCCYPDR
1230     1240     1250     1260     1270     1280

cry1a-105.pe -----VGVTKELEFPETDKVWIEIGETGTFIVDSVELLMEE
1140     1150     1160     1170     1180     1190     1200     1210     1220     1230     1240     1250     1260     1270     1280     1290     1300     1310     1320     1330

VSDGQQLAYVTKSIDLPDPTDKVRIDIGETEGNFRVESVELICMEK
1290     1300     1310     1320     1330

cry1a-105.pep
NRRA: 52145404
```

52145404 source="GENBANK_PROT" Cry3Aa protein [Bacillus thuringiensis]

SCORES Initl: 470 Initn: 843 Opt: 1252 Z-score: 1419.3 E(): 9.2e-71
>>NRRA: 52145404
Initn: 843 Initl: 470 Opt: 1252 Z-score: 1419.3 expect(): 9.2e-71
Smith-Waterman score: 1256; 36.6% identity in 569 aa overlap
(56-607:99-651)

```
cry1a-105.pe GERIETGYTPIIDISLSLQFLLSEFVGAGFVLGLVDIWIIGFQSQMDAFLVQIEQLIN
30      40      50      60      70      80
52145404 TTKDVIQGISVVGOLLGVGFPFGGALVSFYTNFLNTIMPSEDP--WKAFMEQVEALMD
70      80      90      100     110     120

cry1a-105.pe QRIEEFARNOALSRLEGSLNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT
90      100     110     120     130     140
52145404 OKIADAKNAKLAELQGLQNNVEDYVSALUSSQWKPNFVSRPNPQSGRIELFSQAESHFR
130     140     150     160     170     180

cry1a-105.pe TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFGQWGFDAATINSRYNDLRLIGN
150     160     170     180     190     200
52145404 NSMPFAISGYSVEVLFTTYAQAANIHLFLDKQAQIYGEWGYEKEDIAEFYKROKLQTE
190     200     210     220     230     240

cry1a-105.pe YTDHARVNTGLERWGPDSRDMIRYNOFRRELTITVLDIVSLFNYDSRTYPIRTVWSQ
210     220     230     240     250     260
52145404 YTDHCVKYNVGLDLKLGSSYSEVNFNRYRREMTITVLDIALFLYDVRLYPKVEKTE
250     260     270     280     290     300

cry1a-105.pe LTRIEVTNPLV--ENFDGSRFGSAQIGESIRSPHLDILNITITVDARGEY-----
270     280     290     300     310
52145404 LTRDVLTDPIGVANNLRG-YGTFFSNIENYIRKPHLFDYLRHQFTRFRPGYGNDSFN
310     320     330     340     350     360

cry1a-105.pe YWGHQIMASPVGSGPEPTFPLYGTMGNAAPQQRIVAQLGQGVVRLTGST-LYRRPFI
320     330     340     350     360     370
52145404 YWGSNTVSTRPSIGSNDIITSPFYGNK-SSEPQNLEFN-GEKVYRAVANTNLAVPSAV
370     380     390     400     410     420

cry1a-105.pe --GINNQQLSVL-DGTFEYAGTSSNLPSSAVYKSGTV--DSLDEIPQNNVPPRQGFSH
380     390     400     410     420
52145404 YSGVTKVEFSQVNDOTDEA--STQTYDSK--RNVGAVSWDSIDQLPPEITDEPPEKGYSH
430     440     450     460     470

cry1a-105.pe RLSHVSMFRSGFNSSVSIIRAPMFSWIRHSAEFNNIIASDSITQIPLVKAHTLOSQTIV
430     440     450     460     470     480
52145404 QLNMYWCMFLMGSSRGTI-----PVLTWTKHSDVDFNMDSKITQLPLVYKAYKQSGASV
480     490     500     510     520     530

cry1a-105.pe VSGPFTGDIILRRTSGGPATYIVNINQQLPQRYRARIYASTTNLRIYTVVAGERIFA
490     500     510     520     530     540
52145404 VAGPFTGDIIOCTENGSAATYVTPDVYSYQKHARIIHVASTSOITFTLSLDGAPFNQ
540     550     560     570     580     590

cry1a-105.pe GQFNKMTDGTPTQFSFYATINTAFTFPMSQSFVVGADTFSSGNEVYIDREFELPVT
550     560     570     580     590     600
52145404 YTFDKTINKGTLTYSNLFNASFSTPFE--LSGNLQIGVGLSAGDKVYIDKIEFIPVN
600     610     620     630     640     650

cry1a-105.pe ATLEAEYNLERAAQKAVNALFTSTNQLGKTNVTDYHIDQVSNLVTLSDFCLEKRELS
610     620     630     640     650
52145404 YTFDKTINKGTLTYSNLFNASFSTPFE--LSGNLQIGVGLSAGDKVYIDKIEFIPVN
600     610     620     630     640     650

cry1a-105.pep
NRRA: 3965331
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39653331 source="GENBANK_PROT" CryIA [Bacillus thuringiensis]
SCORES Init1: 1242 Inith: 1242 Opt: 1244 z-score: 1415.9 E(): 1.4e-70
>>NRAA:39653331
Initn: 1242 Inith: 1242 Opt: 1244 z-score: 1415.9 expect(): 1.4e-70
Smith-Waterman score: 1248; 36.6% identity in 193 aa overlap
(241-433:1-193)
cry1a-105.pe YNTGLERWGPDSRDWIRNNOFRRLTITLNDYSLFPNNSRPIRTVYSQLTREIYN
39653331
cry1a-105.pe PVLENFDGFRGSAOGIEGSRSPHLMILNSNTYVAHGEASNGHOMASNGEG
39653331
cry1a-105.pe PFTFPLYTGMNAAPQORIVAQLGQGVYRTLSSTLYRPPNIGINNOSLSGDTEAY
39653331
cry1a-105.pe GTSSNPLSAVYKSGTVDLSDEITPPQNNVPPRQGFHRLSHVMFSGFSNVSIIIRA
39653331
cry1a-105.pe PMFSWIRHSAEFNIIASDSITQPLVKAHTIQTGTVTVRPGFGTGDILLRTSGGPAY
cry1a-105.pep
NRAA:45934892
45934892 source="GENBANK_PROT" insecticidal crystal protein [Bacillus
thuringiensis]
SCORES Init1: 467 Inith: 832 Opt: 1244 z-score: 1410.3 E(): 2.9e-70
>>NRAA:45934892
Initn: 832 Inith: 467 Opt: 1244 z-score: 1410.3 expect(): 2.9e-70
Smith-Waterman score: 1248; 36.6% identity in 569 aa overlap
(56-607:99-651)
cry1a-105.pe GERIEGTPTIDISLSTQFLSEFVPGAGFVLGLVDIIMGIFGSPQWDALVQIEQLN
45934892
cry1a-105.pe ORIEEFARNQALSRLEGLNLIQIYAESFREWADPT--NPALREEMIQFNDMNSALT
45934892
cry1a-105.pe TATPLFVQNVQVPLLSVYVQANLHLVLRDVSFQGRGFAATINSYNDLTRLLGN
cry1a-105.pe

45934892 NSMPSFAISGYEVLFTTYAQANHTLFLDLDAQIYGEWYKEDIAEFYKRLKLTQE
cry1a-105.pe YTDHAWNTGLERWGPDSRDWIRNNOFRRLTITLNDYSLFPNNSRPIRTVYSQLTREIYN
45934892
cry1a-105.pe LTRIEYTNVPL--ENFDGFRGSAOGIEGSRSPHLMILNSNTYVAHGEAY
45934892
cry1a-105.pe YWSGHQIMASPVGFGPEFTPLLYGNGNAAPQORIVAQLGQGVYRTLSSTLYRPPNIGINNOSLSGDTEAY
45934892
cry1a-105.pe --GINNOQLSVL--DGTEFAYGTSSNPLSAVYKSGTV--DSLDEIPPONNVPPRQGFH
45934892
cry1a-105.pe RLHSVMSFGSFSNVSIIIRAFMFSWIRHSAEFNIIASDSITQPLVKAHTIQTGTV
45934892
cry1a-105.pe VRPGFGTGDILLRTSGGPAYIIVNINQPLQRYRARIIRASTNRIYIVAGERIFA
45934892
cry1a-105.pe GQFNTMNGDPLTETATINFTMSSQSFVTGADTFSGNEVYIDRFELIPVT
45934892
cry1a-105.pe ATLEAEYNLERAQAVNALNLSNOLGLKQNTVHIDQVSNLWYLSDEFCLDEKRELS
cry1a-105.pep
NRAA:640362
640362 source="GENBANK_PROT" Delta-Endotoxin CryIIa (Bt13)
SCORES Init1: 467 Inith: 832 Opt: 1242 z-score: 1408.7 E(): 1.4e-70
>>NRAA:640362
Initn: 832 Inith: 467 Opt: 1242 z-score: 1408.7 expect(): 3.6e-70
Smith-Waterman score: 1246; 36.6% identity in 569 aa overlap
(56-607:31-583)
cry1a-105.pe GERIEGTPTIDISLSTQFLSEFVPGAGFVLGLVDIIMGIFGSPQWDALVQIEQLN
640362
cry1a-105.pe TTKDVIQKISVVGDLGVGFPFGALVSFYTNFLNTIWPSEDP--WKAFFMEQVEALMD

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SCORES   Initl: 467   Initn: 832   Opt: 1242   z-score: 1408.6 E(): 3.7e-70
>NR0A:312848
Initn: 832   Initl: 467   Opt: 1242   z-score: 1408.6   expect(): 3.7e-70
Smith-Waterman score: 1246;   36.6% identity in 569 aa overlap
(56-607:44-596)

cry1a-105.pe 30 40 50 60 70 80
>NR0A:312848
TTKDVIQKGSVVGDLGVGFPFGGALVSFYTNFLNTWPSDEP--WKAFMEQVEALMD
(56-607:44-596)

cry1a-105.pe 90 100 110 120 130 140
>NR0A:312848
QRIEFAFARNOAISRLGSLNLYQIYAESFREWEADPT--NPALREEMRIQFNDMNSALT
(56-607:44-596)

cry1a-105.pe 150 160 170 180 190 200
>NR0A:312848
NSMPSFAISGIEVFLTTIYQAQANHLFLDKQAIIYGEWEYKEKEDIAEFYKQLKLTQ
(56-607:44-596)

cry1a-105.pe 210 220 230 240 250 260
>NR0A:312848
YTDHAWNTGLRWGPDSDIRYNQFRELTLVLDIVSLFPNYSRTYPIRTVSQ
(56-607:44-596)

cry1a-105.pe 270 280 290 300 310 320
>NR0A:312848
LTRDVLTDIVGVNLRG-YGTTFSENIEYIRKPHLFYDLHRIQFHRFPQGYGNDSPN
(56-607:44-596)

cry1a-105.pe 330 340 350 360 370 380
>NR0A:312848
YWSGHQIMASPVGSGPEFTFPLXGTMGNAAPQQRIVAQLGQGYRTLSST-LYRPPNI
(56-607:44-596)

cry1a-105.pe 390 400 410 420 430 440
>NR0A:312848
YSGVTKVEFSQVNDQTDQEA--STQYDSK--RNVGAVSWDSIDQLPEITDEPLEKGYSH
(56-607:44-596)

cry1a-105.pe 450 460 470 480 490 500
>NR0A:312848
QLNVMCFWLMQSGRTI-----PVLITWTHKSVDFNFMDISKITQLPLVKAYKLGSGASV
(56-607:44-596)

cry1a-105.pe 510 520 530 540 550 560
>NR0A:312848
VRGFGFTGGDIIRRTSGGPFAYTIVNQLPQRVYRARIYASTNLIYTVVAGERIFA
(56-607:44-596)

cry1a-105.pe 570 580 590 600 610 620
>NR0A:312848
YVFDKTIKNGDITLYNSFNLASFTPE--LSGNLQIGVTGSAGDKVIIDKIEFIPVN
(56-607:44-596)

cry1a-105.pe 630 640 650 660 670 680
>NR0A:312848
ATLEAEYNLERAKAVNALFTSTNQLGLKNTVDVHIQDVSNLTVLSDEFCLDEKRELS
(56-607:44-596)

cry1a-105.pe 690 700 710 720 730 740
>NR0A:312848
GQFNKMTDGTDLTQFSFVATINTAFTFPMQSSFTVGADTFSSGNEVYIDRFELIPVT
(56-607:44-596)

cry1a-105.pe 750 760 770 780 790 800
>NR0A:312848
YVFDKTIKNGDITLYNSFNLASFTPE--LSGNLQIGVTGSAGDKVIIDKIEFIPVN
(56-607:44-596)

cry1a-105.pe 810 820 830 840 850 860
>NR0A:312848
ATLEAEYNLERAKAVNALFTSTNQLGLKNTVDVHIQDVSNLTVLSDEFCLDEKRELS
(56-607:44-596)

cry1a-105.pe 870 880 890 900 910 920
>NR0A:312848
GQFNKMTDGTDLTQFSFVATINTAFTFPMQSSFTVGADTFSSGNEVYIDRFELIPVT
(56-607:44-596)

cry1a-105.pe 930 940 950 960 970 980
>NR0A:312848
YVFDKTIKNGDITLYNSFNLASFTPE--LSGNLQIGVTGSAGDKVIIDKIEFIPVN
(56-607:44-596)

cry1a-105.pe 990 1000 1010 1020 1030 1040
>NR0A:312848
ATLEAEYNLERAKAVNALFTSTNQLGLKNTVDVHIQDVSNLTVLSDEFCLDEKRELS
(56-607:44-596)

cry1a-105.pe 1050 1060 1070 1080 1090 1100
>NR0A:312848
GQFNKMTDGTDLTQFSFVATINTAFTFPMQSSFTVGADTFSSGNEVYIDRFELIPVT
(56-607:44-596)

cry1a-105.pe 1110 1120 1130 1140 1150 1160
>NR0A:312848
YVFDKTIKNGDITLYNSFNLASFTPE--LSGNLQIGVTGSAGDKVIIDKIEFIPVN
(56-607:44-596)

cry1a-105.pe 1170 1180 1190 1200 1210 1220
>NR0A:312848
ATLEAEYNLERAKAVNALFTSTNQLGLKNTVDVHIQDVSNLTVLSDEFCLDEKRELS
(56-607:44-596)

cry1a-105.pe 1230 1240 1250 1260 1270 1280
>NR0A:312848
GQFNKMTDGTDLTQFSFVATINTAFTFPMQSSFTVGADTFSSGNEVYIDRFELIPVT
(56-607:44-596)

cry1a-105.pe 1290 1300 1310 1320 1330 1340
>NR0A:312848
YVFDKTIKNGDITLYNSFNLASFTPE--LSGNLQIGVTGSAGDKVIIDKIEFIPVN
(56-607:44-596)

cry1a-105.pe 1350 1360 1370 1380 1390 1400
>NR0A:312848
ATLEAEYNLERAKAVNALFTSTNQLGLKNTVDVHIQDVSNLTVLSDEFCLDEKRELS
(56-607:44-596)

cry1a-105.pe 1410 1420 1430 1440 1450 1460
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GQFNKMTDGTDLTQFSFVATINTAFTFPMQSSFTVGADTFSSGNEVYIDRFELIPVT
(56-607:44-596)

cry1a-105.pe 1470 1480 1490 1500 1510 1520
>NR0A:312848
YVFDKTIKNGDITLYNSFNLASFTPE--LSGNLQIGVTGSAGDKVIIDKIEFIPVN
(56-607:44-596)

cry1a-105.pe 1530 1540 1550 1560 1570 1580
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(56-607:44-596)

cry1a-105.pe 1590 1600 1610 1620 1630 1640
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(56-607:44-596)

cry1a-105.pe 1650 1660 1670 1680 1690 1700
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(56-607:44-596)

cry1a-105.pe 1710 1720 1730 1740 1750 1760
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(56-607:44-596)

cry1a-105.pe 1770 1780 1790 1800 1810 1820
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(56-607:44-596)

cry1a-105.pe 1830 1840 1850 1860 1870 1880
>NR0A:312848
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(56-607:44-596)

cry1a-105.pe 1890 1900 1910 1920 1930 1940
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(56-607:44-596)

cry1a-105.pe 1950 1960 1970 1980 1990 2000
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(56-607:44-596)

cry1a-105.pe 2010 2020 2030 2040 2050 2060
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YVFDKTIKNGDITLYNSFNLASFTPE--LSGNLQIGVTGSAGDKVIIDKIEFIPVN
(56-607:44-596)

cry1a-105.pe 2070 2080 2090 2100 2110 2120
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(56-607:44-596)

cry1a-105.pe 2130 2140 2150 2160 2170 2180
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(56-607:44-596)

cry1a-105.pe 2190 2200 2210 2220 2230 2240
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(56-607:44-596)

cry1a-105.pe 2250 2260 2270 2280 2290 2300
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(56-607:44-596)

cry1a-105.pe 2310 2320 2330 2340 2350 2360
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(56-607:44-596)

cry1a-105.pe 2370 2380 2390 2400 2410 2420
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(56-607:44-596)

cry1a-105.pe 2430 2440 2450 2460 2470 2480
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(56-607:44-596)

cry1a-105.pe 2490 2500 2510 2520 2530 2540
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(56-607:44-596)

cry1a-105.pe 2550 2560 2570 2580 2590 2600
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(56-607:44-596)

cry1a-105.pe 2610 2620 2630 2640 2650 2660
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(56-607:44-596)

cry1a-105.pe 2670 2680 2690 2700 2710 2720
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(56-607:44-596)

cry1a-105.pe 2730 2740 2750 2760 2770 2780
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(56-607:44-596)

cry1a-105.pe 2790 2800 2810 2820 2830 2840
>NR0A:312848
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(56-607:44-596)

cry1a-105.pe 2850 2860 2870 2880 2890 2900
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(56-607:44-596)

cry1a-105.pe 2910 2920 2930 2940 2950 2960
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(56-607:44-596)

cry1a-105.pe 2970 2980 2990 3000 3010 3020
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(56-607:44-596)

cry1a-105.pe 3030 3040 3050 3060 3070 3080
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(56-607:44-596)

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(56-607:44-596)

cry1a-105.pe 3150 3160 3170 3180 3190 3200
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(56-607:44-596)

cry1a-105.pe 3210 3220 3230 3240 3250 3260
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(56-607:44-596)

cry1a-105.pe 3270 3280 3290 3300 3310 3320
>NR0A:312848
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(56-607:44-596)

cry1a-105.pe 3330 3340 3350 3360 3370 3380
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(56-607:44-596)

cry1a-105.pe 3390 3400 3410 3420 3430 3440
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(56-607:44-596)

cry1a-105.pe 3450 3460 3470 3480 3490 3500
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(56-607:44-596)

cry1a-105.pe 3510 3520 3530 3540 3550 3560
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(56-607:44-596)

cry1a-105.pe 3570 3580 3590 3600 3610 3620
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(56-607:44-596)

cry1a-105.pe 3630 3640 3650 3660 3670 3680
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(56-607:44-596)

cry1a-105.pe 3690 3700 3710 3720 3730 3740
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(56-607:44-596)

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(56-607:44-596)

cry1a-105.pe 3810 3820 3830 3840 3850 3860
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(56-607:44-596)

cry1a-105.pe 3870 3880 3890 3900 3910 3920
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cry1a-105.pe 3930 3940 3950 3960 3970 3980
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(56-607:44-596)

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cry1a-105.pe 4050 4060 4070 4080 4090 4100
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(56-607:44-596)

cry1a-105.pe 4110 4120 4130 4140 4150 4160
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(56-607:44-596)

cry1a-105.pe 4170 4180 4190 4200 4210 4220
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cry1a-105.pe 4230 4240 4250 4260 4270 4280
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cry1a-105.pe 4290 4300 4310 4320 4330 4340
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(56-607:44-596)

cry1a-105.pe 4410 4420 4430 4440 4450 4460
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(56-607:44-596)

cry1a-105.pe 4470 4480 4490 4500 4510 4520
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(56-607:44-596)

cry1a-105.pe 4530 4540 4550 4560 4570 4580
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(56-607:44-596)

cry1a-105.pe 4590 4600 4610 4620 4630 4640
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ATLEAEYNLERAKAVNALFTSTNQLGLKNTVDVHIQDVSNLTVLSDEFCLDEKRELS
(56-607:44-596)

cry1a-105.pe 4650 4660 4670 4680 4690 4700
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(56-607:44-596)

cry1a-105.pe 4710 4720 4730 4740 4750 4760
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cry1a-105.pe 4890 4900 4910 4920 4930 4940
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(56-607:44-596)

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(56-607:44-596)

cry1a-105.pe 5070 5080 5090 5100 5110 5120
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(56-607:44-596)

cry1a-105.pe 5130 5140 5150 5160 5170 5180
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(56-607:44-596)

cry1a-105.pe 5190 5200 5210 5220 5230 5240
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(56-607:44-596)

cry1a-105.pe 5250 5260 5270 5280 5290 5300
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(56-607:44-596)

cry1a-105.pe 5310 5320 5330 5340 5350 5360
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(56-607:44-596)

cry1a-105.pe 5370 5380 5390 5400 5410 5420
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(56-607:44-596)

cry1a-105.pe 5430 5440 5450 5460 5470 5480
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(56-607:44-596)

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(56-607:44-596)

cry1a-105.pe 5550 5560 5570 5580 5590 5600
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(56-607:44-596)

cry1a-105.pe 5610 5620 5630 5640 5650 5660
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(56-607:44-596)

cry1a-105.pe 5670 5680 5690 5700 5710 5720
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cry1a-105.pe 5850 5860 5870 5880 5890 5900
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(56-607:44-596)

cry1a-105.pe 5970 5980 5990 6000 6010 6020
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(56-607:44-596)

cry1a-105.pe 6030 6040 6050 6060 6070 6080
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cry1a-105.pe 6150 6160 6170 6180 6190 6200
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(56-607:44-596)

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(56-607:44-596)

cry1a-105.pe 6330 6340 6350 6360 6370 6380
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(56-607:44-596)

cry1a-105.pe 6390 6400 6410 6420 6430 6440
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(56-607:44-596)

cry1a-105.pe 6450 6460 6470 6480 6490 6500
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(56-607:44-596)

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(56-607:44-596)

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(56-607:44-596)

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(56-607:44-596)

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(56-607:44-596)

cry1a-105.pe 6870 6880 6890 6900 6910 6920
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(56-607:44-596)

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(56-607:44-596)

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(56-607:44-596)

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(56-607:44-596)

cry1a-105.pe 7170 7180 7190 7200 7210 7220
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(56-607:44-596)

cry1a-105.pe 7230 7240 7250 7260
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cytla-103-pe ATLEAEVNRRAKQANNAFTSTNQLGKLTNTVDVHDQVSNLYTSLDFCLDEKRELS
620 630 640 650 660

cytla-105 pep
NRAA:471281

471281 source="GENBANK PROT" cytla105 insecticidal crystal protein [synthetic construct]

SCORES Initl: 467 Initn: 832 Opt: 1428 Z-score: 1408.4 E(): 3.7e-70
>>NRAA:471281
initn: 832 initl: 467 opt: 1242 Z-score: 1408.4 E(): 3.7e-70
Smith-Waterman score: 1246; 36.6% identity in 599 aa overlap
(56-607:44-596)

[illegible]

150 160 170 180 190 200
 cyia-105.pe TAIPLEAVONVYPLLSVVQAAANLHSLVRSVFGFDDAATINSRYNDLTRIGN
 471281 NSNPSFAISGYEVLFLITYAAQAAANTHLFLDKDAQIYGEENGVEKEDIAFFYKRLKLTQE
 140 150 160 170 180 190
 cyia-105.pe YTHAVRWNTGLERVGPDSDRWIRYQNFRELTFLVDIVSLFNYSRSTYRTVTSQ
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[illegible][illegible]

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:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
YSGVTWVFVSQNQTDEA--STQTVDSK--RVNGAVSWSDIQLPETTTDEPKRGYSH
370      380      390      400      410      420
```

430 440 450 460 470 480
cry1a-105.pe RLSHVFMFSGFSNVSIIIRAFPMVHRAEFNIIAGSDSIQTPLPAKATIQSGTIV
471281 QLVNVMCFLMQSGRTI-----PVLFWTHKSVDFNFMIDSKITQLPLPAKAYKQSGASV

	490	500	510	520	530	540
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cryla-105.pe VRGPGFTGDILRTSGGPFAYTTWINGOLPORVEARIRVASTINLRIVTVVAGERIFA
471281 VAGPRFTGDDIIOTCTENGSAATIVTDPVSYSKYARLHVASTSQITFLSIDGAPFQNO 530
550 560 570 580 590 600
cryla-105.pe QQNFKNMDTGDPLTFQSFYSYATINTATFFPMSSQSFVGAQTFSSGNEVYIDRFELIPVT
471281 YYFDKTIKNGDITLTYSNPNLASFTPPE--LSGNLQIGVTGLSAGDKVVIDKIEFVNW 590
540 550 560 570 580 590
cryla-105.pe ATLEAENLERAQKAVNALFTSTNQLGKTNVDYHDQVSNLVTYLSDFCLDEKRELS
471281 LRSPTGTELEFIDI 610
600 610
cryla-105.pcp
SW:117325

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117325 description="PESTICIDIAL CRYSTAL PROTEIN CRY3AA PRECURSOR (INSECTICIDAL DELTA-ENDOTOXIN CRYIIIA(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (73 KDA CRYSTAL PROTEIN)." library="NA species="Bacillus thuringiensis serovar san diego" source="swissprot prot" version="NA type=PRT

SCORES Initl: 467 Inltn: 832 Opt: 1242 Z-score: 1408.1 E(): 3.9e-70
 >FW:11725
 Inltn: 832 Initl: 467 Opt: 1242 Z-score: 1408.1 expect(): 3.9e-70
 SmithWaterman score: 1246; 36.6% identity in 569 aa overlap
 (58-607-61-643)

CT1A-105 DE GERIETGYPDISLSUTOFLLSEFVPGAGVGLVDIWMGIFGQSOWDAFLVQIEQLIN
 117325 TTQDMFQZGIGWGDGAGVGFPGFAGLVSYFNFLNTLWPSEDP--WKAFMEQVEALMD
 117326

~~CRYLA-105.pe~~

~~QRIETSAKMOAISRLTALVQITAFSEWEADPT--NPALREENRQFNDMSALT~~

~~90 100 110 120 130 140~~

~~OKIADYAKNALLAAGLQGNFNPNYSALSSQINPVSRRPHSGOGRIRLEIFSOASHPR~~

~~117325~~

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cry1a-105.pe TATPLFAVQNVQLLSVVYQAANHLISVERLSTGQRWGSDDAATINSRYNDLTSLIGN
150      160      170      180      190      200
NSMPSEA TSGVEVELFLTTVAQRAANVTETLTDTQTGEFCEGVYEVENNENAVPOTVIQOP
117325
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cyt1a-105.pe YTDHAYRWNTGLERVGPPDSRDWYRQFRETITVYDIUSVFPYVGRYPIDRVSUC

cyt1a-105.pe LTRTEVTPVL--ENFGSPRGAQIGGSTRSPHMLDILNSITYTDARQY

cr1a-105.pe ywsghoimaspvgsfgeffflpylgtmgnaapoorivaolgogvvtlssst-lyrrpfni
300 310 320 330 340 350 360 370
ltlmdvldtupi gvwnnlag-vgtftsnienlyrkxphllfydlxhrlqftrpfogvyygnsln
11/7325

Monsanto Company
Final Report
Product Characterization Center

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MSL No. 20351
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117325 YWGNVYSTRPSIGSNDIITSPFYGNK--SSEPQVONLEFN-GEKVYRAVANTNLAVWPSAV
360 370 380 390 400 410

cry1a-105.pe --GINNCOQLSVL-DGTEFAYGTSNLPFAVYKSGTV--DSLDEIPQNNVPPROGFSSH
380 390 400 410 420
117325 YSGVKVEFSQVNDQDEA--STQTYDSK--RNVGAVSWDSIDQLPETTDEPLEKGYSH
420 430 440 450 460 470

cry1a-105.pe RLSHVSMFRSGFSNSVSIIRAPMFHSIAEFNIIASDSITQIPLVKAHFLQSGTIV
430 440 450 460 470 480
117325 QLVNVMCFMQSGRGTI-----PVLTWTHKSVDFNMDSKKITQLPLVKAYKLGASV
480 490 500 510 520

cry1a-105.pe VRGPGFTGGDILRRSTGGPFAYTIIVNINQQLPQRYRARIYASTNLRIYTVVAGERIFA
490 500 510 520 530 540
117325 VAGPRFTGGDIIQCTENGSAATIIYVTPDVSYQKYRARIHYASTSQTFTLSLDGAPFNQ
530 540 550 560 570 580

cry1a-105.pe GQFNKMTMDGDLTTFQSPSYATINTAFTPMSSQSFYVADTFSSGNEVYIDRFELIPVT
550 560 570 580 590 600
117325 YFDKTIKNGDILITNSFNLASFTPE--LSGNNLQIGVTGLSAGDKVYIDKIEFIPVN
590 600 610 620 630 640

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

cry1a-105.pep
NR4A:40253

40253 source="GENBANK_PROT" unnamed protein product [Bacillus
thuringiensis]gi|142736|gb|AA50255.1| crystal protein [Bacillus thuringiensis
serovar morrisoni]gi|61221658|sp|P0A380|CR3AA_BACTM Pesticidal crystal protein
cry3Aa precursor (Insecticidal delta-endotoxin CryIIIA(a)) (Cry3Aa)
entomocidal protoxin (73 kDa crystal protein)gi|61221659|sp|P0A381|CR3AA_BACTD
Pesticidal crystal protein cry3Aa precursor (Insecticidal delta-endotoxin . . .

SCORES Initl: 467 Initn: 832 Opt: 1242 Z-score: 1408.1 E(): 3.9e-70
>>NR4A:40253
Initn: 832 Initl: 467 opt: 1242 Z-score: 1408.1 expect(): 3.9e-70
Smith-Waterman score: 1246; 36.6% identity in 569 aa overlap
(56-607:91-643)

cry1a-105.pe GERIETGYTPIDISLSTQFLSEFVGAGFVLGLVDIIMGIFGSPQWDAFLVOIEQLIN
30 40 50 60 70 80
40253 TTKDVKQIGSVVGLDGLGWCFPGGALVSFTNFWLNTWPSDEP--WKAFMEQVEALMD
70 80 90 100 110

cry1a-105.pe QRIEFARNQALSLRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT
90 100 110 120 130 140
40253 OKIADYAKKALAELOGLQNNVEDYVSALLSSWKNPVSRRNPHSQGRILEFSQAESHR
120 130 140 150 160 170

cry1a-105.pe TATPLFAVQNVQVPLLSVYQAAANLHSLVLRDVSFVGQRMGFDAATINSRYNDLTRIGN
150 160 170 180 190 200
40253 NSMPSFAISGVELFLTYAQAAANTHLFLKDAQIYGEENGKEYEKEDIAFYKRQLKLTQE
180 190 200 210 220 230
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210 220 230 240 250 260
cry1a-105.pe YTDHAWFWNTGLERWVGPSRDRIRYNQFRRELITVLIDVSLFFPNYDSRTYPIRTVQO
240 250 260 270 280 290
40253 YTDRCVKNVNGLDKLRSSYESWVNFNRRRMTLITLIDIALFLYDLVRYPKEVKTE
250 260 270 280 290

cry1a-105.pe LTRRIYTNPVL--ENFDSPRSGSAGGIESIRSPHMDILNSITIIYDAHGEV-----
270 280 290 300 310 320
40253 LTRDVLTDPLVGNVNLRG-YGTTFSNIENIYKPKFLFYLRHQFHRFPQPGYGNDSFN
300 310 320 330 340 350

cry1a-105.pe YWSGHQIMASPVGFSGPEFTPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFNI
320 330 340 350 360 370
40253 YWSGNVYSTRPSIGSNDIITSPFYGNK--SSEPQVONLEFN-GEKVYRAVANTNLAVWPSAV
360 370 380 390 400 410

cry1a-105.pe --GINNCOQLSVL-DGTEFAYGTSNLPFAVYKSGTV--DSLDEIPQNNVPPROGFSSH
380 390 400 410 420
40253 YSGVKVEFSQVNDQDEA--STQTYDSK--RNVGAVSWDSIDQLPETTDEPLEKGYSH
420 430 440 450 460 470

cry1a-105.pe RLSHVSMFRSGFSNSVSIIRAPMFHSIAEFNIIASDSITQIPLVKAHFLQSGTIV
430 440 450 460 470 480
40253 QLVNVMCFMQSGRGTI-----PVLTWTHKSVDFNMDSKKITQLPLVKAYKLGASV
480 490 500 510 520

cry1a-105.pe VRGPGFTGGDILRRSTGGPFAYTIIVNINQQLPQRYRARIYASTNLRIYTVVAGERIFA
490 500 510 520 530 540
40253 VAGPRFTGGDIIQCTENGSAATIIYVTPDVSYQKYRARIHYASTSQTFTLSLDGAPFNQ
530 540 550 560 570 580

cry1a-105.pe GQFNKMTMDGDLTTFQSPSYATINTAFTPMSSQSFYVADTFSSGNEVYIDRFELIPVT
550 560 570 580 590 600
40253 YFDKTIKNGDILITNSFNLASFTPE--LSGNNLQIGVTGLSAGDKVYIDKIEFIPVN
590 600 610 620 630 640

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

cry1a-105.pep
SW:61221658

61221658 description="pesticidal crystal protein cry3Aa precursor (Insecticidal
delta-endotoxin CryIIIA(a)) (Crystalline entomocidal protoxin) (73 kDa crystal
protein)." library="NA species="Bacillus thuringiensis serovar morrisoni"
source="swissprot_prot" version="NA type="PRT

SCORES Initl: 467 Initn: 832 Opt: 1242 Z-score: 1408.1 E(): 3.9e-70
>>SW:61221658
Initn: 832 Initl: 467 opt: 1242 Z-score: 1408.1 expect(): 3.9e-70
Smith-Waterman score: 1246; 36.6% identity in 569 aa overlap
(56-607:91-643)

cry1a-105.pe GERIETGYTPIDISLSTQFLSEFVGAGFVLGLVDIIMGIFGSPQWDAFLVOIEQLIN
30 40 50 60 70 80
61221658 TTKDVKQIGSVVGLDGLGWCFPGGALVSFTNFWLNTWPSDEP--WKAFMEQVEALMD
70 80 90 100 110
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cry1a-105.pe ORTEEFANQAIISLEGSLNLYQIYAESFREWEADPT---NPALREEMRIQFNDNMSALT
120 130 140 150 160 170 180 190 200
61221658 SKIADYAKNKALAELOGLNQNVEDYVSALSSWQKPNVSSRNPHSQGRIRLFSQAESHFR
120 130 140 150 160 170 180 190 200
cry1a-105.pe TAIPUFAYONVOVLLSVYVQAAANLHLSVLRDVSFGVPGAGVLGVDIIWGIIFGSPQMDAFVQIEOLIN
120 130 140 150 160 170 180 190 200
61221658 NSMPSFAISGVEVLFTTYAQAANTHLLFKDAQIYGEWGYEKEDIAFFYKROLKLTQE
120 130 140 150 160 170 180 190 200
cry1a-105.pe YTDHVRVYNTGLERVMGDPDRDRIYNOQFRELTLTLDIVLSLFFNRYNDLTRIGN
120 130 140 150 160 170 180 190 200
61221658 YTDHCVKYNVGLKLRGSSYESWVNFNRYRREMTLTVDLIALFLYDVRLYPKEVKTE
120 130 140 150 160 170 180 190 200
cry1a-105.pe LTREIYTPVL--ENFDGSPRGAQIEGSRSPHLMIDILNSITITDAHGEY-----
120 130 140 150 160 170 180 190 200
61221658 LTRDVLTPPIGVNLRG-YGTTFNSIENYIRKPHLFYLRHQFTRFQRYGYNDSFN
120 130 140 150 160 170 180 190 200
cry1a-105.pe YNSGQIMASPVGSGPEFTFPLYGTMNAPOQRIVAQIQQGVYRTLSST-LYRRPFI
120 130 140 150 160 170 180 190 200
61221658 YNSGNYVSTRISGSDNIIITSPYGNK-SSEPVQNLFEF-GEKYVAVANTNLAVWPSAV
120 130 140 150 160 170 180 190 200
cry1a-105.pe --GINNQQLSVL-DGTEFAYGTSSNLPASVYKSGTV--DSLDEIPQNNVPPROGFSH
120 130 140 150 160 170 180 190 200
61221658 YSGVTKVFEFSYNDQIDEA--STQTYDSK--RNVGAVSWDSIQLPPTTDEPLEKGYSH
120 130 140 150 160 170 180 190 200
cry1a-105.pe RLHSHVMSRSGFNSVSIIRAPMFWSWIRHSAFNNIIASDSITQIPLVKAHTLOSQTV
120 130 140 150 160 170 180 190 200
61221658 QLNYYMCFIMQSGSGTI-----PVLITWTKSVDFNFNIDSKKITQLPLVKAHTLOSQTV
120 130 140 150 160 170 180 190 200
cry1a-105.pe VRGPGFTGDLRLRTSGPFAYTIVNINGQLPQRYRARIYASTNLRIYTVVAGERIFA
120 130 140 150 160 170 180 190 200
61221658 VAGPFTGDDIIQCTENGSAATIVTPDVSYQKRYARIHYASTNLRIYTVVAGERIFA
120 130 140 150 160 170 180 190 200
cry1a-105.pe GQFNKTMIDTGPDLTFQSFYATINTAFTFPMSSQSFVAGADTFSSGNEVYIDRELIPIVT
120 130 140 150 160 170 180 190 200
61221658 YVFDKTIKNGDTLTYSNFIASFTPFE--LSGNLQIGVGTGLSAGDKYIDKIEFIPVN
120 130 140 150 160 170 180 190 200
cry1a-105.pe ATLEAEYNLERAKAVNALFTSTNQLKTNVTDYHIDQVSNLVTYLSDFCLDEKRELS
120 130 140 150 160 170 180 190 200
cry1a-105.pep
SW:61221659

61221659 description="Pesticidal crystal protein cry3Aa precursor (Insecticidal
delta-endotoxin CryIIIAa)) (Crystalline entomocidal protoxin) (73 kDa crystal
protein)." library="NA species="Bacillus thuringiensis serovar san diego"
sources="swissprot_prot" version="NA type="PRT

SCORES Init1: 467 Initn: 832 Opt: 1242 z-score: 1408.1 E(): 3.9e-70
>SW:61221659
Initn: 832 Init1: 467 Opt: 1242 z-score: 1408.1 expect(): 3.9e-70
Smith-Waterman score: 1246; 36.6% identity in 569 aa overlap
(56-607:91-643)
cry1a-105.pe GERIEGTPTIDISLSTQTLSEFVPGAGVLGVDIIWGIIFGSPQMDAFVQIEOLIN
61221659 TTKDVIQGISVWGDLGVGPPFGGALVSFTVNFNTIWPSEDP--WKATMEQVEALMD
cry1a-105.pe ORTEEFANQAIISLEGSLNLYQIYAESFREWEADPT---NPALREEMRIQFNDNMSALT
61221659 OKIADYAKNKALAELOGLNQNVEDYVSALSSWQKPNVSSRNPHSQGRIRLFSQAESHFR
cry1a-105.pe TAIPUFAYONVOVLLSVYVQAAANLHLSVLRDVSFGVPGAGVLGVDIIWGIIFGSPQMDAFVQIEOLIN
61221659 NSMPSFAISGVEVLFTTYAQAANTHLLFKDAQIYGEWGYEKEDIAFFYKROLKLTQE
cry1a-105.pe YTDHVRVYNTGLERVMGDPDRDRIYNOQFRELTLTLDIVLSLFFNRYNDLTRIGN
61221659 YTDHCVKYNVGLKLRGSSYESWVNFNRYRREMTLTVDLIALFLYDVRLYPKEVKTE
cry1a-105.pe --GINNQQLSVL-DGTEFAYGTSSNLPASVYKSGTV--DSLDEIPQNNVPPROGFSH
61221659 YSGVTKVFEFSYNDQIDEA--STQTYDSK--RNVGAVSWDSIQLPPTTDEPLEKGYSH
cry1a-105.pe RLHSHVMSRSGFNSVSIIRAPMFWSWIRHSAFNNIIASDSITQIPLVKAHTLOSQTV
61221659 QLNYYMCFIMQSGSGTI-----PVLITWTKSVDFNFNIDSKKITQLPLVKAHTLOSQTV
cry1a-105.pe VRGPGFTGDLRLRTSGPFAYTIVNINGQLPQRYRARIYASTNLRIYTVVAGERIFA
61221659 VAGPFTGDDIIQCTENGSAATIVTPDVSYQKRYARIHYASTNLRIYTVVAGERIFA
cry1a-105.pe GQFNKTMIDTGPDLTFQSFYATINTAFTFPMSSQSFVAGADTFSSGNEVYIDRELIPIVT
61221659 YVFDKTIKNGDTLTYSNFIASFTPFE--LSGNLQIGVGTGLSAGDKYIDKIEFIPVN

61221657 cry1a-105.pe ATLEAEYNLERAKAVNAFTSTNQLGLKTNVTDYHDQVSNLVTLSDEFCLDEKRELS
610 620 630 640 650 660

cry1a-105.pep
SW:61221657

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

SCORES Initl: 467 Initn: 832 Opt: 1242 z-score: 1408.1 E(): 3.9e-70
>>SW:61221657
initn: 832 initl: 467 opt: 1242 z-score: 1408.1 expect(): 3.9e-70
Smith-Waterman score: 1246; 36.6% identity in 569 aa overlap
(56-607:91-643)

61221657 cry1a-105.pe GERIETGTPDISLSLTQFLSEFVPGAGFVLGLVDIIMGIFGPSQMDAFLVQLEOLIN
610 620 630 640 650 660

61221657 cry1a-105.pe QRIEFARNQAIISLEGLSNLYQIVAESFREWADPT---NPALREEMRIQFNDMNSALT
610 620 630 640 650 660

61221657 cry1a-105.pe YTDHCVKWNVGLDKLGGSSYVSWNFRYRREMLTVLDLIALFLDYDRLYKPVKTE
610 620 630 640 650 660

61221657 cry1a-105.pe YTDHCVKWNVGLDKLGGSSYVSWNFRYRREMLTVLDLIALFLDYDRLYKPVKTE
610 620 630 640 650 660

61221657 cry1a-105.pe YTDHCVKWNVGLDKLGGSSYVSWNFRYRREMLTVLDLIALFLDYDRLYKPVKTE
610 620 630 640 650 660

61221657 cry1a-105.pe YTDHCVKWNVGLDKLGGSSYVSWNFRYRREMLTVLDLIALFLDYDRLYKPVKTE
610 620 630 640 650 660

61221657 cry1a-105.pe YTDHCVKWNVGLDKLGGSSYVSWNFRYRREMLTVLDLIALFLDYDRLYKPVKTE
610 620 630 640 650 660

61221657 cry1a-105.pe YTDHCVKWNVGLDKLGGSSYVSWNFRYRREMLTVLDLIALFLDYDRLYKPVKTE
610 620 630 640 650 660

61221657 QLNVMCFMQSGRTI-----PVLTWTHKSVDFENMIDSKKITQLPLVKAYKLGSGASV
480 490 500 510 520

61221657 cry1a-105.pe VRQPGTGDILRTSGPFPAYTIVNINQQLPQRYRARIYASTTNLRIYTVAGERIFA
490 500 510 520 530 540

61221657 cry1a-105.pe GQFNKMTGDPPLTFQSFVATINATFPMSQSFVVGADTFSSGNEVYIDRFELIPVT
490 500 510 520 530 540

61221657 cry1a-105.pe ATLEAEYNLERAKAVNAFTSTNQLGLKTNVTDYHDQVSNLVTLSDEFCLDEKRELS
610 620 630 640 650 660

cry1a-105.pep
NRAA:4688623

4688623 source="GENBANK_PROT" Cry3Aa protein [Bacillus thuringiensis]gi|142734|gb|AAA22336.1| delta-endotoxin
thuringiensis|gi|142734|gb|AAA22336.1| delta-endotoxin
SCORES Initl: 467 Initn: 832 Opt: 1242 z-score: 1408.0 E(): 3.9e-70
>>NRAA:4688623
initn: 832 initl: 467 opt: 1242 z-score: 1408.0 expect(): 3.9e-70
Smith-Waterman score: 1246; 36.6% identity in 569 aa overlap
(56-607:99-651)

61221657 cry1a-105.pe GERIETGTPDISLSLTQFLSEFVPGAGFVLGLVDIIMGIFGPSQMDAFLVQLEOLIN
610 620 630 640 650 660

61221657 cry1a-105.pe QRIEFARNQAIISLEGLSNLYQIVAESFREWADPT---NPALREEMRIQFNDMNSALT
610 620 630 640 650 660

61221657 cry1a-105.pe YTDHCVKWNVGLDKLGGSSYVSWNFRYRREMLTVLDLIALFLDYDRLYKPVKTE
610 620 630 640 650 660

61221657 cry1a-105.pe YTDHCVKWNVGLDKLGGSSYVSWNFRYRREMLTVLDLIALFLDYDRLYKPVKTE
610 620 630 640 650 660

61221657 cry1a-105.pe YTDHCVKWNVGLDKLGGSSYVSWNFRYRREMLTVLDLIALFLDYDRLYKPVKTE
610 620 630 640 650 660

61221657 cry1a-105.pe YTDHCVKWNVGLDKLGGSSYVSWNFRYRREMLTVLDLIALFLDYDRLYKPVKTE
610 620 630 640 650 660

CRY1A-105.pe LTRREIYTPVL--ENFGSPRGAQIEGSIKRSRPHLMDILNSIITYDAHGEY-----
143084 LTRDVLTPVGVANLRG-YGTTFISNIENIRKPHLFDYLRHQFTFRPQGYGNSDFN
300 310 320 330 340 350
CRY1A-105.pe YNSGHOIMASVPGSGPEFTFLYGTMGNAAPQORIVAOGLQGVGYRTLSST-LYRPPNI
320 330 340 350 360 370
143084 YNSGNTVSTRSIGNSDIIITSPFIGNK-SSPEVQNLFFN-GEKVYAVANTNLAWFSAV
360 370 380 390 400 410
CRY1A-105.pe --GINNQQLSVL-DGTEFAYGTSSNLPSSAVRKSQTV--DSLDEIPPPQNNVPPRQGFSH
380 390 400 410 420
143084 YSGVTKVEFSQVNDQDEA--STQTVDSK--RNUGAVSWDSIDQLPETTDEPLEKGYSH
420 430 440 450 460 470
CRY1A-105.pe RLSHVSMFSGSGSSVSIIRAFMFHRSAEFNNIIASDSITQIPLVKAHTLOSQTIV
430 440 450 460 470 480
143084 QLNVMCMFLMQSGRTI-----FVLWTHTKSVDFNFNIDSKITQLPLVKAHKLOSQASV
480 490 500 510 520 530
CRY1A-105.pe VRGPGFTGDIILRTSGSPFAYTIVNINQOLPQRYRARIYASTNLRITVTVAGERIFA
490 500 510 520 530 540
143084 VAGPRFTGGDIIOCTENASATITVTPDVSYSQKYRARIHVASTISQITTLSDGAPPNQ
530 540 550 560 570 580
CRY1A-105.pe GQNKMTDGTDLTFQSFVATINTAFTFPMQSSFTVGADTFSSGNEVYIDRFELIPVT
550 560 570 580 590 600
143084 YYFDKINKGDTLTYNSENLASFSTPFE--LSGNNLQIGVTGLSAGKVVLDKIEFIVN
600 610 620 630 640 650
CRY1A-105.pe ATLEAEYNLERAKAVNALFTSNQLGLKNTVDHIDQVSNLVYLSDEFCLDEKRELS
610 620 630 640 650 660
CRY1A-105.pep
NRAA:143084
143084 source="GENBANK_PROT" insect control protein
SCORES Initl: 467 Initn: 824 Opt: 1234 Z-score: 1399.0 E(): 1.2e-69
>>NRAA:143084
Initn: 824 Initl: 467 Opt: 1234 Z-score: 1399.0 expect(): 1.2e-69
Smith-Waterman score: 1238; 36.4% identity in 569 aa overlap
(56-607:91-643)
CRY1A-105.pe GERIETGYTPIDISLSLTQFLSEFVPGAGFVLGLVDLIWGIFGSPQNDALVQIEQLIN
30 40 50 60 70 80
143084 TTQXDVTKQGISVVGDLGVGFFPGGALVSFYTNFLNTIWSEDP--WKAFMEQVEALMD
70 80 90 100 110
CRY1A-105.pe TAIPLFAVQNYQVPLLSVYQAAHILSLVLRDVSVFCQRMGFDATINSYNDLIRLIGN
90 100 110 120 130 140
143084 QRIEEFARNAQALSRLEGLSNLYQIYAESFREWEADPT--NPALREMRITQFNDNWSALT
120 130 140 150 160 170
CRY1A-105.pe YTHAVRWNTGLRWGPDSDRWIRYNQFRRLTLTVLDIVSLFPPNYSRTVPRTVSQ
150 160 170 180 190 200
143084 NSMPSFAISGYEVLFTTYAQAAHNLFLKDAQIYGBEWGYEKEDAEFYKRLKLTQOE
180 190 200 210 220 230
CRY1A-105.pe YTHAVRWNTGLRWGPDSDRWIRYNQFRRLTLTVLDIVSLFPPNYSRTVPRTVSQ
210 220 230 240 250 260
143084 YTHCQKWNVGLDKLRGSSYSESWNFNRYREMTLTVLDLIALFFLYDVLVPEKVTKE
240 250 260 270 280 290

CRY1A-105.pe LTRREIYTPVL--ENFGSPRGAQIEGSIKRSRPHLMDILNSIITYDAHGEY-----
143084 LTRDVLTPVGVANLRG-YGTTFISNIENIRKPHLFDYLRHQFTFRPQGYGNSDFN
300 310 320 330 340 350
CRY1A-105.pe YNSGHOIMASVPGSGPEFTFLYGTMGNAAPQORIVAOGLQGVGYRTLSST-LYRPPNI
320 330 340 350 360 370
143084 YNSGNTVSTRSIGNSDIIITSPFIGNK-SSPEVQNLFFN-GEKVYAVANTNLAWFSAV
360 370 380 390 400 410
CRY1A-105.pe --GINNQQLSVL-DGTEFAYGTSSNLPSSAVRKSQTV--DSLDEIPPPQNNVPPRQGFSH
380 390 400 410 420
143084 YSGVTKVEFSQVNDQDEA--STQTVDSK--RNUGAVSWDSIDQLPETTDEPLEKGYSH
420 430 440 450 460 470
CRY1A-105.pe RLSHVSMFSGSGSSVSIIRAFMFHRSAEFNNIIASDSITQIPLVKAHTLOSQTIV
430 440 450 460 470 480
143084 QLNVMCMFLMQSGRTI-----FVLWTHTKSVDFNFNIDSKITQLPLVKAHKLOSQASV
480 490 500 510 520 530
CRY1A-105.pe VRGPGFTGDIILRTSGSPFAYTIVNINQOLPQRYRARIYASTNLRITVTVAGERIFA
490 500 510 520 530 540
143084 VAGPRFTGGDIIOCTENASATITVTPDVSYSQKYRARIHVASTISQITTLSDGAPPNQ
530 540 550 560 570 580
CRY1A-105.pe GQNKMTDGTDLTFQSFVATINTAFTFPMQSSFTVGADTFSSGNEVYIDRFELIPVT
550 560 570 580 590 600
143084 YYFDKINKGDTLTYNSENLASFSTPFE--LSGNNLQIGVTGLSAGKVVLDKIEFIVN
600 610 620 630 640 650
CRY1A-105.pe ATLEAEYNLERAKAVNALFTSNQLGLKNTVDHIDQVSNLVYLSDEFCLDEKRELS
610 620 630 640 650 660
CRY1A-105.pep
NRAA:58826238
58826238 source="GENBANK_PROT" Cry1Aa delta endotoxin [Bacillus thuringiensis
serovar tenebrionis]
SCORES Initl: 467 Initn: 832 Opt: 1226 Z-score: 1389.9 E(): 4e-69
>>NRAA:58826238
Initn: 832 Initl: 467 Opt: 1226 Z-score: 1389.9 expect(): 4e-69
Smith-Waterman score: 1230; 36.2% identity in 569 aa overlap
(56-607:91-643)
CRY1A-105.pe GERIETGYTPIDISLSLTQFLSEFVPGAGFVLGLVDLIWGIFGSPQNDALVQIEQLIN
30 40 50 60 70 80
58826238 TTQXDVTKQGISVVGDLGVGFFPGGALVSFYTNFLNTIWSEDP--WKAFMEQVEALMD
70 80 90 100 110 120
CRY1A-105.pe QRIEEFARNAQALSRLEGLSNLYQIYAESFREWEADPT--NPALREMRITQFNDNWSALT
90 100 110 120 130 140
58826238 OKIADYAKNKALAELOGLQNNVEDYVSALSSWQKNPVSRRPHSQGRIRLEFSQAESYFR
120 130 140 150 160 170 180 190 200

Product Characterization Center

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cyla-105.pe TAIPFAVQNYQVPLISVTVQAANLHLSVLVDVSVFGQWGDAAATINSRVNDLTIGN
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
58826238 NSMPSFALSGVEYLFITTTAAQANHLFLAKDAQIQYGEWGYEKEDIAEFYKRLQKITOE
180 190 200 210 220 230

cyla-105.pe YTDHAVRWYNTGLERVMGPDSDRMIRYNQFRRELTITVLIDVLSFPNVDSTYPIRTVSQ
260 270 280 290 300 310
YTDHCVMYVNGLDKLRGSSGVESWVFNRYRREMTITVLIDIALFLYDURLVPKEVKE
240 250 260 270 280 290

cyla-105.pe LTRIYNPVL--ENPDFSGFRGSAQIEGSIKPSHPLMDILNSITITYDAHGEY-----
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
58826238 LTRDLVTDPTIVGNNLRG--YGTTFSENIENTIRKPHLFNLYRRIQPHTRFGPGYGVNDSEFN
300 310 320 330 340 350
YWSGHQIMASPVFGSGPEFTPLXYGTMGNAAPQRIVAQLOGGYRTLSST-LYRPFNI
320 330 340 350 360 370
YWSGNYSTPSIGSNDIITSPFYGNK-SSEPQNLEFN-GEKYRAVAVNTNLAVMPSAV
360 370 380 390 400 410

cyla-105.pe YWSGHQIMASPVFGSGPEFTPLXYGTMGNAAPQRIVAQLOGGYRTLSST-LYRPFNI
320 330 340 350 360 370
YWSGNYSTPSIGSNDIITSPFYGNK-SSEPQNLEFN-GEKYRAVAVNTNLAVMPSAV
360 370 380 390 400 410

cyla-105.pe --GINNQQLSVL--DQTEFAYGTSSNLPSAVYRKSGTV--DSLDEIIPQNNVPPRGFSH
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
58826238 YSGYTKVEFSQYNDQTEA--STQYDQSK--RNVGAVSWDSIDQLPETTDEPLEKGYSH
420 430 440 450 460 470
QLNYMCFELMQSGRTI-----PVLITKHSVDVDFNMIDSKKTIQLPLVKAAYKLSQGSV
480 490 500 510 520

cyla-105.pe RLSHVSMFSGSGNSSVSIIRAPMFSWIHRSAPFNITASQITQIPLVKAHTLQSGTVV
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
58826238 QLNYMCFELMQSGRTI-----PVLITKHSVDVDFNMIDSKKTIQLPLVKAAYKLSQGSV
480 490 500 510 520

cyla-105.pe VRGPGFTGGDIILRTSGGFPAYTIVNTINGQLPORVYRIRVASTNLRIYVTVAGERIFA
530 540 550 560 570 580
VAGPRFTGGDIIOCTENGSAATIVTDPVSYSKYRARIHVASTSQITFLSLDGAFFNQ
530 540 550 560 570 580

cyla-105.pe GQFNKTMWDGDLTTFQSFYATINTAFTPMQSSQTVGADTFSGSENVIDIRFELPYT
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
58826238 YYFDKTINGDGLTITVNSFNLASSTPFE--LSGNNLQIGVTGLSAGDKVYDKIFIPVN
590 600 610 620 630 640

cyla-105.pe ATLEAEYNLERAKQAVNALFTSTNQLGLKNTVDYHDQVSNLYTSLDEFCLEKRELS
610 620 630 640 650 660

cyla-105.pep
SW:8928018

8928018 description="PESTICIDIAL CRYSTAL PROTEIN CRY8AA (INSECTICIDIAL
DELTA-ENDOTOXIN CRV11A(A)) (CRYSTALLINE ENTOMOCIDIAL PROTOXIN) (I31 KDA CRYSTAL
PROTEIN)." library=NA species="Bacillus thuringiensis serovar kumamotoensis"
source="swissprot_prot" version=NA type=prt

SCORES Initl: 601 Initn: 1940 Opt: 1223 Z-score: 1382.6 E(): 1e-68
>>SW:8928018
initn: 1940 initl: 601 opt: 1223 Z-score: 1382.6 expect(): 1e-68
Smith-Waterman score: 2564; 39.4% identity in 1211 aa overlap
[4-1174:39-1154]

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protein|gi|436833|gb|AA21117.1| CryIII delta-endotoxin

SCORES   Init1: 601   Initn: 1940   Opt: 1223   z-score: 1382.6   E(): 1e-68
>>NRAA:8928018
  initn: 1940   init1: 601   Opt: 1223   z-score: 1382.6   expect(): 1e-68
  Smith-Waterman score: 2564;   39.4% identity in 1211 aa overlap
  (4-1174:39-1154)

cryla-105.pe
10      20      30      40      50      60      70      80      90      100      110      120      130      140      150      160      170      180      190      200      210      220      230      240      250      260      270      280      290      300      310      320      330      340      350      360      370      380      390      400      410      420      430      440      450      460      470      480      490      500      510      520      530
YEIDATPSTVSSDSNRYPFANEPTDALQNNNYKDYLKMSGGENPEL--FGNPETFISS
10      20      30      40      50      60      70      80      90      100      110      120      130      140      150      160      170      180      190      200      210      220      230      240      250      260      270      280      290      300      310      320      330      340      350      360      370      380      390      400      410      420      430      440      450      460      470      480      490      500      510      520      530
TPIDISLITQFLSEF--VPGAGFVLGLVDIIMWIFGPGSQ----WDAFVLQVLEQLINORI
10      20      30      40      50      60      70      80      90      100      110      120      130      140      150      160      170      180      190      200      210      220      230      240      250      260      270      280      290      300      310      320      330      340      350      360      370      380      390      400      410      420      430      440      450      460      470      480      490      500      510      520      530
STIQTGIVGRIILGALGVFPASQIASFVSFVLGQLWPSKVDIMGEIMERVEEVLVDQKI
10      20      30      40      50      60      70      80      90      100      110      120      130      140      150      160      170      180      190      200      210      220      230      240      250      260      270      280      290      300      310      320      330      340      350      360      370      380      390      400      410      420      430      440      450      460      470      480      490      500      510      520      530
EAFARQAISRLEGLSNLYQIAYSFREWEADPTNPALREEMRIQFNDWNSALTATPLF
10      20      30      40      50      60      70      80      90      100      110      120      130      140      150      160      170      180      190      200      210      220      230      240      250      260      270      280      290      300      310      320      330      340      350      360      370      380      390      400      410      420      430      440      450      460      470      480      490      500      510      520      530
EKVKDKALAEILKGLNALDVQOQSLIEDMLENDARTSRVSNQFIADLNFVSSIPSF
10      20      30      40      50      60      70      80      90      100      110      120      130      140      150      160      170      180      190      200      210      220      230      240      250      260      270      280      290      300      310      320      330      340      350      360      370      380      390      400      410      420      430      440      450      460      470      480      490      500      510      520      530
AVNQYQVPLLSVYVOAANLHLVSLVRVSGFQWGFDAATINSRYNDLTRILGNVTHAV
10      20      30      40      50      60      70      80      90      100      110      120      130      140      150      160      170      180      190      200      210      220      230      240      250      260      270      280      290      300      310      320      330      340      350      360      370      380      390      400      410      420      430      440      450      460      470      480      490      500      510      520      530
AJSQNEVLLAVYAOAVNLLHLRLDASIFGEENGFTPGESIFSYFNRQVLTAEYSDYCV
10      20      30      40      50      60      70      80      90      100      110      120      130      140      150      160      170      180      190      200      210      220      230      240      250      260      270      280      290      300      310      320      330      340      350      360      370      380      390      400      410      420      430      440      450      460      470      480      490      500      510      520      530
RWNYTGLRWSPEDRWIRXNFOREBLTLVLDIVSLFNPYDSRTYPIRTYSOLTREIY
10      20      30      40      50      60      70      80      90      100      110      120      130      140      150      160      170      180      190      200      210      220      230      240      250      260      270      280      290      300      310      320      330      340      350      360      370      380      390      400      410      420      430      440      450      460      470      480      490      500      510      520      530
KWYKGLIKLQKATTSKSNTHYHOREMTLLVDLVAFPNDYTHMPLETTAQTURDVI
10      20      30      40      50      60      70      80      90      100      110      120      130      140      150      160      170      180      190      200      210      220      230      240      250      260      270      280      290      300      310      320      330      340      350      360      370      380      390      400      410      420      430      440      450      460      470      480      490      500      510      520      530
TPIAFNIVSTGSCNPMSKSGMLFVEVENVIRPHFLFDILSSVEINTS--RGSITLN
10      20      30      40      50      60      70      80      90      100      110      120      130      140      150      160      170      180      190      200      210      220      230      240      250      260      270      280      290      300      310      320      330      340      350      360      370      380      390      400      410      420      430      440      450      460      470      480      490      500      510      520      530
TPNVLNPGSGFR--LGAAGQI-----EGSIRPHMLDINSITIVDAHRG--
10      20      30      40      50      60      70      80      90      100      110      120      130      140      150      160      170      180      190      200      210      220      230      240      250      260      270      280      290      300      310      320      330      340      350      360      370      380      390      400      410      420      430      440      450      460      470      480      490      500      510      520      530
--EY--YWSGHQIMASVPVGGPFTFPIGAGNAPQQRVAGVGQGVYRTLSLTLYR
10      20      30      40      50      60      70      80      90      100      110      120      130      140      150      160      170      180      190      200      210      220      230      240      250      260      270      280      290      300      310      320      330      340      350      360      370      380      390      400      410      420      430      440      450      460      470      480      490      500      510      520      530
NDAYINVWSGHTLKRYRTADSTVTYT--ANYGATQSNNSFALSRDSEF--INSTVA-
10      20      30      40      50      60      70      80      90      100      110      120      130      140      150      160      170      180      190      200      210      220      230      240      250      260      270      280      290      300      310      320      330      
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8928018 source="GENBANK_PROT" Pesticidal crystal protein cry8Aa (Insecticidal delta-endotoxin CrvVIIIA(a) (Crystalline entomocidal protoxin) (131 kDa crystal

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8928018      -----GYTKVTFTPTDQMWIEISETEGTFYIESVELIVDVE
              1120      1130      1140      1150

cryla-105.pep
SW:117538

117538 description="130 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE
ENTOMOCIDAL PROTOXIN)." library="NA species="Bacillus thuringiensis serovar
israelensis" source="swissprot_prot" version="NA type="PRI

SCORES      Init1: 553      Initn: 1546      Opt: 1204      z-score: 1361.2      E(): 1.6e-67
>>SW:117538
      initn: 1546      init1: 553      opt: 1204      z-score: 1361.2      expect(): 1.6e-67
      Smith-Waterman score: 1817;      33.8% identity in 1182 aa overlap
      (49-1177:57-1135)

20      30      40      50      60      70
cryla-105.pe      FEVEVLGGERTGTPTDLSLSLTFLSEFV-FGAGFVL-----GLVDITWIGFGPSQ-
117538
      CENNOQGVNPAAINSSSVSPALKDAGATLKFWNPAGSVTLVLSAVFLPWPNTPTPE
              30      40      50      60      70      80

cryla-105.pe      --WDAFLVQIEQLINORIEEFARNQAIISLEGLSNLQIVAESEFREWADPTNPALREEM
117538
      RVNDFWNTGNGLIDQTVAVRTDANAKMTVVDLYDQVTKTKRENNQSYETAV
              90      100      110      120      130      140

cryla-105.pe      140      150      160      170      180
117538
      RIQFNDMNSALT-TAIPLFAVQNYQVPLLSVYQAANHLISLVDRVSVFGQWGFDAATI
              190      200      210      220      230      240
cryla-105.pe      NSRYNDLITRLIGNYTHDAVRWYATGLERVWGSDSDIRYNQFRELTLVLDTVSLFPN
117538
      DQLNTMVQTYEYTAHSITWYKGLDVLRNKSGQWITNDYKREMTIQVLDLIALFAS
              250      260
cryla-105.pe      250      260      270      280      290      300
117538
      YDSRTYPIRV-----SQTREIYTNPLENDGDFRSGAQIEGSI-RSPHMDILN
              310      320      330      340      350
cryla-105.pe      SITIIYDA-HRGEYVWSHQIMASPVGSGSEFFPIYGYTMGNADQRIIVA-OLGGGVY
117538
      RVDFTWITIIQDLRFELSNKIGFSYTNSSAMQES-GIYGSGGLV--QIYLKFKNLILIVI
              360      370      380      390      400      410      420      430
cryla-105.pe      RTLSGTLTYRRPFIINNQQSLVLDGTGEFAYGTS-SNLPSAVRKSGTVDLSIDPEPQNN
117538
      KLLSQILA--PLLIELQWISTKFDCTLASVNSNITTPESGL-RTTFFGFSNTNP-----
              440      450      460      470      480
cryla-105.pe      NVPPRQGFGRHLSHVSMFRSGNSVSIIRAPMFSIHRSAEFNNIITASDITQIPLVY
117538
      NOPTVNDYTHILSYIKTIDVIDNSNRVS-----FAWNHIVDPNNQIYTDATIQGPVAVK
              490      500

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cryla-105.pe	480	490	500	510	520	530	540
117538	480	490	500	510	520	530	540
cryla-105.pe	540	550	560	570	580	590	600
117538	540	550	560	570	580	590	600
cryla-105.pe	590	600	610	620	630	640	650
117538	590	600	610	620	630	640	650
cryla-105.pe	640	650	660	670	680	690	700
117538	640	650	660	670	680	690	700
cryla-105.pe	700	710	720	730	740	750	760
117538	700	710	720	730	740	750	760
cryla-105.pe	760	770	780	790	800	810	820
117538	760	770	780	790	800	810	820
cryla-105.pe	820	830	840	850	860	870	880
117538	820	830	840	850	860	870	880
cryla-105.pe	870	880	890	900	910	920	930
117538	870	880	890	900	910	920	930
cryla-105.pe	930	940	950	960	970	980	990
117538	930	940	950	960	970	980	990
cryla-105.pe	990	1000	1010	1020	1030	1040	1050
117538	990	1000	1010	1020	1030	1040	1050
cryla-105.pe	1050	1060	1070	1080	1090	1100	1110
117538	1050	1060	1070	1080	1090	1100	1110

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1110      1120      1130      1140      1150      1160
cryla-105.pe YASVTEEKSYDGRREPCFNFGYRDYTPDPGVVTKLELFPPEDDKDWIEIGETGFIF
117538 -----GYITKVDVDFPDTRDRVRIEIGETGGF
1100      1110      1120
cryla-105.pe IVDSVELLMEE
117538 YIESIELICWNE
1130
cryla-105.pep
NRAA:142738
142738 source="GENBANK_PROT".mosquitocidal protein

SCORES      Init1: 553      Initn: 1546      Opt: 1204      Z-score: 1361.2      E(): 1.6e-67
>>NRAA:142738
initn: 1546      init1: 553      opt: 1204      Z-score: 1361.2      expect(): 1.6e-67
Smith-Waterman score: 1817;      33.8% identity in 1182 aa overlap
(49-1177:57-1135)

cryla-105.pe PEVEVLGGERIETGYTPIDISLSTOFLSEFV-PGAGFVL-----GLVDIIWGIFGSGQ-
142738 CENNQQYGVNPAINSSSVSTALADGAKILKEVNPAGSLVLSAVLFLPMTPTTPE
30      40      50      60      70      80
cryla-105.pe --WASLVQLEQLINORIEEFARNQISRLGSLNLIQIVAESFREWEDPTNPALREEM
142738 RVWMDPFMTNENLNQOTVAVRIDANAKTVVKKDYLDQHTTFTWKEKPEPNQSYRTAV
90      100      110      120      130      140
cryla-105.pe RIGENDNMNSALT-TAIFPAVONTQVPLLSVVQAAHLHLSVLRDVSVEFGQWGFDAATI
142738 ITQNLTSAKLRETAALALVGVYELLIIYVAQVANFNLLIRDGPHKCTRMVY-ARSC
150      160      170      180      190      200
cryla-105.pe NSRYNDILRLIGNYTHAQRVNTGLFVWGPDSRDMTRINQFRRETLTIVLDIVSLFPN
142738 DQLYNTWVQVYKEYIAHSITWYNGGLDVLNLSNQTWTFNRYKRENTIQVLDIALFAS
210      220      230      240      250      260
cryla-105.pe YDSRTYPIRV-----SOLTREIYNTNPNENQSGFSGAGIEGSI-LEPHANDLIAN
250      260      270      280      290      300
cryla-105.pe YDPRIYFADKIDNTKLSKTEFTRIYALV----EPFSKSLAALDPAITRQVHLFTVPLN
270      280      290      300      310      320
cryla-105.pe SITTIYVDA-HRGEYVWSHQIMASPVGFSPEFTFLVGTGMNAPQASVA-QIQMA
310      320      330      340      350      360
142738 RYDFWTNIIQDRLRFILSANKIGFYVNTSSAMQES-GIYGSSGLV-QIVLKEFLIDAV
330      340      350      360      370      380
cryla-105.pe RYLSTLYLRFFNIGINNOQLSVLDGTGEFAYGTS-SNLPASVYRKSGTVDSLDSEIPPQN
360      370      380      390      400      410
142738 KLSQILA--PPILELQKWISTKFDGLTASVNSNITTPPEGL-RTTFIFGFSNTENPT-
380      390      400      410      420      430

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1050      1060      1070      1080      1090      1100
cry1a-105.pe TIEHIENNDELKSNCEVEEIIYNNVTCTNDYTVNOEEVGGAYTSRRNGYNEAPSPAD
142738      : : : : : : : : : : : : : : : : : : : : : : : :
TLMDCEENOEKLTTSCEE-----
1080      1090

1110      1120      1130      1140      1150      1160
cry1a-105.pe YASVYEKSYTDGRRENPCFNGYRDYTPLPVGYVTKLEYFPEPTDKVWIEGETGTF
142738      : : : : : : : : : : : : : : : : : : : : : : : :
-----GIIKTVDVDFPDTRDRVEIGETEGSF
1100      1110      1120

1170
cry1a-105.pe IVDSEVLLMEE
142738      : : : : : : : : : : : : : : : : : : : : : : : :
YIESIELICMNE
1130

cry1a-105.pep
NRGA:15988322

15988322 source="GENBANK_PROT" Chain A, Crystal Structure Of The Insecticidal
Bacterial Del Endotoxin Cry3bb1 Bacillus Thuringiensis

SCORES      Initl: 411      Initn: 1070      Opt: 1173      z-score: 1330.2      E(): 8.4e-66
>>NRGA:15988322
      Initn: 1070      Initl: 411      Opt: 1173      Z-score: 1330.2      expect(): 8.4e-66
Smith-Waterman score: 1242;      36.7% identity in 583 aa overlap
(51-607:19-587)

cry1a-105.pe VEVLGGERIETGTPIDISLSLTQFLSFEVPGAG----FVLGLVDIIIMGIFGFSQ---W
15988322      30      40      50      60      70
      10      20      30      40
      DAVGTGISVWGQILGVGVGFAGALTSFYQSFLTNIW----PSDADPW

cry1a-105.pe 80      90      100      110      120      130
      : : : : : : : : : : : : : : : : : : : : : : : :
DAFLVQLINQRIEFPARNQAI SRLEGLSNLYCIITAESEFREWADPTN-PALUREMRI
15988322      50      60      70      80      90      100
      KAFMAQVEVLIDIKIEEYAKSKALAELOGLQNFEDYVNALNSWKTPLSLRKSRQDRI

cry1a-105.pe 140      150      160      170      180      190
      Q--FNDMNSALTTAIPLFAVONYQVPLLSVYQAAHLHLSVLDRSDVFGQRMGFDAATIN
15988322      110      120      130      140      150      160
      RELFSQAESHFNFSMPFSVSKFEVLFTFYAQANTHLLKLDQAQVFGEEWGVSSEDVA

cry1a-105.pe 200      210      220      230      240      250
      SRYNDLTRIGNYDTHAVRYNTGTLERVWGPDSRDWRINQFRRELTITLVDIVSFPNY
15988322      170      180      190      200      210      220
      EFVHQRLKLTQOQYTDHCWNVYVNLGLRGSTYDAWKFNFREREMTLTLDLGLVLPFFY

cry1a-105.pe 260      270      280      290      300
      DSRTYPIRVUSOLTRIETHTPVLE-NFGDSFRGSAQIGESRSPLHMDLINSITIYDHA
15988322      230      240      250      260      270      280
      DIRYSKGVKTELTNRIDFTDPIFSLNTLQOEGYPTFLSIENSIRKKPHLFDYLGQIEFHRL

cry1a-105.pe 310      320      330      340      350      360
      YWSHQHQMASPVGFSPEFTFLPYLGTMGNAAPQORIYAQVGQGVYRTLS
15988322      : : : : : : : : : : : : : : : : : : : : : : : :

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15988322 GPYFGKDFNTNSGKVVETRPISGSKTITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
290 300 310 320 330 340
cry1a-105.pe ST-LYRRP-ENIGINNQQLSVLDTGTFAYGTSNLPFAVYKSGTV--DSLDEIPPO
370 380 390 400 410
15988322 NTDAWAPNPKVKYLQVTVVDSQYDDQK--NETSTQYDSKRNNGHVSQAQSDIQLPPE
350 360 370 380 390
cry1a-105.pe NNVPVPRQGFHRLSHVSMFSGFSNVSIIIRAPMFWSIHRSFAEFNIIASDSITQPL
420 430 440 450 460
15988322 TTDEPLEKAYSHQLNYAECAFMQDRGTI--PFTWTHTRSVDFTIDAETKIQLPV
400 410 420 430 440
cry1a-105.pe LRIVTVAGERIFAGQENKMDIGDPLTFQSPSYATINTATFPMSQSSNTVCATDESG
540 550 560 570 580
15988322 LRUFVQNSNDFVIYINKTNKDDLLTYQTFDLATNSNMFGSGDKNELIIGAESFVSN
520 530 540 550 560
cry1a-105.pe NEVVIDRFEIIPVATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDVHIDQVSNLVTY
600 610 620 630 640
15988322 EKIVDKIEFIPVQL
580
cry1a-105.pe
SW:8469155
8469155 description="PESTICIDIAL CRYSTAL PROTEIN CRY3BB (INSECTICIDIAL
DELTA-ENDOTOXIN CRYIIIB(b)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (74 KDA CRYSTAL
PROTEIN)." library=NA species="Bacillus thuringiensis" source="swissprot_prot"
version=NA type=PRT
SCORES Initl: 411 Initn: 1070 Opt: 1173 Z-score: 1329.6 E(): 9.2e-66
>>SW:8469155
initn: 1070 initl: 411 opt: 1173 Z-score: 1329.6 expect(): 9.2e-66
Smith-Waterman score: 1242; 36.7% identity in 583 aa overlap
(51-607:82-650)
cry1a-105.pe VEVLGGERIETGYTPIDISLSLTQFLSEFVPGAG---FVLGLVDIIMGIFGPSQ---W
30 40 50 60 70
8469155 SSTIEVLDSNTVKDAVGTGIVSGVQGLGVGVFPAGALTSFYQSELTNIW----PSDADPW
60 70 80 90 100
cry1a-105.pe DAEVLQTEQLINQRIEEFARNQALSRLEGLSNLYQIYAESFREWEDPTN-PALREEMRI
80 90 100 110 120 130
8469155 KAFMAQVEVLIDKKIEEYAKKALAELOGLQNNFEDYVNALSNKKPTLSLRKRSQDRI
110 120 130 140 150 160
cry1a-105.pe Q--FNDMNSGALTTAIPFAVQNYQVPLLSVYQVQANLHLSVIRDVSVFGQGWGFDAAIN
140 150 160 170 180 190
8469155 RELFSQAGSHFRNSMPSFAVSKFEVLFLPTYAQAAHTLLLLDKDAQVFGSEWYSSDA
170 180 190 200 210 220

cry1a-105.pe SRVNDLTRIGNYTDHVAWNTGLRVAGPDSRDWRVYQFRRRLTLVLDIVSLFPNY
200 210 220 230 240 250
8469155 EFTHROKLTQQTIDHCNVNINGLNGLRGSTYDAWVAFRRFREMILTVLDIVLVPFY
230 240 250 260 270 280
cry1a-105.pe DSRTYIRVTSQLTREIYVNFVLE-NFDGSRFGSAQAGIESIRSPHMLDILNSITYTDA
260 270 280 290 300
8469155 DIRLSKGVKTELTDRIDTPISLNTLOEYGTPTFLSTENSIKRPKPHLFYDLOGIEFHTRL
290 300 310 320 330 340
cry1a-105.pe YWSGHOIMASPVGFGSPFTFPLTGTMGNAAPQORIVAQQLGQVYRTLS
310 320 330 340 350 360
8469155 OPGYFGKDFNTNSGKVVETRPISGSKTITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400
cry1a-105.pe ST-LYRRP-ENIGINNQQLSVLDTGTFAYGTSNLPFAVYKSGTV--DSLDEIPPO
370 380 390 400 410
8469155 NTDAWAPNPKVKYLQVTVVDSQYDDQK--NETSTQYDSKRNNGHVSQAQSDIQLPPE
410 420 430 440 450 460
cry1a-105.pe NNVPVPRQGFHRLSHVSMFSGFSNVSIIIRAPMFWSIHRSFAEFNIIASDSITQPL
420 430 440 450 460 470
8469155 TTDEPLEKAYSHQLNYAECAFMQDRGTI--PFTWTHTRSVDFTIDAETKIQLPV
470 480 490 500 510
cry1a-105.pe VKAHTLOSCTTVVRGPGTGGDILR-RTSGGPFAVTIYVINGQ-LPQRYEARIRVASTTN
480 490 500 510 520 530
8469155 VKAYALSSGASIEGPGFTGNGLLFLKESNSIARPKVTNLSAALLQRYRVRYASTTN
520 530 540 550 560 570
cry1a-105.pe LRIVTVAGERIFAGQENKMDIGDPLTFQSPSYATINTATFPMSQSSNTVCATDESG
540 550 560 570 580 590
8469155 LRUFVQNSNDFVIYINKTNKDDLLTYQTFDLATNSNMFGSGDKNELIIGAESFVSN
580 590 600 610 620 630
cry1a-105.pe NEVVIDRFEIIPVATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDVHIDQVSNLVTY
600 610 620 630 640 650
8469155 EKIVDKIEFIPVQL
640 650
cry1a-105.pe
NRAA:8469155
8469155 source="GENBANK PROT" Pesticidal crystal protein cry3bb insecticidal
delta-endotoxin CRYIIIB(b)) (CRYSTALLINE entomocidal protoxin) (74 kDa crystal
protein)gi|142730|gb|AAA2234.1| cryIIIB2
SCORES Initl: 411 Initn: 1070 Opt: 1173 Z-score: 1329.6 E(): 9.2e-66
>>NRAA:8469155
initn: 1070 initl: 411 opt: 1173 Z-score: 1329.6 expect(): 9.2e-66
Smith-Waterman score: 1242; 36.7% identity in 583 aa overlap
(51-607:82-650)
cry1a-105.pe VEVLGGERIETGYTPIDISLSLTQFLSEFVPGAG---FVLGLVDIIMGIFGPSQ---W
30 40 50 60 70

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MSL No. 20351
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8469155 SSTEVLNDSTVKDAVGTGIVGVQILGVVGFAGALTSFYQSFLNTLW----PSDADPW
      60      70      80      90      100      110      120      130
cry1a-105.pe DFLVQIQLINQRIEIEFARNQAIISRLGLSNLYQIYAESEFWEADPTN-PALREEMRI
      80      90      100      110      120      130
8469155 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALMSWKTLPLSRKSDRI
      110      120      130      140      150      160
cry1a-105.pe Q--ENDNWSALTATPLFAVQNYQVPLSVVQANLHLSVLVDVSFGQWGFDAATIN
      140      150      160      170      180      190
8469155 RELFSQAESHFNRSMFSAVSKFEVLFLPTVAQAANTHLLLLKDAQVFGEEWGSSEDA
      170      180      190      200      210      220
cry1a-105.pe SRYNDLRLIGNYTDHVRWYNTGLERWGPDSKDWIRYNQFRRELTTLVDIVSLFPNY
      200      210      220      230      240      250
8469155 EYHRLQLTQOYTDHCVMYVNGVGLRGSTDAWKFNFRREWTLLVDLIVLPFY
      230      240      250      260      270      280
cry1a-105.pe DERYPTVSLQTRITRYNTPVLE-NFDGSRGSAQIGSIRSPLHMDILNISIITYDA
      260      270      280      290      300
8469155 DIRLYSGVKTELTRDIFTDPIFSLNTIQEYGTFLSIENSIRKPHLPDYLGIEFHTL
      290      300      310      320      330      340
cry1a-105.pe HRGEY-----YMSGHQINASPVGSGPEFTFLYGTMGNAAPQRIVAQLGQVYRTLS
      310      320      330      340      350      360
8469155 QGYFGKDSFNYSNGYVETRSIGSKTITSFYGDK-SIEPIQKLSFD-GQKVYRTIA
      350      360      370      380      390      400
cry1a-105.pe ST-LYRRP-----FNIGINNQLSVLDGTEFAYGTSNLPASVYRKSGTV---DSLDEIPQ
      370      380      390      400      410
8469155 NTDVAAPNGKVLGVTKVDFSOYDQK--NETSTQYDSKRNGHVSQAQDSIDQLPE
      410      420      430      440      450      460
cry1a-105.pe NNVPYPRQGSHELHSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPL
      420      430      440      450      460      470
8469155 TTDEPLEKAYSHQLNAYAECLMQDRRGTI-----PFFTWHRSVDFNTIDAEEKITQLPV
      470      480      490      500      510
cry1a-105.pe VKAHTLOSQTVVRGPGFTGGDILR-RTSGGPFAYTVNNGQ-LPQRYRIRYASTTN
      480      490      500      510      520      530
8469155 VKAVALSSGASIIIEGPGFTGNLLFLKSSNSIAKPKVTLASALLQRYRIRYASTTN
      520      530      540      550      560      570
cry1a-105.pe LRIYTVAGERIPAGQFNKMTDGLPTFQSPSYATINTAFTFPMSSQSTVGADFPSSG
      540      550      560      570      580      590
8469155 LRLFEVQNSNNDFLVIYINKTNKDDDLTYQTFDLATNSNMWFGSGDKNLIIGAESFVN
      580      590      600      610      620      630
cry1a-105.pe NEUVYIDREFELIYPTATLEAEYNLEBAQKAVNALFTSTNQLGKINVTYDIDQVSNLTVY
      600      610      620      630      640      650
8469155 EKIVYDKIEFIPVQL
      640
cry1a-105.ppe
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SW:117324
117324 description="PESTICIDIAL CRYSTAL PROTEIN CRY3BA (INSECTICIDAL
DELTA-ENDOTOXIN CRYIIIB(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (75 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar tolworthi"
source="swissprot_prot" version="NA type=prt
SCORES Init1: 414 Initn: 1072 Opt: 1168 z-score: 1323.8 E(): 1.9e-65
>>SW:117324
Initn: 1072 Init1: 414 Opt: 1168 z-score: 1323.8 expect(): 1.9e-65
Smith-Waterman score: 1246; 35.4% identity in 636 aa overlap
(1-607:37-658)
cry1a-105.pe
      10      20      30      40      50      60      70      80      90      100      110      120      130
117324 RMKPNRSEVDIKVTPNSELPTHNNOYPLADNPNTLEELNYKEFLMTADNSTEVL
      10      20      30      40      50      60      70      80      90      100      110      120      130
cry1a-105.pe GERIEGT-TPIDISLSLQFLSEFVGAG----FVLGLVDIIWGIQPSQ---WDNFL
      30      40      50      60      70
117324 SSTKADAVGTGISV---VQILGVGVFPFAGALTSFYQSLNAINW---PSDADPWKAFM
      70      80      90      100      110
cry1a-105.pe VOIEQLINQRIEIEFARNQAIISRLGLSNLYQIYAESEFWEADPTNPALR---EEMRIQF
      80      90      100      110      120      130
117324 AQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALMSWKAPVNRSRSDRIELF
      120      130      140      150      160      170
cry1a-105.pe NDMASALTATPLFAVQNYQVPLSVVQANLHLSVLVDVSFGQWGFDAATINSRYN
      140      150      160      170      180      190
117324 SQAESHFNRSMFSAVSKFEVLFLPTVAQAANTHLLLLKDAQVFGEEWGSSEDAIEFVQ
      180      190      200      210      220      230
cry1a-105.pe DLTRLIGNYTDHVRWYNTGLERWGPDSKDWIRYNQFRRELTTLVDIVSLFPNYSRT
      200      210      220      230      240      250
117324 ROLKLTQOYTDHCVMYVNGVGLRGSTDAWKFNFRREWTLLVDLIVLPFYDVL
      240      250      260      270      280      290
cry1a-105.pe YPIRTVSQTRITRYNTPVLE-NFDGSRGSAQIGSIRSPLHMDILNISIITYT---DAH
      260      270      280      290      300      310
117324 YSKGVKTELTRDIFTDPIFSLNTIQEYGTFLSIENSIRKPHLPDYLGIEFHTLRPGY
      300      310      320      330      340      350
cry1a-105.pe RGE---YMSGHQINASPVGSGPEFTFLYGTMGNAAPQRIVAQLGQVYRTLSST-L
      320      330      340      350      360
117324 SQKDSFNYSNGYVETRSIGSKTITSFYGDK-SIEPIQKLSFD-GQKVYRTIANTDI
      360      370      380      390      400      410
cry1a-105.pe VRRP---FNIGINNQLSVLDGTEFAYGTSNLPASVYRKSGTVDSDLEIPQNNVPRR
      370      380      390      400      410      420
117324 AAFPDGKIYGVTKVDFSOYDQKNETSTQYDSKRNGHVSQAQDSIDQLPPTIDPLE
      420      430      440      450      460      470
cry1a-105.pe QGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPLVKAHTLQ
      430      440      450      460      470      480
117324 KAYSHQLNAYAECLMQDRRGTI-----PFFTWHRSVDFNTIDAEEKITQLPVVKAYALS
      480
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CRYIA-105.pe SGTIVVGGTGGDILR-RTSGPPAYTVININGO-LPORYRARIYASTTNRIYVTV
117324 SGAISIEGPGTGGNLLFLKESNNIAKVTLSAALLQRYRIRYASTTNLELVQV
CRYIA-105.pe AGRIFAGQFNKNDTDPITQSPSYATINTAFTPMSQSSFTVGADTFSSGNEVIDR
117324 SNNDLVIVYINKTNIDQTLTQTFDFATSNMGFGSDNDTFLGAEFSVSNKXIYDK
CRYIA-105.pe FELIPVATLEAENLERAQKAVNALFTTNGLKTNVTDYHIDQVSNLYLSDEFCL
117324 IEFIPVQ
CRYIA-105.pep
NRAA:40259
40259 source="GENBANK PROT" unnamed protein product [Bacillus
thuringiensis]g|117324|sp|p17969|CB3BA BACTO Pesticidal crystal protein cryIIAa
(insecticidal delta-endotoxin CryIIIB(a)) (Crystalline entomocidal protein)
KDa crystal protein)
SCORES Initl: 414 Initn: 1072 Opt: 1168 Z-score: 1323.8 E(): 1.9e-65
>>NRAA:40259
initn: 1072 initl: 414 opt: 1168 Z-score: 1323.8 expect(): 1.9e-65
Smith-Waterman score: 1246; 35.4% identity in 636 aa overlap
(1-607:37-658)
CRYIA-105.pe MDNNPNTN-ECIPYNCL----SNPEVVLG
40259 RKMPNRRSEVDTIKVTNSELPTNHNQYPLADNPNSTLELNKFEFLRMADNSTEVL
CRYIA-105.pe GERIEGY-TPIDISLSLTOFLSEFVPCAG---FVLGLVDIIWGFPSQ---WDAFL
40259 SSTVXDVGCTGTSV---VGQILGVGVGPAGALTSFYQSPFLNLIW---PSDADPKAFM
CRYIA-105.pe VQIEQLINORIEEFARNQAIISRLGLSNLYQIYAESFREWADPTNPAIR---EEMRIQF
40259 AQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALDSWKAKFVNLRRSQDRIRLF
CRYIA-105.pe NDWNSALTTAPLEAVQNYQVFLSVVQAAHLVSLVDVSVFGQWGFDAATINSYN
40259 SOAESHRNSMPSFAVSKFEVFLPYAQAAHTLLLLKDAQVFGWEGWSESDIAEYQ
CRYIA-105.pe DLRLTGNVTDHVAEYNTGLERWGPDSRDMIRYNQFRELTLTVIDIVSLFPNVDST
40259 RQKLKIQOYTDHCVNVNNGVLSIRGSTYDANVKENRREMTLTVIDLIVLFPFYDLRL

CRYIA-105.pe YPIRTVSQLTREIYTNVLE-NFDGSRGSAQGLESGIRSPHMLDINSIIYI---DAH
40259 YSKGVKTLTIDFTDFTFALQEQYGFTESSIRKPHLEFYLGRGIEFHTLRPGY
CRYIA-105.pe RGE---YVWSHQIMASPVGSGPTEFLYGTWGNAPQORIVAGQGVVRLTST-L
40259 SGKDSFNWGSNYVETRPSIGSDNLTITSPFGDK-STIEPQKLSFD-GQVYRIANTDI
CRYIA-105.pe YRRP---FNIGINNQQSLVDLTGTEFAYGTSSNLPSAVYRKSQVDSLDRIEPPQNNVPPR
40259 AAFPDGKIYFVGVTVDFSDQVDDOKNETSTQTVDSKRYNGVYLGADSIDQLPETTDEPLE
CRYIA-105.pe QGFSHRLSHVSMFRSGFSNSVSIKAPMFSWIRHSAEFNIIASDSITQIPLUKATLQ
40259 KAYSHQJLVYACFLMQDRRTGI-----PFFTWTHTRSVDFNTIDAETIQLFVVKAVALS
CRYIA-105.pe SGTIVVGGTGGDILR-RTSGPPAYTVININGO-LPORYRARIYASTTNRIYVTV
40259 SGAISIEGPGTGGNLLFLKESNNIAKVTLSAALLQRYRIRYASTTNLELVQV
CRYIA-105.pe AGRIFAGQFNKNDTDPITQSPSYATINTAFTPMSQSSFTVGADTFSSGNEVIDR
40259 SNNDLVIVYINKTNIDQTLTQTFDFATSNMGFGSDNDTFLGAEFSVSNKXIYDK
CRYIA-105.pe FELIPVATLEAENLERAQKAVNALFTTNGLKTNVTDYHIDQVSNLYLSDEFCL
40259 IEFIPVQ
CRYIA-105.pep
NRAA:940200
940200 source="GENBANK PROT" CryIIB2
SCORES Initl: 412 Initn: 1067 Opt: 1167 Z-score: 1322.7 E(): 2.2e-65
>>NRAA:940200
initn: 1067 initl: 412 opt: 1167 Z-score: 1322.7 expect(): 2.2e-65
Smith-Waterman score: 1242; 36.7% identity in 580 aa overlap
(51-607:82-650)
CRYIA-105.pe VEVLGERIETGYTIPIDISLSLTQFLISEFVPCAG---FVLGLVSLIISIFGSG
940200 SSTEVLDSNTVKDVGTVGTSVVGQILGVGVVPFAGALTSFYQSFLOTIW---PSDADPKW
CRYIA-105.pe DAFVLQIEQLINORIEEFARNQAIISRLGLSNLYQIYAESFREWADPTN-PALREEMRI
940200 KAFWAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI

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initn: 1575 init1: 571 opt: 1126 Z-score: 1272.5 expect(): 1.4e-62
Smith-Waterman score: 1983; 33.5% identity in 1198 aa overlap
(34-1177:43-11135)

cryla-105.pe NPINECIPYNCLSPNEVEVLGGERIETGCTPIDISLSLTOFLSEFVPGAGVL---G
10 20 30 40 50
1117541 GSKMNTNYKDLWLCENNOQYGVNPAINSSSVSTAKVKAGALKFVNPAGTAVLTLSLA
20 30 40 50 60 70

cryla-105.pe LVDIWIGIFGSQ---WDAFLVIGIQLINRIEFPARNQAISLEGLSNLYQIYAESFRE
60 70 80 90 100 110
1117541 VLPILMPTWTPPERVNDFTMTNGLIDQTVAVRTDANAKMTVVKQDQDYTKFTNT
80 90 100 110 120 130

cryla-105.pe WEADPTNPALREEMRIQFNDMNSALT-TAIPLFAVQNYQVPLSVVQVANLHLSLVLDV
120 130 140 150 160 170
1117541 WKREPNQSYRTAVITQFNUTSIAKLRETAVFPSNIGVJGELLPLPIYAQVANFNLLSLIRDG
140 150 160 170 180 190

cryla-105.pe SVFGQWGFDAATINRSYNDLTILIGNYTHAVRWNTGLERVWGPDSRDWIRYNQFRE
180 190 200 210 220 230
1117541 LINAQWSLACAG-DQLYMTWQVYKEYIAHSITWYKNGLDLRNKSQGWITFNDYKRE
200 210 220 230 240 250

cryla-105.pe LTLVLVDIVSLFPNYSRTYPIRTV-----SQTREIYTNVLENFDFSGFRSQAQIE
240 250 260 270 280
1117541 MTIQVLDILALFASVDPRLPADKIDNTKLSKTEFTEIYALV----ESPSSKSIAALE
260 270 280 290 300

cryla-105.pe GSI-RSFLHMDLINSITIYDA-HRGEYVWGHQIMASPVGFGPEFTPLTIGTMGNAAP
290 300 310 320 330 340
1117541 AALTRDVHLFTLWKRVPWNTYIQDLRSLKSAIGFYSYNSAMQES-GIYGSGSGFSGN
310 320 330 340 350 360

cryla-105.pe QQRIVAQLOGVYRTLGLSTLYRRPFNIGNNQLSLVDGTEFAYGTS-SNLPSAVYKRS
350 360 370 380 390 400
1117541 LTHQI-QLANSVYKT-SITDTSFSPN-RVTKMDFKIDGTLASYNNSNITPEGI-RTTF
370 380 390 400 410 420

cryla-105.pe TVDSLDEIPQNNVPRQFSLHLSHVMFSGFSNYSVSIIRAPMFVSHRSFAFNNI
410 420 430 440 450 460
1117541 FGFSTNTPP--NQPTVNDYTHLSVIKTDVIDYNSNRVS-----FAWTHKIVDPNQ
430 440 450 460 470

cryla-105.pe IASDSITQPLVAKHTQSGTIVVRQPGTGGDIURRTSGGPEYATI-WNINGQL---PQ
470 480 490 500 510 520
1117541 IYTDATQVPAVKSNFLNATAKVIKPGFGHTGGDLVALTSNGTSLGRMEIQCKTSIFNDPT
480 490 500 510 520 530

cryla-105.pe R-YRARIRVASTNLRIYVTVAGERIFAGQFNKMTD-T-GDP-----LTFOSFSYATIN
530 540 550 560 570
1117541 RSVGLRIIRAAANSPVLNVLSVQLQVWSRGTTITSTFSPRNNIIPDLDKIEEYFKDPP
540 550 560 570 580 590

cryla-105.pe TAFTFWMSQSS---FTVGADTF--SSGNEVYIDRPELIPYATIL--EAE-VNLEBAQAKV
580 590 600 610 620

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117541 DAIV-PWSSNQLTIAOPLANMISNNQVILDIETIPITQSVLDTEQNQLSERVW
618 619 620 630 640 650
cry1a-105.pe NAKTSNQLKXKMYTYHIDQVNLVSLDFCLDEKELSEKXKAKLSDERNLL
630 640 650 660 670 680
117541 NALFTNDKADANIGCTISIDANLVECTIESELYPKERKMLLDDEVAKKQUSGRVL
660 670 680 690 700 710
cry1a-105.pe QDSNFKDINRQPERGWCSTCTIQQGDDVFNKAVTLSSAFD--ECRYPTLYQKIDES
690 700 710 720 730 740
117541 QNGDFESATL---GWTSSDNILOENQDPIEFKSHVHNSGARDIDISTITXIFQKIDES
720 730 740 750 760 770
cry1a-105.pe KLAFTRYQLRGVIEDSQDLEISYIRYNAKHETLNNQGTCSLWPLSAOSPGRGEM
750 760 770 780 790 800
117541 KLEPYTRYLVRGFVGSSKDVLSVSRYGEEIDAIMNVPAQDNLVYFSTED---CEGSN
770 780 790 800 810 820
cry1a-105.pe RCETSAVPANIGTSDMLYSQOYDTGKKHVVC--QDSHQFSTIIDIGALDINENLQWVNF
800 810 820 830 840 850
117541 RCETSAVPANIGTSDMLYSQOYDTGKKHVVC--QDSHQFSTIIDIGALDINENLQWVNF
830 840 850 860 870 880
cry1a-105.pe KIKTQDQHAPLNLFLLEKPLVGEALARKAEKKWKDKREKLEWTNIVYKAEKESVD
850 860 870 880 890 900
117541 KISSPDGASLDNLNLEVEEGPIDGEALSRLVKHMEKKWMDOMEAKRSETQOQAVDAKQAD
890 900 910 920 930 940
cry1a-105.pe ALFVNSQYDQDQADNTNIAHIAADKRVHSREAYLDELVSIPGVNAAIFELGRIPTAF
910 920 930 940 950 960
117541 ALFTNVDQEQALQDTLQIQVAYELVQSIPYVYNDWLSDVPGMWNIDYVELDARVAQAR
950 960 970 980 990 1000
cry1a-105.pe SLYDARVINKGDFNGLSCWNVKGVHDVEEQNNQBSVLVWPEWAEVSEVRCVPCRGY
970 980 990 1000 1010 1020
117541 VLYDTRNLIKNGDFTCGVGMWHVTGNADVO-QIDGYSVLVLSNWSAGVSQNVHLQHNHCY
1010 1020 1030 1040 1050 1060
cry1a-105.pe ILRVATYKGGYGGCVTHIEENNTDELKFSNCVEEIIYPNNVTVCNDYTNQOEYGGAY
1030 1040 1050 1060 1070 1080
117541 VLRVIAKGGPGNGVYVTLMDCEENQEKLTFTSCEE-----
1070 1080 1090
cry1a-105.pe TSNRNGYNEAPSVADYASVVEKSYTDGRENPCFNRGYDYTLFVGVYVTELEYEP
1090 1100 1110 1120 1130 1140
117541 -----GIIKTVDVFP
1100
cry1a-105.pe ETDKWLIEIGETSTFIVDSVELLIMEE
1150 1160 1170
117541 DDDRVRIEIGETSTFIVDSVELLIMEE
1110 1120 1130
cry1a-105.pe

NRAA:216288
216288 source="GENBANK PROT" 130 kDa insecticidal protein (ISRH3) [Bacillus
thuringiensis serovar israelensis]gi|225982|prf|1405201A insecticidal protein
ISRH3
SCORES Initl: 571 Initn: 1575 Opt: 1126 z-score: 1272.5 E(): 1.4e-62
>NRAA:216288
Initn: 1575 Initl: 571 Opt: 1126 z-score: 1272.5 expect(): 1.4e-62
Smith-Waterman score: 1883; 33.5% identity in 1198 aa overlap
(34-1177:43-1135)
cry1a-105.pe NPINECIPVNCISNPEVEVLGGRIETGYTIDISLSLTQFLISEFVPGAGFVL---G
10 20 30 40 50
216288 GSKMNTNYKDWLACMCCNQOYVNPAINSSSVSTALAKVAGAILKFNPPAGTIVTLVLSA
20 30 40 50 60 70
cry1a-105.pe LVDIINGIFGPSQ---WDAFLVQIEQLINQRIEFAFNQAIISRLGSLNLYQIYAESFRE
60 70 80 90 100 110
216288 VLPILWPTNPTPTPERVWDEMTNTGNLIDQTVAVRTDANAKMTVVKVDYLDQYTKENT
80 90 100 110 120 130
cry1a-105.pe WEADPTNPALREEMRIQFNDMNSALT-TAIPFAVQNTQVPLLSVYVQAAHLHSLVLRDV
120 130 140 150 160 170
216288 WKREFNQSVRTAVITQFNLTSAKLRETAIVFNSLVNGVGLLELLPIYAQVANFLLLRIG
140 150 160 170 180 190
cry1a-105.pe SVFGQNGPQAAATIRNSRYNDLRLIGNYTDHVRVYNTGLERVMGPDSDRWIRYNQFRRE
140 150 160 170 180 190
216288 LINAQVSLASG--SGLYNTWVQVTKYIAHSITWYNGLDVLRNKGNGQWITFNDYKRE
160 170 180 190 200 210
cry1a-105.pe QRTVLDISLFPNYSRTYRIN-----SGLTREIYNPVLENFDFGSRGSAQGIE
240 250 260 270 280
216288 MTIQWLDNLFALFASG--KALPADKIDNTTS-SKTEFTREIYALV---ESPSSKSTAAL
240 250 260 270 280 290 300
cry1a-105.pe GSI-RSPHMDIILNLTITWDA-REGVYMSGHQIMASNGFSGPEFTFLYGTMGNAAP
290 300 310 320 330 340
216288 AALTRDVLHETLWLRVYFWNTYDODLRVYVYNTGLERVMGPDSDRWIRYNQFRRE
310 320 330 340 350 360
cry1a-105.pe QQRIVAQOGVYRTLSLTPRRPFIQINNOQSVLDGTEFTFYGTSS-SNDSGAVRKSG
350 360 370 380 390 400
216288 LTHOI-QLNSNVYKT-SITDTSSPSN-RVTKMDFTKIDNTLASVNSNTPPEGL-RTTH
370 380 390 400 410 420
cry1a-105.pe TVDSLEIPPNNNVPPRGFSHRLSHVSNFRGFSNSSVSIIRAFNSVHRSKAFNT
410 420 430 440 450 460
216288 FGFSTNENTP---NQPTVNDYTHILSYIKTDIVDVNSRVS-----FANTRITQDNNQ
430 440 450 460 470 480
cry1a-105.pe IASDSITQIEPLVAHQLTQSGTIVVGRGFTGGDLIRLTSGGFPAYTI-VNINQOL---PQ
470 480 490 500 510 520
216288 IYDTAITQVPAVKSNEFNATYAKVINGPGHTGGDLVALTSGRLSGMEIQCKTSIFNDPT
480 490 500 510 520 530

cryla-105.pe R-YRARTASTNRIYTVAGERIFAGQPKMTGT-GDP-----LTFQSFATIN 530 540 550 560 570
216288 RSYGLRIRYAANSPVIVSVYLVQVGRGTISTESTFRPNMIIPFDLKYEFYRFF 540 550 560 570 580 590
cryla-105.pe TAFTPMSQSS---FTVGADTF--SSGNEVIDRFELIPVITAIL--EAE-YNLERAQKAV 580 590 600 610 620
216288 DAIV-PWELSSNQLITIAIQPLNMTSNQVVIDRIEIIITQSVLDENQNLESREV 600 610 620 630 640 650
cryla-105.pe NALFTSTNQLKNTNVDYHIDQVSNLVYLSDFECLDEKRELSKVHAKRSLDERNLL 630 640 650 660 670 680
216288 NALFTNDKALNIGTIDYIDQANLVVECTISEELYPKPKEMILLDEVNKAKQLSQSRVL 660 670 680 690 700 710
cryla-105.pe QDSNFKDINQPERGGSTGITIQGGDVYKENVYTLSTGTD---ECYPTLYQKIDES 690 700 710 720 730 740
216288 QNGFESATL-----GWTSDNITIOEDDPIPKGHYLDHMSGARDIDGITFFPIYFQKIDES 720 730 740 750 760
cryla-105.pe KKAFTRYQLRGVIEDSQLEIYSIRYNKHETV-NVPGT-GSLWPLSAQSPICKGCEPN 750 760 770 780 790
216288 KKPTRYLVGRFVGSSKDVELWRSYGEIDALMVNPDALNYLPSTFD-----CEGEN 770 780 790 800 810 820
cryla-105.pe RC-----AP-HLEWNPDCSCR--DGEK---CAHHSHFSLDIDVCGTDMEDLGVWVIF 800 810 820 830 840
216288 RCETSAVPANIGNTSDMLYSQYDTGKKHVC-QDSHQSFITDTCALDTNENIGVWVF 830 840 850 860 870 880
cryla-105.pe KIKTODGHARGLNLEFLEKPLVGEALRVKRAEKWRKREKLEWETNIVYKEAKESVD 850 860 870 880 890 900
216288 KISSPDGASLDNLEVEIEGPDIDGEALSRVKHKEKWNQMEAKRSEIQQAYDVAKQAD 890 900 910 920 930 940
cryla-105.pe ALFVNSQVQLQADTNMIAMHAAKRVHSIREAYLPSELGVIPGVNAAIFEELEGRIATF 910 920 930 940 950 960
216288 ALFTNVQDEALQFDITLAIQVAEYLVQSIPIYVNDWLSVDVPMYDIYVELDARVAQAR 950 960 970 980 990 1000
cryla-105.pe SLYDARVYKNGDFNGLSCNVKCHVDVEQNNQSVLVVPEWAEVSQVRVCGRGY 970 980 990 1000 1010 1020
216288 YLIDTRNLIKNGDFTOGVMGHVHTGNADVQ-QIDGVSVLVSNWSAGVSNVHLQHNHG 1010 1020 1030 1040 1050 1060
cryla-105.pe ILRVTAKEGPGGCVTIEIENNTDELKFSNCVEBEIYPNNVTVCNDYTVNQEEYGAY 1030 1040 1050 1060 1070 1080
216288 VLRVIAKEGPGGYVTLMDCEENOEKLTFTSCEE----- 1070 1080 1090
cryla-105.pe TSNRNGYNAPSVPADYASVYEKSYTDGRNFCENRGYDYTFPLGVYTKLEYEYFP 1090 1100 1110 1120 1130 1140
216288 -----GYITKTVDFP 1100 1110

cryla-105.pe ETDKWIEIGETEGTIFVDSVELLMEE 1150 1160 1170
216288 DTDVRVIEIGETEGSYFIESIELICMNE 1110 1120 1130
cryla-105.pep
NRAA:40354
40354 source="GENBANK PROT" unnamed protein product [Bacillus
thuringiensis]gi|21685442|emb|CAD30095.1| pesticidal crystal protein cry4Ba
[Bacillus thuringiensis serovar israelensis]gi|8488969|sp|P05519|CR4BA_BACTI
Pesticidal crystal protein cry4Ba (insecticidal delta-endotoxin CryIVB(a))
(Crystalline entomocidal protoxin) (128 kDa crystal protein)
SCORES Initl: 571 Initn: 1667 Opt: 1126 z-score: 1272.5 E(): 1.4e-62
>>NRAA:40354 (1136 aa)
initn: 1667 initl: 571 Opt: 1126 Z-score: 1272.5 expect(): 1.4e-62
Smith-Waterman score: 1896; 33.5% identity in 1198 aa overlap
(34-1177:43-1136)
cryla-105.pe NPINICEIPYNCLSNPEVEVLGERIETGYTPIDISLSTQFLLESEFVGAGFVL----G 10 20 30 40 50
40354 GSMKNTNYKDWLAMCENNOQYGVNPAALNSSSVSTALKVAGAILKFNVPAGTTLTVLSA 20 30 40 50 60 70
cryla-105.pe LVDIWIIGIFPSQ---WDAPLVQIEQLINRIEERFARNOAISRLSEGLSNLYQIYAESFRE 60 70 80 90 100 110
40354 VLPILPMTPTTPERVWDMFTNGLNLDITVAYVITDANAKMTVVKDYLDQVTKFNT 80 90 100 110 120 130
cryla-105.pe WEADPTPALREEMRIQFNDMNSALT-TAIPLEAVQNYOVPLLSVYVQAAHLHSLVLRDV 120 130 140 150 160 170
40354 WRENNQSVRTAVITQFNLTSAKRETAIVYFNLVGYELLLLPIYAQVAFNLLIRDG 140 150 160 170 180 190
cryla-105.pe SVFGQMGFDAATINSRYNDLRLIGNYTDHVRWYNTGLERVWGDSDRWIRYNQFRE 180 190 200 210 220 230
40354 LINAQEWLSARSAGDOLYNTMVTQYTKYIAHSITWYKGLDLVRNKSQWITFNDYKRE 200 210 220 230 240 250
cryla-105.pe LTLTVLDIVSLFNNYSRTYPTV-----SOLTREIYTPVLENPDGSGFRGSAOGIE 240 250 260 270 280
40354 MTIQVLDILALFASYPDRYPADKIDNTKUSKTEFTREIYTLV-----ESPSSKSTAAL 260 270 280 290 300
cryla-105.pe GSI-RSPHLDILNSITIVTDA-HRGEYVWGHQIMASPVGSGPEFTFLYGTGMNAP 290 300 310 320 330 340
40354 AALTDVHLFTLKRVDFTNTIYQDLRFLLSANKIGFSYTNSSAMQES-GYGSSEGSFN 310 320 330 340 350 360
cryla-105.pe QORIVAQGGQVTRTSSLYRPFNIGINNQQSLVDGTGFAYGTS-SNLPSSAVYRKS 350 360 370 380 390 400
40354 LTHQI-QLNSNVYKT-SITDTSPPSN-RVTMDQFYKIDGTLASVNSNITPTPEGL-RTTF 370 380 390 400 410 420

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[illegible]

8488969 AALTRDWHFTLWKRVDFTWTHIYQDLRLFSANKIGFSTNSAWQES-CIYSSGFSGN
310 320 330 340 350 360
cry1a-105.pe QQRVLAQGGVYRLSTSLYRRPFNIGINNQQLSVLDGFAYGTS-SNLPAVYRKSG
350 360 370 380 390 400
8488969 LTHQI-QLNSNVYKT-SITDTSSPN-RVTKMDFYKIDGTLASVNSNITPTPEGL-RTTF
370 380 390 400 410 420
cry1a-105.pe TVDSLDELPPQNNVPPRQGFESHLSHVMSFRSGFSNSVSIIRAPFMSIHSAPFNNI
410 420 430 440 450 460
8488969 FGFSTNENTP---NQPTVNDYTHLSYIKTDVIDYNSNRVS-----FAWTHIVDPNNQ
430 440 450 460 470
cry1a-105.pe IASDSITQIPLVKAHTLQSGTIVVRGPGFTGGDILARTSGGPFAYTI-VNINQGL---PQ
470 480 490 500 510 520
8488969 IYTDALTQPAVKSFLNATAKVIKPGHTGGDLVALTSGTLGRMEIOCKTSIFENDPT
480 490 500 510 520 530
cry1a-105.pe R-YEARIRYASTNLRKIYVTVAGRIIFAGQFNKMTD-GDP-----LTFQSFYATIN
530 540 550 560 570
8488969 RSYGLRIRYAANSPIVLNVSVYLAQVSRGTTISTESTFRPNNIIPDILKYEFRYKDFP
540 550 560 570 580 590
cry1a-105.pe TAFTPMSQSS---FTVGADTF--SSGNEVYIDRFELIPVATL--EAE-YNLERAQAV
580 590 600 610 620
8488969 DAIV-PMLSSNQLITIAIQLPNNMISNNQVIIDRIEIIPIITQSVDDETENQNLSESRVV
600 610 620 630 640 650
cry1a-105.pe NALFSTNQGLKTNVTDYHDQVSNLVYLSDFCLDEKRLSEKVKHAKRLSDERNLL
630 640 650 660 670 680
8488969 NALFTNADKALMIGTVDIDQAANLVEGISEELYPKEKMLLDEVKNAKQLSQSRNVL
660 670 680 690 700 710
cry1a-105.pe QDSNFKDINQPERGMWGSGTGITIGGDDVFKENYVTLSTGTF---ECYPTLYYQKIDES
690 700 710 720 730 740
8488969 QNGDFESATL---GWTSDNITIQEDDPIFKGHYLHMSGARDIDGTIFTYIFQKIDES
720 730 740 750 760
cry1a-105.pe KKAFTYQLRGVIEDSDLEIYSIRYNKHTV-NVPCT-GSLWPLSAQSPIGKCGEN
750 760 770 780 790
8488969 KKKPTTYLVRGVSGSKDVELVSRIGESIDAIMVPADNLNLYSTPFD---CEGNS
770 780 790 800 810 820
cry1a-105.pe RC-----AP-HLEWNPDLQSCRR--DGEK---CAHSHSHFSLDIDVGCTDNEDLGYWVIF
800 810 820 830 840
8488969 RCETSAPVANIGMTSDMLYSQYDTGKKHVC-QDSHQSFFTIDTGALDNEINIGVWVF
830 840 850 860 870 880
cry1a-105.pe KIKTQDGHARGLNLEFLEKPLVGEALARYKRAEKKKRDKREKLEWETNIVYKEASVD
850 860 870 880 890 900
8488969 KISSPDGYSLDLNLEVEEGPIDGEALSRLVKHMEKKNWDMQMEAKSETQQAIDYAKQAD
890 900 910 920 930 940
cry1a-105.pe ALFVNSQYDQLQADTNIAHHAADKRVHSIREAYLPFLSVIPGVNAAIFEELEGRIFTAF
910 920 930 940 950 960

8488969 ALFTNVODEALQFDITLAIQYAEVLVOSIPYVYNDLSDVPGNVYDIYVELDARVAQAR
950 960 970 980 990 1000
cry1a-105.pe SLYDARNVKNQGFNNGISCNWVKGHVDVEEQNRQSRVSLVLPWEAEVSQEVRCGRGY
970 980 990 1000 1010 1020
8488969 XLYDTRNIKNQDFTQGVMGHVTGNADVQ-QIDGVSVLVLSNMSAGVSNVHLQHNHG
1010 1020 1030 1040 1050 1060
cry1a-105.pe ILRVYATKESYGGCVTTHIENNTDELKFSNCVEEIIYPNNTVTCNDYTVNQEEYGGAY
1030 1040 1050 1060 1070 1080
8488969 VLRVIKKEGPGNGYVITLMDCEEKQEKLTFTSCSE-----
1070 1080 1090
cry1a-105.pe TSNRNGYNEAPSVPADYASVVEEKSYPDGRNCFENRGYRDVTPLPVGVYTKLEYFP
1090 1100 1110 1120 1130 1140
8488969 -----GYITKTVDVFP
1100
cry1a-105.pe ETDKWIEIGETEGTPIVDSVLELLMEE
1150 1160 1170
8488969 DTDVRVIEIGETEGSFYIESIELICMNE
1110 1120 1130
cry1a-105.pe
1150 1160 1170
NRAA:40310
40310 source="GENBANK_PROF" unnamed protein product [Bacillus thuringiensis]
SCORES Initl: 571 Initn: 1666 Opt: 1126 z-score: 1272.5 E(): 1.4e-62
>>NRAA:40310
Initn: 1666 Initl: 571 Opt: 1126 z-score: 1272.5 expect(): 1.4e-62
Smith-Waterman score: 1897; 33.5% identity in 1198 aa overlap
(34-1177:43-1136)
cry1a-105.pe NPINCEIPYNCISNPEVEVLGGRIETGTPIDISLSLTQFLJSEFVPGAGFVL----G
10 20 30 40 50
40310 GSMKNTNYKDWLACENNQYGVNPAAINSSSVSTALKVAGAILKFNVPAGTIVLWSA
20 30 40 50 60 70
cry1a-105.pe LVDIWIIGFQPSQ---WDAFLVQIEQLINQRIEFPARNOAISRLGSLNLYQIYAESFRE
60 70 80 90 100 110
40310 VLPILMTPTTPTPERVNDFTMTGNLIDQTVTAYVVRTDANAKMTVVKDYLDQYTKFNT
80 90 100 110 120 130
cry1a-105.pe WEADPTNPALREEMRIQFNDMSALT-TALPLFAVONQVPLLSVYVQAANLHLSVLRDV
120 130 140 150 160 170
40310 WKRPNNQSVRTAVITQFNLISAKLRETAVYFSNIVGVELLLPLIYQAVANFNLLIRDG
140 150 160 170 180 190
cry1a-105.pe SVFQQRMGDAATINSRYNDLTRLIGNYTDHVRVYNTGLERVWGPDSRWIRYNQFRRE
180 190 200 210 220 230
40310 LINAQESLARSQDQYTMVQVTKYEIAHSITWYKNGLDLVRNKSQGWITFNKYRE
200 210 220 230 240 250

cry1a-105.pe KKTQDGHARLGNLEFLEKPLVGEALRVKRAEKKWRDKREKLEWETNIVYKEAKESVD
40310 KISSPDGASLDNLEVEIEEGFIDGEALSRVMEKKWMDQMEAKRSETQQAQYDAKQAI
910 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800 1810 1820 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940 1950 1960 1970 1980 1990 2000 2010 2020 2030 2040 2050 2060 2070 2080 2090 2100 2110 2120 2130 2140 2150 2160 2170 2180 2190 2200 2210 2220 2230 2240 2250 2260 2270 2280 2290 2300 2310 2320 2330 2340 2350 2360 2370 2380 2390 2400 2410 2420 2430 2440 2450 2460 2470 2480 2490 2500 2510 2520 2530 2540 2550 2560 2570 2580 2590 2600 2610 2620 2630 2640 2650 2660 2670 2680 2690 2700 2710 2720 2730 2740 2750 2760 2770 2780 2790 2800 2810 2820 2830 2840 2850 2860 2870 2880 2890 2900 2910 2920 2930 2940 2950 2960 2970 2980 2990 3000 3010 3020 3030 3040 3050 3060 3070 3080 3090 3100 3110 3120 3130 3140 3150 3160 3170 3180 3190 3200 3210 3220 3230 3240 3250 3260 3270 3280 3290 3300 3310 3320 3330 3340 3350 3360 3370 3380 3390 3400 3410 3420 3430 3440 3450 3460 3470 3480 3490 3500 3510 3520 3530 3540 3550 3560 3570 3580 3590 3600 3610 3620 3630 3640 3650 3660 3670 3680 3690 3700 3710 3720 3730 3740 3750 3760 3770 3780 3790 3800 3810 3820 3830 3840 3850 3860 3870 3880 3890 3900 3910 3920 3930 3940 3950 3960 3970 3980 3990 4000 4010 4020 4030 4040 4050 4060 4070 4080 4090 4100 4110 4120 4130 4140 4150 4160 4170 4180 4190 4200 4210 4220 4230 4240 4250 4260 4270 4280 4290 4300 4310 4320 4330 4340 4350 4360 4370 4380 4390 4400 4410 4420 4430 4440 4450 4460 4470 4480 4490 4500 4510 4520 4530 4540 4550 4560 4570 4580 4590 4600 4610 4620 4630 4640 4650 4660 4670 4680 4690 4700 4710 4720 4730 4740 4750 4760 4770 4780 4790 4800 4810 4820 4830 4840 4850 4860 4870 4880 4890 4900 4910 4920 4930 4940 4950 4960 4970 4980 4990 5000 5010 5020 5030 5040 5050 5060 5070 5080 5090 5100 5110 5120 5130 5140 5150 5160 5170 5180 5190 5200 5210 5220 5230 5240 5250 5260 5270 5280 5290 5300 5310 5320 5330 5340 5350 5360 5370 5380 5390 5400 5410 5420 5430 5440 5450 5460 5470 5480 5490 5500 5510 5520 5530 5540 5550 5560 5570 5580 5590 5600 5610 5620 5630 5640 5650 5660 5670 5680 5690 5700 5710 5720 5730 5740 5750 5760 5770 5780 5790 5800 5810 5820 5830 5840 5850 5860 5870 5880 5890 5900 5910 5920 5930 5940 5950 5960 5970 5980 5990 6000 6010 6020 6030 6040 6050 6060 6070 6080 6090 6100 6110 6120 6130 6140 6150 6160 6170 6180 6190 6200 6210 6220 6230 6240 6250 6260 6270 6280 6290 6300 6310 6320 6330 6340 6350 6360 6370 6380 6390 6400 6410 6420 6430 6440 6450 6460 6470 6480 6490 6500 6510 6520 6530 6540 6550 6560 6570 6580 6590 6600 6610 6620 6630 6640 6650 6660 6670 6680 6690 6700 6710 6720 6730 6740 6750 6760 6770 6780 6790 6800 6810 6820 6830 6840 6850 6860 6870 6880 6890 6900 6910 6920 6930 6940 6950 6960 6970 6980 6990 7000 7010 7020 7030 7040 7050 7060 7070 7080 7090 7100 7110 7120 7130 7140 7150 7160 7170 7180 7190 7200 7210 7220 7230 7240 7250 7260 7270 7280 7290 7300 7310 7320 7330 7340 7350 7360 7370 7380 7390 7400 7410 7420 7430 7440 7450 7460 7470 7480 7490 7500 7510 7520 7530 7540 7550 7560 7570 7580 7590 7600 7610 7620 7630 7640 7650 7660 7670 7680 7690 7700 7710 7720 7730 7740 7750 7760 7770 7780 7790 7800 7810 7820 7830 7840 7850 7860 7870 7880 7890 7900 7910 7920 7930 7940 7950 7960 7970 7980 7990 8000 8010 8020 8030 8040 8050 8060 8070 8080 8090 8100 8110 8120 8130 8140 8150 8160 8170 8180 8190 8200 8210 8220 8230 8240 8250 8260 8270 8280 8290 8300 8310 8320 8330 8340 8350 8360 8370 8380 8390 8400 8410 8420 8430 8440 8450 8460 8470 8480 8490 8500 8510 8520 8530 8540 8550 8560 8570 8580 8590 8600 8610 8620 8630 8640 8650 8660 8670 8680 8690 8700 8710 8720 8730 8740 8750 8760 8770 8780 8790 8800 8810 8820 8830 8840 8850 8860 8870 8880 8890 8900 8910 8920 8930 8940 8950 8960 8970 8980 8990 9000 9010 9020 9030 9040 9050 9060 9070 9080 9090 9100 9110 9120 9130 9140 9150 9160 9170 9180 9190 9200 9210 9220 9230 9240 9250 9260 9270 9280 9290 9300 9310 9320 9330 9340 9350 9360 9370 9380 9390 9400 9410 9420 9430 9440 9450 9460 9470 9480 9490 9500 9510 9520 9530 9540 9550 9560 9570 9580 9590 9600 9610 9620 9630 9640 9650 9660 9670 9680 9690 9700 9710 9720 9730 9740 9750 9760 9770 9780 9790 9800 9810 9820 9830 9840 9850 9860 9870 9880 9890 9900 9910 9920 9930 9940 9950 9960 9970 9980 9990 10000 10010 10020 10030 10040 10050 10060 10070 10080 10090 10100 10110 10120 10130 10140 10150 10160 10170 10180 10190 10200 10210 10220 10230 10240 10250 10260 10270 10280 10290 10300 10310 10320 10330 10340 10350 10360 10370 10380 10390 10400 10410 10420 10430 10440 10450 10460 10470 10480 10490 10500 10510 10520 10530 10540 10550 10560 10570 10580 10590 10600 10610 10620 10630 10640 10650 10660 10670 10680 10690 10700 10710 10720 10730 10740 10750 10760 10770 10780 10790 10800 10810 10820 10830 10840 10850 10860 10870 10880 10890 10900 10910 10920 10930 10940 10950 10960 10970 10980 10990 11000 11010 11020 11030 11040 11050 11060 11070 11080 11090 11100 11110 11120 11130 11140 11150 11160 11170 11180 11190 11200 11210 11220 11230 11240 11250 11260 11270 11280 11290 11300 11310 11320 11330 11340 11350 11360 11370 11380 11390 11400 11410 11420 11430 11440 11450 11460 11470 11480 11490 11500 11510 11520 11530 11540 11550 11560 11570 11580 11590 11600 11610 11620 11630 11640 11650 11660 11670 11680 11690 11700 11710 11720 11730 11740 11750 11760 11770 11780 11790 11800 11810 11820 11830 11840 11850 11860 11870 11880 11890 11900 11910 11920 11930 11940 11950 11960 11970 11980 11990 12000 12010 12020 12030 12040 12050 12060 12070 12080 12090 12100 12110 12120 12130 12140 12150 12160 12170 12180 12190 12200 12210 12220 12230 12240 12250 12260 12270 12280 12290 12300 12310 12320 12330 12340 12350 12360 12370 12380 12390 12400 12410 12420 12430 12440 12450 12460 12470 12480 12490 12500 12510 12520 12530 12540 12550 12560 12570 12580 12590 12600 12610 12620 12630 12640 12650 12660 12670 12680 12690 12700 12710 12720 12730 12740 12750 12760 12770 12780 12790 12800 12810 12820 12830 12840 12850 12860 12870 12880 12890 12900 12910 12920 12930 12940 12950 12960 12970 12980 12990 13000 13010 13020 13030 13040 13050 13060 13070 13080 13090 13100 13110 13120 13130 13140 13150 13160 13170 13180 13190 13200 13210 13220 13230 13240 13250 13260 13270 13280 13290 13300 13310 13320 13330 13340 13350 13360 13370 13380 13390 13400 13410 13420 13430 13440 13450 13460 13470 13480 13490 13500 13510 13520 13530 13540 13550 13560 13570 13580 13590 13600 13610 13620 13630 13640 13650 13660 13670 13680 13690 13700 13710 13720 13730 13740 13750 13760 13770 13780 13790 13800 13810 13820 13830 13840 13850 13860 13870 13880 13890 13900 13910 13920 13930 13940 13950 13960 13970 13980 13990 14000 14010 14020 14030 14040 14050 14060 14070 14080 14090 14100 14110 14120 14130 14140 14150 14160 14170 14180 14190 14200 14210 14220 14230 14240 14250 14260 14270 14280 14290 14300 14310 14320 14330 14340 14350 14360 14370 14380 14390 14400 14410 14420 14430 14440 14450 14460 14470 14480 14490 14500 14510 14520 14530 14540 14550 14560 14570 14580 14590 14600 14610 14620 14630 14640 14650 14660 14670 14680 14690 14700 14710 14720 14730 14740 14750 14760 14770 14780 14790 14800 14810 14820 14830 14840 14850 14860 14870 14880 14890 14900 14910 14920 14930 14940 14950 14960 14970 14980 14990 15000 15010 15020 15030 15040 15050 15060 15070 15080 15090 15100 15110 15120 15130 15140 15150 15160 15170 15180 15190 15200 15210 15220 15230 15240 15250 15260 15270 15280 15290 15300 15310 15320 15330 15340 15350 15360 15370 15380 15390 15400 15410 15420 15430 15440 15450 15460 15470 15480 15490 15500 15510 15520 15530 15540 15550 15560 15570 15580 15590 15600 15610 15620 15630 15640 15650 15660 15670 15680 15690 15700 15710 15720 15730 15740 15750 15760 15770 15780 15790 15800 15810 15820 15830 15840 15850 15860 15870 15880 15890 15900 15910 15920 15930 15940 15950 15960 15970 15980 15990 16000 16010 16020 16030 16040 16050 16060 16070 16080 16090 16100 16110 16120 16130 16140 16150 16160 16170 16180 16190 16200 16210 16220 16230 16240 16250 16260 16270 16280 16290 16300 16310 16320 16330 16340 16350 16360 16370 16380 16390 16400 16410 16420 16430 16440 16450 16460 16470 16480 16490 16500 16510 16520 16530 16540 16550 16560 16570 16580 16590 16600 16610 16620 16630 16640 16650 16660 16670 16680 16690 16700 16710 16720 16730 16740 16750 16760 16770 16780 16790 16800 16810 16820 16830 16840 16850 16860 16870 16880 16890 16900 16910 16920 16930 16940 16950 16960 16970 16980 16990 17000 17010 17020 17030 17040 17050 17060 17070 17080 17090 17100 17110 17120 17130 17140 17150 17160 17170 17180 17190 17200 17210 17220 17230 17240 17250 17260 17270 17280 17290 17300 17310 17320 17330 17340 17350 17360 17370 17380 17390 17400 17410 17420 17430 17440 17450 17460 17470 17480 17490 17500 17510 17520 17530 17540 17550 17560 17570 17580 17590 17600 17610 17620 17630 17640 17650 17660 17670 17680 17690 17700 17710 17720 17730 17740 17750 17760 17770 17780 17790 17800 17810 17820 17830 17840 17850 17860 17870 17880 17890 17900 17910 17920 17930 17940 17950 17960 17970 17980 17990 18000 18010 18020 18030 18040 18050 18060 18070 18080 18090 18100 18110 18120 18130 18140 18150 18160 18170 18180 18190 18200 18210 18220 18230 18240 18250 18260 18270 18280 18290 18300 18310 18320 18330 18340 18350 18360 18370 18380 18390 18400 18410 18420 18430 18440 18450 18460 18470 18480 18490 18500 18510 18520 18530 18540 18550 18560 18570 18580 18590 18600 18610 18620 18630 18640 18650 18660 18670 18680 18690 18700 18710 18720 18730 18740 18750 18760 18770 18780 18790 18800 18810 18820 18830 18840 18850 18860 18870 18880 18890 18900 18910 18920 18930 18940 18950 18960 18970 18980 18990 19000 19010 19020 19030 19040 19050 19060 19070 19080 19090 19100 19110 19120 19130 19140 19150 19160 19170 19180 19190 19200 19210 19220 19230 19240 19250 19260 19270 19280 19290 19300 19310 19320 19330 19340 19350 19360 19370 19380 19390 19400 19410 19420 19430 19440 19450 19460 19470 19480 19490 19500 19510 19520 19530 19540 19550 19560 19570 19580 19590 19600 19610 19620 19630 19640 19650 19660 19670 19680 19690 19700 19710 19720 19730 19740 19750 19760 19770 19780 19790 19800 19810 19820 19830 19840 19850 19860 19870 19880 19890 19900 19910 19920 19930 19940 19950 19960 19970 19980 19990 20000 20010 20020 20030 20040 20050 20060 20070 20080 20090 20100 20110 20120 20130 20140 20150 20160 20170 20180 20190 20200 20210 20220 20230 20240 20250 20260 20270 20280 20290 20300 20310 20320 20330 20340 20350 20360 20370 20380 20390 20400 20410 20420 20430 20440 20450 20460 20470 20480 20490 20500 20510 20520 20530 20540 20550 20560 20570 20580 20590 20600 20610 20620 20630 20640 20650 20660 20670 20680 20690 20700 20710 20720 20730 20740 20750 20760 20770 20780 20790 20800 20810 20820 20830 20840 20850 20860 20870 20880 20890 20900 20910 20920 20930 20940 20950 20960 20970 20980 20990 21000 21010 21020 21030 21040 21050 21060 21070 21080 21090 21100 21110 21120 21130 21140 21150 21160 21170 21180 21190 21200 21210 21220 21230 21240 21250 21260 21270 21280 21290 21300 21310 21320 21330 21340 21350 21360 21370 21380 21390 21400 21410 21420 21430 21440 21450 21460 21470 21480 21490 21500 21510 21520 21530 21540 21550 21560 21570 21580 21590 21600 21610 21620 21630 21640 21650 21660 21670 21680 21690 21700 21710 21720 21730 21740 21750 21760 21770 21780 21790 21800 21810 21820 21830 21840 21850 21860 21870 21880 21890 21900 21910 21920 21930 21940 21950 21960 21970 21980 21990 22000 22010 22020 22030 22040 22050 22060 22070 22080 22090 22100 22110 22120 22130 22140 22150 22160 22170 22180 22190 22200 22210 22220 22230 22240 22250 22260 22270 22280 22290 22300 22310 22320 22330 22340 22350 22360 22370 22380 22390 22400 22410 22420 22430 22440 22450 22460 22470 22480 22490 22500 2

```
cryla-105.pe 760 770 780 790 800 810
|||  |||  |||  |||  |||  |||
DLEIYSRYNAKHETVNPCTGLMPLSAQSPGCKGCPNRCAPHLEWNPDLDCSRDGE
21311715  DLEIYLRYNAXKHETVNPCTGLMPLSAQSPGCKGCPNRCAPHLEWNPDLDCSRDGE
160 170 180
|||  |||  |||  |||  |||  |||
820 830 840 850 860 870
cryla-105.pe KCAHSHHFFSLDIDVGCTDLNEDLGVWVIFKIQDQHARLGNLEFLEKPLVGEALARV
|||  |||  |||  |||  |||  |||
21311715  --AHSHHFFSLDIDVGCTDLNEDLGVWVIFKIQDQHARLGNLEFLEKPLVGEALARV
190 200 210
|||  |||  |||  |||  |||  |||
cryla-105.pep
NRAA:62001772
62001772 source="GENBANK_PROT" CryII toxin [Bacillus thuringiensis]

SCORES  Init1: 672  Initn: 1069  Opt: 1096  z-score: 1242.7 E(): 6.3e-61
>>NRAA:62001772  Initn: 1069  Init1: 672  Opt: 1096  z-score: 1242.7 expect(): 6.3e-61
Smith-Waterman score: 1230; 38.5% identity in 571 aa overlap
(4-549:36-585)

cryla-105.pe 10 20 30
MDNPNINECIPYNCLSNPEVEVLGGERIETGY
62001772  QDKHOSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKISEVENVEFPV-SASTIQIG-
10 20 30 40 50 60
|||  |||  |||  |||  |||  |||
cryla-105.pe 40 50 60 70 80 90
TPIDISLSLTOFLSEFVPGAGVLGVLDIIVGIFGP---SQWDAFLVQIQQLNQRIEE
|||  |||  |||  |||  |||  |||
62001772  ----ISIA-GKILGLVPGAGVASLYSFLGELMPKGNQWEIFMEHVEIINQKIST
70 80 90 100 110
|||  |||  |||  |||  |||  |||
cryla-105.pe 100 110 120 130 140 150
FARNOAISFLSGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMSALTALPLFAV
|||  |||  |||  |||  |||  |||
62001772  YARNKALTDLXGLGDALAVHESLESVGNKRNTRARSVVKSQYIALELMFVQKLPFAV
120 130 140 150 160 170
|||  |||  |||  |||  |||  |||
cryla-105.pe 160 170 180 190 200 210
QNYQVPLLSVYVQAANLHLSVLDRVSFQSGWGFDAATINRSYNDLRLIGNYTDHVAWRW
|||  |||  |||  |||  |||  |||
62001772  SGEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFTYNRQVRAQDYSCHVKW
180 190 200 210 220 230
|||  |||  |||  |||  |||  |||
cryla-105.pe 220 230 240 250 260 270
YNTGLERVWGDSDRMIRYNQFRRELTITVLDIVSLPNYDSITYDIRVSQLTRELYTN
|||  |||  |||  |||  |||  |||
62001772  YSTGLNLRGNAESWRYNQFRKDWMLVLDLVALPSPSYDTLVYPIKITSQLTREVITD
240 250 260 270 280 290
|||  |||  |||  |||  |||  |||
cryla-105.pe 280 290 300 310
PV-LENFGSGFRGSA-----QGIEGSI-RSPHLMIDLINSITITTDHRRGEYWSGH
|||  |||  |||  |||  |||  |||
62001772  AIGTVHPNASFASITWNNNAPSFTIESAVVRPHLLDLEQVTTIYSLR-----WSNT
300 310 320 330 340 350
|||  |||  |||  |||  |||  |||
cryla-105.pe 320 330 340 350 360 370
QIMASPVGFSQPEFTFFLYGTMGNAAPQORIVAQLOGGVYRTLSLTLYRRPFNIGIN---
|||  |||  |||  |||  |||  |||
62001772  QYWM---WGHRLEFRITGGMLNTSQGSTNTSINPVLTLPFTSRDVRSTESLAGLNLF
380 390 400 410 420 430
|||  |||  |||  |||  |||  |||
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cryla-105.pe 380 390 400 410 420
NQQLSVLDGTEFAYG-----TSSNLPNAVYKSGT--VDSLDEIPPNNNVPPROGFSH
|||  |||  |||  |||  |||  |||
62001772  TOPVNGPRVDHFHKVFTPIADSNFYYPGAGIGTQLODSENELPPEITTCQPNYESYSH
420 430 440 450 460 470
|||  |||  |||  |||  |||  |||
cryla-105.pe 430 440 450 460 470 480
RLSHVSMFRSGFSSNSVSIIRAPMFSEWHRSAEFNNIIASDSITQIPLVKAHTLQSGTTV
|||  |||  |||  |||  |||  |||
62001772  RLSHIGLI-----SASHVKALVYSWTHRSADRTNIENSITQIPLVKAFLNLSGAAV
480 490 500 510 520
|||  |||  |||  |||  |||  |||
cryla-105.pe 490 500 510 520 530 540
VRGPGFTGDIILRTSGGPAYTIIVNNGQLPQRYRARIYASTNLRIVYVAGERIFA
|||  |||  |||  |||  |||  |||
62001772  VRGPGFTGDIILRTSGGPAYTIIVNNGQLPQRYRARIYASTNLRIVYVAGERIFA
530 540 550 560 570 580
|||  |||  |||  |||  |||  |||
cryla-105.pe 550 560 570 580 590 600
CQFNKMTDGTPLTFQSFYATINTAFTFPMSSQSFVAGDTFSSGNEVIDRFLIPVT
|||  |||  |||  |||  |||  |||
62001772  GN
590 600
|||  |||  |||  |||  |||  |||
cryla-105.pep
SW:117544
117544 description="PESTICIDIAL CRYSTAL PROTEIN CRY4AA (INSECTICIDAL
DELTA-ENDOTOXIN CRYIVA(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (135 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar israelensis"
sources="swissprot_prot" version="NA type="PRT

SCORES  Init1: 571  Initn: 1577  Opt: 1088  z-score: 1229.1 E(): 3.6e-60
>>SW:117544  Initn: 1577  Init1: 571  Opt: 1088  z-score: 1229.1 expect(): 3.6e-60
Smith-Waterman score: 1735; 33.4% identity in 1213 aa overlap
(40-1177:70-1180)

cryla-105.pe 10 20 30 40 50 60
CIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTOFLSEFVPGAGFV--LGLVDIIVG-
|||  |||  |||  |||  |||  |||
117544  QSTNYKDLNLCQNNQOQYGGDFETFDISGEJSAYTIIVGVTLTGFTGFTPLGLALIGFT
40 50 60 70 80 90
|||  |||  |||  |||  |||  |||
cryla-105.pe 70 80 90 100 110
---IRGPSQ-----WDAFLVQIQQLNQRIEERFARNOAISRLSGLSNLYQIYAESFREWE
|||  |||  |||  |||  |||  |||
117544  LIPVLFPQDOSNTWSDFITQYKNIIKKEIASTYISNANKILNRSFNWISTYHNHLKWE
100 110 120 130 140 150
|||  |||  |||  |||  |||  |||
cryla-105.pe 120 130 140 150 160
ADPTNPALREEMRIQFNDMSALTALPLFA-----VQNYQVPLLSVYVQAANLHL
|||  |||  |||  |||  |||  |||
117544  NNP-NPQNTQDVRTQIQLVHYHPQNVPELVNSCPPNPSPDCDYINILVSSYAQAANLHL
160 170 180 190 200 210
|||  |||  |||  |||  |||  |||
cryla-105.pe 170 180 190 200 210 220
SVLRDVSUF---GQRWGFDA-----ATINSRYNDLRLIGNYTDHVAWRVNTGLERWVG-
|||  |||  |||  |||  |||  |||
117544  TVLNQAVKFEAYLKNKQPFYLEPLFTADYIPVLTAKIEDYTNVCYTYKKGLENLKT
220 230 240 250 260 270
|||  |||  |||  |||  |||  |||
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cry1a-105.pe PDSE---TWIRYNOFSELTIVLSDIVSFLNDSRTYDIRVTSQTSOLTRITVYVFLN
117544 QSNLDGQINWLYNTYRTNTAVLDLVALFNDVGVKPIGVQSELTRITVQ--VL-N
280 290 300 310 320 330

cry1a-105.pe FDGS-FRS-SAGIGG---PSPLMDILNSITVTDARG-EYVWSGQIMASVFGSP
117544 FEESPXYKDYDFQEDSLTRPHLFTLDSLSNFYACCTPNFFTSHTYMHFYH-LDNI
280 290 300 310 320 330

cry1a-105.pe EFTFPLVGTMGNAAPQORIVAGQGVVRLTSLT---VRRPGLGNNQSLVDGT
117544 SOKSSVFGNH-NVTDKLKSLG-LATNIFPDLNVISLNDYNDYN-NLSKMDRLTNGT
340 350 360 370 380 390

cry1a-105.pe ---EFAYGTSNLSFSAVYRKSGTVSDLSDEIPPNNGV---PRQGSFHSRSHVSMFRSG
117544 RLLEKELTAG-SQIITYDVNKNIFGLPILKARENQCNPLFPMDNASHILLS-FNFS
390 400 410 420 430 440 450

cry1a-105.pe FSNSSVLIIPAPMFWSHRSAEFNIIASDSITQIPLVKAHTLQSGTIVYRGSGTQSDI
117544 LSIPTATYKTVYTFATWTHSSVDPKNTIYTHLTQIPAVKANSLSGTASKVQGGTGGSG
440 450 460 470 480 490 500

cry1a-105.pe LRRTSGGFAYTVININGQLPQVRRIRYAS--TTNLR--IYVWAGERIFAGQNKTM
117544 IDEVDH--FKITCOHNFQ--QSVFIRIRYASNGSANTRAVINLSIPGVAELGMAINPFE
500 510 520 530 540 550

cry1a-105.pe DTGD--PLTFQSFYATINTAFTF--PMSQSFVTVGADTFSSGNEVYIDRFELIPVTATLE
117544 SGTDYTNLYKDYQYLEFSENEVKFAPQNISLVFNRSVDYVNTVTLVDIKIEFLPITRSIR
560 570 580 590 600 610 620

cry1a-105.pe AEF--NLEAOKAVNALFTSNOLGLKNTVTDYHIDQVSNLVTLSDFCLDEKRELSE
117544 EDREKQLEIVQQLINTFYANPKNTLQSELTDYDDIQANLVEICISELYPKEKMLLD
620 630 640 650 660 670 680

cry1a-105.pe KYHAKRLSDERNLQDSNFKDINRQPERGWSGTGITIQGGDDVKFNKYVTLSTGTFD--
117544 EVKNAKQLSQSRNVNLQNGDFESATL---GWTSDNITIQEDDPFKFGHYLHMSGARDID
670 680 690 700 710 720 730

cry1a-105.pe EGYTYLYQKIDESKLKAFTRYQLRGVIEDSQDLLEYIRINAKHETV-NWPGT-GSLW
117544 GTIFFTYIFQKIDESKLKFTYRLVGRVSGSKDVELVWSRYGEEIDAIMVADNLYL
730 740 750 760 770 780 790

cry1a-105.pe PLSAQSPGKGGFNRC---AP-HLEWNPDLDCSCH--DGEK---CAHSHHPSFLDIDV
117544 PSTFD-----CESNRCETSAPVANIGMTSDMLYSQDYDTGKGVVC-QDSHQFSTFIDT
790 800 810 820 830 840 850

cry1a-105.pe CSTDLEDELGWVVIKFKITQDGHARGNLNLEFEEKPLVGEALARKKAEKKWDRREKLE
117544 GALTNDENIGVWFMFKISIPDGYASLDNLNLEVEIEEGPIDGEALSFKVMEKKKNDQMEAKR
840 850 860 870 880 890

cry1a-105.pe WETNIVVKEAKESVDALFVNSQVDQDQADTNTAMIAHADKRVHSIREAYLPESLVIPGVN
117544 SETQQAIDVAKQAIDALFTNVQDEALQFDITTLAQIQAIEYLVSIPYVYNDWLSDVPGNN
900 910 920 930 940 950 960 970

cry1a-105.pe AAIFEELEGRIFTAFSLYDARNVKNKGNDFNNGSLSCWNVKGVHDVEEQNNQSRSLVVPWE
117544 YDIVVELDARVAQARYLYDTRNIIKNGSDFTQGVGMGHVHTGNADVQ-QIDGVSVLVLSNWS
960 970 980 990 1000 1010 1020 1030

cry1a-105.pe NEVSGEVRCPGRGYILRVYAKGEGYGGCVTIHEIENNTDELAFSNCVEEIEYPNNTVT
117544 AGVSONVHLOHNGHYLVRYIAKKGPGNGYVTLMDCEENQEKLTFTSCEE-----
1020 1030 1040 1050 1060 1070 1080 1090

cry1a-105.pe CNDYTVNQEEYGGAYTSRNRGNEAPSPADYASVYEEKSYTDGRRENPCFNRGYRDT
117544 -----
1080 1090 1100 1110 1120 1130

cry1a-105.pe PLRNGVTKLEYFPETDKWIEIGETEGTFIVDSVELLMEE
117544 ---GYLVTVGVFPDTRVRIEIGETEGSFYIESIELICMNE
1140 1150 1160 1170 1180

cry1a-105.pe
NRAA: 21685485

21685485 source="GENBANK PROTEIN" pesticidal crystal protein cry4AA (Bacillus
thuringiensis serovar israelensis) [117544] [P16480] [CRAAA BACTI Pesticidal
crystal protein cry4AA (insecticidal delta-endotoxin CryIVA(a)) (Crystalline
entomocidal protoxin) (136 kDa crystal protein) [216290] [db] [BAA00179.1] 130 kDa
insecticidal protein (ISR4) (Bacillus thuringiensis serovar
israelensis) [gi|225983|prf|14052018.1 insc4] [cdal protein ISR4] . . .

SCORES Initl: 571 Initn: 1577 Opt: 1088 Z-score: 1224.1 E(-): 3.6e-60
>NRAA: 21685485
Initn: 1577 Initl: 571 Opt: 1088 Z-score: 1224.1 E(-): 3.6e-60
Smith-Waterman score: 1735; 33.4% identity in 1213 aa overlap
(40-1177:70-1180)

cry1a-105.pe CIPYNCLSNPEVEVLGERIEGTYPIDISLSTQFLSEFVAGGV--LAAVQVNG-
21685485 QSTNYKWLNMCOONOQYGGDEFTFIDSGELSAITVGVTVTGFTVTPSIALIGPAT
10 20 30 40 50 60 70 80 90

cry1a-105.pe ---IFGFSQ-----WDAFVQVQEQLINQRIEFAFNAQASRLGSLNLYQIYAESFREHE
21685485 LIPVLFPADQGSNTWSDFTQTQKIIKKEIASTVISNANKILNRSFNVISYHNHLKWE
100 110 120 130 140 150

```
120 130 140 150 160
cry1a-105.pe ADPTNPALREEMRIQNDMNSALTAIPLEA-----VQNVQVPLLSVYQAANLHL
21685485 NNP-NPQNTQDQATQIQLVHFQNVIPELVNSCPNPDSCDQYNNILVSSYQAANLHL
160 170 180 190 200 210
170 180 190 200 210 220
cry1a-105.pe SVLRDVSF---GQRWGFDA---ATINSRYNDLRLIGNYTDHAKRWNTGLERVWG-
21685485 TVLNAQVKFEAYLKNRQDFVLEPLPTAIDYYPVLTKAEDYTNVCTVTKKGNLIKTT
220 230 240 250 260 270
cry1a-105.pe PDNR-----DWIRYQFRRELTFLVDIVSLFPNYSRTPYRTVSQLTREIYTNVLEN
21685485 PDSNLGDNINWNTYNTYTKMTTAVLDLVALFVNDYGVKYPGVQSELTRFIYQ--VL-N
280 290 300 310 320 330
cry1a-105.pe FDGS-FRG-SAOGIEGSI-RSPHLMIDLNSITITTDHFRG-EYWMSGHQMSPVGFSGP
21685485 FEESPKYKDFQOEDSLTRPHLFTWLDLSNFIYKAKQTPNPFTHYMFHT-LDNI
340 350 360 370 380 390
cry1a-105.pe BFTPLXGTMGNAAPQORIVAQOGVYRTLSSTL-----YRPPNIGINNOQLSLDGT
21685485 SOKSSVFGNH-NVTDKLSLG-LATNIVIFLLNVISLDNKYLDYN-NISKMDFFITNGT
400 410 420 430 440 450
cry1a-105.pe -----FRAYGTSNLSFSAVYKSGTVDSLDEIPQNNVV--PPROGSHRLSHVMSFRSG
21685485 RLLEKEITAG-SQIITYDVKNIFGLPILKRENQGNPTLFFTYDYNVSHLS-----FIKS
460 470 480 490 500
cry1a-105.pe FSNSSVSIIRAPWFSWIHRSAEFNNIATSDSITOPLVKAHTLOSQTVTVRGFGTGGDI
21685485 LSIPATYKTVYTFANTHSSVDPKNTIYTHLTQIIPAVKANSLSGTASKVQGGHGGDL
510 520 530 540 550
cry1a-105.pe LRTSGGPFAYTIVNINGQLPQYRARIYAS--TTNLR--IYVTVAGERIFAQPNKTM
21685485 IDFKDH--FKITCOHSNFO--QSVFIRIRYASNGSANTRAVINLSIPGVAELGHALNPTF
570 580 590 600 610 620
cry1a-105.pe DTGP--PLTFQSFYATINTAFTF-PMSQSFTVAGDTFSSGNEVYIDRELTPVATILE
21685485 SGTDTYTLKYDFQYLEFSEVNEVKFAPQNSLFRNSRDVYNTITVLIDKIEFLPTFSIR
630 640 650 660 670 680
cry1a-105.pe AEY---NLERAQAVNALFTSTNQLGKTNVTDYHDQVSNLVTYLSDEFCLCKRELSE
21685485 EDREKQLEIVQIINTFYANPKNTLQSELTDYDIDQANLVEICISELYPEKMLLD
690 700 710 720 730 740
cry1a-105.pe KYXKAKRLSDERNLQDSNFKDINRQPERGGSGTIGITQGGDDVFKNFYTLSTGTFD--
21685485 EVXNAKQLSQSRNVNLQNGDFESATL---GWTTSNITIQEDDPIFKGHYLNHSGARDID
750 760 770 780 790
670 680 690 700 710 720
cry1a-105.pe QSTNYKDLNMCQONQYGGDPTTFIDSGELSAVTIWTGVTLTGFTTPLGLALIGFTG
40352 40 50 60 70 80 90
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```
730 740 750 760 770 780
cry1a-105.pe ECTPTLYOKIDESKLKAFTRYQIRGYIEDSDLEIYSIRYNAKHETV-NVPGT-GSLW
21685485 GTIFPTTIFOKIDESKLKPYRYLVRGVGSKDVLVSVRGEEDAIIMNVFADLNLYL
800 810 820 830 840 850
790 800 810 820 830
cry1a-105.pe PLSAQSPIGKCGPNRC---AP-HLEWNPDLDCSR---DGEK---CAHSHHFSDIDV
21685485 PSTFD-----CEGSNRCETSAVPANIGNTSDMLYSCDYDTGKKHVC-QDSHOFSTIDT
860 870 880 890 900 910
cry1a-105.pe GCTDLNEDLGVWVIFIKTKQDGHARLGNLFLBEKPLVGEALARVKRAEKKWRDKREKLE
21685485 GALDTNENIGVWVFXKISSPDGYASLDNLVEIEEGPIDGEALSRVKHMEKKWQDMEAKR
920 930 940 950 960 970
cry1a-105.pe WETNIVVYKEAKESVDALFVNSQYDQLOADTNIAHIAADKRVHSIREAYLPESLVIPGVN
21685485 SETQQAQDVAKQAIIDALFTNVQDEALQFDITLQIQYAEYLVSQIPYVYNDWLSVDYPGVN
980 990 1000 1010 1020 1030
cry1a-105.pe AAFEELEGRIFTAFSLYDARNVINGDFNNGLSQWNVKGVHVDVEEQNNQSRVSLVPEWE
21685485 YDIVELDARVAQARYLYLIDTRNIIKNGDFTQGVMGVHVTGNADVQ-QIDGVSVLVLSNWS
1040 1050 1060 1070 1080 1090
cry1a-105.pe AEVQEVRCVPCRGYILRTAYKGYEGCVTTHEIENNTDELAFSNCVREEIYPNNTVT
21685485 AGVSONVHLQHNHGYVLRVIAKKGPGNGVITLMDCEEKQELFTSCSE-----
1100 1110 1120 1130 1140
cry1a-105.pe CNDVTYQNEEYGGAYTSRRNRYGNEAPSVADYASVYEEKSYTDGRENPCFNRGYRDT
21685485 -----
1080 1090 1100 1110 1120 1130
cry1a-105.pe PLPVGYVTKLEYFPETDKVWIEIEGTEGTFIVDSVELLMEE
21685485 ----GYITKTVDFPDTDRVRIEIEGTEGTFIESIELICMNE
1150 1160 1170 1180
cry1a-105.pep
NRAA:40352
40352 source="GENBANK_PROT" unnamed protein product [Bacillus thuringiensis]
SCORES Initl: 570 Initn: 1551 Opt: 1076 z-score: 1215.4 E(): 2.1e-59
>NRAA:40352
initn: 1551 initl: 570 opt: 1076 z-score: 1215.4 expect(): 2.1e-59
Smith-Waterman score: 1725; 33.3% identity in 1213 aa overlap
(40-1177:70-1180)
cry1a-105.pe CIPVNCILSNFEVLGGERIETGYTPIIDISLQTLFLLSEFVPGAGFV--LGLVDIING-
40352 QSTNYKDLNMCQONQYGGDPTTFIDSGELSAVTIWTGVTLTGFTTPLGLALIGFTG
40 50 60 70 80 90
```


(1028-1177:1-150)

cry1a-105.pe 1000 1010 1020 1030 1040 1050
VEEQNNORSVLVPEWEAEVSEVRVCPGRGYILRLVTAYKSYEGCVTHIEIENNTDEL
14537818 GYILRLVTAYKSYEGCVTHIEIENNTDEL 10 20 30

cry1a-105.pe 1060 1070 1080 1090 1100 1110
KFSNCVEEYIPNNVTGNDYVNOQEEYGGAYTSRNRGYNAPSVPADYASVVEEKSYYTD
14537818 KFSNCVEEYIPNNVTGNDYVNOQEEYGGAYTSRNRGYNAPSVPADYASVVEEKSYYTD 40 50 60 70 80 90

cry1a-105.pe 1120 1130 1140 1150 1160 1170
GRRENPCFNRRGYRDTPLPGYVTKLEYFPETDKWTEIGETGTFIVDSVELLMEE
14537818 GRRENPCFNRRGYRDTPLPGYVTKLEYFPETDKWTEIGETGTFIVDSVELLMEE 100 110 120 130 140 150

cry1a-105.pep
SW:8469161

8469161 description="PESTICIDIAL CRYSTAL PROTEIN CRY3CA (INSECTICIDAL DELTA-ENDOTOXIN CRYIIIC(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (73 KDA CRYSTAL PROTEIN)." library=NA species="Bacillus thuringiensis serovar kurstaki" source="swissprot_prot" version=NA type=PRT

SCORES Initl: 370 Initn: 713 Opt: 1008 z-score: 1142.1 E(): 2.6e-55
>>SW:8469161
initn: 713 initl: 370 opt: 1008 z-score: 1142.1 expect(): 2.6e-55
Smith-Waterman score: 1070; 33.4% identity in 572 aa overlap
(56-607:89-648)

cry1a-105.pe 30 40 50 60 70 80
GERIETGYTPIDISLSLTQFLSEFVPGAGFVLGLVDIIVGIFGPSQWDAFLVQIEQLIN
8469161 TTKDAIQKGISIIIGDLLGVVGPYGGALVSYTNLLNTIWP--GEDPLKAFMQQVEALID 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200

cry1a-105.pe 90 100 110 120 130 140
QRIEFARNQAIISRLGLSNLYQIYAESFREWADP--TNPALREEMRIQ--FNDMNSALT
8469161 QKIADYAKDKATAELOGLKNVFKDYVSALDSWDKTPILTRDGRSQGRIRLEFSQAESHR 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350

cry1a-105.pe 150 160 170 180 190 200
TAIPLFAVQNVQVPLLSVYVQAANLHLSVLDRVSVFQGRWGFDAAATINSRYNDLTRIGN
8469161 RSMPSFAVSGYEVFLPTVYAQAANTHLLLLKDAQIYGTWDGYSSTDLINEFTKQDLTIE 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350

cry1a-105.pe 210 220 230 240 250 260
YTDHARVNTGLERWGPDSRDMIRYNQFRRELTITLVDIVSLFPNYDSRTYPIRTVSQ
8469161 YTNHCARKYRAGLDKLRGSTEYEWKFNRYREMTLTITLITLFLPYDVRTYTKGKTE 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350

cry1a-105.pe 270 280 290 300 310
LPREIYNFV--LENFDGFRSQAQIEGSIIRSHLMDILNITITYDAHGEY-----
8469161 LTRDVLTDPIVAVNNMNG-YGTFISNIENYIRKPHLPDYILHAIQFHSRLQPGYFGTDSFN 270 280 290 300 310 320 330 340 350

cry1a-105.pe 320 330 340 350 360 370
YWSCHQIWA--SPVGSGEFTFPLYGTMGNAAPQORIVLAQOGVYRTLSS--TLYRRPFN
8469161 YWSGNYSTRSSIG--SDEILSRPYGNKSTLDVQV--LEFNGEKVFAVANGNLAVPVG 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640

cry1a-105.pe 380 390 400 410 420
IGINNQOLSVLDGTEFAYGTSN--LPSAVT---RKSGTV--DSLDEIPPQNNVPPRQGF
8469161 TGGTKHSQVTKVQFQSOYNDNRKDEVRTQTYDSKRNVGIVFDSIDQLPPTTDESLEKAY 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640

cry1a-105.pe 430 440 450 460 470 480
SHRSHVSMRSGFSNNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPLVKAHTLOSQT
8469161 SHQLNYVRCP---LLQGGRII--PVFTWTKSVDFYNTLSEKITQIPFVKAPILVNST 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640

cry1a-105.pe 490 500 510 520 530 540
TVVRGPGFTGDDILRRTSG--GPFAVTIVNNGQLPORVBARIRYASTNLRIVTVVAGER
8469161 SVVAGPFTGDDIKCTNGSGLTLYVTPAPDLTYSKYTKIRIRYASTSQVRFGLDLSYT 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640

cry1a-105.pe 550 560 570 580 590 600
IPAQQFNKMTDGTPLTFOSFSYATINTAFTFPMSSQSTVVGADTFSSGNEVYIDRPELI
8469161 HSIISYFDKNTDKNTLTYSNLSVSRPIEIS--GGNKIGVSVGGIGSGDEVYIDKIEFI 550 560 570 580 590 600 610 620 630 640

cry1a-105.pe 610 620 630 640 650 660
PVATLAEVNLERAQKAVNALFTSTNQLGKTNVTDYHIDQVSNLYLSDFECLDEKR
8469161 PMD 610 620 630 640 650 660

cry1a-105.pep
NRAA:40288

40288 source="GENBANK PROT" CryIIID [Bacillus thuringiensis]gi|8469161|sp|Q45744|CR3CA_BACTX Pesticidal crystal protein cry3Ca (Insecticidal delta-endotoxin CryIIIC(a)) (Crystalline entomocidal protoxin) (73 kDa crystal protein)

SCORES Initl: 370 Initn: 713 Opt: 1008 z-score: 1142.1 E(): 2.6e-55
>>NRAA:40288
initn: 713 initl: 370 opt: 1008 z-score: 1142.1 expect(): 2.6e-55
Smith-Waterman score: 1070; 33.4% identity in 572 aa overlap
(56-607:89-648)

cry1a-105.pe 30 40 50 60 70 80
GERIETGYTPIDISLSLTQFLSEFVPGAGFVLGLVDIIVGIFGPSQWDAFLVQIEQLIN
40288 TTKDAIQKGISIIIGDLLGVVGPYGGALVSYTNLLNTIWP--GEDPLKAFMQQVEALID 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200

cry1a-105.pe 90 100 110 120 130 140
QRIEFARNQAIISRLGLSNLYQIYAESFREWADP--TNPALREEMRIQ--FNDMNSALT
40288 QKIADYAKDKATAELOGLKNVFKDYVSALDSWDKTPILTRDGRSQGRIRLEFSQAESHR 90 100 110 120 130 140 150 160 170 180 190 200

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

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40288 RSMFPAQSYVLEPTQAQANTHLLKDAQIYGTGWDGYSDDLLNEHFKQKDLTIE
180 190 200 210 220 230
cry1a-105.pe YTHNNAWNTGLRVGPDSDRWVWVNFRELTWLDIVSLFPMYDSRTVPIRTVSO
210 220 230 240 250 260
40288 YTHNCAKWTQADDKLQCYFPAWKNRYNREMTWLDITLFLPYDRTYTKGVKTE
240 250 260 270 280 290
cry1a-105.pe LTRIETNPV--LENFDSFRGAGIESSRSCHLMOLNINIVYDAHGEY-----
270 280 290 300 310
40288 LTRDVLTDPIVAVNMWNG-YGTITSNINRYIRSHHETLHAIOFNSRLDGPVFGTDSN
300 310 320 330 340 350
cry1a-105.pe YWSGHQIMA-SPVFGSGPEFTFLYGTMGNAAPQRTVNOIGVGVYTLSS-TLIRNPM
320 330 340 350 360 370
40288 YWSGNYVSTRSSIG-SDEIIRSPFYGNKSTLDVON--LWNGSKVFRAVAGNLAWPVG
360 370 380 390 400 410
cry1a-105.pe IGINNQQLSVLDGTEFAVCTSSN-LPSAVY---RKSGTV--DSLDEIPQNNVPPROGF
380 390 400 410 420 430
40288 TGGTKHSGVTKVQFSQYNDKRDREVRTQYDTSKRNVGIGVFDSDIDPPTTDELEAY
420 430 440 450 460 470
cry1a-105.pe SHRLSHVSMFSGFSNSSVSIIRAPMFWSHIRGAENFIASDSITQIPVKAHTLQSGT
430 440 450 460 470 480
40288 SHQLNYVRCF---LLQGGRII--PVFTWTHKSVDFNYLTDEKXITQIPVKAFLVNST
480 490 500 510 520
cry1a-105.pe TVVGPFGTGGDLIRRTSG-GPFATVINGQLPQRYARIRASTNRIIVTVAGER
490 500 510 520 530 540
40288 SVVAGPFGTGGDIKCTNGSGLTLYVPAPDLTYSTKYIRIRYASTSVQRFGLDLSYT
530 540 550 560 570 580
cry1a-105.pe IFAGQFNKTMDTGDLTFCFSYATINTAFTFPMSSSTFGADTFSGNEVYIDRFELI
550 560 570 580 590 600
40288 HSIYFDKTMKGNLTLYNSNLSVSRPIEIS-CGNKIGVSGVGGISGDEVIDKIEFI
590 600 610 620 630 640
cry1a-105.pe PVATLEAYNLERAKAVNALFTSTNQLGKTNVTDYHIDQVSNLVLYLSDEFCLDKR
610 620 630 640 650 660
40288 PWD
650 660
cry1a-105.pep
NRAA:62548293
62548293 source="GENBANK_PROT" Cry1A toxin [Bacillus thuringiensis]
SCORES Initl: 875 Initn: 875 Opt: 875 z-score: 1001.3 E(): 1.8e-47
>>NRAA:62548293
initn: 875 initl: 875 opt: 875 z-score: 1001.3 expect(): 1.8e-47
Smith-Waterman score: 875; 99.2% identity in 132 aa overlap
(91-222:1-132)

cry1a-105.pe VDIIMGIFPSOWDAFLVQIBOLINQRIEFAFNOAISRLGLSNLYOYAESFREWAD
130 140 150 160 170 180
62548293 FARNQAIISRLGLSNLYOYAESFREWAD
20 30
cry1a-105.pe PTNPALREMRIOFNDMNSALTATPLFAVQVQVPLLSVTVQAANHLHSLVLRDVSFVGO
130 140 150 160 170 180
62548293 PTNPALREMRIOFNDMNSALTATPLFAVQVQVPLLSVTVQAANHLHSLVLRDVSFVGO
40 50 60 70 80 90
cry1a-105.pe RWGFDAATINSRYNDLTRIGNYTDHAVRWYNTGLRVWGPDSRDWIRYNQFRELTLTV
190 200 210 220 230 240
62548293 RWGFDAATINSRYNDLTRIGNYTDHAVRWYNTGLRVWGPDSRDWIRYNQFRELTLTV
100 110 120 130
cry1a-105.pe LDIVSLFPNDSTYPIRTVSQLTREIYTNPVLENFDSFRGAGIESSIRSPHLMIDL
250 260 270 280 290 300
cry1a-105.pep
NRAA:22122188
22122188 source="GENBANK_PROT" cry8 [Bacillus thuringiensis serovar galleriae]
SCORES Initl: 726 Initn: 2159 Opt: 883 z-score: 996.3 E(): 3.4e-47
>>NRAA:22122188
initn: 2159 initl: 726 opt: 883 z-score: 996.3 expect(): 3.4e-47
Smith-Waterman score: 2660; 40.7% identity in 1211 aa overlap
(4-177:9-1144)
cry1a-105.pe MDNNPNINECIPYNCNLSNPEVEVLGGERTCY
10 20 30
22122188 VEILIASSTVNSDNRVPLANDQTITLONMYKDYLMSEGENPEL--FGNPETFISS
10 20 30 40 50 60
cry1a-105.pe TPIDIGLSET-QFLSEHPPGAGFVLSLVALLMGIFGPSQ----WDAPLVQIQLINQRI
40 50 60 70 80
22122188 STVOTGIGTCOVNCGALGVDEGCGASFSYFSLVGSWPSSSTVSVWEMIMKQVEDLIDQKI
70 80 90 100 110 120
cry1a-105.pe BEFARNQAIISRLGLSNLYOYAESFREWADPTNPALREMRIOFNDMNSALTATPLF
90 100 110 120 130 140
22122188 TDSVRKKTALAGLOGLDGDUVYQKSLKNNENRNRGFRSVVVTQYSLDLDVFAKIPSF
130 140 150 160 170 180
cry1a-105.pe AVONYQVPLLSVTVQAANHLHSLVLRDVSFVGOQVQVPLLSVTVQAANHLHSLVLRDVSFVGO
150 160 170 180 190 200
22122188 AISGQEVPLLSVTVQAANHLHSLVLRDVSFVGOQVQVPLLSVTVQAANHLHSLVLRDVSFVGO
190 200 210 220 230 240
cry1a-105.pe RYNYTGLRVWGPDSRDWIRYNQFRELTLTVLDIVSLFPNDSTYPIRTVYNQFRELTLTV
210 220 230 240 250 260
22122188 RYNYTGLRVWGPDSRDWIRYNQFRELTLTVLDIVSLFPNDSTYPIRTVYNQFRELTLTV
250 260 270 280 290 300
cry1a-105.pe TNPVLENF--GSF--RGSAGQ-----IEGS-IRSPHLMIDLNSITLYTDA-----HRG
270 280 290 300 310
22122188 TNPVLENF--GSF--RGSAGQ-----IEGS-IRSPHLMIDLNSITLYTDA-----HRG
270 280 290 300 310

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22122188 TDPIVFNRTSGCFRRNSLNSDISFSEVESAVIRSPHLPDILSEIEFYTTBAGLPLNNT
310 320 330 340 350 360
cry1a-105.pe EY--YWSGQIMASPVGSGP-EFTPLYGTMGNAPQQRIVAQLOQGYRTLSLTYRR
320 330 340 350 360
22122188 EYLEYVGHSHIKYKNTWASSALERN---YGTITSNKIKYVDLANKDIFQVRSIGLADANY
370 380 390 400 410 420
cry1a-105.pe PFNI-CINNOQLSULD---GTEFAYGTSNLSAAYRK-SGTVDSDLDETPPONNVPRQ
370 380 390 400 410 420
22122188 YAQYGVPSYASFTLLDKNTSGSGVGYTSKPHITMQCTQNTYNTIDEIPPENE--PLSR
430 440 450 460 470 480
cry1a-105.pe GFSHRLSHVSMFRSGFNSSVSIIR--APMFSWHRSAEPNNIIASDSITQIPLVKAHT
430 440 450 460 470 480
22122188 GYSHRLSHITSY--SFSKNASSPARYGNLPVFAWTHRSADVNTNIVYSDKITQIPVKAHT
490 500 510 520 530
cry1a-105.pe LQSGTTVVRGPGFTGSDILARTSGPFIATVINGQLPQRYRIRYASTNLIYTV
490 500 510 520 530
22122188 LVSGTTVVRGPGFTGSDILARTSGPFIATVINGQLPQRYRIRYASTNLIYTV
540 550 560 570 580 590
cry1a-105.pe AGERIFAGQFNKMTDGLTQFSFYATINTAFTFPMSSQSFVGDVTFSSGNEVYDR
550 560 570 580 590 600
22122188 SGTRISYINWNTKMGDDLTFTFIDLIIGTFTFNYSDLSLVGADSFAGSGEYVDK
600 610 620 630 640 650
cry1a-105.pe FELIPVTATLEAYNLRAQKAVNALFTSTNQLGLKTVTVDYHIDQVSLVLYSDEFCL
610 620 630 640 650 660
22122188 FELIPVNATFEAEDLDVAKKAVK-----NLVCLSDLYP
660 670 680 690
cry1a-105.pe DEKRELSEKVKAKRLSDERNLLQDSNFKDINRQPERGWGSGTITIQGDDVFKENTVT
670 680 690 700 710 720
22122188 NEKRLMDAVKAKRLVQARNLLQDTGFNRIN--GENGWGSGTIEVAGSDVLFKDRSLR
700 710 720 730 740 750
cry1a-105.pe LSGTFD---ECYPTLYOKIDESKKAFTRYOLRGYIEDSODLEIYSIRYNAKHETVNP
730 740 750 760 770
22122188 LTSAREIDTETPTLYQOIDESLAKPYTRYKLKGFIGSSODLEIKLIRHRAQIVKNVP
760 770 780 790 800 810
cry1a-105.pe GTSLMPLSAQSPGKCGENRCP--HLEWNPDLDCRDEKCAHSHFSLDIDVGC
780 790 800 810 820 830
22122188 D--NLLPDVYL--PVNSCGGIDRCSEQQYVDANLANNNGNMSD--SHAFSFHDTGE
820 830 840 850 860
cry1a-105.pe TDUNEDLGVWVIFKIKTODGHARIGNLEFLEKPLVGEALARKVRAEKWKDRKLEWE
840 850 860 870 880 890
22122188 IDLNENTGTVVVKIPTNGYATIGNLELVEGSLSGTLEAAQQQOQOQKARKGA
870 880 890 900 910 920
cry1a-105.pe TNIVYKEAVESVDALFVNSQVDQLQADTNIAHHAADKRVHSIREAVLPSELVIGVNAA
900 910 920 930 940 950

22122188 SEKAYYAAQALDRLPADYQDQKLSGVEMSDMLAAQLVQSIPYVYNDALPEIPGMNYT
930 940 950 960 970 980
cry1a-105.pe IFEELEGRIFTAFSLYDARVYKNGDFNNGSCMNKGVHVDVEEQNNQSRSLVLPWEAAE
960 970 980 990 1000 1010
22122188 SFTELTNRQQANMLYDLRNATPNGDFRNGLSDMNATSDVNVQ-QLSDTSVLVIPNMNSQ
990 1000 1010 1020 1030 1040
cry1a-105.pe VSSEVVCPCRGYILRYATAYKEGYGEGCTYIHEIENNTDELKPSNCVEEILPNNVTCTN
1020 1030 1040 1050 1060 1070
22122188 VSQQFTVQNYRYVLRVLRVATKRGVGGYVIRIDGANQTETLTN-----ICD
1050 1060 1070 1080 1090
cry1a-105.pe DYTVNOEEYGGATYSRNGYNEAPSYADYASVYEKSYTDGRENPCFENRGYDTPPL
1080 1090 1100 1110 1120 1130
22122188 DDT-----GVLS-----ADQTS-----
1100
cry1a-105.pe PVGYVTELEYEPETDKVWIEIGETGTIVDSVELLMEE
1140 1150 1160 1170
22122188 ---YITKTVEFTPSTEQWIDMSETEGVFNIESVELVEE
1110 1120 1130 1140
cry1a-105.pe
NPAA:19386614
19386614 source="GENBANK_PROT" mosquitoicidal toxin [Bacillus thuringiensis
serovar aizawai]
SCORES Initl: 146 Initn: 486 Opt: 825 z-score: 934.0 E(): 1e-43
>NRAA:19386614
initn: 486 initl: 146 opt: 825 z-score: 934.0 expect(): 1e-43
Smith-Waterman score: 929; 31.4% identity in 625 aa overlap
(29-630:64-660)
cry1a-105.pe MDNPNINECIPNCLSNPEVEVEIGERIEGTYPIDISLTOFLSEFVPGAGFVL
19386614 SLASMTNXYKDWLTCMDRTDVLSSRGAVSTGVGMLSTLSL--FGIPLIGEGIDL
40 50 60 70 80 90
cry1a-105.pe GLVDIIWGIF-CFSQ--WDAPLVQIQQLINQRIEFARNQAISSLEGLSNLYQVAFSFR
60 70 80 90 100 110
19386614 GAADFLWPESDGGHYTWEDLMNHIELMDERLETERETKTTALDDRLGLKALIGLFRDAPD
100 110 120 130 140 150
cry1a-105.pe EWADPTNIPALREERNRQINDMSALTTPAIP-LFAVQNYQVPLLSVYVQAAHLVLRLD
120 130 140 150 160 170
19386614 SWEKNNDPIAKNRVGVGFEDVTHFVKOMASIFSATNYEVLLPLVYQAAHLHLILRE
160 170 180 190 200 210
cry1a-105.pe VSVFGORWGFDAATINSYNDLRTLIGNVTDHAYVNTGL--ERVWGPDSRDWIRYNOF
180 190 200 210 220 230
19386614 GVIYGRWGI-APAADFYHDQLKLYTAIYANHCVTWYNNGLAQOQKELFAKSPNWRFNAY
220 230 240 250 260 270
cry1a-105.pe
240 250 260 270 280 290

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17385648 LKRALSIYQESFETWIDDENDPELOQDVMRRTSTLPELVTTTETIKYSQGEIALLTVFV
 150 160 170 180 190 200
 cryla-105.pe QANLHLSVLRVSVFGQMGFADATINSRY-ND-----LRLIGNTVDHVAWYNTGLR
 170 180 190 200 210
 17385648 QAADHMLLLOQGVMYGVWVGQFQRTVDFYQNDRGELKNLFPKYSYDZCYTVMYDQGLNR
 210 220 230 240 250
 cryla-105.pe V-----WGPDSE-----DMIRYNQFRRELTVLTVLSVLPFNWDSRT
 220 230 240 250
 17385648 AKNLKAMLSSTVRYPAWALENWSVLQELDNLINDYRDMILVDLVAWPTDYLLH
 270 280 290 300 310 320
 cryla-105.pe YP---IRTVSOLTREIYTNVLENFQDSFRGSAQIEGSIKRSPLHMLILNSTIYTDAAHR
 260 270 280 290 300 310
 17385648 YDNGNYGVQSELSTRISYQOAV-GNVMGTVFTFKQEYVEVSFVRPHLVTLKEMFIQIRPTE
 330 340 350 360 370 380
 cryla-105.pe GEYWSGHQIMASPVGFSGPETFPYXTGMGNAAPOQRIVAQLQGVYRILSTLYRRPFF
 320 330 340 350 360 370
 17385648 -----QGAPIDATMAGVS-----LYYSXGWDNTVDD-----ILLGYPTYSSEIRVLVSKS
 390 400 410 420
 cryla-105.pe NGINNQQLSVLGTEFAYGTSNLPBAYVRKSGTVDSLD-EIPPONNVPPRQGFSGHRL
 380 390 400 410 420 430
 17385648 VYQOEKNRAIYNTDLQHDKLVDKRVFVYQNSGEVYAGNDPSSYKTFAMWDTLITNYS
 430 440 450 460 470 480
 cryla-105.pe SHVSMFSGFSNSSLIRAPMFSWIHRSAE-FNNII-ASDSITQIPLVKAHPLASGTVT
 440 450 460 470 480
 17385648 SONTIIRPWSGHFQIOWAPEWI-PASCEPNNIVDAEDVITQIIPAVKARELYRGARV
 490 500 510 520 530 540
 cryla-105.pe VARGPSTGQDILRRSGSGFAYTIVNNGQIPORVARIRVASTNIRIYTVVAGERIFA
 490 500 510 520 530 540
 17385648 IKGVNGTGDVANSAPHGILSGVYATFN--VVRVYRIVHACODPTKINLIGDSR-HD
 550 560 570 580 590 600
 cryla-105.pe GOFNKMTDGTPLTFOSFSLNIRATFF--MPSSTVQADSS-SGNEVYVDRPEL
 550 560 570 580 590 600
 17385648 IITLPSTY-SGGAUTYDSFGYATSEYKVP-ADFDYKSKTIVLIGNSFSGSDVILDKIEF
 610 620 630 640 650 660
 cryla-105.pe IPWTATLEAVNLERAKAVNALFTSTNQLGKTNVTHNDVQNSNLVTLVLEFQFCDSEK
 610 620 630 640 650 660
 17385648 IPVDIFAYEEOLEKAKAVNALFTNDKAKVALQDVTYVAPQANLVECVDEBFAQSK
 670 680 690 700 710 720
 cryla-105.pe RELSEKVKHAKRLSDENLLQDSNFKDINRQPERMGSGSTGITIGGDDVFNKENTLSSG
 670 680 690 700 710 720
 17385648 MILLQVQFAKRLSQARNLLNYGDPESSDMSSGNGWRTSPHVVASDNPIFKGRYILWGGK
 730 740 750 760 770 780
 cryla-105.pe TF-----DECPTTYLQKIDESKLYKAFTRYQALGYIEDSQDLEIYSRYNAK-HETVNVPP
 730 740 750 760 770 780

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17385648  AMSQPSNNIYPTIYAYOKYDESKLKYTRVIVRGFVGNYSKDLLELLVERYGKDYVEMDVP
      790      800      810      820      830      840
cryla-105.pe  GTGSLWPLSAQSPIGKGEPRCAP-HLEWNPDLDCSCRDGE-----KC-----
      780      790      800      810      820
17385648  ND-----IRYTLPRNECGDFDRCKPASYQTKPHCTCTCDPAVAHTDCQCKGNHTSTN
      850      860      870      880      890
cryla-105.pe  -----AHHS-----
      830      840
17385648  MYTNGPTGSEVSTNGPHAKSCGCDKHMDSKSGTHPHKSCGCKDPHVTYHIDTGCVDTE
      900      910      920      930      940      950
cryla-105.pe  -----
      850      860      870      880      890      900
17385648  EDLGVVIFKIKTQDGHARLGNLEFLEKPLVGEALARKRAEKKWRDKREKLEWETNIV
      960      970      980      990      1000      1010
ENLGLFALKIASENGVANIDNLEIIIEAQLTGEALARKVKEQRKQKQEMTKRLETTA
      960      970      980      990      1000      1010
cryla-105.pe  YKEAKESVDALFVNSOYDQLOQADTNIAHAAKRVHSIREAYLPELS-----VIPGVNAA
      910      920      930      940      950
17385648  VQAAQDAIQNLFTNTQYNELKFETLPHVNAELLVQIIPYVYHPFLSGALPVPVPGMNF
      1020      1030      1040      1050      1060      1070
cryla-105.pe  IFEELEGRIITAFSLYDARNVILKNGDFNGLSCWNVKGVHVDVEEONQORSVLVPEWAE
      960      970      980      990      1000      1010
17385648  IFQQLSLIDTAKRLYEARNIVQNGTFSSGTGSWYTAGVEVRLQNT-SVLVLSNSHE
      1080      1090      1100      1110      1120      1130
cryla-105.pe  VSQEVVPCPGRYILRVYATYKEGEGCVTIHEIENNTDELKFSVCEEIYFNNTVTGN
      1020      1030      1040      1050      1060      1070
17385648  ASQQVRIDSDRGVLRVATRKEGAGKGTVILSDCADYTETLSTFSC-----
      1140      1150      1160      1170      1180
cryla-105.pe  DYTVMQEGYATSRNRCYNEAPSPADYASVYEKSYTDGRRNCPCEFRGRTYPL
      1080      1090      1100      1110      1120      1130
17385648  -----DYNTVGTQ-TWTKGLS-----
      1190
cryla-105.pe  PVGVYKLEVFYFETDKVWIEIGETGTFIVDSVELLMEE
      1140      1150      1160      1170
17385648  --GVYTKLENFDDTRIDRIDGETGTFKVESVELICNEQMEDHLYDMAGNLEQDLT
      1200      1210      1220      1230      1240      1250
cryla-105.pe
NRAA:14537815
14537815 source="GENBANK_PROT" CryI-like protein [Bacillus thuringiensis]
SCORES  Initl: 319  Initn: 746  Opt: 764  z-score: 874.4 E(): 2.1e-40
>>NRAA:14537815
      initn: 746  initl: 319  opt: 764  z-score: 874.4  expect(): 2.1e-40
Smith-Waterman score: 764;  74.7% identity in 154 aa overlap
(1028-1177:1-149)
cryla-105.pe  VEEQNQRSVLVPEWAEVSQEVRCFGRGYILRVYATYKEGEGCVTIHEINNTDEL
      1000      1010      1020      1030      1040      1050
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```
14537815  GYLIRVYATYKEGEGCVTIHEINNTDEL
      10      20      30
cryla-105.pe  KFSNCVBEELYPNNTCTNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEK
      1060      1070      1080      1090      1100      1110
14537815  KFSNCEKEQVPGNTVACNDY--NKNHGACSSRNRRGYDESYESSNSIPADYAPVVEE
      40      50      60      70      80
cryla-105.pe  SYTDGRRNCPCEFRGRTYPLPVGVYTKLEFYFETDKVWIEIGETGTFIVDSVELL
      1120      1130      1140      1150      1160      1170
14537815  AYTDQGRNCFEENRHH--TLPAGYVTALEYFETDTVMWIEIGETGTFIVDSVELL
      90      100      110      120      130      140
cryla-105.pe  LMEE
      111
14537815  LMEE
cryla-105.pep
NRAA:15721993
15721993 source="GENBANK_PROT" crystal protein [Bacillus thuringiensis serovar
Yunnanensis]
SCORES  Initl: 361  Initn: 1756  Opt: 759  z-score: 854.9 E(): 2.5e-39
>>NRAA:15721993
      initn: 1756  initl: 361  opt: 759  z-score: 854.9  expect(): 2.5e-39
Smith-Waterman score: 1799;  31.7% identity in 1215 aa overlap
(57-1177:88-1194)
cryla-105.pe  ERLETGYTPIDISLSLTQFLSEFVPGAGVLGL-VDIILWIGIFGPS---QMDAFLVQIEQ
      30      40      50      60      70      80
15721993  RAALFVANSIIGIMLSKIPVIGPIVSTPFPQIMGVALPFLWPNNAPEQFQSWESLMTAAEE
      60      70      80      90      100      110
cryla-105.pe  LINQRIEIEFARNQAIISRLGLSNLYIAYESFREWEADPTNPALREEMRIQFNDMNSALT
      90      100      110      120      130      140
15721993  TADKKIDAQVRANAALESGVHNAIRLYQDAVCMDQDPTNNAQLAEQLRIQYIATNTVIF
      120      130      140      150      160      170
cryla-105.pe  TAIPLFAYQNYQVPLLSVYVQAAHLHLSVLDSVFGQWGFDAATINSRYNDLTRIGN
      150      160      170      180      190      200
15721993  SRMFSFRVGRFEVPLLSYVQAAHLHILKDGVOFGGEWGMDSATVDRFYSLKSDIEI
      180      190      200      210      220      230
cryla-105.pe  YTDHAVRYNTGL-ERVWG-PDSRDWIRYQCERELTLVLDIVSLFVNDSTRTYRTV
      210      220      230      240      250      260
15721993  YNYCIDWYNGLSDSIESIEPTWNGWNTFNFRDMLVLDLWLVLSIWETYPDRPYLPFTK
      240      250      260      270      280      290
cryla-105.pe  SOLTREIYTPVLENDFGSRGSAQIEGSRSPHMLDILNSITTYT-----DAHRGEVY
      270      280      290      300
15721993  SOLTRELYTQAI-----GSYKSVLEPLPPSPFRMLREIEFFLSDSODEAEQPAGE
      300      310      320      330      340
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~~Product Characterization Center~~

[illegible][illegible]

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cryla-105.pe    160   170   180   190   200   210
PLLSVYQAAANHLSVLRDVSFGQRMGFDAAITNSRYNDLTRLIGNYTHAVRWNTGLG
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QLLTIAQAASNLHLLRLDSSLYGASMGFAQTIONNTRQIRKTAIEYANHCTTWTGTGL
210   220   230   240   250   260   270

cryla-105.pe    220   230   240   250   260   270
ERVWGPSRDMRIYNQGFRETLTVLDIVSLFNPDSRTYPIRVUSOLTREIYTNPVLN
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QRLOGTTASSNLHYHRFREMTLVLDICALFSNDDAKSYPLEVRGELTREIYTDVPAG
270   280   290   300   310   320   330

cryla-105.pe    280   290   300   310   320
FDGSFRG-SAQGEG-SIRSPHMD--ILNSITIYDAHRG---EYTWSCHQIMASPVG
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
TNWDTRAPSAETENIVIPARTVTWISGDLVIYGRLYGYTGNDIWAARLU--DFLET
330   340   350   360   370   380

cryla-105.pe    330   340   350   360   370   380
SGPEFTFLXYTMGNAPQORIVAQLGGQVYRTLSTLYRRPFNGINNOQLSVDLGTEF
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
NGYRFEGTYGSTINISRTDISPWS
380   390   400

cryla-105.pep
NRAA:142759
142759 source="GENBANK_PROT" ORF

SCORES      Initl: 672      Initrn: 721      Opt: 714      Z-score: 811.4 E(): 6.7e-37
>NR0A:142759
initn: 721 initl: 672 opt: 714 Z-score: 811.4 expect(): 6.7e-37
Smith-Waterman score: 784; 37.7% identity in 358 aa overlap
(4-347:36-379)

cryla-105.pe    10   20   30   40   50   60   70   80   90   100
PDKHQSFSNAKVDKISTDSLKNETDIELQNINHDCLKISEVENVEFPV-SASTIQIG-
142759          10   20   30   40   50   60   70   80   90   100
MDNNPNINECIPYCNLCNPEVEVLGGERTETGY

cryla-105.pe    40   50   60   70   80   90   100   110
TPIDISLTSQTFLLSEFVGAGVLGVLDIIWGIF---GPSQDAFIQLQEILNQRIORIE
142759          40   50   60   70   80   90   100   110
----ISIA-GKIILGTIGVPFAGQVASLYSIILGELPWPKGKQWEIFMEHVEEIINGKIST
70   80   90   100   110

cryla-105.pe    100   110   120   130   140   150
FARNQATSRLEGSLNYQIYAESPREWEADPTNPALBEEMRIQFNDMNSALTITAIPLFAV
142759          100   110   120   130   140   150
YARNKAUTDLKGGLGDALAYIHESLESWGKRKTARSVVKSYALELMFVKQLPSFAV
120   130   140   150   160   170

cryla-105.pe    160   170   180   190   200   210
QNYQVPLLVSVVQAAANHLHSVLRDVSFGQRMGFDAAITNSRYNDLTRLIGNYTHAVRW
142759          160   170   180   190   200   210
SGEEVPLLPYQAANHLHLRLDASIFGKEWGLSSSELSTFYRNQVERAGDYSDCHVKW
180   190   200   210   220   230

cryla-105.pe    220   230   240   250   260   270
YNTGLERWGPDSRDWRINYNQPRELTLTVLDIVSLFNPDSRTYPIRVUSOLTREIYTNP
142759          220   230   240   250   260   270
YSTGNLNRGTNAESWVRYNQPRKDMLTAMVLDIALVFPSYDTLVPIKTTSQLTREVYDIT

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cryla-105.pe PLLENVGGSPFSA-----OGIEGSI-RSPHLMIDILNSITITDAHRGEYWSCH
142759 AICSVVHNASFASTWANNAPSPSTIESAVENPHLLDLEQVIYISLSSR-----WSNT
300 310 320 330 340 350
300 310 320 330 340 350
cryla-105.pe QIMASPVGSGPPTFFVGTGNNVPOORIVAQDSOGVRLTSLTYRPFNIGINQQ
142759 CYMMN---WGHRLFRFVGGNNTSTGSG
360 370 380
360 370 380
cryla-105.pep
NRAA:2624006
2624006 source="GENBANK_PROT" unknown protein [Bacillus thuringiensis]
SCORES Initl: 323 Initn: 969 Opt: 696 z-score: 788.8 E(): 1.2e-35
>NRAA:2624006
Initn: 969 Initl: 323 Opt: 696 z-score: 788.8 expect(): 1.2e-35
Smith-Waterman score: 1075; 37.7% identity in 567 aa overlap
(627-1175:1-483)
cryla-105.pe VIIDRFELIPVATILEAYNLERAKAVNALFTSTNQLGKTNVTDYHIDQVSNLVYLS
2624006
cryla-105.pe DEFCLDEKRELSKVKHAKRLSDERNLLQDSNEFKDINRQPERGGSGTGITOGDDVFK
2624006 GEQYSQKQMWQHDIKYAKQLSQARNLLQNGDFEDL-----FSGWTTNSQMSIQADNAIFK
40 50 60 70 80
720 730 740 750 760 770
cryla-105.pe ENYVTLSGTFD---ECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQOLEIYSIRYNAKHE
2624006 GNYLHMSGARDIYGTITFTYIYQKIDESKLFKAFTRYQLRGYIEDSQOLEIYSIRYNAKHE
90 100 110 120 130 140
cryla-105.pe TV-----NVPTGSLWPLSAQSPGKCGEPNRCAPHLEWNP-----DLDCSRDGEK-
2624006 TVMVPNDIIPVPSM-FVGCNELYDGOQFPNHRVGYNPMFVSQFSYTSITCQCTPGKHX
150 160 170 180 190 200
cryla-105.pe --CAHHSHHFLSDIDVGCCTDLNEDLGVMVIFKIKTDGCHARLGNLEFLEKPLVGEALAR
2624006 VVC-HDSHQKFKHIDTGEVDYNTNLGIWLVLFKISSPDGATLDNLVIEEGPVRGEAVTH
210 220 230 240 250 260
880 890 900 910 920 930
cryla-105.pe VKRAEKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQADTNIAHIAADKRVHS
2624006 VKQKEKWNQOMEKMETKRVYDRAKQAVDALFTG---EELNDYDVLISHIKNADLVQS
270 280 290 300 310 320
940 950 960 970 980 990
cryla-105.pe TREAYFELSVIGVNAALFELEGRIFTAFSLYDARNVTKGDFNGLSCWNVKSHVDV
940 950 960 970 980 990

2624006 IPYVHNELPDPFGMNYDIQELNARIMQARYLYDARNVITNGDFAQGLQGWHAEGKVEV
330 340 350 360 370 380
cryla-105.pe EQNQNSVLVWPEAEVSEVVCGRGYILRVYAVKGVGEGCVTIHEIENNTDELK
1000 1010 1020 1030 1040 1050
cryla-105.pe EQNQNSVLVWPEAEVSEVVCGRGYILRVYAVKGVGEGCVTIHEIENNTDELK
1000 1010 1020 1030 1040 1050
2624006 Q-QNNGTSVLVLSNWSGVSQNLAVQHPHGYLLRVSAKESGKGYVTRMSCNGKQETLT
390 400 410 420 430 440
cryla-105.pe FSNCEVEEIPNNVTCNDYTNQEEYGGAYTSRNGRYNEAPSPADYASVEEKSYPD
1060 1070 1080 1090 1100 1110
2624006 FTSC-----DG
1120 1130 1140 1150 1160 1170
cryla-105.pe RRENPCFNRGVDYTPVGYVTKLEYEPETDKVWIEIGETGTFIVDSVELLMEE
1120 1130 1140 1150 1160 1170
2624006 -----GYMTKTVVEFPEDSRVRIEIGETGTFIVDSVELLMEE
450 460 470 480
2624006 TSNNNQNMNMYDQSYSGNSYQNTSDMYDQGSVAKFEKE
490 500 510 520
cryla-105.pep
NRAA:31745045
31745045 source="GENBANK_PROT" hypothetical protein [Bacillus thuringiensis
serovar aizawa]
SCORES Initl: 292 Initn: 984 Opt: 693 z-score: 785.3 E(): 1.9e-35
>NRAA:31745045
Initn: 984 Initl: 292 Opt: 693 z-score: 785.3 expect(): 1.9e-35
Smith-Waterman score: 1051; 37.5% identity in 570 aa overlap
(627-1175:1-483)
cryla-105.pe VYIDRFELIPVATILEAYNLERAKAVNALFTSTNQLGKTNVTDYHIDQVSNLVYLS
31745045 MFTSGAKNTLKIEITDYEIDQAAISIECMS
600 610 620 630 640 650
cryla-105.pe DEFCLDEKRELSKVKHAKRLSDERNLLQDSNEFKDINRQPERGGSGTGITOGDDVFK
31745045 DEHSPKEMMLWDEVKRAKLSQARNLLQNGDFEDL-----MFTSNDIIGSNNSIFK
660 670 680 690 700 710
cryla-105.pe ENYVTLSGTFD---ECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQOLEIYSIRYNAKHE
720 730 740 750 760 770
31745045 GNFLQMRGARDIYGTITFTYIYQKIDESKLFKAFTRYQLRGYIEDSQOLEIYSIRYNAKHE
90 100 110 120 130 140
cryla-105.pe TV-NVPTGSLWPLSAQSPGKCGEPNRC-----APHLEWNPDL-PCSCRPHE
810 820 830 840 850 860 870 880
31745045 AIMDVND-----LSYMQPSPCGD-YRCSSSRVYVNOQYPTPTDGVASDMYACPSNNGE
150 160 170 180 190 200
cryla-105.pe K---CAHHSHHFLSDIDVGCCTDLNEDLGVMVIFKIKTDGCHARLGNLEFLEKPLVGEAL
820 830 840 850 860 870
31745045 KHKVC-HDRPHFPDHIDTGEVDYNTNLGIWLVLFKISSPDGATLDNLVIEEGPVRGEAL
820 830 840 850 860 870

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      210      220      230      240      250      260
cry1a-105.pe 880 890 900 910 920 930
ARVKRAEKKWRDKREKLEWETINIVYKEAESVDALFVNSQYDQLQADNTINAMIAHAAKRV
31745045      270 280 290 300 310 320
THVKQKEKKWKQHEKKEKRWETQQTYPAKQAVDTLFTNEQ--ELHYHITLDHIQNADRLV

      280 290 300 310 320 330
cry1a-105.pe 940 950 960 970 980 990
HSIREAYLPESLVIPGVNAAIFEELEGRIPTAFSLYDARNVTKGDFNGLSCWNVKGV
31745045      320 330 340 350 360 370
OSIPYIHHDLWLPDAPGMNVDGYQGLNARIMQAYNLVDARNVITNGDFTKGLQGWHAAGKA

      380 390 400 410 420 430
cry1a-105.pe 1000 1010 1020 1030 1040 1050
DVEEQNQNSVLVPEWEAEVSQEVRCVPCRGYILRVTAKEGYEGECVTHIEIENNTDE
31745045      380 390 400 410 420 430
AVQ-QIDGASVLVLSNWSAGVSNLHAQDHGVMYLRVIAKKEGPGKGYVTMDCNGQET

      440 450 460 470 480
cry1a-105.pe 1060 1070 1080 1090 1100 1110
LKFSNCVVEEIIYNNVTVCNDYTVNQEEYGGAYTSRNGYNEAPSVPADYASVIEEKSVT
31745045      440 450 460 470 480
LKFTSCCE-----

      490 500 510 520 530
cry1a-105.pe 1120 1130 1140 1150 1160 1170
DGRENPCEFRNGYRDYTPLPVGVYVTKLEYRPETDKVWIEGTEGTFIVDSVELLME
31745045      490 500 510 520 530
GWTKEVVEFPESDRVRIEIGTEGTFIVDSIELLQW

      540 550 560 570 580
cry1a-105.pe 1180 1190 1200 1210 1220 1230
GYASNPNPHTGMNGYQSGYNGYNTNDLHSGCTCNGHSGCTCNGYNR
31745045      540 550 560 570 580
GYASNPNPHTGMNGYQSGYNGYNTNDLHSGCTCNGHSGCTCNGYNR

      590 600 610 620 630 640
cry1a-105.pe 1240 1250 1260 1270 1280 1290
VYIDRFELIPVATLEAYNLERAQKAVNALFTSTNQLGKNTVTDYHIDQVSNLYTILS
16945770      590 600 610 620 630 640
VYIDRFELIPVATLEAYNLERAQKAVNALFTSTNQLGKNTVTDYHIDQVSNLYTILS

      650 660 670 680 690 700
cry1a-105.pe 1300 1310 1320 1330 1340 1350
DEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERKMGSGTGITGGDDVFK
16945770      650 660 670 680 690 700
NEHSSKEEMLMDVEVQAKQLSWRNLLYNGDFEDVSN---GWTSTNIEIRENSVPVK

      710 720 730 740 750 760
cry1a-105.pe 1360 1370 1380 1390 1400 1410
ENYVTLGSFTD---ECYPTLYLQKIDESKLFKAFTRYQLRGYIEDSQDLIYSIRYNAKHE
1360 1370 1380 1390 1400 1410
ENYVTLGSFTD---ECYPTLYLQKIDESKLFKAFTRYQLRGYIEDSQDLIYSIRYNAKHE
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      90 100 110 120 130 140
16945770 CHILHFGARDIDGTLFTFYIYKIEESKLPYTRYRVRGVFGSSKDLKLMVTRYKGEID

      150 160 170 180 190 200
cry1a-105.pe 780 790 800 810 820 830
TV-NVPTGSLWPLSAQSPFGKCGEPNRCAPHLEW-----NPDLD-----CSCRDG
16945770      150 160 170 180 190 200
AMNVVPND-----LAYMPTPSCGD-SRCESSRVVSGYPTPTVDGYASGRVACQSNRG

      210 220 230 240 250 260
cry1a-105.pe 820 830 840 850 860 870
EK---CAHSHHPSLDIDVGTCTDUNEDLGWVIFIKITQDGHARLGNLEFLEKPLVGEA
16945770      210 220 230 240 250 260
TKHVKC-HDRHPFDHIDTIGELDTNTNVGIDVLFKISNPDGYATLGNLVEIEEGPLTGEA

      270 280 290 300 310 320
cry1a-105.pe 880 890 900 910 920 930
LARYKRAEKKWRDKREKLEWETINIVYKEAESVDALFVNSQYDQLQADNTINAMIAHAAKRV
16945770      270 280 290 300 310 320
LTHVQKEKKWKQHEKKEKRWETQQTYPAKQAVDALFTNEQ--ELHYHITLDHIQNADRL

      330 340 350 360 370 380
cry1a-105.pe 940 950 960 970 980 990
VHSIREAYLPESLVIPGVNAAIFEELEGRIPTAFSLYDARNVTKGDFNGLSCWNVKGV
16945770      330 340 350 360 370 380
IQALPYVYHAWLPDAPGMNVDGYQGLNARIMQAYNLVDARNVITNGDFTKGLQGWHAAGK

      390 400 410 420 430 440
cry1a-105.pe 1000 1010 1020 1030 1040 1050
VDVEEQNQNSVLVPEWEAEVSQEVRCVPCRGYILRVTAKEGYEGECVTHIEIENNTD
16945770      390 400 410 420 430 440
AMVQMDGA-SVLVLSNWSAGVSNLHAQDHGVMYLRVIAKKEGPGKGYVTMDCNGNRE

      450 460 470 480 490 500
cry1a-105.pe 1060 1070 1080 1090 1100 1110
ELKFSNCVVEEIIYNNVTVCNDYTVNQEEYGGAYTSRNGYNEAPSVPADYASVIEEKS
16945770      450 460 470 480 490 500
TLKFTSCCE-----

      510 520 530 540 550 560
cry1a-105.pe 1120 1130 1140 1150 1160 1170
TDGRENPCEFRNGYRDYTPLPVGVYVTKLEYRPETDKVWIEGTEGTFIVDSVELLML
16945770      510 520 530 540 550 560
TDGRENPCEFRNGYRDYTPLPVGVYVTKLEYRPETDKVWIEGTEGTFIVDSIELLQW

      570 580 590 600 610 620
cry1a-105.pe 1180 1190 1200 1210 1220 1230
GYASNPNPHTGMNGYQSGYNGYNTNDLHSGCTCNGHSGCTCNGYNR
1180 1190 1200 1210 1220 1230
GYASNPNPHTGMNGYQSGYNGYNTNDLHSGCTCNGHSGCTCNGYNR

      1240 1250 1260 1270 1280 1290
cry1a-105.pe 1300 1310 1320 1330 1340 1350
VYIDRFELIPVATLEAYNLERAQKAVNALFTSTNQLGKNTVTDYHIDQVSNLYTILS
1300 1310 1320 1330 1340 1350
VYIDRFELIPVATLEAYNLERAQKAVNALFTSTNQLGKNTVTDYHIDQVSNLYTILS

      1360 1370 1380 1390 1400 1410
cry1a-105.pe 1360 1370 1380 1390 1400 1410
DEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERKMGSGTGITGGDDVFK
1360 1370 1380 1390 1400 1410
DEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERKMGSGTGITGGDDVFK

      1420 1430 1440 1450 1460 1470
cry1a-105.pe 1420 1430 1440 1450 1460 1470
NEHSSKEEMLMDVEVQAKQLSWRNLLYNGDFEDVSN---GWTSTNIEIRENSVPVK
1420 1430 1440 1450 1460 1470
NEHSSKEEMLMDVEVQAKQLSWRNLLYNGDFEDVSN---GWTSTNIEIRENSVPVK

      1480 1490 1500 1510 1520 1530
cry1a-105.pe 1480 1490 1500 1510 1520 1530
ENYVTLGSFTD---ECYPTLYLQKIDESKLFKAFTRYQLRGYIEDSQDLIYSIRYNAKHE
1480 1490 1500 1510 1520 1530
ENYVTLGSFTD---ECYPTLYLQKIDESKLFKAFTRYQLRGYIEDSQDLIYSIRYNAKHE
```

4168284 source="GENBANK_PROT" hypothetical protein [Bacillus thuringiensis serovar entomocidus]

SCORES Initl: 326 Initn: 978 Opt: 689 z-score: 780.7 E(): 3.4e-35
>NRAA:4168284
Initn: 978 Initl: 326 Opt: 689 z-score: 780.7 expect(): 3.4e-35
Smith-Waterman score: 1089; 38.4% identity in 570 aa overlap
(627-1175:1-484)

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ctyla-105.pep
 NRAA:54695306
 54695306 source="GENBANK_PROT" hypothetical protein [Bacillus thuringiensis]

SCORES Init1: 316 Initn: 1097 Opt: 685 z-score: 776.9 E(): 5.6e-35
 >>NRAA:54695306
 initn: 1097 Init1: 316 opt: 685 z-score: 776.9 expect(): 4.86 aa)
 Smith-Waterman score: 1058; 37.7% identity in 565 aa overlap
 (627-1173:1-482)

	600	610	620	630	640	650
ctyla-105.pe	VYIDRFELIPVIALEAEINLERAQAVNA	LTSTINQLGKTNVTDYIDOVSNLYT	LS	---	---	---
54695306						
	660	670	680	690	700	710
ctyla-105.pe	DEFCLDEKRELSEKVKHAKRLSDERN	LLQDSNFKDINRQPERGWGGSTIG	IQGGDVF	---	---	---
54695306						
	720	730	740	750	760	770
ctyla-105.pe	ENVVILSGTFD--ECYPTLYQKIDSK	LKFAFTYQIRGYIEDSDLEISRYAK	HE	---	---	---
54695306						
	780	790	800	810	820	830
ctyla-105.pe	TV-NVCTGSLWPL-----SAQSP	I--GKCGENRCAPHLEWNPDLDC	ROGCK-	---	---	---
54695306						
	840	850	860	870	880	890
ctyla-105.pe	CHSHSLSDIDVCTDNEGLGWVIFIK	TQDGHARLGNLEFLEKPLVGEAL	AR	---	---	---
54695306						
	900	910	920	930	940	950
ctyla-105.pe	IREAYLPESLVPGVNAALFEELGR	IFTASLQARVNIENGFWNGLS	QNTYKHVDV	---	---	---
54695306						
	960	970	980	990	1000	1010
ctyla-105.pe	EQONNRQSVLVPEWEAEVQSRV	CGRGVILRTVAKSGYGGSTIT	HELENNAL	---	---	---
54695306						
	1020	1030	1040	1050	1060	1070
ctyla-105.pe	FSCNVEEIEIPVNTVTCNDYT	VNOEGYGGVTSRNRGNAPS	ADVAYVEEKSYTDG	---	---	---
54695306						
	1080	1090	1100	1110	1120	1130
ctyla-105.pe	Q-QLNGTIVLVSNWSSGSLNQ	HLVQHQHILLRVSAKKSGRG	VTIVLMQNGKKELEI	---	---	---
54695306						
	1140	1150	1160	1170	1180	1190
ctyla-105.pe	FSCNVEEIEIPVNTVTCNDYT	VNOEGYGGVTSRNRGNAPS	ADVAYVEEKSYTDG	---	---	---
54695306						
	1200	1210	1220	1230	1240	1250
ctyla-105.pe	TV-NVCTGSLWPL-----SAQSP	I--GKCGENRCAPHLEWNPDLDC	ROGCK-	---	---	---
54695306						
	1260	1270	1280	1290	1300	1310
ctyla-105.pe	CHSHSLSDIDVCTDNEGLGWVIFIK	TQDGHARLGNLEFLEKPLVGEAL	AR	---	---	---
54695306						
	1320	1330	1340	1350	1360	1370
ctyla-105.pe	IREAYLPESLVPGVNAALFEELGR	IFTASLQARVNIENGFWNGLS	QNTYKHVDV	---	---	---
54695306						
	1380	1390	1400	1410	1420	1430
ctyla-105.pe	EQONNRQSVLVPEWEAEVQSRV	CGRGVILRTVAKSGYGGSTIT	HELENNAL	---	---	---
54695306						
	1440	1450	1460	1470	1480	1490
ctyla-105.pe	FSCNVEEIEIPVNTVTCNDYT	VNOEGYGGVTSRNRGNAPS	ADVAYVEEKSYTDG	---	---	---
54695306						
	1500	1510	1520	1530	1540	1550
ctyla-105.pe	Q-QLNGTIVLVSNWSSGSLNQ	HLVQHQHILLRVSAKKSGRG	VTIVLMQNGKKELEI	---	---	---
54695306						
	1560	1570	1580	1590	1600	1610
ctyla-105.pe	FSCNVEEIEIPVNTVTCNDYT	VNOEGYGGVTSRNRGNAPS	ADVAYVEEKSYTDG	---	---	---
54695306						
	1620	1630	1			


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cryla-105.pe FSNCVEEIEYPNNTVTCNDYTVNOEEYGAYTSRNRGYNEAPSPADYASVEEKSYTDG
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
FTSC-----DQ
50539656

cryla-105.pe RRENPCEFNAGVDYTPVPGVVTKELEFPETDKWVIEIGETSGTIVDSVELLMEE
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
-----GIYTKTVEPEPSDRVRIEGIEGTSGFYSIELICMNGY
450 460 470 480
50539656 TSNNQNMSMYDOGYNNYNQONTTYEQHAVCTCNQNYNNGGCTCKQG
490 500 510 520 530

cryla-105.pap
SW:8928039
DELTDELTA-ENDOTOXIN CRYXXVIA(A) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (131 KDA CRYSTAL
PROTEIN)." library=NA species="Bacillus thuringiensis serovar finitimus"
source="swissprot_prot" version=NA type=PRT

SCORES Initl: 640 Initn: 1878 Opt: 686 z-score: 772.3 E(): le-34
>>SW:8928039
initn: 1878 initl: 640 opt: 686 z-score: 772.3 expect(): le-34
Smith-Waterman score: 2081; 34.7% identity in 119 aa overlap
(36-1176:68-1162)

cryla-105.pe NINECIPNCLSNPEVEVLGGERTGYTPIDISLSTOFLSEF-VPGAGFVLGLVDII
10 20 30 40 50 60
50 60 70 80 90
8928039 FCADDQLQSGERNMDFNSEPFIDASGAINAVTGTVLGFLGVPFGAULTFYKXL
40 50 60 70 80 90

cryla-105.pe WGIFFGS----QMDAFVIOELINORIEFARNQAISRLGSLNVIAVESFRWEAD
70 80 90 100 110 120
100 110 120 130 140 150
8928039 FGFLFPNNTKQEEFMKVQVEALIDEKISDAVENKAISELQGLVNITLYALEEWLEN
100 110 120 130 140 150

cryla-105.pe PTNPALREEMRIQFDPMNSALTTPAIPFAVONYQVPLLSVYVOAAHLSLVRDVSVFGQ
130 140 150 160 170 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
KENPAVRDLVQLQRWLIDGFFQQMPQSFVKGFVELLLVVYVYQAAHLHLSLRDAVIYGA
160 170 180 190 200 210

cryla-105.pe RMGFDAATINSRYNDLTRILGNYTTHAVRWNTGLERVPWSRDWRXYNQOFRETLTV
190 200 210 220 230 240
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
ENGLPTPIDONTRLRRHSABYTDHCVMNWTGLQLENSDAKSFWFOYFRFRFMTLSV
220 230 240 250 260 270

cryla-105.pe LDIVSLPNDYSRTPIRTVSOLTRREIYNPV----LENDFSFGSA---QGIEGS-IR
250 260 270 280 290
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
LVIALFPADVDMKVPYPIPTNFQLTREVYTDVIGKIGNSDSHWYSANAPSFNLESTLIR
280 290 300 310 320 330

cryla-105.pe SPHLMDILNSTITY-TDAHQGEY----YNSGHQIMASPVGFSGEFTFPLYLGMGNAAP
300 310 320 330 340
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

8928039 A P H V D Y I K L N F A T V D Y I G I V R S G K V G H - I I T S A T S A N T T E T R N - - Y C T I V N H D S
340 350 360 370 380 390
cry1a-105.pe Q R N V A L G S G V R T L S G T L Y R P E N I N N Q L S V D G T E F - - A Y G T S S N L P S A V R K S
350 360 370 380 390 400
8928039 V E - - D E F E K N I V A S G S G V P P V Q L C Y V R I Y F T R A V N F F T V S G S K T S V E K Y Y S K D
400 410 420 430 440 450
cry1a-105.pe V D S D E P P O N N A P P S F S H R L S V S V M R G F S N S V S I I R A P M S
410 420 430 440 450
8928039 R Y Y S E G L F E E Q G V F S T E Q L P N S A P E P T A V S H R L C H V T F A S V G N K Y S K D L P L F S
460 470 480 490 500 510
cry1a-105.pe W H S A E F N N I I A S D I T Q I P L V K A H T L O S T T W G P C T G C D I A R T S G S F A T I V N
460 470 480 490 500 510
8928039 W H S V D F D N Y V P K I T O L P A T K G Y V - - S I V E P S I O S D I - G K N G G I L G K Y V N
520 530 540 550 560
cry1a-105.pe I N G Q L P O R Y A R I R V A S I T N I R I Y V T V A G E R I F A G O F N K T M D T G S L T P S F S Y A T I T A
520 530 540 550 560
8928039 V E - D V S Q K Y F R V R Y A T E T E G E L G I K I D G R T V N L Y O Y K K T A P G D P L T Y A F D N S F S T P
570 580 590 600 610 620
cry1a-105.pe F T F P M S O S S T V G A D F S S G N E V I D R F E L P V T A L E A Y N L E R A Q K A N V A L F T S I N G L
580 590 600 610 620 630
8928039 V K F N N A S T I E L F L O N K T S G T - F Y L A G I E I P V K S Y E E L T E A K A V S S L F T D A R N -
630 640 650 660 670 680
cry1a-105.pe G L K N V T D Y H I D O V S N L V T L S D E F C L D E K R E L S E K V K H A K L S D E R N I L Q D N F K D I N R
640 650 660 670 680 690
8928039 A L K I D V T D Y Q I D O A N L V E C I S G D L Y A K E K I V L L R A V K F A K O L S Q N L S D E F N V N R
690 700 710 720 730 740
cry1a-105.pe O P E R G W G S T I T O G G D V F K E N Y V T L S G T F D C E P T Y L Y O K I D E S K L A F T R Y Q L R G Y
700 710 720 730 740 750
8928039 - - E N S W A S T A S V A I E E G D P L Y K G R A V O L S S A R D E N F T Y L Y O K I D E S T L K P Y T R Y Q L R G F
750 760 770 780 790 800
cry1a-105.pe I E D S Q D L E I V S I R Y N A K H E T V N V P G T S L P L S A Q S P I K C G E P - - - - - N R C A P
760 770 780 790 800
8928039 V E G S E N L D V Y L I R Y G A A V R M V P Y - - N L E I D T S S F V N P C E E V D G L S H R S C N V F D R C K Q
810 820 830 840 850
cry1a-105.pe H L E W N P L D C S C R D G E K C A H S H F S L D I D V G C T D N E D L G V W V I F K I K T O D G H A R L G M L
810 820 830 840 850 860
8928039 S I S V A P D A N T G - - - P Q I D G D P H A F S P H I D T G T V D S T E N L G I W A F K I S E L D G S A I F G N L
860 870 880 890 900 910
cry1a-105.pe E F L E K P L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V Y E A K E S V D A L F V N S Q V D Q L Q A D
870 880 890 900 910 920
8928039 E L I E V G P L S G E A L A Q V R K E E K W Q - - - - - V L A K R E T T A Q T V C S G E A S Q L T N S
920 930 940 950 960
cry1a-105.pe T N I A M I H A A D K - - - - - R V H S I R E A Y L P E L S V I - - - - - P - G V N A A I F E E L G R I F T A S F L Y
930 940 950 960 970

8928039 S Q I L K T R N Y D L I O N F R I F S L E N T L S I K F I Y I T I T N V P Y S R L N Y D L F M E L E N R I O N A - S L Y
970 980 990 1000 1010 1020
cry1a-105.pe D A R N V I K N G D F N N G L S C W N V K G R V D V E E Q N N Q R S V L V P W E A E V S Q E V R V C P G Y I L R
980 990 1000 1010 1020 1030
8928039 M T S N I L O N G G F K S D V T S V T W E T T A N A E V Q - Q I D G A S V L T S N N A S V A Q S V N V Q N D H G Y I L R
1030 1040 1050 1060 1070 1080
cry1a-105.pe V T A Y K E I G Y G C V T H E I N N T D E L K E S V C E E I Y P N N T V T C N D Y T V N Q E Y G G A Y T S R
1040 1050 1060 1070 1080 1090
8928039 V T A K E G I G N G Y V T I L D C A N H I D T L T S A C - - - - - R S D S D T S S N E L T A - - - - -
1090 1100 1110 1120
cry1a-105.pe N R G Y N E A P S V P A D Y A S V V E E K S Y T D G R E N P C F E N R G Y R D V T P L P V G Y V T K E L E Y P E T D
1100 1110 1120 1130 1140 1150
8928039 - - - - - Y V I K T L E I F P D T E
1150 1160 1170
cry1a-105.pe K W I E I G E T E G T F I D S V E L L M B E
1160 1170
8928039 Q I R I E I G E T E G M F Y V E S V E L I R M E N
1140 1150 1160
cry1a-105.pe N I N E C I P V N C L S N P E V N A G G E R S T G T I D I S L S L T O L L S E P - V P G A G F V L G L V D I I
10 20 30 40 50 60
4583416 F C A D D F L Q S Y G E N M D N F O S E P E I D A S G G A A G V T G T I G P A G V F A G A L T T F Y Q K L
40 50 60 70 80 90
cry1a-105.pe W I F I G P S - - - - - Q W D A F L V Q I E O L I N Q R I E S A R Q A I S H L E G E N L Y O I A S P E W E A D
70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240
4583416 F C G L F P P N N T K O W E E F M K Q E A L I D E K I S D A V R N A I S I S L O G L V N N I T Y T A L E S L E N
100 110 120 130 140 150 160 170 180 190 200 210 220 230 240
cry1a-105.pe P T N P A L R E E M R I O F N D M N S A L T A T P L P A V O N Y Q V P L S V Y V O R A N H S V L R N A I S
130 140 150 160 170 180 190 200 210 220 230 240
4583416 K E N P A V D R V L Q W R I D R L F F F Q Q W P S F A V K G F E V L L V V Y T Q A N L H S L S R A Y I K R
160 170 180 190 200 210 220 230 240
cry1a-105.pe R W G F D A A T I N S R Y N D L T R I G N Y T D H A V R Y N T G L E R V G P D S R D W I R V N Q F R E L T V
190 200 210 220 230 240 250 260 270
4583416 E N G L F P T N I D Q N T R L L R S A E Y T D H C V N W N T G L A Q L E N S D A K S W F O Y N F R E M T L S V
220 230 240 250 260 270

SCORES Smith: 640 Smith: 1878 Opt: 686 Z-score: 772.3 E(): 1e-34
>>NR04:4583416 Smith: 640 Smith: 1878 Opt: 686 Z-score: 772.3 E(): 1e-34
Smith: 1878 Smith: 640 Opt: 686 Z-score: 772.3 expect(): 1e-34
Smith-Waterman score: 2081; 71.7% identity in 1194 aa overlap
(36-1176:68-1162)

```
cry1a-105.pe LDIVSLPNDSTYPIRVISQLTREIYNPV-----LENFGSRGSA---QOIGES-IR      250      260      270      280      290
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
LDVIALFPAYDVDMVPIPTNFQLTREIVTDVIGKIGRNDSDHMTSANAPSGNSLESTLIR      280      290      300      310      320      330
4583416      280      290      300      310      320      330

cry1a-105.pe SPHLMDILNSITIIY--TDAHSGEY-----YWSGHQIMASVPGFSGPEFTFLYTCMGNAAP      300      310      320      330      340
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
TPHVVDYIKLKFATVDYVIGYGRSGKWGH-ILITSANTSANTETRN--YGLIWNHDS      340      350      360      370      380      390
4583416      340      350      360      370      380      390

cry1a-105.pe QQRIVAGQGVRVTLSTLYRRPFNIGINNQOLSVDLGTFF--AYGTSNLPSSAVYRKS      350      360      370      380      390      400
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
VE--LNFEKGNIYKTSGLPQGVPPYQIGYVTPYIFLTRAVNFFTVSGSKTSVEKYYSKD      400      410      420      430      440      450
4583416      400      410      420      430      440      450

cry1a-105.pe -----GT-----VDSLEIPQNNNVPPROGFSHRUSHVSMFRSGFNSNSVSIIRAPMFS      410      420      430      440      450
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RYSEGPEQGVSTEQLPNPSIAPEHAYSHRLCHVTFI--SVNGKNKYSKDLPLFS      460      470      480      490      500      510
4583416      460      470      480      490      500      510

cry1a-105.pe WIHRSAEFNIIASDSITQIPLVKAHTLQSGTTVVRGPGTGGDILRTSGGPFATYIN      460      470      480      490      500      510
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
WTHSSVDNIVYVPKTIQLPATKGYNV---SIVKEPGFIGDI-CKNNGQILGKYKN      520      530      540      550      560
4583416      520      530      540      550      560

cry1a-105.pe INGQLPQRVARIYASTNRIYVTVAGERIFAGQFNKMTMDTDLPTFQSFYATINTA      520      530      540      550      560      570
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
VE-DVSKQYRFRVYATETEGELGIKIDGRTVNLVYQYKKAPADPDITYKAFYLSFSTP      570      580      590      600      610      620
4583416      570      580      590      600      610      620

cry1a-105.pe FTEPMSSQSFVGGADTFSSGNEVYIDRFELIPVTATLEAEYNIYLRACKAYNALFTSTNOL      580      590      600      610      620      630
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
VKFNASSITIELFLQNKYSGT-FYLAGIEIIPVKNYEEELTLEEAKKAVSSLTFDARN-      630      640      650      660      670      680
4583416      630      640      650      660      670      680

cry1a-105.pe GLKTNVTDYHIDQVNLVTLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNPKDINR      640      650      660      670      680      690
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
ALKIDVTDYQIDQANLVCEISGLDYAKEKIVLRAVKFAQLSQSONLILSDPEFNVNR      690      700      710      720      730      740
4583416      690      700      710      720      730      740

cry1a-105.pe OPERGWGGSTGTIGQGDVFKENIVTLSTFDECYVYLVYQKIDSKLKAFTRYQLRGY      700      710      720      730      740      750
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
--ENSWTASTVAILEGDPYKGRAVLSSARDENFPTYLYQKIDESTLKYPTRYQLRGF      750      760      770      780      790      800
4583416      750      760      770      780      790      800

cry1a-105.pe IEDSQDLEIYSRYNAKHETVNVPGTSLWPLSAQSPGKCGEP-----NRCAP      760      770      780      790      800
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
VEGSENLDVYLIRYGAARVMNVPI--NLEIIDTSFVNPCEEVVDGLSHRSNCVFDRCQK      810      820      830      840      850
4583416      810      820      830      840      850

cry1a-105.pe HLEWNPDLDCSRDGEKCAHSHHFSLDIDVGCTDLNEDLGVWYIFKIKTODGHARLGNL      810      820      830      840      850      860
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
SISVAPDANTG--PDQIDGDPHAFSHIDTGTVDSTENLGIWVAFKISELDGSAIFGNL      860      870      880      890      900      910
4583416      860      870      880      890      900      910
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cry1a-105.pe EFLEEKLVGELARVKAERKAKKREKLEWNETNIVYKEAKESVDALFVNSQYDQLQAD      870      880      890      900      910      920
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
ELIEVGLPSGEALQVQRKEKWKQ-----VLAKKRETTAQTCVSGSEASOLTNS      920      930      940      950      960
4583416      920      930      940      950      960

cry1a-105.pe NTIAMIHADK---RVHSIREAVLPESLVI-----P-GVNAALFELEGRIFTAFLSY      930      940      950      960      970
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
SOILKIRNYDLIONFRIFSLRNTLSIKFKIYITITNYPYSRLNYDLFMELERNIONA-SLY      970      980      990      1000      1010      1020
4583416      970      980      990      1000      1010      1020

cry1a-105.pe DARNVIKNGDFNNGSLSCNVNKGHVDEEQNNQSRVLVVPMEAEVSOEVRVCPGRGYILR      980      990      1000      1010      1020      1030
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
MTSNILONGGFKSDVTSMETTANAEOV-QIDGASVLVLSNNWNASVQSVNVQNDHGYLR      1030      1040      1050      1060      1070      1080
4583416      1030      1040      1050      1060      1070      1080

cry1a-105.pe VTAYKEGYGEGCVTTHEINNTDELKESNCVEEIPNNVTVCNDYTNQOEYGGAYTSR      1040      1050      1060      1070      1080      1090
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
VTAKKEGIGNGYTILDCANHIDTLTFSAC-----RSDSDTSSNELTA-----      1090      1100      1110      1120
4583416      1090      1100      1110      1120

cry1a-105.pe NRGYNAPSPADYASVVEEKSYYTDGRRENPCFNGYRDYTLPLVGYYVTKLEYEYPETD      1100      1110      1120      1130      1140      1150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
-----YVTKLEIIPDTE      1150
4583416      1150

cry1a-105.pe KVIWIEGETEGTIFVDSVELLIMEE      1160      1170
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QIRIEIGETEGMEFYVESVELIRMEN      1140      1150      1160
4583416      1140      1150      1160

8928007 description="PESTICIDIAL CRYSTAL PROTEIN CRY19AA (INSECTICIDAL
DELTA-ENDOTOXIN CRYIXA(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (75 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar jegathesan"
source="swissprot_prot" version="NA type="PRT

SCORES      Initl: 173      Intln: 396      Opt: 682      z-score: 771.6 E(): 1.1e-34
>>SW:8928007
Initn: 396      initl: 173      Opt: 682      Z-score: 771.6      expect(): 1.1e-34
Smith-Waterman score: 689;      28.0% identity in 624 aa overlap
(7-606:48-646)

cry1a-105.pe      MDNNPNINECIPYNCLSNP-EVEVLGGERIEGTYP      10      20      30
8928007      NDSNMSYTPRYPLANPQQDLMQNTYKWLNVCEGYH-IENPREASVRAGLKGKLGII--      20      30      40      50      60      70
cry1a-105.pe      IDISLSLTQFLSEFVPGAGVGLVDIIWGIFGFSQ--WDAFLVQEQLINRIEFPAR      40      50      60      70      80      90
8928007      --VSTIVGFGGSIILDTIGLYFOISELLWPEDDTQOYTWQDINNHHVEDLIDKRITVEIR      80      90      100      110      120      130
100      110      120      130      140      150
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CRYLA-105.pe NOAISRLEGSLNYQIYAESFREWEADPTNPALREEMRIQFNDMSALTITAIPLFAVON-
8928007 GNAIRTLADQGVDDNNMFKWKDDPKSTGLNLTSLVTKFTALDSFNGAIRTVNNGS
140 150 160 170 180 190
160 170 180 190 200
CRYLA-105.pe --YQVPLLSVYVQAANLHLSVLDSVSGQWGFDAATINSRYNDLT-RLIGNYTDHAVR
8928007 PGYELLPLPVQAANLHLLRDAQVYGDKNWASAFANARDNYQIOLEKTEYTCIN
200 210 220 230 240 250
210 220 230 240 250 260
CRYLA-105.pe WYNTGLE--RWGPDSDRWIRYNFRRELTLDIVISLFPNDSTYPIRTVSQLTREI
8928007 WYNGKLDNFRTAG---QWVNFNRVRENTLTVLGNSMRYDARLNPTEVKTREI
260 270 280 290 300 310
270 280 290 300 310 320
CRYLA-105.pe YTNVPLENFGSGFRG--SAQIEG-SIRSPHLMIDNLSITITDAHGEYVWGHQIMAS
8928007 YSDVINGEILGLMTPIYFSEKASLITRAPHLFTWLKGFRTVNSISYVWFLSGQNKYS
310 320 330 340 350 360
330 340 350 360 370 380
CRYLA-105.pe PVGFSG-PEFTFLYGT-MGNAAPQORIVAGLQGVYRTLSSTL-YRPFN-IGINNOQ
8928007 YTNNSINSGFRGQTDYGGTSSTINIPSN--SVYVNLWENYEYIYPMGDPVNTKMN
370 380 390 400 410 420
380 390 400 410 420 430
CRYLA-105.pe LSVLDGT---EFAYGTS-SNLPASVYKSGTVDSLDEIPQNNVPPRQGFSEHLSVHM
8928007 FSVTDNNSKELIYGAHRTNKP--VVRTD--FDPLTN--KEGTELAKYNDYNHLSYMLI
430 440 450 460 470 480
440 450 460 470 480 490
CRYLA-105.pe FRSGFSSSVSITRAPMFSWHRSAEFNNIIASDSITQIPLVKAHTLQSGTVVRGPGFT
8928007 NGEYFGQKR---HGYSFAPHTSSVDPNNTIAANKITQIPVVKASSINGSISIEKGFPT
490 500 510 520 530 540
500 510 520 530 540 550
CRYLA-105.pe GGDILR-RTSGGPFATYIVNNGQLPQRYRARIYASTNLRIYTV-AGERIFAGQFNK
8928007 GGDILVKNRADSG--LTMRFKAELDKKRVIRYKCNYSKSLILRKWKGEYIQOQIHN
540 550 560 570 580 590
560 570 580 590 600 610
CRYLA-105.pe TWDIGDPLTF-QSFVSATINTAFPPMSQSFVVGADTFSSGNEVYIDRELPVATYLE
8928007 ISPTYGAFVSLESTITTENIFDLTM-EVTYPVGRQFVEDIPSLILDKIEFLPTN
600 610 620 630 640 650
620 630 640 650 660 670
CRYLA-105.pe AEYNLERAKAVNALFTSTNQLGLKTNVTDYHDQVSNLVTLSDEFCLDEKRELSEKVK
8928007
CRYLA-105.pep
NRAA:2624005

2624005 source: "GENBANK PROT" mosquitocidal toxin [Bacillus
thuringiensis]gi|8928007|sp|032307|C19AA BACTJ Pesticidal crystal protein
cry19Aa (Insecticidal delta-endotoxin CryXIXA(a)) (Crystalline entomocidal
protoxin) (75 kDa crystal protein)

SCORES Initl: 173 Initn: 396 Opt: 682 z-score: 771.6 E(): 1.1e-34
>NRAA:2624005
Initn: 396 Initl: 173 Opt: 682 z-score: 771.6 expect(): 1.1e-34
Smith-Waterman score: 689; 28.0% identity in 624 aa overlap
(7-606:48-646)

CRYLA-105.pe 10 20 30
2624005 MNNPNINEPYNCLSNP-EVEVLGGERIETGYTP
20 30 40 50 60 70
CRYLA-105.pe 40 50 60 70 80 90
2624005 IDISLSLTQFLLSEFVGAGFVLGVLDIIVGIFGFSQ--WDAFLVQIEQLINQRIEFPAR
80 90 100 110 120 130
--VSTIVGFFGGSIILDTITGLFYQISELLWPEDDTQCYTWQDINHHVEDLIDKRITVEIR
100 110 120 130 140 150
CRYLA-105.pe NOAISRLEGSLNYQIYAESFREWEADPTNPALREEMRIQFNDMSALTITAIPLFAVON-
2624005 GNAIRTLADQGVDDNNMFKWKDDPKSTGLNLTSLVTKFTALDSFNGAIRTVNNGS
140 150 160 170 180 190
CRYLA-105.pe --YQVPLLSVYVQAANLHLSVLDSVSGQWGFDAATINSRYNDLT-RLIGNYTDHAVR
2624005 PGYELLPLPVQAANLHLLRDAQVYGDKNWASAFANARDNYQIOLEKTEYTCIN
200 210 220 230 240 250
CRYLA-105.pe WYNTGLE--RWGPDSDRWIRYNFRRELTLDIVISLFPNDSTYPIRTVSQLTREI
2624005 WYNGKLDNFRTAG---QWVNFNRVRENTLTVLGNSMRYDARLNPTEVKTREI
260 270 280 290 300
CRYLA-105.pe YTNVPLENFGSGFRG--SAQIEG-SIRSPHLMIDNLSITITDAHGEYVWGHQIMAS
2624005 YSDVINGEILGLMTPIYFSEKASLITRAPHLFTWLKGFRTVNSISYVWFLSGQNKYS
310 320 330 340 350 360
CRYLA-105.pe PVGFSG-PEFTFLYGT-MGNAAPQORIVAGLQGVYRTLSSTL-YRPFN-IGINNOQ
2624005 YTNNSINSGFRGQTDYGGTSSTINIPSN--SVYVNLWENYEYIYPMGDPVNTKMN
370 380 390 400 410 420
CRYLA-105.pe LSVLDGT---EFAYGTS-SNLPASVYKSGTVDSLDEIPQNNVPPRQGFSEHLSVHM
2624005 FSVTDNNSKELIYGAHRTNKP--VVRTD--FDPLTN--KEGTELAKYNDYNHLSYMLI
430 440 450 460 470 480
CRYLA-105.pe FRSGFSSSVSITRAPMFSWHRSAEFNNIIASDSITQIPLVKAHTLQSGTVVRGPGFT
2624005 NGEYFGQKR---HGYSFAPHTSSVDPNNTIAANKITQIPVVKASSINGSISIEKGFPT
490 500 510 520 530 540
CRYLA-105.pe GGDILR-RTSGGPFATYIVNNGQLPQRYRARIYASTNLRIYTV-AGERIFAGQFNK
2624005 GGDILVKNRADSG--LTMRFKAELDKKRVIRYKCNYSKSLILRKWKGEYIQOQIHN
540 550 560 570 580 590
CRYLA-105.pe TWDIGDPLTF-QSFVSATINTAFPPMSQSFVVGADTFSSGNEVYIDRELPVATYLE
2624005 ISPTYGAFVSLESTITTENIFDLTM-EVTYPVGRQFVEDIPSLILDKIEFLPTN
600 610 620 630 640 650
CRYLA-105.pe AEYNLERAKAVNALFTSTNQLGLKTNVTDYHDQVSNLVTLSDEFCLDEKRELSEKVK
2624005

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[illegible]

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SCORES      Initi: 288      Intn: 454      Opt: 668      z-score: 756.6 E(): 7.5e-34
>NRJAA:66360322
      Initi: 454      Intn: 454      Opt: 668      z-score: 756.6 E(): 7.5e-34
      Smith-Waterman score: 721;      28.2% identity in 571 aa overlap
      (73-614:6-557)

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cryla-105.pe TQFLLESEFVGAGFVLGIITWIGIFGPSQWDAFLVQIEQLINQRIEESFARNQAIISRLG
              | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
              TPERVWDFMTNTGNLIDOTVTAxVRTDANAKMTV
66360322

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cryla-105.pe LSNLQIYAESFREWEADPTNPALREEMRIQFNDMNSALT-TAIPLFAVQNYQVPLLSVY
110      120      130      140      150      160

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	40	50	60	70	80	90
170						
180						
190						
200						
210						
220						

100	110	120	130	140	150
230	240	250	260	270	

000000522	SNQWIFNDIKRMIQVLDJIALFASIDFKRIFADRIUNINTSKIEFIREIYIALV--	160	170	180	190	200	210
		280	290	300	310	320	330

220	230	240	250	260	270
340	350	360	370	380	390

	280	290	300	310	320
	400	410	420	430	440
					450

350
340
330
320
310

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cry1a-105.pe MFSWIRH... 490 500 510
66360322 F... 380 390 400 410 420 430 440 450 460 470 480 490 500 510

cry1a-105.pe I-VNINGQL... 490 500 510
66360322 MEIQCKTS... 440 450 460 470 480 490 500 510

cry1a-105.pe --LTFQSFYATINTAFTFMSQSS... 490 500 510
66360322 TDLKYEF... 500 510 520 530 540 550 560 570 580 590 600 610

cry1a-105.pe EYNLER... 620 630 640 650 660 670
66360322 ET

cry1a-105.pep
NRAA:17385646

17385646 source="GENBANK_PROT" crystal protein Cry56L [Bacillus thuringiensis]

SCORES Initl: 316 Initn: 1234 Opt: 653 z-score: 734.2 E(): 1.3e-32
>NRAA:17385646
Initn: 1234 Initl: 316 Opt: 653 z-score: 734.2 expect(): 1.3e-32
Smith-Waterman score: 1592; 31.1% identity in 1256 aa overlap
(51-1177:98-1265)

cry1a-105.pe VEVLGGERIETGTPIDISLSLTQFLSEFVPGAGVGLV-DIIMGIF--GFQO--WD
17385646 TKVQSITISAGIAAIAAGVASVAPPLAIVAGAFALISMFFDVLWPESENNTNSQVWA
70 80 90 100 110 120 130

cry1a-105.pe AFLVQIEQLINQIEFARNQAIISRLGSLNLVQIYAESFREWADPTNPALREMRIOF
17385646 DPAAEEMDEKIADEIKAEAVQLRIVOSRLRDYQQAACNFGSDPNNEYSYALLRDAF
130 140 150 160 170 180 190

cry1a-105.pe NDMNSALTATPLFVQNYQVPLLSVTVQAAHLHSLVLRDVSFVGQRMGDAATINSRYN
17385646 DDADALKEMVILFSREGYEQLLFDVYVQAAHLHLLLDVVRFGVGVGPPGGRVEQYYS
190 200 210 220 230 240 250

cry1a-105.pe D-----LTRIGNYTDHAVRWYNTGLE-RVWGPDSR---DWIRYNQFRRELTUTVID
17385646 NPTNLGPNQVQLAKYNTSTSLCWKGIERRKWMVESYRNEEYAYRYSNTMMWLD
250 260 270 280 290 300 310

cry1a-105.pe IVSLFPNYSRTPIETVSOLTRETYNPNVLENFGDSFRG--SAQIEGSIIRSP-HLMDI
17385646 MWALWTFIDPKVTPYATAVELTREIYSL-----IAGFRDYKGYMPIQYTWEPGSLVIN
250 260 270 280 290

cry1a-105.pe INSITTYDAHREYMSGHQIMASPVFGSGPEFTFPLYGTMGNAAPQORIVAQGG--
17385646 LERFTIYT-----WKNFEYF--P--FAGVETTYQTIGTSGSSSTKQAGVIPSPEGTA
300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510

cry1a-105.pe VRTLSLTLRRRFNIGINNQQLSVLDCGTEFAVGT-SNLPNAV
17385646 WTPGIVNEVHLVESFIYGTITQLLFYDVYNTIPAFKAGSDAVEVPGSIAGTICKNIPILDA
300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510

cry1a-105.pe YRKSGTVDSI-DEIP--PONNVV--PROGFSHRLSHV-----SMERSGFSNSSVSIIRAPM
17385646 NDVNVCVPTLWESPANPEGVCVYRNREMQSNLLSEVIPEDPKLLTLPHVPPLGYIDAF
300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510

cry1a-105.pe FSWHRSAPFN-NIADSIITQIPLVKAHTL-OSGTTVVRGPGFTGDIILRTSGGPFAY
17385646 FAMESITCDTRYNLIPANKIQIPAVKGNWLGQSGSVVRTSGNTGDDVVRVLYEFNGLMG
300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510

cry1a-105.pe TIVNINGQLPQRYRARIYVASTTN-LRIYVTVV--GERIFAGQFNKMTMDGDLT---PO
17385646 PARFSENK---SYILRIYAVADDLNIVVRORGELEYESELPINQTSNNSTTOWKFE
300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510

cry1a-105.pe SFSVATINAFAPMSQSFVFGADTFSS--GNEVIDRFELIPIVTALE---AEYNLER
17385646 DYGVQVGF--DQVSEVEYELWFSVPVGTSLSHMDIDKIEFIPMETSLEAYLANQDIEK
300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510

cry1a-105.pe AKAVNALFTSTNQLG... 640 650 660 670
17385646 ARKAVNALFTSTNQLG... 640 650 660 670

cry1a-105.pe ERNLLQSNFKDINQPRGKSGSTG... 640 650 660 670
17385646 ARNLLNYGDFESPERSRENGKSR... 640 650 660 670

cry1a-105.pe YOKIDESKLAFTFRALRGYIEDSQDLEIYSINNAI-HEIVNPGTGSWPLSQSSIG
17385646 YOKVDESKLASYTRYLVIRGVFGVNSKDLLELVERYGKDVENVDPHDIY--SLOT--N
300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510

cry1a-105.pe KGEFNPACAP-----HLENFPL-----DCSCR-----
17385646 ECGGFDCRVRVSLARSSHACTCKDTASMTDCCQCNKANRTVNTMNTVNSPOSANMDG
300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510

cry1a-105.pe ---EKCA-----HHS-----HFSLDIDVCGCTDLNEOLGVWVIFKIKTQD
17385646 FPAQKSGCKNNMDYQNGTHPKSGCKDPHFVSYHIDTGCVDPEENLGLWFLAKIAGEN
300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510

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17385650      ELEGVYTRILVQLAAERWNQKNDPOAESIRTOFRATNTIIFBAMPFSRVVAGEVDPL
      140      150      160      170      180      190
cry1a-105.pe      SVVYQAAHLHSLVLDVSVFGQRFGDAATINSRYND-LTRELIGNYTDHVAWRYMTGLER
      160      170      180      190      200      210
17385650      NVYAEANQLALLRDVAKFGROWGLPQDEVDIDYSEQLLPRIAEHTDHCVTYFNRGLEE
      200      210      220      230      240      250
cry1a-105.pe      V-----WGP---DSR-----DWRYNQFRRLEITLVLDIVSLFPNVDSTRY
      220      230      240      250
17385650      AKKLANLDYARYPWAQYVNHSHSQIGIENNLNFDYERNMTILVDLVALAFTYDPDRY
      260      270      280      290      300      310
cry1a-105.pe      PIRIVSOLTRREIYTN--PVLENFQGSFRGSAQIGESIRSP-HLMDILANSITIYDAHRG
      260      270      280      290      300      310
17385650      SMTKSELTRREITSVRGAFYGHNDYQDNFEIERNISPHLWTPWPNFIVYT---QN
      320      330      340      350      360      370
cry1a-105.pe      EYTW--SG--HQIMASPVGFGSPFTFPLVGTMGNAQQOIRVIAQLQGQVYTLASTLYR
      320      330      340      350      360      370
17385650      DYVYPMAGLQHKENYETISVS---LESPVGTGTSNLINFEVTAD-----PFLAVTI--
      370      380      390      400      410      420
cry1a-105.pe      370      380      390      400      410      420
17385650      RPFNIGINQLSVLDGTEFAYGTSNLPASVVR-KSGTVDSLDEIPPONNVPPRQFGS
      430      440      450      460      470      480
17385650      ---IGFG-QLGTSIGIYAMSGFRKSGSISHVGDIETIGTDDYLDIV---DRIPVGDSPT
      420      430      440      450      460      470
cry1a-105.pe      HRLSHVSNFSGSGSNSSVSIIRAPMFWSHRSFAENNIASDITOLPLVKAHTLQSG-T
      430      440      450      460      470      480
17385650      NKLWNGAAPTILG--STIFQVSYVAWRHPSVDNSNRISIDKITQIPAKAFPIDDNHV
      480      490      500      510      520      530
cry1a-105.pe      490      500      510      520      530      540
17385650      TVVRPGFTGCDILRRITSG-PFAYTVINNGOLQORVARIRVASTNLRIVTVAGE-
      530      540      550      560      570      580
17385650      KVIKPGSGTGDLVAFSGREGVGLSISVIPGSDLVSFYVRVIRVASSQSAKVTMGFGGV
      530      540      550      560      570      580
cry1a-105.pe      550      560      570      580      590      600
17385650      RIFAGQN-KYMDTGDLPTFQSFYATINT-AFTFPMQSSFTVGADTFSSGNEVYIDRF
      600      610      620      630      640      650
17385650      EESESKNFPAITYSGNLTYSNFGY--INTLAFASQTAQTIIEVYFRQYBEA-EFIVDKL
      590      600      610      620      630      640
cry1a-105.pe      ELIPVATLE---AEVNLERAKAVNALFTSTNQLGLKNTVDYHIDOVSNLVYLSDEF
      610      620      630      640      650
17385650      EPIFEMSLEBYQADQLEKARKAVNALFTSDAKSELKVNITDIXVDQAAANLVCEVCSDF
      650      660      670      680      690      700
cry1a-105.pe      660      670      680      690      700      710
17385650      CLJDEKRELSKVHAARLSDERNLLQDSNFKDINPROPERMGSGTGTIGOGDVDFKENVY
      660      670      680      690      700      710
17385650      HAOEKRIILDOVAFACKLSQARNLLYNGDFESJLDMGSENGNRTSPHYHVASDNPIFGKY
      710      720      730      740      750      760
cry1a-105.pe      720      730      740      750      760      770
17385650      VTLGTFP-----DECYPTLYOKIDESKLAFTRYOLRGYIEDSQDLIEYSIRNAK-H-
      720      730      740      750      760      770

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      480      490      500      510      520      530
cry1a-105.pe LVKHAFLQSGTTVWRPGFTGGDILATSGGPFVATIWNINGOLPORYRARIYASTTNL
               ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
               GOISTLRWNTAPLSQRYSRVRIYASTTNL
46852037

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[illegible]

cy1a-105.pe EVIDRFELIPYATLEAVNLERAKAVNAFLTSTNOGLKTNVTDYHIDQVSNLVTVY
 EVIDRIEFPVAVETFEAYDPLERAKAVNELFTSSNOIGLTKTVDYHIDQVSNLVCEL

CRYIA-105.pe SDFCJDEKKEUSEKVRHAKKUSJDERNNLQDSNF KUJNKUPKRWGGS IG111QGQGDVU
 |||||:||||| SDFCJDEKQELSEVXK 160

~~Cry4A-105.pep
NPAA:16945773
16945773 source="GENBANK_PROT" Cry400RF2 protein [Bacillus thuringiensis~~

```
SCORES initl: 304 Instrn: 980 Opt: 632 Z-score: 715.7 E(): 1.4e-31
>NRX_16945773
initl: 980 instrn: 632 Z-score: 715.7 expect(): 1.4e-31
(558 aa)
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(627-1176-11-483)

16945773

16945773 DEHSPEKXOMLDEWKRAKLQSJULSNGDGFVND---WPKGNNLSIGSNNISFKK

16945773

GNFLOMSGARDIYGFIFTYIYQKIDSKLPTRYRYRGVSGSKDLRLVTPYAKKEID

90 100 110 120 130 140 150

780 790 800 810 820 830 840

cyt18-105.pe iv-nvpqigslmfpaqlgckgepnkc-----afplmwnvfp--dolgscroo
|||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
AMMNVPD----LAVMQNPNSCGD-SKCESSQVYSCGYPTPTDGTAPDRYACRPSGSDN
16945773 150 160 170 180 190 200

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cry1a-105.pe K--CAHSHHSFLDIDVGCTDLNEDLGWVVIKFIQTQDHARGLNLEFLEEEXPLVGL
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[illegible]

[illegible]

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410      420      430      440      450
cryla-105.pe  430      440      450      460      470      480
>:SHLSHVSIMRSGFNSSVSIIRAPMFMIHSAEFNNIIASDISITQIPLVKAHTQSQT
8928008      480      490      500      510
>:THRLFQMMNEVSNVNAQRVFI---LHATHSRLRRITNGLSQDIQIIPAVKTISGGDR
460      470      480      490      500      510

490      500      510      520      530      540
cryla-105.pe  TVVRGPGFTGDIILRTSGSPFAYTIIVINGQLPQRVRIARIVASTNLIIRYIVTVAGERI
8928008      520      530      540      550      560
>:AVVLNYGENTMKLDNLTIGLSYKLTAVDSEAS-NTRFTVRVRYASMMNNKLNVLVINGAQI
520      530      540      550      560

550      560      570      580      590      600
cryla-105.pe  FAGQPNKMTGTDPLT---FQSFYATINTAFTFPMSSQSFVTCADTFSSGNEVIDRFE
8928008      570      580      590      600      610      620
>:ASLANVEHTVQVQSGSLTDQYGNFYATFI--AGNFMVQSQSI-LGIFKEIPNDFIDVLDKIE
570      580      590      600      610      620

610      620      630      640      650      660
cryla-105.pe  LIPVPI-ATLAEAVENLERAQKAVNALFTSINQLGLKTNVTDYDHIDQVSNLVTYVLSDEFCL
8928008      630      640      650      660      670      680
>:LIPSNFSSLEQNTQNTYNQDITYTHNQGYDYTDQNSGMYHQSNNYDQNMWDTTYQPS
630      640      650      660      670      680

410      420      430      440      450
cryla-105.pep
SW:8928008
8928008 description="PESTICIDIAL CRYSTAL PROTEIN CRY20AA (INSECTICIDIAL
DELTA-ENDOTOXIN CRYXXA(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (86 KDA CRYSTAL
PROTEIN). Library=NA species="Bacillus thuringiensis serovar fukuokaensis"
source="Swissprot_prot" version=NA type=PRI

SCORES      Init1: 158      Initn: 410      Opt: 625      z-score: 705.8 E(): 5.1e-31
>>SW:8928008
initn: 410 init1: 158 opt: 625 Z-score: 705.8 expect(): 5.1e-31
Smith-Waterman score: 635; 28.7% identity in 658 aa overlap
(2-616:18-641)

410      420      430      440      450
cryla-105.pe  MDNPNINECIPYNCLSNPEVGLGRIETGYTPIDISLSTQ
8928008      460      470      480      490      500
>:MNPYQNNDIVDVPENYDNNLNR---YPYANDPNVAMQNTNYKQWMNGYEINPFS-SITA
460      470      480      490      500      510

520      530      540      550      560      570
cryla-105.pe  FL-----LSEFVPAGFVIG-----LVDIINGIFG---PSQWDAFLVQIEOLINQRIEFA
8928008      580      590      600      610      620      630
>:ILASGILNRVIALTG-VLIGNTQEVISIQDALGFRNGTGNGLIHVEQLIQOITLQTOY
580      590      600      610      620      630

640      650      660      670      680      690
cryla-105.pe  RNQAIISRLGLESLNLIQIYAESFEREWEDPTNPALREEMRIQFNDMNSALTAT-PLFAV-
8928008      700      710      720      730      740      750
>:RGAATGAIYGISRSDNYLMLFQRMNRRTREN-GQGVSAFTITNIIICLNALAPQASLS
700      710      720      730      740      750

760      770      780      790      800      810
cryla-105.pe  -QNYQVPLSVVQAAANLHLSVLRDVSVEGQWGFDA-ATINSRYNDLTIRLIQNTDHAV
8928008      820      830      840      850      860      870
>:RGFETLLPYMAANFHLRLLRDAVLYRNQWLSNLSISITANVNILRAALIEYTHCT
820      830      840      850      860      870

```

[illegible]

[illegible]

```

37999234 source="GENBANK_PROT" putative mosquitoicidal toxin [Bacillus
thuringiensis serovar entomocidicus]

SCORES Initl: 197 Initn: 352 Opt: 582 z-score: 657.6 E(): 2.5e-28
>>NRAA: 37999234
initn: 352 initl: 197 opt: 582 z-score: 657.6 expect(): 2.5e-28
Smith-Waterman score: 616; 27.5% identity in 643 aa overlap
(34-628:59-681)

cry1a-105.pe NNINECIPNYCLNSNEVEVLGGRIETGVTRIDI-----SLSLTQFLSEFPVGGAG-
10 20 30 40 50
37999234 YPLANNPOVPLQNTSYKWLNNCOTIINPLCTIPINIDISLAASIAVVGSLA-LIPGGE
30 40 50 60 70 80
cry1a-105.pe ---FVLGVADIINGIPGSPQ---WDAFLVQIEQL---INRIEEFARNQAIISLEGLS
60 70 80 90 100
37999234 ALGPFVLGTFTILPILPWNGETKIWTFDAERGQLFRPELQGDIAEILVTGVKSYGNALK
90 100 110 120 130 140
cry1a-105.pe 110 120 130 140 150 160
37999234 NLYQIYAESFREMEADPTNPALREEMRIQFNDMNSALTATPLPFAVQNYQVP-LLSVTVQ
170 180 190 200 210
cry1a-105.pe ANLHLSVLRDVSVFGORGFDA-ATIN-----SRYNDLTFLGNVTDHAWPWNTGLE
210 220 230 240 250 260
37999234 TANIDLILYQRAYGVGDWEKDINGISFPFGWKQDYESLKTKEEYNTVCBAETYSNLS
270 280 290 300 310 320
cry1a-105.pe RVWGPDSDRWIRYNQFRRELITLVIDIVSLFPNVDSRTVPRTYSQLTREIYNVPLENF
330 340 350 360 370 380
37999234 ILKXKNPISWDTYKNYKREATIGALDVLVAFPNVDMLHPYATKTELTRYIM-PSFGLO
390 400 410 420 430 440
cry1a-105.pe DSGFRSGAQGLEGI-RSPHLMIDIINSTIYTAHRGEYWGSHQIMASVPGSGPEFTF
450 460 470 480 490 500
37999234 QSNYFQSLGLENALTHPFSLTWLNELNLYTR--ENFNPALQV-SLSGLQARSRYT
490 500 510 520 530 540 550
cry1a-105.pe PLYGTGNAAPQQR--IVAQLQGQ---VYRTLSTLYRPFN----IGINNQLSVLDGT
560 570 580 590 600
37999234 QNFTILDPAQGVANGTSTOIGLNNLFYK--LSNSQYHHPNDCCSIIAGISDMTIFYKSDIN
610 620 630 640 650
cry1a-105.pe EFAYGTSSNLPASVRYKSGTVGSDLEIPQO---NNNVPRQGFSHRLSHVM--FRSGFS
660 670 680 690 700
37999234 GNASATQTY--QAGRNTNNTVINFWNGPQKASSNNNISIKQT-KHLLSDIKMIFYFTGGM
710 720 730 740 750
cry1a-105.pe NSSVSIIRAPMFSIHRSASFNNIITASDITQIPLVKAHTLQSGTVYVRGPGFTGGDILR
760 770 780 790 800
37999234 YQYVDFGYS--PAMHTSVDPNLIVPNRIQTQIPAVKALGISGTSKVKVKGKGVFVFGDGLL
810 820 830 840 850

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51090233 source="GENBANK_PROT" C-terminal half of Cry protein [Bacillus thuringiensis|gi|51090229|dbj|BAD35158.1 | C-terminal half of Cry protein (Bacillus thuringiensis)]

SCORES Init1: 241 Initn: 902 Opt: 578 Z-score: 652.5 E(1): 4.7e-28
>>NRAA:51090233
Initn: 902 Init1: 241 opt: 578 Z-score: 652.5 expect(1): 4.7e-28
Smith-Waterman score: 961; 35.4% identity in 554 aa overlap
(615-1118:3-550)

```

590      600      610      620      630      640
cry1a-105.pe TVGADTFSSGNEVYIDREFLIPVTATLAEYNIERAKQAVNALSTINQLGLKNTVDYH
51090233      |||:::||||:::||||:::||||:::||||:::
              MNVYTVKAREAVQALFSNPITTLQLK--VTDHH
              10      20      30

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550      650      660      670      680      690      700
cryla-105.pe IDVSNLVTLSDFECLDFKRELSEKVHKAKRLSDERNLLQDSNFKOINPQBERGMGGST
51090233 VNOVARVECTIOADOHPKEKMCLLDOVKLAKRLSRENNLLNNGOFESSDWGVDGDNVNST

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~~C:\yla-105.pe GITI0GGDVFKNVYUUSGT-----FDECIPYL7QKIDESKLKATRQLRGYIEDSQ~~

51080293 NUYTVAOPIFKDHYLNMPSEANNPILSDKIFPYPAYQKVEESRLKPYTRYIVRGFVGS

Szyła 105.pe QLEYSIRYNAK-HETVNVPGTGSIMPLSAQS--PIGKGEPNRCAPHLEWNPDLDCS-C

109023
 DLEINAKQKEVHKRMVNP--DIITPSCTGEPVSQ--PTPYVWVESNTMPDQWNCPCN
 160 170 180 190 200
 820 830 840 850 860
 BHSFSLDVGCTDNLNEDLGVWVIFKTDGQHGRLGN
 cyta1-105-se RDGECA

51090233
GNSVOTANMMVOSTGNCMDPHEPKFHIDIGELDMERNLGIWIFKVKVGTTEGNALDNI

51090233
EVEVGPIGDALFNONETWKKQTKRMKLEKAVGLARDAQTITFCPNOSCLOSAN

51090233
ITLQILRAEKLWKIPYVNOFLOGVLSUPSEAYDI
330 340 350 360 370 380
COLSDAVATPAALNORNI

~~CIVIL-105.pe~~

450	460	470	480	490	500
	1090	1100	1110	1120	1130

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cry1a-105.pe A-----YTSRNGYN-EAPSPADYAS-VYEKSYTDGRRENPCFNRYGRDYT
51090233  TNGVSNQNMVNSSENTGSAHSGNNNMNYQSESGKPYGDSNGMSINGSSNNYFANGY
510          520          530          540          550          560
cry1a-105.pe PLPGVYTKLEYFPETDKVMEIGETEGTFIVDSVELLMEE
51090233  PGNNINDQENYGANAYSSNNMYQSESGFTPYGDENNMTNTPSNMYEMNYPSSDMM
510          570          580          590          600          610          620
cry1a-105.pe
NRAA:31745044
31745044 source="GENBANK PROT" putative mosquitocidal toxin [Bacillus
thuringiensis serovar aizawai]
SCORES   Initl: 163   Initn: 360   Opt: 564   Z-score: 637.3 E(): 3.3e-27
>>NRAA:31745044
Initn: 360 initl: 163 opt: 564 Z-score: 637.3 expect(): 3.3e-27
Smith-Waterman score: 670; 27.1% identity in 661 aa overlap
(14-630:41-666)
cry1a-105.pe
NRAA:31745044
31745044  EILKSSPNNTNINRYPPFANDRDMSPMSWDCQSPWVWSTASTFTG-----IGIDLI
20          30          40          50          60
10          20          30          40
MDNNPNINECIPYNCILSNPEVEVLGGERIETGYTPIDISLST
31745044
cry1a-105.pe
31745044  QFLSEVPQAGVGLGVLDIINGIFGSQWDAFLVQIEGL---INQRIEFARNQAIKSL
50          60          70          80          90          100
100          110          120          130          140          150
31745044  TFLGERSITGINLFSVI-----GKLLPSGQNVASISICDLISIRKVEDSVLSRDYGF
70          80          90          100          110          120
120          130          140          150          160          170
31745044  NGVNNYQTYLTSLTKXKMLDAGKTTTQGLTDVTKHFPSEFEFNALLKSL---SRPKG
130          140          150          160          170
170          180          190          200          210          220
cry1a-105.pe  EQLSNLQIYA-ESPREM--EADPTNPALREEMRIQFN-----DNMSALTATPLFAVQNY
110          120          130          140          150
150          160          170          180          190          200
cry1a-105.pe  QVPLLSYVQANLHLSVLRDVSFQGRW-----GFDAATINSRYN---DLTRLIGNY
160          170          180          190          200
200          210          220          230          240          250
31745044  EILLPPYTCGANLHLLLRDFVQYKAVWEKELRTENVESELISPSDFEGHKEQLAEH
180          190          200          210          220          230
230          240          250          260          270          280
cry1a-105.pe  TDHAVRWNTGLERW--GPSRDWIRYNGFRRELTTLVDIVLSLFNYSRTPRTVS
210          220          230          240          250          260
260          270          280          290          300          310
31745044  INHCITWQAGLNQINKESGTSTENLWKNFRREMTLSVLDLIAIFTYDFENYKSETHI
240          250          260          270          280          290
290          300          310          320          330          340
cry1a-105.pe  OLTRIEITYNPVLEN-PDGSFRCSAGIEGS-IRSPHMLDILNSITITVDHRCVEYWSCH
270          280          290          300          310          320
320          330          340          350          360          370
31745044  ELSREVTIDVGVNGHEQNLNGNTLEANGTGPGLVTLWKKIDITFDIVTEYSGSPV
300          310          320          330          340          350
350          360          370          380          390          400
cry1a-105.pe  QIMASPVGSGPEFTFPLGYTMGNAPQQRIVAQCGGYRTLSLTSYRFPFNGINNOQ
320          330          340          350          360          370
370          380          390          400
31745044  AILR---GWAGTRH-YEIIY--TGSSNTLQRIISGTTSDNVSNI--DFINSRIFI--TSLAR
360          370          380          390          400

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cry1a-105.pe  LSVLDGTEFAYGTSNLSAV-YRKSGTVDLSDEL--P-----PQNNVPPROG
380          390          400          410          420
31745044  YALAGAAAGPGSPRYRVRVEFRSTGYTFLEYVNSPGISMTIESKLEGVKNATGFTD
410          420          430          440          450          460
460          470          480          490          500          510
cry1a-105.pe  FSHLSHVSMFRSGFSSSVSIIRAPMFSMIHRSAEFNMIASDSITQIPLVKAHTLQSG
430          440          450          460          470          480
480          490          500          510          520          530
31745044  YFNLSNACVQFGTS-----RVNYGWHTHISMEGEGYVYPNKIITQIPAVKAMEIRGT
470          480          490          500          510          520
520          530          540          550          560          570
cry1a-105.pe  TVVVRGFGFTGSDILRTSGGPFAYTIIVNINGQLPQRYARIRYASTNRIYTV-AGE
490          500          510          520          530          540
540          550          560          570          580          590
31745044  SSVVAGFGHTGGLNVMKSVHVSWS---IKFTCQQLKRYRVRIRVASDGNQCLAMRRWGG
530          540          550          560          570
570          580          590          600          610          620
cry1a-105.pe  RIFAGQFNKTMDT--GDPLTFQSFYATINTAFTFPMSSQSFYVGAFTFSSGNEVYDRF
550          560          570          580          590          600
600          610          620          630          640          650
31745044  PGYVQEARHTVQRTFGSGMTDPSFKYLDI---FTMPAEDYTFDLTD--LESGLALYDKI
580          590          600          610          620          630
630          640          650          660          670          680
cry1a-105.pe  ELIP---VTATLEAEYNLERAKAVNALFTSTNQLGKTNVTDYHIDQVSNLVTLSDEF
610          620          630          640          650
650          660          670          680          690          700
31745044  EFIPDDLTTLEVEEERNELEKTKNAVDLFTN
640          650          660
660          670          680          690          700          710
cry1a-105.pe  CLDEKRELSKVKHAKRUSDERNLLQDSNFKDINRQPERMGSGTGITIOGGDDVPKENY
660          670          680          690          700          710
710          720          730          740          750          760
cry1a-105.pe
NRAA:1246432
1246432 source="GENBANK PROT" cbm71 mosquitocidal toxin [Clostridium
bifermentans]gi|10719937|sp|Q45882|C16AA CLOBI Pesticidal crystal-like protein
cry16Aa (insecticidal toxin CryXVIA(a)) (Cbm71 mosquitocidal toxin)
SCORES   Initl: 145   Initn: 392   Opt: 558   Z-score: 631.0 E(): 7.5e-27
>>NRAA:1246432
Initn: 392 initl: 145 opt: 558 Z-score: 631.0 expect(): 7.5e-27
Smith-Waterman score: 579; 26.6% identity in 561 aa overlap
(56-580:43-579)
cry1a-105.pe  GERIETGYTIDISLSTQFLSEFVGAGFVLGLV-DIIMGIFGSGWDAFLVQIEQ--
30          40          50          60          70          80
80          90          100          110          120          130
1246432  SKGVASVFKVIDTTHNISKNNNFNIIITQDFIIDTILSLME--DPNENEIFSSMIEDGE
20          30          40          50          60          70
70          80          90          100          110          120
cry1a-105.pe  LLINORIEEFARNQALISLEGISNLYOIAVESFREWEADPTNPALREEMRIQFNDMSAL
90          100          110          120          130          140
140          150          160          170          180          190
1246432  TITNKNLSAQTKSGLLLSNSFGKFKYVYNNAFRSW-IDNYNPTSIDDVVYRFDVNSIC
80          90          100          110          120          130
130          140          150          160          170          180
cry1a-105.pe  TTAIPLEFAYQNYQVPLLSYVQANLHLSVLRDVSFQGRW-----GFDAATINSRYN
150          160          170          180          190
190          200          210          220          230          240
1246432  ENNINEFKVKNYEVTVLPYMQIANLHLLLRDGMITYGDANLRYELGFSQD--DSFYNH
130          140          150          160          170          180
180          190          200          210          220          230

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cr1a-105.pe LTRLGNYTHAVRWYNTGLERWVGPDSRDWIRYNGFRRELTTLVDIVSLFNPYDSRTY
1246432 VLDKTKFYINDCLNYNTGLSKLDPNNSWIDITRYCFMTFYILDMISICPIYTKVY
cr1a-105.pe --PIRTVSQRLTRVYTPVLENF-DGSRFSAQIGSIRSPLMDILNSITTYDAHRG
1246432 DKFI-NMQTLTRKVSDDPV-NFIDEMIPISYEKMYNI-SPELSTLSISFYTN-KSG
cr1a-105.pe EYVMSGH-QIMASPVGSGPEFTPLDYGNGNAAPQQRIVAQCGVYRTLSLYRRP
1246432 NKFLNGHVRHVGDIDLYNGLRETH-YGNVGSNYE---VESMAFDDIKAYSNY---
cr1a-105.pe FNIGINQQLSVLDGTEFAYGTSSNLPSAVYRK--SGTVDSLDEIPPNONNVPPROGFSH
1246432 FNNTONNPTSV---KSIKFLITKNDEWIYGPDSNIDFTNTOGYSLSNLN-NESYTH
cr1a-105.pe RLHVSVMRSGFNSVSIIRAPMFSWIRHSABENNIILASDSITQIPLVKAHTLQSG---
1246432 SLSMDILANDKIQINIDTPHYSYSWIYKGIETNYSIDKLINOIPLVKEVLSKSHYS
cr1a-105.pe --TTVVRGPGFTGGDIL-----RRTSGGPFAY---TIVNINGOLP---ORYRARIRYAST
1246432 ELSVKGPGFTGGDILSKVHKPANOIPAOYMNKNTIPIKTKFPAGSDPKVCLVYASN
cr1a-105.pe TNLRIYTVAGERIFAGQFNKMTDT--GDP-LTFQSFVATINTAFTPMQSSFTVGAD
1246432 HDIGLIRLIAGSKYIITNTQOTFNTENNPSLIYDDPKYFNFTLSITSSGIDELYEF
cr1a-105.pe TFSSGNEVYIDREFELIPVTATLEAEYNLERAKAVNALFTSNQLGLKNTVTDYHIDQVS
1246432 YYSYTDGNFEFDFPKLSIPVTRNYSC
cr1a-105.pep
SW.10719937

10719937 SKGVASVFKVIDTIRHNSKNNFNILTOQFIIDTILSLWE--DPNENEFSSMIEDGE 70
20 30 40 50 60
cr1a-105.pe --LINORIEEFARNOAISRLGSLNLYQIYAESPREWEADPTNPALREEMRIQFNDMSAL 140
90 100 110 120 130
10719937 TITWKNLSAQTKREGILLNSFGKLFKYNNAFRSW-IDNYNPTSIDDVVVRFKDVNSIC 120
80 90 100 110
cr1a-105.pe TTAIPLFAVQYQVPLLSYQVAAANLHLSVLRDVSFVGQW-----GFDAAATINSRYND 190
150 160 170 180
10719937 ENNINEFKVKNYEVTVLPYMQIANLHLLLRDGMIDYGDANLYRELGFSDQ--DSFYNH 180
130 140 150 160 170
cr1a-105.pe LTRLGNYTHAVRWYNTGLERWVGPDSRDWIRYNGFRRELTTLVDIVSLFNPYDSRTY 250
200 210 220 230 240
10719937 VLDKTKFYINDCLNYNTGLSKLDPNNSWIDITRYCFMTFYILDMISICPIYTKVY 240
190 200 210 220 230
cr1a-105.pe --PIRTVSQRLTRVYTPVLENF-DGSRFSAQIGSIRSPLMDILNSITTYDAHRG 310
260 270 280 290 300
10719937 DKFI-NMQTLTRKVSDDPV-NFIDEMIPISYEKMYNI-SPELSTLSISFYTN-KSG 300
250 260 270 280 290
cr1a-105.pe EYVMSGH-QIMASPVGSGPEFTPLDYGNGNAAPQQRIVAQCGVYRTLSLYRRP 370
320 330 340 350 360
10719937 NKFLNGHVRHVGDIDLYNGLRETH-YGNVGSNYE---VESMAFDDIKAYSNY--- 350
310 320 330 340 350
cr1a-105.pe FNIGINQQLSVLDGTEFAYGTSSNLPSAVYRK--SGTVDSLDEIPPNONNVPPROGFSH 420
380 390 400 410 420
10719937 FNNTONNPTSV---KSIKFLITKNDEWIYGPDSNIDFTNTOGYSLSNLN-NESYTH 420
360 370 380 390 400
cr1a-105.pe RLHVSVMRSGFNSVSIIRAPMFSWIRHSABENNIILASDSITQIPLVKAHTLQSG--- 530
430 440 450 460 470 480
1246432 SLSMDILANDKIQINIDTPHYSYSWIYKGIETNYSIDKLINOIPLVKEVLSKSHYS 520
410 420 430 440 450 460
cr1a-105.pe --TTVVRGPGFTGGDIL-----RRTSGGPFAY---TIVNINGOLP---ORYRARIRYAST 530
490 500 510 520 530
1246432 ELSVKGPGFTGGDILSKVHKPANOIPAOYMNKNTIPIKTKFPAGSDPKVCLVYASN 520
470 480 490 500 510 520
cr1a-105.pe TNLRIYTVAGERIFAGQFNKMTDT--GDP-LTFQSFVATINTAFTPMQSSFTVGAD 580
540 550 560 570 580
1246432 HDIGLIRLIAGSKYIITNTQOTFNTENNPSLIYDDPKYFNFTLSITSSGIDELYEF 570
530 540 550 560 570 580
cr1a-105.pe TFSSGNEVYIDREFELIPVTATLEAEYNLERAKAVNALFTSNQLGLKNTVTDYHIDQVS 640
590 600 610 620 630 640
1246432 YYSYTDGNFEFDFPKLSIPVTRNYSC 610
590 600 610
cr1a-105.pep
SW.10719937

10719937 description-"PESTICIDIAL CRYSTAL-LIKE PROTEIN CRY16A (INSECTICIDIAL
TOXIN CRYXIVA(A)) (CBM71 MOSQUITOCIDAL TOXIN)" library=NA species="Clostridium
bifermentans" source="swissprot_prot" version=NA type=PKI

SCORES Init1: 145 Initn: 392 Opt: 558 z-score: 631.0 E(): 7.5e-27
>SW:10719937
initn: 392 init1: 145 opt: 558 z-score: 631.0 expect(): 7.5e-27
Smith-Waterman score: 579; 26.6% identity in 561 aa overlap
(56-580:43-579)

cr1a-105.pe GERIETGTPIDISLSLTQFLSEFVPGAGVGLV-DIIVGIFGSPQMDAFLVQIEQ--
30 40 50 60 70 80

10719937 SKGVASVFKVIDTIRHNSKNNFNILTOQFIIDTILSLWE--DPNENEFSSMIEDGE 70
20 30 40 50 60
cr1a-105.pe --LINORIEEFARNOAISRLGSLNLYQIYAESPREWEADPTNPALREEMRIQFNDMSAL 140
90 100 110 120 130
10719937 TITWKNLSAQTKREGILLNSFGKLFKYNNAFRSW-IDNYNPTSIDDVVVRFKDVNSIC 120
80 90 100 110
cr1a-105.pe TTAIPLFAVQYQVPLLSYQVAAANLHLSVLRDVSFVGQW-----GFDAAATINSRYND 190
150 160 170 180
10719937 ENNINEFKVKNYEVTVLPYMQIANLHLLLRDGMIDYGDANLYRELGFSDQ--DSFYNH 180
130 140 150 160 170
cr1a-105.pe LTRLGNYTHAVRWYNTGLERWVGPDSRDWIRYNGFRRELTTLVDIVSLFNPYDSRTY 250
200 210 220 230 240
10719937 VLDKTKFYINDCLNYNTGLSKLDPNNSWIDITRYCFMTFYILDMISICPIYTKVY 240
190 200 210 220 230
cr1a-105.pe --PIRTVSQRLTRVYTPVLENF-DGSRFSAQIGSIRSPLMDILNSITTYDAHRG 310
260 270 280 290 300
10719937 DKFI-NMQTLTRKVSDDPV-NFIDEMIPISYEKMYNI-SPELSTLSISFYTN-KSG 300
250 260 270 280 290
cr1a-105.pe EYVMSGH-QIMASPVGSGPEFTPLDYGNGNAAPQQRIVAQCGVYRTLSLYRRP 370
320 330 340 350 360
10719937 NKFLNGHVRHVGDIDLYNGLRETH-YGNVGSNYE---VESMAFDDIKAYSNY--- 350
310 320 330 340 350
cr1a-105.pe FNIGINQQLSVLDGTEFAYGTSSNLPSAVYRK--SGTVDSLDEIPPNONNVPPROGFSH 420
380 390 400 410 420
10719937 FNNTONNPTSV---KSIKFLITKNDEWIYGPDSNIDFTNTOGYSLSNLN-NESYTH 420
360 370 380 390 400
cr1a-105.pe TNLRIYTVAGERIFAGQFNKMTDT--GDP-LTFQSFVATINTAFTPMQSSFTVGAD 580
430 440 450 460 470 480
10719937 HDIGLIRLIAGSKYIITNTQOTFNTENNPSLIYDDPKYFNFTLSITSSGIDELYEF 570
410 420 430 440 450 460
cr1a-105.pe TFSSGNEVYIDREFELIPVTATLEAEYNLERAKAVNALFTSNQLGLKNTVTDYHIDQVS 640
590 600 610 620 630 640
1246432 YYSYTDGNFEFDFPKLSIPVTRNYSC 610
590 600 610
cr1a-105.pep
SW.10719937

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cryla-105.pe LE---RVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNDSRTYPIRTVSQLTREIYT--
220      230      240      250      260

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cryla-105.pe LE---RVWGPDSRDWIRYNQFRELTLTVLDIVSIFPNYDSRTYPIRTVSQLTREIYT--
|| : : || : : || : : || : : || : : || : : || : : || : : || : : || : : ||
LEEAKKIKNSDKLDWDFYNOYRRDMLTVLDVIALFTYDVVKYPISTVKVELTREIYTDMD
41688283

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	260	270	280	290	300	310
	260	270	280	290	300	310

320	330	340	350	360	370
320	330	340	350	360	370

41688283
TGIQNTSYRINVEDYPSGPLHGYR-YAGITARSVDNNGKDY-----SIYSTMFPLETN
380 390 400 410 420 430

41688283
NHVHELPCGAYYFGVKGRHDATDRRTGNSQKILGEDSKTGRIATGTSYFISEIPYD
440 450 460 470 480 490

41688283 KEI:NETIRTPTEKYNHRLSYISAYATDCGRISGVGDGCFRTPQMCANTHVSADPYNTIHH

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99						
100						

```

4168283      PDKITQISAVKAFYIWDTEGQVYSGPGFTGGDLVKLPYNARUKIRLKPTSTS--KKYRV
560      570      580      590

```

```
cryla-105.pe RIRYAS--TTNLRIVTVVAGERIFAGQFNKTMTDGDLTFQFSFY-ATINTAFTFFMSQS
```

```
cry1a-105.pe SFTVGADTFSSGNEVYIDRFELIPTATLEAEYNLERAQKAVNALFTSTNQLGLKTIVTD
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
```

cryla-105.pap
NR04-50539655

SCORES Initl: 245 Initn: 541 Opt: 467 z-score: 526.9 E(): 4.7e-21
NDAP: 5053055 (675 aa)

7-628:46-613)

CITY 18-103.PE
50519655
HSNNOKDI PNRYPEFTNPNVAVMKNIGNYKDWNECEGSNVSPSAPAAVTSA-----II

[illegible]

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[illegible]

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SCORES      Initl: 174      Inltn: 351      Opt: 459      z-score: 517.9 E(): 1.5e-20
>>NRAA:16945772
Initn: 351 Inlt: 174 opt: 459 Z-score: 517.9 expect(): 1.5e-20
Smith-Waterman score: 582;   27.1% identity in 683 aa overlap
(3-628:17-664)

cry1a-105.pe          MDNNNINECPY-----NCLSNPEVEVLGGRI-ETGYTPDIS
                  ||| | : : : : : : : : : : : : : : : :
16945772    NSYENKNEYEILESSNNINPNYPFANDRDNSTMSQCGISWDEIWESAEITIGIS
                  10       20       30       40       50       60

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51090240      GHWPELSPAFGHNVPYITSCAAEGWTHLSVERSENEKSDKTIQPAKVAQLSNASV
490      490      500      510      520      530      540
cryla-105.pe  VRGFGFTGGDILR--RTSGG--PFAYIVNINQQLPQRYRIRYASTNLIYVT--VA
|||||      |||||      |||||      |||||      |||||      |||||
51090240      VRGPGSTGGDLVQFSATSSGNKQLWIKWKPITIALGRBFKVRIRYAAAANVTFTVQKCVT
550      560      570      580      590      600
cryla-105.pe  GERIFAGCNFKMTDT-GDPLTFQSFSAVINTAFTFPMSSQSFVQADTFSSGNGVEYIDR
|||||      |||||      |||||      |||||      |||||      |||||
51090240      GVACWETAKSVTITYSTGLTYNAFKYVDI---FEIPANESEFSLEFLS-TSGGPIYIDK
610      620      630      640      650
cryla-105.pe  FELIPVATLEAEYNLEAKQAVNALFTSTNQLGLKTNVTDYHDQVSNLTVLSDEFL
|||||      |||||      |||||      |||||      |||||      |||||
51090240      IEFIVNPPEPVP-EGIIYQIVTALNNSSVDVMDPGTGTGRHNVHLWQNNNTNNKQRF
660      670      680      690      700      710
cryla-105.pep
NSAA:51090236
51090236 source="GENBANK_PROT" cancer cell-killing Cry protein [Bacillus
thuringiensis]
Scores Initn: 360 Initn: 723 Opt: 447 Z-score: 502.9 E(): 1e-19
>>NSAA:51090236
Initn: 723 Initn: 160 Opt: 447 Z-score: 502.9 expect(): 1e-19
Smith-Waterman score: 786 29.2% identity in 681 aa overlap
(15-625:46,698)
cryla-105.pe  MNMNPINCEPIYNCNLSEVLEVGGERIETGYTPIIDLSLSTQ
28      30      40      50      60      70
51090236      GNCVQRRYFFACAPQELQNGKKEKMMNCTSGDPT-VLGGGYSADVKKDAVITSNIAS
50      60      70      80      90      100
cryla-105.pe  FLLSEFVPGAGFVLGMDIIVGFPSS---WDAFQIQIQLINQRIEFAFNQAISRL
|||||      |||||      |||||      |||||      |||||      |||||
51090236      YLLSVPPPPAGVAAIGTICALIGLWPELQVQWFAFMNWEALNOKLDEVARSKAISEL
80      90      100      110      120      130
cryla-105.pe  EGLSNLQIYAESFREWADTNPALREKRL--QFNQNNKMTAIPFENNVQVPLL
|||||      |||||      |||||      |||||      |||||      |||||
51090236      NGLKNLLELYQDADDMNENPGD--LRNKRVVETEPFNVNNGHFNSMPSPVAFNEVALL
140      150      160      170      180      190
cryla-105.pe  SVVYQAAHLHLSVLKDVSVFGORGFDAATINSRYNDLRLG---YTDHVAQVDTG
160      170      180      190      200      210
51090236      PYAEANILHLLLLDAVKFGEHGNSITDGAER--DMWVRLRSRTETVTDKLVNTVGG
200      210      220      230      240      250
cryla-105.pe  LERV-----W-----GPDSRD-----WIRYNQFERELTIVLRI
|||||      |||||      |||||      |||||      |||||      |||||
51090236      LQQAQSLQANVSYSRYTQVQVNOGSGFSYREAKGEYGTENWNLVNAFNRDFTMLVLDI
260      270      280      290      300      310

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250      260      270      280      290
cry1a-105.pe VSLFFPNYSRTY--PIRTVQLTRELYTN--PVLENEDGSRGSAQIEGSI---RSPHL
51090236      IAQFFPYDGLYSREVK--SELTREYTDIRGTWRS DANL--NTIDAIRMWGSRQLQL
320      330      340      350      360

300      310      320      330      340      350
cry1a-105.pe MDILNSITITYT--DAHRGEYVWSGHQIMASPVGF--SGPEFTPLVGTMGNAAPQORTVA
51090236      FTWLTEMKEIYRNTGSIITSYTHGDLVWGLEKKIRKTNNDNDQWLPLEGQNTSITRIDRGI
370      380      390      400      410      420

360      370      380      390      400      400
cry1a-105.pe QLGQGV--YRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSNNLPS--AVYRKSGTVD
51090236      ELGKNVWYVARTQQWFETRLQLWVNTDVLISLNAGTVGNEFWARDVDPVRYNIARS----
430      440      450      460      470      480

410      420      430      440      450      460
cry1a-105.pe SLDEIIPPQNNVPPRQGFSHRLSHVM--FRSG--FSNSSVSIIRAPMSWIHRSAENN
51090236      -----TRNHFE-----NHRLSWIKFPEPVDRNCPCFAMPGYKQLSALLFGWTHNSVDPFN
490      500      510      520      530

470      480      490      500      510      520
cry1a-105.pe IIASDSITQIPVKAHTLQSGTIVVRGEGTGDILRRTS--GGPFAITIVNINGQLPOR-
51090236      TIASDRITQIPAVGVLVNGCATVVRGPGNTGDDLVLPAVYNQWMTOLRVKVRPSTTART
540      550      560      570      580      590

530      540      550      560      570      580
cry1a-105.pe --YRARIRYASTNRIYVTVAGERIPAGFNKMTDGDPLTFQSGSIATINTATFFPMS
51090236      RGVNRIYRASEGNANLEF--GK--YVDTANRFYETGYAVNGTQFSGSMYNSFKY-LD
600      610      620      630      640      650

590      600      610      620      630      640
cry1a-105.pe QSSFTVGADTF-----SSGNEVYIDRFELIPVTATLAEYLNERRAKAVNALFTSTNQL
51090236      AIGFAANEFEFRIELRCNSGGPIYIDKIEFIPNPIPEPPEGIYQIVTALNNSSVTSEE
650      660      670      680      690      700

640      650      660      670      680      690
cry1a-105.pe GLKTNVTDHXIDQVSNLVYLSDEFCLDEKRELSKVHAKRLSDERNLLQDSNFKDINR
51090236      FCMGIGLITTRCGVNLWSNNGNTLQKRFVYNGDQNAFQIKSTPNEDLVLSGNSGTSVTA
710      720      730      740      750      760

cry1a-105.pep
NRAA:8928030

8928030 source="GENBANK_PROT". Pesticidal crystal protein cry27Aa (Insecticidal
delta-endotoxin CryXXVIIA(a)) (Crystalline entomocidal protoxin) (94 kDa crystal
protein)gi|5689049|dbj|BAA82796.1| 94kDa mosquitocidal toxin [Bacillus
thuringiensis]

SCORES      Initi: 70      Initn: 159      Opt: 445      z-score: 500.6 E(): 1.4e-19
>NRAA:8928030
      Initn: 159      Initi: 70      Opt: 445      z-score: 500.6 expect(): 1.4e-19
Smith-Waterman score: 585;      24.9% identity in 655 aa overlap
(36-633:88-712)

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

```
8928030      GLIPSEFWTLNGTVAALTIYVSIVLAGITLVAPVSVTAGLITVLGAGAALLAGITPLIM
60      70      80      90      100      110

cry1a-105.pe GIFGPSQDAFVUQIEQINQRIEIEEFARNQALISRLGSLNLYQIYAESFEWEADPTNPA
120      130      140      150      160      170
8928030      PATYDNTFNKIIDTAEVLLAKKEISEFVRTANTKIDSLQIQLIYYQYNALENKKPNDSA
180      190      200      210      220      230

130      140      150      160      170      180
cry1a-105.pe LREMRIQFNDMSALITATPLFAVQNYQVPLLSVYVQAANLHLSVLSDVSVEGQMGFD
8928030      ARNTVSTRFOIYNAFFVEAMPALSMGFEYVQLGAYAAQANLHLILRLREGIAYADQMNIA
180      190      200      210      220      230

190      200      210      220      230
cry1a-105.pe AATINS----RYNDLTRILIGNYTDHVRVYNTGLERVMGPDSDRDWIRYNO--FRRELITIT
240      250      260      270      280      290
8928030      RDPHMAAGDLHYKEFLDYRQYINHCSTWYNEG-----QNEANLKNGLVYQRTMTLF
240      250      260      270      280      290

240      250      260      270      280      290
cry1a-105.pe VLDIVSLFPNYSRTY--PIRTVSQLTREIYNPVLNFDGSRGSAQIEGSIIRSPHLM
8928030      VLDLIAMFSTYDPRLYTMPIKT-EILTRIYT-----DGVNENEK-----SIHNPGLF
300      310      320      330      340      350

300      310      320      330      340      350
cry1a-105.pe DILNSITITDAHRGEYVWSGHQIMASPVGFSGPEFTPLVGTMGNAAPQORTVAQLGQG
8928030      RLREQMKLHIYEQAGQLSGHQNFIRSNYHNPILIYGPVQGYSSNNIK--ITITNLG
340      350      360      370      380      390

360      370      380      390      400      410
cry1a-105.pe VYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSNNLPSAVYRKSGTVDLSLEIPPON
8928030      DYDKIYS-INTESRNLV--QGSTTFDKINFYGAENWLFVSVYNGQPIIKHSNIPGID
400      410      420      430      440      450

420      430      440      450      460      470
cry1a-105.pe NNVPFPROG-----FSHRLSHVMFPRSGFSNSSVS--IIRAPMSWIHRSAEFNNIASDS
8928030      A---PSTGLNYSNYTHYLSNC-IFQSNRNGSGSAPDYNTQSYVFGMNHYTIDTGTNYVTD
460      470      480      490      500      510

480      490      500      510      520      530
cry1a-105.pe -----ITOIPLVKAHTLQSGTIVR-----GPGFTGDDL---RRTSGGP
540      550      560      570      580      590
8928030      FEVWKNLPESRYVFOISQVPAYKASDIFNPGRVVNAKVESGPEYFTGGDVIKSKAQLDSSG
510      520      530      540      550      560

510      520      530      540      550      560
cry1a-105.pe FAYTIVNINGQLPORYA---RIR--YASTNRIYVTVAGERIFA-GQFNKMTDGDPL
8928030      LARTLITFP-IIPKRYRASGFRVRMYAANHTQGVSYGVANINTGYANFQKTFDGEYF
570      580      590      600      610      620

570      580      590      600      610      620
cry1a-105.pe T--FQSSYATINTATFPMQQS-----SFTVGADTFSSGNEVYI-DRFELIPVTATLE
630      640      650      660      670      680
8928030      RARHEFKYIEFTDTFSLRNSGQLEHLLHIYYPNTTKISGQLLIIDKIEFIPVGIPLN
630      640      650      660      670      680

620      630      640      650      660      670
cry1a-105.pe AE---YNL-ERAQKAVNALFTSTNQLGLKTNVTDHYHIDQVSNLVYLSDEFCLDEKRELS
```

CTVla-105 de	480	490	500
-----ITOIPIWKAHTLOSQTIVR-----	480	490	500
-----GPFGTGGIIL-----			
-----RRTSGGP			

8928030 FEVKNLPESRYVPQISQVPAVKASDIFNPRGVNAKVESGPYFTGGDIVSKAQLDGSGS
510 520 530 540 550 560

```

510      FATIYININGQUPORYA---RIR--YASTTNRLRYIVTAGERIFA-GOFNKTMTDTGDL
cryla-105.pe    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
520      LATLTTP-IIPKRYASGRVRYMYAAHHQGVSYGVANINTTGTYANFQITDGEWVF
                    |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
530      YATTNRLRYIVTAGERIFA-GOFNKTMTDTGDL
540      YATTNRLRYIVTAGERIFA-GOFNKTMTDTGDL
550      YATTNRLRYIVTAGERIFA-GOFNKTMTDTGDL
560      YATTNRLRYIVTAGERIFA-GOFNKTMTDTGDL

```

```

cya1a-105.pe T--FQSGSVATNTAFPMQS:-----SFTVGADTFSSGNEVYI--DRFELIPVTATLE
630          570      580      590      600      610
8928030      RAARHFKIIEFDITFSRNSQGLEHLHIYYPNTWISDGLLIIDKTEIPIVGPIN
630          640      650      660      670      680

```

```
cryIa-105.pe.AE---YNL-ERAQKAVNALFTSTNQLGLKTNTVDYHIDQVNSLVTLSDFCLEKRELS
|| : : || : : ||
8928030 QTSEGYNTYDQNTSNYNQNYYNNQNMDTTYQPNDNYTKNSSGMVTDNPYNQNPKDSYNQ
720 720 720 720
```

CryIa-105 pep
NR_047232.634
22469624 source=GENBANK PROT" insecticidal protein CryIc [Bacillus

SCORES Initl: 173 Initn: 279 Opt: 431 z-score: 494.6 E(): 2.9e-19
>>NR04:23268634 (181 aa)

(238-418-1-151)
cryla-105.pe VRWYNTGSRFGWGPDSHOWYNOFRREATLWLDIVLFNYSRTPIRTVSQUTREI

```

270      YTNPVLEDFGFRSAQG---LEGS-IRSPALMINSITVTAHR-GE-YWWSGCH
cryla-105.pe
280      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
290      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
300      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
310      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

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cr\yla-105.pe QIMASPVGSGEFTFPLVGTMGWAAQQQIVALGQVYKLSST-LAPSPENIGN

cry1a-105.pe NQQLSVLDCTEFAVGTSSNLPASVYRKSGTVDLSLDIIPPQNNVPPROGFSHRKSHVSMF

cryla-105.pe RSGFNSVILIPAFMSWIHSAFFNIASDITQIPVXAHTLQSGTTIVRGPCFTG

cry1a-105.pep
NRAA:51090232

51090232 source="GENBANK PROT" cancer cell-killing Cry protein parasporin-3
[Bacillus thuringiensis]gi|51090228|dbj|BAD35157.1| cancer cell-killing Cry
protein parasporin-3 [Bacillus thuringiensis]

SCORES Initl: 360 Initn: 739 Opt: 437 z-score: 491.5 E(): 4.4e-19
>NRAA:51090232
initn: 739 initl: 360 opt: 437 z-score: 491.5 expect(): 4.4e-19
Smith-Waterman score: 763; 29.3% identity in 655 aa overlap
(15-608:46-675)

cry1a-105.pe MDNNPINEICIPYNCISNEVEVLGGERIETGYTPIDISLSTQ 40

51090232 GKGYCQPRIPFAQAQSGSELQNMGYKEMNMCTSGDPT-VLGEYSADVDAVITSINIAS 70

cry1a-105.pe FLSEFVPGAGFVLGLVDIIWGIFPSQ----WDAFLVQIQELINQRIEFARNQAIISRL 100
51090232 YLLSVPPPPAGVAAGILGALLGLLWPTNTQAVWEAFMTVEALINQKLDYARSAKAISEL 130

cry1a-105.pe EGLSNLYQIYAESFREWADPTNPALREMRI--QFNDMNSALITAIPLFAVQNVQVPLL 150
51090232 NLGNLVLELYQDAADDNENPGD--LRNKNVLTEFRNVNGHFNENSPFAVRNFEVLL 190

cry1a-105.pe SVYVQAANLHLSLRDVSFQGWGFDAAATINSRYNDLTRLIGN---YTDHVARWYNTG 210
51090232 PVYAEANLHLLLRDAVKFGEGMGSTDPGABER-DDMYRLRSRTETIYDHCVTNYNG 250

cry1a-105.pe LERV-----W-----GFDSRD-----WIRYQNFRELTITVLDI 240
51090232 LQAKSLQANVSDYSRYPTWYQNSGGFSYREAKGYRGTEWNLWYNAFRDITILVDI 310

cry1a-105.pe VSLPNDVDSRTY--PIRTVSQLTREIYTN--PVLENFGSFRGSAQIGESI---RSPHL 290
51090232 IAQPIYDPLGYSRPVK--SELTREYVDIRGTWRSANL-NTIDAIERNWGVSRQLQL 360

cry1a-105.pe MDILNSTIYIY-DAHREYYSHQINASVGF--SGPEFTFLYTMGNAAPQORIVA 350
51090232 FTWLTEMKFYIRNTGSIYTHGLDWGLEKKIRKTNDDQMLPLEQNTSYTRIDRPGI 420

cry1a-105.pe QLGQG--VYRTLSSTLYRPNIGINNOQLSLVDGTGTFAYGTSNLSAVYRKSQVDSL 410
51090232 ELGKNYVYARTQWFETRLQLWANTDVLNAGTVGNEFWDRDVPD--YRNIYARST- 480

cry1a-105.pe DEIPQNNVPPQGFSHLSHVM--FRSG--FSNSSVSIIIRPMFSWIHRAEFNNII 460

51090232 -----RNHIE-----NHRLSWIKFEFVNDNCFPAWPGYKQLSALLEFWTHNSVDLNNII 530

cry1a-105.pe ASDSIITQPLVKAHTLQSGTIVVRGPGTGGDILARTSGGPFAYTIVNINGQLPQRYRAR 520
51090232 SQYRITQIPAVKAYWNRGAFSVIRGPGSTGGNLVQLGTGGEVSVK--VRPEQTGSDWYVR 590

cry1a-105.pe IRYASTNLRIVTVAGERIFAG---QFNKTMDTGDLTFQSFYATINTAFTFPMSSQS 580
51090232 IRYAAGSRGRLANVKYKVSIIHASVYDYNNMTSSSTQGTYSFOYLDV---YNFRLAEPE 650

cry1a-105.pe FTVGADTFSSGNEVIDRFEPLIPVYATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDY 640
51090232 FEWL--TNESGGFIWDKIEFIPLSPIPELPVYPGYOIVTALNNSSVVTSEFCMGICL 710

cry1a-105.pep
NRAA:8928014

8928014 source="GENBANK PROT" Pesticidal crystal protein cry21aA (Insecticidal
delta-endotoxin CryXXIA(a)) (Crystalline entomocidal protoxin) (132 kDa crystal
protein)

SCORES Initl: 192 Initn: 688 Opt: 423 z-score: 473.4 E(): 4.5e-18
>NRAA:8928014
initn: 688 initl: 192 opt: 423 z-score: 473.4 expect(): 4.5e-18
Smith-Waterman score: 845; 24.7% identity in 1102 aa overlap
(38-1037:70-1105)

cry1a-105.pe NECIPYNCISNEVEVLGGERIETGYTPIDISLSTQELSEFVPGAG---FVLGLVDI 60
8928014 EEFKTYMDPLKQHLQIANTDTSQNGTVDYLAUTKASISLIGLIPGADAVVPFINMFVDF 90

cry1a-105.pe IWG-IFG-PSQMDA-----FLVQIEQLINQRIEFARNQAIISRLGELS-----NLY 100
8928014 IFPKLFGSGSQQAQAFELIEKVKELAVDEDFRFTLNLLNVLGDMOTALSHFQNDV 150

cry1a-105.pe QIYAESFRE-----WEADPT--NPALRE--EMRIQFNDMNSALTAIPLFA-----VONYQV 150
8928014 QIAICQGEQPLMDQTPACTPTTDLHLSVRESFKDARTTETALPHFKNPLMSTNDNT 210

cry1a-105.pe P-----LSVYVQANLHLSLRDVSFQGW--GFDAATINSRYNDLTRLIGNY 200
8928014 PDFNSDVTLLTLPWITLQATNLILHOGYIQFAERWKSVDNDEFINQTKVDLQRIQDI 270

cry1a-105.pe TDHVARWYNTGLERWGPDSRDW--RYNQFRRELTITVLIDVSLFPYNDYRTPYIRTVSQ 260
8928014 STTWTTFEK-FKPTLNFENSKESVKNYRVRSMTLQSLDIAATWPTLDNWNVPSVDIQ 330

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[illegible]


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cry1a-105.pe TDHAVRWNTGLRVMGPDSDWI-RYNQFRRELTTLVLDIVLSPFNVDGRTYPIRTVSQ
8928014 STTSTTFEK-FKPTLNSKESVKNRYVRSMTLQSDIAATVTLDDVNVPSVDIQ
280 290 300 310 320 330

cry1a-105.pe TTRIYNPVLENFDSFRGSAQIEGSIIRPHMLDILSIITYDAHRGEYWSGHQM
8928014 LDQ---TRLVFSVAGVMEGN---DNITS-NIIDVLPINTGI-----GFQES
340 350 360 370

cry1a-105.pe ASPVFGSGPEFTFLYGTMGNAAPQQRIVAQLGQYRVLSTSLYRPFNIGINQQLSV
8928014 SLLKFTYPRIELQSMQFHGQVMSKSVHCYSDG---LKNYKNTITAGVSNIDEN
380 390 400 410 420 430

cry1a-105.pe LDGTFAYGTSSNLP-SAVYRKSGTVSDLSDEIPQNNVPPRQGFSHLSHVMFSGFS
8928014 QNN-KHNYGPVINSPIITDINVNSQNSQVLDLNSVMYWGQKVTGCGSPSSNGSNNAALP
440 450 460 470 480 490

cry1a-105.pe NSSVSLIRA-----P-----MFSWTHRSAP-----NNLIAS-USITQIP-ILVKAH
8928014 NOKINVIYSVQSNNDKPEKHADYTRKMGYSMSHIPYDLVPENVIGDIDPTKQPSLLKGF
500 510 520 530 540 550

cry1a-105.pe TLQSG---TTVVRGPGTGGDILLRTSGGPFAYTVINGQLPQVRARIVAS--TTN
8928014 PAEKYGDSTAYSEP-LGANAVALTS---YQVLQMEVTNQTQKRIIRATGDTA
560 570 580 590 600 610

cry1a-105.pe LRIYTVAG---ERIFACQFNKMTDGDPLTFQS----FSYATINTAFTFPMQSQSFV
8928014 ASIWFHIIIGPSGNDLTNEGHNFSSVSSRNKMFVQGNNGKYVLNLTDSIELPSGQQTILI
620 630 640 650 660 670

cry1a-105.pe GADTFSSGNEVYIDREELI--PVTAT-----LEAEVNLERAKQAVNALFTSNQLGLKT
8928014 QN---TNSQDLFLDRLEFISLPSISTPTSTNFEPE-SLEKLIINQVNLFSSSSQTELAH
680 690 700 710 720

cry1a-105.pe NVTDYHIDQVSNIVLYLSDFCFLDEKRELSEKVKHAKRLSDERNLLQPSNFKOINRQPER
8928014 TVSDYKIDQVVLKVNALSDDVFGVEKALRKLKVNQAKLSKARNVLUGGNF-----EK
730 740 750 760 770

cry1a-105.pe G-WGGSTGTIGQDDVKENIVTLSTGTFDECPYLYQKIDESKLKAFTRQLRGYIE
8928014 GHEWALSREATMVANHELFGDHLILPPP--TLPSYAYQKIDESKLKSNTRYTVSGFIA
780 790 800 810 820 830

cry1a-105.pe DSQDLIYSIRYNAK-HETVNPVGTGSLWPLSA-QSPIGKCEPNCRAPHLEWNFDLDCS
8928014 QSEHLEVVVSRYGKEVHMDLIPYEEAL-PISSDESP--NCKCPAAC-----QCS
840 850 860 870 880 890 900
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cry1a-105.pe CRDGEKCAHSHHFSLDIDVGCTDLNEDLGWVIFKIKTQDCHARLGNLEFLEKPLVGE
8928014 SCDGSQS--DSHFFSYSDVGSLOSDVNLGLIEFGLEIAKPNQFAKISNLEIKEDRLTEK
890 900 910 920 930 940

cry1a-105.pe ALARVKRAEKWKREKLEWETNIVYKEAESVDALFVNSQYDQLOQADTNIAHIAAK
8928014 EIKKQVQKEQKWKAFNQAEVATVLTQPTLDQINALYQNEWDN-----GSVHPASD
950 960 970 980

cry1a-105.pe RVH--SIREAYLPE-----LSVIGCVNAAIFEELEGRIETAFESLDARNVTKMGDFNNGL
8928014 YOHL SAVVVTLPQRHWMFEGREGEHVVLTPQFQALDRAPQQIEEQNLHNGNLANGL
1000 1010 1020 1030 1040 1050

cry1a-105.pe SCWNVKGHVDVEQNNQRSLVLPWEAEVYSQEVRC--PGRGYILRVYATYKGYGEGCV
8928014 TDWTVTGDAQLT-IPDEDVLELAHWDASISQTIETIMDFEGRHRITQACTWKQRNSYRS
1060 1070 1080 1090 1100 1110

cry1a-105.pe TIHETENNTDELFCVCEVEEYIPNNVTCTDVTNQEYGGAYTSRNRGNRAPSVPAD
8928014 TWKRKLEMTFTNTSTTTOEQTFYFEGTVDVHVQSENNTFLIDSVELIEIEE
1120 1130 1140 1150 1160

cry1a-105.pep
NRAA:8928012

8928012 source="GENBANK_PROT" Pesticidal crystal protein cry24Na (Insecticidal
delta-endotoxin CryXIIA(a)) (Crystalline entomocidal protoxin) (Crystal protein)
(Insecticidal protein Jcg72)gi|366833|gb|AAC61891.1| insecticidal protein Jcg72
[Bacillus thuringiensis serovar jegathesan]

SCORES Initl: 237 Initn: 601 Opt: 419 z-score: 472.4 E(): 5.1e-18
>>NRAA:8928012
initn: 601 initl: 237 opt: 419 z-score: 472.4 expect(): 5.1e-18
Smith-Waterman score: 727; 29.0% identity in 589 aa overlap
(77-828:105-672)

cry1a-105.pe LSEFVPGAGFVLGLVDIHWGIFGPSQMDAFLVQIEQLINQRIEERFARNQAIISLEGSLN
8928012 KAVASSLADSIKSSLGISGISTITENNVSQVSMVQHQIINRIQETILDGESSLNGLVAI
80 90 100 110 120 130

cry1a-105.pe Y-QIYASFEWADTNPALREEMRQFNDMSALTATP-LFAVQNYQVPLLSVYQA
8928012 YNRDYLGALEAWNNKSNINYQTVAAEFKTVVEREFTKLGIVYFTSSSQITLLPTFTA
140 150 160 170 180 190

cry1a-105.pe ANLHLSVLRVSVFGORWGFDAATINSRYNDLTLRLIGNYTDHAVRWNTGLRVMGPDSDR
8928012 ANLHLSMLRDVAVYQSGWNLQSHINYK--ELDDALEDYNTVCVEYTKGLNALRGSTAI
200 210 220 230 240 250

cry1a-105.pe DMIRYNQFRRELTTLVLDIVLSPFNVDGRTYPIRTVSQTLREIYNPVLENFDSF---
8928014 QSEHLEVVVSRYGKEVHMDLIPYEEAL-PISSDESP--NCKCPAAC-----QCS
840 850 860 870 880 890 900
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Monsanto Company
Final Report

Product Characterization Center

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MSL No. 20351
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8928012 DWLEFNFRDMLTALDLVAIFPNVNPVPLSTKISLRKIYTDVGRDTSFSGDWT 270 280 290 300 310

cry1a-105.pe ---RGSA---GTEGSGIR-SPHMDILANSITIT---DAHR---GEY---YWSGHQIMASP 290 300 310 320

8928012 NTGRTLANFNDLERETDPSLVKWLGMNTYTGAIDSYRPTSPGDRIGVWYGNINAFVH 330 340 350 360 370

cry1a-105.pe VGFSGPEFTPLVGTGNGNAAPQORIVAAQLGQGVYR---TLSTLYRRFPNIGINNOQ 330 340 350 360 370

8928012 TGRTDV-VMFRQGTAYEDSTISNLIDYKDLRAAASTIQGAMDTTFGVSSSR 380 390 400 410 420 430

cry1a-105.pe LSVLDGTEFAYGTSNLPASAVRKSGTVDSLEPPQNNVPPRGFSHRLSHVMSFRSG 380 390 400 410 420 430

8928012 FFDIRGNQLYQSNKPYPSLPITIT-----FPGESSEGNANDYSHDCDKIISD 440 450 460 470 480

cry1a-105.pe FSNSSVSIIRAPMFS---WIHRSAPFNIIASDSITQIPLVKAHTLSGTIVRGFATQS 440 450 460 470 480 490

8928012 SSN-ICEGRSSLSLHAWTHASLDENNTILPDELTQIPAVTAYELRGNSVWAGSGTGS 490 500 510 520 530 540

cry1a-105.pe DILARTSGGPFATVINGQLPQRYRARIYASTTNLRIVY---TVAGERIFAGQFN 500 510 520 530 540 550

8928012 DLVKMSVHVSVMSEFKVYC--SEL-KNYRVRIRYASHGNCQFLMKRWPFSTGVAPQWA-RHN 550 560 570 580 590

cry1a-105.pe KMTDGTPLTFQSFYSATINTAFTPPMSQSFVAGDTSSGNEVYIDRFLPVTAT-- 550 560 570 580 590 600 610

8928012 VOGTFSNMYEAFKYLDI---FTITPEENNFAFTID-LESGGDLFDKIEFIPVSGSAP 600 610 620 630 640 650

cry1a-105.pe LEAEYNLERAQKAVNALFTSTNQLGLKNTVDYHDIDQVSNLVTVLSDEFCLDEKRLSE 620 630 640 650 660

8928012 EYEGKQNIETQKAVNDLFIN 660 670

cry1a-105.pep
SW:8928012

8928012 description="PESTICIDIAL CRYSTAL PROTEIN CRY24AA (INSECTICIDIAL DELTA-ENDOTOXIN CRYXXIVA(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (CRYSTAL PROTEIN) (INSECTICIDIAL PROTEIN JEG72)" library=NA species="Bacillus thuringiensis serovar jegathesan" source="swissprot_prot" version=NA type=PRT

SCORES Initl: 237 Initn: 601 Opt: 419 z-score: 472.4 E(): 5.1e-18
>>SW:8928012
Initn: 601 Initl: 237 Opt: 419 z-score: 472.4 expect(): 5.1e-18
Smith-Waterman score: 727; 29.0% identity in 589 aa overlap
(77-628:105-672)

cry1a-105.pe LSEFVPGAGFVLGLVDIINGIFGPGQWDAFLVQIEQLINQRIEERFARNQASRLLEGISNL 80 90 100 110 120 130
8928012 KAVASSLADSIKSSLGISKTIITENNVSQVSWQVQHVIINRIQETILDGLGSSJLGLVAI 80 90 100 110 120 130

©01

Protein Information

Protein Information of Monsanto Company

cry1a-105.pe Y-QIYAESFREWEADPTPALREEMRIQFNDMNSALITTAIP-LEAVQNVQVPLLSVYVQA 110 120 130 140 150 160

8928012 YNRDYLGALEANNKNSNINQVTNVAEAFKIVEREFFTKLKGIVYRTSSQITLLPTFTQA 140 150 160 170 180 190

cry1a-105.pe ANHLSLVRDVSFGORGVDAATINSRYNDLTRLIGNYTDHAYRWNTGLERVWGPDSR 170 180 190 200 210 220

8928012 ANHLSMLRDVWYQEGNLOSHINYSK--ELDDALEDTYNYCEVYTKGLNALRGSTAI 200 210 220 230 240 250

cry1a-105.pe DWIRYNQFRRLTLVLDIVSLFNPYDSRTYPIRTVSOLTRITNPNVLENFDGSE--- 230 240 250 260 270 280

8928012 DWLEFNFRDMLTALDLVAIFPNVNPVPLSTKISLRKIYTDVGRDTSFSGDWT 260 270 280 290 300 310

cry1a-105.pe ---RGSA---QIEGSGIR-SPHMDILANSITIT---DAHR---GEY---YWSGHQIMASP 290 300 310 320

8928012 NTGRTLANFNDLERETDPSLVKWLGMNTYTGAIDSYRPTSPGDRIGVWYGNINAFVH 320 330 340 350 360 370

cry1a-105.pe VGFSGPEFTPLVGTGNGNAAPQORIVAAQLGQGVYR---TLSTLYRRFPNIGINNOQ 330 340 350 360 370

8928012 TGRTDV-VMFRQGTAYEDSTISNLIDYKDLRAAASTIQGAMDTTFGVSSSR 380 390 400 410 420 430

cry1a-105.pe LSVLDGTEFAYGTSNLPASAVRKSGTVDSLEPPQNNVPPRGFSHRLSHVMSFRSG 380 390 400 410 420 430

8928012 FFDIRGNQLYQSNKPYPSLPITIT-----FPGESSEGNANDYSHDCDKIISD 440 450 460 470 480

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

8928012 VOGTFSNMYEAFKYLDI---FTITPEENNFAFTID-LESGGDLFDKIEFIPVSGSAP 490 500 510 520 530 540

cry1a-105.pe LEAEYNLERAQKAVNALFTSTNQLGLKNTVDYHDIDQVSNLVTVLSDEFCLDEKRLSE 500 510 520 530 540 550

8928012 EYEGKQNIETQKAVNDLFIN 550 560 570 580 590

cry1a-105.pe KMTDGTPLTFQSFYSATINTAFTPPMSQSFVAGDTSSGNEVYIDRFLPVTAT-- 560 570 580 590 600 610

8928012 VOGTFSNMYEAFKYLDI---FTITPEENNFAFTID-LESGGDLFDKIEFIPVSGSAP 560 570 580 590 600 610

cry1a-105.pe LEAEYNLERAQKAVNALFTSTNQLGLKNTVDYHDIDQVSNLVTVLSDEFCLDEKRLSE 620 630 640 650 660 670

8928012 EYEGKQNIETQKAVNDLFIN 660 670

cry1a-105.pep
NRAA:1922253

1922253 source="GENBANK_PROT" cbm72 mosquitoicidal toxin [Clostridium

bifermentans/gi|10719926|sp|005102|C17AA_CLOBI_Pesticidal crystal-like protein
cry17Aa (Insecticidal toxin cryXVIIA(a)) (CbM72 mosquitocidal toxin)

SCORES Initl: 215 Initn: 389 Opt: 403 z-score: 454.8 E(): 4.9e-17
>>NRAA:1922253
initn: 389 initl: 215 opt: 403 z-score: 454.8 expect(): 4.9e-17
Smith-Waterman score: 515; 24.4% identity in 651 aa overlap
(3-606:2-616)

cry1a-105.pe MNPNVLI-NECIPYNC---LSNPEVILGGERIETGYTPIDISLSLTQFLSFEVPGAG
1922253 MNKKIQONKIVEYNSNDIQPRELNTLGL-VFTGAT---VSIILPLIGTTAVVPGVG
10 20 30 40 50

cry1a-105.pe FVLGLV----DIWIGFQSQ---WDAFLVQIEQLINRIEIEFARNQAIISLEGLSNLYQ
1922253 GVIGIIAALLPVIMPAGTSSNDNLFDAVMKDTMIMDEKISEVYVNDAMTLESLYNILD
60 70 80 90 100 110

cry1a-105.pe IYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVONYQVPLLSVYVQAANLH
1922253 YRLSKDFWEKNKDDPLATAELKERFSKLHSQFIESMAYFKRANYEVLLLPAYANAANLH
120 130 140 150 160 170

cry1a-105.pe LSVLRDVSFGQWGFDAATINSRYNDLTRIGNYTDHVRVNTGLERVGPDSDMRIR
1922253 LLLREGLLLNKVID-NFITEGLHVEEFTKRSYIIAHSTWYNGLENINKK-TRDPNK
180 190 200 210 220 230

cry1a-105.pe YNQFRRELTLLVDIVSLFPNDSTRTYPIRTVSQ-LTREIYNPVLNFDGSGFRGSAQGI
1922253 INKYDAYMNLVSLDIISLFLSDPYQYDKATKLTQTLTRTVFSDPLQD-----APRDL
240 250 260 270 280

cry1a-105.pe EGSISRPHLMDILNSITIIDAHGEYVWSGHQIMASPVGSGPDEFTPLIGTMGNAAPQ
1922253 YISPKETLFKNLGLRAFFA--EGDLVLTGFRNYFRNTYINDQIEGDLFGYTN--N
290 300 310 320 330 340

cry1a-105.pe QRIVAQLGQGVYRTLSLTVRRPFNIGNNQOLSVLDGTGEFAYGTSNLPASVYRKSGTV
1922253 ERYKLFSDSKYIKV---TVFIDNVALAIVKLIIPHDTNKEWDFSKTDLTDINKRKEEYV
350 360 370 380 390 400

cry1a-105.pe DSLDEIPQNNVPPRGFSHRLSHVSMFRSGNSVSIIRAPMFSWIRHS-AEFNII
1922253 LNLN-----SNNEIQKEP--SHYLYKMHYGDYNDYSY-----LPQWIIHQSIQSPENLYF
410 420 430 440 450 460 470 480 490 500

cry1a-105.pe ASDS-----ITQIPLVKHTLQS-----GTTVVRGPGTGGD-ILKRTS-----GGP
1922253 DKDKDNNYIITQIPAKSELNGLSELQAKGPRFTGNGVTLSSVSKINDNDPLVGGT
450 460 470 480 490 500

cry1a-105.pe FAYTIVNNGQLPQRYEARIRYASTTN-----LRIYTVVAGERIFAGQFNKMTDGD--P
510 520 530 540 550 560

1922253 IKAILPLTAFNNT-SKEKILYYAANHNVDYICALLTINSQHANFKFKQTFSGEDYSN
510 520 530 540 550 560

cry1a-105.pe LTFQFSYATINTAFTFPMSSQSFVTGADTFSSG---NE---VYIDREFELIPVTATLEA
1922253 LSYNNYQFDVLVQTVAFPQNTSDVTNLNQFFYDFPKFLNDYKQIVLIDKIEPIPN
570 580 590 600 610

cry1a-105.pe EYNLERAKAVNALFTSTNQLGKINVTYDHYDIDQVSNLVTYLSDEFCLDEKRELSKVKH
cry1a-105.pep
SW:10719926

10719926 descriptions="PESTICIDIAL CRYSTALL-LIKE PROTEIN CRY17AA (INSECTICIDIAL
TOXIN CRYXVIIA(a)) (CBM72 MOSQUITOCIDAL TOXIN)." library=NA species="Clostridium
bifermentans" source="swissprot_prot" version=NA type=PRT

SCORES Initl: 215 Initn: 389 Opt: 403 z-score: 454.8 E(): 4.9e-17
>>SW:10719926
initn: 389 initl: 215 opt: 403 z-score: 454.8 expect(): 4.9e-17
Smith-Waterman score: 515; 24.4% identity in 651 aa overlap
(3-606:2-616)

cry1a-105.pe MNPNVLI-NECIPYNC---LSNPEVILGGERIETGYTPIDISLSLTQFLSFEVPGAG
10719926 MNKKIQONKIVEYNSNDIQPRELNTLGL-VFTGAT---VSIILPLIGTTAVVPGVG
10 20 30 40 50

cry1a-105.pe FVLGLV----DIWIGFQSQ---WDAFLVQIEQLINRIEIEFARNQAIISLEGLSNLYQ
10719926 GVIGIIAALLPVIMPAGTSSNDNLFDAVMKDTMIMDEKISEVYVNDAMTLESLYNILD
60 70 80 90 100 110

cry1a-105.pe IYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVONYQVPLLSVYVQAANLH
10719926 YRLSKDFWEKNKDDPLATAELKERFSKLHSQFIESMAYFKRANYEVLLLPAYANAANLH
120 130 140 150 160 170

cry1a-105.pe LSVLRDVSFGQWGFDAATINSRYNDLTRIGNYTDHVRVNTGLERVGPDSDMRIR
10719926 LLLREGLLLNKVID-NFITEGLHVEEFTKRSYIIAHSTWYNGLENINKK-TRDPNK
180 190 200 210 220 230

cry1a-105.pe YNQFRRELTLLVDIVSLFPNDSTRTYPIRTVSQ-LTREIYNPVLNFDGSGFRGSAQGI
10719926 INKYDAYMNLVSLDIISLFLSDPYQYDKATKLTQTLTRTVFSDPLQD-----APRDL
240 250 260 270 280

cry1a-105.pe EGSISRPHLMDILNSITIIDAHGEYVWSGHQIMASPVGSGPDEFTPLIGTMGNAAPQ
10719926 YISPKETLFKNLGLRAFFA--EGDLVLTGFRNYFRNTYINDQIEGDLFGYTN--N
290 300 310 320 330 340

cry1a-105.pe QRIVAQLGQGVYRTLSLTVRRPFNIGNNQOLSVLDGTGEFAYGTSNLPASVYRKSGTV
350 360 370 380 390 400


```
21685444 AGNFASSETIVGVSGAGIIVVGTMLGFAFPAVLAAAGIISFGTLLPFIWQGSDFPANNWQDLL
      70      80      90      100      110      120
cryla-105.pe VQIEQLNQRIEIEFARNQAISELEGLSNLYQIYAESFRWEADPTNPALREEMRIQFNDM
      80      90      100      110      120      130
21685444 -NIGRPQIEIDKNIINVLTSIVTPIKQDKYQEFDFKWEPAATHANAKAVHDL-FTTL
      130      140      150      160      170
cryla-105.pe NSALTAIPFAVQ-NYQVPLISVTVQANLHLSVLDSVFGQW-----GFDAAIINSR
      140      150      160      170      180      190
21685444 EPIIDKDLMLKNNASRYIPTLPAYAQIATWHLNLLKHAATYINWLNQGNIPSTFNS
      180      190      200      210      220      230
cryla-105.pe --YND-LTRLIGNYTDHAVRYNTGLERVWGPDSDRWIRYNQFRRELTTLVLDIVSLFPN
      200      210      220      230      240
21685444 NYQYGLKARKIOEYDYCIOTYNAGLTWIRNTNATWNNYTYRLEMTLVLDLIAIFN
      240      250      260      270      280      290
cryla-105.pe YDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIGSIRSPLHMDILNSITIYDA
      250      260      270      280      290      300
21685444 YDPEKYPIGVKSELIREVTNV---NSD-TFRITILENGLTRNPTLTFTWLNQGRFYTRN
      300      310      320      330      340      350
cryla-105.pe HRGEYWSGHQIMASPVGSGPEFTFPLYGTGN---AAPQRIVAQLGQGVYTLSSTL
      310      320      330      340      350      360
21685444 SRD--ILDPIYDIFS----FTGNQMAFTTDDRNIIWGAHGNIIISQDTSKV-----PF
      360      370      380      390      400
cryla-105.pe YR-RPFN-IGINQQQLSLVDGTGFAYGTSSNLPSAVYKSGTVDLSIDIPQNNVPPRQ
      370      380      390      400      410      420
21685444 YNKPDKVEIVRHRYSVDIIYEMIFFSNS---SEVFRYSSNSTIENNYKRTDSYMPKO
      410      420      430      440      450      460
cryla-105.pe G-----FSHRLSHVSMFRSGFNSVSIIRAPMFSWTHRSAEFNIIASDSITQIPLVKA
      430      440      450      460      470      480
21685444 TWKNEGYHTLSVIKT--DNYIFSVMRERRRVAFSWTHSVDFONTIDLDNIQIHAKA
      470      480      490      500      510
cryla-105.pe HTLQSGITTVRGPGFTGGDILRRTSGGPFATIV-NINGQLPQRYRARIYASTNLIY
      480      490      500      510      520      530
21685444 LKVSDDSKIVKPGHGTGGDLVILKDSMDFRVFLKNVSRQ-----YQVRIATNAP-KIT
      490      500      510      520      530      540
cryla-105.pe VTVAGERIFAGQNKMTMDGDP----LTFQSFYATINAP---TFPMSSQSFYTGADTF
      540      550      560      570      580      590
21685444 VFLTGIDTISVELPSTTSRQNPNDLTLYADFGVIFPPTVPNKTFEGEDTLMLTYGTP
      580      590      600      610      620      630
cryla-105.pe SSGNEVIYDRFELIPVATL---EAYNLEPAQKAVNALFTSNGLKTNVTYDHDQV
      600      610      620      630      640
21685444 NHSYNIYDKIEFIPITQSVLDYTEKQIEXTQKIVNDLFVN
      640      650      660      670
cryla-105.pe SNLVITYLSDFECLDEKRELSEKVKHAKELSDERNLLQDSNFKDINRQPERGWSGTGITI
      650      660      670      680      690      700
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cryla-105.pep
NRAA:117329

117329 source="GENBANK_PROT" Pesticidal crystal protein cry10Aa (Insecticidal delta-endotoxin CryXA(a)) (Crystalline entomocidal protoxin) (78 kDa crystal protein)gi|143229|gb|AAA25614.1| insecticidal endotoxin (put.); putative

SCORES Initl: 230 Initn: 419 Opt: 385 Z-score: 433.7 E(): 7.3e-16
>NRAA:117329
initl: 419 initl: 230 opt: 385 Z-score: 433.7 expect(): 7.3e-16
Smith-Waterman score: 636; 28.3% identity in 612 aa overlap
(51-630:91-675)

cryla-105.pe VEVLGERIETGYTPIDISLSLTQFLSEFVPGGFV-LG-LVDIIMGIFGPSQ-WDAFL
 30 40 50 60 70
117329 AGNFASSETIVGVSGAGIIVVGTMLGFAFPAVLAAAGIISFGTLLPFIWQGSDFPANNWQDLL
 70 80 90 100 110 120

cryla-105.pe VQIEQLNQRIEIEFARNQAISELEGLSNLYQIYAESFRWEADPTNPALREEMRIQFNDM
 80 90 100 110 120 130
117329 -NIGRPQIEIDKNIINVLTSIVTPIKQDKYQEFDFKWEPAATHANAKAVHDL-FTTL
 130 140 150 160 170

cryla-105.pe NSALTAIPFAVQ-NYQVPLISVTVQANLHLSVLDSVFGQW-----GFDAAIINSR
 140 150 160 170 180 190
117329 EPIIDKDLMLKNNASRYIPTLPAYAQIATWHLNLLKHAATYINWLNQGNIPSTFNS
 180 190 200 210 220 230

cryla-105.pe --YND-LTRLIGNYTDHAVRYNTGLERVWGPDSDRWIRYNQFRRELTTLVLDIVSLFPN
 200 210 220 230 240
117329 NYQYGLKARKIOEYDYCIOTYNAGLTWIRNTNATWNNYTYRLEMTLVLDLIAIFN
 240 250 260 270 280 290

cryla-105.pe YDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIGSIRSPLHMDILNSITIYDA
 250 260 270 280 290 300
117329 YDPEKYPIGVKSELIREVTNV---NSD-TFRITILENGLTRNPTLTFTWLNQGRFYTRN
 300 310 320 330 340 350

cryla-105.pe HRGEYWSGHQIMASPVGSGPEFTFPLYGTGN---AAPQRIVAQLGQGVYTLSSTL
 310 320 330 340 350 360
117329 SRD--ILDPIYDIFS----FTGNQMAFTTDDRNIIWGAHGNIIISQDTSKV-----PF
 360 370 380 390 400

cryla-105.pe YR-RPFN-IGINQQQLSLVDGTGFAYGTSSNLPSAVYKSGTVDLSIDIPQNNVPPRQ
 370 380 390 400 410 420
117329 YNKPDKVEIVRHRYSVDIIYEMIFFSNS---SEVFRYSSNSTIENNYKRTDSYMPKO
 410 420 430 440 450 460

cryla-105.pe G-----FSHRLSHVSMFRSGFNSVSIIRAPMFSWTHRSAEFNIIASDSITQIPLVKA
 430 440 450 460 470 480
117329 TWKNEGYHTLSVIKT--DNYIFSVMRERRRVAFSWTHSVDFONTIDLDNIQIHAKA
 470 480 490 500 510

cryla-105.pe HTLQSGITTVRGPGFTGGDILRRTSGGPFATIV-NINGQLPQRYRARIYASTNLIY
 480 490 500 510 520 530

117329 LKVSZGKVKGFNGGSLVILKSDMDFVRFLKNVSRQ-----YQVRIYATNAP-KTT
520 530 540 550 560 570
cryla-105.pe VVAGEHIFAGGKQKQKPGDP---LPSFSYATINTAF---TFPMQSSFTVGADIF
540 550 560 570 580 590
117329 VFLGIDNIVLPSFTSSTQKFNATPLAYAFSGNTPFRTVPNKTFEGEDLLTLTYGTP
580 590 600 610 620 630
cryla-105.pe SSGNEVVIDRFELIPVTNKL---EAEYNEFANKVNALESTNGLKTNVTDYHDQV
600 610 620 630 640
117329 NHSVNIIDKIEPIPIQSVLDYFEKNIENKTKYKNDYEVN
640 650 660 670 680
cryla-105.pe SNLVYLSDEFCLDEKRELSEKVKHAKELSDERLQDSNKKDINRQPEKMGSGQYH
650 660 670 680 690 700
cryla-105.pep
NRAA:17977981
17977981 source="GENBANK_PROT" Cry30Aa protein [Bacillus thuringiensis serovar medellin]
SCORES Initl: 176 Initn: 360 Opt: 372 z-score: 418.8 E(): 4.9e-15
>>NRAA:17977981
initn: 360 opt: 372 z-score: 418.8 expect(): 4.9e-15
Smith-Waterman score: 508; 25.7% identity in 637 aa overlap
(34-607:59-678)
cryla-105.pe NFNINECLPYNCLSNPEVEVLGGERIETGYTPIDISLSLTOFLLS-----EFVPGAGFV
10 20 30 40 50
17977981 YPLTNPKVPLQNTNYKDWLNMCQTITPLCTPIDTDSKLVAITAIKVGAIKSPGPGAA
30 40 50 60 70 80
cryla-105.pe LGLV-----DIWIGFQPSQWDAFLVQIOLINORIE---EFARNOAISREGLSN
60 70 80 90 100
17977981 VGLVLKSFSTIIPILPNDKTPIMKEFTKQGLQFLPELGRDAIILIGNDVQAEYNSLEI
90 100 110 120 130 140
cryla-105.pe LYQIYAESFREWADPTNPALREEMRIQFNDMSALTTAIPLFAYQNYQVP-LLSVYVQA
110 120 130 140 150 160
17977981 MMRDENKFNANWESNTR-ANAIAVTTFSTVNTQIRLKERFLIAPENRPAFLNLYAQT
150 160 170 180 190 200
cryla-105.pe ANLHLSVLRDVSVFGQMGFDAQINSP-----YNDLTRIGNYTDHVRVNTG
170 180 190 200 210
17977981 ANIDLILYQSGSVIGDKW---VADINNRSISPFSSVDYQSLGKIKDYITNYCAETRNS
210 220 230 240 250 260
cryla-105.pe LERVWGPDSDRYRNQFRRELTTLVLDIVSLFPNYDSRTYPTVSOVLTREIYTNVLE
220 230 240 250 260 270
17977981 LTLANKPHQMDIYNYRYREAILCALDLVALFENYDICIYPTQFTELTRKVM-PSFY
270 280 290 300 310 320
cryla-105.pe NPDGSGFRGSAQIEGSI-RSPLMDILNSITTYDARHGE-----YVWSGHQIMASPVGF
280 290 300 310 320

17977981 -LQALQORDIETVENOLTHPPSLFTWLNELNLYTIRERNFVPLQVASLSGLQA-TSRYTQ
330 340 350 360 370 380
cryla-105.pe SCPEFTFLYGTWGNAAPOQRIVAOLQGQYRILSTLYRRFNI-----GINNQLSVLD
330 340 350 360 370 380
17977981 NTTTISNPVQGPVREGTPPK--ISLANYIYIKLFMSQ-YRHPNDCPLISGINEMSFYRSD
390 400 410 420 430
cryla-105.pe GTEFAYGTSNLSFSAVYRKSG---TVDSLDEIPPN---NNVPPROGFSHRLSHVSMF
390 400 410 420 430
17977981 ---YYGAGG--PAPVHYSAGESPNTVILKTYMNGPONALISINDISINET-SHILSDIKNN
440 450 460 470 480 490
cryla-105.pe RSGFNSSVSIIIRAPMFSWIHSAEFNNIIASDSITQIPLVKAHTLQSGTIVVRGPGFTG
440 450 460 470 480 490
17977981 YSRTGGVPLYDFGYSFAWHTSVDPDNLIVPNRITQIPAVKAYSLTSPARVIVGPGHTG
500 510 520 530 540 550
cryla-105.pe GDILRRTSGGPFAYT--IVNINGQL--PQR-YRARIRYASTTNLRI---YVTVAGER---
500 510 520 530 540
17977981 GDLVALNSGTQSGTWIOCKTGSTGTFPSROYGLRWRYAANSFAVLSVLYLQTRGTS
560 570 580 590 600 610
cryla-105.pe -IFAQCFNKMTDT-GDPLTFQFSYATINTAFPPMSQSSFTVGADTFSSG---NEVYID
550 560 570 580 590 600
17977981 PTNTNFSRNNIIPTDLKVEFKYKDYLIQIITWTPANTLITISMQCATGLNNOLIID
620 630 640 650 660 670
cryla-105.pe REELIPVATDREKLEAKVNALETSINQLKTNVTDYHDQVSNLVYLSDEF
640 650 660 670
17977981 RIEEAMMGVACTVN
680
cryla-105.pep
NRAA:22002424
22002424 source="GENBANK_PROT" Cry2Aa [Bacillus thuringiensis serovar roskildensis]
SCORES Initl: 191 Initn: 652 Opt: 373 z-score: 415.9 E(): 7.2e-15
>>NRAA:22002424
initn: 652 opt: 373 z-score: 415.9 expect(): 7.2e-15
Smith-Waterman score: 729; 23.6% identity in 1207 aa overlap
(40-1060:70-1244)
cryla-105.pe CIPYNCISNPEVEVLGGERIETGYTPIDISLSLTOFLLS-EFVPGAGFV
10 20 30 40 50 60
22002424 EEFKTYGKDFLEQHLKIANNASQNGTIDYLAITKASISFISGLIPADANVPPFIMVMDI
40 50 60 70 80 90
cryla-105.pe IWG-IFGP-----SOMDAELVOIEQ---LINORIEEFARNOAISREGLSNLYQVIAEST
70 80 90 100 110
22002424 IFPKFLGSGSQQSQAQGFQFFVQDEQFRFTNLTDLNDLGWQTLLEHFONDV
100 110 120 130 140 150

```
cry1a-105.pe R-----EWEADTPNALREMIQ---FNDMSALTTAIFL--AVONQVP-
22002424 QIAICQEGPGLILDEKHPCTFTKNHLVSKSFKNARTSETVLPHPKMPNKNKTPD
160 170 180 190 200 210

cry1a-105.pe -----LSVVQAAHLHLSVLDSVFGQW---GFAATINRSYNDLTRIGNYTD
22002424 FNSDTVLLTLPMTTAAATNLHLHOGYIQFVERKWSVDDEAFINQTKADLQRIQEYST
220 230 240 250 260 270

cry1a-105.pe HAVRWNTGLRWGPDSDRWIRYNQFRRLTLTVLDIVSLFPNVDSTYPIRTVSOL--
22002424 TVSTTFEK-EKPTLSNKKSSINTYKTVRSWTLNCLDIAATWPTLNDVNPSPVEIQDQ
280 290 300 310 320 330

cry1a-105.pe TREIYTN---PVLENFD-----GFRGSAQGIERSIRSPHLMILNITTY
22002424 TRLVFSLNGLVFPFGNDISTYTRRSIMNYSKGTDPGDVNSAIQSRLYPRLE--LSKVQFY
340 350 360 370 380 390

cry1a-105.pe TDARGE---YWSHQI-----MASPVGSG-----PETFLIGTMNAAPQOR--
22002424 THDQRSNGVRHCYTGFLNFTNDSSMSAKODESATADSPPLTAPFKNMNANSONSCYYD
400 410 420 430 440 450

cry1a-105.pe -----IVAQLGQGV-----YRLSLSTLYRRFPNI-----GINNOQL---SVLDGTEAYG-
22002424 YSSNIDNQGSGCSAFPYSQSNPILPNQKINVFYPGSSAHPIDHDTPDPTWKLGY
460 470 480 490 500 510

cry1a-105.pe TSSNLPASVYRKS--GTVDLSDETPQN--NNVPPRGFGSHRLSHVSMFRGFSNVSVI-
22002424 VSSHIPYDLTPQNVIGEIDQDTKQPSLILKGFPAGRYGSGSYEVYSEPLANGANAALTLN
520 530 540 550 560 570

cry1a-105.pe -----IRAPMFSWHRSAEFNNIIAS-----DSLTQIP-----
22002424 QILYMQVNTTQKYOIRLRATKNDTASWPHIIGPNQNDIINHSPDIPPRSNKMFV
580 590 600 610 620 630

cry1a-105.pe -----LYKAHTLQSG--TTVVRGPGFTGGDILARTSGGPFAYTIWNINGQLPOR
22002424 OGENGKYLVDLTLVDSIELPSGQLTILONINPDQDLFLDRIEFVPIPLPTNINISIPKT
640 650 660 670 680 690

cry1a-105.pe -----YRARIRYASTNLRIRY--VTVAG-----ERIFAGQFNKMTDGDPL-----
22002424 DTSPPKSKVLWEASPDIPANTITLTGVSVDYFADITFELYKNGNNTVSYPIKGGPIPHR
700 710 720 730 740 750

cry1a-105.pe ---TFQS-----PSYATINTAFTFMSQSSFTVGAD--TF---SSGNEVIDRELIPVTA
22002424 SHGNVSCSGILSYNYENKPVLDGFDQLRININSDPSYNSCOTKQKQYSAEIKNP
760 770 780 790 800 810

610 620 630 640 650 660
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cry1a-105.pe TLREYNLERAQAVNALFTSTNQLGKTNVTYHIDQVSNLVTYLSDEFCLDEKRELSE
22002424 NLSATTDLEKITQVNLQFTSSQTELANITYDIRIDQIVMKVDALSNNVFGVEKKALRK
820 830 840 850 860 870

cry1a-105.pe KYVHAKRLSDERNLLODSNFDINRQPERG--WGGSTGITIQGDDVFKENYVLTSGTFD
22002424 LVNQAKOLSKARIVLAGGNF-----EKGHEWLGREATMIANHELFGKHLLPPP--
880 890 900 910 920

cry1a-105.pe EGYPTYLYQKIDESKLFATRYQLRGYDVSQDLEIYSIRYNK--HETVNVPGTGSWLPL
22002424 TLTPSYAQKIDESKLSNTRYVSGFIAQSEHLEIVISRYGKEVHMDLDVPEEAL---
930 940 950 960 970 980

cry1a-105.pe SAQSPIGKCGENRCAPHLEWMPDLDCSDGKCAHSHHFSLDIDVGCTDLNEDLGYW
22002424 ---PISDESPPCKPATCQCP---SC-DGSG--PDSHFFSYSDVGSVQSDVNLGIE
990 1000 1010 1020 1030

cry1a-105.pe VIFKIKIQDGHARLGNLEFLEKPLVGEALARVKRAEKWRDKREKLEWETNIVYKEAKE
22002424 FGLRIAKPENGFAKISNLEIKEDRPLTDQEIKKIQKQKKAQFQEQAEVAATFQFTLD
1040 1050 1060 1070 1080 1090

cry1a-105.pe SVDALFVNSQDLOADNTMINAHADKRVHSIREAYLPELSVPGVNAALFELEGRIFF
22002424 QINALLYQEDWNG--SLHPVTYQHLSSAVLPTLPKORHWFMEDREGEHYGVTOQFOQALD
1100 1110 1120 1130 1140 1150

cry1a-105.pe TAFSLYDARNVIKNGDFNNGSNVKNVGHVDVEEQNNQSRSLVLPWEAEVSVQVRVCPFG
22002424 RGFOQIEEONLIHNGSFANGLTDMVTGDAQLT--IFEDPVDLELAHMDASVSQTIEMDF
1160 1170 1180 1190 1200 1210

cry1a-105.pe RG---YILRVTAKEGIGGCVTTHEIENNTDELKFSNCVEEIIYNNVTVCNDYTVNOE
22002424 EETETYLKRV-----RGKGKGVTVVQHGSEELTMTFTTTSFTTQGTFFEGDTVDVHVQ
1220 1230 1240 1250 1260

cry1a-105.pe EYGGAYTSNRNGVNEAPSVPADYASVVEEKSYYTDGRRENPCFNRGYDYDTPLPVGVYTK
22002424 SENNTFLVDSVELLIEVVEE
1270 1280

cry1a-105.pep
SW:8927990
8927990 description="PESTICIDIAL CRYSTAL PROTEIN CRY5AB (INSECTICIDAL
DELTA-ENDOTOXIN CRVA (B)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (142 KDA CRYSTAL
PROTEIN)." library=NA species="Bacillus thuringiensis serovar darmstadtensis"
source="swissprot_prot" version=NA type=PRI

SCORES Initl: 186 Initn: 484 Opt: 338 z-score: 376.1 E(): 1.2e-12
>SW:8927990
Initn: 484 Initl: 186 Opt: 338 Z-score: 376.1 expect(): 1.2e-12
```

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8927990	PIFQINFAS	TVDNNTG	VQANGVY	VVKSIAT	TDNSFT	VKIPAK	TINVHL	TNQGS	SDVFL
610	620	630	640	650	660				

cryla-105.pe TIVNINGQLPQRYRARIRYAST---NLRIYV---TVAGERIFAGQFN---KTMDTGDP

8927990
DRIEVPILESNTVTFNNSYTTGSANLIPALAPLWSTSSDKALTGSMITGRTPNSDD

670	680	690	700	710	720
570	580	590	590	590	600

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ccryla-105.pe LTFQSFYSYATINTAFTFPMSQSSFT-----VGADTFSGNEWIDRFELIP
      370      380      390      400
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8927990 ALLRFFKTYNDTQTIPGSGKDFNTLEIQDIVSIDFVGSLHGSDGSIKLDFTNNNS
730 740 750 760 770 780

610 620 630 640 650 660

8927890
GSGSXPSETEONDYENITTOVNAALFTSNTOBALATDVSDHDEFEVVKVALSDEVEKG
:: :: :: :: ||| ||| ||| ||| :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
VTAEAYNLERAKQAVNALFTSNQLGKRNVDYHIDQVSNLVLYLSDEFCLL

822/550: 790 800 810 820 830 840

crv1a-105.pe EKRELSKVKAHAKRLSDERNLLQDSNFKDINRQPERGWSGTGITIQGDDVFKENYVTL

8927990
EKKTLRFVNQAKRLSKARNLLVGGNFNDLID-----AWYGRNVTVSVNHELLKSDHVL

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CRY1A-105.pe SGTDFECYPTLYQKIDESKLKAFTRYQLRGYIEDSQDLEIYSIRYNAK-HETVNVPGTG

89077990
 99P GLSPSYIFQKVEESKLKRNTRYTVSGFIAHATDLEIVVSRYGQEIFKVVQVP-YG

790 800 810 820 830 840

8927990
EAFSSPC-
CIPHSTNGTLG
NPHEFSYIDVGALPVDI

980 990 1000

~~crýla-105.pe DLGVNTHPIKTOGCHAPSNLEFLSEKPAVGEALARVKRAEKKWRDRKLEWETNIVY~~

8927990
NPGIEGLKLVNFTGMAVRSNDE REDRPLANEINTEQVQRVARNRWTEYEKERAETSLI
1010 1000 1000 1000 1050 1050

1010 910 1020 920 1030 930 1040 940 1050 950 1060 960 1070 970 1080 980

ccryla-105.pe KEAKESVDALFVNSQYD-QDQADTNIAIMTA-ADCRVHSIREAYSPELSVPVGNAAIFE

8927990 QPVINRGLYDNGNWNGSIFSDISYQNDIAVLPLPKLRHWFMDRFSQQG---DIMA
1070 1080 1090 1100 1110 1120

960 970 980 990 1000 1010

city ia 100. pe
8927990
KFOGALNRVAOALEONTLLPHNGHETKDAANWTVEGAHOWLECKRLEKRLUPDSSVSO

1130 1140 1150 1160 1170 1180

1020 1030 1040 1050 1060 1070
cry1a-105.pe EVRVC---PGRGYILRVTAKEYGEGGCVTIHEIENN---TDELKFSNCVEEETYPNNK

[illegible]

Year	1190	1200	1210	1220	1230
1080	1090	1100	1110	1120	1130

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cryla-105.pe VTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEKSYTDGRRENPCFENRGYRD

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8927990 FESGKVTVTIISSEGEFLVDNIALVEAP-LPTDDONSEGNTASSTNSDTSMMNNQ
1240 1250 1260 1270 1280

cryla-105.pe YTELPVGYTKLEYFPEPTDKWIEIGETEGFIVDSVELLMEE
1140 1150 1160 1170

cryla-105.pep
NRAA:8927990

8927990 source="GENBANK_PROT" Pesticidal crystal protein crysAB (Insecticidal
delta-endotoxin CryVA(b)) (Crystalline entomocidal protoxin) (142 kDa crystal
protein)gi|142770|gb|AA67693.1| delta-endotoxin

SCORES Init1: 186 Initn: 484 Opt: 338 z-score: 376.1 E(): 1.2e-12
>NRAA:8927990 (1289 aa)
Initn: 484 Init1: 186 Opt: 338 z-score: 376.1 expect(): 1.2e-12
Smith-Waterman score: 725; 23.4% identity in 1263 aa overlap
(6-1105:45-1267)

cryla-105.pe
10 20 30
MDNNPNIECIPNCLSNPEVEVLGGERIET--GY
8927990 VLAYTPSPFLPDAGTQATPADLTAAYEQLLKNLEKINAGTYSKAIADVLKGFIDDTINY
20 30 40 50 60 70

cryla-105.pe -TPIDISLSLTOFLISE---FVPGAGFVLGLVDIIWIGIFGSPQMDAFLVQ---ISOLINQ
40 50 60 70 80
8927990 QTVVNLGSLIITLAVPEIGIFTFGLFFAALNKHNDAPPNNAKDIFEAKPAIOEMIDR
80 90 100 110 120 130

cryla-105.pe RI---BEFARNQAIISRLGSLNLYQIYAESFREWEA-DPTNPALREMRIRQFNQDNWNSALT
90 100 110 120 130 140
8927990 TLTADEQTLFNGEISGLQNLAAARYQSTMDIQSHGGFNKVDGLIKKFTDEVLNSFYT
140 150 160 170 180 190

cryla-105.pe TAIPLEAVONY-OVELLSV-YVQANLHLSVLRDVSFVGQRM---GFDAAITNSRYND
150 160 170 180 190
8927990 DRLPVITDNTADRTLLGLPYAILASMLMLRDIITKGTWDSKINTFTPDIAISFKID
200 210 220 230 240 250

cryla-105.pe LTRILIGNYTDHAVRWNTGLERWGP-DSGRDWIRYNQPRELITLVIDIVSLFPNYSRT
200 210 220 230 240 250
8927990 IKNNIKLYSKTIYDVFQKGLASYGTSPDLESFAKKQKVIEMTHICLDFARLFTFPDPL
260 270 280 290 300 310

cryla-105.pe YP-----IRTVSOLT---RIIYN--PVLENPDGSPFGSGAGI--
260 270 280
8927990 YPTGSGDISLQKTRILSPFPIRTADGLTLNNTSIDTSNPNYENGNGAFNPKERILK
320 330 340 350 360 370

cryla-105.pe -----EGSIRSPHL--MDIINSI--TIY-----TDARGEYWS---GHQIM-
290 300 310 320
8927990 QFKLYSWRAAQYGGGLQPYLMAIEVQDSVETRLGQLPADVDPAGNPNYVSDSNPLIQ
380 390 400 410 420 430

cryla-105.pe -----ASPVGSGPEFTFPLVGTWGNAAPOOR-----IVAQOGQVYRTLST-----
330 340 350 360
8927990

8927990 INMDTWKTPPOGASGWNINL-MRGSVSGLSFLQRDGTLSAGMGGGFADTIYSLPATHYL
440 450 460 470 480 490

cryla-105.pe --LYRPFN-----IGNNQLSVLD---GTEFAYGTSNLPASVYRKS--GT
370 380 390 400
8927990 SYLYGTPYQTSNDYSGHVGALVGSTPOEATLPIIIGQPDQGNVSTMGTFPEFKASYGTT
500 510 520 530 540 550

cryla-105.pe V-----DSLDETPPONNVPPROGFSHRLSHVSMERSGF-SNSSVSII-----RA
410 420 430 440 450
8927990 VVKEWINGANAVKLSFGQSIGIP-----ITNVTSGEYICRYASNDNINVFVNDTGGAN
560 570 580 590 600

cryla-105.pe PMFSWIHRSAEFNNIIASDSITQIPLVKAHTLQSGTTVVRGPGFTGDIILRTSGGPFAY
460 470 480 490 500 510
8927990 PIFQINFASVTVDNNTGVQGVVYVVKSIATTDNSFTVKIPAKTINVHLTQGGSDVFL
610 620 630 640 650 660

cryla-105.pe TIVNQQLPQRYRARIKYSTT---NLRIYV-----TVAGERIPAGQFN---KTMDTGD
520 530 540 550 560
8927990 DRIEFPILESNTVTFNNSYTTGSANLPAIAPLWSTSSDKALTGSMSTIGRTTTPNSDD
670 680 690 700 710 720

cryla-105.pe LTFQFSYATINTAFTFPMSQST-----VGADTFSSGNEVVIDREFLIP
570 580 590 600
8927990 ALIRFKNYDQTFPIPGSKQFTNTLIDQIVSIDIFVGSGLHSGDSISIKLDTNNNS
730 740 750 760 770 780

cryla-105.pe VTA---TLEAFNLEAKQAVNALETNTNQLKXNTVDYHIDQVSNLVYLSDFCLD
610 620 630 640 650 660
8927990 GSGSPKSTEQNDLENTTQVNALETNTQDALATDVSDHDIEEVVLKVDALSDEVFGK
790 800 810 820 830 840

cryla-105.pe EKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGSGSTGITQGGDDVFKENYTL
670 680 690 700 710 720
8927990 EKTILRFVNOAKRLSKARNLLVGGNFDNLD-----AWYGRNVVNVSNHELKSDHVL
850 860 870 880 890 900

cryla-105.pe SGTFDECYTYLYQKIDSKLAFTRYQYRGVIEDSOOLEIYSIRYNAK-HETVNVPGTG
730 740 750 760 770 780
8927990 PPP--GLSPYSIFQKVEESKLKXNTVTVSGFIAHTDLEIVSVRYGQEKKKVQVP-YG
910 920 930 940 950 960

cryla-105.pe SLNPISAQSPICKCEPNRCAPHLEWNPDLDCSDRGEKCAHSHHFLSDIDVGCTDLNE
790 800 810 820 830 840
8927990 EAFPLTSSGPV--C-----CIPHSTNSGTIG-----NPHFFSYSIDVGDVDT
970 980 990 1000

cryla-105.pe DLGWWIFIKITQDGHARLNLBELEKPLVGEALARYKRAEKWKRKREKLEWETNIYV
850 860 870 880 890 900
8927990 NPGIEFLRIVNPTQMARVSLNIREDRPLAANEIRQVQVARNWRTEYKEKRAEAVTSLI
1010 1020 1030 1040 1050 1060

cryla-105.pe KEAKESVDALFVNSOYD-OLQADNTIAMTHA-ADKRVHSIREAYLPESLVIPGNAALFE
910 920 930 940 950
8927990

800 810 820 830 840 850
 try1a-105.pe GEPNRCAPHLEWNPDLDCSDRGEKCAHSHHFLSDIDVGCTDLNEDLGWVVFIKITQD

ryla-105.pe L5DERNILLQDSFNKDNROPEFGWGSGTGITIQGGDDVFNKYVILSTFDECPYLYQ

9327991
LSRARNLLIGGSFENWD-----AWYKGRNVVTVSDHELKSDHVLPPP--GLSPSYIFQ
960 970 980 990 1000 1010

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cryla-105.pe 740 750 760 770 780 790
KIDSKLAFTRQLRGYIEDSDLEIYIRYNAK-HETVNVPGTSLWPSAOSPICK
8927991 1020 1030 1040 1050 1060
KVEESKLPNTRIVSGFIAHGKLEIVVSRYGOEVQKVVQVP-YGEAPLTSNGPV-C

cryla-105.pe 800 810 820 830 840 850
GEPNCAHLEWPDLDSCROGKCAHSHFSLDIDVCGCTDLNEDGVVVFIKITQD
8927991 1070 1080 1090 1100 1110
-----CPRSTSGTL-----GDP-----HFFSYSDVGALDQANPGEIEGURVNP

cryla-105.pe 860 870 880 890 900 910
GHARLGNLEFLEKPLVGEALARKVRAEKWRDKREKLEWETNIVVYKEAKESVDALFVNS
8927991 1120 1130 1140 1150 1160 1170
GMARVSNLEIREDRPLAANEIROVORVARNWRTEYERAEVTSLLIQPVINRGLYENG

cryla-105.pe 920 930 940 950 960 970
QVD-QLQADTNIAIHA-ADKRVHSIREAYLPELSVIPGNAIAIFEELEGRIFTASLYD
8927991 1180 1190 1200 1210 1220 1230
NNGSIRSDISYQNIADILVPLKLRHWFMSDRFSQG---DIMAKFGALNRAYAOLE

cryla-105.pe 980 990 1000 1010 1020 1030
ARNVKNKGDFNNGLSVWVKGHVDEEONNORSVLVVPWEAEVSOEVRV---CPGRGYI
8927991 1240 1250 1260 1270 1280 1290
QSTLLHNGHFTKDAANWTIEGDAHQITLEDGERVLRIDPDSSVSQMSQIEIENFNPDKYEN

cryla-105.pe 1040 1050 1060 1070 1080
LRVATYKGEYGEVCVTHIEENN---TDELFKSNCEVEEIIYFNNTVTCNDYTNQBEYG
8927991 1300 1310 1320 1330 1340
LVF---HQGEETVLEHGEETKYEIETHHFANFTTSQ-ROGLTFESKNKVTIISSED

cryla-105.pe 1090 1100 1110 1120 1130 1140
GAYTSRNGYNEAPSVADYASVYEEKSYTGRRNCPENRGYRDTPLFVGVTYKELE
8927991 1350 1360 1370 1380
GEFLVDNIALVEAP-LPTDDQNSEGTASSTNSDTSNNNQ

cryla-105.pe
SW:8927987

8927987 description="PESTICIDIAL CRYSTAL PROTEIN CRY5AC (INSECTICIDAL
DELTA-ENDOTOXIN CRYVA(C)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (135 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis" source="swissprot_prot"
version="NA type="PRT

SCORES Initl: 162 Initn: 449 Opt: 325 z-score: 361.7 E(): 7.5e-12
>>SW:8927987
initn: 449 initl: 162 opt: 325 z-score: 361.7 expect(): 7.5e-12
Smith-Waterman score: 765; 23.8% identity in 1212 aa overlap
(6-1105:45-1198)

cryla-105.pe 10 20 30
MDNNPINEICIPYNCISNPEVEVLGGERIE--TGY
8927987 VLAYTPPSFLPDAGTQATPADLTAYEQLKLNLEKGINAGTYSKAIADVLKGFIDDTINY
20 30 40 50 60 70 80
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cryla-105.pe 80 90 100 110 120 130
QYVNIIGLSLITLAVPEIGIFPFIIGLFAALNKHDPAPPNAKDIIFAMPAIQCEWIDR
8927987 140 150 160 170 180 190
TLTADQETFLNGELSGQLNLAARYOSTWDDIQSHGGFNKVDGSLGKIKFTDEVLSNGFYT

cryla-105.pe 200 210 220 230 240 250
YPIRT--VS-QUTREIYTN--PV-----LEN-FDGSFRGSAQIGESIRSHPLMDIL
8927987 260 270 280 290 300 310
IKNNIKLSKIYDVFOKGLASGVTPSDLESFAKKKXIEMITHCLDFARLFTFPDPL

cryla-105.pe 320 330 340 350 360 370
YPTGSGDISLOKTRILSPPIRTADGLTLNNTSIDTSMNPYENGANGAFPNPK-ERIL
8927987 380 390 400 410 420 430
KQKLYPWRAGQYGGLLQYLWAEVQDSVETR--LYGQLPAVDPAQPNYVSDSNP

cryla-105.pe 360 370 380 390 400 410
VYTLSSLTLYRRPNL-GIN-NOOLSVLDGTEFAVGTSSNLPSAVYRKSGTVDLSLEIPP
8927987 420 430 440 450 460 470
IIQINMDTWKTPGAGSGWNTNLMRGVSUGLSFLQDGTSLSGM--GGGFADTIYSLPA

cryla-105.pe 480 490 500 510 520 530
THYLSYLVGTQVTSNDYSGHVGAL-VGVSTPQ---EATLPNIIGOPDEQGNV---ST
8927987 540 550 560 570 580 590
MGFPPEKA---SYGGTVVK-EWJLNGANAKLSPGQSIGIPITNVT---KHNYQVACRYAS

cryla-105.pe 600 610 620 630 640 650
NSNPVFNVDTGGANIFQOINFASTVDNSWNGVEKNGVYV-VKSIKIVEIPAGSFYVH
8927987 660 670 680 690 700 710
V-INQSSDLFLDRIEFVFKIQFQCDNNNLHCDNNPVDTDCTFCVCCTSLTDCDNNP

cryla-105.pe 590 600
ADTFSSGNEVIDRFEIIP-----
8927987 V-INQSSDLFLDRIEFVFKIQFQCDNNNLHCDNNPVDTDCTFCVCCTSLTDCDNNP
660 670 680 690 700 710
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~~Product Characterization Center~~

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[illegible]

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

Monsanto Company

Final Report

Product Characterization Center

Study No. 06-01-62-04

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cryla-105.pe ITNLRIVTV---AGERIFAG-QFNKWTMDTGDPLTFOSFYATINTATFFPMSSQSTVIG 540 550 560 570 580 590
8927987 NSDNVFFNVDTGCAPIFOQINFASIVDSNMGVKEENGIVV-VKSIKIVIPAGSYFVH 600 610 620 630 640 650
cryla-105.pe ADTFSSGNEVYIDRFELIP----- 590
8927987 V-TNGSSDLFLDRIEFVKIQFCDDNNLHDCDNPVDTCTCCVCTSLTDCDCNPP 660 670 680 690 700 710
cryla-105.pe --VTATLEAEY-----NLERAQKAVNALFTSTNQLGKTNVTDYHIDOVSLVT 610 620 630 640 650
8927987 RGIDCTLCQVENQLPSFVLTDLRNITSQVGLFAPGTQNLQNIADHIEEVLKVD 720 730 740 750 760 770
cryla-105.pe YLSDFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINROPERGWGGSTGITIQGDD 660 670 680 690 700 710
8927987 ALSDEIFGNTKALKRLVNAQKRLSRAENLLIGGFENWD-----AWYKGRNVVTVSDHE 780 790 800 810 820
cryla-105.pe VFKENYVLTSTFDECYPTVLYOKIDESKKAFTRYOLRGYLEDSDLEIYSIERVNAK-H 720 730 740 750 760 770
8927987 LFKSDHVLPPP--GLSPSYIFQVKEESKLANTRYVSGFIHAHTDLEIVSVYQGEIK 830 840 850 860 870 880
cryla-105.pe ETVNVPTGSLWPLSAQSPIGKCGEPNCPAPHLEWNPDLDCSRDGEKCAHSHHFFSLDI 780 790 800 810 820 830
8927987 KVVQVP-YGEAFPLTSSGPV--C-----CIPHSTSNGLTG-----NPHFFSYSI 890 900 910 920
cryla-105.pe DVGCTDLEDIGVWVIFKIKTODGHARLGNLEFLEKPLVGEALARYKRAKKWRKREK 840 850 860 870 880 890
8927987 DVGALDVTNPGIEFGLRVNFTGMARVSNLEIREDRPLAANEIRQVQVARNWRTEYK 930 940 950 960 970 980
cryla-105.pe LEWETNIVYKEAKESVDALFVNSQYD-OLQADTNIAHIA-ADKRVHSIRAYIPELSVI 900 910 920 930 940 950
8927987 ERAEVTSLIQVINRINGLYENENWNGSIRSDISYQNIIDAIVLPTLRLRHWFMDSRFSF 990 1000 1010 1020 1030 1040
cryla-105.pe FGVNNAIFEELGRIATFSLDARNVIRKGDFFNGLSCWNVKGHVDEEQNORSVLV 960 970 980 990 1000 1010
8927987 QG---DIMAKFQALNARYAQLQESTLLHGHFTKDAANWTIEGDAHQITLEDGRVRL 1050 1060 1070 1080 1090 1100
cryla-105.pe PEWEAEISQEVVRV---CPGRGYILRVAYKEGYEGCVIHIEN-----NTDELKSNVCV 1020 1030 1040 1050 1060
8927987 PDWSSVSQMIENIENPNPKYNLVF---HQQEGGVTLIEHGEETKYIETHHHFANFT 1110 1120 1130 1140 1150
cryla-105.pe EEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGVNEAPSPADYVSEKSYTDGRREN 1070 1080 1090 1100 1110 1120
8927987 TSQ-RQGLTRESKNVTVTISSEDEGEFLVDNALVEAP-LPTDDQNSEGNATFSTNSDTSM 1130 1140 1150

cryla-105.pe CEFNRYGRDYTPLVGVVTKLEYFPETDKVNIIEGTEGTFIVDSVELLMEE 1130 1140 1150 1160 1170 1180 1190 1200 1210
8927987 NNNQ 1220
cryla-105.pep
NRAA:8928013
8928013 source="GENBANK_PROT" Pesticidal crystal protein cry25Aa (Insecticidal delta-endotoxin CryXXVA(a)) (Crystalline entomocidal protoxin) (76 kDa crystal protein) (Insecticidal protein Jeg74)gi|3668335|gb|AAC61892.1| insecticidal protein Jeg74 [Bacillus thuringiensis serovar jegathesan]
SCORES Init1: 165 Initn: 385 Opt: 308 z-score: 346.2 E(): 5.4e-11
>>NRAA:8928013
initn: 385 init1: 165 opt: 308 z-score: 346.2 expect(): 5.4e-11
Smith-Waterman score: 571; 26.9% identity in 620 aa overlap
(52-628:76-673)
cryla-105.pe EVLGERIETGYTPIDISLSLTQFLSEFVPGAGFVLGLVDIHWGIFGQSOMDAF---LV 30 40 50 60 70
8928013 NECDITPSIFGTGLVGLASIVISTINLATSPISIGDAFALVSSI-GEYWPETKTSFPLSVA 50 60 70 80 90 100
cryla-105.pe QIEQLINQRIEEFARNQALSRLGSLNYQ-IYAESFREWEAD--PTNPA----LREEMR 80 90 100 110 120 130
8928013 DVNRLIREALDQNAIRATKGNKFMMDTNTVYLNKLQMDYTRIPANPGDSOLREAR 110 120 130 140 150 160
cryla-105.pe IQFNDMSALTTAIP-LEAVQNYQVPLISVYVQANLHLSVLSDVSVFGQWGFDP---AA 140 150 160 170 180
8928013 RSLIEIERDFKALAGEFAEGSQVLLPIYQAANLHLLILDKDAWQFTDLGLIRPVGV 170 180 190 200 210 220
cryla-105.pe TINSRYND-----LTRLIGNYTDHAVRWNTGLERVW--GPDSRDWIRYNQFRRELTLT 190 200 210 220 230
8928013 PITTSADPESEFLLR-IKKYTDHCISYDDGLAKIRSGSDGETWFEFNKFRREMTLT 230 240 250 260 270 280
cryla-105.pe VLDIVSLFPNDTSRTPIKTVSQLTREIYNPVL-----ENFDGSRGSAQIGESIRSPH 240 250 260 270 280 290
8928013 VLDLVALYPTNKLPIPTQELSRVYTDVPGCFGNKRSKDFISRLNFDYLENRLRPR 290 300 310 320 330 340
cryla-105.pe L-MDLINSITIIY---TDAHRGEYWSG-HQIWASPVGSGPEFTFPLYGTGNAAPQOR 300 310 320 330 340
8928013 EFPNVLNSVQLFASVTSNNGNEVLRGNLKNIM-----FEGWATASRGDGVITGTTFST 350 360 370 380 390
cryla-105.pe IVAIQGQGVRTLSLSLYRRPNI-GINNQLSVLDGTFE-AYGTSSNLPSAVYKSGTV 350 360 370 380 390 400
8928013 MDWSYGVYPRKHYAEITSRQALPLNNSIHVIGIDSFRALFGPGGODHTFSLPG-- 400 410 420 430 440 450

[illegible]

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cry1a-105.pe 640 650 660 670 680 690
: : : : :
: : : : :
SYEELAKVSSYQINQVALKWMALSDKFC-EEKRLRLRYKANKQLENNLLVGGN-
750 760 770 780 790

cry1a-105.pe 700 710 720 730 740
DINRQPERGGSGTGITIOGGDDVPEKNYVTL--SGTDECYFTYLYQKIDSKLKAFT
: : : : :
: : : : :
---ETTONWLVGNAYINYSDFNGFNYSLOPASGFT---SYAYQKIDESTLKPYT
800 810 820 830 840 850

cry1a-105.pe 750 760 770 790 800
RYQLRGVIEDSODLEIYSIRYNKXHTV-NVPGTSLWPLSAQSPGKCGEPRNRCAPHLE
: : : : :
: : : : :
RYKVSFGTSGNQVEVLISRYGKEIDKLNVVAGPL-PITADASI-TC-----CAPEID
860 870 880 890 900

cry1a-105.pe 810 820 830 840 850 860
WNPDDLCSRDGKCAHHSHFSLDIDVGCTDINELDGMWIFIKITQDGHARLGNLEFL
: : : : :
: : : : :
-----QCDDGQS---DSHFNTSIDVGAHPELNPGIEGLKIVGNSGYITISNLEII
910 920 930 940 950

cry1a-105.pe 870 880 890 900 910 920
EEKPLVGEALARYKRAEKKWRDKREKLEWETNI--VYKEAKESVDALFVNSQDQLQADT
: : : : :
: : : : :
EERPLTMEIQAVNRKDKW--KREKLLECAVSSELLQPIINQIDSLFKDANW-----Y
960 970 980 990 1000

cry1a-105.pe 930 940 950 960 970
NLMTHAADKRVHSIREAYLPEL--SVIPGVNAAIFEELEGRIETAFSLDYARNVLIK
: : : : :
: : : : :
NDILPHYTYQTLANIIVPDLPKLKHWTIDHLPGEVHEIQWKKEALXHAFTOLDEKNLH
1010 1020 1030 1040 1050 1060

cry1a-105.pe 980 990 1000 1010 1020 1030
NGDFNGLSCWNKYGHDVVEEQNRQSVLVVPEWEAEYSQEVRC---PGRGYILRVLTAY
: : : : :
: : : : :
NGHFATNLIDWQVEGDARKMKVLNNALALQSNWSDSVSQSIDILEDFEDKAYKLRV--Y
1070 1080 1090 1100 1110 1120

cry1a-105.pe 1040 1050 1060 1070 1080 1090
KEGVGECVTIHEIENNTDELKFSNCVBEISYPNNTVTINDYTNQGEYGGAYTSNRRGY
: : : : :
: : : : :
AQSGST-----IQFGNCDEAAIQFNNTNSFVYKEKIIYFDTPTPSINLHQSEG
1130 1140 1150 1160

cry1a-105.pe 1100 1110 1120 1130 1140 1150
NEARVPADYAVYEEKSYTDGRENPCFNRCGRDYTFLPVGVYKVEYFETDKWVI
: : : : :
: : : : :
SEFVVSSIDLVELSDDE
1170 1180

cry1a-105.pep
SW:8928020

```

8928020 description="PESTICIDIAL CRYSTAL PROTEIN CRV14AA (INSECTICIDAL DELTA-ENDOTOXIN CRX14A(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (132 KDA CRYSTAL PROTEIN)." library="NA species="Bacillus thuringiensis serovar sotto" source="swissprot prot" version=NA type=PRT

SCORES Init1: 155 Initn: 558 Opt: 308 z-score: 342.5 E(): 8.7e-11

>>8:8928020 (1186 aa)
initia: 148 opt: 108 2-score: 342.5 expect(): 8.7e-11
Smith-Waterman score: 75; 34.9% identity in 1144 aa overlap
(46-1070 vs 1443)

cry1a-105.pe LNPFEVFGGERIPGTHNDISLSLQFLSEFVGAGFVGLVDIWIIGFSGQ---
50 50 60 70
8928020 SFLSLAQGSASGGAFFNLTLQSGISLAGEFVGCGTFVAPVIMVIGLPHKNTK
50 60 70 80 90 100
cry1a-105.pe WDAF-LVO-----TEOLINGNEEARNOASRLSTSNLYQVAF--REWE--ADPT
110 120 130 140 150 160 170
8928020 AUTENLIKLIIDEEIOKQINKALIDQSRNNTSFLESFIDGATVSNADADAGWSTVDTT
110 120 130 140 150 160 170
cry1a-105.pe N-----PALREEMRI--QFNDMSALTTAIPFAVQVQVLLSVYVQANHLHSLRQV
180 190 200 210 220
8928020 NROQKPTTSDYLVNWKGFDSADSSITINQIMNGFVDAAPFVIGACVRSINSGY
170 180 190 200 210 220
cry1a-105.pe SVEGQW-----GDDAATINSFYNDLTEL-----IGNYTHAVRWY--NIGLENWGPD
230 240 250 260 270 280
8928020 IFPCNSIDAWGFSTNDANTOKANLARTKLWRTTINEYTORVWVKVDSKNMPTT-GTN
230 240 250 260 270 280
cry1a-105.pe SRDWIRYQFRELTLVLDIVSLFPNYSRTYPIRTVSQLTREITNV--LENFGDSF
290 300 310 320 330 340
8928020 KFSVDAYVYVKGMTLVLDVMAVMSLVPNDYTSOTAIQTRVTFESNVWGOEGTGTL
290 300 310 320 330 340
cry1a-105.pe RGAQIGESIRSPHLM---DILNSITITDAHGEYVWGHQIMASPVGSGPEFTFPL
350 360 370 380 390
8928020 K-IYNTFDSLSYQHSIFPNNNVNLISFYVDELONL-----ELAVYTPKGGSG--YAYP-
350 360 370 380 390
cry1a-105.pe YGTFILNAN-----SNKYGDNDPTGKLNKODGPIQOQINAAQNSKYLDG-ETINGIGA
400 410 420 430 440
8928020 YGTFILNAN-----SNKYGDNDPTGKLNKODGPIQOQINAAQNSKYLDG-ETINGIGA
400 410 420 430 440
cry1a-105.pe NLP-----SAV---YRKSGTVDLSIDE-IPPQNNN--VPPQCGFSHRLSHVSMFRSGFS
450 460 470 480 490 500
8928020 SLPGYCTTGCSATQPSCTSTANSYKASCPNSDINQINKALYAFQTQVWKGSTGKGLVL
450 460 470 480 490 500
cry1a-105.pe NSSVSLIRAPMFSIHRSAEFNNIIASDSITQIPLVKAHTLQSGTIVRGPGFTGDLRL
510 520 530 540 550 560
8928020 ASLVPLDLNPKNVFGEILSDTNVVI-----LKGIPAEKGYFPFNARPTVVKWEINGASAVP
510 520 530 540 550 560
cry1a-105.pe RTSGGPFATVINGQLPQRYBARIRYA---STTNLRIVTVVAGERIFAGF-----N
570 580 590 600
8928020 FYSGNLFMTATNLTAT---QYKIRIRYANPNSDTQIGVLITQNGSQISNSNLTYSTTD
570 580 590 600 610 620

cry1a-105.pe KTWMDGDELTFQSFSEYATINTAFTFMQSQSFTVGADTF--SSGNE-VYIDRFELIP-
630 640 650 660 670 680
8928020 SSMSSNLQNVVTVGNGVNTLLDLYSTNVLTSGDITLKLGTGNGKQKFIQRIEFTMP
630 640 650 660 670 680
cry1a-105.pe -----VTAT-----LEAYNLERAQKAVNALFTST
690 700 710 720 730 740
8928020 VPAPTNTNNNGDNGNNPPHGGCAIAGTQOLCGPPKEFQVSDLEKITTVQVYMLFKSS
690 700 710 720 730 740
cry1a-105.pe NQLGKTNVTDYHIDQVSNLVTVLSDE-FCLEKRELSKVKHAKRLSDERNLLQDSNFK
750 760 770 780 790
8928020 SYEELALVUSSYQIQINQVAKVMAWSDEKFC-EKRLRLKLVNFANQLLEARNLLVGNF-
750 760 770 780 790
cry1a-105.pe DINRQPERGSGSTGITIOGDDVFKENYVTL---SGTFDECYPTYLYQKIDESKLKRAFT
800 810 820 830 840 850
8928020 ---ETTONWLVGTNAINYDSFLFNGLYLSLQPASGFT---SVAYQKIDESTLKPYT
800 810 820 830 840 850
cry1a-105.pe RYOLRCYIEDSQDLEIYSIRYNAKHETV-NVPGTGLMPLSAQSPICKGCEPNRCAPHLE
860 870 880 890 900
8928020 RYKVSFGFGQSNQVELLIISRYGKEIDKILNVPYAGPL-PIITADASI-TC-----CAPEID
860 870 880 890 900
cry1a-105.pe WPLDPCSCROGEXCAHSHHFLDIDVCGTDLNEDLGVMVFIKIKTQDGHARLGNLEFL
910 920 930 940 950
8928020 ---QDSGQS---DSHFNYSIDVGAHPNLNPGIEIGLKIVQSGNYITTSNLEII
910 920 930 940 950
cry1a-105.pe EEAIVGGAARVRKAKKRDREKLEWETNI--VYKEAKESVDALFVNSQYDQLOQADT
960 970 980 990 1000
8928020 FERSJTEMEIOAVVADQKW-KRKLLECASVSELLQPIINOISLFDKDNW-----Y
960 970 980 990 1000
cry1a-105.pe NIAMIHADSVIRKIRAYAPEL---SVAGUNDAIFEELESGRIFATFSLYDARNVIK
1010 1020 1030 1040 1050 1060
8928020 NDILPHVITQTKNTVYPSKPKLNADIDNPGETHYTESCKMEKALKHAFTOLDKKNLIH
1010 1020 1030 1040 1050 1060
cry1a-105.pe NGDFNGLSCWNVKGVHDVEEQNQSVAIVPEVEVSRVVC--PQGYILRVYAT
1070 1080 1090 1100 1110 1120
8928020 NGHFATNLIDMQVEGDARMKVLNNAALQSSNQSVAIDILEFDEDAVYQV--Y
1070 1080 1090 1100 1110 1120
cry1a-105.pe KEGYGGCVTHIEIENNTDKLSCVBEETIYPNNVTVCNTVVOEEYGVYVSGNNGY
1130 1140 1150 1160
8928020 AQSGGT-----IQFGNCEDAIQFNTNSFVYKKEIITFDTSSINLHISEF
1130 1140 1150 1160
cry1a-105.pe NEAPSVADYASVVEEKSYYDGRNPNCFNGYRDYTLFVGVYVTKLEYEPEDKVM
1170 1180
8928020 SEFVSSIDLVELSDDE
1170 1180

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      430 440 450 460 470 480
cry1a-105.pe URLHGWMPGSGNSVSYTRAPMFWIHSRAEFNNIAS-DSITOLPLVKAHTI-
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
8928021 -VLPIETVYKGTGNLGVISA---YVPMELVPENVICGNADTKLPLTQKGGPFPEK

```

cry1a-105.pe	490	500	510	520	530	540	550	560
8928021	570	580	590	600	610	620	630	640
cry1a-105.pe	540	550	560	570	580	590	600	610
8928021	630	640	650	660	670	680	690	700
cry1a-105.pe	600	610	620	630	640	650	660	670
8928021	690	700	710	720	730	740	750	760
cry1a-105.pe	620	630	640	650	660	670	680	690
8928021	750	760	770	780	790	800	810	820
cry1a-105.pe	660	670	680	690	700	710	720	730
8928021	810	820	830	840	850	860	870	880
cry1a-105.pe	720	730	740	750	760	770	780	790
8928021	860	870	880	890	900	910	920	930
cry1a-105.pe	780	790	800	810	820	830	840	850
8928021	920	930	940	950	960	970	980	990
cry1a-105.pe	840	850	860	870	880	890	900	910
8928021	960	970	980	990	1000	1010	1020	1030
cry1a-105.pe	900	910	920	930	940	950	960	970
8928021	1020	1030	1040	1050	1060	1070	1080	1090
cry1a-105.pe	960	970	980	990	1000	1010	1020	1030
8928021	1070	1080	1090	1100	1110	1120	1130	1140
cry1a-105.pe	1020	1030	1040	1050	1060	1070	1080	1090
8928021	1100	1110	1120	1130	1140	1150	1160	1170
cry1a-105.pe	1060	1070	1080	1090	1100	1110	1120	1130
8928021	1140	1150	1160	1170	1180	1190	1200	1210

cryla-105.pe 11130 11140 11150 11160 11170 11180
1088 1090 1100 1110 1120
cryla-105.pe 11130 11140 11150 11160 11170 11180
1088 1090 1100 1110 1120
8928021 11130 11140 11150 11160 11170 11180
1088 1090 1100 1110 1120
cryla-105.pe 11130 11140 11150 11160 11170 11180
1088 1090 1100 1110 1120
8928021 11130 11140 11150 11160 11170 11180
1088 1090 1100 1110 1120

cryla-105.pe 11130 11140 11150 11160 11170 11180
1088 1090 1100 1110 1120
8928021 11130 11140 11150 11160 11170 11180
1088 1090 1100 1110 1120

8928021 NNNQ

cryla-105.pep

SW:8928021

8928021 description="PESTICIDIAL CRYSTAL PROTEIN CRISBA (INSECTICIDAL
DELTA-ENDOTOXIN CRYB(A)) (CRYSTALLINE ENTOMOCIDAL PROTEIN) 440 KDA CRYSTAL
PROTEIN." library="NA species="Bacillus thuringiensis" source="spisport prot"
version="NA type="PRT

SCORES Initl: 167 Initn: 509 Opt: 293 z-score: 325.2 E(1) 8.1e-10
>>SW:8928021
initn: 509 initl: 167 opt: 293 z-score: 325.2 expect(1): 8.1e-10
Smith-Waterman score: 693; 23.3% identity in 1215 aa overlap
(39-1108:71-1226)

cryla-105.pe 110 20 30 40 50 60
EGIPNCLSNPEVEVLGGERIETGTPIDISLSLQFLSEFVPGA---GFVLGLVDII
8928021 110 20 30 40 50 60
EWGKTGQKLFEDHLTIAMNLYKGLDYFALTKASISLIGFIPGAEAAPFINMFVDFV

cryla-105.pe 110 20 30 40 50 60
WG-IEGSPQ-----WDAFLVQIEQLINQRIEF---ARNQAISELEGLNLVQ---
8928021 110 20 30 40 50 60
WPKLFANTEGKQQLFNALMDAVNKNVNDKFLSYNLSTLNTKTEGLQNLGLFQNAIQV

cryla-105.pe 110 20 30 40 50 60
-IYAESFRE-----WEADPTNPAL--REEM-RI--QFNDMNSALITAIPLF-----A
8928021 110 20 30 40 50 60
AICQGSTPERVFNQDCTPCNPNQPKDDLDVARSRTANSQTOHLPEKPNWSDENS

cryla-105.pe 110 20 30 40 50 60
VPL-LSVYVQANLHLSVLRDVSFQCRWGF-DAATINSRYNDLTILIGNYT
8928021 110 20 30 40 50 60
TOEFRTISVELTLPMTTATLHLLLYEGYIEFTMTKNWFNEQYLNKLKVELQQLHSYS

cryla-105.pe 110 20 30 40 50 60
DHAVERWNTGLERWVGDSRDIMRNQFRRELTITLVDIVSLFVNDSTYPIRTVSQLT
8928021 110 20 30 40 50 60
EIVRTSFLQFLTLNNKSSVNAVRNMTVNCILDIATWFTFDHNVHQSGKLDLT

cryla-105.pe 110 20 30 40 50 60
PVLNFDGSRFGSAQIGSIRSPH-LMDILNLSITITVDAHGEYWSG--
8928021 110 20 30 40 50 60
RIILSDTAGPIEEYTTGD---KTSGEHSNITPNILDTSPPTYQHSFVSDSVISRKE

cryla-105.pe 320 330 340 350 360 370
-HQIMASVPGSGPEFFPLYGTMGNAAPQORIVVAQLGGVYRTLSSTL---YERPFNI
8928021 320 330 340 350 360 370
LAQLODIATYSNNNSNCHP-YGLRLSYTDGSDYDQNDQDFTTSNNYCHNSYTABITL

cryla-105.pe 320 330 340 350 360 370
GINNQOLSVDGTGFAVGTSSNLPNAVYKSGTV--DS-LDEI-PPQN--NNVPPRGFS
8928021 320 330 340 350 360 370
-NARHLNAGKS--LONVESLVSTVANGSGSCICDAMINYLRRPPTSKNESRPDQKIN

cryla-105.pe 320 330 340 350 360 370
HRLSHVSMFRSGFSNVSSTIRAPMFSMIHRSAEFNMIAS-DSITOLPLVKAHTL---
8928021 320 330 340 350 360 370
-VLYPITETVNGTGGNGLVISA---YVPMELVPENVIGDUNADTKLPLTLQKGFPEK

cryla-105.pe 320 330 340 350 360 370
-QSGTIVVPGFTGGDILRTSGGPAYTIIVNINGQLPQRYRARIYASTTNLR
8928021 320 330 340 350 360 370
YGEYNNRIGISLVR-EWINGNNAVKLSNSQSVGIQITN---QTKQYIEIRCYASKGDNN

cryla-105.pe 320 330 340 350 360 370
IYVTVG-GERIFAG--QFNKMTDGTDLTFOFSFYATINTAFTFPMSSQSSFTVGADTFSS
8928021 320 330 340 350 360 370
VFNVDLSNFRNRSISFSGSTESSVVGVGNGKYYI-LKSITIVPEPAGSFVHI--TNQG

cryla-105.pe 320 330 340 350 360 370
GNNYVIRFELIP-----VTATLAEYN-----
8928021 320 330 340 350 360 370
SSDLFLDAIEHPKIQFCDNNNLCDDNPNVDTCFCVCTSLTDCDNNRPGDCT

cryla-105.pe 320 330 340 350 360 370
-DRAKAVNALFTSNOLGKNTVDYHIDQVSNLTVLSDEF
8928021 320 330 340 350 360 370
LDCQVNLQPSFVYVLTQNTITQNVAVASSEHDTLATDVSDEIEEVLKVDALSCEV

cryla-105.pe 320 330 340 350 360 370
CLDEKRELSERKHAELSDKALSSNFNDNRO-ERGWSGTITIGQDDVFKENY
8928021 320 330 340 350 360 370
FGKEKALKRLVNTKESSEENLLIGQNTID---ANRGRNVNVSDHELFKSDH

cryla-105.pe 320 330 340 350 360 370
VTLSTDFECPTLYOKIDESKLPARYRGYINQD-EIYSIRNAN-HETVNVVP
8928021 320 330 340 350 360 370
VLLPPP--TLYSSYMFQKVEESKLANTRYTVSGFAHREDLEIVVSGQEVAKVQVP

cryla-105.pe 320 330 340 350 360 370
GTGSLWPLSAGSPGKCGEPNRCAPHEWNFDLDCRCRGERGRHSHFSLTSTDT
8928021 320 330 340 350 360 370
-YGEAPLITSRGAI--C---CPPR-----STSNKPA--DPIEFSSASIDSL

cryla-105.pe 320 330 340 350 360 370
LNEDLGVWVIFKIKTOGHARLGNLEFEEPLVGEALAFVRAEKWRDKREKLEWEN
8928021 320 330 340 350 360 370
VEANFGIELGRIVERTCGWARVSNLEIEDPFLAKNELRNVOEAAARNWRTAYDQERAEVT

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[illegible]

31872007 source="GENBANK_PROT" crystal delta-endotoxin Cry2ab-HB [Bacillus thuringiensis]

SCORES Init1: 128 Initn: 128 Opt: 288 z-score: 323.9 E(): 9.5e-10
>NRAA:31872007
Initn: 128 Init1: 128 opt: 288 z-score: 323.9 expect(): 9.5e-10
Smith-Waterman score: 294; 21.2% identity in 600 aa overlap
(41-610:56-630)

cry1a-105.pe IPYCNLSNEVEVLGGERIETGTPIDISLSTOFLSER--VPGAGFVLGLVDIINGIF
31872007 FQKSLDITVQKEMTEKNNHSLYLDPIVGTVASFLLKKVGSVGVKRLSELRLNLIFFSG
70 80 90 100 110 120 130 140
cry1a-105.pe GPSQWDAFLVQEQINORIEEFARNQAIISRLGSLNLYQIYAESFREWEADPTNP---A
31872007 STNLQDILRETEKFLNRLNTDTLARVNAELTGL---QANVEEFNRQVDNLFNPNNA
90 100 110 120 130 140
cry1a-105.pe LREEMRIQDNMSALTATPLFAVQNYQVPLLSVYQAAHLHSLVLDVSVFGORGF
31872007 VPLSITSSVNTMOQLFNRPLQFQOMQGYQLLLPLFAQAAHLHSLFIRVDILNADWGIS
130 140 150 160 170 180 190 200
cry1a-105.pe ANINSRYNDLTRIGNYTDHVRNVTGLERWGPDSR--DWIRYNQFRRLTITVLDI
31872007 AATRLTYDYLNRVTRDYSNYCINTYQAFR--GLNTRLHDM---EERTYMFNLVFEY
190 200 210 220 230 240 250
cry1a-105.pe VSEFPHYDSRTPIRTVSQLTREIYTNVLENFDFGSPRGAQIEGSIIRSPHMDIINSI
31872007 VSIWLSFYQSLVSSGANL---YASGSGPQOQSTQSDWPFYSLFQVNSNYLNGF
250 260 270 280 290 300 310
cry1a-105.pe T-----IYDAHRGEYWSGHQIMASPVGSGPEFTFPLYG--TMGNAAPQQRIVAAQ
31872007 SGARLSNTPFNIGLPSSTTHLHILHIVNYSGLSS---GDIGASPFNQFNCSF---
320 330 340 350 360
cry1a-105.pe VYTLSSITLYRRFPNIGNQOQ--SYLDGTEFATGTTNLPFSANWRKSTVDSLEIPPO
31872007 FLPELLTPFVRSWLDSSDREGVATVNTQTSFETTLRLSGAFTARONSNRPDYFIR
370 380 390 400 410 420
cry1a-105.pe N-NVNP--PROCFSHRLSHVSMRSGFSNSSV-SIIRAPMFSWIHR---SAEFNNII-
31872007 NISGVLVVRNEDRLRLHYNGIRNIAISPSGTPGGRAYMVSVNNTNINIAHAFSSSMI
420 430 440 450 460 470 480
cry1a-105.pe -IASDSITQIPLVKAHTLQSGT---TVVRGPGFTG-GDLIRTSGGPFATVINGQUPQ
31872007 HLAENDYTGFTISPIHATQVNNQTRTFISEKFGNGGSLRFEQSNNTARYTLRNGEN-
490 500 510 520 530 540 550
cry1a-105.pe RYRARIYASTTNLRIVTVVAGERIFAGQFNKMTDGTPLTFQSFYATINTAFTFPMNQ
560 570 580 590 600 610 620 630 640 650

31872007 source="GENBANK_PROT" crystal delta-endotoxin Cry2ab-HB [Bacillus thuringiensis]

SCORES Init1: 128 Initn: 128 Opt: 288 z-score: 323.9 E(): 9.5e-10
>NRAA:31872007
Initn: 128 Init1: 128 opt: 288 z-score: 323.9 expect(): 9.5e-10
Smith-Waterman score: 294; 21.2% identity in 600 aa overlap
(41-610:56-630)

cry1a-105.pe IPYCNLSNEVEVLGGERIETGTPIDISLSTOFLSER--VPGAGFVLGLVDIINGIF
31872007 FQKSLDITVQKEMTEKNNHSLYLDPIVGTVASFLLKKVGSVGVKRLSELRLNLIFFSG
70 80 90 100 110 120 130 140
cry1a-105.pe GPSQWDAFLVQEQINORIEEFARNQAIISRLGSLNLYQIYAESFREWEADPTNP---A
31872007 STNLQDILRETEKFLNRLNTDTLARVNAELTGL---QANVEEFNRQVDNLFNPNNA
90 100 110 120 130 140
cry1a-105.pe LREEMRIQDNMSALTATPLFAVQNYQVPLLSVYQAAHLHSLVLDVSVFGORGF
31872007 VPLSITSSVNTMOQLFNRPLQFQOMQGYQLLLPLFAQAAHLHSLFIRVDILNADWGIS
130 140 150 160 170 180 190 200
cry1a-105.pe ANINSRYNDLTRIGNYTDHVRNVTGLERWGPDSR--DWIRYNQFRRLTITVLDI
31872007 AATRLTYDYLNRVTRDYSNYCINTYQAFR--GLNTRLHDM---EERTYMFNLVFEY
190 200 210 220 230 240 250
cry1a-105.pe VSEFPHYDSRTPIRTVSQLTREIYTNVLENFDFGSPRGAQIEGSIIRSPHMDIINSI
31872007 VSIWLSFYQSLVSSGANL---YASGSGPQOQSTQSDWPFYSLFQVNSNYLNGF
250 260 270 280 290 300 310
cry1a-105.pe T-----IYDAHRGEYWSGHQIMASPVGSGPEFTFPLYG--TMGNAAPQQRIVAAQ
31872007 SGARLSNTPFNIGLPSSTTHLHILHIVNYSGLSS---GDIGASPFNQFNCSF---
320 330 340 350 360
cry1a-105.pe VYTLSSITLYRRFPNIGNQOQ--SYLDGTEFATGTTNLPFSANWRKSTVDSLEIPPO
31872007 FLPELLTPFVRSWLDSSDREGVATVNTQTSFETTLRLSGAFTARONSNRPDYFIR
370 380 390 400 410 420
cry1a-105.pe N-NVNP--PROCFSHRLSHVSMRSGFSNSSV-SIIRAPMFSWIHR---SAEFNNII-
31872007 NISGVLVVRNEDRLRLHYNGIRNIAISPSGTPGGRAYMVSVNNTNINIAHAFSSSMI
420 430 440 450 460 470 480
cry1a-105.pe -IASDSITQIPLVKAHTLQSGT---TVVRGPGFTG-GDLIRTSGGPFATVINGQUPQ
31872007 HLAENDYTGFTISPIHATQVNNQTRTFISEKFGNGGSLRFEQSNNTARYTLRNGEN-
490 500 510 520 530 540 550
cry1a-105.pe RYRARIYASTTNLRIVTVVAGERIFAGQFNKMTDGTPLTFQSFYATINTAFTFPMNQ
560 570 580 590 600 610 620 630 640 650

31872007 SYNLVRSSIGNSITRVING-RVYATATWNTTNDGVNDGARFSDINIGNVVASSN
550 560 570 580 590

cryla-105.pe SSFTVGAD-TFSSGNEVYIDRFELIPVATLEAYNLERAQAKAVNAFLTSTNQLGKLTNV
590 600 610 620 630 640

31872007 SDVPLDINVTLSGTQFDLMIMLVPTNISPLY
610 620 630

cryla-105.pep
NRAA:4239730

4239730 source="GENBANK_PROT" Cry2Aa protein [Bacillus thuringiensis]

SCORES Init1: 163 Initn: 163 Opt: 284 Z-score: 319.4 E(): 1.7e-09
>NRAA:4239730
Initn: 163 Init1: 163 Opt: 284 Z-score: 319.4 expect(): 1.7e-09
Smith-Waterman score: 285; 21.3% identity in 597 aa overlap
(41-606:56-626)

cryla-105.pe IPYNCLSNPEVEVLGERIETGYTPIDISLSLQFLLESFVPGAGFVLG--LVDIIWIGF
30 40 50 60 70 80

4239730 FEHKSLOTIQKEMEWRRDHSLVAPVGVTVSSFLKK---VGSLLIGRIILSEILWGI
30 40 50 60 70 80

cryla-105.pe GPSQ-----WDAFIVQIEQLINRIEEFARNQAISRLGLESLNYIYAESFREWEADPTNP
70 80 90 100 110 120 130 140

4239730 PFSGSTNLMQDILRETEQFLNRLTDTLARNVAELIGLOANREFNQVDNFLNPOTNP
90 100 110 120 130 140

cryla-105.pe ALREEMRIQNDNNNSALITAPLFAVQNYVPLSVYQAAHLSLVLRDVSVFQGRGWF
130 140 150 160 170 180 190 200

4239730 A-PLSITTSVNTMQQLFNRLFPQIQGYQLLLPLFAQAANMHLSFIRDVLINADWGI
150 160 170 180 190 200

cryla-105.pe DAATINRGYNDLTRLIGNYTDHAVRWNTGLERVMGDSR--DWIRYNQFRRELTLVLD
190 200 210 220 230 240

4239730 SAAITRTVDYLENTYRDSYNYCINTQTAFR---GLNTRLHML---EFTYMFLENLWFE
210 220 230 240 250

cryla-105.pe IVSLFPNYSRTYPIRTVYSQLTREIYTNFVLENFDGSPRGAQIEGIRSPLHMDILNS
250 260 270 280 290 300

4239730 YVSTWSLFKYQSLMVSNGANL---YASSGSGPQQTSTAQNWFFLYSLFQVNSNYLLSG
260 270 280 290 300 310

cryla-105.pe IT-----ITYDAHGEYWGSHQIMASPVGSGPEFTFLPYGTMGNAAPQQRIVAQGLQG
310 320 330 340 350

4239730 ISGTRLISITPPNIGGIPGSTTTHSLNARVNYSGGVSS---GLIGATNLNINFNCSL--
320 330 340 350 360

cryla-105.pe GVTYLTSLTYLRPPNIGINNQQLSV-LDGTFAVGTSSNLPFSAVKYKSGTVDSDLEIPP
360 370 380 390 400 410

4239730 -VLPPSLTPFVRSWLDSDIGREGVATSTNMWQTESQTTLSURCAFSAAGNSNYFPDYFI
370 380 390 400 410 420

420 430 440 450 460

[illegible]

cry1a-105.pe --SIRSPHMDLMSITIT--DAHRGEYWSGHQIMASPVGSGPEFTPLYGTMGN-AA
4239728 PLSITPNIIGLPGSTTTHSLNSARVNY--SGG-VSSGLIGATNLNHNFCSTVLPPLST
cry1a-105.pe POORIVAGLGGQVYR--TLSSLYRPPENGINNQLSVLDGTGTFAYGTSNLPASVYR
4239728 PFVR--SWLDSGTDRGVATSTWQTESPT--TLSSRCGAFSARGNSNYFPDYFIR
cry1a-105.pe K-SGT---VDSLDEIPP-QNNVPPRQGFHSRHSLSHVSFSGFSNVSIIIRA-PMFSWI
4239728 NISGVLVIRNEDLTRPLHYNQIRNIESPSGPGARAYLVSVHNKNNIYAANGTMI
cry1a-105.pe HRSAE-FNNIADSITQIPLVKAHTLQSGTIVVAGERIPAGQFNKMTDGTGDLRTSGGPFAYTIYNI
4239728 HLAPEDTGTF---TISPIHATQVNN-QTRTFISEKFG-NOGSLRFEQSNTPARHARG
cry1a-105.pe NGOLPORYEARIRYASTINRIVYTVAGERIPAGQFNKMTDGTGDLRTSGGPFAYTIYNI
4239728 NGN---SYNLYLRVSSIGNSTIRVTING-RVVTYSNNVTNNNDGVNDNGARFSDINIGN
cry1a-105.pe GLKATNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKHAKRUSDERNLQDSNFKDINR
NRAA:47678765
47678765 sources="GENBANK PROT" insecticidal crystal protein Cry2aA [Bacillus
thuringiensis serovar kurstaki]
SCORES Init1: 166 Initn: 166 Opt: 282 z-score: 317.1 E(): 2.3e-09
>>NRAA:47678765
initn: 166 init1: 166 opt: 282 z-score: 317.1 expect(): 2.3e-09
Smith-Waterman score: 285; 22.9% identity in 602 aa overlap
(41-606:56-626)
cry1a-105.pe IPYNCLSNEVEVLGGERIETGYTPIDISLSTQFLSEFPVCGAGVLG--LVDIIMGIF
47678765 FEHKSIDTIQKEMEWKRTDHSLYVAPVGVTSFLEKK---VGSILGRILSELWGII
cry1a-105.pe GPSSQ---WDAPLVQIEQLINRIEFAFNQAIISLEGLSNLVGIVAESFREWADPTNP
47678765 FPGSINLWQDILRETEQFLNQLNTDLARNAELIGLQANIREFNQVQDNF-LNPTON

cry1a-105.pe ALREEMRIQVNDMNSALTTPALFAVQNYQVPLLSVTVQAANHLSDVLRDVSFQGRWG
47678765 PVLSTISSTVNTMOQLNPLPQFQIQGVQLLLPLFAQANWHLSDIFRDLVILNADWGI
cry1a-105.pe DAATINSRYNDLTRELIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNGFRRLTLVLD
47678765 SAATLRTDRLRYNTDYSCINTYQAFR---GLNTRLDHML---EFRTYMLFNWFE
cry1a-105.pe IVSL--FNLYDS-----RTYPIRTVSQLTREIYTN--PVLEN-FDGSFRGSAQIEG-
47678765 YVINSFFKYQSLMVSSGANLYASGSGPQQTOSTTAQWPFYLSLFOVNSNYILSGISGT
cry1a-105.pe --SIRSPHMDLMSITIT--DAHRGEYWSGHQIMASPVGSGPEFTPLYGTMGN-AA
47678765 RLSITPNIIGLPGSTTTHSLNSARVNY--SGG-VSSGLIGATNLNHNFCSTVLPPLST
cry1a-105.pe POORIVAGLGGQVYR--TLSSLYRPPENGINNQLSVLDGTGTFAYGTSNLPASVYR
47678765 PFVR--SWLDSGTDRGVATSTWQTESPT--TLSSRCGAFSARGNSNYFPDYFIR
cry1a-105.pe K-SGT---VDSLDEIPP-QNNVPPRQGFHSRHSLSHVSFSGFSNVSIIIRA-PMFSWI
47678765 NISGVLVIRNEDLTRPLHYNQIRNIESPSGPGARAYLVSVHNKNNIYAANGTMI
cry1a-105.pe HRSAE-FNNIADSITQIPLVKAHTLQSGTIVVAGERIPAGQFNKMTDGTGDLRTSGGPFAYTIYNI
47678765 HLAPEDTGTF---TISPIHATQVNN-QTRTFISEKFG-NOGSLRFEQSNTPARHARG
cry1a-105.pe NGOLPORYEARIRYASTINRIVYTVAGERIPAGQFNKMTDGTGDLRTSGGPFAYTIYNI
47678765 NGN---SYNLYLRVSSIGNSTIRVTING-RVVTYSNNVTNNNDGVNDNGARFSDINIGN
cry1a-105.pe TFPMSSOSTTGAD-TFSSGNEVYIDRFELIPVATLEAEYNLERAKVNAALFTSTNQL
47678765 IVASDNTNVTLIDINVTLNSGTTPFDLMNMFVPTNPLLY
cry1a-105.pe GLKATNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKHAKRUSDERNLQDSNFKDINR
SW:117326

117326 description="PESTICIDIAL CRYSTAL PROTEIN CRY2AA (INSECTICIDIAL
DELTA-ENDOTOXIN CRYIIA(A)) (CRYSTALLINE ENTOMOCIDIAL PROTOXIN) (71 KDA CRYSTALL
PROTEIN) (P2 CRYSTAL PROTEIN) (MOSQUITO FACTOR) " library=NA species="Bacillus
thuringiensis serovar kurstaki" source="swissprot_prot" version=NA type=PRT

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SCORES Initl: 166 Initn: 166 Opt: 282 z-score: 317.1 E(): 2.3e-09
>>SW:117326
initn: 166 initl: 166 opt: 282 z-score: 317.1 expect(): 2.3e-09
Smith-Waterman score: 284; 21.6% identity in 597 aa overlap
(41-606:56-626)

cry1a-105.pe IPYNCLSNPEVEVLGERIETGTPIDISLTQFLSEFVPGAGVLG-LVDIIMGIF
NRAA:33314185
117326 FEKSLDTIQKEMWETDHSYVAVPVGTSSFLAK---VGSIGKRIELSELWGII
30 40 50 60 70 80

cry1a-105.pe GPQSQ----WDAFLVQIEQLINQRIEFARNQAIISLEGLSNLYQIYAEFSREWEADPTNP
117326 FPGSGTNLMQDILRETEQFLNQRINTDTLARVNAELIGLOANIREFNOQVDNF-LNPTON
90 100 110 120 130 140

cry1a-105.pe ALREEMRIQNDMSALTTAIPFAVQNYQVLLSVYQOANLHLSVLDRVSVFGQRMGF
117326 PVPLSITSSVTMQQLFLNRLPQIQGYQLLLPLFAQAAANHLSPFIRVILNADWGI
150 160 170 180 190 200

cry1a-105.pe DAATINSRYNDLTRIGNYTDHVRVNTGLERVMPDSR--DWIRYNOFRRELTITLVD
117326 SAATLATRYDYLNRVTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMLNVE
210 220 230 240 250

cry1a-105.pe IVSLFNYDSRTPIRTVQSQITREIYTNVLENFPGSPRGAQIEGSTRSPLMDILNS
117326 YVSIWLSLFYQSLWVSSGANL---YASGSGPQQTQSFTAQNWPFYLSFQVNSNYILSG
260 270 280 290 300 310

cry1a-105.pe IT-----IYTDHGRGEYWSGQIMASPVGSGPEFTFLYG--TMGNAAPQQRIVAQ
117326 ISGTRLSITFPNIGGLPGSTTHSLNSARVNSGG-VSSGLIGATNLNENFNCSTVLPL
320 330 340 350 360

cry1a-105.pe GQGVYRT-LSSTLVRRPFGNINQO-----LSVLDGTEFAYGTSNLPSPAYRK-SGT
117326 STPFVRSWLDSDGTREGVATSTNQWTESFQTTLSLRCCAFSARGNSNYPDPYFIRNIGSV
370 380 390 400 410 420

cry1a-105.pe ---VDSLEIPP-QNNVPPROGFSHRLSHVSMFSGSNSSVSIIRA-PMSFWTHRSAR
117326 PLVIRNEDLTRPHYNQIRNIESPGSTPGARAYLVSVHKKNIIVAAENENGTMIHLAPE
430 440 450 460 470 480

cry1a-105.pe -FNNIADSIQIPLVKAHTQSQTIVVRGPGFTGGIILRTSGGPFAYTIWINGQLP
117326 DYTGPF---TISPIHATQVNN-OTRTFISEKEG-NOGDSLFQSGNTARYILRNGN--
490 500 510 520 530 540

cry1a-105.pe QRYRARIRVASTNLRIYTVAGERIFAQGFNKMTDGLPTLQFSYSYATINTAFTFMS
117326 -SYNLYLRVSSIGNSTIRVING-RVYTVSNVNTTTNNDGVNONGARFSDIMIGNIVASD
550 560 570 580 590

cry1a-105.pe QSSFTVQAD-TSSQNEVYIDRPELIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
117326 NTNVTLDINVLNLSGTFPDLNMNMFVPTNPLPY
600 610 620 630

cry1a-105.pep
NRAA:33314185
33314185 source="GENBANK_PROT" Cry2a [Bacillus
thuringiensis]gi|27447976|gb|AAO13750.1| Cry2a [Bacillus
thuringiensis]gi|61221653|sp|POA37|CR2AA BACTX Pesticial crystal protein
cry2a (insecticidal delta-endotoxin CryIIa(a)) (Crystalline entomocidal
protoxin) (71 kDa crystal protein) (p2 crystal protein) (Mosequito
factor)gi|142746|gb|AAA83516.1| insecticidal crystal

cry1a-105.pe IPYNCLSNPEVEVLGERIETGTPIDISLTQFLSEFVPGAGVLG-LVDIIMGIF
33314185 FEKSLDTIQKEMWETDHSYVAVPVGTSSFLAK---VGSIGKRIELSELWGII
30 40 50 60 70 80

cry1a-105.pe GPQSQ----WDAFLVQIEQLINQRIEFARNQAIISLEGLSNLYQIYAEFSREWEADPTNP
33314185 FPGSGTNLMQDILRETEQFLNQRINTDTLARVNAELIGLOANIREFNOQVDNF-LNPTON
90 100 110 120 130 140

cry1a-105.pe ALREEMRIQNDMSALTTAIPFAVQNYQVLLSVYQOANLHLSVLDRVSVFGQRMGF
33314185 PVPLSITSSVTMQQLFLNRLPQIQGYQLLLPLFAQAAANHLSPFIRVILNADWGI
150 160 170 180 190 200

cry1a-105.pe DAATINSRYNDLTRIGNYTDHVRVNTGLERVMPDSR--DWIRYNOFRRELTITLVD
33314185 SAATLATRYDYLNRVTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMLNVE
210 220 230 240 250

cry1a-105.pe IVSLFNYDSRTPIRTVQSQITREIYTNVLENFPGSPRGAQIEGSTRSPLMDILNS
33314185 YVSIWLSLFYQSLWVSSGANL---YASGSGPQQTQSFTAQNWPFYLSFQVNSNYILSG
260 270 280 290 300 310

cry1a-105.pe IT-----IYTDHGRGEYWSGQIMASPVGSGPEFTFLYG--TMGNAAPQQRIVAQ
33314185 ISGTRLSITFPNIGGLPGSTTHSLNSARVNSGG-VSSGLIGATNLNENFNCSTVLPL
320 330 340 350 360

cry1a-105.pe GQGVYRT-LSSTLVRRPFGNINQO-----LSVLDGTEFAYGTSNLPSPAYRK-SGT
33314185 STPFVRSWLDSDGTREGVATSTNQWTESFQTTLSLRCCAFSARGNSNYPDPYFIRNIGSV
370 380 390 400 410 420

61221653	:: : : : :: : : : :: : : : :: : : : :: : : : :: : : : :: : : : :: : : :
YVTSWLFKYSIMVSSCANL----	YASGSGQQTQSFTQQNWPFLYSFQVNSNYILSG
260	270 280 290 300 310

```
cryla-105.pe IT-----IYDAHRGEYYGSHQIWASPVGSPEFTFLYG--TWGNAPQQRIVAOQL
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
ISGRUSIFPNIGGLPGSTTHLSNSARVNYSGG-VSSGLIGATNLNUNFNCSTVLPP
```

cr1a-105.pe GGGVRT-LSSTLYRRPNIINNOQ-----LSVLDCTEFAVGTSSNIPSAVVRK-SGT

61221653
STTPEFVSILDSGTDREGVATSTNNQTESQTTLSLRCCAFSARGNSVPPDYFIRNISGV
370 380 390 400 410 420 430 440 450 460

```
cryla-105.pe ---VDSLDEIPP-QNNVVPRQGFSHRLSHVMFSGFSNSSVSIIIRA-PMFSTIHRSAE  
61221653 PLVI RNEDLT RPLHYNQIRNIESPFGTGGARAYLVSVHNRKNNYIAANENGCTWHLAPE
```

Cy1a-105.pe -FNNITASDISIQIPLVKAHTLOSQTTVVRGPGFTGGDIARRTSGGPFAYTWINQGLP
::: :| | :::::: :| | :| | :| | :| | :| :

6222453 490 500 510 520 530 540
DYTGF----TSPHATQWN-OTRIFISEKFG-NOEDSLRFQNSNTARYTLRGN--
QVADRTVAQMTNTRIVMVRIGDPTRECDTWRVQWQDGRS MRCQCCGCTNTMTRMDSG

61221653 -SULUVRUSSLESTIRVING-RYVTVSVNVTITNDGNDGAPSDINIGIVASD
558 560 560 570 580 590

61221653
 KNTVTLSS NVTLNSGTPEBLSMCMFFVPTNLPPL
 QSSFTYGAG-TFSSSNVYIDREFLIPVATLEAEYNLERAQKAVNALFTSTNQLGKTN
 590 600 610 620 630
 cryla-105.pe

600 610 620 630

9622198 source="GENBANK PRO" parasitol crystal protein Cry18Ba1 [Paeniba
popillialis]gi|10719329|sp|P57091 CNGA PAPO Parasitol crystal protein cry
[Parasitol gi10719329|sp|P57091 CNGA PAPO Parasitol crystal protein cry
[Parasitol gi10719329|sp|P57091 CNGA PAPO Parasitol crystal protein cry

[illegible]

>NRRAA:9622198
initn: W19 init1: 76 opt: 281 Z-score: 315.5 expect (): 2.8e-09 (875 aa)
Smith-Waterman score: 284; 22.3% identity in 605 aa overlap
(56-607:101-674)

```

cry1a-105.pe  GERIETGTPIDISLSLTQFLSEFVPGAGFVLGIVDIIWGIFGSPQAREFNQITQDAK
30          40          50          60          70          80

```

9622198
ENGPSFTAPIVGVVTTJLEALKQVRSRLLLLMTLLFPNNSTWEEILRLTEQVO
80 90 100 110 120 130 140

CALYA I0J:PE QABER ARNVALSRUEGUSNDIYU PABCFKEN-----EAFUFINFAKCEMLQ UNWUNSH
9622198 EQLDITVNRVSQELEGIKNLATENDQIDDFLQNRVEISPTA-----MDSINTMQOV

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```
version=NA type=PRT

SCORES   Init1: 76   Initn: 119   Opt: 281   z-score: 315.5 E(): 2.8e-09
>>SW:10719929
Initn: 119 Init1: 76 Opt: 281 z-score: 315.5 expect(): 2.8e-09
Smith-Waterman score: 284; 22.3% identity in 605 aa overlap
(56-607:101-674)

cryla-105.pe GERITGYTIDISLISLTQFLISEFPGAGVLGLVDIITWIGFGSQMDAFLVQIEQLIN
10719929 ENSPSLFTAPIGVVSTLLEALKKQVQSRLLLMLNLPNNSTSTMEELRATEQYVQ
30 40 50 60 70 80
cryla-105.pe QRIEFARNOAISRLGLNLQIYVAESFREW----EADPTNPALREEMRIQFNDMNSA
10719929 EQLDVTWNRVSQELGKNNLRTNQDIDDFLQNRVELSPTA-----MDSINTMQOV
90 100 110 120 130 140
cryla-105.pe LTTAIPFAVONQVPLLSVYQAAHLHLSVLSDVSFGQRMGFDAAATINSRYNDLTRLI
10719929 FVNRLPQQLSDVQLLLPLFAQGATLHLEFIRDIINAGENWNIPEAQLNTCKRYLKQYV
150 160 170 180 190 200
cryla-105.pe GNYTDHVRVNTGLERVGPDSRDWIRYQFRRELTITVLDIVSLFPNYSRTYPIRTV
10719929 AQSYNALSITYEGAFRFRYPAT--LENNLOFRTFMTLVNLDVLSIMSLKYNMXYLISTS
210 220 230 240 250 260
cryla-105.pe SOLTREIYTPVLENFDGFRSGAQIEGSI---RSPHLMIDLNSITI---YTDARHGEY
10719929 VPIYACNFQELTS--SGTA---GTGGRFSDVFRSEDNICGLGTGYASAWTSYP----DYV
270 280 290 300 310
cryla-105.pe LSHVSMFRSGFNSSVSIIRAPM--FSW---IHRSAEFNNIIASDSITQIPLVKAHTLQSG
10719929 ITNIS---ATVQVDGINIDITPLCFEGEDRAITSTHGVNKA---VYNRKANAGTNQNG
320 330 340 350 360 370
cryla-105.pe TTVVRGP---GFT-----GGDILRRTSGGPFAYTIVNINQO
10719929 TMIHQAPNDGTGFTVSPLHLASFTHPSEAHIOENYCNDSLSRLT--GPTAITYMLSGD
380 390 400 410 420 430
cryla-105.pe LPQRYRARIYASTTNLRIVTVVAGERIFAGQFNKTMGTGDLT-----FQSFYSY-ATIN
10719929 GRTYIKLVLRVSGVIT--RITAKVRGNSIGYLEYINTVNNQGITDNGSKFDQDFEFPRTIT
440 450 460 470 480 490
cryla-105.pe TAFTFPMQSQSFVGVADTFSSGNEVYIDREFLIPVTATLAEAYNLRAQAVNALETSTN
10719929 IDAQTPIVLE--FSATSN--FDLMNLIFIPYDT--PIY
500 510 520 530 540 550
cryla-105.pe QLGKLTWYTDYHIDQVSNLVTVLSDFCLDEKRELSEKVKHAKRLSDERNLQDSNFKDI
560 570 580 590 600 610
cryla-105.pep
SW:10719929
10719929 description="PARASPORAL CRYSTAL PROTEIN CRY18BA (PARASPORAL
DELTA-ENDOTOXIN CRYXIIIB(A)) (CRYSTALLINE PARASPORAL PROTOXIN) (76 KDA CRYSTAL
PROTEIN)." library=NA species="Paenibacillus popilliae" source="swissprot_prot"
```

```
140 150 160 170 180
cryla-105.pe LTTAIPFAVONQVPLLSVYQAAHLHLSVLSDVSFGQRMGFDAAATINSRYNDLTRLI
9622198 FVNRLPQQLSDVQLLLPLFAQGATLHLEFIRDIINAGENWNIPEAQLNTCKRYLKQYV
190 200 210 220 230 240
cryla-105.pe GNYTDHVRVNTGLERVGPDSRDWIRYQFRRELTITVLDIVSLFPNYSRTYPIRTV
9622198 AQSYNALSITYEGAFRFRYPAT--LENNLOFRTFMTLVNLDVLSIMSLKYNMXYLISTS
250 260 270 280 290 300
cryla-105.pe SOLTREIYTPVLENFDGFRSGAQIEGSI---RSPHLMIDLNSITI---YTDARHGEY
9622198 ANL--YNIQDNKQVNE---GEYSISYWPFFNSYIQTKSNYVLSGVGYAIRWYLYNTFGEY
310 320 330 340 350
cryla-105.pe YMSG-HQIMASPVG--FSGPEFTFPLYGTMGNAAPQORIVAOLGQGVYRTLSSTLYRPFN
9622198 IQDNLYNIASVYGVNGPKIGVQLSTELDKQIKQAARAGMPTGLDLSFNCTLRNPTT
360 370 380 390 400 410
cryla-105.pe I---GINNQQLSVLDGTEFAYGTSNLPSSAVYKSGTVSDLSDEIPPQNNVPPRGFSHR
9622198 VPIYACNFQELTS--SGTA---GTGGRFSDVFRSEDNICGLGTGYASAWTSYP----DYV
420 430 440 450 460 470
cryla-105.pe LSHVSMFRSGFNSSVSIIRAPM--FSW---IHRSAEFNNIIASDSITQIPLVKAHTLQSG
9622198 ITNIS---ATVQVDGINIDITPLCFEGEDRAITSTHGVNKA---VYNRKANAGTNQNG
480 490 500 510 520
cryla-105.pe TTVVRGP---GFT-----GGDILRRTSGGPFAYTIVNINQO
9622198 TMIHQAPNDGTGFTVSPLHLASFTHPSEAHIOENYCNDSLSRLT--GPTAITYMLSGD
530 540 550 560 570 580
cryla-105.pe LPQRYRARIYASTTNLRIVTVVAGERIFAGQFNKTMGTGDLT-----FQSFYSY-ATIN
9622198 GRTYIKLVLRVSGVIT--RITAKVRGNSIGYLEYINTVNNQGITDNGSKFDQDFEFPRTIT
590 600 610 620 630 640
cryla-105.pe TAFTFPMQSQSFVGVADTFSSGNEVYIDREFLIPVTATLAEAYNLRAQAVNALETSTN
9622198 IDAQTPIVLE--FSATSN--FDLMNLIFIPYDT--PIY
650 660 670 680
cryla-105.pe QLGKLTWYTDYHIDQVSNLVTVLSDFCLDEKRELSEKVKHAKRLSDERNLQDSNFKDI
690
cryla-105.pep
SW:10719929
10719929 description="PARASPORAL CRYSTAL PROTEIN CRY18BA (PARASPORAL
DELTA-ENDOTOXIN CRYXIIIB(A)) (CRYSTALLINE PARASPORAL PROTOXIN) (76 KDA CRYSTAL
PROTEIN)." library=NA species="Paenibacillus popilliae" source="swissprot_prot"
```

10619929 CRTIYKAVLEVSCHYF-RITAKVRGNSIGLEYINTVONNOGIDTNGSKFQDFEFPFTIT
570 600 610 620 630 640
cry1a-105.pe VAPFPMNSGSSVADTFSSGNEVVDREFLIPVTATLEAYNLERAQKAVNALFTSTN
590 600 610 620 630
10719929 IDAQPRIVE-FSNFN-TLMLNLIPTPTPT-PIY
650 660 670
cry1a-105.pe QLGKLTNVDYHIDQVSNNTVLSDFSDVDEKRELSENKAKRLSDERNLLQDSNFKDI
640 650 660 670 680 690
cry1a-105.pep
NRAA:27447952
27447952 source="GENBANK_PROT" insecticidal crystal protein Cry2Aa (Bacillus
thuringiensis)
SCORES Initl: 166 Initn: 166 Opt: 278 Z-score: 312.6 E(1): 8.5e-09
>NRAA:27447952
Initn: 166 Initl: 166 Opt: 278 Z-score: 312.6 expect(1): 4.4e-09
Smith-Waterman score: 280; 21.6% identity in 597 aa overlap
(41-606:56-626)
cry1a-105.pe IPYNCLNPEVEVLGGERIETGTPIDISLSTQFLLSFVFGAGFLVG-LVDIIWGF
20 30 40 50 60
27447952 FEHKSLDTIQKEMWKRTHSLXVAPVGVGTSSVFLKK- VGSIGIKRILSELWGLI
30 40 50 60 70 80
cry1a-105.pe GPSQ----WDAFLVOIEQLINORIEEFARNAQISRLGGLSNLYQIYAESFREWADPTNP
70 80 90 100 110 120
27447952 PFSSSTNLMDILRETEQFLNRLNTDILARVNAELIGLQANREFNQVDNF-LNPTON
90 100 110 120 130 140
cry1a-105.pe ALREEMRIQFNDMNSALTTAIPFVAVQNYQVPLLSVYVQAANLHLSVLRVSVFGQWGF
130 140 150 160 170 180
27447952 PVPLSITSSVNTMQQLFNRLPFQIQGYQLLLPLFAQANMHLSTFIRVILNADWGI
150 160 170 180 190 200
cry1a-105.pe DAATINSRYNDLTRLIGNYTHAVRWNTGLERWGPDSR--DWIRYNQFRRLTLTVLD
190 200 210 220 230 240
27447952 SAATLRTRDYLRNTRDYSNYCINTYTQAFR---GLNTRLHDML---EFTYMLNLFVE
210 220 230 240 250
cry1a-105.pe IVSLFFPNDSRTYPIRTVSOLTRITNVPVLENFDSFRGSAQIGEGSIRSPHMLDILNS
250 260 270 280 290 300
27447952 YVSIWSLFKKYQGLMVSSGNL-----YASGSGPQQTQSFTAQNWPFLLSLFQVNSNVLSSG
260 270 280 290 300 310
cry1a-105.pe IT-----IYTDHARGEYVWSGHQIMASPVGFGPEFTFPLYG--TWGNAAPQQRVAOL
310 320 330 340 350
27447952 ISGTRLSITFPNIGGLPGSTTHSINARVNSYSG-VSSGLIGATNLNHNFNCSVTLVPL
320 330 340 350 360
cry1a-105.pe GGGVYRT-LSTLYRRFPFNIGNNQ-----LSVLGDTEFGAYGSSNLSAVYRK-SGT
360 370 380 390 400
27447952 STPFVRSWLDGSDTREGVATSTNMTQTESFQTLTLRLCGAFSARGNSNYFPDYFIRNSGV
380 390 400

370 380 390 400 410 420
cry1a-105.pe ---VDSIDEIIPP-QNNYPPRQGFSHLSHVSMRSGFSSSVSIIIRA-PWFSWIHRSAE
410 420 430 440 450 460
27447952 PLVIRNEDLTRPLHYNQIRNIESPSGTPGGRAYLVSVNKRNNIYAANENGTMHIAPE
430 440 450 460 470 480
cry1a-105.pe -FNNIIASDSITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLP
470 480 490 500 510 520
27447952 DYTGF---TISPIHATQVNN-QRTTFISEKFG-NGDLSLRFEOSTNTARTYTLRNGN--
490 500 510 520 530 540
cry1a-105.pe ORYRARIRYASTNLRILVTVAGRIIFAGQFNKMTMDTGLTFQSFATINTAFTFPMWS
530 540 550 560 570 580
27447952 -SYNLYLRVSSIGNSTIRVING-RVTVSVNVNTTINDGVNDNGARFSDINIGNIVASD
550 560 570 580 590
cry1a-105.pe OSSFTVGAD-TFSSGNEVVDREFLIPVTATLEAYNLERAQKAVNALFTSTNQLGKTN
590 600 610 620 630
27447952 NTNVLDINVTLSNGTTPFDLMNMFVPTNPLPY
600 610 620 630
cry1a-105.pep
SM:117328
117328 description="PESTICIDIAL CRYSTAL PROTEIN CRY2AB (INSECTICIDAL
DELTA-ENDOTOXIN CRY2AB(B)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (71 KDA CRYSTAL
PROTEIN) library name="Bacillus thuringiensis serovar kurstaki"
source="Swissprot Prot" version="NA type="PRT
SCORES Initl: 128 Initn: 128 Opt: 273 Z-score: 306.9 E(1): 8.5e-09
>SM:117328
Initn: 128 Initl: 128 Opt: 273 Z-score: 306.9 expect(1): 8.5e-09
Smith-Waterman score: 281; 21.0% identity in 600 aa overlap
(41-610:56-630)
cry1a-105.pe IPYNCLNPEVEVLGGERIETGTPIDISLSTQFLLSFVFGAGFLVG-LVDIIWGF
20 30 40 50 60
117328 FOHKSLDTIQKEMWKRTHSLXVAPVGVGTSSVFLKK- VGSIGIKRILSELNLIFFSG
30 40 50 60 70 80
cry1a-105.pe GPSQWDAFLVOIEQLINORIEEFARNAQISRLGGLSNLYQIYAESFREWADPTNP---A
70 80 90 100 110 120 130 140
117328 STNLMQDILRETEQFLNRLNTDILARVNAELIGLQANREFNQVDNF-LNPTON
90 100 110 120 130 140
cry1a-105.pe LREEMRIQFNDMNSALTTAIPFVAVQNYQVPLLSVYVQAANLHLSVLRVSVFGQWGF
130 140 150 160 170 180 190 200
117328 VPLSITSSVNTMQQLFNRLPFQIQGYQLLLPLFAQANMHLSTFIRVILNADWGS
150 160 170 180 190 200
cry1a-105.pe DAATINSRYNDLTRLIGNYTHAVRWNTGLERWGPDSR--DWIRYNQFRRLTLTVLD
190 200 210 220 230 240
117328 SAATLRTRDYLRNTRDYSNYCINTYTQAFR---GLNTRLHDML---EFTYMLNLFVE
210 220 230 240 250

```
cry1a-105.pe 250 260 270 280 290 300
VSLFPNYSRTPIRTVSQLTREIYNFVLENFVDFGSGAAGIEGSIKSPHLMILNSI
117328 90 100 110 120 130 140
STWLMODILRETFKFLQRLNTLTARVNAELTGL---QANVEEFNRQVDNLFNPNRA
cry1a-105.pe 130 140 150 160 170 180
LREEMIQDNMNSGALTALPLFAVONQVPLLSVYVQAANLHLSVLRDVSVEFGWGF
40312 150 160 170 180 190 200
VPLSITSSVNTWQQLFNRLPQOMOGQQLLLPLFAQANLHLSFIRDVILNADWGIS
117328 210 220 230 240 250 260
AATLRTYRDLKANTRYSNVCINTVOSAPK---GLNLRHLDML---EFTVMFLNVEY
cry1a-105.pe 190 200 210 220 230 240
AATINSRYNDLTRIGNYTDHAVRYNTGLERVGPDSR--DMIRYNQFRRELTITVLDI
40312 210 220 230 240 250 260
AATLRTYRDLKANTRYSNVCINTVOSAPK---GLNLRHLDML---EFTVMFLNVEY
cry1a-105.pe 250 260 270 280 290 300
VSLFPNYSRTPIRTVSQLTREIYNFVLENFVDFGSGAAGIEGSIKSPHLMILNSI
40312 260 270 280 290 300 310
VSIWLFKYQSLLVSSGANL---YASGGPQQTOSTQDWPFLYSLFQVNSNYLNGF
cry1a-105.pe 310 320 330 340 350
T-----IYDAHRGEYVWSGHOIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAGLQGG
40312 320 330 340 350 360
SGARLSNTPFNIVGLPGSTTTHALLAARVNYSGISS---GDIGASPFNQFNCSF---
cry1a-105.pe 360 370 380 390 400 410
VYRTLSSTLYRRPNIGINNQQQL--SVLDGTEFAYGTSSNLPFSAYRKSGTVDLSDEIPPO
117328 370 380 390 400 410 420
FLPPLLTFFVRSLDSDGREGVATVNMQTESFETTLGLRSGAFTARGNSNYFPDYFIR
cry1a-105.pe 420 430 440 450 460
N-NNVP--PROGFSHRLSHVSMRSGFSNSSV-SIIRAPMFSIHSAEFNNI-----
117328 430 440 450 460 470 480
NISGVLVVRNEDLRRLPHYNEIRNIASPSGPGGARAYMVSVHNRKNNIHAVHENGSMI
cry1a-105.pe 470 480 490 500 510 520
-IASDSITQIPLVKAHTLQSGT---TVVRGPGFTGGDILRTSGGPFAYTIIVNINGQLPQ
117328 490 500 510 520 530 540
HLAPNDYTGFTISPIHATQVNNOTRTFISEKFGNGDSLRFEGONNTTARYTLRNGN---
cry1a-105.pe 510 520 530 540 550 560 570 580
RYPARIRASTNNRIYVTVAGERIPAGQFNKMTGDTGTLTOSFSYATINTAFTFPMQ
117328 550 560 570 580 590 600 610
SYNLXLRVSSIGNSTIRVTING-RVYTATNVNTTNDGNGARFSDINIGNVASSN
cry1a-105.pe 590 600 610 620 630 640
SSFTVGAD--TFSSGNEVYIDRFELIPVTATLEAEYNLERAKAVNALFTSTNQLGKTNV
117328 610 620 630 640 650 660
SDVPLDINVTLSGTFQDLNMLVPTNISPLY
cry1a-105.pep
NRAA:40312
40312 sources="GENBANK_PROT" crystal protein CryIIB [Bacillus
thuringiensis]gi|11526737|gb|AAG36762.1| Cry2Ab [Bacillus
thuringiensis]gi|117328|sp|P21254|CR2AB BACTK Pesticidal crystal protein cry2Ab
(Insecticidal delta-endotoxin CryIIA(b)) (Crystalline entomocidal protoxin) (71
kDa crystal protein)gi|142748|gb|AA22342.1| crystal protein B2
SCORES Init1: 128 Initn: 128 Opt: 273 z-score: 306.9 E(): 8.5e-09
>>NRAA:40312
initn: 128 init1: 128 opt: 273 z-score: 306.9 expect(): 8.5e-09
Smith-Waterman score: 281; 21.0% identity in 600 aa overlap
(41-610:56-630)
cry1a-105.pe 20 30 40 50 60
IPVNCILSNPEVEVLGGRIETGYTPIDISLSLTQFLSEF--VPGAGFVLGLVDIIMGIF
40312 30 40 50 60 70 80
FOHKSIDTVQKEWTEWKNHNSLYDPIVGTVASGLLKKVGLKVGSLVGRILSELNLIIPSG
70 80 90 100 110 120
```

```
cry1a-105.pe GPSONDAFLVQIEQLINRIEIEFARNQAISLEGISNLIYQIYAESFEWEADPTNP---A
40312 90 100 110 120 130 140
STWLMODILRETFKFLQRLNTLTARVNAELTGL---QANVEEFNRQVDNLFNPNRA
cry1a-105.pe 130 140 150 160 170 180
LREEMIQDNMNSGALTALPLFAVONQVPLLSVYVQAANLHLSVLRDVSVEFGWGF
40312 150 160 170 180 190 200
VPLSITSSVNTWQQLFNRLPQOMOGQQLLLPLFAQANLHLSFIRDVILNADWGIS
cry1a-105.pe 190 200 210 220 230 240
AATINSRYNDLTRIGNYTDHAVRYNTGLERVGPDSR--DMIRYNQFRRELTITVLDI
40312 210 220 230 240 250 260
AATLRTYRDLKANTRYSNVCINTVOSAPK---GLNLRHLDML---EFTVMFLNVEY
cry1a-105.pe 250 260 270 280 290 300
VSLFPNYSRTPIRTVSQLTREIYNFVLENFVDFGSGAAGIEGSIKSPHLMILNSI
40312 260 270 280 290 300 310
VSIWLFKYQSLLVSSGANL---YASGGPQQTOSTQDWPFLYSLFQVNSNYLNGF
cry1a-105.pe 310 320 330 340 350
T-----IYDAHRGEYVWSGHOIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAGLQGG
40312 320 330 340 350 360
SGARLSNTPFNIVGLPGSTTTHALLAARVNYSGISS---GDIGASPFNQFNCSF---
cry1a-105.pe 360 370 380 390 400 410
VYRTLSSTLYRRPNIGINNQQQL--SVLDGTEFAYGTSSNLPFSAYRKSGTVDLSDEIPPO
40312 370 380 390 400 410 420
FLPPLLTFFVRSLDSDGREGVATVNMQTESFETTLGLRSGAFTARGNSNYFPDYFIR
cry1a-105.pe 420 430 440 450 460
N-NNVP--PROGFSHRLSHVSMRSGFSNSSV-SIIRAPMFSIHSAEFNNI-----
40312 430 440 450 460 470 480
NISGVLVVRNEDLRRLPHYNEIRNIASPSGPGGARAYMVSVHNRKNNIHAVHENGSMI
cry1a-105.pe 470 480 490 500 510 520
-IASDSITQIPLVKAHTLQSGT---TVVRGPGFTGGDILRTSGGPFAYTIIVNINGQLPQ
40312 490 500 510 520 530 540
HLAPNDYTGFTISPIHATQVNNOTRTFISEKFGNGDSLRFEGONNTTARYTLRNGN---
cry1a-105.pe 510 520 530 540 550 560 570 580
RYPARIRASTNNRIYVTVAGERIPAGQFNKMTGDTGTLTOSFSYATINTAFTFPMQ
40312 550 560 570 580 590 600 610
SYNLXLRVSSIGNSTIRVTING-RVYTATNVNTTNDGNGARFSDINIGNVASSN
cry1a-105.pe 590 600 610 620 630 640
SSFTVGAD--TFSSGNEVYIDRFELIPVTATLEAEYNLERAKAVNALFTSTNQLGKTNV
40312 610 620 630 640 650 660
SDVPLDINVTLSGTFQDLNMLVPTNISPLY
cry1a-105.pep
NRAA:27436036
27436036 source="GENBANK_PROT" crystal delta-endotoxin [Bacillus thuringiensis]
```

SCORES Init1: 128 Initn: 128 Opt: 272 z-score: 305.7 E(): 9.8e-09
>NRAA-2436036
initn: 128 init1: 128 opt: 272 z-score: 305.7 expect(): 9.8e-09
Smith-Waterman score: 272; 21.0% identity in 600 aa overlap
(41-610:56-630)

cry1a-105.pe IPNCLSNPEVVGKRIETGTPIDISLSLTQELLSEF--VPGAGFVLGLVDIINGIF
NRAA:33316454
33316454 source="GENBANK_PROT" Cry2Ab [Bacillus thuringiensis]

SCORES Init1: 128 Initn: 128 Opt: 271 z-score: 304.6 E(): 1.1e-08
>NRAA-33316454
initn: 128 init1: 128 opt: 271 z-score: 304.6 expect(): 1.1e-08
Smith-Waterman score: 279; 20.7% identity in 600 aa overlap
(41-610:56-630)

cry1a-105.pe IPNCLSNPEVVGKRIETGTPIDISLSLTQELLSEF--VPGAGFVLGLVDIINGIF
33316454
FOHKSLSITVQKEMTEWKKNNHSLYLDPIGVIVASFLKKVGSVLGKRIELSELRLIPPSG

cry1a-105.pe GPSQMDAFLVQIQLINQRI--EELFAR-NQALSLGLSLNLYQIYAESFREWADPTNPA
33316454
STNLMDILRETEKFLNQLNTDTLARNVAELTQANVEEFNRQVDNF---LNPRNA

cry1a-105.pe VPLSTSSVNTMQQLFLNLPQFQMOGYQLLLPLFAAANLHSEF--DVILNLADEWGIS
33316454
VPLSTSSVNTMQQLFLNLPQFQMOGYQLLLPLFAAANLHSEF--DVILNLADEWGIS

cry1a-105.pe VPLSTSSVNTMQQLFLNLPQFQMOGYQLLLPLFAAANLHSEF--DVILNLADEWGIS
33316454
VPLSTSSVNTMQQLFLNLPQFQMOGYQLLLPLFAAANLHSEF--DVILNLADEWGIS

cry1a-105.pe T-----IYDAHGEYVWGHQIMASPVGSGPEFTFPLVGTMGNAAPQRIVAQLGOG
33316454
SGARLSNTPFPNIVGLPGSTTHALLAARVNYSGGIS--GDIGASPPNQFNCGT---

cry1a-105.pe VPLSTSSVNTMQQLFLNLPQFQMOGYQLLLPLFAAANLHSEF--DVILNLADEWGIS
33316454
VPLSTSSVNTMQQLFLNLPQFQMOGYQLLLPLFAAANLHSEF--DVILNLADEWGIS

cry1a-105.pe N-NNVP--PROGFSHRLSHVSMRSGFSSSV-SLIIRAPMFSWIHSAEFNNI-----
27436036
NLSGVLVVRNEDLRRLPHYNEIRNIAFGSGTGGARAYMVSVHNNKNNIHAVHNGSMI

cry1a-105.pe -IASDSITQILPVKAHTLQSGT---TVVRGPGFTGGDILRTSGGPFATVINGNQLPQ
27436036
HIAPDYTGFTISPIHATQVNNQRTFISEKFGNQGSRLFRGNTTARTYLRNGN---

cry1a-105.pe RYEARIRVASTNLRIVYVAGERIFAGQFNKTMDTGDLTFQSFYATVNTAFTFPMQ
27436036
SYNLIRVSSIGNSTIRVING--RVITAINVNTTNDGVDNGARFSDINIGNVAVSSN

cry1a-105.pe SSVTVGAD-TFSSGNEYVIDRFELIPVATLEAEYNLERAKAVNALFTSTNQLGLKTNV
27436036
SDVPLDINVTLNLSGTQFDLMNIMLVPTNISPLY

cry1a-105.pe
NRAA:33316454
33316454 source="GENBANK_PROT" Cry2Ab [Bacillus thuringiensis]

SCORES Init1: 128 Initn: 128 Opt: 271 z-score: 304.6 E(): 1.1e-08
>NRAA-33316454
initn: 128 init1: 128 opt: 271 z-score: 304.6 expect(): 1.1e-08
Smith-Waterman score: 279; 20.7% identity in 600 aa overlap
(41-610:56-630)

cry1a-105.pe IPNCLSNPEVVGKRIETGTPIDISLSLTQELLSEF--VPGAGFVLGLVDIINGIF
33316454
FOHKSLSITVQKEMTEWKKNNHSLYLDPIGVIVASFLKKVGSVLGKRIELSELRLIPPSG

cry1a-105.pe GPSQMDAFLVQIQLINQRI--EELFAR-NQALSLGLSLNLYQIYAESFREWADPTNPA
33316454
STNLMDILRETEKFLNQLNTDTLARNVAELTQANVEEFNRQVDNF---LNPRNA

cry1a-105.pe VPLSTSSVNTMQQLFLNLPQFQMOGYQLLLPLFAAANLHSEF--DVILNLADEWGIS
33316454
VPLSTSSVNTMQQLFLNLPQFQMOGYQLLLPLFAAANLHSEF--DVILNLADEWGIS

cry1a-105.pe T-----IYDAHGEYVWGHQIMASPVGSGPEFTFPLVGTMGNAAPQRIVAQLGOG
33316454
SGARLSNTPFPNIVGLPGSTTHALLAARVNYSGGIS--GDIGASPPNQFNCGT---

cry1a-105.pe VPLSTSSVNTMQQLFLNLPQFQMOGYQLLLPLFAAANLHSEF--DVILNLADEWGIS
33316454
VPLSTSSVNTMQQLFLNLPQFQMOGYQLLLPLFAAANLHSEF--DVILNLADEWGIS

cry1a-105.pe N-NNVP--PROGFSHRLSHVSMRSGFSSSV-SLIIRAPMFSWIHSAEFNNI-----
27436036
NLSGVLVVRNEDLRRLPHYNEIRNIAFGSGTGGARAYMVSVHNNKNNIHAVHNGSMI

cry1a-105.pe -IASDSITQILPVKAHTLQSGT---TVVRGPGFTGGDILRTSGGPFATVINGNQLPQ
27436036
HIAPDYTGFTISPIHATQVNNQRTFISEKFGNQGSRLFRGNTTARTYLRNGN---

cry1a-105.pe RYEARIRVASTNLRIVYVAGERIFAGQFNKTMDTGDLTFQSFYATVNTAFTFPMQ
27436036
SYNLIRVSSIGNSTIRVING--RVITAINVNTTNDGVDNGARFSDINIGNVAVSSN

cry1a-105.pe N-NNVP--PROGFSHRLSHVSMRSGFSSSV-SLIIRAPMFSWIHSAEFNNI-----
33316454
NLSGVLVVRNEDLRRLPHYNEIRNIAFGSGTGGARAYMVSVHNNKNNIHAVHNGSMI

Monsanto Company
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Product Characterization Center

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cry1a-105.pe -TASDITQIPLVKAHTLQSGT---TVRGQFGTGGDILRRTSGGPFATVUNINGLPQ
33316454 HAPNDYTGFTISPIHATQVNNQITRIFSEKFGNGDLSLRFQNNNTTARTYTLRNGN---
470 480 490 500 510 520
cry1a-105.pe RYRAIRVASTNLRIVTVAGERIFAGQFNKMTDGTPLTFOSFSYATINTAFETPMQ
530 540 550 560 570 580
33316454 SYNLVLRVSSIGNSTIRVTING-RVYTATVNTTNDGVNDGARFSDINIGNVASSN
590 600 610 620 630
cry1a-105.pe SFTVAGD-TFSSQNEVYIDRFELIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTV
640
33316454 SDVPLDINVLTNSGTQFDLMNIMLVPTNISPLY
610 620 630
cry1a-105.pep
NRAA:6457578
6457578 source="GENBANK_PROT" crystal protein [Bacillus
thuringiensis]gi|8927992|sp|Q9RMG3|CR2AD_BACTU Pesticidal crystal protein
cry2Ad (insecticidal delta-endotoxin CryIIA(d)) (Crystalline entomocidal
protoxin) (71 kDa crystal protein)
SCORES Initl: 130 Inltn: 130 Opt: 270 z-score: 303.5 E(): 1.3e-08
>NRAA:6457578
initn: 130 inltn: 130 opt: 270 z-score: 303.5 expect(): 1.3e-08
Smith-Waterman score: 276; 21.7% identity in 609 aa overlap
(41-610:56-630)
cry1a-105.pe IPYNCLSNPEVEVLGGERIETGYTIDISLSLTQFLSEF--VPGAGFVLGLVDIINGIF
20 30 40 50 60
6457578 FOHKSLDITQKEMWEKKDNHSLYVDPIVGTVASFLKLGSLGKILSELRLNLFPSG
30 40 50 60 70 80
cry1a-105.pe GFSQMDALVQIQLINRIEFAFNQAISRLGSLNLYQIYAESFREWEADPTNP---A
70 80 90 100 110 120
6457578 STNLMEDILRETEKFLNQKLTNLTSLRVNAELTGL---QANVEEFNRQVDFNLPNRNA
90 100 110 120 130 140
cry1a-105.pe LREEMRIQDNMSALTATPLFAVQNYQVPLSVYQAAHLHSLVLRDVSFQGRGFD
130 140 150 160 170 180
6457578 VPLSTISVTNMQQLFLNLSQFMQGTQLLLPLFAQAANLHLSFIRDVILNAEENGIS
150 160 170 180 190 200
cry1a-105.pe AATINSRYNDLTRIGNYTDHVRVNTGLERVWGPDSR--DWIRNQFRRELTLVLDI
190 200 210 220 230 240
6457578 AATLTYQNHLRNRYTRDYSNYCIDTYQAFR---GLNTRLDML---EFTYMEFLNVEFY
210 220 230 240 250
cry1a-105.pe VSLFNYDSRYPIRTVQSLTREITNTP-----VLENFDGFRGSAQGLEGRSPLHMDI
250 260 270 280 290
6457578 VSIWLSFYQSLVSSGANLYAS--GSGPQQLFTSQDWPFLYSLF---QVNSNYVLSG
260 270 280 290 300 310
300 310 320 330 340 350
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cry1a-105.pe LNSITLIYTD-AHRCGEYWSG--HQIMASPVGFSGPETFFLYGTMGNAAPQORIVQAQLGQ
6457578 FSGASLFTTFNIGGLPGSTTQALLAARVNYSGGITS-----SGISGNSFNQNFNCNT--
320 330 340 350
cry1a-105.pe GYVRTLSSTLVRRPFNIGINNQOL-SVLDTGTEFAYGTSNLPASVYRKSGTVDSLSDEIPP
360 370 380 390 400 410
6457578 -ISPPLSTSVFVRSWLDSSGSDRGQVNTVNTWQTESFETSLGRCGAFTPGNSNVYGVFI
370 380 390 400 410 420
cry1a-105.pe QNNNVPPRQGFSHLSVMSFRSGNSVSI-----IAPMFSWIHSABFNII
420 430 440 450 460
6457578 RNIS-----GVSLVRNEDLKRPLYYNEKRNIESPSTPGGARAYWS-VHNKK--NNIY
430 440 450 460 470
cry1a-105.pe A-SDSITQIPL-----VKAHTLQSGTIVVRGPGF-TGGDILRRTSGGPFAYTI
470 480 490 500 510
6457578 AVHENGTMHILAPEDNTGFTISPIHATQVNNQITRIFSEKFGNGDLSLRFQSNNTTARTY
480 490 500 510 520
cry1a-105.pe VNINGQLPQRYRARIRVASTNLRIVTVAGERIFAGQFNKMTDGTPLTFOSFSYATIN
520 530 540 550 560 570
6457578 LRNGN---SYNLVLRVSSIGNSTIRVTING-RVYTASVNTTNTNDGVNDGARFSDIN
540 550 560 570 580 590
cry1a-105.pe TAITFPMQSSFTVAGD-TFSSQNEVYIDRFELIPVTATLEAEYNLERAKAVNALFTST
580 590 600 610 620 630
6457578 IGNVASSNSDVPDLNLTNSGTQFDLMNIMLVPTNISPLY
600 610 620 630
cry1a-105.pe NQLGLKTNVTVDYHIDQVSNLVLSLDEFCLDEKSELSEKVKHAKRLSDERNLLQDSNFKD
640 650 660 670 680 690
cry1a-105.pep
SW:8927992
8927992 description="PESTICIDIAL CRYSTAL PROTEIN CRY2AD (INSECTICIDAL
DELTA-ENDOTOXIN CRYIIA(D)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (71 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis" source="swissprot_prot"
version="NA type="PRT
SCORES Initl: 130 Inltn: 130 Opt: 270 z-score: 303.5 E(): 1.3e-08
>SW:8927992
initn: 130 inltn: 130 opt: 270 z-score: 303.5 expect(): 1.3e-08
Smith-Waterman score: 276; 21.7% identity in 609 aa overlap
(41-610:56-630)
cry1a-105.pe IPYNCLSNPEVEVLGGERIETGYTIDISLSLTQFLSEF--VPGAGFVLGLVDIINGIF
20 30 40 50 60
8927992 FOHKSLDITQKEMWEKKDNHSLYVDPIVGTVASFLKLGSLGKILSELRLNLFPSG
30 40 50 60 70 80
cry1a-105.pe GFSQMDALVQIQLINRIEFAFNQAISRLGSLNLYQIYAESFREWEADPTNP---A
70 80 90 100 110 120
8927992 STNLMEDILRETEKFLNQKLTNLTSLRVNAELTGL---QANVEEFNRQVDFNLPNRNA
90 100 110 120 130 140
```


cry1a-105.pe HSLVLDVSVFGQWGFDAATINSRYNDLRLIGNYTHAVRWNTGLERWGPDSRWI
8928024 HILLRLDAIVNAEKLGFSDKEVDTHKKYIKMTIHNHTAIVKAPLNGLDFKSLDVSYN
200 210 220 230 240 250
260 270 280 290 300 310
cry1a-105.pe RYNGFRRLTLVLDIVSLFNYSRTYPIRTVSQLTREIVT--NPVLENFDGS----
8928024 KXANYIKGTWMLVDLVALMFTDPDHYQKEVEIEFTTISPIYQVPKMNQNTSSSIV
260 270 280 290 300 310
cry1a-105.pe -----FRGAQIEGSIIRSPH--LMDILNSI--TIYTDHARGYYW-----SGHQ
8928024 PSDLFHQGDVLKLEFSTRDNDGLAKIFTGIRNTFYKSPNTHETVHDFSYNTQSSGNI
320 330 340 350 360 370
cry1a-105.pe IMAS-----PVGSGPEFTF-----PLY-----GTMGNA--AP-----QKRI
8928024 SRGSSNPIDILNPIIISTCIRNSFYKAIAGSVLVNFKDGTQGYAFAPQAQPTGAWDHSF
380 390 400 410 420 430
cry1a-105.pe VAQLG--QG-----VVRTLSSTLYRRPFNI-----GINQQLSVLDGTGEFAYGTSSNL
8928024 IESDGAPEGHKLNLYITSPGDTL--RDFINIVYTLISTPTINELSTEKIKGFEPAEKGYIKN-
440 450 460 470 480 490
cry1a-105.pe PSAYRKSGTVSLDEIPQNNVPPRQGFHSLHVSNFR-----SGF---SN
8928024 -QGIMMYKGEYINGAOFVNLNQOQLIFEFHASKAQYIRIRYASTOGTGYEFLN
500 510 520 530 540 550
cry1a-105.pe SSVSIIIRAPMSFWIHRSAEFNNI-----IASOSITQ--IPLVKAHTLQSTTVRGP
8928024 QELQTLNIFTS---ENGIVTGNIGENVLYTIGSTYITIEGHNHTLQIQHNDKNGWILDRIE
560 570 580 590 600 610
cry1a-105.pe GFTGGDLIRRT--SGPFAY--TIVNINGQLPQYRARIYASTTNLRIYVTVAG---ERI
8928024 -FVFKDSLODQSDQSPPEVHESHTIIFDKSSPTIWSNKHSHIHLGGSYTSQGSYPHNL
620 630 640 650 660 670
cry1a-105.pe FAGQFNKT-----MDTQDPLTFQSFYSATINTATFFPMSSQSTTVGADTFSSGNEV
8928024 LINLFIHTDPNRNHTIHVNGD-----MNVDYGDSDVADGLNFKITATIPSDAWVSGTIT
680 690 700 710 720
cry1a-105.pe VIDREF---LIPVTATLEAYNLERAQAVNALFTSNQGLKNTVDVHIDOVSNLTY
8928024 SMHLFNDNNFKYITIKFELSNELENTITQVNALFASSAQDITLIVNSVSDIYEWVWKVDA
730 740 750 760 770 780
cry1a-105.pe LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSFNINQROPERGWSGTGTITQGGDV
8928024 LSDEVFGKEKKALKRLVNOAKRLSKIRNLLIGGNFNLV-----AWYMGKDVVKESDHEL
790 800 810 820 830 840

cry1a-105.pe FKENYVTLSS--TFDECYTYLYQKIDESKLKAFTRQYLRGVIEDSQLEIYSIRNAK--H
8928024 FKSHVLLPPPTF--HPSYIFQKVEESKLKPNTRYTISGFIAGHEDVELWVSRYQGEIQ
850 860 870 880 890 900
cry1a-105.pe ETNVNPTGSLMPLSAQSPIGKCEPNRCAPHLEWNPDLDCSCRDGKCAHHSHHFSLDI
8928024 KVMQVPEEAL--PLISEN--SSC-----CVPNLINETLA-----DHPFESYSI
910 920 930 940
cry1a-105.pe DVGCTDLNEDLGVWVIFKTKQDGHARLGNLEFLEEKPLVGEALARVKAERKWRDKREK
8928024 DVGSLEMANPGIEFGLRIVKPTGMAVSNLEIREDRPLTAKEIROVORAARDWKONYEQ
950 960 970 980 990 1000
cry1a-105.pe LEWETNIVYKEAKESYDALFNVSQ-----YDQLOADNTIAMIAADKRVHSIREA
8928024 ERTETAITQPVNLQINALYENEDMNGSIRSNVSYHDLEQIMLPTLLKTEINCNCDHPA
1010 1020 1030 1040 1050 1060
cry1a-105.pe YLPE-----LSVIPGVNAAIPEELEGRIFTAFSLYDARNVKNKGDFNNGLSQWNVKGVHD
8928024 FLLKVIHFMPTDRIGEHGTILARQEQALDRAYTQLESNMLLNHGHFTTDANTWITIGSDAH
1070 1080 1090 1100 1110 1120
cry1a-105.pe VEEQNQRSVLVVPEWEAEVQEVVCP---GRGYILRVYAKGEGYEGCVTTHIEENNT
8928024 HTILEDGRRVLRPLPQSSNATQTEIEDFDQEQQLTHAK---GKGSITITLQHEENE
1130 1140 1150 1160 1170
cry1a-105.pe DELAFSCNVEEIEYPNVITCNDYTVNQEEYGGAYTSNRNGVNEAPSPADYASVYEKS
8928024 YVETHTHNDFITSONIPFTFKGNQIEVHITSEDEGEFLIDHITVIEVSKTDTNTNIEN
1180 1190 1200 1210 1220 1230
cry1a-105.pep
SW:8928024
8928024 description="PESTICIDIAL CRYSTAL PROTEIN CRY12AA (INSECTICIDIAL
DELTA-ENDOTOXIN CRY1A(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (142 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis" source="swissprot_prot"
version="NA type="PRT
SCORES Initl: 207 Initn: 664 Opt: 266 z-score: 294.4 E(): 4.2e-08
>>SW:8928024
Initn: 664 Initl: 207 Opt: 266 z-score: 294.4 expect(): 4.2e-08
Smith-Waterman score: 715; 23.2% identity in 1169 aa overlap
(29-1053:60-1177)
cry1a-105.pe MDNNFINECIPNCLSNPEVEVLGGERIETG-YTPIDISLSLTQFLLSSEFVGAGFV
8928024 SKYDEMIKAFKKWKKGAKGKDLDDVAVTYITTEIDPLNIVKGVLSVLT--LIPEVGVV
30 40 50 60 70 80 90 100

cry1a-105.pe LG-----VDLNG-IG-PSOMDAFLV---QIEQLINQRIEFPARNQAIISLEGLSNLY
8928024 ASAAQVLSKIPKIFSKNAKNIIEELKPOIEALIOODITQYDAINQKIFDSLOKTI
cry1a-105.pe QIVAFKRWEDPFAPEEMRIQNDMSALITAIPLFAVQNVQVPLLSVYQAAANL
8928024 NLTVVAI-----LNDYVTC-ANQLENLNLSLQISLPIGVEYETGLSPYAMVANA
cry1a-105.pe HLSVLRDVSFQRMGFDAKINSVNDLTGLIGKTDHVRNNTGLERVMGQPSRDWI
8928024 HILLRDAIVNAEKLGFSDKEVDTHKYNMTIHNTPKNAKFLNLSOKKASLDVNSYN
cry1a-105.pe RYNOFRREITLVLDSLPFNDSRTYPIRTVSQNTREYNT--NPLVJNFDGS-----
8928024 KCANYIKGTEWMLDLVALMPTDPDHYQYKEVEIEFTTISGPTLOPVKQKQVQVSSNAV
cry1a-105.pe FRGSAQIGESIRSPH-LMDILNSI--TIYDARGHYW-----SGHQ
8928024 PSDLFYQGLLVKLEFSTRDNDGLAKIFITGRNFIYKSPNTHETHVDFESYNTOSGNI
cry1a-105.pe IMAS-----PVGSGPEFTF-----PLY-----GTMGNA--AP-----QORI
8928024 SRGSSNFIPIDLNNPIISTCIRNSFYKAIAGSSVLNVNFKDGTQGYAFAPQATGGAWDSF
cry1a-105.pe VAQIG--QG-----VYRTLSLTYRPFNI-----GINNQQLSVLDGTGEFAYGTSNL
8928024 IESDGAPEGHKLNLYTSPGDTL-RDFINVYTLISTPTINELSTELKIKGFPAKGYIKN-
cry1a-105.pe PSAVYRKSGTVDLSLDEIPPNQNNVPPRQGFHRLSHVSMFR-----SGF-----SN
8928024 -QGIMKYKPEYINGAQPVNLENQOQLIFEHASKTAQYTIIRIRYASQTQGYFRLDN
cry1a-105.pe SSVSIIRAPMFSWIHRSAPFNI-----IASDSITQ--IPLVKAHLQSGTTVVRGP
8928024 QELQTLNPTS---HNGVYTCNGENYDLYTIGSYTIEGHNHTLQIHDNKNMGVLDRIE
cry1a-105.pe GFTGGLIRRT--SGGPAY-TIVNINGQLPQRYPARIRYASTINLEIVTVAG---ERI
8928024 -FVPKDLSQDQSPQSPPEVHESIIFDKSSPTIWSNKHYSYSHIHLEGSYTSQGSYPHNL
cry1a-105.pe FAGQFNKT-----MDTGDPLTFQSFYSYATINTAFTFPMQSSPTGATGDFSSGNEV
8928024 LNLHFTDPNENHTIHVNGD-----MNVGYKDSVADGLNFKNTAITIPSAWISGTTI

cry1a-105.pe YIDRFE---LIPVTATLAEAYNLRAQKAVNALFTSNQLGLKTNVTDYHIDQVSNLTV
8928024 SMHLFNDNNFKITITPKFELSNELENTITTOVNALFASSAQDTLASVSDYVIEQVVMKVDA
cry1a-105.pe LSEDFCLDEKRELSEKVKHAKRLSDERNILODSNFKDINROPEKRGSGSTGITIGGGDV
8928024 LSEDFVGEKKALKRLVKNQAKRLKRNLLIGGNFDNLV-----AWYMGKDVVVKESDHSL
cry1a-105.pe FKNYVTLSG-TFDECYFTLYOKIDESKLKAFTRYQYLRGVIEDSDOLEIYSIRYNAK-H
8928024 FKSDHVLPPPTF---HPSYIFQKVESKLNTRYTISGFIAGHEDVELVSRYGQELQ
cry1a-105.pe ETVNVFTGSLMPLSAQSPIGKGEPRNRCAPHEWNPLDLCSDRGCEKCAHSHHFSLDI
8928024 KVMQVPEEAL-PLTSES-SSC-----CVPNLINNETLA-----DPHFFYSYI
cry1a-105.pe DVGCTDLNEDLGVWVIFKIKTODGHARLGNLFELEKPLVGEALARKVKAEEKWRDKREK
8928024 DVGSLMEANPGIEFGLRIVKPTGMARVSNLEIREDRPLTAKEIRQVQRAARDWKONYEQ
cry1a-105.pe LEVNTNIVYKAKESVDALFVNSO-----YDQLQADTNAMIHAADKRVHSIREA
8928024 ERTEETALQPVNLQINALYENEDWNGSIRSNSVSVHDLQMLPTLILKTEECNVDHPA
cry1a-105.pe YLEP---CVVIPQNDNFEELGRITFAFLSDYDARNVKNKGDFNGLSCWNVKGVHD
8928024 FLNVYHMTMDTRI--HGTTIARQCALDRAYTQLESNLLHNGHFTTITANWTIEGDAH
cry1a-105.pe VESQNNORSNLYVREWEALSSERVCP---GRGMILVYAYKEGYEGCVTIHEINNT
8928024 HTILEDGRVRLPLPSSNMACTITLADFDQDETOLINAK-----GKSIILQHGEENE
cry1a-105.pe DELKFSNCVEEIIYNNVTICNDYTNNOFEYGGAY--SNRGYNEANRVPDYASVVEEKS
8928024 YVETHHTNDFTITSONIPPTFFKGNQIEVNTLSDEGEPLAHTIVIEVSKNTNNNIEN
cry1a-105.pep
NRAA:1429252
1429252 source="GENBANK PROT" parasporal crystal protein (parasporal crystal protein)
popilliae|gil10719336|sp|Q45358|C18AA PAEPP Parasporal crystal protein (parasporal crystal protein) (Parasporal delta-endotoxin CryXVIIIa(a)) (Crystalline parasporal protein) (kDa crystal protein)

SCORES Initl: 93 Initn: 131 Opt: 262 z-score: 293.7 E(): 4.6e-08
>NRAA:1429252
initn: 131 initl: 93 opt: 262 z-score: 293.7 expect(): 4.6e-08

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MSL No. 20351
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Smith-Waterman score: 262; 26.8% identity in 257 aa overlap
(2-247:84-332)

cry1a-105.pe MNNP-NINECIPNCLSNPEVEVLGGERIE 10 20 30
1429252 PLYNNNDNDAICDELGLTPIDNNITCSTDFPINVMTDPFRKSKQELTREWEKKE 60 70 80 90 100 110

cry1a-105.pe TG---YTPIDISLSLTOFLSEFVPGA-GFVLG-LVDIIMGIFGSQMDAFLVQIEQLIN 40 50 60 70 80
1429252 NSPSLFTPAIVGV-VTSFLQSLKQKATSFLKLTLDLFPNNSLTMEELIRATEQIVQ 120 130 140 150 160 170

cry1a-105.pe QRIEEFARNQALSRLGLSN---LYQIYAESFREWEADPTNPALREEMRIQFNDMNSALT 90 100 110 120 130 140
1429252 ERLDITDANRVSQELVGLKNNLTTFNDQVEDFLQNRVIGISPLAIDSI---NTMQQLFV 180 190 200 210 220

cry1a-105.pe TAIPLFAYONVQVPLLSVYVQAAHLHLSVLRDVSFGQWGFDAATINSRYNDLTRIGN 150 160 170 180 190 200
1429252 NRLFQFQVSGQVLLFLFQAATLHLTFLRDVIINADENWIPTAQLNTYTRYFKEYIAE 230 240 250 260 270 280

cry1a-105.pe YTDHAVRWNTGLERVMGPD--RDWIRYNQFRRLTLTVLDIVSLFFPNYDSRTYPIRTV 210 220 230 240 250 260
1429252 YSNYALSTYDDGFRTRFVPNTLEDML---QKTFMTLNALDIVSWSLLKYVNLVYSTS 290 300 310 320 330 340

cry1a-105.pe SQTREIYNFVLENFDGSRGSAQIEGSRSHPLMDILNSITITVDAHRGEYVWSGHQ 270 280 290 300 310 320
1429252 ANLYNGDKNKGAYPISYGPFNSYIQTNSYLVSGVSGIGARFTYSTVLGRYLHDDL 350 360 370 380 390 400

cry1a-105.pep
SW:10719936
10719936 description="PARASPORAL CRYSTAL PROTEIN CRY18AA (PARASPORAL DELTA-ENDOTOXIN CRYXIII(A)) (CRYSTALLINE PARASPORAL PROTOXIN) (79 KDA CRYSTAL PROTEIN)." library=NA species="Paenibacillus popilliae" source="swissprot_prot" version=NA type=PRT

SCORES Init1: 93 Initn: 131 Opt: 262 z-score: 293.7 E(): 4.6e-08
>SW:10719936
initn: 131 initl: 93 opt: 262 z-score: 293.7 expect(): 4.6e-08
Smith-Waterman score: 262; 26.8% identity in 257 aa overlap
(2-247:84-332)

cry1a-105.pe MNNP-NINECIPNCLSNPEVEVLGGERIE 10 20 30
10719936 PLYNNNDNDAICDELGLTPIDNNITCSTDFPINVMTDPFRKSKQELTREWEKKE 60 70 80 90 100 110

cry1a-105.pe TG---YTPIDISLSLTOFLSEFVPGA-GFVLG-LVDIIMGIFGSQMDAFLVQIEQLIN 40 50 60 70 80
10719936 NSPSLFTPAIVGV-VTSFLQSLKQKATSFLKLTLDLFPNNSLTMEELIRATEQIVQ 120 130 140 150 160 170

cry1a-105.pe QRIEEFARNQALSRLGLSN---LYQIYAESFREWEADPTNPALREEMRIQFNDMNSALT 90 100 110 120 130 140
10719936 ERLDITDANRVSQELVGLKNNLTTFNDQVEDFLQNRVIGISPLAIDSI---NTMQQLFV 180 190 200 210 220

cry1a-105.pe TAIPLFAYONVQVPLLSVYVQAAHLHLSVLRDVSFGQWGFDAATINSRYNDLTRIGN 150 160 170 180 190 200
10719936 NRLFQFQVSGQVLLFLFQAATLHLTFLRDVIINADENWIPTAQLNTYTRYFKEYIAE 230 240 250 260 270 280

cry1a-105.pe YTDHAVRWNTGLERVMGPD--RDWIRYNQFRRLTLTVLDIVSLFFPNYDSRTYPIRTV 210 220 230 240 250 260
10719936 YSNYALSTYDDGFRTRFVPNTLEDML---QKTFMTLNALDIVSWSLLKYVNLVYSTS 290 300 310 320 330 340

cry1a-105.pe SQTREIYNFVLENFDGSRGSAQIEGSRSHPLMDILNSITITVDAHRGEYVWSGHQ 270 280 290 300 310 320
10719936 ANLYNGDKNKGAYPISYGPFNSYIQTNSYLVSGVSGIGARFTYSTVLGRYLHDDL 350 360 370 380 390 400

cry1a-105.pep
SW:10719930
10719930 description="PARASPORAL CRYSTAL PROTEIN CRY18CA (PARASPORAL DELTA-ENDOTOXIN CRYXIII(A)) (CRYSTALLINE PARASPORAL PROTOXIN) (78 KDA CRYSTAL PROTEIN)." library=NA species="Paenibacillus popilliae" source="swissprot_prot" version=NA type=PRT

SCORES Init1: 71 Initn: 130 Opt: 259 z-score: 290.3 E(): 7e-08
>SW:10719930
initn: 130 initl: 71 opt: 259 z-score: 290.3 expect(): 7e-08
Smith-Waterman score: 259; 22.6% identity in 367 aa overlap
(54-410:114-472)

cry1a-105.pe LGGERIETGYTPIDISLSLTOFLSEFVPGAFLV-LGLVDIIMGIFGSQMDAFLVQIEQ 30 40 50 60 70 80
10719930 EWKESASLFTAPIVGVITSTLEALKKLVAGRVLSLTLNLLFPNNSLTMEELIRATEQ 90 100 110 120 130 140

cry1a-105.pe LINQRIEFARNQALSRLGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALT 90 100 110 120 130 140
10719930 YIQEQLDVTWNRVSQELGLEKNDLRTFNDQIDDFLQNRVIGISPLAID-SINTMQQLFV 150 160 170 180 190 200

cry1a-105.pe TAIPLFAYONVQVPLLSVYVQAAHLHLSVLRDVSFGQWGFDAATINSRYNDLTRIGN 150 160 170 180 190 200
10719930 NRLFQFQVSDQVLLFLFQAATLHLTFVRDIIINADENWIPAEQLNTYTRYKQVQAQ 210 220 230 240 250 260

cry1a-105.pe YTDHAVRWNTGLERVMGPDSDWRIR-YNQFRRLTLTVLDIVSLFFPNYDSRTYPIRTVS 210 220 230 240 250 260
10719930 YSNYALSTYEEAFRARP-P-RNTVENMLEKFTMTLNVLVDLSVMSLLKYVNLVYSTSA 270 280 290 300 310 320

310

CRYIA-105.pe QLTREIYTNVPLENFDGSRGSAQIEGS---IRSPHMLDILNSITI---YTDHAGREYY
10719930 NL-YNIGONKYNVE---GEYSISYWPFFNTYIQTKSNYVLGSGVSYAMRWSYTNPPFGEYI
330 340 350 360 370

CRYIA-105.pe WSG-HQIMASPVG-FSGPTEFLYXGTMGNAAPQORIVAOLGQGVYRTLSLTYRRPNI
10719930 QDHLYNITASTYGVNGPQIGQQLSTTELDQVQQARADIPVDFTQIPINCITLENFLEV
380 390 400 410 420 430

CRYIA-105.pe GINNQQLSVLDCGTEFAYGTSNLSAVYKSGTVDLSDEIPQNNVPPRQGFSHLSHV
10719930 PYATRFNELTSLGTA-GVGGFVRSDFVFNDSVGLTNYSSGQTFYDDYVITNISATV
440 450 460 470 480 490

CRYIA-105.pe SMFRGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPLVKAHTLQSGTTVVRGPG
10719930 QVNGTNDISPLFYGENRAITSTNGVKNVIAIYNKKNYDDFTNIRGTIVHEAPTDTSTGF
500 510 520 530 540 550

CRYIA-105.pep
NRAA:17977979

9622200 source="GENBANK PROT" parasporeal crystal protein CryI8Cai (Paenibacillus
popilliae)gi|10719930|sp|P57092|c18CA PAEPP Parasporeal crystal protein cryI8C
(Parasporeal delta-endotoxin CryXVIIIc(a)) (Crystalline parasporeal protoxin) (8
kDa crystal protein)

SCORES Initl: 71 Initn: 130 Opt: 259 2-score: 290.3 E(): 7e-08
>>NRAA:9622200
initn: 130 inil: 71 opt: 259 2-score: 290.3 expect(): 7e-08
Smith-Waterman score: 259; 22.6% identity in 367 aa overlap
(54-410:114-472)

CRYIA-105.pe LGGERTGCTPIDISLSTQFLSEFVGAGFVL-GLAVDIINGIFGSPQWDAFLVQIEQ
9622200 EWKESASLFTAPIVGVITSTLLEALKLVAGRVLMSTLNLFFNNSTSTMEILRATEQ
90 100 110 120 130 140

CRYIA-105.pe LINQRIEEFARNQALISRLGLSNLYQIYAESFREWEDPTNPALREEMRIQFNDMSALT
9622200 YIQEQLDTVTNRVSOEGLKNDLATFNDQIDDLQNRVGISPLAID-SINTWQQLFV
150 160 170 180 190 200

CRYIA-105.pe TAIPLFVQNVQVPLLSVYQAAHLHSLVRDVSFVGQWGFDAATINSRYNDLRLIGN
9622200 NRIPLQVSDQVLLPLFAQAVTLHLTFVRDIIINADEMNIPEAQNTYKRYLQYVAAQ
210 220 230 240 250 260

CRYIA-105.pe YTDHAYRWNTGLERVWGPDSRWIR-YNQRRELTTLVLDIVSLFNNYDSRTYPIRTVS
9622200 YSNVALTYEEAFRFRFP--RNIVENMLFEKTFPLMLNVLVSWLSLXNLYVTSISA
270 280 290 300 310 320

CRYIA-105.pe QLTREIYTNVPLENFDGSRGSAQIEGS---IRSPHMLDILNSITI---YTDHAGREYY
330 340 350 360 370

9622200 NL-YNIGONKYNVE---GEYSISYWPFFNTYIQTKSNYVLGSGVSYAMRWSYTNPPFGEYI
330 340 350 360 370

CRYIA-105.pe WSG-HQIMASPVG-FSGPTEFLYXGTMGNAAPQORIVAOLGQGVYRTLSLTYRRPNI
9622200 QDHLYNITASTYGVNGPQIGQQLSTTELDQVQQARADIPVDFTQIPINCITLENFLEV
380 390 400 410 420 430

CRYIA-105.pe GINNQQLSVLDCGTEFAYGTSNLSAVYKSGTVDLSDEIPQNNVPPRQGFSHLSHV
9622200 PYATRFNELTSLGTA-GVGGFVRSDFVFNDSVGLTNYSSGQTFYDDYVITNISATV
440 450 460 470 480 490

CRYIA-105.pe SMFRGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPLVKAHTLQSGTTVVRGPG
9622200 QVNGTNDISPLFYGENRAITSTNGVKNVIAIYNKKNYDDFTNIRGTIVHEAPTDTSTGF
500 510 520 530 540 550

CRYIA-105.pep
NRAA:17977979

17977979 source="GENBANK PROT" Cry29Aa protein (Bacillus thuringiensis serovar
medellin)

SCORES Initl: 113 Initn: 310 Opt: 257 2-score: 288.5 E(): 8.9e-08
>>NRAA:17977979
initn: 310 inil: 113 opt: 257 2-score: 288.5 expect(): 8.9e-08
Smith-Waterman score: 662; 27.8% identity in 597 aa overlap
(53-625:62-648)

CRYIA-105.pe VLGCRIPGTPPIDISLSTQFLSEFVGAGFVLGLVDIINGIFGSPQW---DAFLV
17977979 QNSLVGLFAITAAIISLSSNITIGTISIAAGTAIAAAIPIILM---PSQENNLDPKLLA
80 90 100 110 120

CRYIA-105.pe QIEQLINQREERENQALISRLGLSNLYQIYAESFREWEDPTNPALREEMRIQFNDMN
17977979 ISEATLYSFQDQVRVEDNTRLESLSSVSYFENANTFTNPNP-NSNTTITVRERFQVN
130 140 150 160 170 180

CRYIA-105.pe SALTATPILFVQNVQVPLLSVYQAAHLHSLVRDVSFVGQWGF---DAATINSRYN
17977979 GRFVGSMAFFRAKNVEPILSTVAQAARLLEHEDGLVWAEKNLSRGCSQMPDILLYK
190 200 210 220 230 240

CRYIA-105.pe DLTRLIGNYTDHAYRWNTGLERVWGPDSRWIRYNQFRRELSTVLDIUSFFYDSRT
17977979 EFNKYCNIEHCIKWYNESILSLKSVGA-NWLEYNOYRVTLTATSLVLDIVSLFSSVPR
250 260 270 280 290 300

CRYIA-105.pe YPIR-YVSQITREIYTNVPLENFDGSRGSAQIEGSIRSPHMLDILNSITIYDAHRE
17977979 YKELSLTRKRLTDIPI--NVHRGISLEADESKYTLIE-PFLFTQITLYITFYSNIF---
310 320 330 340 350 360 370

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cry1a-105.pe YWNGHGMASPVGSGPEFTFLYGTGMAPOORIVAGLGGVRLTSLSTLYRRPNI
17977979 YNMGH---TWYRILSPD-----KIFASRSG---KOSSTYDKVPV--
360 370 380 390

cry1a-105.pe GINNQQSLVDGTEFAYGTSSNLPASVYRK--SGTVDSLDEIPPONNVPRQGFSHRLS
17977979 -IPNDK-SIIYKIR-AVDNHNGLFNVMYFGWDGCKDQIKQIIGSGSTIYIKNCHRLA
400 410 420 430 440

cry1a-105.pe HYSMFRSGFSNVSIIIRAPMSWHRSAEFNNIIASDSITQIPLVKAHTLQSGTTVVRG
17977979 DVISHDLDEKNKCY-----FAWSTTISLENEIKNDIITQIPAVKAYOLGVQSVQVING
450 460 470 480 490 500

cry1a-105.pe PGFTGGDILRTSGGPEAYTIVNINGQLPORVARIYAS--FTNLR--IVTVAGERIF
17977979 PGHTGGDILNKSDNLRISCQHLN-VTKYFVRIYATNGSLNTRPIINIPGHTPQ
510 520 530 540 550 560

cry1a-105.pe AGQFNKTMW-TG-DPLTFQSFYATINTAFTFPMQS- SFTVGADTFSSGNEVIDRFEL
17977979 GMVLNDFSGTGYSNLEYQNGYKEFLKEVTLNPNQISILTNRSQNSNILLDRIEF
570 580 590 600 610 620

cry1a-105.pe IPVTATL--EAENYLERAKAVNALFTSTNQLGKNTVDYHIDQVSNLVTYLSDFEL
17977979 LPITFSIRKSKEQONLEKNQTKNKLFFN
630 640 650

cry1a-105.pap
NRAA:66734543
66734543 source="GENBANK_PROT" Cry2Ac [Bacillus thuringiensis]
```

```
SCORES Initl: 128 Initn: 163 Opt: 251 z-score: 282.0 E(): 2.1e-07
>>NRAA:66734543
Initn: 163 Initl: 128 Opt: 251 z-score: 282.0 expect(): 2.1e-07
Smith-Waterman score: 266; 22.2% identity in 553 aa overlap
(81-607:98-612)
```

```
cry1a-105.pe VFGAGFVLGLVDIIWIGFQSGQWDAFLVQIEQLINQRIEFARNQAIISLEGL-SNLYQI
66734543 LVGKILSELONLFFSGSIDLMQELIRATEQFINQRLNADTLGRVNAELAGLQANVAEF
70 80 90 100 110 120

cry1a-105.pe --YAESFREMADPTNPALREEMRIQFNDMNSALTATPLFAVQNVQVPLSVVQAAANL
110 120 130 140 150 160
17977979 NQVDNFLNPNQVPLAIDSV---NLQQLFLSLFQFQIQYQLLLPLFAQAAANL
130 140 150 160 170 180

cry1a-105.pe HLSVLRDVSFGQRMGWFDAATINSRYNDLTRIGNYTDHAVRWYNTGLERVWGDSR--D
170 180 190 200 210 220
66734543 HLSFRDVLNADENWGISAAVTVRDHLNFRNFRDYSYNTCYOTAFR--GLNTLHD
190 200 210 220 230 240
```

```
cry1a-105.pe WIRNQFRETLLVILDIVSLFNDYDSRTYPIRVSQL-----TREIYTN--PVLEN-
66734543 ML---EFRTYFLNVEFYIWSLKFYQSLVSSGANLYASGSGPTQSFQANWPFYLSL
250 260 270 280 290

cry1a-105.pe FDGSRGSAQGIEG---SIRSPHLMDILNSITTYDAHRGEYWSGHQIMASPVCFSGPE
66734543 FQVNSYVLNGLSGARTITTFNFGGLPGSTTQT-LHFAFINRGV-VSSSRICQANLN
300 310 320 330 340 350

cry1a-105.pe FTFFLYGTMGNAAPQQRIVAGLGGVRLTSLSTLYRRPFGNINNOQLSLVDGTEF-AYG
66734543 QNFNI-STLFPNLOTPTFIRSLDSDGTDEGVAT---STNWQSGAFETTLRFSIFSARG
360 370 380 390 400 410

cry1a-105.pe TSSNLPASVYRK-SGTVDSLDEIPPONNVPRQGFSHRLSHVSMFRSGFSNVSIIIRA
66734543 NSNFPDFIRNISGVVGTIS-----NADLA-----RELHFEIRDIGITAVASLVTV
420 430 440 450

cry1a-105.pe PMF-SWHRSAEFNNII--ASDSITQIPLVKAHTLQSGT---TVVRGPGFTGGDILRRTS
66734543 HNRKNNIYDTHENGTMHLAPNDYTGFTVSIPIATQVNNQIRTFISEKYNGQGSLSRLEL
460 470 480 490 500 510

cry1a-105.pe GGFAYTIVNINGQLPORVARIYASTTNRIYTVAGERIFAGQFNKTMIDGDLPTPQ
66734543 SNTTARYTLRGNGN---SYNLYRVSSIGSSTIRVTING-RVYVANVTNN-DGVLDN
520 530 540 550 560 570

cry1a-105.pe SFSYATINTAFTFPMQS SFTVGADTFSSGNEVIDRFELIPVTATLEAEYNLERAKAV
66734543 GARFSDINIGNVASANTNVPLDIQVTFNGNP-----QFELNMIMFVPTNLPLPY
580 590 600 610 620

cry1a-105.pe NALFTSTNQLGKNTVDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKELSDERNLL
cry1a-105.pap
SW:8469156
```

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

```
SCORES Initl: 106 Initn: 141 Opt: 244 z-score: 274.0 E(): 5.7e-07
>>SW:8469156
Initn: 141 Initl: 106 Opt: 244 z-score: 274.0 expect(): 5.7e-07
Smith-Waterman score: 250; 21.4% identity in 552 aa overlap
(81-607:98-611)
```

```
cry1a-105.pe VFGAGFVLGLVDIIWIGFQSGQWDAFLVQIEQLINQRIEFARNQAIISLEGL-SNLYQI
8469156 LVGKILSELONLFFSGSIDLMQELIRATEQFINQRLNADTLGRVNAELAGLQANVAEF
70 80 90 100 110 120
```

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```
cry1a-105.pe --VAESFREWEADPTNPALEEMRIQFNDMSALTATPLFAVQYVPLLSVYQAAANL
8469156 NRQVDNFLNPNQNPFLAIDSV---NTLOQLFUSRLPQFQIGQQLLLPLFAQAAAF
130 140 150 160 170 180
170 180 190 200 210 220
cry1a-105.pe HLSVLRDVSFGQRMGFDATINSNDLTRIGNNDHVRWYNTGLERVGPDSR--D
8469156 NLSFIRGVILNADENGLISAATVTRTDRHLKPHRDYNYCINPYQTAFR---GLNHRLPD
130 140 150 160 170 180
230 240 250 260 270 280
cry1a-105.pe WIRYNOFRRLTLVLDIVLFFNYSRTYPIRTVSQI-----TREIYTN---PVLEN-
8469156 ML---EFRTYPLANVFEVYSWLSFKYQSDLVSSGANLYASPSPTQSTPAQNWPFYLSL
250 260 270 280 290 300
cry1a-105.pe FDCSFRGSAQEGSIRSPLMDILNSITIIDTA--HRGEVYWSGHQIMASVPFGSPF
8469156 FQVNSYVNLGSLGA-KITITFENIGGLPVHNSTLHAFINRYRGV-VSSSRIGQANLNG
300 310 320 330 340 350
360 370 380 390 400 410
cry1a-105.pe TFLYGTGMAAPQRIVAQIQGVYRTLSLTLRRPNIGINNQLSVLDGTEF-AVGT
8469156 NFNI-STLFNPLQTFPIRSLWDSITDREGVAI-----STNWOSGAFETTLIRFSIFSARGN
360 370 380 390 400 410
420 430 440 450
cry1a-105.pe SSNLPSAVYRK-SGTVDLSDEIPQNNVPPRQGFHSRLSHVSMFSGNSVSIIRAP
8469156 SNFFPDYIRNISGVGTIS-----NADLA-----RPLHFNEDIRDTTAVASLVTVH
420 430 440 450
460 470 480 490 500
cry1a-105.pe MF-SMHSRSEFNII--ASDSITQIPLVKATLQSGT---TVVRGPGFTGDILRTSG
8469156 NRKNNIYDTHENGTMHILAPNDYGTFTVSPHATQVNNQIRTFISEKYGNQSDSLRFELS
460 470 480 490 500
510 520 530 540 550 560
cry1a-105.pe GPFAITVINGQLPQRYRARIYASTTNLRIYTVVAGERIFAFQFNKMTDGTQFQS
8469156 NPTARYTLRNGN---SYNLYLRVSSIGSSTIRVTING-RVYVANVTITNN-DGVLDNG
520 530 540 550 560 570
570 580 590 600 610 620
cry1a-105.pe FSYATINTAFTFPMSSQSFVAGDFTSSGNEVIDRRELIPVTATLEAYNLRAQAVN
8469156 ARFSDINCNVVASANTVPLDIQVTFNGNP-----QPELMNIMFVPTNLPPLY
580 590 600 610 620
630 640 650 660 670 680
cry1a-105.pe ALFTSTNGLKLTNVTYDHDQVSNLVTVLSDEFCLDEKSELSEKVKHAKRLSDERNLQ
8469156
NRAA:40286
40286 source="GENBANK PROT" CryIIIC delta-endotoxin [Bacillus
thuringiensis]gi|8469156|sp|Q45743|CR2AC BACTU pesticidal crystal protein
cry2Ac (insecticidal delta-endotoxin CryIIA(c)) (Crystalline entomocidal
protoxin) (70 kDa crystal protein)gi|228281|prf|1802281A delta endotoxin
```

```
SCORES Initl: 106 Initn: 141 Opt: 244 z-score: 274.0 E(): 5.7e-07
>NRAA:40286
Initn: 141 Initl: 106 Opt: 244 z-score: 274.0 expect(): 5.7e-07
Smith-Waterman score: 250; 21.4% identity in 552 aa overlap
(81-607:98-611)
cry1a-105.pe VPAGFVLGVLDIINGIFGSDQDAFLVQIQLINRIEFPARNQAISREGL-SNLYQI
40286 LVKGRILSELQNLFFPGSSIDLMOEILRATEQFINORLNADTLGRVNAELAGLQANVAEF
70 80 90 100 110 120
130 140 150 160 170 180
cry1a-105.pe --VAESFREWEADPTNPALEEMRIQFNDMSALTATPLFAVQYVPLLSVYQAAANL
40286 NRQVDNFLNPNQNPFLAIDSV---NTLOQLFUSRLPQFQIGQQLLLPLFAQAAAF
130 140 150 160 170 180
170 180 190 200 210 220
cry1a-105.pe HLSVLRDVSFGQRMGFDATINSRYNDLTRIGNNDHVRWYNTGLERVGPDSR--D
40286 NLSFIRGVILNADENGLISAATVTRTDRHLKPHRDYNYCINPYQTAFR---GLNHRLPD
190 200 210 220 230 240
250 260 270 280 290
cry1a-105.pe WIRYNOFRRLTLVLDIVLFFNYSRTYPIRTVSQI-----TREIYTN---PVLEN-
40286 ML---EFRTYPLANVFEVYSWLSFKYQSDLVSSGANLYASPSPTQSTPAQNWPFYLSL
250 260 270 280 290
300 310 320 330 340 350
cry1a-105.pe FDCSFRGSAQEGSIRSPLMDILNSITIIDTA--HRGEVYWSGHQIMASVPFGSPF
40286 FQVNSYVNLGSLGA-KITITFENIGGLPVHNSTLHAFINRYRGV-VSSSRIGQANLNG
300 310 320 330 340 350
360 370 380 390 400 410
cry1a-105.pe SSNLPSAVYRK-SGTVDLSDEIPQNNVPPRQGFHSRLSHVSMFSGNSVSIIRAP
40286 SNFFPDYIRNISGVGTIS-----NADLA-----RPLHFNEDIRDTTAVASLVTVH
420 430 440 450
460 470 480 490 500
cry1a-105.pe MF-SMHSRSEFNII--ASDSITQIPLVKATLQSGT---TVVRGPGFTGDILRTSG
40286 NRKNNIYDTHENGTMHILAPNDYGTFTVSPHATQVNNQIRTFISEKYGNQSDSLRFELS
460 470 480 490 500
510 520 530 540 550 560
cry1a-105.pe GPFAITVINGQLPQRYRARIYASTTNLRIYTVVAGERIFAFQFNKMTDGTQFQS
40286 NPTARYTLRNGN---SYNLYLRVSSIGSSTIRVTING-RVYVANVTITNN-DGVLDNG
520 530 540 550 560 570
570 580 590 600 610 620
cry1a-105.pe FSYATINTAFTFPMSSQSFVAGDFTSSGNEVIDRRELIPVTATLEAYNLRAQAVN
40286 ARFSDINCNVVASANTVPLDIQVTFNGNP-----QPELMNIMFVPTNLPPLY
580 590 600 610 620
630 640 650 660 670 680
```

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```

crys1a-105.pep
NR04:73540082

73540082 source="GENBANK_PROT" Twin-arginine translocation pathway signal
[Ralstonia eutropha JMP134]gi|72117495|gb|AA259758.1|Twin-arginine
translocation pathway signal [Ralstonia eutropha JMP134]

SCORES   Init1: 123   Initn: 123   Opt: 241   Z-score: 272.1 E(): 7.3e-07
>>NR04:73540082
initn: 123 init1: 123 opt: 241 Z-score: 272.1 expect(): 7.3e-07
Smith-Waterman score: 241; 24.6% identity in 362 aa overlap
(35-373;39-368)

crys1a-105.pe PNINECIPNCLSNPEVEVLGERIEGTYPIDISLTSQFLSEFVPGAGFLV-LVDI
10 20 30 40 50 60
73540082 RSIFSALMAMGAPPAHADGALGKLPVTPDMDEKLTILEVLAIE-VPVVGAMSAALVGL
10 20 30 40 50 60

crys1a-105.pe IWGIFGSDWDAFLVQIEQLINQRIIEFARNQAIISREGLSNLYQIYAESFFREWEADPTN
70 80 90 100 110 120
73540082 LWPVEPADWEEIRQKVEALTEQKINDAVVYSLKSLKLDGTGNTLKLYLNA--AATGDISN
70 80 90 100 110 120

crys1a-105.pe PALREEMRIQFNMNSALTTAIPLFAVQNYQ--VPLLSVYVQAANLHLSVLRDVSVFGQ
130 140 150 160 170 180
73540082 -----NRMQFIATNTQMTLAASEFRNPDFOMWLAPLFAIFSQ---LHAVLRDCVLHGR
130 140 150 160 170

crys1a-105.pe EWGFDATINSRY---NDLTLEIGNYTDHAVRYNTGLERVW--GPDSDWIRYN---QF
190 200 210 220 230
73540082 DWGNTATYEGVYRVLASDTINEXHAYLDVAVKEQDLAPAAPTSFGKHYYAIYVWQSF
180 190 200 210 220 230

crys1a-105.pe RRELTFLVLDIVSLPNYDSRTPIRTVSQLTREIYTNVLENFDGSGSGAQTG---
240 250 260 270 280
73540082 SOKQVLFEGDYMLLNALD---PIRNPQG---VKTIIPDFVFSAAI-GTADOMDATCR
240 250 260 270 280

crys1a-105.pe ---GSIRSPHLMDLINSITYTDHAGREYWGSHQIMAS-PVGSGPEFTFLYGTWGN
290 300 310 320 330 340
73540082 AWAGAVATPFSIPAANISEIYIEL---ENFTPIRDVDSYPAG-SGPK-----VWG--GNR
290 300 310 320 330

crys1a-105.pe APOQRIVAQGGV-YRFLS--STLYRRFPNFINNQOLSVLDGTGFAYGTSNNLPSAVY
350 360 370 380 390 400
73540082 QDRTGIADRVSGVEQKTIISIPRSTDGKTFNLAGASIRAGSIPTAVSLVMDQKSKIALWD
340 350 360 370 380 390

crys1a-105.pe RKSGTVDLSDELTPQNNNVPRQGFHRLSHVSMRFGFNSVSIIIRAPMFSWIKHSAE
410 420 430 440 450 460
73540082 RRDGLGQQFVSVVPGKRLTTLNMMWSRFDYNDLGCIFGFSRDPDIPPAVREALYVTA
400 410 420 430 440 450

crys1a-105.pep

```

~~NR0A:20091447~~

20091447 source="GENBANK PROT" hypothetical protein MA2621 [Methanosarcina acetivorans C2A|gi19916390|gb|AAW06802.1| hypothetical protein [Methanosarcina acetivorans str. C2A]

SCORES Init1: 102 InitInt: 177 Opt: 191 z-score: 222.2 E(): 0.00044
>NRRA:20091447
Init1: 177 InitInt: 102 Opt: 191 z-score: 222.2 expect(): 0.00044
Smith-Waterman score: 191: 2% identity in 113 aa overlap
(167-272)-(112)

cry1a-105.pe MNSALTTPILFAVQNYQVPLLSVYNOANLHLSVRDVSFGCRWGFDAATINSRYNDL
 140 150 160 170 180 190
 20091447 HELLLRDGALICFSGWNEEISQHTSEGI

```

200      210      220      230      240      250
cryla-105.pe  TRLGIVYTDHVRWYNTGLERVW--GPDSDRWIR----YNGFRRLTLVLDIVSLFRNY
: ||| : : : : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

40 50 60 70 80 90
 260 270 280 290 300 310
 DSRTPRTVSQITREIYNPVLENFDSRGSAOGIEGSRPSDHIMJINSITINDAN
 CIVJ1A-105 DE

2003144 / DFVKIFPAEVI LSKEIISDAVGIA DNSGALNF PQHFKASRSQKWKSGPGIGLMPVKLLIR 100 110 120 130 140 150

crv1a-105 nen

NRAA: 66800187

66800187 source="GENBANK_PROT" hypothetical protein DB0192018 [Dictyostelium discoideum]gi|60462380|gb|EAL60601.1| hypothetical protein DB0192018 [Dictyostelium discoideum]

SCORES Init1: 54 Opt: 181 z-score: 202.0 E(): 0.0059
 >NRRA:66800187
 Init1: 54 Opt: 181 z-score: 202.0 expect(): 0.0059
 Smith-Waterman score: 185; 20.6% identity in 243 aa overlap
 (51-279;61-303)

```
cryla-105.pe VEVLGRIGETYPIDISLQTLSEVPVCGAVFLG-LVDIIMG-IFGSQ-----  
              :|   |   |   |   |   |   |   |:|   |   |   |   |   |:  
68800187    PIISDYQTNSNVNDYTELIIIVVGGLSIPTIGNPLSVLSVAWHAHSITNETTVFVV  
            40      50       60        70
```

```
cryla-105.pe WDAFLVQIQLNQIRAEFARNQAISLEGSLNYVAESFREWEDPTNPALREMRI  
::: | :: | : : : : | : | : : : : : : : : : : : : : : :  
YNSYREMIMATIONSIDMYDASTIKAVLTAKNALVIDTKAKNKYLTPNQAIPVKRLVD
```

```

cylinder-105.pe QFDMNSALT-TAIPLFAV--QNYQVPLSVVYQQAHLHLSVLRDVSFQCRMGFDAATI
140      150      160      170      180
AHNLLYIEURGSGLLPLSDIRKEGYEAOLGAFALMATTAHLLLLKEGSGTNGKIGWISSEKI
190      200      210
66800187

```

```

190 200 210 220 230 240
cryla-105.pe NSRYNDLTRLIGNYTDHVRWYNTGLERV--WGPDS-RDWIRYNQFRRELTTLTVLDIVSL

```

66800187
ETFEQFNKNWEYAQHCKLAYKGVAKIKALGIDGMQFNKLTFRSFCARYVFDVYNL
:: ::::: : :::: | | :: | | :: : | | : | ::

cry1a-105.pe FPNYDSRTYPPIRTVSQLTREIYTNVPVLENFDGSRGSAQIEGSI RSPHLM DILNSITTY

	280	290	300	310	320	330
--	-----	-----	-----	-----	-----	-----

cryla-105.pe TDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGGVYRTLSSL

[illegible]

cryla-105.pép
SW:8928023

8928023 description="PESTICIDIAL CRYSTAL PROTEIN CRY11BA (INSECTICIDAL DELTA-ENDOTOXIN CRY11BA) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (81 KDA CRYSTAL PROTEIN)." library="NA species="Bacillus thuringiensis serovar jegathesan" source="swissprot prot" version="NA type="prt

SCORES Init1: 60 Initn: 86 Opt: 178 Z-score: 198.0 E(): 0.0098
 P>SW: 8428623
 Init1: 86 Initn: 60 Opt: 178 Z-score: 198.0 E(): 0.0098
 P>SW: 8428623
 Smith-Waterman score: 199; 18.0% identity in 655 aa overlap
 47 605.1-633.1

89280623 MON-NTTTEINWTFP--MYNG-RLEPSLAPALAVAPIAKYLATATAKAWVKQGF
:
MDNNENINFCINCLNSPEVEVLGGERITGVTPIDISLS-LTQFL--LSSEFVGAG

[illegible]

```

cry1a-105.pe      MEADPTNPALREEMRIQNDSSALTTATFQAVQNYCPRLQYVQAAHLHSVLSDVS
8928023           SKFE-TGVANR-----LFFDTSNOLLRLPQFAGKGVNISFTQCTMCTHGLLKKDGI
                  120      130      140      150      160

```

```

cryla-105.pe      VFGORWGFDAATINGSYNDLRLIGNYTHDVAWVNSGLERWGPDSQZIRUYNFREL
                    :   :   |   :   :   :   :   :   :   :   :   :   :   :   :   :
8928023           LAGSDWGFADAPKDIALICOFNRVFNEYNTLMVLVSFGSLAKNHEWTINRMCSSX
                    :   :   :   :   :   :   :   :   :   :   :   :   :
170              170    180    190    200    210    220    230
```

```

cryla-105.pe  TLTVLIVSLFPPWYDSRTVPYITVSQLTREIYNPNVLENFSGRSGAGTSSISL
8928023      VFPFSEAWSLRYEGTKLNTLSLWNFVGESINNISPNDWGALYKLLMGAPG---RL
230 240 250 260 270 280 290

```

```

cryla-105.pe MDIINSITYTDA---HRGEY-----WSGQINASPVG---FSGEFTTPLYGMGNA
               : : : : | | : : : : | | : : : : | | : : : :
8928023      NNKVFNYSFSDTQATIHRENIHGVLPTNGGGTTIGWIGNRFGS-LSPPCSNEILEIT

```

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```

290      300      310      320      330      340
cry1a-105.pe APOQRIVVAQGGVATLSSLYRR-----PF--NIGINNQOLS--VLDGTEF
350      360      370      380      390      400
8928023 KIKQETIYNDKGNFNSIVPAATREILITATVPTSADPFKATADINMKYFSPGLYSGWNI
350      360      370      380      390      400
390      400      410      420      430      440
cry1a-105.pe AYTSSNLPSAVYRK-SGTVDSLDEIPQNNVPRQ---GFSH---RLSHVSMFRSGFS
410      420      430      440      450      460
8928023 KFDITVLKSRVPSIIPSNILKYDDYIVRAVSACPKGVSLAYNHDFTLTYNKLEYDAFT
410      420      430      440      450      460
450      460      470      480      490      500
cry1a-105.pe NSSVSIIRAPMSWIHRSAEFNIIASDSITQIPLVKAHTLQSGTTVVVRGP-FTGDDIL
470      480      490      500      510      520
8928023 TQNIIVGFSFNDTKSFYRSNSHYLSITDDAVVIPALQFSTVSDRSFLEDPDQATDGSIK
470      480      490      500      510      520
510      520      530      540      550      560
cry1a-105.pe RRTS--GGPAYTI-VNINGQLPQRYRARIYASTTNRIYTVVAGERIFAGQNKMTDT
510      520      530      540      550      560
8928023 FTDTVLGNEAKYSIRLNTGFNTATRYRLIIRFKAPARLAAGIRVRSON--SGN-NKLLG-
530      540      550      560      570      580
560      570      580      590      600      610
cry1a-105.pe GDPLTFQSFYATINTATFP---MSQSS-----FTVGADTFSSGNEVIYDRFELIPIVAT
580      590      600      610      620      630
8928023 GIPVEGNSGWIDYITDSFTDGLGITTSTNAFFSIDSDGVNASQQWYLSKLILVKRESSF
580      590      600      610      620      630
620      630      640      650      660      670
cry1a-105.pe LEAEYNLERAQKAVNALETSTNQLGLKNTVDYHIDQVSNLVTLSDEFCLDEKRELSK
640      650      660      670      680      690
8928023 TTQIPLKPYVIVRCPTDFVSNSSSYEQGYNNYNNQNSSSMYDQGYNNSYNPNSGCTC
640      650      660      670      680      690
cry1a-105.pep
NRAA:971347
971347 source="GENBANK PROT" mosquito toxin [Bacillus
thuringiensis]gi|8928023|sp|Q45730|C11BA_BACTO_Pesticidal crystal protein
cry11Ba (Insecticidal delta-endotoxin CryXIb(a)) (Crystalline entomocidal
protoxin) (81 kDa crystal protein)
SCORES   Initl: 60   Initn: 86   Opt: 178   z-score: 198.0   E(): 0.0098
>NRAA:971347
Initn: 86   Initl: 60   Opt: 178   z-score: 198.0   expect(): 0.0098
Smith-Waterman score: 199; 18.0% identity in 655 aa overlap
(1-605:1-633)
```

```

10      20      30      40      50
cry1a-105.pe MDNNPNINECIPVNCLSNPEVEVLGGERIETGYTPIDISLS-LTQFL---LSFEVPGAGF
10      20      30      40      50
971347 MQNN-NFNTTEINMINFP---MYNG-RLEPSLAPALIAVAPIAKYALATALAKWVKQGF
10      20      30      40      50
60      70      80      90      100      110
cry1a-105.pe VLGLVDIIMGIFGPGSQDVAFLVQIEQLINRIEERFARNOAISREGLSNLYQYIAESFRE
60      70      80      90      100      110
971347 AKLKEIFFPGNT-PATMDKVRIVETLLDQRLQDDRVKLLGEYKGIIDYKVFDTYVNO
60      70      80      90      100      110
```

```

120      130      140      150      160      170
cry1a-105.pe WEADPTPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYQAAHLHSLVLRDVS
120      130      140      150      160      170
971347 SKFE-TGTANR-----LFFDTSNQLISRLPQFEIAGYEGVISLSLTQMTCTFHLGLLKOGI
120      130      140      150      160      170
180      190      200      210      220      230
cry1a-105.pe VFGQRMGFDAATINSYNDLIRLLGNVTHAVRWNTGLRWGPDSDRWIRYNQFRRL
180      190      200      210      220      230
971347 LAGSDMGFAPADKALICQNRKFVNEYNTRLMWLYSKFGLKANNLEALNFRNMCSLY
180      190      200      210      220      230
240      250      260      270      280      290
cry1a-105.pe TLTVLDIVSLFPNYDSRTVPRTVSQLTREIYTNVLENFDSFRGSAQIEGSIIRPHL
240      250      260      270      280      290
971347 VFPSEAWSLRVEGTKLENTLSLWNFVGSINNISPNDWKALYKLLMGAPNQ----RL
240      250      260      270      280      290
300      310      320      330      340      350
cry1a-105.pe MDILNIIITYDA---HRGEY-----WSGHQIMASPVG---FSGPEFTFLYGTMGNA
300      310      320      330      340      350
971347 NNKVFNSYFSDTQATIHRENHGVLTNGGTTITGWTGNFRFSG--LSFPGCSNELEIT
290      300      310      320      330      340
350      360      370      380      390      400
cry1a-105.pe APOQRIVVAQGGVATLSSLYRR-----PF--NIGINNQOLS--VLDGTEF
350      360      370      380      390      400
971347 KIKQETIYNDKGNFNSIVPAATREILITATVPTSADPFKATADINMKYFSPGLYSGWNI
350      360      370      380      390      400
390      400      410      420      430      440
cry1a-105.pe AYTSSNLPSAVYRK-SGTVDSLDEIPQNNVPRQ---GFSH---RLSHVSMFRSGFS
390      400      410      420      430      440
971347 KFDITVLKSRVPSIIPSNILKYDDYIVRAVSACPKGVSLAYNHDFTLTYNKLEYDAFT
410      420      430      440      450      460
450      460      470      480      490      500
cry1a-105.pe NSSVSIIRAPMSWIHRSAEFNIIASDSITQIPLVKAHTLQSGTTVVVRGP-FTGDDIL
450      460      470      480      490      500
971347 TQNIIVGFSFNDTKSFYRSNSHYLSITDDAVVIPALQFSTVSDRSFLEDPDQATDGSIK
470      480      490      500      510      520
510      520      530      540      550      560
cry1a-105.pe RRTS--GGPAYTI-VNINGQLPQRYRARIYASTTNRIYTVVAGERIFAGQNKMTDT
510      520      530      540      550      560
971347 FTDIVLGNEAKYSIRLNTGFNTATRYRLIIRFKAPARLAAGIRVRSON--SGN-NKLLG-
530      540      550      560      570      580
560      570      580      590      600      610
cry1a-105.pe GDPLTFQSFYATINTATFP---MSQSS-----FTVGADTFSSGNEVIYDRFELIPIVAT
560      570      580      590      600      610
971347 GIPVEGNSGWIDYITDSFTDGLGITTSTNAFFSIDSDGVNASQQWYLSKLILVKRESSF
580      590      600      610      620      630
620      630      640      650      660      670
cry1a-105.pe LEAEYNLERAQKAVNALETSTNQLGLKNTVDYHIDQVSNLVTLSDEFCLDEKRELSK
620      630      640      650      660      670
971347 TTQIPLKPYVIVRCPTDFVSNSSSYEQGYNNYNNQNSSSMYDQGYNNSYNPNSGCTC
640      650      660      670      680      690
cry1a-105.pep
NRAA:66805043
66805043 source="GENBANK PROT" hypothetical protein DB0188332 [Dictyostelium
discoideum]gi|60464685|gb|EAL62812.1| hypothetical protein DB0188332
```

ID:tyestellum discideum

SCORES Initl: 50 Inltn: 50 Opt: 175 z-score: 195.5 E(): 0.013
>>NRAA:66805043
inltn: 50 inltn: 50 opt: 175 z-score: 195.5 expect(): 0.013
Smith-Waterman score: 175; 20.9% identity in 216 aa overlap
(73-279;91-296)

cryla-105.pe TOFLLEFVPGAGVGLVWIIWIGIFETQWAFVQEQDINQRIEFARNQAISSLE
66805043 IPTYGAFISNAISCVFLEYTSKGNKTKNEFMDFSKIEELADYRQSF-----LSEVF
70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300

cryla-105.pe GLSNLYQIYAESFREWEADPTNPALRENRQFNMNSALTTATPLFAVQNVQVPLLSV
66805043 GIDTHLKFLAKLAFKIDPGEAAYCLO--EYNDVQRNDYDKLMMNDTRFKTTCI
110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300

cryla-105.pe YVOANLHLSVLVDVSGQWVG---FDAATNGSYNDLRLIGNTYDHAHRYWNGKSLR
66805043 FGLMATIHLIILNEGIKYSGKMGWREFYKVEITKCYDS--IPRVIECHTSYAGVAVR
170 180 190 200 210 220 230 240 250 260 270 280 290 300

cryla-105.pe WGFPSRD-----WRYNQFRELTLVLDIVSLFPNIDRTYPIRVISQLTREIYNPVL
66805043 IKDIDYMSAKFRAYNDYRNFCAITRVDFINGWIGLDENKFPDSINLENRYLWNGPYG
220 230 240 250 260 270 280 290 300 310 320 330 340 350

cryla-105.pe ENFDGSRGSAQGIERSIRSPHMLDILNSITTYDHAHRYWNGKSLR
66805043 IPVDNKSVPNVIDYQEEPYDFSPAKINDYMALEVDLNLVAKSCFENVDSEFINHR
280 290 300 310 320 330 340 350

cryla-105.pep
NRAA:21685428
21685428 source="GENBANK PROT" pesticidal crystal protein cryIIAA (Bacillus
thuringiensis serovar israelensis)gi|117327|sp|P21256|CilAA BACTI pesticidal
crystal protein cryIIAA (Insecticidal delta-endotoxin CryIIA(a)) (Crystalline
entomocidal protein) (72 kDa crystal protein)gi|142763|gb|AA22352.1|
mosquito-toxic crystal protein

SCORES Initl: 119 Inltn: 119 Opt: 175 z-score: 195.4 E(): 0.014
>>NRAA:21685428
inltn: 119 inltn: 119 opt: 175 z-score: 195.4 expect(): 0.014
Smith-Waterman score: 234; 20.9% identity in 646 aa overlap
(30-609;25-633)

cryla-105.pe MNNPNINECIYPNCLSNPEVVLGERIETGYTPIIDISUS-ITQPL---USEFVPGAGF
21685428 MEDSSLDLTSIVNETDFELVYNNYTEPTIAPALIAVAPTAQYLAIGKWAAKAF
10 20 30 40 50

cryla-105.pe VLGLVDIIWIGIFPSOWDAFLVQIQEOLINQRIEFARNQAISSLEGLSNLYQIYAESFRE
21685428 S-KVLSLIFPGSQPATMEKVRTEVELINQKLSQDRVNIILNAEYRGLIEVSDVDFATIKQ
60 70 80 90 100 110

cryla-105.pe WEADPTNPALRENRQFNMNSALTTATPLFAVQNVQVPLLSVQVAAANLHLSVLVDVS
21685428 PGFTATA-----KGFIPLNSGAILQIRPOEVQTEGVSIALLFTQMCTILALILKKDGI
120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300

cryla-105.pe VFQQRWGFDAATINSRNDTRLIGNYTDHVRWNTYDHAHRYWNGKSLR
21685428 LAGSAMGFTQADVDSFIKLQKQVLDYRRLMRMYTEEFGRGLCKVSLKDGKLTFRMCMNLY
170 180 190 200 210 220 230 240 250 260 270 280 290 300

cryla-105.pe W-----W--IRYQFRELTLVLDIVSLFPNIDRTYPIRVISQLTREIYNPVL
21685428 VFFFAEAWSLMRYEGLKQSSLSLDYGVGSIPVNYNEWGLVYKL--LMGEVNRQLTTV
230 240 250 260 270 280 290 300 310 320 330 340 350

cryla-105.pe NFQDGSFRGSAQGIERSIRSPH-LMDILNSITTYDHAHRYWNGKSLR
21685428 KFNYSFTNEPADIPARENIRGVPIYDPSGSLTGWINGRNNFNADNNGNEINEVTRQ
280 290 300 310 320 330 340 350

cryla-105.pe VGFSGPEFTPLGYTMGNAAPQORIVAQOGCVVRLTSSLYRPFNIGINNQOL--SVL
21685428 TPQNFN-NEPI-----APRD-IINQI--LTAPAPADLFFKNADINVKFTOWFSTL
330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500

cryla-105.pe DGEFAYGSSNLSAVYKSGTVDSLDDEIPQNNVPPRQGFSGHLSHVMSFRSGFSNS
21685428 YGHITLTIYQIEYDSITDENIIVGFAPQNTYDFYSKSHVLSLSEINDSYVIALQFAEV
440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990

cryla-105.pe SVSLINAPMFSWI--HAFEFNNIT--ASDSITQIPLVKARTIQSGTIVRPGPGTGGDI
21685428 YNHDLTITLYQIEYDSITDENIIVGFAPQNTYDFYSKSHVLSLSEINDSYVIALQFAEV
440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990

cryla-105.pe LRR-----TSGG-PRATIVNINPQPRVRRNRYASTNLRIVYTVAGERIFA
21685428 SDRSFLDTPDQATDGSIFKARFETISNEAKYSILNYSFNTATNVLKIRVRVP-YRLPA
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

cryla-105.pe GQNKMTDGTQPLTFQFSVAT-----INTATFEL--MSOSS--TVVGNTPGSG
21685428 GIRVQSGNSGNRMGLSGFTANANPENWDFVDTATFNDAGINSSINMLTSSLSLNSG
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

cryla-105.pe NEVYIDREFLIPVTATLEAEYNLERAQKAVNALFTSNQGLKNTVTDHIDQSNVAV
21685428 EEWYLSQLFLVKESAFITQINPLLK
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

cryla-105.pep
SW:117327

117327 description="PESTICIDIAL CRYSTAL PROTEIN CRY11AA (INSECTICIDAL DELTA-ENDOTOXIN CRYXIA(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (72 KDA CRYSTAL PROTEIN)." library="NA species="Bacillus thuringiensis serovar israelensis" source="swissprot_prot" version="NA type="PRT

SCORES Initl: 119 Initn: 119 Opt: 175 z-score: 195.4 E(): 0.014
>>SW:117327
initn: 119 initl: 119 opt: 175 z-score: 195.4 expect(): 0.014
Smith-Waterman score: 234; 20.9% identity in 646 aa overlap
(30-609:25-633)

cry1a-105.pe MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTIDISLS-LTQFL---LSEFVPGAGF
117327 MEDSSDLSLTSIVNETDFPLYNNYTEPTIAPALIAVAPIAQYLATAIGKAAKAAF
10 20 30 40 50
60 70 80 90 100 110

cry1a-105.pe VLGIVDIINGIFGSPQNDALFVQIEQLINORIEEFARNQAIISRLGSLNLYQIYAESFRE
117327 S-KVLSLIFPGSQPAIMEKVEITVELINQKUSQORVILNNAEYRGIIIEVSDVFAYIKQ
60 70 80 90 100 110
120 130 140 150 160 170

cry1a-105.pe WEADPTNPALREEMRIQFNDMNSALTAIPLFAVQVQVPLLSVYVQAAHLHLSVLRDVS
117327 LAGSANGFTQADVDSFIKFLNQKVDYRLRMRYTEEFGLCKVSLKDGSLFRMNCNLY
170 180 190 200 210 220
230 240 250 260 270 280

cry1a-105.pe VFGQWGFDAATINSRYNDLTRLIGNVTHAVRWYNTGLRWGPDSDR-----
117327 LAGSANGFTQADVDSFIKFLNQKVDYRLRMRYTEEFGLCKVSLKDGSLFRMNCNLY
170 180 190 200 210 220
230 240 250 260 270 280

cry1a-105.pe -----W--IRYNQFRELTLVLDIVSL-PP-NYDSRTYPIRTVSQLTREIYNPVLE
117327 VFPFAEAMSLMRYEGLKQSLSLWDYGVGSIPTVNYNEWGLVYKL--LMGEVNRLLTV
230 240 250 260 270 280
290 300 310 320 330 340

cry1a-105.pe NFDGSRGSAQGIEG--SIRSPH-LMDILNSITTYTDAHRGEYYW---SGHQIMA--SP
117327 KFNYSFTNEPADIPARENIRGVHPIDYDPSGLTGWINGRTNNFNADNNGNEIMEVRTQ
290 300 310 320 330 340
350 360 370 380 390 400

cry1a-105.pe VFGSGFEFTPLVGLTGMNAPOQRIVAOIGQGVYRTLSLTYRPFNIGINNQQDL--SVL
117327 IFTONEN-NEPI-----APRD-IINQI---LTAPADLFFKNADINVKTFQWQSTL
350 360 370 380 390 400
410 420 430 440 450 460

cry1a-105.pe DGTFAYGTSNLSAVYKSGTVDSLDEIPQNNNVPPRGFHSRLHVSFMFRSGFNS
117327 YGNWIKLQGTQVLSS-----RGT-----IPP---NYLAYDGYIRA--ISACPRGVSLA
400 410 420 430 440 450
460 470 480 490 500 510

cry1a-105.pe SVSIIIRAPMFSWI-HRSAEFNNII---ASDSITQIPLVKAHTLQSGTGVTVRPGFTGGDI
117327 YNHDLTATYNRIEYDPTTNIIVGFAPDNTKDFYSKKSHYLSSETSDSVIPLAQFAEV
440 450 460 470 480 490
500 510 520 530 540 550

cry1a-105.pe LRR-----TSGG-PFAYTIVNIGQLPQRYARIRVASTNRIYTVVAGERIPA
117327 SDRSFLETPDQATDGSIKFARTFISNEAKYSIRLNTGFTATRYKLIIRVRVP-YRLPA
500 510 520 530 540 550

cry1a-105.pe GQFNKTMDTGDPILTFQSFYSAT-----INTAFTEP--MSQSS---FTWCADTFSSG
117327 GIRVQSONGNRMMLGFTANAPENWVDFTDAFTFNDLGIITSTTALFSISSDLSNSG
560 570 580 590 600 610
620 630 640 650 660 670

cry1a-105.pe NEVVIDRFELIPVTATLEAEYNIERQAQVNALFTSTNQLGKTNVTDYHIDQVSNLVTY
117327 EEWYLSQLFLVKESAFITQINPLLK
600 610 620 630 640 650
660 670 680 690 700 710

cry1a-105.pep
NRAA:9798640

9798640 source="GENBANK_PROT" 81-kDa leukemia toxin [Bacillus thuringiensis]

SCORES Initl: 99 Initn: 99 Opt: 166 z-score: 184.4 E(): 0.056
>>NRAA:9798640
initn: 99 initl: 99 opt: 166 z-score: 184.4 expect(): 0.056
Smith-Waterman score: 224; 22.1% identity in 633 aa overlap
(38-608:149-723)

cry1a-105.pe NECIPYNCLSNPEVEVLGGERIETGYTIDISLSLTQFLSEFVPGAGFVLGVDIINGI
9798640 QTSFSALTQSNMNGGTIDNPLISTFFKVASLLPPLFSSLGALASFVV--TDSQTGA
120 130 140 150 160 170
180 190 200 210 220 230

cry1a-105.pe FGPSQWDAFLVQIEQLINORIEEFARNQAIISRLGSLNLYQIYAESFREWAD-----P
9798640 MA-NLARQWVDYVEKRIDSKILDYHFMGAELAAALNASLKEYARVVKIFENDMNRMAEP
180 190 200 210 220 230
240 250 260 270 280 290

cry1a-105.pe TNPALREEMRIQFNDMNSALTAIPLFAVO-NYQVPLLS--VYVQAAHLHLSVLRDV--S
9798640 PSTGVITQFRI-LNDFIKYIAKLOFSTNQSDLOYPVLTPLRAQACVMHMLLKDATTS
240 250 260 270 280 290
300 310 320 330 340 350

cry1a-105.pe VFGQWGFDAATINSRYNDLTRLIGNVTHAVRWYNTGL-----RVWG
9798640 VWGQQ--IDSQQLNGYKAEILIRLIKVTYNDVNTVYNGLELEKAKPLNYSDEEYLOAGR
300 310 320 330 340 350
360 370 380 390 400 410

cry1a-105.pe PDSR-----DWIRYNQFRELTLVLDIVSLFPNYSRTYPIRTVSQLTREIYT
9798640 PDISVLSRNFKEWMKNVAKYKFGKGMASALSALAAFFFTGFP-NYPKQALKVQVSRQIFA
360 370 380 390 400 410
420 430 440 450 460 470

cry1a-105.pe NPVLENFDSGRGSAQGIEGSIR---SPLMDILNSIT-IYTDHARGEYYW---SGHQI
9798640 -PWIGPGITSQDHSHTGSGFRFDVKTVDQIDALRLRMELYIQPLKSAFYIYESDKV
420 430 440 450 460 470
480 490 500 510 520 530

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Product Characterization Center

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cry1a-105.pe MASPGSGGFTPLPNTSNAAPQRIIVAOLOGQVYRTLSSTLYRRPFINGINNOOLS 350 360 370 380
9798640 RAYVN-----YIYIKRGSGNTG-----LAWGWSDDPSPVIVTSA-LGAAGVAPN 400 410 420 430
cry1a-105.pe VLDGTEFAYGSSNLPSPARKSGVDSIDELRQNNVPPROGFSH---RLSHVMSFRS 440 450 460 470
9798640 VV-GVRYSHGGS-----YTKGMA-----PPTNTNAPPE-FKYPYKILHSVAY-- 480 490 500 510
cry1a-105.pe GFSNSVSIIRAPMSW--IHRSAENNNIASDSNIOIYVKAHTLSGGTVVVRGPGFT 520 530 540 550
9798640 GLSKAP-DTADSVNMGFRPVLLENANOLLTDALQIPAEIOTDVPAPQSTERP-IN 560 570 580 590
cry1a-105.pe GQDIL-----RETSGCPATYININGQLPQRYRARIYASVNRD---IYQVGEREFA 600 610 620 630
9798640 GQDAIIWESFTSGFGFTYVDS-----PQKYKIYRIANNLSASTVSTYNNATFF 640 650 660 670
cry1a-105.pe GQFNKIMTDGDLTFOSFSVATINTAFTFPMSSQSFVGDGF---SSGNEVYIDNDEL 680 690 700 710
9798640 DILNTSLDP-NGVRNGVGYTLVEG-----PIIE--FSQINIFKLRSGGEFALDSIFFS 720 730 740 750
cry1a-105.pe PVTATLEAYNLERAKAVNALFTSTNGLTKNTVDYHIDQVSNLVTYLSDFECLDEKR 760 770 780 790
9798640 PVS
cry1a-105.pep
NRAA:8928042
8928042 source="GENBANK PROT" Pesticidal crystal protein cry1Bb (Insecticidal
delta-endotoxin Cry1B(b)) (Crystalline entomocidal protoxin) (84 kDa crystal
protein)/gi|4033727|gb|AAC97162.1| d-endotoxin [Bacillus thuringiensis]
SCORES Initl: 65 Initn: 65 Opt: 163 Z-score: 180.7 E(): 0.09
>NRAA:8928042
Initn: 65 Initl: 65 Opt: 163 Z-score: 180.7 expect(): 0.09
Smith-Waterman score: 182; 19.0% identity in 662 aa overlap
(13-605:6-633)
cry1a-105.pe MDNPNINECIPYCNLSNPEVEV--LGGRIETGYTPIDISLS-LTQFLSEFVPGAGVF 10 20 30 40 50
9798640 MENNSFNVLANNMSSPFLNSKIEPSIAPALIAVAPIAKYLATALAKWA-LK 60 70 80 90 100 110
cry1a-105.pe LGLVDITWIGFQSONDAFL-----VQIEQLINQRIEFAFNQALSRLEGLSNLYQIYAES 120 130 140 150 160 170
9798640 QGFALKESEIF-PGNETATMEKVRLEVTILNQTLDQDRVATLKAEGFIHLGKVFTDY 180 190 200 210 220 230
cry1a-105.pe FREWEADPTNPALREEMRIQFNDMNSALTTTAPLFAVQYQVPLLSVIVQANLHLSVLR 240 250 260 270 280 290
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8928042 VQSFTFTATA-----KTHFLMNSLLIQRLOFEIAGYEGVSISLFTQMCTLHLGLLK 120 130 140 150 160
cry1a-105.pe DYSVFGQSGWGF--DAATINSRYNDL-----TRLIGNYT-----DHAVRWYNTG 180 190 200 210
9798640 DGLAGSDMGFTPEDKSDLSICQPNRYVNEYNTMMGLYSIEFGRLAKNLKNEALNFRNMC 170 180 190 200 210 220
cry1a-105.pe LERVVGPDSRDW--IRYNQFRRELTLTVLDIVS-----LFPNVDSTYPIRTVSQLTRE 220 230 240 250 260
9798640 SLVVF-PFSEAWYLLRVEGCKLENTLSLWNFVGEDIGLHNDWKGLYKLLMGA----- 230 240 250 260 270
cry1a-105.pe IYTNPVLEN--FDGSRGSAQIGESIRSPLMDILNSIITYDHRGEYWSGHQIMAS 270 280 290 300 310 320
9798640 --TNORLANVFNYSFSDTQG-----TIHRENILGAHPTY-NGEQTPTGWNIGRGLGR 280 290 300 310 320 330
cry1a-105.pe PVGFSGP-----EFTFPLYCTMGNAAPQRIIVAOLOGQVYRTLSSTLYR--- 330 340 350 360
9798642 ---FSAPYSNELEITKVEQETIYNNKSDHSISVNPANTRNEILTATVPTADPFKTDADI 340 350 360 370 380
cry1a-105.pe RPFNIGIN-NOQLSVLDGTEFAFGTSSNLPSSAVVRKSGT-VDSLDEIPQNNVPPRQ 370 380 390 400 410 420
9798642 NRVFSSGLYYGNWIKFDRDVLNLSRVPGGIPSNRLELDGYVIRAVSACP---RNVPLSY 390 400 410 420 430 440
cry1a-105.pe GFSPFSLSHUSMPSGNSNSVSIIRAP--MFSWIHRSAEFNIIASDSITQIPLVKAHT 430 440 450 460 470 480
9798642 RNYLTLYARLEYDAPTQNTLVGFSFNNTKSFYARNSHY--LSATNDVAVIPALQFAT 450 460 470 480 490 500
cry1a-105.pe LQSGTTVARGG-FTGSDI--ARRTSGRFAKTI-VNINGQLPQRYRARIYASTNL-- 490 500 510 520 530
9798642 VSDRSFLEDTPDSDTSCIKFTFVQVWEAKYSRLNMGFNFTATFRLVIRFKATARLAA 510 520 530 540 550 560
cry1a-105.pe RYIVVAGERIFACQFNKNTMG--DPLTQSSFAATINTAFPMSSQSFVGDGF 540 550 560 570 580 590
9798642 GIRVRSQNSGNRLLGIPVEGNSGWTAVILDSFTANIGS-IITASRNAPSIDSDGV 570 580 590 600 610 620
cry1a-105.pe SSGNEVIDFELIPVTATLEAYNLERAKAVNALFTSTNGLSKNTVYHIDQVSNL 600 610 620 630 640 650
9798642 NASQQWLSKLILVLDKDFVNNSGFRNPVPLAPYVIARCPNTFFVNNSSGVGEGDNNYN 620 630 640 650 660 670
cry1a-105.pep
SW:8928042
8928042 description="PESTICIDIAL CRYSTAL PROTEIN CRY1IBB (INSECTICIDAL
DELTA-ENDOTOXIN CRY1B(b)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (84 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar medellin"
source="swissprot_prot" version="NA type="PRT"
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cyla-105.pe --RIYVTVAGERIFAGQFNKMTDGT--DPLTFOFSYATINTAFTFPMSQSSTFGVDGTF
      :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
8928042 GIRVRSONSGNELLGGIPVEGNSGDVYIT-DSFTFDLIG--ITTASTNAFFSIDSDGV
      570   580   600   610

cyla-105.pe SSGNEVIDRFELIPVTATLEAYNLERAQAKVNALFTSTNQLGLKNTVDYHIDQVSNL
      :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
8928042 NASQQWLSKLILVKDFVNNSGFRNQVPLAPYVIARCPNTPFVSNNTSSGYEQGYNDYN
      620   630   640   650   660   670

cyla-105.pcp
NRAA:68348789

68348789 source="GENBANK_PROT" cya4A insecticidal protein [Bacillus
thuringiensis]

SCORES   Initl: 77   Inltn: 109   Opt: 151   z-score: 177.8 E(): 0.13
>>NRAA:68348789
inltn: 109 initl: 77 opt: 151 Z-score: 177.8 expect(): 0.13
Smith-Waterman score: 172; 27.% identity in 137 aa overlap
(521-647:7-143)

cyla-105.pe GPGFTGGDIILRTSGPFAYTVINGQLPQRVARIRVAS--TTNLR--IYVTVAGERI
      500   510   520   530   540
68348789 SSSLNFQSQSYFIIRIVASNGSANTRAVINLSIPGVAE
      10   20   30

cyla-105.pe FAGQFNKMTDGT--DLPTFOFSYATINTAFTFPMSQS--SFTVGADTFSSGNEVYIDRFE
      550   560   570   580   590   600
68348789 LGMALNPTFGTDYTNLKYKFQYLEFSNEVKFAPQNISLVFNRSDVYTNLTLLDKIE
      40   50   60   70   80   90

cyla-105.pe LIPIVTATLEAYN--LEREAQAKVNALFTSTNQLGLKNTVDYHIDQVSNLVTLVSLDFEC
      610   620   630   640   650   660
68348789 FLPTIRSIREDKQLETVQQLINTFYANPKNTLQSELTYDYLDQGG
      100   110   120   130   140

cyla-105.pe LDEKRELSEKVHKAKELSDERNLLQDSNFKNIDINROPERGWGGTGITIOGGDDVFKEVYV
      670   680   690   700   710   720

cyla-105.pcp
NRAA:75812162

75812162 source="GENBANK_PROT" hypothetical protein [Bacillus thuringiensis]

SCORES   Initl: 99   Inltn: 99   Opt: 155   z-score: 176.1 E(): 0.16
>>NRAA:75812162
inltn: 99 initl: 99 opt: 155 Z-score: 176.1 expect(): 0.16
Smith-Waterman score: 178; 24.1% identity in 274 aa overlap
(38-273:97-362)

cyla-105.pe NECIPYCNLSNPEVEVLGERIETGYTPIDISLSLTFLSEFVPGAGFVLGIWDIINGI
      10   20   30   40   50   60
75812162 QTGSFSAITOSNNWGDTINPMLIISTIFFFKVASILLPPFLSSLGALASFYII--TDSOTGA

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cryla-105.pe FGSQWDAFLVQIEOLINRIEFAFNQALISLEGLSNLYOIAESFREWAD-----P
75812162 MA-NLARQWVDVFAIDSKILDYHNFNGAELALNASLKEAYARVVKIFENDMNRMAEP
130 140 150 160 170 180
cryla-105.pe TNPALREERIQDNMSALTATTAIPFAVQ-NYQVPLLSV--VYQAAHLHLSVLRDV--S
75812162 PSTGVITQFRI-LNDNFYKYLAKIQFSTNQSLQVPLVLTPLRAQACVHMLMLLDATTS
130 140 150 160 170 180
cryla-105.pe VFQGRWGFDAATINSRYNDLTRLLIGNYTHAVRWNTGLE-----RVWG
75812162 WMQOQ--IDSQQLNGYKAEILRLIKVYINDVNTYNOGLELEKAKPLINSDPEEYLQAGR
180 190 200 210 220 230 240 250 260 270 280 290 300
cryla-105.pe PD-----SRDWIRYNQFRRELTATVLDIVSLFPNYSRTYPTVSOL-TREIYT
75812162 PDISVLRSNFKKEMKWNVAKYKGMAMSAALSIAALFTTFCP-NYPKQALKVQSRQIFA
230 240 250 260 270 280 290 300 310 320 330 340 350
cryla-105.pe NPVLENFDGSRFGSAGGIEGSIRSPHLMILANSITYTDAHRGEYVWSGHQIMASPVGFS
75812162 -PVIGIPGGITSQDHSHTFG
270 280 290 300 310 320 330 340 350 360 370
cryla-105.pe
75812164
75812164 source="GENBANK_PROT" hypothetical protein [Bacillus thuringiensis]
SCORES Initl: 99 Initn: 99 Opt: 154 z-score: 174.7 E(): 0.2
-->NRAA:75812164
Initn: 99 Initl: 99 Opt: 154 z-score: 174.7 expect(): 0.2
Smith-Waterman score: 177; 24.1% identity in 274 aa overlap
(38-273:116-381)
```

```
75812164 WMQOQ--IDSQQLNGYKAEILRLIKVYINDVNTYNOGLELEKAKPLINSDPEEYLQAGR
270 280 290 300 310
cryla-105.pe PD-----SRDWIRYNQFRRELTATVLDIVSLFPNYSRTYPTVSOL-TREIYT
230 240 250 260
75812164 PDISVLRSNFKKEMKWNVAKYKGMAMSAALSIAALFTTFCP-NYPKQALKVQSRQIFA
320 330 340 350 360 370
cryla-105.pe NPVLENFDGSRFGSAGGIEGSIRSPHLMILANSITYTDAHRGEYVWSGHQIMASPVGFS
270 280 290 300 310 320
75812164 -PVIGIPGGITSQDHSHTFG
380 390
cryla-105.pe
75812164
75812164 source="GENBANK_PROT" 83-KDa crystal protein [Bacillus thuringiensis]
SCORES Initl: 99 Initn: 99 Opt: 156 z-score: 172.9 E(): 0.25
-->NRAA:37543234
Initn: 99 Initl: 99 Opt: 156 z-score: 172.9 expect(): 0.25
Smith-Waterman score: 220; 21.7% identity in 628 aa overlap
(38-687:168-741)
```

75812164 source="GENBANK_PROT" hypothetical protein [Bacillus thuringiensis]

SCORES Initl: 99 Initn: 99 Opt: 154 z-score: 174.7 E(): 0.2
-->NRAA:75812164
Initn: 99 Initl: 99 Opt: 154 z-score: 174.7 expect(): 0.2
Smith-Waterman score: 177; 24.1% identity in 274 aa overlap
(38-273:116-381)

```
cryla-105.pe FGSQWDAFLVQIEOLINRIEFAFNQALISLEGLSNLYOIAESFREWAD-----P
75812164 MA-NLARQWVDVFAIDSKILDYHNFNGAELALNASLKEAYARVVKIFENDMNRMAEP
130 140 150 160 170 180 190 200
cryla-105.pe TNPALREERIQDNMSALTATTAIPFAVQ-NYQVPLLSV--VYQAAHLHLSVLRDV--S
75812164 PSTGVITQFRI-LNDNFYKYLAKIQFSTNQSLQVPLVLTPLRAQACVHMLMLLDATTS
130 140 150 160 170 180 190 200
cryla-105.pe VFQGRWGFDAATINSRYNDLTRLLIGNYTHAVRWNTGLE-----RVWG
75812164 WMQOQ--IDSQQLNGYKAEILRLIKVYINDVNTYNOGLELEKAKPLINSDPEEYLQAGR
180 190 200 210 220 230 240 250 260 270 280 290 300
```

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cryla-105.pe PD-----SRDWIRYQFRRLTLTVLDIVSLFPNYDSRTPRTVSOL-TREIYT
|||
75812158 PDISVLSRNFKEVMKWEVAKYKRGWAMGALSIALPFTFGP-NYPKQALKVQSRQIFA
320 330 340 350 360 370

cryla-105.pe NPVLNFDGSRFGSAQIGESIRSPHLMIDLINSITITYTDAHRGEYVWSGHQIMASPVGFGS
|||
75812158 -PVIGIPGGITSDQHSGETFG
380 390

cryla-105.pep
NRAA:75812160

75812160 source="GENBANK_PROT" hypothetical protein [Bacillus thuringiensis]

SCORES Initl: 99 Initn: 99 Opt: 150 z-score: 170.1 E(): 0.35
>>NRAA:75812160
initn: 99 initl: 99 opt: 150 z-score: 170.1 expect(): 0.35
Smith-Waterman score: 170; 23.1% identity in 273 aa overlap
(38-273;116-381)

cryla-105.pe NECIPYNCLSNPEVEVLGERIETGYPIDISLSLTQLLSEFVPGAGFVLGLVDLIIMG
10 20 30 40 50 60
75812160 QTGSFSALTQSNMNOGTDINPLISAFFKAVAGSLPPLFSSLCALASFYV-TDSQTGA
90 100 110 120 130 140

cryla-105.pe FGPSQWDAFLVQIEQLINQRIEFPARNQALSRLEGSLNLYQIYAESFREWAD-----P
70 80 90 100 110 120
75812160 MA-NLRQWVDYVEKRIDSKILDYHFMGAELAAINLASKEYARVVKVIFENDMNRRIAPP
150 160 170 180 190 200

cryla-105.pe TNPALREWRICQDNMSALTTPALPFAVQYQVPLSV--YVQAAHLHLVLRDV--SV
130 140 150 160
75812160 PSTGVITQFRILLHDFIKYIAKIQFSTNQSDLOYVULPILPRAQCVMHMLMLKDRITTSV
210 220 230 240 250 260

cryla-105.pe FGQRWGFDAATINSRYNDLTILIGNYTDHAVRWYNTGLE-----RVWGP
180 190 200 210
75812160 WGQQ--IDSQQLNGYKAEILRIKIVTNDVNTTNYQGLEKAKPLNSYPPEYLQAGRP
270 280 290 300 310 320

cryla-105.pe DS-----RD---WIRNQFRRLTLTLDIVSLFPNYDSRTPRTVSOL-TREIYN
230 240 250 260
75812160 DISVLSRNFKEVMKWEVAKYKRGWAMGALSIALPFTFGP-NYPKQALKVQSRQIFA-
330 340 350 360 370

cryla-105.pe PVLENFDGSRFGSAQIGESIRSPHLMIDLINSITITYTDAHRGEYVWSGHQIMASPVGFGS
280 290 300 310 320 330
75812160 -PVIGIPGGITSDQHSGETFG
380 390

cryla-105.pep
NRAA:4565920

```

45655920 source="GENBANK PROT" DNA gyrase subunit A [Leptospira interrogans
serovar Copenhagen str. Floc22 11-130]gi|24212706|ref|NP_710187.1| DNA gyrase
subunit A [Leptospira interrogans serovar Lai str.
56601]gi|45559153|gb|AA566593.1| DNA gyrase subunit A [Leptospira
serovar Copenhagen str. 813272 Li-130]gi|24193337|gb|AA47205.1| DNA gyrase
subunit A [Leptospira interrogans serovar lai str.]

SCORES Initl: 64 Initn: 64 Opt: 143 Z-score: 157.3 E(): 1.8
>NR44:45655920
Initn: 64 Initl: 64 Opt: 143 Z-score: 157.3 expect(): 1.8
Smith-Waterman score: 143; 22.3% identity in 421 aa overlap
(809-1021:86-295)

cryla-105.pe GTGSLWPLSAQSPGKCGEPNCAPHLEWNNOLDCRDEGELAHSHHFSLNDVCTD
780 790 800 810 820 830 840
45655920 RALPDVRDGLKPVHRRILHAMMERAWRSRDREYKCKAKICEVIGNYHPHDAVYEAR
60 70 80 90 100 110 120

cryla-105.pe LNEIDGVVVFVKIKQDGHARLGNLEFLEKPLVGE-ALARYKR-ARKND-KKAKL
840 850 860 870 880 890 900
45655920 MYQFSL----RVPLIDGOGFSGID--GONPAAYRYEARLEKVAEELLEAEIKETVSF
120 130 140 150 160 170 180

cryla-105.pe ETNIVYKEAKESVDALFVNSQYDQADTNIAHIAADKRVHSIREAYLPESLVPVNA
900 910 920 930 940 950
45655920 SPN--YDITKEQPDVLPANFNLLVNGSSGTAVMATNPPPHNLRTTDAVIAVIRNPEI
170 180 190 200 210 220

cryla-105.pe AIFELSGRIFTAFSLYDARNVIRKGD-----FNLGLSCWNVKGVHDVEENQORSVLV
960 970 980 990 1000 1010
45655920 TIPFLL--KIIPGD--FPTSGIIGGGLISAYSGKIRIRSKVEIEKKNGRVIVV
230 240 250 260 270 280

cryla-105.pe PEWAESVQEVRCVPGRYLRTVAYKEGYGEGCVTIHEIENNTDLKFSNCVEEIIYN
1020 1030 1040 1050 1060 1070
45655920 TEIPYQNVKKVLEKIGDLVNEKQIEGISEILDSPKGIIRVEIHIKKDANAQVILNQLY
290 300 310 320 330 340

cryla-105.pep
SW:14195066

14195066 description="PROBABLE OUTER MEMBRANE PROTEIN PMP8 PRECURSOR
(POLYMORPHIC MEMBRANE PROTEIN 8) [OUTER MEMBRANE PROTEIN 11." library=NA
species="Chlamydomophila pneumoniae" source="swissprot_prot" version=NA type=PRT

SCORES Initl: 46 Initn: 46 Opt: 137 Z-score: 149.8 E(): 4.8
>SW:14195066
Initn: 46 Initl: 46 Opt: 137 Z-score: 149.8 expect(): 4.8
Smith-Waterman score: 137; 24.0% identity in 371 aa overlap
(371-723:335-687)

cryla-105.pe MGNAAPQORIVAQLGGVYRTLSSTLYRFPNIGNNQOLSVDLGTFAFGTSSNLPNAV
350 360 370 380 390 400
14195066 AAGTFLFSNNRCNTAAGKGAIAIADSGLSLSANQGDITFLGNTLTSTTSAPTSTRNAI
310 320 330 340 350 360

cryla-105.pe YR-KSGTVDLSDELIPQNNNV-PPQGFSHRLSHVMSFGSGNSVSIIRAPMFSWIHR
410 420 430 440 450
14195066 YGSAKINLURAAQGSIFYVDPIASNTTGCASDLVTINQPDNSPLDYSGTIVFSGEKL
370 380 390 400 410 420

cryla-105.pe SAEFNNIIASDIQTPLVKAHTLOSQTTVVVRGFGTGDILLRRTSGGPPFAYTIWINGQ
460 470 480 490 500 510
14195066 SADEAK--AADNFTSI-LKQPLALASGTLAKGNVLDVNGFTQEGS---TLLMQPGT
430 440 450 460 470

cryla-105.pe LPQRYRIRIYASTNRIYVT-VAGER---IFAGQFNKMTDGTPLTFQSFs---YA--
520 530 540 550 560
14195066 ---KLKADTEALSLTLVVDLSALEGNKSVSIETAGANKTITLTPLVFQDSSGNFYESH
480 490 500 510 520 530

cryla-105.pe TINTAFTFPMSSQSSFTVGADTFSSGNEVYIDRELPVTVTATLEAEVNLERAQKAVNALET
570 580 590 600 610 620
14195066 TINGAFTQPLV--VFATA---TAASDIYIDALLTFVQV-TPEPHYGQGHWEATWAD-T
540 550 560 570 580

cryla-105.pe STNQLGKTNVTDYHIDQVSNLVTVLSDEF--CLDEKRELS-KVKHAKRLSDERNILQD
630 640 650 660 670 680
4195066 STAKSGMTWTVTGTGYNPNERRASVVPDSLWASFTDIRLQOIMTSQANSIYQOGLWAS
590 600 610 620 630 640

cryla-105.pe SNE-KDINRQPERGNGSGTIGTIGQDDVFKENIVTSLGTDECPTVLYVQKIDESK
690 700 710 720 730 740
14195066 GTANFFHRSKQNTQAFKHSYGVIVGSSAEDEFSENFSAFCQLFGKDKDLFVENTISH
650 660 670 680 690 700

cryla-105.pe KAFTRVLRGYEDSDQELIAGRYNAKHETVNVFGTSLWPLSAQSPGKCGEPNCA
750 760 770 780 790 800
14195066 NPLASVLOHRAFLVAVMPFSGSITMLKDIPLILNAQLSYSTYNDMDTRTYSPEAQ
710 720 730 740 750 760

cryla-105.pep
NR44:15835979

15835979 source="GENBANK PROT" polymorphic outer membrane protein G family
[Chlamydomophila pneumoniae J138]gi|33236305|gb|AA3394.1| outer membrane protein
11 [Chlamydomophila pneumoniae TW-183]gi|24193337|gb|AA47205.1| polymorphic outer
membrane protein G family [Chlamydomophila pneumoniae J138]gi|7189235|gb|AA338164.1| polymorphic membrane protein G family
[Chlamydomophila pneumoniae AR39]gi|33241796|ref|NP_876737.1| outer membrane

SCORES Initl: 46 Initn: 46 Opt: 137 Z-score: 149.8 E(): 4.8
>NR44:15835979
Initn: 46 Initl: 46 Opt: 137 Z-score: 149.8 expect(): 4.8
Smith-Waterman score: 137; 24.0% identity in 371 aa overlap
(371-723:335-687)

cryla-105.pe MGNAAPQORIVAQLGGVYRTLSSTLYRFPNIGNNQOLSVDLGTFAFGTSSNLPNAV
350 360 370 380 390 400
15835979 AAGTFLFSNNRCNTAAGKGAIAIADSGLSLSANQGDITFLGNTLTSTTSAPTSTRNAI
310 320 330 340 350 360

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```
cry1a-105.pe 410 420 430 440 450
: : : : :
YR-KSGTVDSLSDEIPPNV-PPROGFHRLSHVSMFRSGFNSVSIIRAPMSWIHR
: : : : :
YLGSSAKITNLRAAQGSIIYPDIASNTGASDLTINQPDNSPLDYSGTIVFSGEKL
370 380 390 400 410 420

cry1a-105.pe 460 470 480 490 500 510
: : : : :
SAEFNNIIASDSITOIPLVKAHTLOSQTIVVRGPGFTGDDLRTSGGPFATVININGQ
: : : : :
SADPAK--AADNFTSI-LKQPLALASGTLALGNVELDVNGFTQTEGS---TLLMQPGT
430 440 450 460 470

cry1a-105.pe 520 530 540 550 560
: : : : :
LPORYRARIRYASTTNLRIVT-VAGER---IFAGQFNKMTDGTPLTQSFPS---YA--
: : : : :
---KLKADTEAISLTKLVVDLSALEGNKSVSIETAGANKTITLTSPLVFQDSSGNFYESH
480 490 500 510 520 530

cry1a-105.pe 570 580 590 600 610 620
: : : : :
TINTATFPMSSOSTGADTFSSGNEVYIDRFELIPVATLEAEYNLEAAQKAVNALFT
: : : : :
TINQATQPLV--VFATA---TAASDIYDALLTSPVQ-TPEPHYGYQGHWEATWAD-T
540 550 560 570 580

cry1a-105.pe 630 640 650 660 670 680
: : : : :
STNQLGLKTNVDYHIDQVSNLVTLSDEF--CLDEKRELSE-KVXKAKLSDERNLQD
: : : : :
STAKSGTMTVTGTYNPNPERRASVVPDLSLWASFTDITLQOINTSQANSIYQQRLWAS
590 600 610 620 630 640

cry1a-105.pe 690 700 710 720 730 740
: : : : :
--SNF--KDINRQPERGSGSTGTTIOGGDDVFKENYVTLSGTDFECYPTLYQKIDESH
: : : : :
GTANFFHKDKSGTQNAFRHKSXGYIVGGSADFSNIFSVAFQQLFGKDKDLFIVENTSH
650 660 670 680 690 700

cry1a-105.pe 750 760 770 780 790 800
: : : : :
LKAFTRYQLRGVIEDSDLEIYSIRYNKHEVTVNVPGTGSLMPLSAQSPIGKCGEPNRC
: : : : :
NYLASIYLOHRAFLGGLPMPSPGSIITDMLKDIPILNNAQLSYSTYKNDMDTRYTSYPEAQ
710 720 730 740 750 760

cry1a-105.pep
NRAA:15618361

15618361 source="GENBANK PROT" Polymorphic Outer Membrane Protein G Family
[Chlamydomonas reinhardtii] gi|4455883|emb|CAB37068.1| outer membrane
protein 11 [Chlamydomonas reinhardtii] gi|4376729|gb|AA18590.1| Polymorphic Outer
Membrane Protein G Family [Chlamydomonas reinhardtii]
CWL0291gi|14195066|sp|Q22393|FMP8_CHLPP Probable outer membrane protein pmp8
precursor (Polymorphic membrane protein 8) (Outer membrane protein 11) . . .

SCORES Initl: 46 Initn: 46 Opt: 137 z-score: 149.8 E(): 4.8
>>NRAA:15618361
initn: 46 initl: 46 opt: 137 z-score: 149.8 expect(): 4.8
Smith-Waterman score: 137; 24.0% identity in 371 aa overlap
(371-723:335-687)

cry1a-105.pe 350 360 370 380 390 400
: : : : :
MGNAPQQRIVVAQLGGVYRVLSTLTPNFGINQQLSVLDGTFEAYGTSSNLPASV
350 360 370 380 390 400

15618361 AAGPTLFSNNRCNNTAAGKGAIAADSSLSLSANQGDITFLGNTLTSTAPTSTNAI
310 320 330 340 350 360
```

```
cry1a-105.pe 410 420 430 440 450
: : : : :
YR-KSGTVDSLSDEIPPNV-PPROGFHRLSHVSMFRSGFNSVSIIRAPMSWIHR
: : : : :
YLGSSAKITNLRAAQGSIIYPDIASNTGASDLTINQPDNSPLDYSGTIVFSGEKL
370 380 390 400 410 420

cry1a-105.pe 460 470 480 490 500 510
: : : : :
SAEFNNIIASDSITOIPLVKAHTLOSQTIVVRGPGFTGDDLRTSGGPFATVININGQ
: : : : :
SADPAK--AADNFTSI-LKQPLALASGTLALGNVELDVNGFTQTEGS---TLLMQPGT
430 440 450 460 470

cry1a-105.pe 520 530 540 550 560
: : : : :
LPORYRARIRYASTTNLRIVT-VAGER---IFAGQFNKMTDGTPLTQSFPS---YA--
: : : : :
---KLKADTEAISLTKLVVDLSALEGNKSVSIETAGANKTITLTSPLVFQDSSGNFYESH
480 490 500 510 520 530

cry1a-105.pe 570 580 590 600 610 620
: : : : :
TINTATFPMSSOSTGADTFSSGNEVYIDRFELIPVATLEAEYNLEAAQKAVNALFT
: : : : :
TINQATQPLV--VFATA---TAASDIYDALLTSPVQ-TPEPHYGYQGHWEATWAD-T
540 550 560 570 580

cry1a-105.pe 630 640 650 660 670 680
: : : : :
STNQLGLKTNVDYHIDQVSNLVTLSDEF--CLDEKRELSE-KVXKAKLSDERNLQD
: : : : :
STAKSGTMTVTGTYNPNPERRASVVPDLSLWASFTDITLQOINTSQANSIYQQRLWAS
590 600 610 620 630 640

cry1a-105.pe 690 700 710 720 730 740
: : : : :
--SNF--KDINRQPERGSGSTGTTIOGGDDVFKENYVTLSGTDFECYPTLYQKIDESH
: : : : :
GTANFFHKDKSGTQNAFRHKSXGYIVGGSADFSNIFSVAFQQLFGKDKDLFIVENTSH
650 660 670 680 690 700

cry1a-105.pe 750 760 770 780 790 800
: : : : :
LKAFTRYQLRGVIEDSDLEIYSIRYNKHEVTVNVPGTGSLMPLSAQSPIGKCGEPNRC
: : : : :
NYLASIYLOHRAFLGGLPMPSPGSIITDMLKDIPILNNAQLSYSTYKNDMDTRYTSYPEAQ
710 720 730 740 750 760

! Distributed over 4 threads.
! Start time: Wed Sep 6 08:28:52 2006
! Completion time: Wed Sep 6 08:33:45 2006
! CPU time used:
! Database scan: 0:10:05.9
! Post-scan processing: 0:01:11.3
! Total CPU time: 0:11:17.2
! Output File: /usr/people/seqstore/ebits_prod/jsmccla/cry1a105_allpeps_Tmp
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