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Title

**Bioinformatics Evaluation of the Cry1A.105 Protein Utilizing the AD6, TOXIN5,
and ALLPEPTIDES Databases**

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Completion Date

September 21, 2006

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Submitter


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Sponsor Representative

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21-Sept-2006


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Sept 21 2006

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This report was checked to ensure that it accurately reflects the raw data. The raw data were audited for compliance with the Monsanto Company Guidelines for Keeping Research Records (GRR 10/1/99), and where applicable, to Monsanto SOPs.

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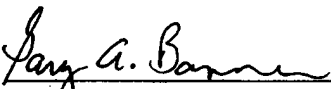
Study Certification

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

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Abbreviations and Definitions

aa	Amino acid
AD6	Allergen, gliadin, and glutenin protein sequence database
ALLPEPTIDES	Protein sequence database comprised of GenBank and SwissProt
BLOCKS	A database of amino acid motifs found in protein families
BLOSUM	BLOcks SUBstitution Matrix, used to score similarities between pairs of distantly related protein or nucleotide sequences
DATASET	Command used to create a GCG data library from a set of sequences in GCG format
EMBL	A public genetic database maintained by the European Molecular Biology Laboratory at the European Bioinformatics Institute, Hinxton, England
FASTA	Algorithm used to find local high scoring alignments between a pair of protein or nucleotide sequences
GCG	Genetics Computer Group, part of Accelrys and called the Wisconsin Package
GenBank	A public genetic database maintained by the National Center for Biotechnology Information at the National Institutes of Health, Bethesda, MD, USA
GI	Gene sequence identification number
NCBI	National Center of Biotechnology Information at the National Institutes of Health, Bethesda, MD, USA
NRAA	Non-redundant amino acid databased sourced from GenBank
PubMed	A public MEDLINE citation database maintained by the National Center for Biotechnology Information at the National Institutes of Health, Bethesda, MD, USA
STRINGSEARCH	Algorithm used to identify sequence entries by searching for character patterns, such as "toxin", in the annotation section of database flatfiles
SeqLab	The graphical X Windows-based interface for the GCG Wisconsin Package
SwissProt	A public protein database maintained by the Swiss Institute of Bioinformatics, Geneva, Switzerland, and the European Molecular Biology Laboratory at the European Bioinformatics Institute, Hinxton, England
TOXINS	Toxin protein sequence database, version 5
UNIX	A computer operating system originally termed "UNiplexed Information and Computing Service"

1.0 Summary

Bacillus thuringiensis Cry1A.105 insecticidal protein was expressed in corn to provide protection against feeding damage by lepidopteran insect pests. Cry1A.105 is a modified Cry1A protein with overall amino acid sequence identity to Cry1Ac, Cry1Ab, and Cry1F of 93.6, 90.0, and 76.7 %, respectively. The Cry1A.105 protein consists of domains I and II from Cry1Ab, domain III from Cry1F, and substantially all of the C-terminal domain of Cry1Ac.

The safety assessment of genetically enhanced crops evaluates potential health effects through a comprehensive approach, which includes bioinformatic analysis of the amino acid sequence of the introduced protein to ensure the protein is not similar to allergenic, toxic, or other biologically active proteins that may adversely affect animal or human health. Bioinformatic analyses were performed to assess the potential for allergenicity, toxicity, or bioactivity of the Cry1A.105 protein sequence. The comparison was performed with the allergen (AD6), toxin (TOXIN5), and public domain (ALLPEPTIDES) database sequences using bioinformatic tools.

The FASTA sequence alignment tool was used to assess structural similarity. Although the FASTA program directly compares amino acid sequences (i.e., primary protein structure), the alignment data may be used to infer higher order structural similarities (i.e., secondary and tertiary protein structures). Proteins that share a high degree of similarity throughout their entire lengths are often homologous. Homologous proteins share secondary structure and common three-dimensional folds. Therefore, proteins homologous to allergens are more likely to share linear and/or conformational cross-reactive allergenic epitopes than are unrelated proteins. Structural similarities between the Cry1A.105 protein sequence and the aligned allergen (AD6) database sequences were examined. The extent of each similarity was evaluated by visual inspection of the alignment, the calculated percent identity, and the *E* score value for that alignment. The current allergen, gliadin, and glutenin sequence database (AD6) was assembled from sequences found on the FARRP allergen database dated January 2006 located at <http://www.allergenonline.com> (FARRP, 2006).

The Cry1A.105 protein sequence was also screened against the AD6 sequence database using a pair-wise comparison algorithm (ALLERGENSEARCH). In these analyses, any sequences of eight linearly contiguous amino acids that were found to be identical between the Cry1A.105 protein and proteins in the AD6 database were defined as immunologically relevant, in that they may indicate the presence of potentially cross-reactive allergenic epitopes.

These bioinformatic search results indicate that no biologically relevant structural similarities to allergen proteins were observed for the Cry1A.105 protein sequence. Furthermore, no short (eight amino acid) polypeptide matches were shared between the

Cry1A.105 protein sequence and proteins in the allergen database. No other biologically relevant structural correlation with human and animal toxins or other proteins that may adversely affect animal or human health was observed for the Cry1A.105 protein sequence. Taken together, these bioinformatic search data indicate the lack of both structurally and immunologically relevant similarities between the Cry1A.105 protein sequence and proteins that may have an adverse effect on the health of animals or humans.

2.0 Introduction

Bacillus thuringiensis Cry1A.105 insecticidal protein was expressed in corn to provide protection against feeding damage by lepidopteran insect pests. Cry1A.105 is a modified Cry1A protein with overall amino acid sequence identity to Cry1Ac, Cry1Ab, and Cry1F of 93.6, 90.0, and 76.7 %, respectively. The Cry1A.105 protein consists of domains I and II from Cry1Ab, domain III from Cry1F, and substantially all of the C-terminal domain of Cry1Ac.

The safety assessment of genetically enhanced crops evaluates potential health effects through a comprehensive approach, which includes bioinformatic analysis of the amino acid sequence of the introduced protein to ensure the protein is not similar to allergenic, toxic, or potentially bioactive proteins that are known to cause adverse health effects. Bioinformatic analyses were performed to assess the potential for toxicity, allergenicity, or bio-activity of the Cry1A.105 protein sequence. The comparison was performed with the allergen (AD6), toxin (TOXINS), and public domain (ALLPEPTIDES) database sequences using bioinformatic tools.

Exposure to allergens in foods may cause sudden, severe life-threatening reactions in susceptible individuals. Gliadins and glutenins are suspected to cause celiac disease, a non-IgE mediated allergic disorder (gluten-sensitive enteropathy), and are also considered important immunologically active proteins. Screening the amino acid sequences of proteins introduced into plants by modern biotechnology for similarity to sequences of known allergens, gliadins, and glutenins is one of many assessments performed to support product safety. Similarly, the amino acid sequences of introduced proteins are also screened against a toxin-enriched dataset as well as all known proteins in publicly available genetic databases.

The FASTA algorithm can be used to evaluate the extent of sequence alignment between a query protein sequence and a database sequence. In principle, if two proteins share sufficient linear sequence similarity and identity, they will also likely share three-dimensional structure and, therefore, functional homology. By definition, homologous proteins share secondary structure and common three-dimensional folds (Pearson, 2000). Because the degree of relatedness between homologs varies widely, the data need to be carefully evaluated in order to maximize their potential predictive value. The

allergenicity assessment is used to identify known allergens or potentially cross-reactive proteins. While related (homologous) proteins may share 25% amino acid identity in a 200 amino acid overlap (Pearson, 2000), this is not generally sufficient to indicate IgE mediated cross-reactivity (Aalberse et al., 2001). Indeed, allergenic cross-reactivity caused by proteins is rare at 50% identity and typically requires >70% amino acid identity across the full length of the protein sequences (Aalberse, 2000). A conservative approach is currently applied by which related protein sequences are identified as potentially cross-reactive if linear identity is 35% or greater in an 80 amino acid overlap (Thomas et al, 2005). Such levels of identity are readily detected using FASTA. Additionally, proteins closely related to gliadins or glutenins, the proteins that trigger celiac disease, can be easily identified using FASTA.

A second bioinformatics tool, an eight amino acid sliding window search, is used to specifically identify short linear polypeptide matches to known or suspected allergens. It is possible that proteins structurally unrelated to allergens, gliadins, and glutenins may still contain smaller immunologically significant epitopes. A query sequence may be considered allergenic if it has an exact sequence identity of at least eight linear and contiguous amino acids with a potential allergen epitope (Metcalf et al., 1996; Hileman et al., 2002; Goodman et al., 2002). However, most allergen epitopes have not been confirmed and the amino acid length for those that have been identified can vary widely, thus the relevance of an exact match of eight amino acids may have limited immunological relevance (Thomas et al., 2005). The eight amino acid bioinformatic strategy is currently an *in silico* search that can produce matches containing significant uncertainty depending on the length of the query sequence (Silvanovich et al., 2006).

This report describes the bioinformatics assessment of the Cry1A.105 protein. Inspection of the bioinformatic analysis data can be used to indicate whether the Cry1A.105 protein sequence is structurally congruent with known allergens, toxins, or other bioactive proteins.

3.0 Purpose

The purpose of this study was to evaluate, using bioinformatics techniques, the amino acid sequence structural relatedness of the Cry1A.105 protein sequence to known allergens, toxins, or other bioactive proteins. Sequence identity and amino acid similarities to allergens, toxins, and other proteins were assessed using the sequence alignment tools FASTA and ALLERGENSEARCH.

4.0 Methods

- 4.1 Sequence database preparation.** The Allergen database has been updated to include recently characterized allergens, gliadins, and glutenin sequences. The intent is that the Allergen database contain relevant protein sequences. The current allergen, gliadin, and glutenin sequence database (AD6) was assembled from sequences found on the FARRP allergen database dated January 2006 located at <http://www.allergenonline.com> (FARRP, 2006). Gene identification (GI) numbers for each of the 1537 sequences found on the FARRP database were used to assemble a list, and this list was used to batch query the NCBI protein sequence database located at <http://www.ncbi.nlm.nih.gov/entrez/batchentrez.cgi>. For obsolete GI numbers found using the batch search, the GenPept format flat file associated with each obsolete GI number was examined and an up to date GI number was used to replace the obsolete GI number. Due to the collation of short peptide sequences into a single protein sequence, a total of 1,511 GI numbers were found to be valid as of February 13, 2006. These 1511 GI numbers were used to assemble a searchable database AD6 (Appendix 1, release date; March 6, 2006).

The toxin sequence database (TOXINS) was assembled from public sequence databases, including GenBank and EMBL release 124 and SwissProt release 1. Protein sequences were retrieved using the STRINGSEARCH function (keyword = toxin) of the Wisconsin Package version 10). This search was used to identify and retrieve 12,771 separate entries containing the word toxin within the flatfile annotation section. The list data file was loaded into the editor window of SeqLab, selected, and compiled into a sub-database using the DATASET database utility. The actual number of unique toxin sequences is fewer than 12,771 because of the redundancy of these public databases and because some entries may contain the word toxin, but are not confirmed protein toxins.

The ALLPEPTIDES sequence database was used to represent all currently known publicly available protein sequences and consisted of SwissProt release 40.0 (May 4, 2005) and PIR release 65.0 (October 24, 2005).

- 4.2 Sequence Database Searches.** All search analyses were performed using the UNIX-based Wisconsin Package software, Genetics Computer Group (GCG, version 10.3, Madison, WI) on a personal computer supported with Reflection X Client Manager network software (version 7.20, WRQ, Inc. Seattle, WA). The DNA sequence was supplied in (Rice *et al.*, 2006) and translated to the amino acid sequence with DNASTar, SeqBuilder software, version 7.00 (Fig. 1). The structural similarity of the translated protein sequences to sequences in each database (AD6, TOXINS, and ALLPEPTIDES) was assessed using the FASTA algorithm (Lipman and Pearson, 1985; Pearson and Lipman, 1988). FASTA comparisons are initiated

by aligning the first match of a specific wordsize. The alignment is then extended based on the chosen scoring matrix. Specific FASTA comparison parameters used in this study included a wordsize (*k-tuple*) of two, a gap creation penalty of 12, a gap extension penalty of two, and an expectation threshold (*E* score) of ten. The *E* score (expectation score) is a statistical measure of the likelihood that the observed similarity score could have occurred by chance in a search. A larger *E* score indicates a lower degree of similarity between the query sequence and the sequence from the database. Typically, alignments between two sequences will need to have an *E* score of less than 1×10^{-5} to be considered to have significant homology. FASTA comparisons were performed using the BLOSUM50 scoring matrix (Henikoff and Henikoff, 1992). Multiple alignments are made between the query sequence and each sequence in the database with a score calculated for each alignment. Only the best scoring alignment is extensively analyzed for each database sequence. The BLOSUM matrix series (Henikoff and Henikoff, 1992) was derived from a set of aligned, ungapped regions from protein families, called the BLOCKS database. Sequences from each block were clustered based on the percent of identical residues in the alignments (Henikoff and Henikoff, 1996). The BLOSUM50 matrix will identify blocks of conserved residues that are at least 50% identical. BLOSUM50 works well for identifying sequence similarities that include gaps, and thus recognizes distant evolutionary relationships (Pearson, 2000).

The extent of structural relatedness was evaluated by visual inspection of the aligned sequences, the calculated percent identity, and *E* score. The *E* score reflects the degree of amino acid similarity between a pair of sequences and can be used to evaluate the significance of the alignment. Similar amino acids are structurally related and share polar, hydrophobic, or charged states. Such substitutions are referred to as "conservative" since they are unlikely to change the structure of the protein and, by inference, the function of homologous proteins. The calculated *E* score depends on the overall length of joined (gapped) local sequence alignments, the quality (percent identity, similarity) of the overlap, and the size of the database (Pearson and Lipman, 1988; Baxeavanis and Ouellette, 1998). For a pair of sequences, a very small *E* score may indicate a structurally relevant similarity. Conversely, large *E* scores are typically associated with alignments that do not represent a biologically relevant correlation.

In addition to the FASTA comparisons of the Cry1A.105 protein sequence to allergens (to assess overall structural congruence), an eight amino acid sliding-window search was performed. An algorithm (ALLERGENSEARCH) was developed to identify whether or not a linearly contiguous match of eight amino acids existed between the query sequence and sequences within the allergen database (AD6). This program compares the query sequence to each protein sequence in the allergen database using a sliding-window of eight amino acids; that

is, with a seven amino acid overlap relative to the preceding window. While there have been recommendations for using a shorter scanning window (Gendel, 1998; Kleter and Peijnenburg, 2002), only a few studies have actually investigated the ability of six, seven, or eight amino acid search windows to identify allergens (Hileman et al., 2002; Goodman et al., 2002; Stadler and Stadler, 2003). In these studies, randomly or specifically selected protein sequences were used as query sequences in FASTA and six, seven, and eight amino acid window searches against allergen databases. The results demonstrated that searches with six and seven amino acid windows led to high rates of false positive matches between non-allergenic query sequences and allergen database sequences. Additionally, searches with a six or seven amino acid window identified apparently random matches between totally unrelated proteins, such that the matched proteins were not likely to share any structural or sequence similarities that could act as cross-reactive epitopes. These studies concluded that six or seven amino acid sliding-window searches yielded such a high rate of false positive hits that they were of no predictive value. Furthermore, Silvanovich et al. (2006) recently demonstrated the lack of value for six or seven amino acid sliding-window searches in a comprehensive analysis of short peptide match frequencies by analyzing the match frequencies of peptides derived from ~1.95 million published protein sequences. In order to provide the best predictive capability to identify potentially cross-reactive proteins, a window of eight contiguous amino acids was used in the current study to represent the smallest immunologically relevant sequential, or linear IgE binding epitope (Metcalf et al., 1996).

- 4.3 Significance of the Alignment.** An *E* score of 1×10^{-5} was set as an initial high cut-off value for alignment significance. Although all alignments were inspected visually, any aligned sequence that yielded an *E* score less than 1×10^{-5} was analyzed further to determine if such an alignment represented relevant sequence homology.

5.0 Results and Discussion

Bioinformatics analysis was performed on the Cry1A.105 protein sequence (Figure 1) to assess the potential for structural correlation with allergens, toxins, or other bioactive proteins. Summaries of the significant alignments from the analysis are shown in Tables 1-3. The supporting dataset output files for the analysis are presented in Appendices 2-5.

- 5.1 Assessment of Potential Allergenicity:** Potential structural identity and similarity shared between the Cry1A.105 protein and proteins in the allergen database were evaluated using the FASTA sequence alignment tool. Identified proteins were ranked according to their degree of similarity (Appendix 2). None of these proteins had an *E* score of less than 1×10^{-5} indicating that no homology with protein allergens was observed.

The most significant alignment was to a Kiwi fruit allergen, actinidin (GI number 166317). This alignment demonstrated 24.2% identity over a 318 amino acid window with an *E* score of 2.3. The *E* score of 2.3 observed in this alignment is not reflective of homology between Cry1A.105 and actinidin, as *E* scores of ~1 or greater are expected to occur for alignments between random, non-homologous sequences (Pearson, 2000). Therefore, this low quality alignment is not considered relevant from an allergenic assessment perspective.

The length of the overlap (318) is 27% compared to full length (1177 amino acids) Cry1A.105 protein and twenty-one gaps were required to optimize the alignment. Consequently, no structural and/or functional homology between the Cry1A.105 protein and the Kiwi fruit allergen, actinidin can be inferred. This alignment neither met nor exceeded the Codex recommended threshold of 35% identity over 80 amino acids (Codex, 2003). The minimum similarity required for allergenic cross-reactivity is likely $\geq 50\%$ identity across the entire length of the protein (Aalberse, 2000). Therefore, it is extremely unlikely that cross-reactivity exists between the Cry1A.105 protein and the Kiwi fruit allergen, actinidin. Inspection of the remaining 22 alignments also did not show any significant similarities between the Cry1A.105 protein and allergens.

No immunologically relevant sequences of eight contiguous amino acid identities, as assessed from the ALLERGENSEARCH data (Appendix 3), were detected when the Cry1A.105 protein sequence (Figure 1) was compared to the AD6 sequence database (Appendix 1).

5.2 *Assessment of Potential Toxicity:* Potential structural identity and similarity shared between the Cry1A.105 protein and proteins in the toxin database were evaluated using the FASTA sequence alignment tool. Identified proteins were ranked according to their degree of similarity (Appendix 4). As expected, the most significant similarity observed (Table 2) was to the *Bacillus thuringiensis* pesticidal crystal protein, Cry1Ac (Accession no. U89872), demonstrating 92.0% identity over 1,182 aa with an *E* score of zero. This alignment is expected because the Cry1A.105 protein contains a significant portion of the Cry1Ac protein, which is listed within GenBank as an insecticidal toxin and, as such, was included in the TOXIN5 database during its construction. The Cry1A.105 protein did not demonstrate any structural similarity with any proteins that may present toxicity to humans and animals.

5.3 *Assessment of Potential Adverse Biological Activity to Humans and Animals:* Potential structural similarities shared between the Cry1A.105 protein and proteins in the ALLPEPTIDES database were evaluated using the FASTA sequence alignment tool. Identified proteins were ranked according to their degree of

similarity (Appendix 5). As expected, the best similarity observed (Table 3) was to pesticidal crystal protein Cry1A (GI no. 37048803), demonstrating 92.1% identity over 1,177 aa with and an *E* score of zero. All of the remaining alignments with significant *E* scores are to Cry protein homologues except one hypothetical amino acid sequence; the hypothetically translated sequence, JMP 134, from the bacteria *Ralstonia eutropha*. Upon further examination, none of the Cry protein homologues or the *Ralstonia eutropha* bacterial sequence indicated any concern for adverse biological activity. Therefore, based on these data, the Cry1A.105 protein does not share any structural congruence with any proteins that may have adverse biological activity to humans and animals.

6. Conclusions

Bioinformatics analyses were performed on the Cry1A.105 protein sequence to assess its structural correlation with allergens, toxins, and bioactive proteins. No biologically relevant sequence correlates were observed between the Cry1A.105 protein coding sequence and any allergens, human and animal toxins, or other proteins that may adversely affect animal or human health.

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Figure 1. Amino acid sequence of the Cry1A.105 protein

MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG
LVDIIWGIFGPSQWDAFLVQIEQLNQRIEEFARNQAISRLEGLSNLYQIYAESFREWE
ADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRD
VSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIR
YNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGI
EGSIRSPHLMIDILNSITIYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNA
APQQRIVAQLGQGVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVY
RKSGTVDSLDEIPPQNNNVPPRQGFHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRS
AEFNIIASDSITQIPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQ
LPQRYRARIRYASTTNLRIYVTVAGERIFAGQFNKTMDTGDPLTFQSFSYATINTAFT
FPMSQSSFTVGADTFSSGNEVYIDRFELIPVTATLEAEYNLERAQKAVNALFTSTNQ
LGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNF
KDINRQPERGWGGSTGITIQQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLKAF
TRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAP
HLEWNPDLDCSCRIDGEKCAHSHHFSLDIDVGCTDLNEDLGWVWVIFKIKTQDGH
RLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFV
NSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSL
YDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVLVVPWEAEVSQEV RVCP
GRGYILRVTA YKEGYGEGCVTIHEIENNTDELKFSNCVEEEIYPNNTVTCNDYTVNQ
EEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGYRDTPLP
VGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE

Table 1. Top alignment observed for the Cry1A.105 protein sequence from a FASTA search against the AD6 allergen database.

Database	GI #	Description	E-score	% Identity	aa Overlap
AD6	166317	actinidin	2.3	24.2	318

Table 2. Top alignment observed for the Cry1A.105 protein sequence from a FASTA search against the TOXIN5 database.

Database	Accession #	Description	E-score	% Identity	aa Overlap
TOXIN5	U89872	<i>Bacillus thuringiensis</i> Cry1Ac delta-endotoxin gene	0	92.0	1182

Table 3. Top alignment observed for the Cry1A.105 protein sequence from a FASTA search against the ALLPEPTIDES database.

Database	GI #	Description	E-score	% Identity	aa Overlap
ALLPEPTIDES	37048803	Cry1A toxin <i>Bacillus thuringiensis</i>	0	92.1	1177

Appendix 1. Allergen, gliadin, and glutenin protein sequence database (AD6)

Venoms

Species	Comments	GI #	AA
<i>Aedes aegypti</i>	D7 protein precursor (Allergen Aed a 2).	118216	321
<i>Aedes aegypti</i>	putative 30 kDa allergen-like protein [<i>Aedes aegypti</i>].	18568322	215
<i>Aedes aegypti</i>	putative 18.2 kDa secreted protein [<i>Aedes aegypti</i>].	18568332	158
<i>Aedes aegypti</i>	30 kDa salivary gland allergen Aed a 3 [<i>Aedes aegypti</i>].	2114497	253
<i>Aedes aegypti</i>	apyrase.	556272	562
<i>Aedes albopictus</i>	putative 30 kDa allergen-like protein 30k-1 [<i>Aedes albopictus</i>].	56417500	210
<i>Aedes albopictus</i>	30 kDa salivary gland allergen 30k-2 [<i>Aedes albopictus</i>].	56417502	210
<i>Aedes albopictus</i>	30 kDa salivary gland allergen 30k-3 [<i>Aedes albopictus</i>].	56417504	271
<i>Aedes albopictus</i>	GE-rich salivary protein 30k-4 [<i>Aedes albopictus</i>].	56417506	266
<i>Aedes albopictus</i>	putative salivary secreted 30 kDa allergen-like protein 30k-5	56417508	204
<i>Anopheles gambiae</i>	30 kDa protein [<i>Anopheles gambiae</i>].	18389879	182
<i>Apis dorsata</i>	Melittin.	126955	26
<i>Apis mellifera</i>	venom protease precursor [<i>Apis mellifera</i>].	22724911	405
<i>Apis mellifera</i>	Phospholipase A2 precursor (Phosphatidylcholine 2-acylhydrolase)	24418862	167
<i>Apis cerana</i>	Phospholipase A2 (Phosphatidylcholine 2-acylhydrolase).	24638082	134
<i>Apis mellifera</i>	Allergen Api m 6.	34921475	71
<i>Apis dorsata</i>	Phospholipase A2 (Phosphatidylcholine 2-acylhydrolase).	47117012	134
<i>Apis mellifera</i>	prepromelittin [<i>Apis mellifera</i>].	5622	70
<i>Apis mellifera</i>	Hyaluronoglucosaminidase precursor (Hyaluronidase) (Hya) (Allergen	585279	382
<i>Apis mellifera</i>	profilin [<i>Apis mellifera</i>].	58585250	126
<i>Apis mellifera</i>	venom acid phosphatase precursor [<i>Apis mellifera</i>].	61656214	388
<i>Apis mellifera</i>	PREDICTED: similar to allergen Bla g 5, partial [<i>Apis mellifera</i>].	66534655	157
<i>Apis mellifera</i>	melittin, minor - honeybee.	69552	27
<i>Apis cerana</i>	phospholipase A2 (EC 3.1.1.4), venom - Indian honeybee.	7435005	134
<i>Bombus terrestris</i>	Phospholipase A2 (Phosphatidylcholine 2-acylhydrolase) (Allergen	14423832	136
<i>Crotalus durissus</i>	phospholipase A2 inhibitor [<i>Crotalus durissus terrificus</i>].	501050	200
<i>Ctenocephalides felis</i>	FS-H precursor.	1575479	98
<i>Ctenocephalides felis</i>	salivary antigen 1 precursor [<i>Ctenocephalides felis</i>].	4336703	176
<i>Ctenocephalides felis</i>	salivary allergen 2 [<i>Ctenocephalides felis</i>].	7638032	264
<i>Dolichovespula maculata</i>	Hyaluronoglucosaminidase (Hyaluronidase) (Allergen Dol m 2) (Dol m	1346322	331
<i>Dolichovespula maculata</i>	Venom allergen 5.01 precursor (Antigen 5 form 2) (Ag5-2) (Allergen	137395	227
<i>Dolichovespula maculata</i>	Phospholipase A1 2 (Allergen Dol m 1.02) (Dol m I).	1709542	303
<i>Dolichovespula arenaria</i>	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Dol a 5) (Dol a V).	465052	203
<i>Dolichovespula maculata</i>	Phospholipase A1 1 precursor (Allergen Dol m 1.01) (Dol m I).	548449	317
<i>Dolichovespula maculata</i>	Venom allergen 5.02 precursor (Antigen 5 form 3) (Ag5-3) (Allergen	549186	215
<i>Myrmecia pilosula</i>	major allergen Myr p II.	1587177	75
<i>Myrmecia pilosula</i>	Pilosulin-2 precursor (Allergen Myr p 2) (Myr p II).	2498604	75
<i>Myrmecia pilosula</i>	major allergen [<i>Myrmecia pilosula</i>].	312284	112
<i>Myrmecia pilosula</i>	Pilosulin-1 precursor (Major allergen Myr p 1) (Myr p I) [Contains:	730091	112
<i>Phlebotomus papatasi</i>	28 kDa salivary protein precursor [<i>Phlebotomus papatasi</i>].	15963511	254
<i>Phlebotomus papatasi</i>	30 kDa salivary protein precursor [<i>Phlebotomus papatasi</i>].	15963513	253
<i>Polistes annularis</i>	Hyaluronoglucosaminidase precursor (Hyaluronidase) (Allergen Pol a	14423735	367
<i>Polistes annularis</i>	Phospholipase A1 (Allergen Pol a 1).	14423833	301
<i>Polistes annularis</i>	allergen 5.	160780	209
<i>Polistes gallicus</i>	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Pol g 5).	25091511	206
<i>Polistes dominulus</i>	venom serine protease precursor [<i>Polistes dominulus</i>].	30909091	277
<i>Polistes gallicus</i>	Phospholipase A1 (Allergen Pol g 1).	41017429	42
<i>Polistes dominulus</i>	venom phospholipase A1 1 precursor [<i>Polistes dominulus</i>].	45510887	337
<i>Polistes dominulus</i>	venom phospholipase A1 2 precursor [<i>Polistes dominulus</i>].	45510889	316
<i>Polistes dominulus</i>	venom phospholipase A1 3 precursor [<i>Polistes dominulus</i>].	45510891	316
<i>Polistes dominulus</i>	venom phospholipase A1 4 precursor [<i>Polistes dominulus</i>].	45510893	316
<i>Polistes exclamans</i>	allergen Pol e 5 precursor [<i>Polistes exclamans</i>].	51093375	226
<i>Polistes dominulus</i>	allergen Pol d 5 precursor [<i>Polistes dominulus</i>].	51093377	227
<i>Polistes exclamans</i>	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Pol e 5) (Pol e V).	549187	205
<i>Polistes fuscatus</i>	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Pol f 5) (Pol f V).	549188	205
<i>Polybia scutellaris</i>	venom allergen 5 [<i>Polybia scutellaris</i>].	31747352	206
<i>Polybia scutellaris</i>	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Pol s 5) (Pol s V).	47117356	207
<i>Psoroptes ovis</i>	allergen A precursor [<i>Psoroptes ovis</i>].	14388619	143

Psoroptes ovis	Derp1 antigen [Psoroptes ovis].	23450237	263
Psoroptes ovis	glutathione S-transferase [Psoroptes ovis].	6625158	219
Sarcoptes scabiei	cathepsin L-like protease [Sarcoptes scabiei type hominis].	27462834	245
Sarcoptes scabiei	glutathione S-transferase [Sarcoptes scabiei type hominis].	27462836	219
mitochondrion Sarcoptes	cytochrome oxidase subunit I [Sarcoptes scabiei type hominis].	27462838	275
mitochondrion Sarcoptes	cytochrome oxidase subunit II [Sarcoptes scabiei type hominis].	27462840	157
Sarcoptes scabiei	cytochrome Bcl complex chain B-like protein [Sarcoptes scabiei type hominis].	27462842	131
Sarcoptes scabiei	vitellogenin-like protein [Sarcoptes scabiei type hominis].	27462844	174
Sarcoptes scabiei	paramyosin [Sarcoptes scabiei type hominis].	27462846	638
Sarcoptes scabiei	major allergen 1 [Sarcoptes scabiei type hominis].	27462848	330
Sarcoptes scabiei	Sar s 3 allergen Yv7016G03 [Sarcoptes scabiei type hominis].	38202313	260
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv4005B08 [Sarcoptes scabiei type hominis].	38202315	271
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv4005G12 [Sarcoptes scabiei type hominis].	38202317	251
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv4031D03 [Sarcoptes scabiei type hominis].	38202319	264
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv5004E08 [Sarcoptes scabiei type hominis].	38202321	256
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv5018H10 [Sarcoptes scabiei type hominis].	38202323	251
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv5026E07 [Sarcoptes scabiei type hominis].	38202325	242
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv5027C11 [Sarcoptes scabiei type hominis].	38202327	259
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv6017G11 [Sarcoptes scabiei type hominis].	38202329	248
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv6018H06 [Sarcoptes scabiei type hominis].	38202331	262
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv6023A04 [Sarcoptes scabiei type hominis].	38202333	257
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv6028G11 [Sarcoptes scabiei type hominis].	38202335	250
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv7016C10 [Sarcoptes scabiei type hominis].	38202337	259
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv7003F10 [Sarcoptes scabiei type hominis].	38202339	259
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv7004A06 [Sarcoptes scabiei type hominis].	38202341	263
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv5001A04 [Sarcoptes scabiei type hominis].	38202343	233
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv9017F05 [Sarcoptes scabiei type hominis].	38202345	261
Solenopsis invicta	Sol i 1=antigen (N-terminal) [Solenopsis invicta=imported fire ant venom allergen Sol i 1 precursor [Solenopsis invicta].	1336809	58
Solenopsis invicta	Sol i 1=antigen (N-terminal) [Solenopsis invicta=imported fire ant venom allergen Sol i 1 precursor [Solenopsis invicta].	1336811	25
Solenopsis invicta	Sol i 1=antigen (N-terminal) [Solenopsis invicta=imported fire ant venom allergen Sol i 1 precursor [Solenopsis invicta].	1336812	26
Solenopsis invicta	Sol i 1=antigen (N-terminal) [Solenopsis invicta=imported fire ant venom allergen Sol i 1 precursor [Solenopsis invicta].	1336813	26
Solenopsis richteri	phospholipase (EC 3.1.1.32), venom - black imported fire ant venom allergen Sol i 1 precursor [Solenopsis invicta].	321043	20
Solenopsis invicta	allergen Sol i 1 precursor [Solenopsis invicta].	4038411	137
Solenopsis invicta	allergen Sol i 1 precursor [Solenopsis invicta].	51093373	346
Solenopsis invicta	Venom allergen 1 precursor (Allergen Sol i 2) (Sol i II).	549179	138
Solenopsis richteri	venom allergen Sol r 2 - black imported fire ant.	7512067	119
Solenopsis geminata	venom allergen Sol g 4.01 precursor [Solenopsis geminata].	7638028	137
Solenopsis geminata	venom allergen Sol g 4.02 precursor [Solenopsis geminata].	7638030	137
Solenopsis invicta	Venom allergen IV precursor (Allergen Sol i 4) (Sol i IV).	14424465	137
Solenopsis invicta	Venom allergen 3 precursor (Venom allergen III) (Allergen Sol i 3).	14424466	234
Solenopsis richteri	Venom allergen 3 (Venom allergen III) (Allergen Sol r 3) (Sol r 3).	6136163	211
Tityus serrulatus	Tityustoxin-6 (Tityustoxin VI) (TsTX-VI) (TsTXVI) (Toxin VI) (TsTX-VI) (Tityus protracta).	1173399	62
Triatoma protracta	procalin [Triatoma protracta].	15426413	169
Vespa crabro	Venom allergen 5.01 (Antigen 5-1) (Ag5-1) (Allergen Vesp c 5.01).	549184	202
Vespa crabro	Venom allergen 5.02 (Antigen 5-2) (Ag5-2) (Allergen Vesp c 5.02).	549185	202
Vespa mandarinia	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Vesp m 5).	6136165	202
Vespula vulgaris	Chain A, Ves V 5, An Allergen From Vespula Vulgaris Venom.	11514279	209
Vespula vulgaris	hyaluronoglucosaminidase (Hyaluronidase) (Allergen Ves v 2) (Ves v 2).	1346323	331
Vespula vulgaris	allergen 5.	162551	227
Vespula maculifrons	phospholipase A1 (EC 3.1.1.32), allergen Ves m 1 - eastern.	482382	300
Vespula vulgaris	allergen 5; antigen 5 [Vespula vulgaris].	4826574	204
Vespula flavopilosa	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves f 5) (Ves f V).	549189	204
Vespula germanica	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves g 5) (Ves g V).	549190	204
Vespula maculifrons	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves m 5) (Ves m V).	549191	204
Vespula pennsylvanica	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves p 5) (Ves p V).	549192	204
Vespula squamosa	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves s 5) (Ves s V).	549193	205
Vespula vidua	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves vi 5) (Ves vi V).	549194	206
Vespula vulgaris	hyaluronidase b [Vespula vulgaris].	62147665	340
Vespula vulgaris	allergen and phospholipase A1.	897647	336

Aeroallergens animals

Species

Canis familiaris

Comments

precursor Can f II [Canis familiaris].

GI #

29292272

AA

177

Canis familiaris	precursor Can f II [Canis familiaris].	29292274	179
Canis familiaris	Major allergen Can f 1 precursor (Allergen Dog 1).	3121745	174
Canis familiaris	Minor allergen Can f 2 precursor (Allergen Dog 2).	3121746	180
Canis familiaris	albumin [Canis familiaris].	3319897	585
Canis familiaris	epithelial dog allergen - Canis familiaris (fragment).	60729635	13
Canis familiaris	albumin [Canis familiaris].	633938	265
Canis familiaris	albumin [Canis familiaris].	6687188	608
Cavia porcellus	Eosinophil granule major basic protein 1 precursor (MBP-1).	119238	233
Cavia porcellus	Major allergen Cav p 2.	32363133	15
Cavia porcellus	Major urinary protein (MUP) (Allergen Cav p 1).	32469617	15
Cavia porcellus	Eosinophil granule major basic protein 2 precursor (MBP-2).	544241	234
Felis catus	Major allergen I polypeptide chain 1 precursor (Allergen Fel d 1-A)	1169665	92
Felis catus	fel d I chain 1 precursor with leader B [Felis catus].	1364212	88
Felis catus	fel d I chain 1 precursor with leader A [Felis catus].	1364213	92
Felis catus	major allergen I.	163823	109
Felis catus	major allergen I.	163827	88
Felis catus	prostaglandin FP receptor [Felis catus].	17224444	366
Felis catus	cystatin [Felis catus].	17939981	98
Felis catus	Chain A, Crystal Structure Of Fel D 1- The Major Cat Allergen.	38492847	170
Felis catus	Fel d 4 allergen [Felis catus].	45775300	186
Felis catus	albumin precursor [Felis catus].	886485	608
Felis catus	Major allergen I polypeptide chain 2 precursor (Allergen Fel d 1-B)	232086	109
Macaca mulatta	encephalitogenic peptide M.	229507	14
Mus musculus	androgen-binding protein eta [Mus musculus].	10181188	93
Mus sp.	DEC-205=205 kda protein allergen {N-terminal} [mice, outbred CD-1	1174278	25
Mus musculus	Major urinary protein 6 precursor (MUP 6) (Alpha-2U-globulin)	20178291	180
Mus musculus	TPA_exp: allergen dI chain C2A [Mus musculus].	28476845	112
Mus musculus	TPA_exp: allergen dI chain C2C [Mus musculus].	28476849	108
Mus musculus	TPA_exp: allergen dI chain C2D [Mus musculus].	28476851	112
Mus musculus	TPA_exp: allergen dI chain C2Y [Mus musculus].	28476853	46
Mus musculus	androgen binding protein zeta [Mus musculus].	30315676	112
Mus musculus	androgen binding protein gamma [Mus musculus].	30315678	112
Mus musculus	androgen binding protein gamma [Mus musculus].	45331198	112
Mus musculus	androgen binding protein beta [Mus musculus].	45331208	112
Mus musculus	cysteine-rich secretory protein [Mus musculus].	56694673	250
Mus musculus	lacrimal androgen-binding protein delta [Mus musculus].	8926324	112
Rattus norvegicus	Major urinary protein precursor (MUP) (Alpha-2u-globulin)	127533	181
Rattus norvegicus	Niemann Pick type C2 [Rattus norvegicus].	27465565	149
Rattus norvegicus	PREDICTED: similar to Major urinary protein precursor (MUP)	62649086	181
Rattus norvegicus	Alpha-2u globulin.	81890324	181
Thaumatococcus ptyocarpa	Tha p 1.	74798355	18

Aeroallergens fungi

Species	Comments	GI #	AA
Alternaria alternata	proteindisulfidomerase [Alternaria alternata].	1006624	433
Alternaria alternata	Aldehyde dehydrogenase (ALDDH) (Allergen Alt a 10) (Alt a X).	1169290	495
Alternaria alternata	60S acidic ribosomal protein P1 (Allergen Alt a 12) (Alt a XII).	1350779	110
Alternaria alternata	Alt a 1 [Alternaria alternata].	1421808	135
Alternaria alternata	Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate	14423684	438
Alternaria alternata	Heat shock 70 kDa protein (Allergen Alt a 3).	14423730	152
Alternaria alternata	major allergen Alt a 1 subunit [Alternaria alternata].	1842045	157
Alternaria alternata	ribosomal P2 phosphoprotein [Alternaria alternata].	1850540	113
Alternaria brassicicola	major allergen-like protein precursor [Alternaria brassicicola].	20279107	158
Alternaria alternata	putative nuclear transport factor 2 [Alternaria alternata].	21748153	124
Alternaria alternata	major allergen alt a 1 [Alternaria alternata].	21913174	115
Alternaria alternata	allergen r Alt a 2 [Alternaria alternata].	4097481	190
Alternaria alternata	major allergen Alt a 1 subunit [Alternaria alternata].	45680856	157
Alternaria alternata	minor allergen, ribosomal protein [Alternaria alternata].	467617	113
Alternaria alternata	minor allergen [Alternaria alternata].	467619	204
Alternaria cetera	major allergen alt a 1 [Alternaria cetera].	49476471	138
Alternaria mouchaccae	major allergen alt a 1 [Alternaria mouchaccae].	49476473	138
Alternaria argyranthemii	major allergen alt a 1 [Alternaria argyranthemii].	49476475	138
Alternaria conjuncta	major allergen alt a 1 [Alternaria conjuncta].	49476477	138
Alternaria photistica	major allergen alt a 1 [Alternaria photistica].	49476479	138

Alternaria oregonensis	major allergen alt a1 [Alternaria oregonensis].	49476481	128
Alternaria metachromatica	major allergen alt a1 [Alternaria metachromatica].	49476485	137
Alternaria radicina	major allergen alt a1 [Alternaria radicina].	49476487	137
Alternaria carotiincultae	major allergen alt a1 [Alternaria carotiincultae].	49476489	137
Alternaria petroselini	major allergen alt a1 [Alternaria petroselini].	49476491	137
Alternaria smyrnii	major allergen alt a1 [Alternaria smyrnii].	49476493	137
Alternaria cheiranthi	major allergen alt a1 [Alternaria cheiranthi].	49476495	137
Alternaria blumeae	major allergen alt a1 [Alternaria blumeae].	49476497	137
Alternaria dauci	major allergen alt a1 [Alternaria dauci].	49476499	137
Alternaria crassa	major allergen alt a1 [Alternaria crassa].	49476501	137
Alternaria macrospora	major allergen alt a1 [Alternaria macrospora].	49476503	137
Alternaria pseudorostrata	major allergen alt a1 [Alternaria pseudorostrata].	49476505	137
Alternaria porri	major allergen alt a1 [Alternaria porri].	49476507	137
Alternaria tagetica	major allergen alt a1 [Alternaria tagetica].	49476509	137
Alternaria capsici	major allergen alt a1 [Alternaria capsici].	49476511	137
Alternaria solani	major allergen alt a1 [Alternaria solani].	49476513	137
Alternaria cucumerina	major allergen alt a1 [Alternaria cucumerina].	49476515	137
Alternaria tenuissima	major allergen alt a1 [Alternaria tenuissima].	49476519	137
Alternaria arborescens	major allergen alt a1 [Alternaria arborescens].	49476521	137
Alternaria longipes	major allergen alt a1 [Alternaria longipes].	49476523	137
Alternaria dumosa	major allergen alt a1 [Alternaria dumosa].	49476525	137
Alternaria limoniasperae	major allergen alt a1 [Alternaria limoniasperae].	49476527	137
Alternaria sonchi	major allergen alt a1 [Alternaria sonchi].	49476529	138
Alternaria cinerariae	major allergen alt a1 [Alternaria cinerariae].	49476531	137
Alternaria brassicae	major allergen alt a1 [Alternaria brassicae].	49476533	137
Alternaria mimica	major allergen alt a1 [Alternaria mimica].	49476535	137
Alternaria japonica	major allergen alt a1 [Alternaria japonica].	49476539	137
Alternaria eryngii	major allergen alt a1 [Alternaria eryngii].	49476541	137
Alternaria euphorbiicola	major allergen alt a1 [Alternaria euphorbiicola].	49476543	137
Arthroderma benhamiae	tri m 4 allergen [Arthroderma benhamiae].	23894232	726
Arthroderma benhamiae	tri m 2 allergen [Arthroderma benhamiae].	23894240	292
Arthroderma benhamiae	tri m 2 allergen [Arthroderma benhamiae].	23894244	404
Arthroderma benhamiae	tri m 2 allergen [Arthroderma benhamiae].	23894248	405
Aspergillus oryzae	Alpha-amylase A precursor (Taka-amylase A) (TAA)	113779	499
Aspergillus oryzae	Oryzin precursor (Alkaline proteinase) (ALP) (Aspergillus)	129235	403
Aspergillus fumigatus	enolase [Aspergillus fumigatus].	13925873	438
Aspergillus fumigatus	manganese superoxide dismutase [Aspergillus fumigatus].	1648970	221
Aspergillus fumigatus	Possible pathogenesis-related protein precursor [Aspergillus]	19309414	164
Aspergillus fumigatus	large subunit ribosomal protein L3 [Aspergillus fumigatus].	21215170	392
Aspergillus fumigatus	cellular serine proteinase [Aspergillus fumigatus].	2143220	495
Aspergillus niger	xylosidase [Aspergillus niger].	2181180	804
Aspergillus fumigatus	peroxisomal-like protein [Aspergillus fumigatus].	2769700	168
Aspergillus fumigatus	rAsp f 7 [Aspergillus fumigatus].	2879888	112
Aspergillus fumigatus	rAsp f 9 [Aspergillus fumigatus].	2879890	302
Aspergillus niger	serine protease.	289172	533
Aspergillus fumigatus	IgE-binding protein [Aspergillus fumigatus].	2980819	197
Aspergillus fumigatus	rAsp f 4 [Aspergillus fumigatus].	3005839	286
Aspergillus fumigatus	rAsp f 13 [Aspergillus fumigatus].	3005841	152
Aspergillus fumigatus	Asp f1 allergen [Aspergillus fumigatus].	3021324	125
Aspergillus fumigatus	IgE-binding protein [Aspergillus fumigatus].	3219530	185
Aspergillus fumigatus	allergen [Aspergillus fumigatus].	3643813	427
Aspergillus fumigatus	metalloprotease (MEP) [Aspergillus fumigatus].	3776613	634
Aspergillus niger	beta-xylosidase [Aspergillus niger].	4235093	804
Aspergillus fumigatus	suppressor protein spt23-related, with ankyrin repeats [Aspergillus]	42820661	1407
Aspergillus flavus	Oryzin precursor (Alkaline proteinase) (ALP) (Elastase)	464318	403
Aspergillus fumigatus	PPase [Aspergillus fumigatus].	5019414	178
Aspergillus fumigatus	Asp FII [Aspergillus fumigatus].	664852	250
Aspergillus fumigatus	rAsp f 8 [Aspergillus fumigatus].	6686524	111
Aspergillus flavus	Allergen Asp f1.	74665726	403
Aspergillus fumigatus	Major allergen Asp f 2 precursor (Asp f II).	83300352	310
Aspergillus fumigatus	Heat shock protein 90 (Heat shock protein hsp1) (65 kDa IgE-binding	83303658	706
Aspergillus fumigatus	major allergen 118kDa antigen [Aspergillus fumigatus].	9280360	150
Aspergillus fumigatus	aspergillopepsin i [Aspergillus fumigatus].	963013	395
Aspergillus fumigatus	Ribonuclease mitogillin precursor (Major allergen Asp f 1) (Asp f	54039254	176

Candida albicans	Alcohol dehydrogenase 1 (40 kDa allergen) (Allergen Cand a 1) (Can	1168348	350
Candida boidinii	Putative peroxiredoxin-A (Thioredoxin reductase) (Peroxisomal	130360	167
Candida boidinii	Putative peroxiredoxin-B (Thioredoxin reductase) (Peroxisomal	130361	167
Candida albicans	Fructose-bisphosphate aldolase (37 kDa major allergen) (IgE-binding	18203509	40
Candida albicans	Enolase 1 (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate	232054	440
Candida albicans	putative aminoacid permease protein [Candida albicans].	24461764	648
Candida albicans	29 kDa IgE-binding protein [Candida albicans].	37548637	236
Candida albicans	hypothetical protein CaO19.557 [Candida albicans SC5314].	46431500	341
Candida albicans	hypothetical protein CaO19.8192 [Candida albicans SC5314].	46431509	341
Coprinus comatus	Cop c1 allergen [Coprinus comatus].	4538529	81
Coprinus comatus	thioredoxin [Coprinus comatus].	5689669	106
Coprinus comatus	rCop c3 [Coprinus comatus].	5689671	328
Coprinus comatus	rCop c5 [Coprinus comatus].	5689673	141
Coprinus comatus	rCop c7 [Coprinus comatus].	5689675	152
Cryptococcus neoformans	allergen, putative [Cryptococcus neoformans var. neoformans JEC21].	57227639	234
Cryptococcus neoformans	thioredoxin (allergen cop c 2) [Cryptococcus neoformans var.	58265022	104
Davidiella tassiana	ribosomal protein P1 [Davidiella tassiana].	1143425	110
Davidiella tassiana	Minor allergen Cla h 7 (Cla h 5) (Cla h V).	1168970	204
Davidiella tassiana	60S acidic ribosomal protein P2 (Allergen Cla h 3) (Cla h III).	1173074	111
Davidiella tassiana	60S acidic ribosomal protein P2 (Minor allergen Cla h 4) (Cla h	21542440	111
Davidiella tassiana	putative nuclear transport factor 2 [Davidiella tassiana].	21748151	125
Davidiella tassiana	hydrophobin [Davidiella tassiana].	22796153	105
Davidiella tassiana	enolase; phosphopyruvate hydratase [Davidiella tassiana].	467660	440
Davidiella tassiana	Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate	6015094	440
Davidiella tassiana	Heat shock 70 kDa protein (Allergen Cla h 4) (Cla h IV).	729764	643
Davidiella tassiana	aldehyde dehydrogenase (NAD+) [Davidiella tassiana].	76666769	496
Embellisia allii	major allergen alt a1 [Embellisia allii].	49476559	138
Embellisia indefessa	major allergen alt a1 [Embellisia indefessa].	49476561	137
Embellisia novae-zelandiae	major allergen alt a1 [Embellisia novae-zelandiae].	49476563	136
Embellisia telluster	major allergen alt a1 [Embellisia telluster].	49476565	138
Epicoccum nigrum	[Segment 1 of 2] Major allergen Epi p 1 (Epi n 14625*).	24636821	12
Fusarium culmorum	60S acidic ribosomal protein P2 [Fusarium culmorum].	19879657	109
Fusarium culmorum	thioredoxin-like protein [Fusarium culmorum].	19879659	121
Fusarium culmorum	helix-loop-helix protein [Fusarium culmorum].	25361513	450
Fusarium culmorum	hypothetical protein [Fusarium culmorum].	27965571	342
Gibberella zeae	ENO_ALTAL Enolase (2-phosphoglycerate dehydratase)	46108928	438
Gibberella zeae	RLA2_ALTAL 60S acidic ribosomal protein P2 (Minor allergen Alt a 6)	46122455	109
Gibberella zeae	RLA1_CLAHE 60S acidic ribosomal protein p1 (allergen cla h 12) (CLA	46137705	108
Haematonectria haematococca	Allergen Fus s I3596*.	3122132	8
Lewia ethzedia	major allergen alt a1 [Lewia ethzedia].	49476483	138
Macrospora scirpicola	major allergen alt a1 [Macrospora scirpicola].	49476555	138
Malassezia sympodialis	allergen [Malassezia sympodialis].	1261972	350
Malassezia furfur	Major allergen Mal f 1 precursor (Pit o 1).	13959403	350
Malassezia sympodialis	allergen [Malassezia sympodialis].	19069920	342
Malassezia sympodialis	manganese superoxide dismutase [Malassezia sympodialis].	28569698	237
Malassezia furfur	MF1 [Malassezia furfur].	3445490	177
Malassezia furfur	MF2 [Malassezia furfur].	3445492	166
Malassezia sympodialis	allergen [Malassezia sympodialis].	4138171	172
Malassezia sympodialis	allergen [Malassezia sympodialis].	4138173	162
Malassezia sympodialis	allergen [Malassezia sympodialis].	4138175	187
Malassezia furfur	major allergenic protein Mal f4 [Malassezia furfur].	4587985	342
Malassezia sympodialis	allergen [Malassezia sympodialis].	7271239	179
Malassezia furfur	allergen Mal f3 - Malassezia furfur.	7514251	166
Malassezia sympodialis	mala s 12 allergen precursor [Malassezia sympodialis].	78038796	618
Neurospora crassa	probable rAsp f 9 allergen [Neurospora crassa].	28949979	301
Neurospora crassa	related to rasp f 7 allergen [Neurospora crassa].	28950043	265
Nimbya caricis	major allergen alt a1 [Nimbya caricis].	49476557	138
Penicillium oxalicum	vacuolar serine protease [Penicillium oxalicum].	12005497	503
Penicillium citrinum	vacuolar serine protease [Penicillium citrinum].	12005501	358
Penicillium citrinum	enolase [Penicillium citrinum].	13991101	438
Penicillium chrysogenum	vacuolar serine protease [Penicillium chrysogenum].	14215732	494
Penicillium citrinum	Heat shock 70 kDa protein (Allergen Pen c 19).	14423733	503
Penicillium chrysogenum	alkaline serine protease [Penicillium chrysogenum].	21069093	398
Penicillium citrinum	unknown [Penicillium citrinum].	38326693	228

Penicillium citrinum	Pen c 1; alkaline serine protease [Penicillium citrinum].	4587983	397
Penicillium citrinum	alkaline serine protease Pen c2 [Penicillium citrinum].	4588118	457
Penicillium citrinum	peroxisomal membrane protein [Penicillium citrinum].	5326864	167
Penicillium chrysogenum	allergen Pen n 13 [Penicillium chrysogenum].	6684788	397
Penicillium chrysogenum	allergen Pen n 18 [Penicillium chrysogenum].	7963902	494
Penicillium chrysogenum	68 kDa allergen [Penicillium chrysogenum].	999009	117
Pleospora tarda	major allergen alt a1 [Pleospora tarda].	49476463	137
Pleospora herbarum	major allergen alt a1 [Pleospora herbarum].	49476469	137
Rhodotorula mucilaginosa	Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate	7078092	439
Saccharomyces cerevisiae	Chain A, Yeast Profilin, Cubic Crystal Form.	15988101	125
Schizophyllum commune	pSc7 protien [Schizophyllum commune].	169865	204
Schizophyllum commune	pSc14 protein [Schizophyllum commune].	386678	214
Scomber japonicus	parvalbumin [Scomber japonicus].	29420793	109
Stemphylium vesicarium	major allergen alt a1 [Stemphylium vesicarium].	49476465	137
Stemphylium callistephi	major allergen alt a1 [Stemphylium callistephi].	49476467	137
Trichophyton tonsurans	83 kDa hypersensitivity protein (Protein IV).	1708296	26
Trichophyton schoenleinii	tri s 4 allergen [Trichophyton schoenleinii].	23894227	726
Trichophyton schoenleinii	tri m 2 allergen [Trichophyton schoenleinii].	23894260	405
Trichophyton rubrum	Tri r 4 allergen [Trichophyton rubrum].	5813788	726
Trichophyton rubrum	Tri r 2 allergen [Trichophyton rubrum].	5813790	412
Ulocladium cucurbitae	major allergen alt a1 [Ulocladium cucurbitae].	49476545	137
Ulocladium alternariae	major allergen alt a1 [Ulocladium alternariae].	49476547	138
Ulocladium botrytis	major allergen alt a1 [Ulocladium botrytis].	49476549	137
Ulocladium atrum	major allergen alt a1 [Ulocladium atrum].	49476551	137
Ulocladium chartarum	major allergen alt a1 [Ulocladium chartarum].	49476553	137
Verticillium dahliae	allergen rAsp f9-like protein [Verticillium dahliae].	42742375	403
Verticillium dahliae	allergen Asp f2-like protein [Verticillium dahliae].	42742377	297

Aeroallergens mites

Species	Comments	GI #	AA
Acarus siro	lipid binding protein [Acarus siro].	4049356	64
Blomia tropicalis	allergen [Blomia tropicalis].	1377859	130
Blomia tropicalis	cysteine protease precursor [Blomia tropicalis].	14276828	221
Blomia tropicalis	paramyosin allergen [Blomia tropicalis].	21954740	875
Blomia tropicalis	trypsin [Blomia tropicalis].	25989482	266
Blomia tropicalis	allergen Blo t Mag 1 [Blomia tropicalis].	25989484	338
Blomia tropicalis	major IgE-binding protein Blo t 5 [Blomia tropicalis].	4204917	134
Blomia tropicalis	allergen precursor [Blomia tropicalis].	902012	144
Blomia tropicalis	allergen [Blomia tropicalis].	915347	73
Chironomus thummi	Globin CTT-III precursor (Erythrocrucorin III).	121219	151
Chironomus thummi	Globin CTT-IV precursor.	121227	151
Chironomus thummi	Globin CTT-VIII.	121237	151
Chironomus thummi	Globin CTT-VIIB-3 precursor.	121244	161
Chironomus thummi	Globin CTT-VIIB-6 precursor.	121248	161
Chironomus thummi	Globin CTT-VIIB-7 precursor.	121249	162
Chironomus thummi	Globin CTT-III A.	121256	151
Chironomus thummi	Globin CTT-X.	121259	151
Chironomus thummi	Globin CTT-II beta precursor.	1707908	160
Chironomus thummi	Globin CTT-IX precursor.	1707911	161
Chironomus thummi	Globin CTT-I/CTT-IA precursor (Erythrocrucorin).	2506460	158
Chironomus thummi	Globin CTT-VI precursor.	2506461	162
Chironomus thummi	Globin CTT-VIIB-4 precursor (Erythrocrucorin).	56405052	161
Chironomus thummi	Globin CTT-VIIB-5/CTT-VIIB-9 precursor.	56405054	161
Chironomus thummi	Globin CTT-VII A precursor.	56405306	161
Chironomus thummi	tropomyosin [Chironomus thummi].	7321108	285
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	10189811	215
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	10189816	213
Dermatophagoides pteronyssinus	group III allergen - house-dust mite (Dermatophagoides	102832	18
Dermatophagoides pteronyssinus	Der p 7 allergen polypeptide.	1045602	215
Dermatophagoides microceras	Major mite fecal allergen Der m 1 (Der m I).	127205	30
Dermatophagoides farinae	Der f 3 mite allergen.	1314736	232
Dermatophagoides pteronyssinus	Alpha-amylase (Allergen Der p 4) (Der p IV).	1351935	19
Dermatophagoides pteronyssinus	Mite group 2 allergen Der p 2 precursor (Der p II) (DPX).	1352237	146

Dermatophagoides pteronyssinus	Mite allergen Der p 5 (Der P V) (IgE-binding allergen).	1352238	132
Dermatophagoides pteronyssinus	Mite allergen Der p 6 (Der p VI) (DP5).	1352239	20
Dermatophagoides farinae	allergen Def f II precursor [Dermatophagoides farinae].	13560629	170
Dermatophagoides farinae	Mag44 [Dermatophagoides farinae].	1359436	299
Dermatophagoides farinae	paramyosin-like allergen [Dermatophagoides farinae].	13785807	692
Dermatophagoides farinae	Mite allergen Der f 6 precursor (Der f VI) (DF5).	14424450	279
Dermatophagoides pteronyssinus	ferritin heavy chain-like protein [Dermatophagoides pteronyssinus].	15072346	180
Dermatophagoides farinae	Mag3 [Dermatophagoides farinae].	1545803	349
Dermatophagoides farinae	major Der f 2 isoform [Dermatophagoides farinae].	17978844	129
Dermatophagoides pteronyssinus	group 14 allergen protein [Dermatophagoides pteronyssinus].	20385544	1662
Dermatophagoides pteronyssinus	Chain A, X-Ray Structure Of Der P 2, The Major House Dust Mite	21465915	129
Dermatophagoides farinae	gelsolin-like allergen Der f 16 [Dermatophagoides farinae].	21591547	480
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725560	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725562	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725564	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725566	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725568	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725570	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725572	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725574	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725576	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725578	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725580	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725582	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725584	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725586	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725588	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725590	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725592	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725594	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725596	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725600	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725602	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725604	129
Dermatophagoides farinae	mite allergen Der f II precursor [Dermatophagoides farinae].	217306	146
Dermatophagoides farinae	mite allergen Der f II precursor [Dermatophagoides farinae].	217308	138
Dermatophagoides pteronyssinus	serine protease [Dermatophagoides pteronyssinus].	22595342	244
Dermatophagoides pteronyssinus	tropomyosin [Dermatophagoides pteronyssinus].	2353266	284
Dermatophagoides pteronyssinus	tropomyosin [Dermatophagoides pteronyssinus].	2440053	284
Dermatophagoides farinae	Mite allergen Der f 7 precursor (Der f VII).	2498299	213
Dermatophagoides farinae	Mite allergen Der f 3 precursor (Der f III).	2507248	259
Dermatophagoides farinae	trypsin-like protease=Der f III allergen homolog {N-terminal}	259012	20
Dermatophagoides farinae	Der f 1 allergen preproenzyme [Dermatophagoides farinae].	27530349	321
Dermatophagoides farinae	60 kDa allergen Der f 18p [Dermatophagoides farinae].	27550039	462
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	28798085	132
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	29786835	302
Dermatophagoides pteronyssinus	trypsin-like serine protease [Dermatophagoides pteronyssinus].	31745576	273
Dermatophagoides pteronyssinus	serine protease LM-1 [Dermatophagoides pteronyssinus].	37654735	261
Dermatophagoides pteronyssinus	HDM allergen [Dermatophagoides pteronyssinus].	37778944	875
Dermatophagoides pteronyssinus	Tertiary Structure Of The Major House Dust Mite Allergen Der P 2,	3891991	129
Dermatophagoides farinae	DF5=allergen {N-terminal} [Dermatophagoides farinae=mites, Peptide	404371	20
Dermatophagoides pteronyssinus	alpha-amylase [Dermatophagoides pteronyssinus].	5059162	496
Dermatophagoides pteronyssinus	Der p 3 allergen.	511476	261
Dermatophagoides pteronyssinus	Der p 1 allergen preproenzyme [Dermatophagoides pteronyssinus].	511953	320
Dermatophagoides farinae	Der f II [Dermatophagoides farinae].	546852	142
Dermatophagoides farinae	mite allergen Der f 2 [Dermatophagoides farinae].	55859466	146
Dermatophagoides farinae	Der f 2 [Dermatophagoides farinae].	55859468	146
Dermatophagoides farinae	mite allergen Der f 2 [Dermatophagoides farinae].	55859470	146
Dermatophagoides farinae	group 2 allergen [Dermatophagoides farinae].	56378069	146
Dermatophagoides farinae	98kDa HDM allergen [Dermatophagoides farinae].	5815436	555
Dermatophagoides pteronyssinus	Der p 1 allergen [Dermatophagoides pteronyssinus].	61608445	216
Dermatophagoides farinae	allergen Der f1 precursor - house-dust mite (Dermatophagoides	627141	319
Dermatophagoides farinae	Allergen MAG29.	729970	145
Dermatophagoides farinae	Allergen Mag.	729979	341

Dermatophagoides farinae	Major mite fecal allergen Der f 1 precursor (Der f I).	730035	321
Dermatophagoides pteronyssinus	Major mite fecal allergen Der p 1 precursor (Der p I).	730036	320
Dermatophagoides pteronyssinus	Major fecal allergen Der p 1-associated protein.	74798156	23
Dermatophagoides farinae	Major Der f 2 isoform.	74820084	129
Dermatophagoides pteronyssinus	major allergen p Dp 15 [Dermatophagoides pteronyssinus].	807138	219
Dermatophagoides pteronyssinus	IgE-binding protein C-terminal fragment (148 AA) [Dermatophagoides pteronyssinus].	9072	148
Dermatophagoides pteronyssinus	Der p V allergen [Dermatophagoides pteronyssinus].	913785	132
Euroglyphus maynei	Mite group 2 allergen Eur m 2 precursor.	14423649	145
Euroglyphus maynei	Mite allergen Eur m 3 precursor.	14423685	261
Euroglyphus maynei	group 2 allergen Eur m 2 0102 [Euroglyphus maynei].	3941386	135
Euroglyphus maynei	group 1 allergen Eur m 1 0101 precursor [Euroglyphus maynei].	3941388	321
Euroglyphus maynei	group 1 allergen Eur m 1 0102 [Euroglyphus maynei].	3941390	327
Euroglyphus maynei	alpha-amylase precursor [Euroglyphus maynei].	5059164	521
Euroglyphus maynei	high molecular weight allergen M-177 precursor [Euroglyphus maynei].	6492307	1668
Glycyphagus domesticus	Gly d 2 [Glycyphagus domesticus].	6179520	128
Glycyphagus domesticus	gly d 2.02 isoform [Glycyphagus domesticus].	7160811	125
Lepidoglyphus destructor	Mite allergen Lep d 7 precursor.	14423650	216
Lepidoglyphus destructor	Mite allergen Lep d 5.	14423651	110
Lepidoglyphus destructor	Fatty acid-binding protein (Allergen Lep d 13).	14423714	131
Lepidoglyphus destructor	Tropomyosin (Allergen Lep d 10).	14423956	284
Lepidoglyphus destructor	allergen Lep d 1.01.	1582222	141
Lepidoglyphus destructor	allergen Lep d 1.02.	1582223	141
Lepidoglyphus destructor	alpha tubulin [Lepidoglyphus destructor].	19702131	450
Lepidoglyphus destructor	Lep D 2 precursor [Lepidoglyphus destructor].	21213898	141
Lepidoglyphus destructor	Lep D 2 precursor [Lepidoglyphus destructor].	21213900	141
Lepidoglyphus destructor	allergen Lep d 1.02 precursor - Lepidoglyphus destructor.	2147108	141
Lepidoglyphus destructor	Lep D 2 allergen [Lepidoglyphus destructor].	999462	141
Tyrophagus putrescentiae	group 2 allergen [Tyrophagus putrescentiae].	2182106	141
Tyrophagus putrescentiae	fatty acid-binding protein [Tyrophagus putrescentiae].	51860756	131

Aeroallergens insects

Species

Species	Comments	GI #	AA
Argas reflexus	Arg r 1 precursor [Argas reflexus].	58371884	159
Blattella germanica	allergen Bla g 4.	1166573	182
Blattella germanica	Aspartic protease Bla g 2 precursor (Allergen Bla g II).	1703445	352
Blattella germanica	major allergen Bla g 1.02 [Blattella germanica].	4240395	492
Blattella germanica	major allergen Bla g 1.0101 [Blattella germanica].	4572592	412
Blattella germanica	36 kda allergen (peptide 143-111) [Blattella germanica=German].	544618	20
Blattella germanica	36 kda allergen (peptide 143-115) [Blattella germanica=German].	544619	25
Blattella germanica	Glutathione S-transferase (GST class-sigma) (Major allergen Bla g 2).	6225491	204
Blattella germanica	Chain A, The Structure Of Mutant (N93q) Of Bla G 2.	62738637	330
Blattella germanica	tropomyosin [Blattella germanica].	8101069	284
Ixodes ricinus	allergen-like protein [Ixodes ricinus].	28564461	116
Lepisma saccharina	tropomyosin [Lepisma saccharina].	20387027	284
Lepisma saccharina	tropomyosin [Lepisma saccharina].	20387029	243
Periplaneta americana	allergen [Periplaneta americana].	1531589	631
Periplaneta americana	allergen [Periplaneta americana].	1580792	685
Periplaneta americana	allergen [Periplaneta americana].	1580794	470
Periplaneta americana	allergen [Periplaneta americana].	1580797	393
Periplaneta fuliginosa	tropomyosin [Periplaneta fuliginosa].	19310971	284
Periplaneta americana	ribosomal protein S12 [Periplaneta americana].	21217441	139
Periplaneta americana	Rab11 [Periplaneta americana].	21217443	204
Periplaneta americana	Cr-P11 allergen [Periplaneta americana].	2231297	446
Periplaneta americana	Cr-P11 allergen [Periplaneta americana].	2253610	274
Periplaneta americana	Cr-P11 [Periplaneta americana].	2580504	395
Periplaneta americana	allergen [Periplaneta americana].	2897849	228
Periplaneta americana	major allergen Per a 1.0105 [Periplaneta americana].	30144660	124
Periplaneta americana	major allergen Per a 1.0101 [Periplaneta americana].	4240399	231
Periplaneta americana	tropomyosin [Periplaneta americana].	4378573	284
Periplaneta americana	tropomyosin [Periplaneta americana].	4468639	284
Pieris rapae	nitrile-specifier protein [Pieris rapae].	40288346	632
Plodia interpunctella	arginine kinase [Plodia interpunctella].	15886861	355
Plodia interpunctella	unnamed protein product [Plodia interpunctella].	21335404	285

Plodia interpunctella	unnamed protein product [Plodia interpunctella].	21335406	705
Plodia interpunctella	unnamed protein product [Plodia interpunctella].	21335408	254
Polypedilum nubifer	Pol n 1 component MV=allergenic monomeric hemoglobin {N-terminal}	1703681	37
Tenebrio molitor	cockroach allergen-like protein [Tenebrio molitor].	32967475	595

Aeroallergens pollen

Species	Comments	GI #	AA
Agrostis alba	pollen allergen Agr a 1 - bent grass (fragment).	320606	26
Agrostis alba	Group I allergen Agr a 1 (Form 2), pollen.	75139987	35
Agrostis alba	Group I allergen Agr a 1 (Form 1), pollen.	75139989	35
Alnus glutinosa	Aln g 1 [Alnus glutinosa].	261407	160
Alnus glutinosa	pollen allergen Aln g 4 [Alnus glutinosa].	3319651	85
Ambrosia artemisiifolia	Pollen allergen Amb a 1.1 precursor (Antigen E) (AgE) (Antigen Amb	113475	396
Ambrosia artemisiifolia	Pollen allergen Amb a 1.2 precursor (Antigen E) (Antigen Amb a I)	113476	398
Ambrosia artemisiifolia	Pollen allergen Amb a 1.3 precursor (Antigen E) (Antigen Amb a I).	113477	397
Ambrosia artemisiifolia	Pollen allergen Amb a 1.4 precursor (Antigen E) (Antigen Amb a I).	113478	392
Ambrosia elatior	Pollen allergen Amb a 5 (Amb a V) (Allergen Ra5).	114090	45
Ambrosia trifida	Pollen allergen Amb t 5 precursor (Amb t V) (Allergen Ra5G).	114091	73
Ambrosia artemisiifolia	Nonspecific lipid-transfer protein precursor (LTP) (Pollen allergen	14285595	118
Ambrosia artemisiifolia	antigen E.	166443	397
Ambrosia artemisiifolia	profilin-like protein [Ambrosia artemisiifolia].	34851178	131
Ambrosia artemisiifolia	profilin-like protein [Ambrosia artemisiifolia].	34851180	131
Ambrosia artemisiifolia	profilin-like protein [Ambrosia artemisiifolia].	34851182	133
Ambrosia elatior	Pollen allergen Amb a 3 (Amb a III) (Allergen Ra3).	416636	101
Ambrosia psilostachya	Amb p V allergen.	515953	77
Ambrosia psilostachya	Amb p V allergen.	515954	77
Ambrosia psilostachya	Amb p V allergen.	515955	77
Ambrosia psilostachya	Amb p V allergen.	515956	77
Ambrosia psilostachya	Amb p V allergen.	515957	77
Ambrosia artemisiifolia	allergen Amb a 1.2 precursor - common ragweed.	539048	398
Ambrosia artemisiifolia	allergen Amb a 1.3 precursor - common ragweed.	539049	397
Ambrosia artemisiifolia	Pollen allergen Amb a 2 precursor (Antigen K) (Antigen Amb a II).	113479	397
Anthoxanthum odoratum	pollen allergen Ant o 1 - sweet vernal grass (fragment).	320607	26
Anthoxanthum odoratum	Group I allergen Ant o 1 (Form 1), pollen.	75139986	32
Anthoxanthum odoratum	Group I allergen Ant o 1 (Form 2), pollen.	75139990	32
Artemisia vulgaris	major pollen allergen Art v 1 precursor [Artemisia vulgaris].	27818335	132
Betula pendula	allergenic isoflavone reductase-like protein Bet v 6.0102 [Betula	10764491	308
Betula pendula	Chain A, Birch Pollen Allergen Bet v 1 Mutant N28t, K32q, E45s,	11514622	159
Betula pendula	Calcium-binding allergen Bet v 3 (Bet v III).	1168696	205
Betula pendula	Major pollen allergen Bet v 1-B (Bet v I-B).	1168701	160
Betula pendula	Major pollen allergen Bet v 1-C (Bet v I-C).	1168702	160
Betula pendula	Major pollen allergen Bet v 1-D/H (Bet v I-D/H).	1168703	160
Betula pendula	Major pollen allergen Bet v 1-E (Bet v I-E).	1168704	160
Betula pendula	Major pollen allergen Bet v 1-F/I (Bet v I-F/I).	1168705	160
Betula pendula	Major pollen allergen Bet v 1-G (Bet v I-G).	1168706	160
Betula pendula	Major pollen allergen Bet v 1-J (Bet v I-J).	1168707	160
Betula pendula	Major pollen allergen Bet v 1-K (Bet v I-K).	1168708	160
Betula pendula	Major pollen allergen Bet v 1-L (Bet v I-L).	1168709	160
Betula pendula	Major pollen allergen Bet v 1-M/N (Bet v I-M/N).	1168710	160
Betula platyphylla	Bet vl jap1 [Betula platyphylla var. japonica].	12583681	160
Betula platyphylla	Bet vl jap2 [Betula platyphylla var. japonica].	12583683	160
Betula platyphylla	Bet vl jap3 [Betula platyphylla var. japonica].	12583685	160
Betula pendula	Profilin (Pollen allergen Bet v 2) (Bet v II).	130975	133
Betula pendula	major allergen Bet v 1 [Betula pendula].	1321714	160
Betula pendula	major allergen Bet v 1 [Betula pendula].	1321716	160
Betula pendula	major allergen Bet v 1 [Betula pendula].	1321718	160
Betula pendula	major allergen Bet v 1 [Betula pendula].	1321720	160
Betula pendula	major allergen Bet v 1 [Betula pendula].	1321722	160
Betula pendula	major allergen Bet v 1 [Betula pendula].	1321724	160
Betula pendula	major allergen Bet v 1 [Betula pendula].	1321726	160
Betula pendula	major allergen Bet v 1 [Betula pendula].	1321728	160
Betula pendula	pollen allergen Bet v 1 [Betula pendula].	1542857	160
Betula pendula	pollen allergen Bet v 1 [Betula pendula].	1542861	160
Betula pendula	pollen allergen Bet v 1 [Betula pendula].	1542863	160

Betula pendula	pollen allergen Bet v 1 [Betula pendula].	1542863	160
Betula pendula	pollen allergen Bet v 1 [Betula pendula].	1542867	160
Betula pendula	pollen allergen Bet v 1 [Betula pendula].	1542869	160
Betula pendula	pollen allergen Bet v 1 [Betula pendula].	1542871	160
Betula pendula	pollen allergen Bet v 1 [Betula pendula].	1542873	160
Betula pendula	Birch Pollen Profilin.	1942360	133
Betula pendula	peptidylprolyl isomerase (cyclophilin) [Betula pendula].	21886603	173
Betula pendula	Bet v I=major allergen [Betula verrucosa=birch trees, pollen,	239734	43
Betula pendula	major allergen Bet v 1 [Betula pendula].	2414158	160
Betula pendula	pollen allergen Betv1 [Betula pendula].	2564220	160
Betula pendula	pollen allergen Betv1 [Betula pendula].	2564222	160
Betula pendula	pollen allergen Betv1 [Betula pendula].	2564224	160
Betula pendula	pollen allergen Betv1 [Betula pendula].	2564228	160
Betula	isoallergen {N-terminal} [birch, pollen, Peptide Partial, 51 aa].	298736	51
Betula	isoallergen {N-terminal} [birch, pollen, Peptide Partial, 51 aa].	298737	51
Betula pendula	allergen Bet v 1x [Betula pendula].	30908931	21
Betula pendula	major pollen allergen Bet v I - European white birch (fragment).	320545	51
Betula pendula	major pollen allergen Bet v II - European white birch (fragment).	320546	51
Betula pendula	Chain A, Birch Pollen Allergen Bet V 1 Mutant E45s.	38492423	159
Betula pendula	pollen allergen Betv1, isoform at8 [Betula pendula].	4006928	160
Betula pendula	pollen allergen Betv1, isoform at10 [Betula pendula].	4006945	160
Betula pendula	pollen allergen Betv1, isoform at14 [Betula pendula].	4006947	120
Betula pendula	pollen allergen Betv1, isoform at37 [Betula pendula].	4006953	160
Betula pendula	pollen allergen Betv1, isoform at42 [Betula pendula].	4006955	160
Betula pendula	pollen allergen Betv1, isoform at44 [Betula pendula].	4006957	160
Betula pendula	pollen allergen Betv1, isoform at56 [Betula pendula].	4006959	160
Betula pendula	pollen allergen Betv1, isoform at59 [Betula pendula].	4006961	160
Betula pendula	pollen allergen Betv1, isoform at87 [Betula pendula].	4006963	120
Betula pendula	pollen allergen Betv1, isoform at85 [Betula pendula].	4006965	160
Betula pendula	pollen allergen Betv1, isoform at7 [Betula pendula].	4006967	160
Betula pendula	pollen allergen, Betv1 [Betula pendula].	4376216	159
Betula pendula	pollen allergen, Betv1 [Betula pendula].	4376219	159
Betula pendula	pollen allergen, Betv1 [Betula pendula].	4376220	159
Betula pendula	pollen allergen, Betv1 [Betula pendula].	4376221	159
Betula pendula	pollen allergen, Betv1 [Betula pendula].	4376222	159
Betula pendula	isoallergen bet v1 b1 [Betula pendula].	4590392	160
Betula pendula	isoallergen Bet v 1 b2 [Betula pendula].	4590394	160
Betula pendula	isoallergen bet v 1 b3 [Betula pendula].	4590396	160
Betula pendula	Chain A, Solution Structure Of The Birch Pollen Allergen Bet V 4.	46014884	84
Betula pendula	1 Sc-3 [Betula pendula].	534898	160
Betula pendula	1 Sc2 [Betula pendula].	534900	159
Betula pendula	1-Sc1 [Betula pendula].	534910	160
Betula pendula	Chain A, Birch Pollen Allergen Bet V 1.	6980540	159
Betula pendula	Polcalcin Bet v 4 (Calcium-binding pollen allergen Bet v 4).	14423850	85
Carpinus betulus	pollen allergen Car b 1 [Carpinus betulus].	1545875	160
Carpinus betulus	pollen allergen Car b 1 [Carpinus betulus].	1545877	160
Carpinus betulus	pollen allergen Car b 1 [Carpinus betulus].	1545879	160
Carpinus betulus	pollen allergen Car b 1 [Carpinus betulus].	1545887	160
Carpinus betulus	pollen allergen Car b 1 [Carpinus betulus].	1545891	160
Carpinus betulus	pollen allergen Car b 1 [Carpinus betulus].	1545893	160
Carpinus betulus	pollen allergen Car b 1 [Carpinus betulus].	1545895	161
Carpinus betulus	pollen allergen Car b 1 [Carpinus betulus].	1545897	161
Carpinus betulus	Car b I=major allergen [Carpinus betulus=hornbeam trees, pollen,	239735	40
Carpinus betulus	Car b I [Carpinus betulus].	402745	159
Carpinus betulus	Major pollen allergen Car b 1 isoforms 1A and 1B (Car B I).	730048	160
Carpinus betulus	Major pollen allergen Car b 1 isoform 2 (Car b I).	730049	160
Catharanthus roseus	Intracellular pathogenesis related protein.	75279798	140
Chamaecyparis obtusa	Chao1 [Chamaecyparis obtusa].	1514943	375
Chamaecyparis obtusa	Polygalacturonase precursor (PG) (Pectinase) (Major pollen allergen	47606004	514
Chenopodium album	Che a 1 allergen precursor [Chenopodium album].	22074346	168
Chenopodium album	pollen allergen Che a 2 [Chenopodium album].	29465666	131
Chenopodium album	pollen allergen Che a 3 [Chenopodium album].	29465668	86
Crocus sativus	profilin [Crocus sativus].	58700651	131
Cryptomeria japonica	Cry j 1 precursor [Cryptomeria japonica].	19570315	374

Cryptomeria japonica	isoflavone reductase-like protein CJP-6 [Cryptomeria japonica].	19847822	306
Cryptomeria japonica	thaumatin-like protein [Cryptomeria japonica].	22830593	232
Cryptomeria japonica	thaumatin-like protein [Cryptomeria japonica].	22830595	233
Cryptomeria japonica	thaumatin-like protein [Cryptomeria japonica].	22830597	230
Cryptomeria japonica	allergen Cry j 2 [Cryptomeria japonica].	24898904	514
Cryptomeria japonica	allergen Cry j 2 [Cryptomeria japonica].	24898906	514
Cryptomeria japonica	allergen Cry j 2 [Cryptomeria japonica].	24898908	514
Cryptomeria japonica	class IV chitinase [Cryptomeria japonica].	56550550	281
Cryptomeria japonica	pollen major allergen No.121 isoform 1 [Cryptomeria japonica].	62149368	278
Cryptomeria japonica	pollen major allergen No.121 isoform 2 [Cryptomeria japonica].	62149370	290
Cryptomeria japonica	pollen allergen CJP38 [Cryptomeria japonica].	62149372	348
Cryptomeria japonica	Polygalacturonase precursor (PG) (Pectinase) (Major pollen allergen	1171004	514
Cryptomeria japonica	Sugi basic protein precursor (SBP) (Major allergen Cry j 1) (Cry j	1173367	374
Cupressus arizonica	putative allergen Cup a 1 [Cupressus arizonica].	19069497	367
Cupressus sempervirens	PR5 allergen Cup s 3.2 precursor [Cupressus sempervirens].	38456228	225
Cupressus sempervirens	PR5 allergen Cup s 3.3 precursor [Cupressus sempervirens].	38456230	225
Cupressus arizonica	cup a 1 protein [Cupressus arizonica].	6562326	346
Cupressus sempervirens	Cup s 1 pollen allergen precursor [Cupressus sempervirens].	8101711	367
Cupressus sempervirens	Cup s 1 pollen allergen precursor [Cupressus sempervirens].	8101713	367
Cupressus sempervirens	Cup s 1 pollen allergen precursor [Cupressus sempervirens].	8101715	367
Cupressus sempervirens	Cup s 1 pollen allergen precursor [Cupressus sempervirens].	8101717	367
Cupressus sempervirens	Cup s 1 pollen allergen precursor [Cupressus sempervirens].	8101719	367
Cupressus arizonica	Cup a 3 protein [Cupressus arizonica].	9929163	199
Cynodon dactylon	acidic Cyn d 1 isoallergen isoform 1 precursor [Cynodon dactylon].	10314021	244
Cynodon dactylon	B1 protein allergen [Cynodon dactylon].	1247373	71
Cynodon dactylon	B4 protein allergen [Cynodon dactylon].	1247375	73
Cynodon dactylon	B2 protein allergen [Cynodon dactylon].	1247377	247
Cynodon dactylon	Major pollen allergen Cyn d 1.	14423757	246
Cynodon dactylon	acidic allergen Cyn d 1 precursor [Cynodon dactylon].	15384338	244
Cynodon dactylon	acidic Cyn d 1 isoallergen isoform 2 precursor [Cynodon dactylon].	16076693	262
Cynodon dactylon	acidic Cyn d 1 isoallergen isoform 3 precursor [Cynodon dactylon].	16076695	262
Cynodon dactylon	acidic Cyn d 1 isoallergen isoform 4 precursor [Cynodon dactylon].	16076697	262
Cynodon dactylon	calcium-binding pollen allergen [Cynodon dactylon].	1871507	82
Cynodon dactylon	profilin 1 [Cynodon dactylon].	2154730	131
Cynodon dactylon	pollen allergen Cyn d 23 [Cynodon dactylon].	32344779	118
Cynodon dactylon	pollen allergen Cyn d 15 [Cynodon dactylon].	32344781	112
Cynodon dactylon	pollen 2-phosphoglycerate dehydrogenase 2 precursor [Cynodon	37222051	446
Cynodon dactylon	pollen allergen (group II) [Cynodon dactylon].	4006978	122
Cynodon dactylon	FAD-linked oxidoreductase BG60 [Cynodon dactylon].	41393750	522
Cynodon dactylon	major allergen Cyn d 1=34 kda polypeptide {N-terminal} [Cynodon	451274	25
Cynodon dactylon	major allergen Cyn d 1=29 kda polypeptide {N-terminal} [Cynodon	451275	38
Cynodon dactylon	Cyn d 24 [Cynodon dactylon].	51950706	153
Cynodon dactylon	Cyn d 1b isoallergen {N-terminal} [Cynodon dactylon=Bermuda grass,	691726	34
Cynodon dactylon	Acidic Cyn d 1 isoallergen isoform 4 precursor.	75249708	262
Dactylis glomerata	allergen Dac g II.	1093120	196
Dactylis glomerata	group 5 allergen precursor [Dactylis glomerata].	14423124	290
Dactylis glomerata	unnamed protein product [Dactylis glomerata].	18093971	265
Dactylis glomerata	unnamed protein product [Dactylis glomerata].	18093991	264
Dactylis glomerata	Dac gIII allergen.	1825459	96
Dactylis glomerata	pollen allergen DG3 - orchard grass (fragment).	280409	28
Dactylis glomerata	{Segment 1 of 4} Major pollen allergen Dac g 4.	32363464	12
Dactylis glomerata	{Segment 2 of 4} Major pollen allergen Dac g 4.	32363465	11
Dactylis glomerata	{Segment 3 of 4} Major pollen allergen Dac g 4.	32363466	17
Dactylis glomerata	{Segment 4 of 4} Major pollen allergen Dac g 4.	32363467	15
Dactylis glomerata	group 1 allergen Dac g 1.01 precursor [Dactylis glomerata].	33149333	240
Dactylis glomerata	pollen allergen (group II) [Dactylis glomerata].	4007040	122
Dicranopteris linearis	2S storage protein-like albumin precursor [Dicranopteris linearis].	6573243	125
Dicranopteris curranii	2S storage protein-like albumin precursor [Dicranopteris curranii].	6573245	125
Dicranopteris linearis	2S storage protein-like albumin precursor [Dicranopteris linearis].	6573247	125
Festuca arundinacea	pollen allergen Fes e 1 type A - reed fescue (fragment).	320610	17
Festuca arundinacea	pollen allergen Fes e 1 type B - reed fescue (fragment).	320611	20
Festuca arundinacea	Group I allergen FeS e 1, pollen.	75139991	35
Fraxinus excelsior	allergen Fra e 1.0101 [Fraxinus excelsior].	33327133	145
Fraxinus excelsior	allergen Fra e 1 [Fraxinus excelsior].	34978692	146

Fraxinus excelsior	Fra e 1.0102 major allergen [Fraxinus excelsior].	56123478	145
Holcus lanatus	protein with incomplete signal sequence [Holcus lanatus].	1167836	248
Holcus lanatus	pollen allergen Hol 1 5b [Holcus lanatus].	11991229	296
Holcus lanatus	group V grass pollen allergen [Holcus lanatus].	2266623	240
Holcus lanatus	group V allergen [Holcus lanatus].	2266625	264
Holcus lanatus	major group I allergen Hol 1 I [Holcus lanatus].	3860384	263
Holcus lanatus	pollen allergen (group II) [Holcus lanatus].	4807084	122
Holcus lanatus	allergen Hol-II [Holcus lanatus].	4114703	265
Holcus lanatus	30K allergen.	75140046	20
Humulus japonicus	Humj1 [Humulus japonicus].	33113263	155
Humulus scandens	profilin-like protein [Humulus scandens].	34851174	131
Humulus scandens	profilin-like protein [Humulus scandens].	34851176	131
Juniperus oxycedrus	putative allergen jun o 1 [Juniperus oxycedrus].	15139849	367
Juniperus ashei	elongation factor [Juniperus ashei].	21632054	172
Juniperus rigida	PR5 allergen Jun r 3.1 precursor [Juniperus rigida].	38456222	225
Juniperus rigida	PR5 allergen Jun r 3.2 precursor [Juniperus rigida].	38456224	225
Juniperus ashei	pollen major allergen 1-1 [Juniperus ashei].	4138877	367
Juniperus virginiana	Pathogenesis-related protein precursor [Putative major pollen	51316532	110
Juniperus oxycedrus	pollen allergen Jun o 4 [Juniperus oxycedrus].	5391446	165
Juniperus ashei	allergen Jun a 3 [Juniperus ashei].	6940772	225
Juniperus virginiana	pollen major allergen 1-2 [Juniperus virginiana].	8843917	367
Juniperus virginiana	pollen major allergen 1-1 [Juniperus virginiana].	8843921	367
Juniperus ashei	pollen major allergen 2 protein [Juniperus ashei].	9955725	507
Ligustrum vulgare	major allergen [Ligustrum vulgare].	3256210	145
Ligustrum vulgare	major allergen [Ligustrum vulgare].	3256212	145
Lilium longiflorum	profilin 1 [Lilium longiflorum].	6425105	131
Lilium longiflorum	profilin 2 [Lilium longiflorum].	6425107	131
Lilium longiflorum	profilin 3 [Lilium longiflorum].	6425109	131
Lolium perenne	pollen allergen p1b precursor - perennial ryegrass.	100639	308
Lolium perenne	Pollen allergen Lol p 2-A (Lol p II-A).	126386	97
Lolium perenne	Pollen allergen Lol p 3 (Lol p III).	126387	97
Lolium perenne	pollen allergen.	168314	252
Lolium perenne	Major pollen allergen Lol p 5a precursor (Lol p Va) (Lol p Ib).	2498581	308
Lolium perenne	Major pollen allergen Lol p 5b precursor (Lol p Vb).	2498582	339
Lolium italicum	pollen allergen (group II) [Lolium italicum].	4007636	122
Lolium perenne	pollen allergen Lol p VA precursor; major allergen [Lolium	4416516	301
Lolium perenne	Major pollen allergen Lol p 11 (Lol p XI).	47605808	134
Lolium perenne	pollen allergen Lol p 9 [Lolium perenne].	55859464	423
Lolium perenne	pollen allergen [Lolium perenne].	6634467	301
Lolium perenne	50K allergen.	75140048	20
Lolium perenne	Allergen Lol p 1k.	75220940	88
Lolium perenne	Pollen allergen.	75274600	263
Lolium perenne	allergen Lol p II [Lolium perenne].	939932	88
Lolium perenne	Pollen allergen Lol p 1 precursor (Lol p I) (Allergen R7).	126385	263
Lupinus luteus	Chain A, Crystal Structure Of Pathogenesis-Related Protein	22218768	155
Lupinus luteus	Chain B, Crystal Structure Of Pathogenesis-Related Protein	22218772	155
Lupinus luteus	Chain B, Crystal Structure Of Pathogenesis-Related Protein Llpr-	61680377	157
Mercurialis annua	Profilin [Mercurialis annua].	2959898	133
Olea europaea	main olive allergen [Olea europaea].	13195753	130
Olea europaea	major allergen OLE16 - common olive (fragment).	1362128	137
Olea europaea	major allergen OLE17 - common olive (fragment).	1362129	136
Olea europaea	major allergen OLE19 - common olive (fragment).	1362130	136
Olea europaea	major allergen OLE1c - common olive (fragment).	1362131	145
Olea europaea	major allergen OLE20 - common olive (fragment).	1362132	137
Olea europaea	major allergen OLE26 - common olive (fragment).	1362133	136
Olea europaea	major allergen OLE33/OLE37 - common olive (fragment).	1362134	136
Olea europaea	major allergen OLE3c - common olive.	1362135	145
Olea europaea	major allergen OLE5c - common olive.	1362136	145
Olea europaea	major allergen OLE6 - common olive (fragment).	1362137	136
Olea europaea	beta-1,3-glucanase-like protein [Olea europaea].	14279169	460
Olea europaea	Pollen allergen Ole e 6.	14423643	50
Olea europaea	Calcium-binding allergen Ole e 8 (PCA18/PCA23).	14423648	171
Olea europaea	Pollen allergen Ole e 7 (Ole e VII).	22002032	21
Olea europaea	Ole e 1.0102 protein [Olea europaea].	2465127	146

Olea europaea	Ole e 1.0103 protein [Olea europaea].	2465129	146
Olea europaea	Ole e 1 protein [Olea europaea].	2465131	146
Olea europaea	Superoxide dismutase [Cu-Zn] (Allergen Ole e 5) (Ole e V).	2500822	29
Olea europaea	allergen Ole e 10 [Olea europaea].	29465664	123
Olea europaea	[Segment 1 of 2] Major pollen allergen Ole e 4 (Ole e IV).	32363448	10
Olea europaea	[Segment 2 of 2] Major pollen allergen Ole e 4 (Ole e IV).	32363449	14
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33325111	132
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33325115	132
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33329732	132
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33329738	132
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33329744	131
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33329748	129
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33329750	131
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33329752	131
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33329754	132
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33329756	132
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33329758	131
Olea europaea	calcium-binding pollen allergen [Olea europaea].	3337403	84
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	37548753	132
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	37724593	135
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	37724597	134
Olea europaea	Ole e 6 allergen [Olea europaea var. sylvestris].	37725369	38
Olea europaea	Ole e 3 allergen [Olea europaea].	37725377	52
Olea europaea	Profilin-1 (Pollen allergen Ole e 2).	3914426	134
Olea europaea	Profilin-2 (Pollen allergen Ole e 2).	3914427	134
Olea europaea	Profilin-3 (Pollen allergen Ole e 2).	3914428	134
Olea europaea	Cu/Zn super-oxide dismutase [Olea europaea].	39840779	152
Olea europaea	calcium-binding protein [Olea europaea].	6901654	171
Olea europaea	Major pollen allergen (Allergen Ole e 1) (Ole e I).	14424429	145
Parietaria officinalis	mAb 2F9-reactive major allergen {N-terminal} [Parietaria	1311509	17
Parietaria officinalis	mAb 8C7-reactive major allergen {N-terminal, band 1} [Parietaria	1311510	15
Parietaria officinalis	mAb 8C7-reactive major allergen {N-terminal, band 2} [Parietaria	1311511	15
Parietaria officinalis	mAb 3F8-reactive major allergen {N-terminal} [Parietaria	1311512	15
Parietaria officinalis	mAb 8B6-reactive major allergen {N-terminal} [Parietaria	1311513	30
Parietaria judaica	Profilin-2 (Pollen allergen Par j 3.0102).	14423869	131
Parietaria judaica	Profilin-1 (Pollen allergen Par j 3.0101).	14423876	132
Parietaria judaica	P8 protein [Parietaria judaica].	1532056	133
Parietaria judaica	P9 protein [Parietaria judaica].	1532058	176
Parietaria officinalis	Par o 1a=acidic allergen isoform {N-terminal} [Parietaria	1836010	25
Parietaria officinalis	Par o 1b=basic allergen isoform {N-terminal} [Parietaria	1836011	24
Parietaria judaica	Probable nonspecific lipid-transfer protein 1 precursor (LTP)	2497749	138
Parietaria judaica	Probable nonspecific lipid-transfer protein 2 precursor (LTP 2)	2497750	133
Parietaria judaica	Probable nonspecific lipid-transfer protein (LTP) (Major pollen	3915783	139
Parietaria judaica	major allergen Par j I.	741844	143
Parietaria officinalis	Pollen major allergen Par o I.	75139847	12
Phalaris aquatica	Major pollen allergen Pha a 1 precursor (Pha a I).	2498576	269
Phalaris aquatica	Major pollen allergen Pha a 5.1 precursor (Pha A 5) (Clone 28).	2498577	320
Phalaris aquatica	Major pollen allergen Pha a 5.2 precursor (Pha a 5) (Clone 14).	2498578	305
Phalaris aquatica	Major pollen allergen Pha a 5.3 precursor (Pha a 5) (Clone 29).	2498579	294
Phalaris aquatica	Major pollen allergen Pha a 5.4 (Pha a 5) (Clone 5).	2498580	175
Phalaris aquatica	Pha a I=34 kda pollen allergen {N-terminal} [Phalaris	409328	20
Phleum pratense	major allergen Phl p Va.	1092249	285
Phleum pratense	group V allergen Phl p 5 precursor [Phleum pratense].	13430402	275
Phleum pratense	Polcalcin Phl p 7 (Calcium-binding pollen allergen Phl p 7) (P7).	14423846	78
Phleum pratense	major allergen Phl p 5 [Phleum pratense].	1684718	281
Phleum pratense	major allergen Phl p 5 [Phleum pratense].	1684720	276
Phleum pratense	unnamed protein product [Phleum pratense].	21725606	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725608	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725610	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725612	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725614	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725616	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725618	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725620	287

Phleum pratense	unnamed protein product [Phleum pratense].	21725622	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725624	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725626	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725628	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725630	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725632	287
Phleum pratense	pollen allergen Phl p 11 [Phleum pratense].	22452313	143
Phleum pratense	Major Pollen Allergen Phl p Va [Phleum pratense].	2308757	286
Phleum pratense	profilin 3 [Phleum pratense].	2415700	131
Phleum pratense	profilin 4 [Phleum pratense].	2415702	131
Phleum pratense	Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen	28373838	241
Phleum pratense	Chain N, Crystal Structure Of Phl P 6, A Major Timothy Grass Pollen	28374072	111
Phleum pratense	Pollen allergen Phl p 5b precursor (Phl p Vb).	2851457	284
Phleum pratense	Chain A, Crystal Structure Of The Functional Domain Of The Major	28948464	102
Phleum pratense	phl p5a allergen precursor [Phleum pratense].	29500897	284
Phleum pratense	Phl p6 allergen [Phleum pratense].	3004465	138
Phleum pratense	Phl p6 allergen [Phleum pratense].	3004467	138
Phleum pratense	Phl p6 IgE binding fragment [Phleum pratense].	3004469	106
Phleum pratense	major allergen Phl p 5 [Phleum pratense].	3135497	276
Phleum pratense	major allergen Phl p 5 [Phleum pratense].	3135499	276
Phleum pratense	major allergen Phl p 5 [Phleum pratense].	3135501	276
Phleum pratense	major allergen Phl p 5 [Phleum pratense].	3135503	276
Phleum pratense	group V allergen Phl p 5.0103 precursor [Phleum pratense].	3309039	312
Phleum pratense	group V allergen Phl p 5.0203 precursor [Phleum pratense].	3309041	295
Phleum pratense	group V allergen Phl p 5.0206 precursor [Phleum pratense].	3309045	290
Phleum pratense	group V allergen Phl p 5.0207 precursor [Phleum pratense].	3309047	287
Phleum pratense	pollen allergen Phl p1 [Phleum pratense].	3901094	263
Phleum pratense	Phl p 3 allergen [Phleum pratense].	39841264	97
Phleum pratense	Phlp5 [Phleum pratense].	398830	312
Phleum pratense	PHL P11, pollen allergen [Phleum pratense].	415896	122
Phleum pratense	PHLP5A protein - common timothy (fragment).	422005	257
Phleum pratense	unnamed protein product [Phleum pratense].	45108967	500
Phleum pratense	unnamed protein product [Phleum pratense].	45108973	500
Phleum pratense	unnamed protein product [Phleum pratense].	45823012	240
Phleum pratense	Profilin-1 (Pollen Allergen Phl p 12) (Phl p 11).	464471	131
Phleum pratense	Phl p 1 allergen [Phleum pratense].	473360	263
Phleum pratense	allergen Phl p Vb - common timothy.	481397	280
Phleum pratense	polygalacturonase [Phleum pratense].	4826572	394
Phleum pratense	pollen allergen Phl p 4 [Phleum pratense].	54144332	508
Phleum pratense	pollen allergen Phl p 4 [Phleum pratense].	54144334	508
Phleum pratense	Pollen allergen Phl p V.	75139900	24
Phleum pratense	Pollen allergen Phl p1 precursor.	75221090	263
Phoenix dactylifera	profilin [Phoenix dactylifera].	21322677	131
Pinus radiata	Pollen allergen.	75099285	293
Platanus x	phatate invertase inhibitor precursor [Platanus x acerifolia].	26190140	179
Platanus x	polygalacturonase [Platanus x acerifolia].	49523394	377
Poa pratensis	Pollen allergen KBG 31 precursor (Pollen allergen Poa p 9) (Poa p	113560	373
Poa pratensis	Pollen allergen KBG 41 precursor (Pollen allergen Poa p 9) (Poa p	113561	333
Poa pratensis	pollen allergen Poa p 5 [Poa pratensis].	11991227	303
Poa pratensis	pollen allergen Poa-pl - Kentucky bluegrass (fragment).	280414	20
Poa pratensis	pollen allergen Poa p 1 - Kentucky bluegrass (fragment).	320620	26
Poa pratensis	pollen allergen (group II) [Poa pratensis].	4007655	122
Poa pratensis	group I pollen allergen [Poa pratensis].	4090265	263
Poa pratensis	pollen allergen (clone 7.2) - Kentucky bluegrass (fragment).	539056	131
Poa pratensis	Pollen allergen KBG 60 precursor (Pollen allergen Poa p 9) (Poa p	113562	307
Poa pratensis	major pollen allergen Que a 1 - white oak (fragment).	543675	24
Quercus alba	major antigen-like protein [Salsola kali].	22726221	320
Salsola kali	[Segment 1 of 4] Pollen allergen Sal k 1.	25090948	11
Salsola kali	[Segment 2 of 4] Pollen allergen Sal k 1.	25090949	8
Salsola kali	[Segment 3 of 4] Pollen allergen Sal k 1.	25090950	9
Salsola kali	[Segment 4 of 4] Pollen allergen Sal k 1.	25090951	14
Sambucus nigra	allergen-like protein BR5n20 [Sambucus nigra].	6561156	159
Syringa vulgaris	Polcalcin Syr v 3 (Calcium-binding pollen allergen Syr v 3).	14423847	81
Syringa vulgaris	allergen-like protein Syr v 1 isoform 1 - Syringa vulgaris.	631911	145

Syringa vulgaris	allergen-like protein Syr v I isoform 2 - Syringa vulgaris.	631912	145
Syringa vulgaris	allergen-like protein Syr v I isoform 3 - Syringa vulgaris.	631913	145
Taraxacum officinale	root allergen protein [Taraxacum officinale].	2707295	157

Food allergens animals

Species	Comments	GI #	AA
Batillus cornutus	major allergen Tur c1 - Turbo cornutus.	7441399	146
Bos taurus	allergen Bos d 2.0103 [imported] - bovine.	11277082	156
Bos taurus	allergen Bos d 2.0102 [imported] - bovine.	11277083	156
Bos taurus	kappa-casein [Bos taurus].	1228078	190
Bos taurus	Myelin basic protein (MBP) (Myelin A1 protein) (20 kDa	126796	169
Bos taurus	alpha-lactalbumin precursor (EC 2.4.1.22).	162644	142
Bos taurus	albumin [Bos taurus].	162648	607
Bos taurus	alpha-s1-casein.	162650	93
Bos taurus	beta-lactoglobulin.	162748	151
Bos taurus	beta-lactoglobulin.	162750	14
Bos taurus	alpha-s1-casein precursor.	162792	214
Bos taurus	alpha-S1-casein.	162794	214
Bos taurus	beta-casein precursor.	162797	224
Bos taurus	beta-casein.	162805	224
Bos taurus	kappa-casein precursor.	162811	190
Bos taurus	alpha-s1-casein.	162927	76
Bos taurus	alpha-s2-like casein precursor.	162929	222
Bos taurus	beta-casein precursor.	162931	224
Bos taurus	S100 calcium-binding protein A7 (Allergen Bos d 3) (Dander minor	2493414	101
Bos taurus	MD-2 protein [Bos taurus].	27806539	160
Bos taurus	Niemann-Pick disease, type C2 [Bos taurus].	27806881	149
Bos taurus	alpha-lactalbumin [Bos taurus].	295774	142
Bos taurus	bovine serum albumin [Bos taurus].	3336842	607
Bos taurus	beta-casein A3 [Bos taurus].	459292	224
Bos taurus	beta-lactoglobulin [Bos taurus].	520	178
Bos taurus	PREDICTED: similar to Odorant-binding protein precursor (OBP) [Bos	61819907	171
Bos taurus	beta-lactoglobulin variant B precursor [Bos taurus].	669061	178
Bos taurus	PREDICTED: similar to Odorant-binding protein precursor (OBP) [Bos	76677407	152
Bos taurus	PREDICTED: similar to Odorant-binding protein precursor (OBP) [Bos	76686423	215
Bos taurus	major allergen BDA20 [Bos taurus].	886215	172
Charybdis feriatus	heat stable allergen tropomyosin [Charybdis feriatus].	7024506	264
Crassostrea gigas	tropomyosin [Crassostrea gigas].	15419048	233
Crassostrea virginica	tropomyosin [Crassostrea virginica].	3668408	160
Cyprinus carpio	parvalbumin [Cyprinus carpio].	17977825	109
Cyprinus carpio	parvalbumin [Cyprinus carpio].	17977827	109
Farfantepenaeus aztecus	muscle tropomyosin, Pen a 1=36 kda major allergen	632782	21
Gadus callarias	Parvalbumin beta (Allergen Gad c 1) (Gad c I) (Allergen M).	131112	113
Gadus morhua	parvalbumin beta [Gadus morhua].	14531014	109
Gadus morhua	parvalbumin beta [Gadus morhua].	14531016	109
Gallus gallus	Ovomucoid precursor (Allergen Gal d 1) (Gal d I).	124757	210
Gallus gallus	Lysozyme C precursor (1,4-beta-N-acetylmuramidase C) (Allergen Gal	126608	147
Gallus gallus	Ovalbumin (Plakalbumin) (Allergen Gal d 2) (Gal d II).	129293	386
Gallus gallus	Ovotransferrin precursor (Conalbumin) (Allergen Gal d 3) (Gal d	1351295	705
Gallus gallus	Chain A, Loop-Inserted Structure Of P1-P1' Cleaved Ovalbumin Mutant	15826578	385
Gallus gallus	very low density lipoprotein II precursor.	211156	106
Gallus gallus	lysozyme protein.	212279	24
Gallus gallus	vitellogenin.	212881	1852
Gallus gallus	ovalbumin [Gallus gallus].	212900	388
Gallus gallus	Chain D, Crystal Structure Of S-Ovalbumin At 1.9 Angstrom	34811333	385
Gallus gallus	PREDICTED: similar to MD-2 [Gallus gallus].	50731634	155
Gallus gallus	unnamed protein product [Gallus gallus].	63052	155
Gallus gallus	preproalbumin (serum albumin) [Gallus gallus].	63748	615
Gallus gallus	vitellogenin [Gallus gallus].	63885	81
Gallus gallus	vitellogenin [Gallus gallus].	63887	1850
Gallus gallus	ovotransferrin [Gallus gallus].	757851	705
Gallus gallus	unnamed protein product [Gallus gallus].	808969	386
Haliotis diversicolor	tropomyosin [Haliotis diversicolor].	9954249	284
Helix aspersa	tropomyosin [Helix aspersa].	4468224	284

Homarus americanus	Tropomyosin (Allergen Hom a 1).	14285796	284
Homarus americanus	fast tropomyosin isoform [Homarus americanus].	1660868	284
Kryptolebias marmoratus	parvalbumin 1 [Rivulus marmoratus].	50953781	109
Kryptolebias marmoratus	parvalbumin 2 [Rivulus marmoratus].	50953783	109
Metapenaeus ensis	tropomyosin.	607623	274
Mimachlamys nobilis	tropomyosin [Chlamys nobilis].	9954253	284
Panulirus stimpsoni	Tropomyosin (Allergen Pan s 1) [Pan s I].	14285797	274
Penaeus monodon	allergen Pen m 2 [Penaeus monodon].	27463265	356
Perna viridis	tropomyosin [Perna viridis].	9954251	284
Rana esculenta	parvalbumin alpha [Rana esculenta].	20796729	110
Rana sp.	parvalbumin alpha [Rana sp. CH-2001].	20796733	110
Rana esculenta	parvalbumin beta protein [Rana esculenta].	20797081	109
Rana sp.	parvalbumin beta protein [Rana sp. CH-2001].	20797085	109
Salmo salar	Parvalbumin beta 2 [Major allergen Sal s 1].	18281421	108
Salmo salar	Parvalbumin beta 1 [Major allergen Sal s 1].	2493445	109
Theragra chalcogramma	parvalbumin [Theragra chalcogramma].	14531018	109
Theragra chalcogramma	parvalbumin [Theragra chalcogramma].	14531020	109

Food allergens plants Species

	Comments	GI #	AA
Actinidia chinensis	Actinidain precursor (Actinidin) (Allergen Act c 1).	113285	380
Actinidia deliciosa	unnamed protein product [Actinidia deliciosa].	15984	380
Actinidia deliciosa	actinidin.	166317	380
Actinidia deliciosa	phytolectin [Actinidia deliciosa].	40807635	116
Actinidia deliciosa	pKIWI501.	450239	184
Actinidia deliciosa	thaumatin-like protein [Actinidia deliciosa].	71057064	225
Anacardium occidentale	vicilin-like protein [Anacardium occidentale].	21666498	536
Anacardium occidentale	vicilin-like protein [Anacardium occidentale].	21914823	538
Anacardium occidentale	2s albumin [Anacardium occidentale].	24473800	138
Anacardium occidentale	allergen Ana o 2 [Anacardium occidentale].	25991543	457
Ananas comosus	profilin [Ananas comosus].	14161637	131
Apium graveolens	Major allergen Api g 1 (Api g 1.0101) (Api g I).	1346568	154
Apium graveolens	Chlorophyll a-b binding protein, chloroplast precursor (Allergen	14423661	264
Apium graveolens	Api g 1.0201 allergen [Apium graveolens].	1769847	159
Apium graveolens	[Segment 2 of 4] Allergen Api g 5.	32363124	30
Apium graveolens	[Segment 3 of 4] Allergen Api g 5.	32363125	24
Apium graveolens	[Segment 4 of 4] Allergen Api g 5.	32363126	10
Apium graveolens	[Segment 1 of 4] Allergen Api g 5.	33300921	22
Apium graveolens	profilin [Apium graveolens].	4761578	134
Apium graveolens	cofactor-independent phosphoglyceromutase [Apium graveolens].	6706331	559
Apium graveolens	NADP-dependent malate dehydrogenase (decarboxylating) [Apium	6706333	570
Arachis hypogaea	Allergen Ara h 1, clone P17 precursor (Ara h I).	1168390	614
Arachis hypogaea	Allergen Ara h 1, clone P41B precursor (Ara h I).	1168391	626
Arachis hypogaea	oleosin variant A [Arachis hypogaea].	13161005	176
Arachis hypogaea	oleosin variant B [Arachis hypogaea].	13161008	176
Arachis hypogaea	unnamed protein product [Arachis hypogaea].	14347293	207
Arachis hypogaea	conglutin [Arachis hypogaea].	17225991	144
Arachis hypogaea	allergen Ara h 3/Ara h 4 [Arachis hypogaea].	21314465	538
Arachis hypogaea	trypsin inhibitor [Arachis hypogaea].	22135348	219
Arachis hypogaea	peanut agglutinin precursor; prePNA [Arachis hypogaea].	253289	273
Arachis hypogaea	allergen Ara h 2.02 [Arachis hypogaea].	26245447	172
Arachis hypogaea	allergen Ara h 2 isoform [Arachis hypogaea].	31322017	169
Arachis hypogaea	glycinin [Arachis hypogaea].	3703107	507
Arachis hypogaea	Ara h 8 allergen [Arachis hypogaea].	37499626	157
Arachis hypogaea	conarachin [Arachis hypogaea].	46560472	303
Arachis hypogaea	conarachin [Arachis hypogaea].	46560474	299
Arachis hypogaea	conarachin [Arachis hypogaea].	46560476	428
Arachis hypogaea	oleosin isoform [Arachis hypogaea].	47156059	176
Arachis hypogaea	glycinin [Arachis hypogaea].	47933675	510
Arachis hypogaea	Ara h 6 allergen [Arachis hypogaea].	57118278	124
Arachis hypogaea	glycinin [Arachis hypogaea].	5712199	530
Arachis hypogaea	profilin [Arachis hypogaea].	5902968	131
Arachis hypogaea	allergen Ara h 6 [Arachis hypogaea].	5923742	129
Arachis hypogaea	allergen [Arachis hypogaea].	5931948	160

Arachis hypogaea	mannose/glucose-binding lectin precursor.	951118	254
Bertholletia excelsa	2S sulfur-rich seed storage protein precursor (Allergen Ber e 1)	112754	146
Bertholletia excelsa	2S albumin [Bertholletia excelsa].	17713	154
Bertholletia excelsa	11S globulin [Bertholletia excelsa].	30313867	465
Beta vulgaris	RS2 protein [Beta vulgaris subsp. vulgaris].	11691639	158
Brassica rapa	Thioredoxin H-type (TRX-H).	11135129	123
Brassica napus	pollen allergen group II (clone 42) - rape.	2129801	83
Brassica napus	pollen allergen group II (clone 44) - rape.	2129802	83
Brassica rapa	pollen allergen group II (clone 4) - turnip (fragment).	2129805	80
Brassica napus	recombinant 1b pronapin precursor [Brassica napus].	26985163	109
Brassica rapa	Lipid transfer protein [Brassica rapa].	3062791	86
Brassica rapa	[Segment 1 of 5] Chitin-binding allergen Bra r 2.	32363457	33
Brassica rapa	[Segment 2 of 5] Chitin-binding allergen Bra r 2.	32363458	34
Brassica rapa	[Segment 3 of 5] Chitin-binding allergen Bra r 2.	32363459	13
Brassica rapa	[Segment 5 of 5] Chitin-binding allergen Bra r 2.	32363461	8
Brassica juncea	Bra j 1E small chain=allergen [Brassica juncea=oriental-mustard,	407609	37
Brassica juncea	Bra j 1E large chain=allergen [Brassica juncea=oriental-mustard,	407610	92
Brassica napus	Polcalcin Bra n 1 (Calcium-binding pollen allergen Bra n 1).	59800143	79
Brassica rapa	Polcalcin Bra r 1 (Calcium-binding pollen allergen Bra r 1).	59800144	79
Brassica napus	Polcalcin Bra n 2 (Calcium-binding pollen allergen Bra n 2).	59800145	83
Brassica rapa	Polcalcin Bra r 2 (Calcium-binding pollen allergen Bra r 2).	59800146	83
Brassica rapa	PCP-1 family.	75099036	83
Capsicum annuum	profilin [Capsicum annuum].	16555785	131
Capsicum annuum	osmotin-like protein [Capsicum annuum].	16609959	246
Capsicum annuum	profilin [Capsicum annuum].	40287498	18
Carica papaya	papain precursor.	167391	345
Carya illinoensis	putative allergen II [Carya illinoensis].	28207731	143
Castanea sativa	chitinase 1b [Castanea sativa].	1359600	316
Castanea sativa	yp10 [Castanea sativa].	16555781	160
Castanea sativa	CAS S 1 major allergen.	75199059	24
Citrus sinensis	lipid transfer protein [Citrus sinensis].	50199132	91
Citrus sinensis	Germin-like protein (Allergen Cit s 1).	52782810	25
Citrus limon	Nonspecific lipid-transfer protein (LTP) (Allergen Cit l 3).	52783176	20
Citrus sinensis	Nonspecific lipid-transfer protein (LTP) (Allergen Cit s 3.0101).	52783177	20
Citrus sinensis	Profilin (Allergen Cit s 2).	54036219	10
Citrus sinensis	profilin [Citrus sinensis].	56000996	131
Corylus avellana	putative luminal binding protein [Corylus avellana].	10944737	668
Corylus avellana	major allergen variant Cor a 1.0402 [Corylus avellana].	11762102	161
Corylus avellana	major allergen variant Cor a 1.0403 [Corylus avellana].	11762104	161
Corylus avellana	major allergen variant Cor a 1.0404 [Corylus avellana].	11762106	161
Corylus avellana	minor allergen hazelnut profilin [Corylus avellana].	12659206	131
Corylus avellana	minor allergen hazelnut profilin [Corylus avellana].	12659208	131
Corylus avellana	major allergen Cor a 1 [Corylus avellana].	1321731	160
Corylus avellana	major allergen Cor a 1 [Corylus avellana].	1321733	160
Corylus avellana	lipid transfer protein precursor [Corylus avellana].	13507262	115
Corylus avellana	putative LEA III protein isoform 1 [Corylus avellana].	14148979	109
Corylus avellana	putative LEA III protein isoform 2 [Corylus avellana].	14148981	87
Corylus avellana	11S globulin-like protein [Corylus avellana].	18479082	515
Corylus avellana	48-kDa glycoprotein precursor [Corylus avellana].	19338630	448
Corylus avellana	major allergen [Corylus avellana].	22684	160
Corylus avellana	major allergen [Corylus avellana].	22686	160
Corylus avellana	major allergen [Corylus avellana].	22688	160
Corylus avellana	major allergen [Corylus avellana].	22690	160
Corylus avellana	oleosin [Corylus avellana].	29170509	140
Corylus avellana	major allergen Cor a 1.0401 [Corylus avellana].	5726304	161
Corylus avellana	Major pollen allergen Cor a 1 isoforms 5, 6, 11 and 16 (Cor a 1).	584968	160
Cucumis melo	profilin [Cucumis melo].	31559374	131
Cucumis melo	[Segment 1 of 3] Pathogenesis-related protein (PR-1) (Allergen Cuc	46396596	21
Cucumis melo	[Segment 2 of 3] Pathogenesis-related protein (PR-1) (Allergen Cuc	46396597	10
Cucumis melo	[Segment 3 of 3] Pathogenesis-related protein (PR-1) (Allergen Cuc	46396598	10
Cucumis melo	profilin [Cucumis melo].	58263793	131
Cucumis melo	pre-pro-cucumisin [Cucumis melo].	807698	731
Cucumis melo	profilin [Cucumis melo var. reticulatus].	57021110	131
Daucus carota	pathogenesis-related protein.	1335877	168

Daucus carota	cr16 [Daucus carota].	1663522	154
Daucus carota	major allergen isoform Dau c 1.0201 [Daucus carota].	8651047	154
Daucus carota	minor allergen Dau c 4 profilin [Daucus carota].	18652049	134
Daucus carota	pathogenesis-related protein-like protein 1 [Daucus carota].	19912791	154
Daucus carota	major allergen [Daucus carota].	2154732	154
Daucus carota	major allergen [Daucus carota].	2154734	154
Daucus carota	major allergen Dau c 1/1 [Daucus carota].	2154736	154
Fagopyrum esculentum	BW8KD allergen protein [Fagopyrum esculentum].	17907758	133
Fagopyrum tataricum	allergenic protein [Fagopyrum tataricum].	22353013	195
Fagopyrum esculentum	legumin-like protein [Fagopyrum esculentum].	2317670	565
Fagopyrum esculentum	legumin-like protein [Fagopyrum esculentum].	2317674	504
Fagopyrum esculentum	major allergenic storage protein [Fagopyrum esculentum].	4895075	538
Fagopyrum esculentum	BW 16kDa allergen [Fagopyrum esculentum].	61970231	127
Fagopyrum gracilipes	22kDa storage protein [Fagopyrum gracilipes].	6979766	191
Fragaria x	major allergen Mal d 1 [Fragaria x ananassa].	54306612	80
Fragaria x	[Segment 1 of 3] Allergen Fra a 1.	60389903	12
Fragaria x	[Segment 2 of 3] Allergen Fra a 1.	60389904	14
Fragaria x	[Segment 3 of 3] Allergen Fra a 1.	60389905	74
Glycine max	34 kDa maturing seed vacuolar thiol protease precursor [Glycine	1199563	379
Glycine max	Hydrophobic seed protein (HPS) (Allergen Gly m 1).	123506	80
Glycine max	allergen Gly m Bd 28K [Glycine max].	12697782	473
Glycine max	P34 probable thiol protease precursor.	129353	379
Glycine max	hull allergen Gly m 2 - soybean (fragment).	1362049	20
Glycine max	beta-conglycinin-alpha subunit.	169927	218
Glycine max	beta-conglycinin storage protein [Glycine max].	169929	639
Glycine max	glycinin.	169969	516
Glycine max	glycinin precursor.	169971	240
Glycine max	lectin prepeptide.	170006	285
Glycine max	unnamed protein product [Glycine max].	18536	605
Glycine max	unnamed protein product [Glycine max].	18609	485
Glycine max	unnamed protein product [Glycine max].	18615	495
Glycine max	glycinin subunit G1 [Glycine max].	18635	495
Glycine max	glycinin subunit G2 [Glycine max].	18637	485
Glycine max	glycinin subunit G3 [Glycine max].	18639	481
Glycine max	glycinin [Glycine max].	18641	562
Glycine max	unnamed protein product [Glycine max].	18744	158
Glycine max	trypsin inhibitor subtype A [Glycine max].	18770	217
Glycine max	trypsin inhibitor subtype B [Glycine max].	18772	217
Glycine max	CG4 beta-conglycinin [Glycine max].	256427	439
Glycine max	Kunitz trypsin inhibitor; KTi [Glycine max].	256429	216
Glycine max	Kunitz trypsin inhibitor KTi1 [Glycine max].	256635	203
Glycine max	Kunitz trypsin inhibitor KTi2 [Glycine max].	256636	204
Glycine max	profilin [Glycine max].	3021373	131
Glycine max	Bd 30K [Glycine max].	3097321	379
Glycine max	Profilin-1 (GmPRO1) (Allergen Gly m 3.0101).	3914435	131
Glycine max	Kunitz trypsin inhibitor [Glycine max].	510515	208
Glycine max	unnamed protein product [Glycine max].	732706	562
Glycine soja	Gys [Glycine soja].	736002	517
Glycine max	Cytokinin induced message.	75102126	277
Glycine soja	ASA4B3 subunit [Glycine soja].	806556	563
Glycine max	Gly m 1A allergen, HPS=hydrophobic seed protein {N-terminal}	999355	42
Helianthus annuus	pre-pro-seed albumin [Helianthus annuus].	18821	141
Helianthus annuus	profilin [Helianthus annuus].	3581965	133
Hordeum vulgare	trypsin inhibitor cme precursor [Hordeum vulgare].	1405736	144
Hordeum vulgare	amylase/protease inhibitor.	167077	117
Hordeum vulgare	alpha-amylase/trypsin inhibitor preprotein [Hordeum vulgare subsp.	18869	147
Hordeum vulgare	alpha-amylase inhibitor [Hordeum vulgare subsp. vulgare].	18955	144
Hordeum vulgare	monomeric alpha-amylase [Hordeum vulgare subsp. vulgare].	19003	146
Hordeum vulgare	CMe [Hordeum vulgare subsp. vulgare].	19009	148
Hordeum vulgare	LTP 1 [Hordeum vulgare].	19039	134
Hordeum vulgare	Alpha-amylase inhibitor BMAI-1 precursor (Allergen Hor v 1)	2506771	146
Hordeum vulgare	BDAL-1; Barley dimeric alpha-amylase inhibitor [Hordeum vulgare	3367714	152
Hordeum vulgare	CMA, component of tetrameric alpha-amylase inhibitor [Hordeum	439275	145
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Hordeum vulgare	CMd component of tetrameric alpha-amylase inhibitor [Hordeum	452325	171
Hordeum vulgare	pollen allergen Hor v 4 [Hordeum vulgare].	55859462	518
Hordeum vulgare	Alpha-amylase/trypsin inhibitor CMb precursor	585290	149
Hordeum vulgare	BAKER'S ASTHMA allergen BDP.	75198868	20
Hordeum vulgare	Pollen allergen precursor.	75219009	313
Juglans regia	albumin seed storage protein precursor [Juglans regia].	1794252	139
Juglans nigra	2S albumin seed storage protein [Juglans nigra].	31321942	161
Juglans nigra	vicilin seed storage protein [Juglans nigra].	31321944	481
Juglans regia	vicilin-like protein precursor [Juglans regia].	6580762	593
Lens culinaris	allergen Len c 1.0101 [Lens culinaris].	29539109	418
Lens culinaris	allergen Len c 1.0102 [Lens culinaris].	29539111	415
Litchi chinensis	profilin [Litchi chinensis].	15809696	131
Lycopersicon esculentum	Anther-specific protein LAT52 precursor.	125887	161
Lycopersicon esculentum	profilin [Lycopersicon esculentum].	16555787	131
Lycopersicon esculentum	profilin [Lycopersicon esculentum].	17224229	131
Lycopersicon esculentum	minor allergen beta-fructofuranosidase precursor [Lycopersicon	18542113	553
Lycopersicon esculentum	minor allergen beta-fructofuranosidase precursor [Lycopersicon	18542115	636
Malus x	thaumatin-like protein [Malus x domestica].	10334651	246
Malus x	major allergen {N-terminal} [apples, Golden Delicious, Peptide	1174276	37
Malus x	major allergen Mal d 1 [Malus x domestica].	1313966	159
Malus x	major allergen Mal d 1 [Malus x domestica].	1313968	160
Malus x	major allergen Mal d1 [Malus x domestica].	1313970	160
Malus x	major allergen Mal d1 [Malus x domestica].	1313972	160
Malus x	Major allergen Mal d 1 (Mal d 1).	1346478	159
Malus x	Profilin-1 (GD4-1) (Pollen allergen Mal d 4.0301).	14423873	131
Malus x	Profilin-2 (GD4-2) (Pollen allergen Mal d 4.0201).	14423874	131
Malus x	Profilin-3 (GD4-5) (Pollen allergen Mal d 4.0101).	14423875	131
Malus x	18 kda major allergen/Bet v 1 homolog {N-terminal} [Malus	1478292	25
Malus x	31 kda major allergen/disease resistance protein homolog	1478293	26
Malus x	ypr10 [Malus x domestica].	16555783	159
Malus x	major allergen d 1 [Malus x domestica].	21685277	158
Malus x	major allergen Mal d 1 [Malus x domestica].	2443824	159
Malus x	major allergen Mal d 1 [Malus x domestica].	27922941	159
Malus x	profilin [Malus x domestica].	28881453	131
Malus x	profilin [Malus x domestica].	28881455	131
Malus x	profilin [Malus x domestica].	28881457	131
Malus x	Mal d 1-associated protein [Malus x domestica].	32709122	190
Malus x	major allergen Mal d 1 [Malus x domestica].	3309647	159
Malus x	allergen Mal d 3 [Malus x domestica].	38492338	115
Malus x	major allergen mal d 1 [Malus x domestica].	4590364	159
Malus x	major allergen mal d 1 [Malus x domestica].	4590366	159
Malus x	major allergen mal d 1 [Malus x domestica].	4590368	159
Malus x	major allergen mal d 1 [Malus x domestica].	4590376	159
Malus x	major allergen mal d 1 [Malus x domestica].	4590378	159
Malus x	major allergen mal d 1 [Malus x domestica].	4590380	159
Malus x	major allergen mal d 1 [Malus x domestica].	4590382	159
Malus x	major allergen mal d 1 [Malus x domestica].	4590388	159
Malus x	lipid transfer protein precursor [Malus x domestica].	50659859	115
Malus x	lipid transfer protein precursor [Malus x domestica].	50659879	115
Malus x	lipid transfer protein precursor [Malus x domestica].	50659885	115
Malus x	lipid transfer protein precursor [Malus x domestica].	50659889	115
Malus x	lipid transfer protein precursor [Malus x domestica].	50659891	115
Malus x	lipid transfer protein precursor [Malus x domestica].	6715522	115
Malus x	Mal d 1 [Malus x domestica].	747852	159
Manihot esculenta	allergenic-related protein Pt2L4 [Manihot esculenta].	21585695	177
Musa acuminata	profilin [Musa acuminata].	14161635	131
Oryza sativa	beta-expansin [Oryza sativa].	11346546	271
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	1304216	111
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	1304217	109
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	1304218	113
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	1398913	166
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	1398915	160
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	1398916	157
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	1398918	160

Oryza sativa	Bet v I allergen-like [Oryza sativa (japonica cultivar-group)].	15624049	208
Oryza sativa	glyoxalase I [Oryza sativa (japonica cultivar-group)].	6580747	291
Oryza sativa	putative pollen allergen Jun o 4 [Oryza sativa (japonica	19386816	185
Oryza sativa	putative allergen Amb a 1.2 precursor [Oryza sativa (japonica	20146453	364
Oryza sativa	Putative pollen allergen [Oryza sativa (japonica cultivar-group)].	20502989	289
Oryza sativa	expansin Os-EXPA2 [Oryza sativa (japonica cultivar-group)].	21104587	251
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	248193	165
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	218195	162
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	218197	157
Oryza sativa	beta-expansin [Oryza sativa].	2224915	261
Oryza sativa	putative allergenic protein [Oryza sativa (japonica	23616947	160
Oryza sativa	Major pollen allergen Ory s 1 precursor (Ory s I).	2498586	263
Oryza sativa	allergenic protein [Oryza sativa].	2827316	157
Oryza sativa	Pollen allergen Ory s 2-A.	32363197	15
Oryza sativa	seed allergen RA17 [Oryza sativa (japonica cultivar-group)].	34900094	163
Oryza sativa	seed allergen RAG2 [Oryza sativa (japonica cultivar-group)].	34900098	166
Oryza sativa	allergen RA16 [Oryza sativa (japonica cultivar-group)].	34900104	157
Oryza sativa	allergen RASB precursor [Oryza sativa (japonica cultivar-group)].	34900132	160
Oryza sativa	putative pollen allergen [Oryza sativa (japonica cultivar-group)].	37536544	275
Oryza sativa	putative Cup s 1 pollen allergen [Oryza sativa (japonica	38175617	384
Oryza sativa	glyoxalase I [Oryza sativa (japonica cultivar-group)].	4126809	291
Oryza sativa	putative latex protein allergen [Oryza sativa (japonica	42408062	430
Oryza sativa	putative latex protein allergen [Oryza sativa (japonica	42408066	431
Oryza sativa	putative polcalcin Phl p 7 [Calcium-binding pollen allergen Phl p	45736119	82
Oryza sativa	putative expansin 11 precursor [Oryza sativa (japonica	45736177	269
Oryza sativa	Bet v I allergen-like [Oryza sativa (japonica cultivar-group)].	49388537	207
Oryza sativa	Bet v I allergen-like [Oryza sativa (japonica cultivar-group)].	50251668	180
Oryza sativa	pollen Ole e 1 allergen and expansin family protein-like [Oryza	50251728	155
Oryza sativa	Bet v I allergen-like [Oryza sativa (japonica cultivar-group)].	50252014	204
Oryza sativa	putative group 3 pollen allergen [Oryza sativa (japonica	51536378	117
Oryza sativa	putative group 3 pollen allergen [Oryza sativa (japonica	52075909	118
Oryza sativa	putative group 3 pollen allergen [Oryza sativa (japonica	52075910	118
Oryza sativa	putative group 3 pollen allergen [Oryza sativa (japonica	52075913	117
Oryza sativa	putative group 3 pollen allergen [Oryza sativa (japonica	52075914	113
Oryza sativa	putative group 3 pollen allergen [Oryza sativa (japonica	52075915	117
Oryza sativa	putative group 3 pollen allergen [Oryza sativa (japonica	52075917	117
Oryza sativa	putative group 3 pollen allergen [Oryza sativa (japonica	52075924	117
Oryza sativa	Bet v I allergen-like [Oryza sativa (japonica cultivar-group)].	52077086	146
Oryza sativa	Bet v I allergen-like [Oryza sativa (japonica cultivar-group)].	52077087	158
Oryza sativa	Bet v I allergen-like [Oryza sativa (japonica cultivar-group)].	53791938	206
Oryza sativa	Bet v I allergen-like [Oryza sativa (japonica cultivar-group)].	53791944	206
Oryza sativa	Bet v I allergen-like [Oryza sativa (japonica cultivar-group)].	53792800	207
Oryza sativa	putative pollen allergen Phl p 11 [Oryza sativa (japonica	53792960	175
Oryza sativa	pollen allergen-like [Oryza sativa (japonica cultivar-group)].	54291022	313
Oryza sativa	Seed allergenic protein RA5 precursor.	548657	157
Oryza sativa	Seed allergenic protein RA14 precursor.	548658	165
Oryza sativa	Seed allergenic protein RA17 precursor.	548660	162
Oryza sativa	Seed allergenic protein RAG2 precursor.	548671	166
Oryza sativa	allergen-like protein [Oryza sativa (japonica cultivar-group)].	57900264	139
Oryza sativa	putative expansin [Oryza sativa (japonica cultivar-group)].	6069656	284
Oryza sativa	Allergenic protein.	75102358	160
Oryza sativa	Allergenic protein.	75102382	111
Oryza sativa	Allergenic protein.	75102383	109
Oryza sativa	Allergenic protein.	75102384	113
Oryza sativa	Allergenic protein.	75219561	157
Oryza sativa	Allergenic protein.	75221023	166
Oryza sativa	Allergenic protein.	75221024	157
Oryza sativa	Allergenic protein.	75221025	160
Oryza sativa	beta-expansin [Oryza sativa].	8118421	267
Oryza sativa	beta-expansin [Oryza sativa].	8118423	268
Oryza sativa	beta-expansin [Oryza sativa].	8118425	286
Oryza sativa	beta-expansin [Oryza sativa].	8118428	275
Oryza sativa	beta-expansin [Oryza sativa].	8118430	275
Oryza sativa	beta-expansin [Oryza sativa].	8118432	327

Oryza sativa	beta-expansin [Oryza sativa].	8118437	269
Oryza sativa	beta-expansin [Oryza sativa].	8118439	267
Persea americana	endochitinase [Persea americana].	3201547	326
Petroselinum crispum	pathogenesis-related protein 1 [Petroselinum crispum].	1843451	155
Phaseolus vulgaris	pathogenesis-related protein 1 (PvPR1) [Phaseolus vulgaris].	21044	156
Phaseolus vulgaris	pathogenesis-related protein 2 (PvPR2) [Phaseolus vulgaris].	21048	155
Pisum sativum	Vicilin [Pisum sativum].	42414627	415
Pisum sativum	Vicilin [Pisum sativum].	42414629	415
Pisum sativum	Orf protein.	75221106	258
Plantago lanceolata	plantain pollen major allergen, Pla l 1.0101 [Plantago lanceolata].	14422359	131
Plantago lanceolata	plantain pollen major allergen, Pla l 1.0102 [Plantago lanceolata].	14422361	131
Plantago lanceolata	plantain pollen major allergen, Pla l 1.0103 [Plantago lanceolata].	14422363	131
Plantago lanceolata	unnamed protein product [Plantago lanceolata].	29163771	65
Plantago lanceolata	unnamed protein product [Plantago lanceolata].	29163773	65
Prunus avium	thaumatin-like protein precursor.	1144346	245
Prunus avium	Chain A, Solution Structure Of The Major Cherry Allergen Pru Av 1.	13787043	159
Prunus avium	cherry-allergen PRUA1.	1513216	160
Prunus persica	pru p 1 [Prunus persica].	17974195	91
Prunus dulcis	profilin [Prunus dulcis].	24473794	131
Prunus armeniaca	major allergen protein homolog [Prunus armeniaca].	2677826	160
Prunus persica	profilin [Prunus persica].	27528310	131
Prunus persica	profilin [Prunus persica].	27528312	131
Prunus persica	Nonspecific lipid-transfer protein 1 (LTP 1) (Major allergen Pru p	3287877	91
Prunus avium	Chain A, Solution Structure Of The Major Cherry Allergen Pru Av 1	34809853	159
Prunus avium	major cherry allergen Pru av 1.0201 [Prunus avium].	44409451	160
Prunus avium	major cherry allergen Pru av 1.0202 [Prunus avium].	44409474	160
Prunus avium	major cherry allergen Pru av 1.0203 [Prunus avium].	44409496	160
Prunus avium	profilin [Prunus avium].	4761582	131
Prunus armeniaca	putative allergen protein [Prunus armeniaca].	4887129	168
Prunus avium	lipid transfer protein precursor [Prunus avium].	6715520	117
Prunus armeniaca	Nonspecific lipid-transfer protein 1 (LTP 1) (Major allergen Pru ar	7404406	91
Prunus domestica	Nonspecific lipid-transfer protein 1 (LTP 1) (Major allergen Pru d	9297015	91
Pyrus communis	Nonspecific lipid-transfer protein precursor (LTP) (Allergen Pyr c	14423813	115
Pyrus communis	major allergen Pyrc1 [Pyrus communis].	3044216	159
Pyrus communis	isoflavone reductase related protein [Pyrus communis].	3243234	308
Pyrus communis	profilin [Pyrus communis].	4761580	131
Ricinus communis	2S albumin precursor (Allergen Ric c 1/3) [Contains: Allergen Ric c	112762	258
Secale cereale	pollen allergen Sec c 4 [Secale cereale].	55859454	518
Secale cereale	pollen allergen Sec c 4 [Secale cereale].	55859456	520
Secale cereale	30K allergen.	75140047	16
Secale cereale	Major BAKER'S ASTHMA allergen SEC C 1.	75198875	26
Sesamum indicum	2S albumin [Sesamum indicum].	13183175	153
Sesamum indicum	7S globulin [Sesamum indicum].	13183177	585
Sesamum indicum	2S albumin precursor [Sesamum indicum].	5381323	148
Sinapis alba	allergen sin a 1.0104 [Sinapis alba].	1009434	145
Sinapis alba	allergen sin a 1.0105 [Sinapis alba].	1009436	145
Sinapis alba	allergen sin a 1.0106 [Sinapis alba].	1009438	145
Sinapis alba	allergen sin a 1.0107 [Sinapis alba].	1009440	145
Sinapis alba	allergen sin a 1.0108 [Sinapis alba].	1009442	145
Sinapis alba	Allergen Sin a 1 precursor (Sin a 1) [Contains: Allergen Sin a 1	51338758	145
Sinapis alba	major allergen Sin a 1 [Sinapis alba].	7545129	145
Solanum tuberosum	Aspartic protease inhibitor 11 (Cathepsin D inhibitor PDI)	124148	188
Solanum tuberosum	Patatin B1 precursor (Potato tuber protein).	129641	377
Solanum tuberosum	patatin.	169500	386
Solanum tuberosum	Cysteine protease inhibitor 1 precursor (PCPI 8.3) (P340) (P34021).	20141344	222
Solanum tuberosum	Serine protease inhibitor 7 precursor (PIG) (PIGEN1) (Allergen Sola	20141714	221
Solanum tuberosum	aspartic proteinase inhibitor [Solanum tuberosum].	21413	217
Solanum tuberosum	unnamed protein product [Solanum tuberosum].	21510	386
Solanum tuberosum	patatin [Solanum tuberosum].	21512	386
Solanum tuberosum	patatin [Solanum tuberosum].	21514	386
Triticum aestivum	hypothetical 11.8K protein - wheat.	100794	106
Triticum turgidum	alpha-amylase inhibitor, tetrameric, chain CM3 precursor - durum	100834	168
Triticum aestivum	profilin [Triticum aestivum].	1008443	141
Triticum aestivum	profilin [Triticum aestivum].	1008445	140

Triticum aestivum	profilin [Triticum aestivum].	1052817	138
Triticum aestivum	gamma-gliadin precursor [Triticum aestivum].	063170	279
Triticum aestivum	triosephosphat-isomerase [Triticum aestivum].	11124572	253
Triticum aestivum	allergenic peptide=low-molecular-weight glutenin chain [wheat,	1168171	30
Triticum aestivum	Endogenous alpha-amylase/subtilisin inhibitor (WASI).	123975	180
Triticum aestivum	alpha-gliadin [Triticum aestivum].	1304264	259
Triticum aestivum	IgE-binding polypeptide 4[major allergen {N-terminal} [wheat,	1311642	16
Triticum aestivum	agglutinin isolectin A precursor.	170666	212
Triticum turgidum	wheat germ agglutinin.	170668	186
Triticum aestivum	agglutinin isolectin D precursor.	170670	213
Triticum aestivum	gamma gliadin precursor.	170702	302
Triticum aestivum	gamma-gliadin B precursor.	170708	291
Triticum aestivum	alpha-type gliadin precursor protein.	170710	318
Triticum aestivum	pre-alpha-/beta-gliadin A-II.	170712	291
Triticum aestivum	pre-alpha-/beta-gliadin A-V.	170716	319
Triticum aestivum	alpha/beta-gliadin precursor.	170718	313
Triticum aestivum	alpha/beta-gliadin precursor [Triticum aestivum].	170720	286
Triticum aestivum	pre-alpha-/beta-gliadin A-I.	170722	262
Triticum aestivum	pre-alpha-/beta-gliadin A-IV.	170724	297
Triticum aestivum	pre-alpha-/beta-gliadin A-III.	170726	282
Triticum aestivum	alpha-type gliadin.	170728	186
Triticum aestivum	gamma-gliadin B-I precursor [Triticum aestivum].	170730	304
Triticum aestivum	gamma-gliadin.	170732	323
Triticum aestivum	gamma gliadin B-III.	170734	244
Triticum aestivum	gamma-gliadin.	170736	251
Triticum aestivum	gamma-gliadin.	170738	327
Triticum urartu	gliadin.	170740	296
Triticum aestivum	HMW glutenin subunit Ax2 [Triticum aestivum].	170743	815
Triticum aestivum	serpin [Triticum aestivum].	1885350	399
Triticum aestivum	unnamed protein product [Triticum aestivum].	21673	307
Triticum aestivum	unnamed protein product [Triticum aestivum].	21701	145
Triticum aestivum	CM 17 protein precursor [Triticum aestivum].	21711	143
Triticum aestivum	unnamed protein product [Triticum aestivum].	21713	168
Triticum aestivum	high molecular weight glutenin subunit 1Ax1 [Triticum aestivum].	21743	830
Triticum aestivum	high molecular weight glutenin subunit 10 [Triticum aestivum].	21751	648
Triticum aestivum	unnamed protein product [Triticum aestivum].	21755	286
Triticum aestivum	unnamed protein product [Triticum aestivum].	21757	296
Triticum aestivum	unnamed protein product [Triticum aestivum].	21761	286
Triticum aestivum	unnamed protein product [Triticum aestivum].	21765	313
Triticum aestivum	seed storage protein (154AA) [Triticum aestivum].	21769	154
Triticum aestivum	unnamed protein product [Triticum aestivum].	21773	307
Triticum aestivum	unnamed protein product [Triticum aestivum].	21779	660
Triticum aestivum	unnamed protein product [Triticum aestivum].	21783	356
Triticum aestivum	unnamed protein product [Triticum aestivum].	21793	39
Triticum turgidum	precursor (AA -24 to 119) [Triticum turgidum subsp. durum].	21916	143
Triticum turgidum	CM2 protein [Triticum turgidum subsp. durum].	21920	145
Triticum turgidum	unnamed protein product [Triticum turgidum subsp. durum].	21926	295
Triticum turgidum	LMW glutenin [Triticum turgidum subsp. durum].	21930	285
Triticum aestivum	HMW glutenin subunit 1By9 [Triticum aestivum].	22090	705
Triticum turgidum	tetrameric alpha-amylase inhibitor 16 kDa subunit, CM16* [Triticum	244610	18
Triticum aestivum	27K protein [Triticum aestivum].	30793446	203
Triticum aestivum	Allergen C-C.	3913017	27
Triticum aestivum	pollen allergen (group II) [Triticum aestivum].	4007852	122
Triticum aestivum	putative pollen allergen precursor [Triticum aestivum].	40644792	178
Triticum aestivum	putative group V allergen [Triticum aestivum].	40644794	119
Triticum aestivum	putative major allergen Phi p 5 [Triticum aestivum].	40644796	231
Triticum aestivum	pollen allergen homolog [Triticum aestivum].	4099919	271
Triticum aestivum	alpha-gliadin.	473876	287
Triticum aestivum	pollen allergen Tri a 4 [Triticum aestivum].	55859458	518
Triticum aestivum	pollen allergen Tri a 4 [Triticum aestivum].	55859460	518
Triticum aestivum	putative gamma-gliadin [Triticum aestivum].	62484809	285
Triticum aestivum	putative LMW-glutenin subunit [Triticum aestivum].	62550933	326
Triticum aestivum	putative omega-gliadin [Triticum aestivum].	63252971	375
Triticum aestivum	glutenin [Triticum aestivum].	736319	838

Triticum aestivum	Gliadin omega-5.	75139902	32
Triticum turgidum	16K protein.	75140060	10
Triticum aestivum	LMM glutenin 1.	75219081	285
Triticum aestivum	LMM glutenin 3.	75317968	373
Triticum urartu	unknown protein.	806315	106
Triticum aestivum	low molecular weight glutenin [Triticum aestivum].	886963	229
Triticum aestivum	low molecular weight glutenin [Triticum aestivum].	886965	261
Triticum aestivum	low molecular weight glutenin [Triticum aestivum].	886967	276
Triticum aestivum	unnamed protein product [Triticum aestivum].	897811	101
Triticum aestivum	pollen allergen-like protein [Triticum aestivum].	972513	118
Vitis sp.	Nonspecific lipid-transfer protein P2 (LTP P2).	462717	38
Vitis sp.	Nonspecific lipid-transfer protein P3 (LTP P3).	462718	37
Vitis sp.	Nonspecific lipid-transfer protein P4 (LTP P4).	462719	37
Zea mays	Nonspecific lipid-transfer protein precursor (LTP) (Phospholipid	128388	120
Zea mays	Zm13.	1588669	170
Zea mays	beta-expansin 1a precursor (Pollen allergen Zea m 1) (Zea m 1).	20138191	269
Zea mays	profilin [Zea mays].	2642324	131
Zea mays	beta-expansin 9 protein [Zea mays].	28630919	269
Zea mays	beta-expansin 1 protein [Zea mays].	28630923	269
Zea mays	group 3 pollen allergen [Zea mays].	33188338	120
Zea mays	pectate lyase homolog [Zea mays].	405535	438
Zea mays	Bet v 1 allergen [Zea mays].	54111527	154
Zea mays	Pectate lyase homolog.	75221515	104

Other contact allergens

Species	Comments	GI #	AA
Acanthamoeba castellanii	Acanthamoeba Castellani Profilin Ia.	2781014	125
Acanthamoeba castellanii	Chain B, Crystal Structure Of Acanthamoeba Castellani Profilin Ii,	9257090	125
Equus caballus	latherin [Equus caballus].	20143977	228
Equus caballus	Dander allergen Equ c 2.0101.	3121755	29
Equus caballus	Dander allergen Equ c 2.0102.	3121756	19
Equus caballus	Major allergen Equ c 1 precursor.	3121758	187
Equus caballus	preproalbumin [Equus caballus].	399672	607
Hevea brasiliensis	IgE-binding protein MnSOD [Hevea brasiliensis].	10862818	205
Hevea brasiliensis	Chain A, Latex Profilin Hevb8.	11513601	131
Hevea brasiliensis	beta-1,3-glucanase.	1184668	374
Hevea brasiliensis	Pro-hevein precursor (Major hevein) [Contains: Hevein (Allergen Hev	123062	204
Hevea brasiliensis	Rubber elongation factor protein (REF) (Allergen Hev b 1).	132270	138
Hevea brasiliensis	Profilin-6 (Pollen allergen Hev b 8.0204).	14423856	131
Hevea brasiliensis	Profilin-5 (Pollen allergen Hev b 8.0203).	14423858	131
Hevea brasiliensis	Profilin-4 (Pollen allergen Hev b 8.0202).	14423859	131
Hevea brasiliensis	Profilin-3 (Pollen allergen Hev b 8.0201).	14423860	131
Hevea brasiliensis	Profilin-2 (Pollen allergen Hev b 8.0102).	14423868	131
Hevea brasiliensis	Small rubber particle protein (SRPP) (22 kDa rubber particle	14423933	204
Hevea brasiliensis	putative class I chitinase [Hevea brasiliensis].	14575525	295
Hevea brasiliensis	latex allergen.	1480457	151
Hevea brasiliensis	latex patatin homolog [Hevea brasiliensis].	1916805	388
Hevea brasiliensis	lipid transfer precursor protein [Hevea brasiliensis].	20135538	116
Hevea brasiliensis	class I chitinase [Hevea brasiliensis subsp. brasiliensis].	27526732	295
Hevea brasiliensis	prohevein [Hevea brasiliensis].	2832430	187
Hevea brasiliensis	latex allergen [Hevea brasiliensis].	3087805	388
Hevea brasiliensis	ENSP-like protein [Hevea brasiliensis].	30909057	391
Hevea brasiliensis	profilin [Hevea brasiliensis].	3183706	131
Hevea brasiliensis	beta-1,3-glucanase [Hevea brasiliensis].	32765543	374
Hevea brasiliensis	latex allergen [Hevea brasiliensis].	3288200	388
Hevea brasiliensis	superoxide dismutase (manganese).	348137	233
Hevea brasiliensis	putative latex allergen hev b 7.02 [Hevea brasiliensis].	41581137	387
Hevea brasiliensis	major latex allergen Hev b 4 [Hevea brasiliensis].	46410859	366
Hevea brasiliensis	MnSOD [Hevea brasiliensis].	5777414	205
Hevea brasiliensis	latex protein allergen Hev b 7 [Hevea brasiliensis].	6707018	388
Hevea brasiliensis	enolase, isoform 1 [Hevea brasiliensis].	9581744	445
Hevea brasiliensis	enolase, isoform 2 [Hevea brasiliensis].	9581746	445
Methanococcus maripaludis	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal	45047603	217
Nicotiana tabacum	beta-expansin-like protein [Nicotiana tabacum].	12330698	273

Nicotiana tabacum	villin 1 [Nicotiana tabacum].	57263177	579
Nicotiana tabacum	villin 2 [Nicotiana tabacum].	67283139	520
Nicotiana tabacum	Polcalcin Nic t 1 (Calcium-binding pollen allergen Nic t 1).	50798467	84
Nicotiana tabacum	Polcalcin Nic t 2 (Calcium-binding pollen allergen Nic t 2).	59798468	86
Plasmodium falciparum	conserved protein [Plasmodium falciparum 3D7].	23509219	171
Styela plicata	major allergen [Styela plicata].	58257626	126

Nematodes and worms

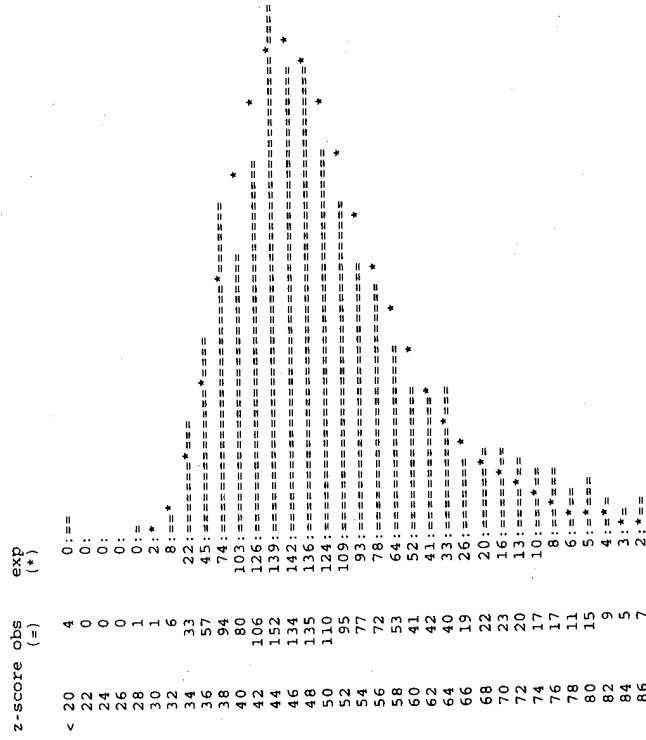
Species	Comments	GI #	AA
Acanthocheilonema viteae	ladder protein [Acanthocheilonema viteae].	4102959	131
Ancylostoma caninum	secreted protein ASP-2 precursor [Ancylostoma caninum].	3608493	218
Ancylostoma duodenale	ancylostoma-secreted protein 1 precursor [Ancylostoma duodenale].	3719257	425
Ancylostoma caninum	ancylostoma-secreted protein 1 precursor; ASP-1 [Ancylostoma	4884851	424
Ancylostoma caninum	Aspartic protease.	74936004	442
Anisakis simplex	Tropomyosin (Allergen Ani s 3).	14423976	284
Anisakis simplex	21k allergen [Anisakis simplex].	31339067	194
Anisakis simplex	Allergen Ani s 4.	47605398	14
Anisakis simplex	Major allergen Ani s 1 precursor (Excretory gland allergen Ani s 1)	47605452	194
Anisakis simplex	troponin-like protein [Anisakis simplex].	6065738	161
Anisakis simplex	putative nucleosome binding protein [Anisakis simplex].	6065744	321
Anisakis simplex	paramyosin [Anisakis simplex].	8117843	869
Anisakis simplex	paramyosin isoform [Anisakis simplex].	8453086	473
Ascaridia galli	fatty acid binding protein [Ascaridia galli].	3152922	135
Ascaris suum	allergen [Ascaris suum].	159653	395
Ascaris lumbricoides	ABA-1 allergen [Ascaris lumbricoides].	2735096	134
Ascaris lumbricoides	ABA-1 allergen [Ascaris lumbricoides].	2735098	134
Ascaris lumbricoides	ABA-1 allergen [Ascaris lumbricoides].	2735100	134
Ascaris lumbricoides	ABA-1 allergen [Ascaris lumbricoides].	2735102	133
Ascaris lumbricoides	ABA-1 allergen [Ascaris lumbricoides].	2735106	133
Ascaris lumbricoides	ABA-1 allergen [Ascaris lumbricoides].	2735108	267
Ascaris lumbricoides	ABA-1 allergen [Ascaris lumbricoides].	2735110	267
Ascaris lumbricoides	ABA-1 allergen [Ascaris lumbricoides].	2735112	267
Ascaris lumbricoides	ABA-1 allergen [Ascaris lumbricoides].	2735114	134
Ascaris lumbricoides	ABA-1 allergen [Ascaris lumbricoides].	2735118	134
Ascaris suum	polypeptide allergen/antigen [Ascaris suum].	2970629	1095
Ascaris suum	major allergen ABA-1/TBA-1 allergen homolog (N-terminal) [Ascaris	299550	68
Brugia malayi	venom allergen antigen-like protein 1 [Brugia malayi].	13095442	220
Brugia malayi	major allergen [Brugia malayi].	13310414	227
Brugia malayi	larval allergen [Brugia malayi].	24711753	248
Dictyocaulus viviparus	DVA-1 polypeptide precursor (Antigen 1) (Allergen 1) (Nematode	2498317	1557
Dirofilaria immitis	venom allergen antigen 5-like protein [Dirofilaria immitis].	2245508	221
Heterodera glycines	secreted venom allergen-like protein vap2 [Heterodera glycines].	13447461	212
Heterodera glycines	venom allergen-like protein [Heterodera glycines].	14211968	212
Heterodera glycines	vap-1 [Heterodera glycines].	14326230	215
Heterodera glycines	probable polypeptide allergen Hgg-14 [Heterodera glycines].	18677166	288
Litomosoides carinii	ladder protein [Litomosoides carinii].	4102911	132
Loa loa	ladder protein [Loa loa].	4102951	132
Loa loa	LL20 15kDa ladder antigen.	414553	588
Meloidogyne incognita	secreted protein MSP-1 [Meloidogyne incognita].	4102596	231
Necator americanus	ancylostoma secreted protein 1 precursor [Necator americanus].	3396070	424
Necator americanus	calreticulin [Necator americanus].	3687326	403
Onchocerca volvulus	activation-associated secreted protein-2 [Onchocerca volvulus].	11762066	224
Onchocerca volvulus	myosin-like antigen.	159881	343
Onchocerca volvulus	vespid allergen antigen homolog [Onchocerca volvulus].	2796175	220
Onchocerca cervicalis	ladder protein [Onchocerca cervicalis].	4102953	133
Onchocerca volvulus	beta-galactoside-binding lectin.	433317	280
Onchocerca volvulus	activation-associated secreted protein-1 [Onchocerca volvulus].	5868902	220
Schistosoma japonicum	22.6 kDa tegumental antigen [Schistosoma japonicum].	2739154	191
Schistosoma japonicum	hypothetical protein, putative Profilin/allergen [Schistosoma	29841461	129
Setaria cervi	ladder protein [Setaria cervi].	4102957	133
Strongyloides stercoralis	IgG and IgE immunoreactive antigen recognized by sera from patients	2290388	152
Strongyloides stercoralis	IgG and IgE immunoreactive antigen recognized by sera from patients	2290390	90
Strongyloides stercoralis	IgG and IgE immunoreactive antigen recognized by sera from patients	2290392	128
Strongyloides stercoralis	IgG and IgE immunoreactive antigen recognized by sera from patients	2290394	144

Strongyloides stercoralis	IgG immunoreactive antigen [Strongyloides stercoralis].	2801529	156
Strongyloides stercoralis	allergen polypeptide homolog [Strongyloides stercoralis].	2801531	95
Stylonychia lemnae	unnamed protein product [Stylonychia lemnae].	10142	104
Toxocara canis	TBA-1 precursor [Toxocara canis].	1731859	140
Toxocara canis	ladder protein [Toxocara canis].	4102955	133
Toxocara canis	Allergen TBA-1.	74827032	36
Trichostrongylus colubriformis	aspartyl protease inhibitor precursor [Trichostrongylus	28274792	228
Wuchereria bancrofti	translationally controlled tumor protein-like protein [Wuchereria	14700054	181
Wuchereria bancrofti	vespid allergen antigen homolog [Wuchereria bancrofti].	4324680	220
Wuchereria bancrofti	vespid allergen antigen homolog [Wuchereria bancrofti].	4704758	220
Wuchereria bancrofti	cuticular endochitinase [Wuchereria bancrofti].	7673688	504

Appendix 2 FASTA Sequence Alignments of
CryIAA-105 Protein Against AD6 database

!!SEQUENCE_LIST 1.0
(Peptide) FASTA of: cryIAA-105 from: 1 to: 1177 September 6, 2006 08:28
cryIAA-105
TO: AD6: * Sequences: 1,511 Symbols: 333,422 Word Size: 2
Databases searched: 1,511 Symbols: 333,422 Word Size: 2
Monsanto, Release 1.0, Released on 6/28/2006, Formatted on 6/28/2006
Minimum search sequence length: 1
Maximum search sequence length: 350000
Scoring matrix: genrundata:biosum50.cmp
Variable pamfactor used
Gap creation penalty: 12 Gap extension penalty: 2

Histogram Key:
Each histogram symbol represents 3 search set sequences
Each inset symbol represents 1 search set sequences
Z-scores computed from opt scores



Joining thres	opt.	ashold: 27, opt. width: 16, reg.-scaled	initl	initn	opt	z-sc E(1507)...
88	4	2:*=				
90	1:*	1:*=				
92	1:*	1:*=				
94	1:*	1:*=				
96	1:*	1:*=				
98	0	0				
100	0	0				
102	0	0				
104	0	0				
106	0	0				
108	0	0				
110	0	0				
112	0	0				
114	0	0				
116	0	0				
118	0	0				
>120	0	0				
The best score are:						
AD6:GI-166317	Begin: 28	End: 318	40	40	91	96.2 2.3
! actinidin						
AD6:GI-22690	Begin: 54	End: 144	52	52	83	94.2 2.9
! major allergen [Corylus avellana]						
AD6:GI-584968	Begin: 54	End: 144	48	48	81	92.1 3.8
! Major pollen allergen Cor a 1 isofo...						
AD6:GI-118704	Begin: 54	End: 139	47	47	81	92.1 3.8
! Major pollen allergen Bet v 1-E (Be...						
AD6:GI-545891	Begin: 54	End: 144	36	36	81	92.1 3.8
! pollen allergen Car b 1 [Carpinus b...						
AD6:GI-24628	Begin: 54	End: 144	48	48	81	92.1 3.8
! major allergen [Corylus avellana]						
AD6:GI-24684	Begin: 54	End: 144	53	53	80	91.0 4.4
! major allergen [Corylus avellana]						
AD6:GI-315581	Begin: 86	End: 134	35	35	83	90.1 4.9
! major allergen Phl p 5 [Pleum bra...						
AD6:GI-1545877	Begin: 54	End: 144	36	36	79	90.0 5
! pollen allergen Car b 1 [Carpinus b...						
AD6:GI-1545887	Begin: 54	End: 144	36	36	79	90.0 5
! pollen allergen Car b 1 [Carpinus b...						
AD6:GI-2259342	Begin: 83	End: 106	75	100	80	87.9 6.6
! serine protease [Dermatophagoides p...						
AD6:GI-22686	Begin: 54	End: 144	52	52	77	87.9 6.6
! major allergen [Corylus avellana]						
AD6:GI-1545893	Begin: 54	End: 144	36	36	77	87.9 6.6
! pollen allergen Car b 1 [Carpinus b...						
AD6:GI-170730	Begin: 200	End: 255	59	70	81	87.3 7.1
! gamma-gliadin B-I precursor [Tritic...						
AD6:GI-402745	Begin: 53	End: 143	36	36	76	86.9 7.5
! Car b 1 [Carpinus betulus]						
AD6:GI-170732	Begin: 219	End: 274	59	59	81	86.9 7.5
! gamma-gliadin						
AD6:GI-730048	Begin: 54	End: 128	41	41	76	86.8 7.5
! Major pollen allergen Car b 1 isofo...						
AD6:GI-15984	Begin: 28	End: 318	40	40	82	88.7 7.7
! unnamed protein product [Actinidia ...]						
AD6:GI-113285	Begin: 28	End: 318	40	40	82	86.7 7.7
! Actinidin precursor [Actinidin] (A...						
AD6:GI-6706331	Begin: 488	End: 553	42	42	84	85.9 8.3
! cofactor-independent phosphoglycero...						
AD6:GI-1545879	Begin: 54	End: 144	36	36	74	84.7 9.8
! pollen allergen Car b 1 [Carpinus b...						
AD6:GI-1545875	Begin: 54	End: 144				

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! pollen allergen Car b 1 [Carpinus b... 36 36 74 84.7 9.8
AD6:GI-422005 Begin: 45 End: 216
! PHLPSA protein - common timothy (fr... 42 42 77 84.3 10
cryla-105.pep
AD6:GI-166317
gi|166317|gb|AAA32629.1| actinidin
SCORES Initl: 40 Initn: 40 Opt: 91 Z-score: 96.2 E(): 2.3
>>AD6:GI-166317
Initn: 40 Initl: 40 Opt: 91 Z-score: 96.2 expect(): 2.3
Smith-Waterman score: 91; 24.2% identity in 318 aa overlap
(869-1159:28-318)
cryla-105.pe LNEDLGVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARYKRAEKKWRDKREKL-----
GI-166317 MGLPKSVSNLSLFFSTLLILSLAFNAKNLTORTNDEVKAMYESWLKYGKSYNSLG
10 20 30 40 50
840 850 860 870 880 890
cryla-105.pe EWEINI-VYKEAKESVDALFNFSYDQLQADTN-----IAMIHADKKVHSIREAYLPELS
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
GI-166317 EWERFEIFKETLR-----FI-----DEHNADTNRSYKVLGNQFADLTDEEFRSTYLGTS
60 70 80 90 100
900 910 920 930 940
cryla-105.pe VIPGVN-AAIFEELEGRIPTAFSLY-DARNV-----IKNGDFNNGLSQWNVKGVHDVEEQ
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
GI-166317 ---GSNKTIVSNRYEPRVQVLPYSYVDMSAGAVVDIKSQGECG--CWAFSAIATVEGI
110 120 130 140 150 160
1010 1020 1030 1040 1050
cryla-105.pe NNQSRVLVPEWEAEV-----SQEVRVCPGRGYILRVYAYKEGEGCVTIHEIENNTDE
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
GI-166317 NKIVTGLVLSLEQELDCGRTQNCNG-GYI--TDGFQFIINNGINTEE--NYPYT
170 180 190 200 210
1060 1070 1080 1090 1100 1110
cryla-105.pe LKFSNCVVEEIIYPNNTVTCNDYTNQEEYGGAYTSRNRGYNEAPSPADYASVVEEKSYS
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
GI-166317 AODSEC-NVELONEKVTIDTY--ENVYPNNEWALOTAVTYQPVSVVALDAAG-DAFKQYS
220 230 240 250 260 270
1120 1130 1140 1150 1160 1170
cryla-105.pe DGRNENPCENRGYR-DVTPLPVGYVTKK-LEYF---PETDKVMIEGTETGTFIVDSVE
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
GI-166317 SGIFTGPC-----GTADHAVTIVGYTGEGIDYIWKVNSMDTTWGEEGYNRIILRVNGGAG
280 290 300 310 320 330
cryla-105.pe LLLMEE
GI-166317 TCGIATWPSVPYKYNQNPPEYSSLINPPAFSMKSDGPGVDEGQRYSA
340 350 360 370 380
cryla-105.pep
AD6:GI-22690
gi|22690|emb|CAA50328.1| major allergen [Corylus avellana]
SCORES Initl: 52 Initn: 52 Opt: 83 Z-score: 94.2 E(): 2.9
```

```
>>AD6:GI-22690
Initn: 52 Initl: 52 Opt: 83 Z-score: 94.2 expect(): 2.9
Smith-Waterman score: 83; 28.6% identity in 98 aa overlap
(978-1067:54-144)
cryla-105.pe SVIPGVNAAIFEELEGRIPTAFSLYDARNVTKNGDFNNGLSQWNVKGVHD-VVEQNNQRS
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
GI-22690 VLDGDKLIPKVPQAITSVENVEGNGGPGTIKNITFEGSRYKYVYKERVDEVDTNFTKYS
30 40 50 60 70 80
1010 1020 1030 1040 1050
cryla-105.pe VLVVP-----EWEAEVSQEVRC--PGRGYILRVYAYKEGEGCVTIHEIENNTDELRF
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
GI-22690 YTVIEGDVLGDKLEKVCSELKIVAAPGGGSLKISSKFHAKGD-----HEI--NAEEMKG
90 100 110 120 130
1060 1070 1080 1090 1100 1110
cryla-105.pe SNCVEEIIYPNNTVTCNDYTNQEEYGGAYTSRNRGYNEAPSPADYASVVEEKSYSYDGR
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
GI-22690 AKEMAELLRRAVETYLIAHSAEYN
140 150 160
cryla-105.pep
AD6:GI-584968
gi|584968|sp|Q08407|MPAC1_CORAV Major pollen allergen Cor a 1 isoforms 5, 6, 11
and 16 (Cor a I)
SCORES Initl: 48 Initn: 48 Opt: 81 Z-score: 92.1 E(): 3.8
>>AD6:GI-584968
Initn: 48 Initl: 48 Opt: 81 Z-score: 92.1 expect(): 3.8
Smith-Waterman score: 81; 28.6% identity in 98 aa overlap
(978-1067:54-144)
cryla-105.pe SVIPGVNAAIFEELEGRIPTAFSLYDARNVTKNGDFNNGLSQWNVKGVHD-VVEQNNQRS
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
GI-584968 VLDGDKLIPKVPQAITSVENVEGNGGPGTIKNITFEGSRYKYVYKERVDEVDTNFTYS
30 40 50 60 70 80
1010 1020 1030 1040 1050
cryla-105.pe VLVVP-----EWEAEVSQEVRC--PGRGYILRVYAYKEGEGCVTIHEIENNTDELRF
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
GI-584968 YTVIEGDVLGDKLEKVCSELKIVAAPGGGSLKISSKFHAKGD-----HEI--NAEEMKG
90 100 110 120 130
1060 1070 1080 1090 1100 1110
cryla-105.pe SNCVEEIIYPNNTVTCNDYTNQEEYGGAYTSRNRGYNEAPSPADYASVVEEKSYSYDGR
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
GI-584968 AKEMAELLRRAVETYLIAHSAEYN
140 150 160
cryla-105.pep
AD6:GI-1168704
gi|1168704|sp|P43178|BEVIE_BETVE Major pollen allergen Bet v 1-E (Bet v I-E)
SCORES Initl: 47 Initn: 47 Opt: 81 Z-score: 92.1 E(): 3.8
>>AD6:GI-1168704
Initn: 47 Initl: 47 Opt: 81 Z-score: 92.1 expect(): 3.8
Smith-Waterman score: 81; 26.7% identity in 86 aa overlap
```

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978-105554-139)	950	960	970	980	990	1000
cr1yla-105.pe	SVIEGVNA	ITNELEGRT	ITAFSLYDARNV	IKNGDFNNGJSCMNV	KGHVD-VEEQNNORS	
GI-1168704	ITDGNLFFPKW	PEFA	ASSVENIEBNG	QSEGTIKKISFPEGI	PFKVVKGREVDVHTNFNYS	80
	30	40	50	60	70	
cr1yla-105.pe	VLVV--PEWEA-	102X	103X	1040	1050	
GI-1168704	YSVIEGFGVD	TLEKTSNEIM	IVATWGS	AKINKYHTKGS	HEVKAQIKASKEGME	140
	90	100	110	120	130	
cr1yla-105.pe	1060	1070	1080	1090	1100	
GI-1168704	LLRAVESI	LLAHSDAYN				
	150	160				
cr1yla-105.pep						
ADG:GI-1545891						

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gi|1545891|emb|CAB02214.1| pollen allergen Car b 1 [Carpinus betulus]

SCORES      Initi: 36      Initn: 36      Opt: 81      Z-score: 92.1      E(): 3.8
>AD6:GI-1545891
      Initi: 36      Initn: 36      Opt: 81      Z-score: 92.1      expect(): 3.8
Smith-Waterman score: 81; 28.6% identity in 98 aa overlap
(978-1067:54-144)

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          950      960      970      980      990      1000
cyla-105.pe SVIPGVNAAIFELEGRIFTAFSLYDARNVNNKFNGLSCMNVKGHV-VEEQNNRS
          30      40      50      60      70      80
GI-1545891 VLDFDKLIPKVAQIAISSVNVNGVGQPGTINKITFAESGPFKEVKEVDEVDFNANFFKS

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 cyIa-105-pe SNCVEEYPPNNTVTCNDYTNQEEYGGATSRNRYGNEAPSPADYASVYEKSYTDGR
 : : : : :
 GI-1545891 AKENAEKLLRAVESVLLAHTAEYN
 140 150 160

cry1a-105.pep
 AD6:GI-22688
 gi|22688|emb|CA50327.1| major allergen [Corylus avellana]

SCORES Init1: 48 Initn: 48 Opt: 81 z-score: 92.1 E(): 3.8
 >>AD6.GI-22688
 Initn: 48 Init1: 48 Opt: 81 z-score: 92.1 expect(): 3.8
 Smith-Waterman score: 81; 28.6% identity in 98 aa overlap.
 (978-1067:54-144)

950 960 970 980 990 1000
cryla-105.pe SVTPGVNAAIFEELEGRIFTAFSLDYDARNVINGDFNNGUSCWNVKCHVD-VEEQNNQRS

GI-22688
VLDGDKLIPKVAQAITSVENVEGNGPGTIKNITFGEGRYKYVKERVDVNTNFTYS
||| ||:| ||:| ||:| ||:|

[illegible]

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cry1a-105.pe  SNCVEEIIYNNITVCNDYTNQEEYGGAYSTRNGKNEAPSDYASVYEKSYTDGR
:::|:::
GI-22688      AKEMAELLRAVETVILLAHSAEYN
140          150          160

```

cry1a-105.pap
AD6:GI-22684

gi|22684|emb|CAA50325.1|major allergen [Corylus avellana]

```

SCORES      In1tl: 53      In1tn: 53      Opt: 80      Z-score: 91.0      E(): 4.4
              (160 aa)
>ad6:GI-22684
ad6:GI-22684 In1tl: 53 In1tn: 53 Opt: 80 Z-score: 91.0 expect(): 4.4
              (160 aa)
Smith-Waterman score: 80; 28.6% identity in 98 aa overlap
              (978-1067:54-144)

```

950 960 970 980 990 1000
 cyrla-105.pe SYNGVNAIIEEGRIPTAFSYDARNVINGFNNGLSCMNVUGHD-VEEONNORS
 91-22694 VLDSEKILRVAPOAITSVENVEGNGPGTIKNITFGYKKVKKVVERDEVINTFNFTYS
 30 40 50 60 70 80

cryla-105.re vLMD---EWEANUSURVC--PGRVILRVAYKEGEGCVTHIEHNNTDEIKF
 :
 GI-22684 YNTEGVLDKLEIVCHELVIAVAPGGSLUKISSKFKAGD-----HEI--NAEEIKG
 90 100 110 120 130

~~SECRET~~

cryla-105.pe SNCVEEESIPNNNAVTNDYITWCEFGGATSRNGYNARSVPDASVYEKSYTDGR
:: :: ::
GI-22684 AKENAEKLRLAVEVTLNLSAEYTH
1060 1070 1090 1100 1110

cry1a-105.pap
AD6:GI-3135501

qi 3135501 | qb | AAC16527.1 | major allergen phl p 5 | phleum pratense

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SCORES Init1: 35 Initn: 35 Opt: 83 z-score: 90.1 B019
>>AD6:GI-3135501
Initn: 35 Init1: 35 Opt: 83 Z-score: 90.1 expect(): 4.9
Smith-Waterman score: 83; 22.7% identity in 154 aa overlap
(890-1038:86-234)
```

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cryla-105.pe LGNIJEELEKPLVGEALARVKAERKKWRDKREKLEWENIVYVKEAESVDALFVNSODQ
860 870 880 890 900 910
GI-313501 TTVATFGAANKAFAGLSAPKGAESSKAALTSKLDAAVKLAVYKAGTTPBAKYDA
60 70 80 90 100 110

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cry1a-105.pe LQADNTIAM: IHAADKRVHSIREAYLPGLSVIPGYNAAIFEELEGRIFTAFSLYDARNVI
GI-3135501 YVALSEALRIAGTLELVHAKPAA--EEVKVIPAGELQVIEKVDVSFAKVAATAAPAA--
120 130 140 150 160 170
cry1a-105.pe KNGDFNGLSCMNKGVHDVEEQNNQSRSLVLPPEWEAEVSQ----EVRVCPGRGYILRVIT
GI-3135501 -NDRFTVFEAAFN--NAIKASTGGAYESYKFTIPALEAAVKQAAVATVATAPEVKYTVFET
180 190 200 210 220 230
cry1a-105.pe AYKGYGEGCVTHIEENNTDELFSNCVEEIIYFNNTVTCNDTVNQEEYGAITSNR
GI-3135501 ALKKAITAMSEAQAAPAAATATATSAVGAATGATTAAGGYKV
240 250 260 270
cry1a-105.pep
AD6:GI-1545877
gi|1545877|emb|CAB02207.1| pollen allergen Car b 1 [Carpinus betulus]
SCORES Initl: 36 Initn: 36 Opt: 79 z-score: 90.0 E(): 5
>>AD6:GI-1545877
Initn: 36 initl: 36 opt: 79 z-score: 90.0 expect(): (160 aa)
Smith-Waterman score: 79; 26.5% identity in 98 aa overlap
(978-1067:54-144)
cry1a-105.pe SVIFGVNAAIFEELEGRIFTAFSLYDARNVKNNGDFNGLSCMNKGVHDVEEQNNQSRV
GI-1545877 VLDDKILPKVAPQAISSEVNGGPGGTIKNITFAEGSPFKFVKERVDEVNDANFKYN
30 40 50 60 70 80
cry1a-105.pe LVVPPEWEA-----EVSQEVRC--PGRGYILRVYAYKEGEGCVTHIEENNTDELK
GI-1545877 YTVIEGVLGDNLEKVSHELKIVAAPGGGSIKISKFHAKGD----HEV--NAEEMKG
90 100 110 120 130
cry1a-105.pe SNCYVEEIIYFNNTVTCNDTVNQEEYGAITSNRGYNEAPSPADYASVYEKSYTDGR
GI-1545877 AKEMAELLRAVESYLLAHTDEYN
140 150 160
cry1a-105.pep
AD6:GI-1545877
gi|1545887|emb|CAB02212.1| pollen allergen Car b 1 [Carpinus betulus]
SCORES Initl: 36 Initn: 36 Opt: 79 z-score: 90.0 E(): 5
>>AD6:GI-1545887
Initn: 36 initl: 36 opt: 79 z-score: 90.0 expect(): (160 aa)
Smith-Waterman score: 79; 26.5% identity in 98 aa overlap
(978-1067:54-144)
cry1a-105.pe SVIFGVNAAIFEELEGRIFTAFSLYDARNVKNNGDFNGLSCMNKGVHDV-VEEQNNQSR
GI-1545887 VLDDKILPKVAPQAISSEVNGGPGGTIKNITFAEGSPFKFVKERVDEVNDANFKYN
950 960 970 980 990 1000

cry1a-105.pe VLWVP-----EWEAEVSQEVRC--PGRGYILRVYAYKEGEGCVTHIEENNTDELK
GI-1545887 YTVIEGVLGDNLEKVSHELKIVAAPGGGSIKISKFHAKGD----HEV--NAEEMKG
90 100 110 120 130
cry1a-105.pe SNCYVEEIIYFNNTVTCNDTVNQEEYGAITSNRGYNEAPSPADYASVYEKSYTDGR
GI-1545887 AKEMAELLRAVESYLLAHTAEYN
140 150 160
cry1a-105.pep
AD6:GI-22595342
gi|22595342|gb|AA02510.1|AF409110_1 serine protease [Dermatophagoides
pteronysinus]
SCORES Initl: 75 Initn: 100 Opt: 80 z-score: 87.9 E(): 6.6
>>AD6:GI-22595342
Initn: 100 initl: 75 opt: 80 z-score: 87.9 expect(): (244 aa)
Smith-Waterman score: 81; 26.2% identity in 126 aa overlap
(905-1004:83-208)
cry1a-105.pe ALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLOADTNIAHIAADK
GI-22595342 ILDEYWTIAHCVDQTSKILRSKVLGEKISVKIFAHEKYDSRLDNDIALIKLSP
60 70 80 90 100 110
cry1a-105.pe RVHSIREAYLPGLSVIP-GYNAAIFEELEGRIFTA-----FSLYD
GI-22595342 RLNSKNAAVLPGSDVVKDQGVQSVMGYLEGYSYLPPELRVDIGGASRKECNELYSKYN
120 130 140 150 160 170
cry1a-105.pe AR---NVIKNGDFNNG--LSCMNKGVHDVEEQNNQSRSLVLPPEWEAEVSQEVRCVCPGRG
GI-22595342 AEVTDMICGSDVANGKDSGCGDGGGLVDVKNQVGNVSWGVCERKCYPGVTVRVG
180 190 200 210 220 230
cry1a-105.pe YILRVYAYKEGEGCVTHIEENNTDELFSNCVEEIIYFNNTVTCNDTVNQEEYGA
GI-22595342 NFIDWIESKRFPQ
240
cry1a-105.pep
AD6:GI-22686
gi|22686|emb|CAA50326.1| major allergen [Corylus avellana]
SCORES Initl: 52 Initn: 52 Opt: 77 z-score: 87.9 E(): 6.6
>>AD6:GI-22686
Initn: 52 initl: 52 opt: 77 z-score: 87.9 expect(): (160 aa)
Smith-Waterman score: 77; 27.6% identity in 98 aa overlap
(978-1067:54-144)
950 960 970 980 990 1000

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cry1a-105.pe SVIPGNAAIFEELEGRIPTAFSLYDARNVKNKDFNGLSCWNKGVHD-VBEQNNQRS
GI-1545893 VLDGKLIKVPAPQAISSVENGVGGPGTIKNITFAEGSPFKFVKRVEDVDNANFKYN
30 40 50 60 70 80

cry1a-105.pe VLWVPE---EWEAEVSOEVKVC--PGRGYILRVTAKEGEGCVTHIENNTDELKF
GI-22686 YTVIEGDVLDGKLEKVSLELTVAAAPGGSSILKISGFHAKGD-----HEV--NAEEMK
90 100 110 120 130

cry1a-105.pe SMCVEEIPNNTVTCNDYVNVQEEYGGATSNRGYNAPSPADYASVYEKSVDGR
GI-22686 AKEMAELKILRAVESYLLAHTAEN
140 150 160

cry1a-105.pe
AD6:GI-1545893

gi|1545893|emb|CA802215.1| pollen allergen Car b 1 [Carpinus betulus]

SCORES Initl: 36 Inltn: 36 Opt: 77 z-score: 87.9 E(): 6.6
>>AD6:GI-1545893
initn: 36 initl: 36 opt: 77 z-score: 87.9 expect(): 6.6
Smith-Waterman score: 77; 28.6% identity in 98 aa overlap
(978-1067:54-144)

cry1a-105.pe SVIPGNAAIFEELEGRIPTAFSLYDARNVKNKDFNGLSCWNKGVHD-VBEQNNQRS
GI-1545893 VLDGKLIKVPAPQAISSVENGVGGPGTIKNITFAEGSPFKFVKRVEDVDNANFKYS
30 40 50 60 70 80

cry1a-105.pe VLWVPE---EWEAEVSOEVKVC--PGRGYILRVTAKEGEGCVTHIENNTDELKF
GI-1545893 YTVIEGDVLDGKLEKVSLELTVAAAPGGSSILKISGFHAKGD-----HEV--NAEEMK
90 100 110 120 130

cry1a-105.pe SMCVEEIPNNTVTCNDYVNVQEEYGGATSNRGYNAPSPADYASVYEKSVDGR
GI-1545893 AKEMAELKILRAVESYLLAHTAEN
140 150 160

cry1a-105.pe
AD6:GI-170730

gi|170730|gb|AA34285.1| gamma-gliadin B-1 precursor [Triticum aestivum]

SCORES Initl: 59 Inltn: 70 Opt: 81 z-score: 87.3 E(): 7.1
>>AD6:GI-170730
initn: 70 initl: 59 opt: 81 z-score: 87.3 expect(): 7.1
Smith-Waterman score: 81; 31.7% identity in 60 aa overlap
(327-386:200-255)

cry1a-105.pe MDILNSITTYDAHGEYWSGHQIMASPVGSGSEFPFLYGTWNAAPQRIWOLGQ
GI-170730 CQLOQIPQGSRYEARIRAIILYILQEQQQGFVQPOQQQGGVSGVSGQQQQLGQ
170 180 190 200 210 220

cry1a-105.pe GVRTLSSTLYRRPFGNIGINNQLSVLDGTEFAYGTSNLPASVYKSGTVDLSDEIPPO
GI-170730 CSFQPOQOOLGOOP-----QQQQQQVLOQGTFLQPHQIAHLEAVTSTIALRTLTFTMCSVNV
230 240 250 260 270 280

cry1a-105.pe
AD6:GI-402745

gi|402745|emb|CAA47357.1| Car b I [Carpinus betulus]

SCORES Initl: 36 Inltn: 36 Opt: 76 z-score: 86.9 E(): 7.5
>>AD6:GI-402745
initn: 36 initl: 36 opt: 76 z-score: 86.9 expect(): 7.5
Smith-Waterman score: 77; 27.0% identity in 100 aa overlap
(978-1067:53-143)

cry1a-105.pe SVIPGNAAIFEELEGRIPTAFSLYDARNVKNKDFNGLSCWNKGVHD-VBEQNNQRS
GI-402745 VLDGKLIKVPAPQAISSVENGVGGPGTIKNITFAEGSPFKFVKRVEDVDNANFKYN
30 40 50 60 70 80

cry1a-105.pe VLWVPE---EWEAEVSOEVKVC--PGRGYILRVTA--YKEGEGCVTHIENNTDEL
GI-402745 YTVIEGDVLDGKLEKVSLELTVAAAPGGSSIVKISSKFHAKGY-----HEV--NAEEM
90 100 110 120 130

cry1a-105.pe KFSNCVEEIPNNTVTCNDYVNVQEEYGGATSNRGYNAPSPADYASVYEKSVD
GI-402745 KGFEWAELKILRAVESYLLAHTAEN
1060 1070 1080 1090 1100 1110

cry1a-105.pe
AD6:GI-170732

gi|170732|gb|AAA34286.1| gamma-gliadin

SCORES Initl: 59 Inltn: 59 Opt: 81 z-score: 86.8 E(): 7.5
>>AD6:GI-170732
initn: 59 initl: 59 opt: 81 z-score: 86.8 expect(): 7.5
Smith-Waterman score: 81; 31.7% identity in 60 aa overlap
(327-386:219-274)

cry1a-105.pe MDILNSITTYDAHGEYWSGHQIMASPVGSGSEFPFLYGTWNAAPQRIWOLGQ
GI-170732 CQLOQIPQGSRYEARIRAIILYILQEQQQGFVQPOQQQGGVSGVSGQQQQLGQ
190 200 210 220 230 240

cry1a-105.pe GVRTLSSTLYRRPFGNIGINNQLSVLDGTEFAYGTSNLPASVYKSGTVDLSDEIPPO
GI-170732 CSFQPOQOOLGOOP-----QQQQQQVLOQGTFLQPHQIAHLEAVTSTIALRTLTFTMCSVNV
250 260 270 280 290 300

cry1a-105.pe
AD6:GI-730048

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cry-ia-105.pe CVEEEEIYNNVTCTNDVYNQEEYGGAAYTSNRNGNEAPSPADYASVKEEYSYTDGRRRE  
| : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
C-NLPLONEKXWITDITY--ENVPYNNWALQTAVTVQPVSVALDAAG--DAFXHYSGSIFT
```

```

cry1a-105.pe  NCCFNRRGTR  DYTPIPGSYTKK  LEYF---PDTKWVILGTEGTFIVDSVLLME
GFC-----GTAIDHAVTIGVYGEGIDVWIKNSMDTWTGGEYMRIRNVGAGTCCGIA
GI-15984

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cr1a-105.pe E
GT-15984 TWPSYEVKYNQNHKPKYSSLINPAPFMSKDGFGVDDGORYSA

cryIa-105.pap
AD6:GI-113285

SCORES In11: 40 In1rn: 40 Opt: 82 z-score: 86.7 E(): 7.7
>>AD6:GI-113285 (380 aa)

(869-1159:28-318)

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cry1a-105.pe      LNEDLGVWVIFKIKTQDGHARGLNLEFEKKPLVGELARVKRAEKKWRDKREKL-----
GI-113285        MGLPKSVSMLLFPFTLLIISLAFNAKNITQTNDVKVMYMSLKCYKCKSYNSLG
                                10    20    30    40    50
                                900   910   920   930   940
cry1a-105.pe      EWETNI-VYKEAKESVDALFVNSQYDQADTN---IAMIIAADKVHVSIRRAYLPELS
                                : :::::
                                : :::::
                                : :::::

```

GA-113203	60	70	80	90	100
EWGAFKFNIGIA-133-F1	DEHINBIDNINSGVGR	ADGIDDEGGR	133-100		
950	960	970	980	990	1000
GVIA-105-pe	VGIVGNAAI-1	FEELGRIPTAF-SLYDARNV	IKNGDFNNGS	CMNVKGVHVDVEEQNNORS	

	110	120	130	140	150	160
cr1a-105.pe	VLVPEAEV----	1010	1020	1030	1040	1050
	QSEVCPGPGVILRTAY	1060	1070	1080	1090	1100
	REGGECVTHIEINNTDEL	1110	1120	1130	1140	1150
	KFSN	1160	1170	1180	1190	1200
GI-113295	GVISLSEGLDCTQNTBNG	1210	1220	1230	1240	1250
	GVY	1260	1270	1280	1290	1300
	TTGCFPIITNGGINTVE	1310	1320	1330	1340	1350
	-NYPVTAQDGE	1360	1370	1380	1390	1400

	170	180	190	200	210	220
CRY1-105.pe	CVEEEYLPNNVT	CNDVTYNQEEY	GAYTSRNRCY	NEASVPADYAS	VEEKSVYTDGR	EE
CRY11209	CNIDLEKVVYTDY	FNIDYNNWAI	CGATVQWISVA	IRAG	DFPKYVSSGIT	TT

```

cryla-105.pe NPCEFNGR-DYFLBVGVIKE-LEVF---PDTXVIECTEGTFFVDSVLLME
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
      230  233  236  239  242  245  248  251  254  257  260  263  266  269  272

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cryla-105.pep
AD6:GI-1545875
gi|113285|emb|CA66002.1| cofactor-independent phosphotransferase (Apium graveolens)
CRYLA-105-PEP
TAPSGVYNNNDP...EYSSLLINPAFNSMDGPGVGVDDGQRYSA
340 350 360 370 380
CRYLA-105-PEP
AD6:GI-6706331
gi|6706331|emb|CA66002.1| cofactor-independent phosphotransferase (Apium graveolens)
CRYLA-105-PEP
440 450 460 470 480 490 500 510 520 530 540 550
CRYLA-105-PEP
GDLRLT-SGG-PFAYTIWINGQL-PQYRARIYASTNLRIVTVVAGERIFAGQF
500 510 520 530 540 550
CRYLA-105-PEP
GVRYKDVPSGLANVAATVNNLHGFVAPDDYETILLIEVVND
520 530 540 550
CRYLA-105-PEP
NKTMDTGDPLTFQSFYATINTAFTFPMSSQSFVGVADTFSSGNEGYIDREFELIPVTATL
560 570 580 590 600 610
CRYLA-105-PEP
AD6:GI-1545879
gi|1545879|emb|CA602208.1| pollen allergen Car b 1 [Carpinus betulus]
CRYLA-105-PEP
INITN: 36 Initn: 36 Opt: 74 Z-score: 84.7 E(): 9.8
>>AD6:GI-1545879
initn: 36 initn: 36 opt: 74 Z-score: 84.7 expect(): 9.8
Smith-Waterman score: 74; 25.5% identity in 98 aa overlap
(978-1067:54-144)
CRYLA-105-PEP
SVLPFGVNAALFEELEGRIPTAFSLYDARNVIRKNGDFNGLSCWNVKGVHD-VEEQNNORS
950 960 970 980 990 1000
GI-1545879
VLDFDKLIPKVAPOAISVENVGNGGPGTINKITFAEGSPFKFVKERVDEVDNANFKYN
30 40 50 60 70 80
CRYLA-105-PEP
VLDFDKLIPKVAPOAISVENVGNGGPGTINKITFAEGSPFKFVKERVDEVDNANFKYN
1010 1020 1030 1040 1050
GI-1545879
YTVIEGDLGDKLEKVSHELKVAAPGGGSIKISSKFHAKG-----HEV--NAEKMKG
90 100 110 120 130
CRYLA-105-PEP
SNVVEEIEYNNVTTCNDYTVNQEYGGAYTSRNGVNEAPSPADYASVVEEYSYTDGR
1060 1070 1080 1090 1100 1110
GI-1545879
AKEMAEKLLRAVESYLLAHTDEYN
1020 1030 1040 1050 1060 1070
CRYLA-105-PEP
EVSQS-----VRVCPGRGYLLRVITAYKEGEGGCVTIHEINNTDELAFSCNVEEIEYIPNN
1020 1030 1040 1050 1060 1070

cryla-105.pep
AD6:GI-1545875
gi|1545875|emb|CA602206.1| pollen allergen Car b 1 [Carpinus betulus]
CRYLA-105-PEP
INITN: 36 Initn: 36 Opt: 74 Z-score: 84.7 E(): 9.8
>>AD6:GI-1545875
initn: 36 initn: 36 opt: 74 Z-score: 84.7 expect(): 9.8
Smith-Waterman score: 74; 25.5% identity in 98 aa overlap
(978-1067:54-144)
CRYLA-105-PEP
SVLPFGVNAALFEELEGRIPTAFSLYDARNVIRKNGDFNGLSCWNVKGVHD-VEEQNNORS
950 960 970 980 990 1000
GI-1545875
VLDFDKLIPKVAPOAISVENVGNGGPGTINKITFAEGSPFKFVKERVDEVDNANFKYN
30 40 50 60 70 80
CRYLA-105-PEP
VLDFDKLIPKVAPOAISVENVGNGGPGTINKITFAEGSPFKFVKERVDEVDNANFKYN
1010 1020 1030 1040 1050
GI-1545875
YTVIEGDLGDKLEKVSHELKVAAPGGGSIKISSKFHAKG-----HEV--NAEKMKG
90 100 110 120 130
CRYLA-105-PEP
SNVVEEIEYNNVTTCNDYTVNQEYGGAYTSRNGVNEAPSPADYASVVEEYSYTDGR
1060 1070 1080 1090 1100 1110
GI-1545875
AKEMAEKLLRAVESYLLAHTDEYN
1020 1030 1040 1050 1060 1070
CRYLA-105-PEP
EVSQS-----VRVCPGRGYLLRVITAYKEGEGGCVTIHEINNTDELAFSCNVEEIEYIPNN
1020 1030 1040 1050 1060 1070

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```

! Distributed over 4 threads.
! Start time: Wed Sep 6 08:28:48 2006
! Completion time: Wed Sep 6 08:29:26 2006

! CPU time used:
!   Database scan: 0:00:00.3
!   Post-scan processing: 0:00:15.9
!   Total CPU time: 0:00:16.1
! Output File: /usr/people/sequester/ebits_prod/jsmccla/crysal05.ad6_tmp

```

©01

Appendix 3. Search for immunologically relevant
sequences in the cryIA.105 protein

allergensearch -infile=/usr/people/seqstore/ebits_prod/jsmccla/upload/cryla-105.pep
-INFILE2=AD6.* -
OUTfile=/usr/people/seqstore/ebits_prod/jsmccla/cryla105_allnsearch_tmp -
WINDOWsize=8

Query sequence(s) : /usr/people/seqstore/ebits_prod/jsmccla/upload/cryla-105.pep
Search sequence(s) : AD6.*
Window size: 8

/usr/people/seqstore/ebits_prod/jsmccla/cryla105_allnsearch_tmp Wed Sep 6 08:30:06
2006 ..

No hits found

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[illegible]

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! A07236 Bacillus thuringiensis B.thu...	635	2653	2684	2956.3	9.2e-159
TXNS:AF077326_1 Begin: 72 End: 1227					
! AF077326 Bacillus thuringiensis Bac...	1817	3239	2680	2951.4	1.7e-158
TXNS:CIBB BACTU Begin: 72 End: 1227					
! Q05805 Bacillus thuringiensis. pest...	1817	3239	2680	2951.4	1.7e-158
TXNS:L32020_1 Begin: 72 End: 1229					
! L32020 Bacillus thuringiensis Bacil...	1824	3419	2667	2937.1	1.1e-157
TXNS:CIBB BACTU Begin: 72 End: 1229					
! Q45739 Bacillus thuringiensis. pest...	1824	3419	2667	2937.1	1.1e-157
TXNS:X06711_1 Begin: 67 End: 1228					
! X06711 Bacillus thuringiensis B. th...	1835	3007	2661	2930.4	2.5e-157
TXNS:AF363025_1 Begin: 67 End: 1228					
! AF363025 Bacillus thuringiensis sub...	1835	3008	2661	2930.4	2.5e-157
TXNS:AKS1084 Begin: 67 End: 1228					
! AKS1084 Bacillus thuringiensis (su...	1835	3008	2661	2930.4	2.5e-157
TXNS:CIBA BACTK Begin: 67 End: 1228					
! P05517 Bacillus thuringiensis (subs...	1835	3007	2661	2930.4	2.5e-157
TXNS:CIBD BACT2 Begin: 40 End: 1231					
! Q92a25 Bacillus thuringiensis (subs...	1809	3175	2652	2920.5	9.1e-157
TXNS:CIBC BACTM Begin: 72 End: 1233					
! Q45774 Bacillus thuringiensis (subs...	1760	3383	2550	2807.9	1.7e-150
TXNS:246442_1 Begin: 72 End: 1233					
! 246442 Bacillus thuringiensis B.thu...	1760	3383	2550	2807.9	1.7e-150
TXNS:G9EA BACTA Begin: 57 End: 1150					
! Q2n19 Bacillus thuringiensis (subs...	434	1436	2084	2294.1	7.1e-122
TXNS:X96682_1 Begin: 1 End: 756					
! X96682 Bacillus thuringiensis B.thu...	1104	2337	1851	2039.7	1.1e-107
TXNS:X99103_1 Begin: 1 End: 630					
! X99103 synthetic construct Artificial...	1104	1598	1823	2010.0	4.8e-106
TXNS:X75019_1 Begin: 29 End: 1144					
! X75019 Bacillus thuringiensis B.thu...	533	2179	1773	1950.8	9.3e-103
TXNS:Q45745 Begin: 29 End: 1144					
! Q45745 Bacillus thuringiensis. delt...	533	2179	1773	1950.8	9.3e-103
TXNS:Q9FDC0 Begin: 23 End: 1128					
! Q9f4c0 bacillus thuringiensis (subs...	519	1660	1741	1915.6	8.6e-101
TXNS:CLIB BACTE Begin: 76 End: 719					
! Q45709 Bacillus thuringiensis (subs...	895	1625	1716	1891.0	2e-99
TXNS:C9DA BACTP Begin: 57 End: 1169					
! Q06014 bacillus thuringiensis (subs...	756	2154	1715	1886.7	3.5e-99
TXNS:CLIA BACTK Begin: 36 End: 719					
! Q45752 Bacillus thuringiensis (subs...	896	1603	1712	1886.6	3.5e-99
TXNS:X08920_1 Begin: 36 End: 719					
! X08920 Bacillus thuringiensis B.thu...	889	1600	1709	1883.3	5.4e-99
TXNS:AAK66742 Begin: 36 End: 719					
! Aak66742 bacillus thuringiensis. cr...	896	1603	1707	1881.1	7.2e-99
TXNS:Q85796 Begin: 36 End: 719					
! Q85796 bacillus thuringiensis (subs...	889	1596	1705	1878.8	9.6e-99
TXNS:C9AA BACTG Begin: 26 End: 1156					
! Q90931 Bacillus thuringiensis (subs...	457	1750	1706	1876.8	1.2e-98
TXNS:X58120_2 Begin: 26 End: 1156					
! X58120 Bacillus thuringiensis B.thu...	457	1750	1706	1876.8	1.2e-98
TXNS:X62821_1 Begin: 36 End: 719					
! X62821 Bacillus thuringiensis B.thu...	896	1592	1701	1874.4	1.7e-98
TXNS:CLID BACTU Begin: 41 End: 719					
! Q9xd11 bacillus thuringiensis. pest...	888	1589	1695	1867.8	3.9e-98
TXNS:Q9F0P8 Begin: 76 End: 719					
! Q9f0p8 bacillus thuringiensis. cryl...	896	1580	1689	1861.2	9.2e-98
TXNS:C9CA BACTO Begin: 59 End: 1157					
! Q45733 Bacillus thuringiensis (subs...	702	2140	1686	1854.8	2.1e-97
TXNS:AF056933_1 Begin: 76 End: 719					
! AF056933 Bacillus thuringiensis Bac...	862	1515	1604	1767.4	1.5e-92
TXNS:CLIC BACTU Begin: 76 End: 719					
! Q87404 Bacillus thuringiensis. pest...	862	1515	1604	1767.4	1.5e-92
TXNS:C8CA BACTP Begin: 59 End: 1160					
! Q45706 Bacillus thuringiensis (subs...	503	1400	1542	1695.8	1.5e-88
TXNS:U04366_1 Begin: 59 End: 1160					

! U04366 Bacillus thuringiensis Bacil...	503	1400	1542	1695.8	1.5e-88
TXNS:U04365_1 Begin: 59 End: 1166					
! U04365 Bacillus thuringiensis Bacil...	801	2006	1542	1695.8	1.5e-88
TXNS:C8BA BACUK Begin: 59 End: 1166					
! Q45705 Bacillus thuringiensis (subs...	801	2006	1542	1695.8	1.5e-88
TXNS:X13620_1 Begin: 1 End: 823					
! X13620 Bacillus thuringiensis Bacil...	1300	2802	1489	1639.6	2e-85
TXNS:AF132928_1 Begin: 23 End: 1109					
! AF132928 Bacillus thuringiensis sub...	519	1580	1478	1625.5	1.2e-84
TXNS:CSAA BACTF Begin: 23 End: 1109					
! Q94682 Bacillus thuringiensis (subs...	519	1580	1478	1625.5	1.2e-84
TXNS:Q45789 Begin: 1 End: 297					
! Q45789 Bacillus thuringiensis. delt...	1355	1355	1355	1498.4	1.5e-77
TXNS:X16315_1 Begin: 1 End: 297					
! X16315 Bacillus thuringiensis Bacil...	1355	1355	1355	1498.4	1.5e-77
TXNS:M84650_1 Begin: 44 End: 596					
! M84650 synthetic construct Syntheti...	467	832	1242	1369.1	2.4e-70
TXNS:C3AA BACTT Begin: 91 End: 643					
! P07130 Bacillus thuringiensis (subs...	467	832	1242	1368.6	2.5e-70
TXNS:Q9S6N9 Begin: 99 End: 651					
! Q946n9 bacillus thuringiensis. cry3...	467	832	1242	1368.5	2.6e-70
TXNS:M22472_1 Begin: 99 End: 651					
! M2472 Bacillus thuringiensis B.thu...	467	832	1242	1368.5	2.6e-70
TXNS:U04364_1 Begin: 39 End: 1154					
! U04364 Bacillus thuringiensis Bacil...	601	1940	1223	1343.8	6.1e-69
TXNS:C8AA BACUK Begin: 39 End: 1154					
! Q45704 Bacillus thuringiensis (subs...	601	1940	1223	1343.8	6.1e-69
TXNS:C3BB BACTU Begin: 82 End: 650					
! Q06117 Bacillus thuringiensis. pest...	411	1070	1173	1292.3	4.5e-66
TXNS:A07234_1 Begin: 29 End: 650					
! A07234 Bacillus thuringiensis B.thu...	414	1072	1168	1286.8	9e-66
TXNS:C3BA BACTO Begin: 37 End: 658					
! P1969 Bacillus thuringiensis (subs...	414	1072	1168	1286.8	9.1e-66
TXNS:X17123_1 Begin: 37 End: 658					
! X17123 Bacillus thuringiensis Bacil...	414	1072	1168	1286.8	9.1e-66
TXNS:U31633_1 Begin: 82 End: 650					
! U31633 Bacillus thuringiensis Bacil...	412	1067	1167	1285.7	1e-65
TXNS:C4BA BACTI Begin: 43 End: 1136					
! P05519 bacillus thuringiensis (subs...	571	1667	1126	1236.8	5.5e-63
TXNS:X07423_1 Begin: 43 End: 1136					
! X07423 Bacillus thuringiensis Bacil...	571	1667	1126	1236.8	5.5e-63
TXNS:X07082_1 Begin: 43 End: 1136					
! X07082 Bacillus thuringiensis Bacil...	571	1666	1126	1236.8	5.5e-63
TXNS:C4AA BACTI Begin: 70 End: 1180					
! P16480 Bacillus thuringiensis (subs...	571	1577	1088	1194.6	1.2e-60
TXNS:Y00423_1 Begin: 70 End: 1180					
! Y00423 Bacillus thuringiensis Bacil...	570	1551	1076	1181.4	6.8e-60
TXNS:AF093107_1 Begin: 48 End: 638					
! AF093107 Bacillus thuringiensis Bac...	410	1018	1037	1142.4	1e-57
TXNS:O87654 Begin: 48 End: 638					
! O87654 bacillus thuringiensis. delt...	410	1018	1037	1142.4	1e-57
TXNS:C3CA BACTK Begin: 99 End: 648					
! Q45744 bacillus thuringiensis (subs...	370	713	1008	1110.3	6.2e-56
TXNS:Q45740 Begin: 36 End: 379					
! Q45740 bacillus thuringiensis. inse...	672	721	714	789.3	4.7e-38
TXNS:AF122897_1 Begin: 68 End: 1162					
! AF122897 Bacillus thuringiensis sub...	640	1878	686	751.1	6.3e-36
TXNS:COAA BACTF Begin: 68 End: 1162					
! Q9X597 Bacillus thuringiensis (subs...	640	1878	686	751.1	6.3e-36
TXNS:Y07603_1 Begin: 48 End: 646					
! Y07603 Bacillus thuringiensis B.thu...	173	396	682	750.5	6.8e-36
TXNS:CJAA BACTJ Begin: 48 End: 646					
! Q32307 Bacillus thuringiensis (subs...	173	396	682	750.5	6.8e-36
TXNS:CJBA BACTH Begin: 79 End: 658					
! O86170 Bacillus thuringiensis (subs...	157	237	632	695.0	8.4e-33
TXNS:U082518_1 Begin: 18 End: 641					

Q9RMG3	Bacillus thuringiensis. pest...	130	130	270	295.9	1.4e-10
TXNS:AFZ00816_1	Begin: 56 End: 630					
AFZ00816	Bacillus thuringiensis Bac...	130	130	270	295.9	1.4e-10
TXNS:Q9M869	Begin: 56 End: 275					
Q9M869	Bacillus thuringiensis. cry2...	166	166	267	293.5	1.9e-10
TXNS:L07027_1	Begin: 60 End: 1177					
L07027	Bacillus thuringiensis Bacil...	207	664	266	287.0	4.4e-10
TXNS:CBA_BACTU	Begin: 60 End: 1177					
Q45754	Bacillus thuringiensis. pest...	207	664	266	287.0	4.4e-10
TXNS:CIAA_PAEPP	Begin: 84 End: 332					
Q45358	paenibacillus popilliae (bac...	93	131	262	286.4	4.8e-10
TXNS:CICA_PAEPP	Begin: 114 End: 472					
P57092	paenibacillus popilliae (bac...	71	130	259	283.2	7.3e-10
TXNS:C2AC_BACTU	Begin: 98 End: 611					
Q45743	Bacillus thuringiensis. pest...	106	141	244	267.3	5.5e-09
TXNS:X57252_3	Begin: 98 End: 611					
X57252	Bacillus thuringiensis B.thu...	106	141	244	267.3	5.5e-09
TXNS:CBA_BACTU	Begin: 1 End: 633					
Q45730	Bacillus thuringiensis (subs...	60	86	178	193.5	7.2e-05
TXNS:X86902_1	Begin: 1 End: 633					
X86902	Bacillus thuringiensis B.thu...	60	86	178	193.5	7.2e-05
TXNS:CBA_BACTU	Begin: 25 End: 633					
P21256	Bacillus thuringiensis (subs...	119	119	175	191.0	9.9e-05
TXNS:A031065_1	Begin: 149 End: 723					
A031065	Bacillus thuringiensis Bac...	99	99	166	180.3	0.00039
TXNS:Q9EVR2	Begin: 149 End: 723					
Q9EVR2	Bacillus thuringiensis. 8l-k...	99	99	166	180.3	0.00039
TXNS:CBA_BACTV	Begin: 6 End: 633					
Q9Z1U	Bacillus thuringiensis (subs...	65	65	163	176.7	0.00062
TXNS:AF017416_1	Begin: 6 End: 633					
AF017416	Bacillus thuringiensis Bac...	65	65	163	176.7	0.00062
TXNS:Q9J591	Begin: 3 End: 20					
Q9J591	Bacillus thuringiensis. inse...	97	97	101	132.1	0.19
TXNS:D01041_1	Begin: 12 End: 12					
D01041	Cloning vector pBUD2.Bt ClO...	92	92	92	125.5	0.44
TXNS:D01049_1	Begin: 1 End: 12					
D01049	Cloning vector pACN235.Bt Cl...	92	92	92	125.5	0.44
TXNS:CDA_BACTU	Begin: 92 End: 691					
Q45755	Bacillus thuringiensis. pest...	60	60	115	123.3	0.58
TXNS:L07023_1	Begin: 92 End: 691					
L07023	Bacillus thuringiensis Bacil...	60	60	115	123.3	0.58
TXNS:BAB38741	Begin: 199 End: 341					
BAB38741	Escherichia coli O157:H7... 341	36	36	104	116.7	1.4
TXNS:BA33795	Begin: 107 End: 338					
BA33795	Escherichia coli O157:H7... 338	34	34	97	109.6	3.4
TXNS:Q9X389	Begin: 225 End: 341					
Q9X389	Bacillus anthracis. pXO1132...	40	40	93	104.3	6.7
TXNS:Z23281_1	Begin: 26 End: 261					
Z23281	Clostridium novyi C.novyi at...	66	66	90	103.6	7.3
TXNS:BA38402	Begin: 355 End: 410					
BA38402	Escherichia coli O157:H7... 410	62	62	94	103.2	7.6
TXNS:O45843	Begin: 253 End: 407					
O45843	Clostridium botulinum. p-47 ...	50	50	91	101.2	9.9

cryla-105.pep
TXNS:U89872_1

Description: U89872 Bacillus thuringiensis CryIAC delta-endotoxin gene
Accession/ID: U89872

LOCUS U89872.1 [EU089872]
DEFINITION Bacillus thuringiensis CryIAC delta-endotoxin gene, complete cds.

====General comments=====

SCORES Initl: 3919 Intn: 7211 Opt: 7222 z-score: 7964.5 E(): 0

Description: U89872 Bacillus thuringiensis Bacillus thuringiensis
delta-endotoxin gene
Accession/ID: U89872
=====General comments=====

LOCUS U89872.1 [BTU89872]
DEFINITION Bacillus thuringiensis CrvIAC delta-endotoxin gene, complete cds.

>>TXN5:U89872_1 (1178 aa)
Smith-Waterman score: 7222; 92.0% identity in 1182 aa overlap
(1-1177:1-1178)

10 20 30 40 50 60
cry1a-105.pe MDNPNNEICIPYCNLSNPEVEVLGGRIETGTPIDISLSLTQLSLSEFVPGAGVLGL
U89872_1 MDNPNNEICIPYCNLSNPEVEVLGGRIETGTPIDISLSLTQLSLSEFVPGAGVLGL
10 20 30 40 50 60
70 80 90 100 110 120
cry1a-105.pe VDIIWGIFGSPQWDAPLQIEQLINQRIEFAFARNOAISRLGSLNLYQIYAESFREWAD
U89872_1 VDIIWGIFGSPQWDAPLQIEQLINQRIEFAFARNOAISRLGSLNLYQIYAESFREWAD
70 80 90 100 110 120
130 140 150 160 170 180
cry1a-105.pe PTPNPALEERIRIQFNDMNSALTTPILFAVQNYQVPLLSVYVQAANHLVSLRDSVFGQ
U89872_1 PTPNPALEERIRIQFNDMNSALTTPILFAVQNYQVPLLSVYVQAANHLVSLRDSVFGQ
130 140 150 160 170 180
190 200 210 220 230 240
cry1a-105.pe RWGFDAAITNSRYNDLTRIGNYTDHAWRWYNTGLERVWGSPDSRDWIRNQFRRELTIV
U89872_1 RWGFDAAITNSRYNDLTRIGNYTDHAWRWYNTGLERVWGSPDSRDWIRNQFRRELTIV
190 200 210 220 230 240
250 260 270 280 290 300
cry1a-105.pe LDIIVLPNDSDRYPIRTVSQLTREIYTNVLENFDGSRGSAQGTESIRSPHLMIL
U89872_1 LDIIVLPNDSDRYPIRTVSQLTREIYTNVLENFDGSRGSAQGTESIRSPHLMIL
250 260 270 280 290 300
310 320 330 340 350 360
cry1a-105.pe NSIITYDAHRGYWGSQIMASPVGSGPEFTPLGTGNGNAAPQORIYLAQLQGQYVR
U89872_1 NSIITYDAHRGYWGSQIMASPVGSGPEFTPLGTGNGNAAPQORIYLAQLQGQYVR
310 320 330 340 350 360
370 380 390 400 410 420
cry1a-105.pe TISSTLYRRFPNIGINNOQLSVLDGTEFAFGTSSNLPNAVYKSGTVDLSDEIPQNNV
U89872_1 TISSTLYRRFPNIGINNOQLSVLDGTEFAFGTSSNLPNAVYKSGTVDLSDEIPQNNV
370 380 390 400 410 420
430 440 450 460 470 480
cry1a-105.pe PPRQGFHRLSHVSMFPRGFSNNSVSIIRAPMFWTHRSABFNIIASDSITQIPVAKH
U89872_1 PPRQGFHRLSHVSMFPRGFSNNSVSIIRAPMFWTHRSABFNIIASDSITQIPVAKH
430 440 450 460 470 480
490 500 510 520 530
cry1a-105.pe TLQSGTIVVRGPGFTGDDILARTSGGPFAYT--IYNINGQLPQ--RYRARIYASTNL
U89872_1 FLFNGS-VISGPGFTGDDILRLNLSGNNIQMRGYIEVPIHPFTSTRYRVRVRYASVTPI
490 500 510 520 530
540 550 560 570 580 590
cry1a-105.pe RIYVTVAGERIFAGQNKMTMDGPTLFQSFYSATINTAFTFPMQSQSFVAGADTFSSGN
U89872_1 HLNWNGNSSIFNSFTPATATSLDNLQSDFGYFESANFTSSLGN--IVGVNFSGTA
540 550 560 570 580 590
600 610 620 630 640 650

660 670 680 690 700 710
cry1a-105.pe SDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGGSGTITIGGDDVF
U89872_1 SDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGGSGTITIGGDDVF
660 670 680 690 700 710
720 730 740 750 760 770
cry1a-105.pe KENYVTLSTGTEDECYPTLYLQKIDSKLAFTRYQLRGVIEDSODLEIYSIRYNAKHETV
U89872_1 KENYVTLSTGTEDECYPTLYLQKIDSKLAFTRYQLRGVIEDSODLEIYSIRYNAKHETV
720 730 740 750 760 770
780 790 800 810 820 830
cry1a-105.pe NVFPGTSLWPLSAQSPIGKCGPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVG
U89872_1 NVFPGTSLWPLSAQSPIGKCGPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVG
780 790 800 810 820 830
840 850 860 870 880 890
cry1a-105.pe CTDLNEDELGVWVIFKIKTQDGHARGNLNLEFLEEKPLVGEALARYKRAEKKWRDKRELEW
U89872_1 CTDLNEDELGVWVIFKIKTQDGHARGNLNLEFLEEKPLVGEALARYKRAEKKWRDKRELEW
840 850 860 870 880 890
900 910 920 930 940 950
cry1a-105.pe ETNIVYKEAKESVDALFVNSQVDQLQADTNIAHAAKRVHSIREAYLPVPGVNA
U89872_1 ETNIVYKEAKESVDALFVNSQVDQLQADTNIAHAAKRVHSIREAYLPVPGVNA
900 910 920 930 940 950
960 970 980 990 1000 1010
cry1a-105.pe AIFEELEGRIITAFSLYDARNVTKNGDFNGLSCMNVKGVHVDVEEQNNQRSLVVPWEWA
U89872_1 AIFEELEGRIITAFSLYDARNVTKNGDFNGLSCMNVKGVHVDVEEQNNQRSLVVPWEWA
960 970 980 990 1000 1010
1020 1030 1040 1050 1060 1070
cry1a-105.pe EVSQEVRCVPCRGYILRVATYKEGYEGECVTIHEIENNTDELKFSNCVEEIIYPNNTVTC
U89872_1 EVSQEVRCVPCRGYILRVATYKEGYEGECVTIHEIENNTDELKFSNCVEEIIYPNNTVTC
1020 1030 1040 1050 1060 1070
1080 1090 1100 1110 1120 1130
cry1a-105.pe NDTVTNQEEYGAYTSNRNGYNEAFSPADYASVYEEKSYTDGRRENCFENRGYRDTTP
U89872_1 NDTVTNQEEYGAYTSNRNGYNEAFSPADYASVYEEKSYTDGRRENCFENRGYRDTTP
1080 1090 1100 1110 1120 1130
1140 1150 1160 1170
cry1a-105.pe LPVGVTYKLEVPFETDKWIEGTETGTFIVDSVELLMEE
U89872_1 LPVGVTYKLEVPFETDKWIEGTETGTFIVDSVELLMEE
1140 1150 1160 1170
TXN5:CIAC_BACTK
Description: P05068 bacillus thuringiensis (subsp. kurstaki), pesticidal
crystal protein cry
Accession/ID: P05068

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=====
ID      CLAC_BACTK  STANDARD  PRT;  1178 AA.
AC      P03068
=====
SCORES  Initl 394  Initl 391  Opt 722  z-score: 7964.5 E(): 0
>>>XNS:CLAC_BACTK
initn: 7211 initl: 3919 opt: 722 z-score: 7964.5 expect(): 0
Smith-Waterman score: 7221 92% identity in 1182 aa overlap
(1-1177:1-1178)

cryla-105.pe  MONNPNINECIPYCNLSNPEVEVLSGEEVLTADISLSQPLSEFVPGAGFVLGL  60
CLAC_BACTK  MONNPNINECIPYCNLSNPEVEVLSGEEVLTADISLSQPLSEFVPGAGFVLGL  60
(1-1177:1-1178)

cryla-105.pe  VDIINGIFGSPQMDAFIVQIOLINQRIEFPARNONLSNREGSLNVOIIESFREHLD  130
CLAC_BACTK  VDIINGIFGSPQMDAFIVQIOLINQRIEFPARNONLSNREGSLNVOIIESFREHLD  130

cryla-105.pe  PTNPALREEMRIQFNDMSALTAIPLEAVQNVQVPLLSVYQVAAHLHSVREDSVFGQ  140
CLAC_BACTK  PTNPALREEMRIQFNDMSALTAIPLEAVQNVQVPLLSVYQVAAHLHSVREDSVFGQ  140

cryla-105.pe  RMGFOAAATNSRNDLTRILGNYTHAVRWYNTGLERVAGPDSRDWRIRYNOFRRELTIV  240
CLAC_BACTK  RMGFOAAATNSRNDLTRILGNYTHAVRWYNTGLERVAGPDSRDWRIRYNOFRRELTIV  240

cryla-105.pe  LDIVSLFVNDYSRTPYPIRTVSQLTREIYTNVLENFDFGSRGAGIERSIRSPHLMIDL  300
CLAC_BACTK  LDIVSLFVNDYSRTPYPIRTVSQLTREIYTNVLENFDFGSRGAGIERSIRSPHLMIDL  300

cryla-105.pe  NSITIYDAHGEYVWYSGHOIMASPVGSGPEFTFPLYGTMGNAAPQORIQAQGGQVYR  360
CLAC_BACTK  NSITIYDAHGEYVWYSGHOIMASPVGSGPEFTFPLYGTMGNAAPQORIQAQGGQVYR  360

cryla-105.pe  TLSSTLYRPPNIGINNQQLSVLDGTEFAYGTSSNLPASVYRKSCTVDSLDEIPPNQNV  420
CLAC_BACTK  TLSSTLYRPPNIGINNQQLSVLDGTEFAYGTSSNLPASVYRKSCTVDSLDEIPPNQNV  420

cryla-105.pe  PPRQGFSLHSHVMSFRSGFSNSSVSIIRAPMFSWIHRSAFNNIIASDSITQIPAKGN  480
CLAC_BACTK  PPRQGFSLHSHVMSFRSGFSNSSVSIIRAPMFSWIHRSAFNNIIASDSITQIPAKGN  480

cryla-105.pe  TLOGSTTVVRGFGTGGDILLRTSGGPFAYT--IWNINGOLPQ--RYRARIIRASTTNL  530
CLAC_BACTK  FLNFGS-VISGFGTGGDVLRLNSSGNNIIQNRGIEVPIFFSTSTRVIRVRYASVTPI  530
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cryla-105.pe  RIYVTVAGERIPAGQFNKNTWDTGDLPTQSFYSYATINTAFTPMSSQSFYVAGDTFSSGN  540
CLAC_BACTK  HLNVMNGSSIFSNVTPATATSLDNLQSSDFYFESANFTSLGN---IVGVNFSGTA  590

cryla-105.pe  EVVIDREFELIPVUTATLEAEVNLERAKVNAALFTSTNQLGLKNTVTDVHIDQVSNLVYL  630
CLAC_BACTK  GVIDRFEFIPVUTATLEAEVNLERAKVNAALFTSTNQLGLKNTVTDVHIDQVSNLVYL  630

cryla-105.pe  SDEFCLDEKREISEKVKHAKRLSDERNLLQSNFKNRQPERGWSGTGTITIOGGDDVF  710
CLAC_BACTK  SDEFCLDEKREISEKVKHAKRLSDERNLLQSNFKNRQPERGWSGTGTITIOGGDDVF  710

cryla-105.pe  KENVYVLTSGTDECYPTVLYOKIDESKAKFTRVQLRGYIEDSDLEIYSIRYNAKHETV  770
CLAC_BACTK  KENVYVLTSGTDECYPTVLYOKIDESKAKFTRVQLRGYIEDSDLEIYSIRYNAKHETV  770

cryla-105.pe  NVPTGSLMPLSAQSPIGKCGEPCNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVG  830
CLAC_BACTK  NVPTGSLMPLSAQSPIGKCGEPCNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVG  830

cryla-105.pe  CTDLNLSLQVWIFIKITQDGHARLGNLFLEEKPLVGEALARKVPAEKKWDRKREKLEW  890
CLAC_BACTK  CTDLNLSLQVWIFIKITQDGHARLGNLFLEEKPLVGEALARKVPAEKKWDRKREKLEW  890

cryla-105.pe  ETNVAVKEKESVDIAFNQVQLOADNMIAMHAADKRVHSIREAYLPESLVPGVNA  950
CLAC_BACTK  ETNVAVKEKESVDIAFNQVQLOADNMIAMHAADKRVHSIREAYLPESLVPGVNA  950

cryla-105.pe  AIFEELEGRIFTASLYDKRWYINGDFNNLSCNVKGVHVDVEEQNNORSVLVVPWEA  1010
CLAC_BACTK  AIFEELEGRIFTASLYDKRWYINGDFNNLSCNVKGVHVDVEEQNNORSVLVVPWEA  1010

cryla-105.pe  EVSDEVPCRGYILRTVAKCEGEGGCTHEIANTDELKFSNVESELYPNNTVTC  1070
CLAC_BACTK  EVSDEVPCRGYILRTVAKCEGEGGCTHEIANTDELKFSNVESELYPNNTVTC  1070

cryla-105.pe  NDTVWNOEEYGAITSRRNGVNEAPSVPADYASVYEEKSYTGRNPNCEKADYTP  1130
CLAC_BACTK  NDTVWNOEEYGAITSRRNGVNEAPSVPADYASVYEEKSYTGRNPNCEKADYTP  1130

cryla-105.pe  LPVGVTKELEFPETDKWIEIGETGTFIVDSVELLIMEE  1170
CLAC_BACTK  LPVGVTKELEFPETDKWIEIGETGTFIVDSVELLIMEE  1170
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Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-04
MSL No. 20351
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cry1a-105.pep
TXM5:U87793_1
Description: U87793 Bacillus thuringiensis subsp. kurstaki Bacillus
thuringiensis kurstaki in
Accession/ID: U87793
=====General comments=====
LOCUS U87793.1 [BTU87793]
DEFINITION Bacillus thuringiensis kurstaki insecticidal delta-endotoxin . .
.
.
.
SCORES Initl: 3919 Initn: 7211 Opt: 7222 Z-score: 7964.5 E(): 0
>TXM5:U87793_1
Initn: 7211 Initl: 3919 Opt: 7222 Z-score: 7964.5 expect(): 0
Smith-Waterman score: 7222; 92.0% identity in 1182 aa overlap
(1-1177:1-1178)

cry1a-105.pe MDNPNINECIPNCLSNPEVEVLGGERIETGYTPIDISLSLTOQLLSEFVPGAGFVLGL 60
U87793_1 MDNPNINECIPNCLSNPEVEVLGGERIETGYTPIDISLSLTOQLLSEFVPGAGFVLGL 60
10 20 30 40 50
70 80 90 100 110 120

cry1a-105.pe VDIIWGIFGSPQWDAFLVQIEQLINQRIEEFARNQALSKLGLSNLYQIYAESFREWAD 120
U87793_1 VDIIWGIFGSPQWDAFLVQIEQLINQRIEEFARNQALSKLGLSNLYQIYAESFREWAD 120
70 80 90 100 110 120

cry1a-105.pe PTPNALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLSVVQAAHLHLSVLRDVSFVG 180
U87793_1 PTPNALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLSVVQAAHLHLSVLRDVSFVG 180
130 140 150 160 170 180

cry1a-105.pe RWGDDAATINSRYNDLTRIGNYTDHAVRWYNTGLERWGPDSRDMIRYNQFRRELTITV 240
U87793_1 RWGDDAATINSRYNDLTRIGNYTDHAVRWYNTGLERWGPDSRDMIRYNQFRRELTITV 240
190 200 210 220 230 240

cry1a-105.pe LDIVSLFPNVDGRTPIRTVSOLTREIYNPVLNFDGSPRGAQIGGSIIRSPHLMIDL 300
U87793_1 LDIVSLFPNVDGRTPIRTVSOLTREIYNPVLNFDGSPRGAQIGGSIIRSPHLMIDL 300
250 260 270 280 290 300

cry1a-105.pe NSITITVDARHGYWYSGHQIMASPVFGSGPEFTPLPYGTGNGNAAPQQRIVLAQLQGQYVR 360
U87793_1 NSITITVDARHGYWYSGHQIMASPVFGSGPEFTPLPYGTGNGNAAPQQRIVLAQLQGQYVR 360
310 320 330 340 350 360

cry1a-105.pe TLSSTLYRRPFGNIGNNOQLSVLDGTEFAYGTSNNLPSAVYKSGTVDSLDEIIPQNNNV 420
U87793_1 TLSSTLYRRPFGNIGNNOQLSVLDGTEFAYGTSNNLPSAVYKSGTVDSLDEIIPQNNNV 420
370 380 390 400 410 420

cry1a-105.pe PPRQGFHRLSHVSMFRSGFSNNSVIRAPMFSWIRHSAFNNIIASDSITQIPLVKAH 480
U87793_1 PPRQGFHRLSHVSMFRSGFSNNSVIRAPMFSWIRHSAFNNIIASDSITQIPLVKAH 480
430 440 450 460 470 480
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cry1a-105.pe TLQSGTIVVRGPGTGTGDLRETSGPPAVT--IVNINQLPQ---RYRARIYASTNL
U87793_1 FLNFGS-VISGPGTGTGDLRLNLSGNNIGNRGYIEVPHPFSTSTRVRVRYASVTPI
490 500 510 520 530

cry1a-105.pe RIYIVTAGERIFAGQFNKMTDGTDLTFQSFYATINTAFTIPMSQSFVTGADTFSSGN
U87793_1 HLNWNMGSSIFSNVTVPATSLDNLQSSDGYFESANFTSSLCN---IVGVNRFSGTA
540 550 560 570 580 590

cry1a-105.pe EYVYIDFELIIVTATLEAEYNLERAKAVNALFTSTNQLGKTNVTDYHDQVSNLVTYL
U87793_1 GVIIDRFEFIVTATLEAEYNLERAKAVNALFTSTNQLGKTNVTDYHDQVSNLVTYL
600 610 620 630 640 650

cry1a-105.pe SDFECLDEKRELSEKVKHAKRLSDERNLQDSNFKDINRQPERGGSGTGITIQGGDDVF
U87793_1 SDFECLDEKRELSEKVKHAKRLSDERNLQDSNFKDINRQPERGGSGTGITIQGGDDVF
660 670 680 690 700 710

cry1a-105.pe KENYVTLSTGTFDECYTYLYQKIDESKLKAPTIRYQLRGHIEDSQDLEIYSIRYNAKHETV
U87793_1 KENYVTLSTGTFDECYTYLYQKIDESKLKAPTIRYQLRGHIEDSQDLEIYSIRYNAKHETV
720 730 740 750 760 770

cry1a-105.pe NYPGTGSLWPLSQSPGKCGPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVG
U87793_1 NYPGTGSLWPLSQSPGKCGPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVG
780 790 800 810 820 830

cry1a-105.pe CTDLNEDLGWVWIFPKIKTODGHARLGNLEFLEEKPLVGEALARVRAEKWKRDREKLEW
U87793_1 CTDLNEDLGWVWIFPKIKTODGHARLGNLEFLEEKPLVGEALARVRAEKWKRDREKLEW
840 850 860 870 880 890

cry1a-105.pe ETNIVYKEAKESVDALFVNSQYDQLQADTNAMTHAADKRVHSIREAYLPELSVIEGVNA
U87793_1 ETNIVYKEAKESVDALFVNSQYDQLQADTNAMTHAADKRVHSIREAYLPELSVIEGVNA
900 910 920 930 940 950

cry1a-105.pe AIFELEGRIEFTAFSLYDARNYIKNGDFNGLSCWNVKGVHVDVEEQNNQSVLVVPEWEA
U87793_1 AIFELEGRIEFTAFSLYDARNYIKNGDFNGLSCWNVKGVHVDVEEQNNQSVLVVPEWEA
960 970 980 990 1000 1010

cry1a-105.pe EYSQEVRCRGYVILRVYKXEGYEGECVTIHEIENNTDELKFSNCVVEEIPNNVTVC
U87793_1 EYSQEVRCRGYVILRVYKXEGYEGECVTIHEIENNTDELKFSNCVVEEIPNNVTVC
1020 1030 1040 1050 1060 1070

cry1a-105.pe NQYTVNOQEYGGAYTSNRNGYNEAPSPADYASVYEKSYTDGRRPCFNFRGYDYTP
U87793_1 NQYTVNOQEYGGAYTSNRNGYNEAPSPADYASVYEKSYTDGRRPCFNFRGYDYTP
1080 1090 1100 1110 1120 1130

cry1a-105.pe NQYTVNOQEYGGAYTSNRNGYNEAPSPADYASVYEKSYTDGRRPCFNFRGYDYTP
U87793_1 NQYTVNOQEYGGAYTSNRNGYNEAPSPADYASVYEKSYTDGRRPCFNFRGYDYTP
1140 1150 1160 1170 1180 1190
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cr1a-105.pe LPVGVYKLEPPEDKWKIEIGETEGTIVDSVELLMEE
U87793_1 LPVGVYKLEPPEDKWKIEIGETEGTIVDSVELLMEE
1140 1150 1160 1170
cr1a-105.pep
TXN5:W73249_1
Description: M73249 Bacillus thuringiensis Bacillus thuringiensis gene,
complete CDS. 4/1993
Accession/ID: M73249
LOCUS M73249_1 [BACKURS]
DEFINITION Bacillus thuringiensis gene, complete cds.
SCORES Initl: 3919 Initn: 7204 Opt: 7215 Z-score: 7956.8 E(-): 0
>TXN5:W73249_1
initn: 7204 initl: 3919 opt: 7215 Z-score: 7956.8 expect (1): 0
Smith-Waterman score: 7215; 92.0% identity in 1182 aa overlap
(1-1177:1-1178)
cr1a-105.pe MDNPNNECIPYNCLSNPEVEVLGGERIETGTPIDISLSLTOFLSEFVPCAGVILGL
M73249_1 MDNPNNECIPYNCLSNPEVEVLGGERIETGTPIDISLSLTOFLSEFVPCAGVILGL
10 20 30 40 50 60
70 80 90 100 110 120
cr1a-105.pe VDIITWIGFGSQWDAFLVQIEQLINQRIEFAFNQAIKRLGSLNLYQIYAFSFEWAD
M73249_1 VDIITWIGFGSQWDAFLVQIEQLINQRIEFAFNQAIKRLGSLNLYQIYAFSFEWAD
70 80 90 100 110 120
cr1a-105.pe PTNPALREEMRIQFNDMSALTTAIPLLAVONVQVPLLSVYVQAAHLHSLVLDYSVFGQ
M73249_1 PTNPALREEMRIQFNDMSALTTAIPLLAVONVQVPLLSVYVQAAHLHSLVLDYSVFGQ
130 140 150 160 170 180
cr1a-105.pe RWGFDAAATINSRYNDLTRIGNYTHAVRWYNTGLERVWGPDSDRWYRINQFRRELTIV
M73249_1 RWGFDAAATINSRYNDLTRIGNYTHAVRWYNTGLERVWGPDSDRWYRINQFRRELTIV
190 200 210 220 230 240
cr1a-105.pe LDIIVSLFPNDYSRTYPIRTVSQLTREIYTNPVLENFDSFGSAQGTGSIIRSPHMDIL
M73249_1 LDIIVSLFPNDYSRTYPIRTVSQLTREIYTNPVLENFDSFGSAQGTGSIIRSPHMDIL
250 260 270 280 290 300
cr1a-105.pe NSIITYDAHREGYWSGHQIMASPVGSGPEFTPLPYGTMGNAAPQORIVAQLOGGYVR
M73249_1 NSIITYDAHREGYWSGHQIMASPVGSGPEFTPLPYGTMGNAAPQORIVAQLOGGYVR
310 320 330 340 350 360
cr1a-105.pe TILSSTLVRFPNIGINNQLSVLDGTEFAVGTSSNLPASVAVRKSGTSDLSLDEIPQNNNV
M73249_1 TILSSTLVRFPNIGINNQLSVLDGTEFAVGTSSNLPASVAVRKSGTSDLSLDEIPQNNNV
370 380 390 400 410 420
430 440 450 460 470 480

cr1a-105.pe PPRQGFSHRLSHVSMFASGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPLVKAH
M73249_1 PPRQGFSHRLSHVSMFASGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPLVKAH
430 440 450 460 470 480
cr1a-105.pe TLQSGTIVRGPGFTGDILRLRTSGPEAYT--IVNINQOLPQ--RYRARIYASTTNL
M73249_1 FLNNGS-VISGPGFTGDILRLRTSGPEAYT--IVNINQOLPQ--RYRARIYASTTNL
490 500 510 520 530
cr1a-105.pe RIYTVVAGERIFAGQFNKMTDGTDELTFQSFSAITINTAFTPFMSQSFVGTGADTFSSGN
M73249_1 HLNVMNGSSIFSNTPATATSLDNLQSSDFGYFESANAFSTSLGN--IVGVNFSGTA
540 550 560 570 580 590
cr1a-105.pe EYVIOREFELIPVTATLEAEVNLERAQKAVNALFTSTNOLGLXNTVDYHIDQVSNLTYL
M73249_1 GVIIIDREFEIPVTATLEAEVNLERAQKAVNALFTSTNOLGLXNTVDYHIDQVSNLTYL
600 610 620 630 640 650
cr1a-105.pe SDFECLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWSGTGITIQGGDDVF
M73249_1 SDFECLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWSGTGITIQGGDDVF
660 670 680 690 700 710
cr1a-105.pe KENVILSGTDECPYLYQIKIDESKUKATRIQLRGVIEDSQDLEIYSIRYNAKHTV
M73249_1 KENVILSGTDECPYLYQIKIDESKUKATRIQLRGVIEDSQDLEIYSIRYNAKHTV
720 730 740 750 760 770
cr1a-105.pe NVQSGTSAQSPICGCGPNRCAPHLEWNPDLDCSCROGECAHSHHFSLDIDVG
M73249_1 NVQSGTSAQSPICGCGPNRCAPHLEWNPDLDCSCROGECAHSHHFSLDIDVG
780 790 800 810 820 830
cr1a-105.pe CTDLNEDSIVVYKIKYDQVTHIRIGNLEFLENPLVGEALARVRAEKWKROKREKLEW
M73249_1 CTDLNEDSIVVYKIKYDQVTHIRIGNLEFLENPLVGEALARVRAEKWKROKREKLEW
840 850 860 870 880 890
cr1a-105.pe ETNIVVKEAKESVDALFVNSQVDLQANTIAMHAADKXHSISIRYAPLSVIRGVNA
M73249_1 ETNIVVKEAKESVDALFVNSQVDLQANTIAMHAADKXHSISIRYAPLSVIRGVNA
900 910 920 930 940 950
cr1a-105.pe AIFEELEGRIITAFSLYDARNYKNGDFNGLSCWNVKSHNDVFEONNQSIVYFWEA
M73249_1 AIFEELEGRIITAFSLYDARNYKNGDFNGLSCWNVKSHNDVFEONNQSIVYFWEA
960 970 980 990 1000 1010
cr1a-105.pe EYVSOVRVPCGRGIVLTAAYKEGEGECVTIHEINNNTDELKFSNCEEIYFNNTVC
M73249_1 EYVSOVRVPCGRGIVLTAAYKEGEGECVTIHEINNNTDELKFSNCEEIYFNNTVC
1020 1030 1040 1050 1060 1070
1080 1090 1100 1110 1120 1130

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cryla-105.pe NDYVNOBEYGGAYTSBNGYNEAPSVADYASVYEKSYDGRBNCENRGYRDYTP
W73249_1 1080 1090 1100 1110 1120 1130
cryla-105.pe LPVGYVTRELFFPETDKWIEIGETGTFIVDSVELLMEE
W73249_1 1140 1150 1160 1170
LPVGYVTRELFFPETDKWIEIGETGTFIVDSVELLMEE
Description: Q45768 bacillus thuringiensis. hypothetical 133.3 kda protein.
Accession/ID: Q45768
ID Q45768 PRELIMINARY;
AC Q45768; . . .

SCORES Init1: 3919 Initn: 7204 Opt: 7215 Z-score: 7956.8 E(): 0
>>TXNS:Q45768
Initn: 7204 init1: 3919 opt: 7215 Z-score: 7956.8 expect(): 0
Smith-Waterman score: 7215; 92.0% identity in 1182 aa overlap
(1-1177:1-1178)

cryla-105.pe MDNNPNIENICIPYCNLSNPEVEVLGERIETGYTPIDISLITQFLSEFVPGAGFVLGL
Q45768 10 20 30 40 50 60
MDNNPNIENICIPYCNLSNPEVEVLGERIETGYTPIDISLITQFLSEFVPGAGFVLGL
cryla-105.pe VDIINGIFGPSQWDAFLVQIEQLINQRIIEEFARNQAISRLGLSNLYQIYAESFREWAD
Q45768 70 80 90 100 110 120
VDIINGIFGPSQWDAFLVQIEQLINQRIIEEFARNQAISRLGLSNLYQIYAESFREWAD
cryla-105.pe PTNPALREEMRIQFNDWNSALTTAIPLEAVONQVPLSVYVQAANHLSLVLRDVSFVQ
Q45768 130 140 150 160 170 180
PTNPALREEMRIQFNDWNSALTTAIPLEAVONQVPLSVYVQAANHLSLVLRDVSFVQ
cryla-105.pe RWGFDAAATNSRYNDLTRILGNHTYDVAVRWYNTGLERVWGPDSRDWRYNQFRRELTIV
Q45768 190 200 210 220 230 240
RWGFDAAATNSRYNDLTRILGNHTYDVAVRWYNTGLERVWGPDSRDWRYNQFRRELTIV
cryla-105.pe LDIVSLFENYDSRTYPIRTVQSOLTREIYNPVENFDGSRSAQIGSIRSHLMDIL
Q45768 250 260 270 280 290 300
LDIVSLFENYDSRTYPIRTVQSOLTREIYNPVENFDGSRSAQIGSIRSHLMDIL
cryla-105.pe NSITTYTDAHRGYWWSGHQINWASPVGSGPEFTFLYGTMGNAAPQORIWAQLGQGVYR
Q45768 310 320 330 340 350 360
NSITTYTDAHRGYWWSGHQINWASPVGSGPEFTFLYGTMGNAAPQORIWAQLGQGVYR

cryla-105.pe TLSTLYRRPFNIGINNQLSVLDCTEFAYGTSSNLSAVYRSGTVDSLDLDEIPQNNNV
Q45768 370 380 390 400 410 420
TLSTLYRRPFNIGINNQLSVLDCTEFAYGTSSNLSAVYRSGTVDSLDLDEIPQNNNV
cryla-105.pe PPROGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIASDSITQIPLVKAH
Q45768 430 440 450 460 470 480
PPROGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIASDSITQIPLVKAH
cryla-105.pe TLQSGTTVVRGPGFTGGDILRRTSGGPFAT--IVNINGQLPQ---RYRARIYASTTNL
Q45768 490 500 510 520 530
FLNNGS-VISGFGFTGGDLVRLNSSGNINQNGYIEVPIHFPSTSTRYRVRYASVTPI
cryla-105.pe RIYVTVAGERIPAGOFNKMTDGTPLTFOSFSYATINTAFTFPMSSOSFTVGADTFSSGN
Q45768 540 550 560 570 580 590
HLNVWGNSSIFSNVTVPATATSLDNLOSDFGYPESANAFSTSLGN---IVGVNFSGTA
cryla-105.pe EYIDREFELIPVATLEAEYNLERAQKAVNALFTSTNQLGKTNVTDYHIDQVSNLVTYL
Q45768 600 610 620 630 640 650
GVIIIDREFELIPVATLEAEYNLERAQKAVNALFTSTNQLGKTNVTDYHIDQVSNLVTYL
cryla-105.pe SDEFLDKREISEKVKHAKELSDSNFKDINRPERGWSGSGITIQGDDVF
Q45768 660 670 680 690 700 710
SDEFLDKREISEKVKHAKELSDSNFKDINRPERGWSGSGITIQGDDVF
cryla-105.pe KENVTLTSGTDFDECYPTLYQKIDESKLAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
Q45768 720 730 740 750 760 770
KENVTLTSGTDFDECYPTLYQKIDESKLAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
cryla-105.pe NVPGTSLMPLSAQSPICKCEPNRCAPHLEWNPDLDCSDGKCAHSHHFSLDIDVG
Q45768 780 790 800 810 820 830
NVPGTSLMPLSAQSPICKCEPNRCAPHLEWNPDLDCSDGKCAHSHHFSLDIDVG
cryla-105.pe CTDLNEGLGVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARVKAERKWKREKLEW
Q45768 840 850 860 870 880 890
CTDLNEGLGVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARVKAERKWKREKLEW
cryla-105.pe ETNIVYKEAKESVDALFVNSQDQLQADTNIAHIAADKRVHSTREAYLPESLVPGVNA
Q45768 900 910 920 930 940 950
ETNIVYKEAKESVDALFVNSQDQLQADTNIAHIAADKRVHSTREAYLPESLVPGVNA
cryla-105.pe AIFEELEGRIFTAFSLYDARNVKNKGDFNNGISCNWVKGVHVDVEEQNNORSVLVVPWEA
Q45768 960 970 980 990 1000 1010
AIFEELEGRIFTAFSLYDARNVKNKGDFNNGISCNWVKGVHVDVEEQNNORSVLVVPWEA
cryla-105.pe AIFEELEGRIFTAFSLYDARNVKNKGDFNNGISCNWVKGVHVDVEEQNNORSVLVVPWEA
Q45768 1020 1030 1040 1050 1060 1070
AIFEELEGRIFTAFSLYDARNVKNKGDFNNGISCNWVKGVHVDVEEQNNORSVLVVPWEA

cry1a-105.pe EVSQEVCPQGTNRVATYKGYGECVTHIEIENNTDELKFNCEVEEIPNNVTTC
Q45768 EYSQVAVGPGRGYILNVAKEGYGECVTHIEIENNTDELKFNCEVEEIPNNVTTC
1020 1030 1040 1050 1060 1070

cry1a-105.pe NDYNNQYGVGATSENGYNEAPSVAASVYEEKSYDGRRENCFENRGYRDYTP
Q45768 NDYVNOEEGATISNRKATNENSVPADYATVYEEKSYDGRRENCFENRGYRDYTP
1080 1090 1100 1110 1120 1130

cry1a-105.pe LPGVYTKELVFFETDKVMEISGTEGTVDSNELLMEE
Q45768 LPGVYTKELVFFETDKVMEISGTEGTVDSNELLMEE
1140 1150 1160 1170

cry1a-105.pe
TXN5: Q9R826

Description: Q9R826 bacillus thuringiensis. crystal toxin protein

Accession/ID: Q9R826

ID Q9R826 PRELIMINARY; PRT: 1178 AA.

AC Q9R826;

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

SCORES Init1: 3919 Initn: 7189 Opt: 7200 z-score: 7940.3 E(): 0
>>TXN5-Q9R826
Initn: 7189 Init1: 3919 Opt: 7200 Z-score: 7940.3 expect(): 0
Smith-Waterman score: 7200; 91.8% identity in 1182 aa overlap
(1-1177:1-1178)

cry1a-105.pe MDNNPINECIPNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVFGAGFVLGL
Q9R826 MDNNPINECIPNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVFGAGFVLGL
10 20 30 40 50 60

cry1a-105.pe VDIINGIFGFSQWDAFLVQIEQLINQRIEEFARNQALSRLEGLSNLYQIYAESFREWEAD
Q9R826 VDIINGIFGFSQWDAFLVQIEQLINQRIEEFARNQALSRLEGLSNLYQIYAESFREWEAD
70 80 90 100 110 120

cry1a-105.pe PTFPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAAHLNLSVLRDVSVFQ
Q9R826 PTFPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAAHLNLSVLRDVSVFQ
130 140 150 160 170 180

cry1a-105.pe RWGFDAAATNSRYNDLTRLIGNYTHAVRWYNTGLERWGPDSRDWRINQFRRELTIV
Q9R826 RWGFDAAATNSRYNDLTRLIGNYTHAVRWYNTGLERWGPDSRDWRINQFRRELTIV
190 200 210 220 230 240

cry1a-105.pe LDIVSLFPNDSRTYPIRTYSQLTREIYNVLENFDFGSRGSAQIGERSIRSPHLMIDL
Q9R826 LDIVSLFPNDSRTYPIRTYSQLTREIYNVLENFDFGSRGSAQIGERSIRSPHLMIDL
250 260 270 280 290 300

cry1a-105.pe LDIVSLFPNDSRTYPIRTYSQLTREIYNVLENFDFGSRGSAQIGERSIRSPHLMIDL
Q9R826 LDIVSLFPNDSRTYPIRTYSQLTREIYNVLENFDFGSRGSAQIGERSIRSPHLMIDL
310 320 330 340 350 360

cry1a-105.pe NSITITDHRGEYTWGSHQIMASPVGFSGPEFTFPLLYGTWGNAAPOQRIVAQLGQGVYR
Q9R826 NSITITDHRGEYTWGSHQIMASPVGFSGPEFTFPLLYGTWGNAAPOQRIVAQLGQGVYR
310 320 330 340 350 360

cry1a-105.pe TLSSTLYRRPFNIGINNQLSLVDGTEFAYGTSSNLPASVYRKSGTVDLSLEIPQNNV
Q9R826 TLSSTLYRRPFNIGINNQLSLVDGTEFAYGTSSNLPASVYRKSGTVDLSLEIPQNNV
370 380 390 400 410 420

cry1a-105.pe PPRQGFSHRLSHVSMFRSGSSNSVSIIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGN
Q9R826 PPRQGFSHRLSHVSMFRSGSSNSVSIIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGN
430 440 450 460 470 480

cry1a-105.pe TLOSSTTVVRGPGFTGGDILARTSGGPFAYT-IIVNINQOLPO---RYRARIYASTTNL
Q9R826 TLOSSTTVVRGPGFTGGDILARTSGGPFAYT-IIVNINQOLPO---RYRARIYASTTNL
490 500 510 520 530

cry1a-105.pe RIYTVAGERIFAGQFNKMTDGLTFTQSFYATINTAFTFPMSSQSTVGAADTFSSGN
Q9R826 RIYTVAGERIFAGQFNKMTDGLTFTQSFYATINTAFTFPMSSQSTVGAADTFSSGN
540 550 560 570 580 590

cry1a-105.pe EVADRFEITPVATLEAEYNLEAQAQVNAVNLFTSTNOLGKTNVTDYHIDQVSNLVTYL
Q9R826 EVADRFEITPVATLEAEYNLEAQAQVNAVNLFTSTNOLGKTNVTDYHIDQVSNLVTYL
600 610 620 630 640 650

cry1a-105.pe SDPCLDEKEISENFKHANLSBERNLLQDSNFMKDINRQPERGWGSGTGITIQGDDVF
Q9R826 SDPCLDEKEISENFKHANLSBERNLLQDSNFMKDINRQPERGWGSGTGITIQGDDVF
660 670 680 690 700 710

cry1a-105.pe KENYVTLSEFECYPTKQVQDESGLKATYERQOLGYIEDSODLEIYSIRYNAKHTV
Q9R826 KENYVTLSEFECYPTKQVQDESGLKATYERQOLGYIEDSODLEIYSIRYNAKHTV
720 730 740 750 760 770

cry1a-105.pe NVPYGTSLWPLSAQSPIGKCGEPNRCAPLEWNPJDCSCRDGKSNHSHFSLDIDVG
Q9R826 NVPYGTSLWPLSAQSPIGKCGEPNRCAPLEWNPJDCSCRDGKSNHSHFSLDIDVG
780 790 800 810 820 830

cry1a-105.pe CTDLNEDLGWVIFIKITQDGHARLGNLEFLEKEPLVGEALRVNLEKSWMDKREJEN
Q9R826 CTDLNEDLGWVIFIKITQDGHARLGNLEFLEKEPLVGEALRVNLEKSWMDKREJEN
840 850 860 870 880 890

cry1a-105.pe ETNIVYKEAKESVDALFVNSOYDQLOQADTNIAHAAKRVHSIREAYLPESLVPGVNA
Q9R826 ETNIVYKEAKESVDALFVNSOYDQLOQADTNIAHAAKRVHSIREAYLPESLVPGVNA
900 910 920 930 940 950

cry1a-105.pe ETNIVYKEAKESVDALFVNSOYDQLOQADTNIAHAAKRVHSIREAYLPESLVPGVNA
Q9R826 ETNIVYKEAKESVDALFVNSOYDQLOQADTNIAHAAKRVHSIREAYLPESLVPGVNA
960 970 980 990 1000 1010

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cryla-105.pe LDIVSLFPNYDSRTPTPTVTSQULTRIITYNPVLENFQDPSRFGSAQIGESIRSPHLMJLII
AJI30970_1 LDIVSLFPNYDSRTPTPTVTSQULTRIITYNPVLENFQDPSRFGSAQIGESIRSPHLMJLII
250 260 270 280 290 300
cryla-105.pe NSIITVDAHRGEYWSGQIMASPVGFSGPEFTFLPYGTMGNAAPQORIVAAQLQGQVYR
AJI30970_1 NSIITVDAHRGEYWSGQIMASPVGFSGPEFTFLPYGTMGNAAPQORIVAAQLQGQVYR
310 320 330 340 350 360
cryla-105.pe TLSSTLYRRFPNIGINNQLSVLDGTEFAYGTSNNLPSAVYRSGTVDSLDEIPPONNVV
AJI30970_1 TLSSTLYRRFPNIGINNQLSVLDGTEFAYGTSNNLPSAVYRSGTVDSLDEIPPONNVV
370 380 390 400 410 420
cryla-105.pe PPRQGFSHRLSHVSMFRSGNSGVSIIIRAPMFSWIHRSAEFNIIIASDSITQIPLVKAAH
AJI30970_1 PPRQGFSHRLSHVSMFRSGNSGVSIIIRAPMFSWIHRSAEFNIIIASDSITQIPLVKAAH
430 440 450 460 470 480
cryla-105.pe TLOSGTIVRGPGFTGGDILIRTSGGPFAYT--IYVINGQLPQ---RYPARIRYASNTNL
AJI30970_1 TLOSGTIVRGPGFTGGDILIRTSGGPFAYT--IYVINGQLPQ---RYPARIRYASNTNL
490 500 510 520 530
cryla-105.pe RIYTVAGERIFAGFNKMTDGLPTFQFSYATINTATFTPMSSGTSFTVCAGDFSSGN
AJI30970_1 RIYTVAGERIFAGFNKMTDGLPTFQFSYATINTATFTPMSSGTSFTVCAGDFSSGN
540 550 560 570 580 590
cryla-105.pe HLVNWNCGNSISFNTVPATSLDNLQSDGFCYFESANATSSIGN--IYGVNRFSGTGA
AJI30970_1 HLVNWNCGNSISFNTVPATSLDNLQSDGFCYFESANATSSIGN--IYGVNRFSGTGA
540 550 560 570 580 590
cryla-105.pe EYVIDRFEIPIVATLEAEYNLERAKQAVNALFTSTNQLGKNTVDYHI DOVSNLVTYL
AJI30970_1 EYVIDRFEIPIVATLEAEYNLERAKQAVNALFTSTNQLGKNTVDYHI DOVSNLVTYL
600 610 620 630 640 650
cryla-105.pe SDFECLDKRELSKVKHAKLSDENLQSDNFKDINROPERGWGSGTGITIOGGDDVF
AJI30970_1 SDFECLDKRELSKVKHAKLSDENLQSDNFKDINROPERGWGSGTGITIOGGDDVF
660 670 680 690 700 710
cryla-105.pe KENYVTLTSGTFDECPTYLYOKIDESKKAFTRYQLRGYIEDSODLEIYSIRYNAKHETV
AJI30970_1 KENYVTLTSGTFDECPTYLYOKIDESKKAFTRYQLRGYIEDSODLEIYSIRYNAKHETV
720 730 740 750 760 770
cryla-105.pe NVPQTGSLMPLSAQSPICKGCEPNRCAPLHWNPLDSCRDEKCAHSHHFSLSLIDVG
AJI30970_1 NVPQTGSLMPLSAQSPICKGCEPNRCAPLHWNPLDSCRDEKCAHSHHFSLSLIDVG
780 790 800 810 820 830
cryla-105.pe CTDLNEDLGWVWIFIKITQDGHARLGNLFELEKPLVGEALARVKAEEKWRDKREKLEW
AJI30970_1 CTDLNEDLGWVWIFIKITQDGHARLGNLFELEKPLVGEALARVKAEEKWRDKREKLEW
840 850 860 870 880 890
cryla-105.pe 900 910 920 930 940 950

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cry1a-105.pe ETTNIVYKAEKESVDNFVNSQYDQLOADTNMIAMHAAKRVHSTREAYLPELSVPGVNA
AJ130970_1 ETTNIVYKAEKESVDNFVNSQYDQLOADTNMIAMHAAKRVHSTREAYLPELSVPGVNA
900 910 920 930 940 950

cry1a-105.pe ALFEELEGRFIFSLYDARVINKNGFNGLSCMNKGVHVDVEEQNQSVLVVPEWEA
AJ130970_1 ALFEELEGRFIFSLYDARVINKNGFNGLSCMNKGVHVDVEEQNQSVLVVPEWEA
960 970 980 990 1000 1010

cry1a-105.pe EYSQEVRCVCGRYVILRVAYKYGEGCTHIEENNTDEKSNVCEVEEIPNNVTVC
AJ130970_1 EYSQEVRCVCGRYVILRVAYKYGEGCTHIEENNTDEKSNVCEVEEIPNNVTVC
1020 1030 1040 1050 1060 1070

cry1a-105.pe NDYTYNOEYGGATSRNGYNEAPSVPADVASVEENYTDGRENPCNRYRNTVP
AJ130970_1 NDYTYNOEYGGATSRNGYNEAPSVPADVASVEENYTDGRENPCNRYRNTVP
1080 1090 1100 1110 1120 1130

cry1a-105.pe LPGVYVTELEYPFETDKWIEIGETGTFIVDSVELLMEE
AJ130970_1 LPGVYVTELEYPFETDKWIEIGETGTFIVDSVELLMEE
1140 1150 1160 1170

cry1a-105.pep
TXNS:M73248_1
Description: M73248 Bacillus thuringiensis Bacillus thuringiensis (cry1A(c)3)
gene, complete
Accession/ID: M73248
=====General comments=====

LOCUS M73248.1 (BACCRYIACC)
DEFINITION Bacillus thuringiensis (cry1A(c)3) gene, complete CDS. . . .
(1-1177:1-1177)

SCORES Init1: 6688 Initn: 6688 Opt: 7185 Z-score: 7923.7 E(): 0
>>TXN5:M73248_1
initn: 6688 init1: 6688 opt: 7185 Z-score: 7923.7 expect(): 0
Smith-Waterman score: 7185; 91.7% identity in 1182 aa overlap
(1-1177:1-1177)

cry1a-105.pe MDNNPINCIPYCNCLNSPEVILGGERIETGYTPIDISLSLTFQFLSEFVPGAGFVLGL
M73248_1 MDNNPINCIPYCNCLNSPEVILGGERIETGYTPIDISLSLTFQFLSEFVPGAGFVLGL
70 80 90 100 110 120

cry1a-105.pe VDIWIFGPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLSNLYQIYAESFREWEAD
M73248_1 VDIWIFGPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLSNLYQIYAESFREWEAD
130 140 150 160 170 180

cry1a-105.pe PTNPALREEMRIQFNDMNSALTITPAFLAVQNYQVPLISVVVOAANHLISVLRDVSFVGQ
M73248_1 PTNPALREEMRIQFNDMNSALTITPAFLAVQNYQVPLISVVVOAANHLISVLRDVSFVGQ
190 200 210 220 230 240

cry1a-105.pe RWGFDAAATINSRVNDLTRIGNVTDHAVRWYNTGLERVAGPDSRDWIRYNOFRELTIV
M73248_1 RWGFDAAATINSRVNDLTRIGNVTDHAVRWYNTGLERVAGPDSRDWIRYNOFRELTIV
190 200 210 220 230 240

cry1a-105.pe LDIVSFFPNYSRYPRTVQSQTREITNTVPLENFGSGFRSAQIEGSIIRSHPLMDIIL
M73248_1 LDIVSFFPNYSRYPRTVQSQTREITNTVPLENFGSGFRSAQIEGSIIRSHPLMDIIL
250 260 270 280 290 300

cry1a-105.pe NSITITVDHARGVYWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQORI VAQLGQGVYR
M73248_1 NSITITVDHARGVYWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQORI VAQLGQGVYR
310 320 330 340 350 360

cry1a-105.pe TLSSTLYRRPFNIGINNQQLSVLDTGTFAYGTSSNLPASVYRKSGTVDSLDEIIPPQNNV
M73248_1 TLSSTLYRRPFNIGINNQQLSVLDTGTFAYGTSSNLPASVYRKSGTVDSLDEIIPPQNNV
370 380 390 400 410 420

cry1a-105.pe PPRQGSFRLSHVSMFRSG-SSSSSVIIIPAPFMSWIRHSAEFNNIIASDSITQIPAVKGN
M73248_1 PPRQGSFRLSHVSMFRSG-SSSSSVIIIPAPFMSWIRHSAEFNNIIASDSITQIPAVKGN
430 440 450 460 470 480

cry1a-105.pe TLRGTTVVRGPGFTGGDILARTSGGPFAYT--IVNNGQLPQ---RYPARIRYASTNLL
M73248_1 TLRGTTVVRGPGFTGGDILARTSGGPFAYT--IVNNGQLPQ---RYPARIRYASTNLL
490 500 510 520 530 540

cry1a-105.pe RIRYPARIRYASTNLLTGTGPFQSFYATINTAFTFPMSSQSFYVAGDTFSSGN
M73248_1 RIRYPARIRYASTNLLTGTGPFQSFYATINTAFTFPMSSQSFYVAGDTFSSGN
550 560 570 580 590 600

cry1a-105.pe EYVIDRFEIPVATLEASVYPAKAVNALFTSTNQLGKTNVDYHIDQVSNLVTYL
M73248_1 EYVIDRFEIPVATLEASVYPAKAVNALFTSTNQLGKTNVDYHIDQVSNLVTYL
610 620 630 640 650 660

cry1a-105.pe SDEFCLDEKLESEKVKHAKRLSDRNLQDSNFYATNROPKRGSGSLITIOGGDDVF
M73248_1 SDEFCLDEKLESEKVKHAKRLSDRNLQDSNFYATNROPKRGSGSLITIOGGDDVF
660 670 680 690 700 710

cry1a-105.pe KENVYVLSGTFDECYPTLYLQKIDESKLKAFTRYQLRGYEDSDLEIYVYAKHETV
M73248_1 KENVYVLSGTFDECYPTLYLQKIDESKLKAFTRYQLRGYEDSDLEIYVYAKHETV
720 730 740 750 760 770

cry1a-105.pe NYVFGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGEKCAHHSHHFSNDING
M73248_1 NYVFGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGEKCAHHSHHFSNDING
780 790 800 810 820 830

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cry1a-105.pe CTDLNEDLGWVIFKIKTODGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
M73248_1 CTDLNEDLGWVIFKIKTODGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
          840 850 860 870 880 890
cry1a-105.pe ENINIVYKAKESVDALFVNSQYDQLOADNTIAMHAADKRVHSIREAYLPELSVIPGVNA
M73248_1 ENINIVYKAKESVDALFVNSQYDQLOADNTIAMHAADKRVHSIREAYLPELSVIPGVNA
          900 910 920 930 940 950
cry1a-105.pe AIFEELLEGRIITAFESLYDARNVKNKGFNNGLSVMVKGHVDEVEQNNQRNSVLVVPWEA
M73248_1 AIFEELLEGRIITAFESLYDARNVKNKGFNNGLSVMVKGHVDEVEQNNQRNSVLVVPWEA
          960 970 980 990 1000 1010
cry1a-105.pe EYSQEVRCPCRGYILRVATAYKEGEGECVTHIEIENNIDELKFSNCVEEIEYPNNVTVC
M73248_1 EYSQEVRCPCRGYILRVATAYKEGEGECVTHIEIENNIDELKFSNCVEEIEYPNNVTVC
          1020 1030 1040 1050 1060 1070
cry1a-105.pe NDVTYNQEEYGGAYTSNRNGYNEAPSVADVASVYEKSYTDGRENPCFENRGYDYTP
M73248_1 NDVTYNQEEYGGAYTSNRNGYNEAPSVADVASVYEKSYTDGRENPCFENRGYDYTP
          1080 1090 1100 1110 1120 1130
cry1a-105.pe LPVGVTYKELGYFFETDKWIEIGETGTFIVDSVELLMEE
M73248_1 LPVGVTYKELGYFFETDKWIEIGETGTFIVDSVELLMEE
          1140 1150 1160 1170
cry1a-105.pep
TXNS: Q03743
Description: Q03743 bacillus thuringiensis. 135 kda crystal protein (delta
endotoxin) (cry3ca
Accession/ID: Q03743
=====General comments=====
ID Q03743 PRELIMINARY; PRT: 1177 AA.
AC Q03743; . . .
SCORES Init1: 6688 Initn: 6688 Opt: 7185 z-score: 7923.7 E(): 0
>>TXNS-Q03743
Initn: 6688 Init1: 6688 Opt: 7185 z-score: 7923.7 expect(): 0
Smith-Waterman score: 7185; 91.% identity in 1182 aa overlap
(1-1177:1-1177)
cry1a-105.pe MDNPNINECIPYNCLSNPEVEVLGGERIETGTPIDISLSLTQFLSEFVPGAGFVLGL
Q03743 MDNPNINECIPYNCLSNPEVEVLGGERIETGTPIDISLSLTQFLSEFVPGAGFVLGL
          10 20 30 40 50 60
cry1a-105.pe VDIINGIFGQSDAFVLQIEQLINQRIEEFARNQAIISRLGSLNLIQIYAESFREWEAD
Q03743 VDIINGIFGQSDAFVLQIEQLINQRIEEFARNQAIISRLGSLNLIQIYAESFREWEAD
          70 80 90 100 110 120
cry1a-105.pe
Q03743
          130 140 150 160 170 180
```

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cry1a-105.pe PTPALREEMRIQFNDMNSALTITAIPLFAVQNYQVPLLSVYVQAANLHLSVLSDVSFVGQ
Q03743 PTPALREEMRIQFNDMNSALTITAIPLFAVQNYQVPLLSVYVQAANLHLSVLSDVSFVGQ
          130 140 150 160 170 180
cry1a-105.pe RWGFDAATINSRYNDLRELIGNYTDHAYVNTGLERWVGPSQSDMIRYNQFRRELITLV
Q03743 RWGFDAATINSRYNDLRELIGNYTDHAYVNTGLERWVGPSQSDMIRYNQFRRELITLV
          190 200 210 220 230 240
cry1a-105.pe LDIVSLFPNYDSRTYPIRTVSQSLTREIYTNPVLENFQDSFRGSAQIEGSIKRSPLMDIL
Q03743 LDIVSLFPNYDSRTYPIRTVSQSLTREIYTNPVLENFQDSFRGSAQIEGSIKRSPLMDIL
          250 260 270 280 290 300
cry1a-105.pe NSIITITDAHREYVMSCHOIMASPVGFSQPEFTPELYGTNGVNAAPQORIVAOLGQVYR
Q03743 NSIITITDAHREYVMSCHOIMASPVGFSQPEFTPELYGTNGVNAAPQORIVAOLGQVYR
          310 320 330 340 350 360
cry1a-105.pe TLSSTLYRRPFPNIGINNQOLSVLDGTEFAYGTSSNLPASVYKSGTVDSLDEIPQNNNV
Q03743 TLSSTLYRRPFPNIGINNQOLSVLDGTEFAYGTSSNLPASVYKSGTVDSLDEIPQNNNV
          370 380 390 400 410 420
cry1a-105.pe PPROGFSHRLSHVSMFRSGFNSVSIIRAPMFSWIHRSAEFNIIIASDSITQIPLVKAH
Q03743 PPROGFSHRLSHVSMFRSGFNSVSIIRAPMFSWIHRSAEFNIIIASDSITQIPLVKAH
          430 440 450 460 470 480
cry1a-105.pe TLQSGTIVVRGPGFTGGDILRRTSGGPFAYT-IIVNINGQLPQ---RYRARIRYASTTNL
Q03743 FLFNGS-VISGEGFTGGDLVFLNSSGNIIQNEGYIEVPIHEPSTSTRYRVRYASVTPI
          490 500 510 520 530 540
cry1a-105.pe RIYTVVAGERIFAGQFNKMTDGLPTFOSFYATINTAFTFPMSSQSTTVGADTFSSGN
Q03743 HLNVMNGNSIFSNTPATATSLDNLQSDDFGYFESANAFSTSLGN---IVGVRNFSGTA
          540 550 560 570 580 590
cry1a-105.pe EVIDIDREFLIPVTATLEAYNLERAQKAVNALFTSTNOLGKTNVTDYHIDQVSNLVTYL
Q03743 GVILDRFEFIPVTATLEAYNLERAQKAVNALFTSTNOLGKTNVTDYHIDQVSNLVTYL
          600 610 620 630 640 650
cry1a-105.pe SDEFCLDEKRELSKVKYHAKLSDEKLNLDQSNFQDINRQPERGWGSGTGIITIQGDDVF
Q03743 SDEFCLDEKRELSKVKYHAKLSDEKLNLDQSNFQDINRQPERGWGSGTGIITIQGDDVF
          660 670 680 690 700 710
cry1a-105.pe KENVYTLSTGTFDECYPTLYOKIDESKLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
Q03743 KENVYTLSTGTFDECYPTLYOKIDESKLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
          720 730 740 750 760 770
cry1a-105.pe KENVYTLSTGTFDECYPTLYOKIDESKLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
Q03743 KENVYTLSTGTFDECYPTLYOKIDESKLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
          780 790 800 810 820 830
```

001
cry1a-105.pe NVPTGSLMPTARQSDIGKGEPRNRCAPLHWNPLDSCRDCEKCAHSHHFSLDIDVG
Q03743 NVPTGSLMPTARQSDIGKGEPRNRCAPLHWNPLDSCRDCEKCAHSHHFSLDIDVG
780 790 800 810 820 830
cry1a-105.pe CTDNEDGVWTFIKOCHGARLGNLEKEKPLGEALAVKKAEEKWDRKRELEW
Q03743 CTDNEDGVWTFIKOCHGARLGNLEKEKPLGEALAVKKAEEKWDRKRELEW
840 850 860 870 880 890
cry1a-105.pe ETNIVYKEAKESVDALFVNSQYDQLOQADTIAMAAADKRVHSIRAYLPESLVPVGVNA
Q03743 ETNIVYKEAKESVDALFVNSQYDQLOQADTIAMAAADKRVHSIRAYLPESLVPVGVNA
900 910 920 930 940 950
cry1a-105.pe AIPEELEGRIFTAFSLYDARNVKNKGFNNGLSQWNVKGVHVDVEEQNCKSLVVPKKEA
Q03743 AIPEELEGRIFTAFSLYDARNVKNKGFNNGLSQWNVKGVHVDVEEQNCKSLVVPKKEA
960 970 980 990 1000 1010
cry1a-105.pe EVSOEVRVCPGRGYILRVTAKEGYEGGCVTHIEIENNTDELKFSNCVEEYIPNTVTC
Q03743 EVSOEVRVCPGRGYILRVTAKEGYEGGCVTHIEIENNTDELKFSNCVEEYIPNTVTC
1020 1030 1040 1050 1060 1070
cry1a-105.pe NDYTVNOEEYGAYTSRNRGNEAPSVADYASVVEEKSYTDGRRNCPCEFRNGRYDTP
Q03743 NDYTVNOEEYGAYTSRNRGNEAPSVADYASVVEEKSYTDGRRNCPCEFRNGRYDTP
1080 1090 1100 1110 1120 1130
cry1a-105.pe LPVGYVTKELVFPETDKVWIEIGETGFIVDSVELLMEE
Q03743 LPVGYVTKELVFPETDKVWIEIGETGFIVDSVELLMEE
1140 1150 1160 1170
cry1a-105.pe LPVGYVTKELVFPETDKVWIEIGETGFIVDSVELLMEE
Q03743 LPVGYVTKELVFPETDKVWIEIGETGFIVDSVELLMEE
1180 1190 1200
cry1a-105.pe LPVGYVTKELVFPETDKVWIEIGETGFIVDSVELLMEE
Q03743 LPVGYVTKELVFPETDKVWIEIGETGFIVDSVELLMEE
1210 1220 1230
Description: Q45735 bacillus thuringiensis. delta-endotoxin. 6/2001
Accession/ID: Q45735
ID Q45735 PRELIMINARY; PRT; 1177 AA.
AC Q45735;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
=====General comments=====

SCORES Initl: 6670 Initn: 6670 Opt: 7167 z-score: 7903.9 E(): 0
>TXNS:Q45735
Initn: 6670 opt: 7167 z-score: 7903.9 expect(): 0
Smith-Waterman score: 7167; 91.6% identity in 1182 aa overlap
(1-1177;1-1177)

cry1a-105.pe MDNPNINECIPNCLSNPEVEVLGGERIETGTPTDIDSLTSLTFLISFVPGAGFVLGL
Q45735 MDNPNINECIPNCLSNPEVEVLGGERIETGTPTDIDSLTSLTFLISFVPGAGFVLGL
10 20 30 40 50 60
10 20 30 40 50 60
70 80 90 100 110 120

cry1a-105.pe VDIINGIFGSDWDAFLVOIQLINQRIEIEFARNQAIIRLEGLSLNLYIYIAESFREWEAD
Q45735 VDIINGIFGSDWDAFLVOIQLINQRIEIEFARNQAIIRLEGLSLNLYIYIAESFREWEAD
70 80 90 100 110 120
cry1a-105.pe PTNPALREEMRIQNDMNSALTALPLFAVONYOVPELLSVVQAANLHLSVLSDVSFQ
Q45735 PTNPALREEMRIQNDMNSALTALPLFAVONYOVPELLSVVQAANLHLSVLSDVSFQ
130 140 150 160 170 180
cry1a-105.pe RMGFDAAATINSRYNDLTRIGNYTDHARVWNTGLERVMGPDSDRWIRYNOFRRELTIV
Q45735 RMGFDAAATINSRYNDLTRIGNYTDHARVWNTGLERVMGPDSDRWIRYNOFRRELTIV
190 200 210 220 230 240
cry1a-105.pe LDIVSLFPNDYSRTYPIRTVSQLTREIYTNPVLNFDGSRGSAAGIEGSIIRSPHLMIDL
Q45735 LDIVSLFPNDYSRTYPIRTVSQLTREIYTNPVLNFDGSRGSAAGIEGSIIRSPHLMIDL
250 260 270 280 290 300
cry1a-105.pe NSITIIDDAHGEYWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQORIVAOQLGQVYR
Q45735 NSITIIDDAHGEYWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQORIVAOQLGQVYR
310 320 330 340 350 360
cry1a-105.pe TISSFTYPPENGINNOQLSLDGTPEAYTSNLPSSAVYRKSGTVDLSDEIPPNNNV
Q45735 TISSFTYPPENGINNOQLSLDGTPEAYTSNLPSSAVYRKSGTVDLSDEIPPNNNV
370 380 390 400 410 420
cry1a-105.pe PPQGFSGSHVSRSSNSVSIIIRAPMFSWIHRSAEFNNIIASDSITQIPVKAH
Q45735 PPQGFSGSHVSRSSNSVSIIIRAPMFSWIHRSAEFNNIIASDSITQIPVKAH
430 440 450 460 470 480
cry1a-105.pe TIOSGTTVWGHSTGTGDIKASGCPFAT--TUNINGQLPQ---RYRARIASITNL
Q45735 TIOSGTTVWGHSTGTGDIKASGCPFAT--TUNINGQLPQ---RYRARIASITNL
490 500 510 520 530
cry1a-105.pe RIYVTVAGERIFAGQFNKMTDGLITQSFATNTAFTFPNSQSSNVGADTFSSGN
Q45735 RIYVTVAGERIFAGQFNKMTDGLITQSFATNTAFTFPNSQSSNVGADTFSSGN
540 550 560 570 580 590
cry1a-105.pe EVVIDRFELIPVATLAEAYNLERAQKAVNALFTSNQISLRNTVDYHDAEINLVTVY
Q45735 EVVIDRFELIPVATLAEAYNLERAQKAVNALFTSNQISLRNTVDYHDAEINLVTVY
600 610 620 630 640 650
cry1a-105.pe SDEFCLEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWSGTITIQGGDVF
Q45735 SDEFCLEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWSGTITIQGGDVF
660 670 680 690 700 710
720 730 740 750 760 770

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cryla-105.pe KENVYLSGTDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLIYSIRYNAKHETV
Q45735 KENVYLSGTDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLIYSIRYNAKHETV
720 730 740 750 760 770

cryla-105.pe NVPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLDIDVG
Q45735 NVPGTSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLDIDVG
780 790 800 810 820 830

cryla-105.pe CTDLNEDLGWVWIFKIKTQGHARLGNLEFLEKPLVGEALARVKAEEKWRDKREKLEW
Q45735 CTDLNEDLGWVWIFKIKTQGHARLGNLEFLEKPLVGEALARVKAEEKWRDKREKLEW
840 850 860 870 880 890

cryla-105.pe ETNIVYKEAKESVDALFVNSQYDQLQADNTIAMTHAADKRVHGISREAYLPELSVIPGVNA
Q45735 ETNIVYKEAKESVDALFVNSQYDQLQADNTIAMTHAADKRVHGISREAYLPELSVIPGVNA
900 910 920 930 940 950

cryla-105.pe AIFEELEGRIFFAFSLYDARNVIKNGDFNNGLSQWNVKGVHDVEEQNNORSVIAVPEWEA
Q45735 AIFEELEGRIFFAFSLYDARNVIKNGDFNNGLSQWNVKGVHDVEEQNNORSVIAVPEWEA
960 970 980 990 1000 1010

cryla-105.pe EVSQEVRVCPGGRYILRVTAKEGEGCVTHIEIENNTDELKFSNCVEEIIYFNNTVTC
Q45735 EVSQEVRVCPGGRYILRVTAKEGEGCVTHIEIENNTDELKFSNCVEEIIYFNNTVTC
1020 1030 1040 1050 1060 1070

cryla-105.pe NDVTNQEYGGAYTSNRNGYNEAPSPADVASVYEKSYTDGRRNCPENRGYRDYTP
Q45735 NDVTNQEYGGAYTSNRNGYNEAPSPADVASVYEKSYTDGRRNCPENRGYRDYTP
1080 1090 1100 1110 1120 1130

cryla-105.pe LPVGVTKELEYFPETDKWIEIGETEGTFIVDSVELLLMEE
Q45735 LPVGVTKELEYFPETDKWIEIGETEGTFIVDSVELLLMEE
1140 1150 1160 1170

cryla-105.pep
TXN5.M35524_1

Description: M35524 Bacillus thuringiensis B.thuringiensis delta-endotoxin
gene, complete cds
Accession/ID: M35524
Locus M35524_1 [BACCRYIA]
DEFINITION B.thuringiensis delta-endotoxin gene, complete cds; . . .

SCORES Initl: 6670 Initn: 6670 Opt: 7167 Z-score: 7903.9 E(): 0
>TXN5:M35524_1
initn: 6670 initl: 6670 opt: 7167 Z-score: 7903.9 expect(): 0
Smith-Waterman score: 7167; 91.6% identity in 1182 aa overlap
(1-1177:1-1177)
```

```
cryla-105.pe MDNPNINECIPYNCISNPEVEVLGGRIETGYTIPIDISLSLTQFLLSFVFAGFVLGL
M35524_1 MDNPNINECIPYNCISNPEVEVLGGRIETGYTIPIDISLSLTQFLLSFVFAGFVLGL
10 20 30 40 50 60

cryla-105.pe VDIITWIFGGSQMDAPLVOIQEQLINORIEEFARNQAIISRIEGLISNLVYIYAESFREWEAD
M35524_1 VDIITWIFGGSQMDAPLVOIQEQLINORIEEFARNQAIISRIEGLISNLVYIYAESFREWEAD
70 80 90 100 110 120

cryla-105.pe PTNPALREEMRIQFNDMMSALTATPILFAVONQVPLLSVYVQAANHLHSLVRDVSFVGQ
M35524_1 PTNPALREEMRIQFNDMMSALTATPILFAVONQVPLLSVYVQAANHLHSLVRDVSFVGQ
130 140 150 160 170 180

cryla-105.pe PTNPALREEMRIQFNDMMSALTATPILFAVONQVPLLSVYVQAANHLHSLVRDVSFVGQ
M35524_1 PTNPALREEMRIQFNDMMSALTATPILFAVONQVPLLSVYVQAANHLHSLVRDVSFVGQ
130 140 150 160 170 180

cryla-105.pe RWGFDAAATINSRYNDLTRIGNYTHAVRWNTGLERVWGPDSDWIRYNQFRRELTITV
M35524_1 RWGFDAAATINSRYNDLTRIGNYTHAVRWNTGLERVWGPDSDWIRYNQFRRELTITV
190 200 210 220 230 240

cryla-105.pe LDIVSLFPNDVSRPTVIRTSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHMLDIL
M35524_1 LDIVSLFPNDVSRPTVIRTSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHMLDIL
250 260 270 280 290 300

cryla-105.pe NSITITVDAHRGYVWSHQIMASPVGSGPEFTPLYGTMGNAAPQOIRIVAQLOGGVYR
M35524_1 NSITITVDAHRGYVWSHQIMASPVGSGPEFTPLYGTMGNAAPQOIRIVAQLOGGVYR
310 320 330 340 350 360

cryla-105.pe TLSSFTVRRFPNIGINNQLSVLDGTFEYAGTSNNLPASAVYRKSGTVDLSDEIPQNNV
M35524_1 TLSSFTVRRFPNIGINNQLSVLDGTFEYAGTSNNLPASAVYRKSGTVDLSDEIPQNNV
370 380 390 400 410 420

cryla-105.pe PPRQGFGRHLSHVMSFRSGFNSSVSIIRAPMFSWTHRSAEFNNIIASDSITQIPLVKAH
M35524_1 PPRQGFGRHLSHVMSFRSGFNSSVSIIRAPMFSWTHRSAEFNNIIASDSITQIPLVKAH
430 440 450 460 470 480

cryla-105.pe TLQSGTVVPGFGTGGDLRLRTSGGPFAYT--IYVINGQLQFQ--RYRARIYASTNVL
M35524_1 TLQSGTVVPGFGTGGDLRLRTSGGPFAYT--IYVINGQLQFQ--RYRARIYASTNVL
490 500 510 520 530

cryla-105.pe RIYVTVAGERIFAGQNKMTDGTPLTFQSFVATINTAFTFPMSSQSFVGTGADTFSSGN
M35524_1 RIYVTVAGERIFAGQNKMTDGTPLTFQSFVATINTAFTFPMSSQSFVGTGADTFSSGN
540 550 560 570 580 590

cryla-105.pe HLVNWNMGSSIFSNTPATATSLDNLQSSDFGYFESANAFSTSLGN--IVGVYRPFSGTA
M35524_1 HLVNWNMGSSIFSNTPATATSLDNLQSSDFGYFESANAFSTSLGN--IVGVYRPFSGTA
540 550 560 570 580 590

cryla-105.pe EYVIDREFLIPVATLAEYNLERAQKAVNALFTSNQGLKTNVTYDHYHDQVSNLVYL
M35524_1 EYVIDREFLIPVATLAEYNLERAQKAVNALFTSNQGLKTNVTYDHYHDQVSNLVYL
600 610 620 630 640 650

cryla-105.pe GVIIDREFLIPVATLAEYNLERAQKAVNALFTSNQGLKTNVTYDHYHDQVSNLVYL
M35524_1 GVIIDREFLIPVATLAEYNLERAQKAVNALFTSNQGLKTNVTYDHYHDQVSNLVYL
600 610 620 630 640 650

cryla-105.pe GVIIDREFLIPVATLAEYNLERAQKAVNALFTSNQGLKTNVTYDHYHDQVSNLVYL
M35524_1 GVIIDREFLIPVATLAEYNLERAQKAVNALFTSNQGLKTNVTYDHYHDQVSNLVYL
660 670 680 690 700 710
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007
cry1a-105.pe SDFCLDEKRLSEKVKHAKRLSDERNLQDSNFKDINROPERGMGSGTITIGGGDDVF
M35524_1 SDFCLDEKRLSEKVKHAKRLSDERNLQDSNFKDINROPERGMGSGTITIGGGDDVF
710
cry1a-105.pe KENYVTSCTEDCEVPELYOKIDESKKAETRYOLRGYIESODLEIYSRYNAKHETV
M35524_1 KENYVTSCTEDCEVPELYOKIDESKKAETRYOLRGYIESODLEIYSRYNAKHETV
770
cry1a-105.pe NVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCGKCAHSHHFFSLDIDVG
M35524_1 NVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCGKCAHSHHFFSLDIDVG
830
cry1a-105.pe CTDLNEDLGWVWIFKIKTODGHARLGNLEFLEEKPLVGENLANKRAEKYARDREHIEW
M35524_1 CTDLNEDLGWVWIFKIKTODGHARLGNLEFLEEKPLVGENLANKRAEKYARDREHIEW
890
cry1a-105.pe ETNIVVYKEAKESVDALFVNSQYDQLQADNTIAMIHAADKRVHSIREAVLPELSVPGVNA
M35524_1 ETNIVVYKEAKESVDALFVNSQYDQLQADNTIAMIHAADKRVHSIREAVLPELSVPGVNA
950
cry1a-105.pe AIFEELEGRIFFATSLYDAARNVINGDFNGLSCWNVKHVDVVEEONQORSLVVPWEWA
M35524_1 AIFEELEGRIFFATSLYDAARNVINGDFNGLSCWNVKHVDVVEEONQORSLVVPWEWA
1010
cry1a-105.pe EVSQEVRVCPGRGVLAVTAYKEGCGCVTHIEIENNTDELKFSNCVEEIEIYNNVTVC
M35524_1 EVSQEVRVCPGRGVLAVTAYKEGCGCVTHIEIENNTDELKFSNCVEEIEIYNNVTVC
1070
cry1a-105.pe NDYTVNQEEYGGAYTSRNGYNEAPSPADYASVYEKSYTDGRNCPENRGYRDYTP
M35524_1 NDYTVNQEEYGGAYTSRNGYNEAPSPADYASVYEKSYTDGRNCPENRGYRDYTP
1130
cry1a-105.pe LPGVYKTELEFFETDKWIEIGETGTFIVDSVELLMEE
M35524_1 LPGVYKTELEFFETDKWIEIGETGTFIVDSVELLMEE
1170

Description: M65252 Bacillus thuringiensis Bacillus thuringiensis alesti delta
endotoxin gene
Accession/ID: M65252
*****General comments*****
LOCUS M65252_1 (BACENIAB)
DEFINITION Bacillus thuringiensis alesti delta endotoxin gene, complete cds. . .

SCORES Initl: 6520 Initn: 6986 Opt: 6987 2-score: 7705.2 E(): 0

>TXN5:M65252_1
Initn: 6986 Opt: 6987 2-score: 7705.2 expect(): 0
Smith-Waterman score: 6987; 88.3% identity in 1181 aa overlap
(1-1177:1-1181)
cry1a-105.pe MDNNPINEICIPVNCISLPEVEVLGERITGTPTIDISLSITOFLLSEFVPGAGFVLGL
M65252_1 MDNNPINEICIPVNCISLPEVEVLGERITGTPTIDISLSITOFLLSEFVPGAGFVLGL
10 20 30 40 50 60
cry1a-105.pe VDIIWGFQSQWDAFLVQIEQLINQRIEFARNQAIISRLSEGLSNLYQIYAEAFREWEAD
M65252_1 VDIIWGFQSQWDAFLVQIEQLINQRIEFARNQAIISRLSEGLSNLYQIYAEAFREWEAD
70 80 90 100 110 120
cry1a-105.pe PTNPFALREERNRQFNDMNSALTTPAIFLFAVQNYVPLISVYVQAVNLHLSVLDRVSEGG
M65252_1 PTNPFALREERNRQFNDMNSALTTPAIFLFAVQNYVPLISVYVQAVNLHLSVLDRVSEGG
130 140 150 160 170 180
cry1a-105.pe RWGFDAAITINSRYNDLTRLIGNYTDHAWRYNTGLERVWGPDSRDMRYNQFRRELTITV
M65252_1 RWGFDAAITINSRYNDLTRLIGNYTDHAWRYNTGLERVWGPDSRDMRYNQFRRELTITV
190 200 210 220 230 240
cry1a-105.pe LDIVSLFPNDSTRTYPIRTVSQLTREIYNPVLNFDGSPGSAQIEGSIIRSPHMDIL
M65252_1 LDIVSLFPNDSTRTYPIRTVSQLTREIYNPVLNFDGSPGSAQIEGSIIRSPHMDIL
250 260 270 280 290 300
cry1a-105.pe NSLTITIDANGGEYWSHQMASPVGSGPFTPLVGTMGNAAPQORIVAGLQGVYR
M65252_1 NSLTITIDANGGEYWSHQMASPVGSGPFTPLVGTMGNAAPQORIVAGLQGVYR
310 320 330 340 350 360
cry1a-105.pe TLISSTLRNFPNGINNCGLYDGTGFAYGTSSNLPSAVYKSGTVDSLDEIPQNNNV
M65252_1 TLISSTLRNFPNGINNCGLYDGTGFAYGTSSNLPSAVYKSGTVDSLDEIPQNNNV
370 380 390 400 410 420
cry1a-105.pe PPROGFSRHLVSHVMSFRSGFSNSGSTRAPMSWHSRPFNNVNSSTITDILVKAH
M65252_1 PPROGFSRHLVSHVMSFRSGFSNSGSTRAPMSWHSRPFNNVNSSTITDILVKAH
430 440 450 460 470 480
cry1a-105.pe TLQSGTIVVRGPGFTGGDILRRTSQGPAYTIWNGQILRSQRIARIRASITRIYVI
M65252_1 TLQSGTIVVRGPGFTGGDILRRTSQGPAYTIWNGQILRSQRIARIRASITRIYVI
490 500 510 520 530 540
cry1a-105.pe VAGERIFAGQFNKMTDGTDLTFQSFYATINTATTFPMSSOSTTCGATFFSGNEVND
M65252_1 VAGERIFAGQFNKMTDGTDLTFQSFYATINTATTFPMSSOSTTCGATFFSGNEVND
550 560 570 580 590 600
cry1a-105.pe IDGRPNQMGNSATMSSGNGSQSGSFTFTFPNFNGSSVFTLSAHVFNSGNEVID
M65252_1 IDGRPNQMGNSATMSSGNGSQSGSFTFTFPNFNGSSVFTLSAHVFNSGNEVID
610 620 630 640 650 660

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cryla-105.pe VAGRIAPGQNKIYKIDTGLTFOFSYATINTAFTPMSSQSFYVAGTSSGNEVYID
CIAE_BACTL IDGRIKNGFATMSGCGNQSOSFTFTFPFNSGSSVFTLSAHSVNGNEVYID
cryla-105.pe RFENIPVATLEAFLEPRAKAVNAFTSTNOLGLKTNVDHIDQVNLVYLSDEFEC
CIAE_BACTL RIEFVPAEVEAEVLENAQEAALFTSMQIKTKIDVDHIDQVNLVYLSDEFEC
cryla-105.pe LDEKREUSEKVKHAKLSDERNLSDNPNRGINKRDPDARGSTDIHQGDDVFEKNYV
CIAE_BACTL LDEKREUSEKVKHAKLSDERNLSDNPNRGINKRDPDARGSTDIHQGDDVFEKNYV
cryla-105.pe TLSCITFDECYTYLYOKIDESKKAFTYQLRGYEDSDLEIYSIRYVSHETVNRGT
CIAE_BACTL TLPGTFDECYTYLYOKIDESKKAFTYVELRGYIEDSDLEIYRYVSHETVNRGT
cryla-105.pe GSLMPLSAGSPIGKCEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSNIDGCTDIN
CIAE_BACTL GSLMPLSAGSPIGKCEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSNIDGCTDIN
cryla-105.pe EDLGVMWIFKIKTODGHARLGNLEFLEPELNGEALAKVKAEPKDFREKLEWETIV
CIAE_BACTL EDLGVMWIFKIKTODGHARLGNLEFLEPELNGEALAKVKAEPKDFREKLEWETIV
cryla-105.pe YKEAKESVDALFVNSQYDQLOADTNIAHAAKRVHIREAYLPELSVPGVNAAFEE
CIAE_BACTL YKEAKESVDALFVNSQYDQLOADTNIAHAAKRVHIREAYLPELSVPGVNAAFEE
cryla-105.pe LEGRIFTAFSLYDARNVINKGDFNGLSCMNKGVHDVVEEONNORSVLVPEWEAEVSQE
CIAE_BACTL LEGRIFTAFSLYDARNVINKGDFNGLSCMNKGVHDVVEEONNORSVLVPEWEAEVSQE
cryla-105.pe VRVCPGRGYLRVTAKEGYGEGCVTTHEIENNTDELKFSNCEVEEYNNVTVCNDYTV
CIAE_BACTL VRVCPGRGYLRVTAKEGYGEGCVTTHEIENNTDELKFSNCEVEEYNNVTVCNDYTV
cryla-105.pe NOEYGGAYTSNRGNNEAP-----SVDPADYASVYEKSYTDGRNCPFNKGIDYTPPL
CIAE_BACTL NOEYGGAYTSNRGNNEAP-----SVDPADYASVYEKSYTDGRNCPFNKGIDYTPPL
cryla-105.pe PVGVVTKLEYPETDKWVIEIGETGTFIVDSVLLMEE
CIAE_BACTL PVGVVTKLEYPETDKWVIEIGETGTFIVDSVLLMEE

cryla-105.pep
TXNS:Y09663_1
Description: Y09663 Bacillus thuringiensis B.thuringiensis mRNA for
delta-endotoxin. 1/2000
Accession/ID: Y09663
LOCUS Y09663.1 [BTRVNS3]
DEFINITION B.thuringiensis mRNA for delta-endotoxin.
SCORES Initl: 4298 Initn: 6544 Opt: 6844 Z-score: 7547.4 E(): 0
>TXNS:Y09663_1
Initn: 6544 Initl: 4298 Opt: 6844 Z-score: 7547.4 expect(): 0
Smith-Waterman score: 6844; 86.9% identity in 1179 aa overlap
(1-1177:1-1176)
cryla-105.pe MDNNPINECIPYCNLSNVEVEVLGERIETGTPIDISLSTQFLISEFVPGAGFVLGL
Y09663_1 MDNNPINECIPYCNLSNVEVEVLGERIETGTPIDISLSTQFLISEFVPGAGFVLGL
cryla-105.pe VDIINGIFGQSDAFVIOEQLINQRIEFPARNOAISLEGLSNLYQIYAESFREWEAD
Y09663_1 VDIINGIFGQSDAFVIOEQLINQRIEFPARNOAISLEGLSNLYQIYAESFREWEAD
cryla-105.pe FVNDALREMIQNDNMSALITATPAFVONVOVPLSVYVQANLHLSVLROVSFVQ
Y09663_1 FVNDALREMIQNDNMSALITATPAFVONVOVPLSVYVQANLHLSVLROVSFVQ
cryla-105.pe RWEADYVNSRVNATRNIGNYTDHVAVRVNTGLERVNGPDSRDWRYNQFRRLTLTV
Y09663_1 RWEADYVNSRVNATRNIGNYTDHVAVRVNTGLERVNGPDSRDWRYNQFRRLTLTV
cryla-105.pe LDIVSLFVNSRVNATRNIGNYTDHVAVRVNTGLERVNGPDSRDWRYNQFRRLTLTV
Y09663_1 LDIVSLFVNSRVNATRNIGNYTDHVAVRVNTGLERVNGPDSRDWRYNQFRRLTLTV
cryla-105.pe NSITTYTDHAGEYVNSGHIQIMASVNGSGPEFTFLYGTMGNAARQONVAOLGQGVYR
Y09663_1 NSITTYTDHAGEYVNSGHIQIMASVNGSGPEFTFLYGTMGNAARQONVAOLGQGVYR
cryla-105.pe TLSSLYLRP-FNIGINNOLSVLGTETAYGT-SSNLPSRVYKSGTVAQVSPNN
Y09663_1 TLSSLYLRP-FNIGINNOLSVLGTETAYGT-SSNLPSRVYKSGTVAQVSPNN
cryla-105.pe NVPPQGSFHRLSHVMSFRSGNSVSIIRAPMFWIHRSAEFNNIISDSTGTPAK
Y09663_1 NVPPQGSFHRLSHVMSFRSGNSVSIIRAPMFWIHRSAEFNNIISDSTGTPAK
cryla-105.pe SVPPRAGSHRLSHVMTLSQ--AAGAVVTLRPTFWQHRSAEFNNIIPSSQITPLIN
Y09663_1 SVPPRAGSHRLSHVMTLSQ--AAGAVVTLRPTFWQHRSAEFNNIIPSSQITPLIN

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cryla-105.pe	GVVTELEYPETDKVWIEIGETGTFIVDSVELLMEE	1140	1150	1160	1170
Y09663_1	GVVTELEYPETDKVWIEIGETGTFIVDSVELLMEE				
cryla-105.pep					
TXN5:X13535_1					
Description: X13535 Bacillus thuringiensis Bacillus thuringiensis cryA gene for parasporal cr					
Accession/ID: X13535					
=====General Comments=====					
LOCUS	X13535_1 [BFCRYAG]				
DEFINITION Bacillus thuringiensis cryA gene for parasporal crystal toxin;					
SCORES	Initl: 4298	Initn: 6535	Opt: 6835	2-score: 7537.4	E(): 0
>>TXN5:X13535_1	Initn: 6535	Intl: 4298	opt: 6835	Z-score: 7537.4	expect(): 0
Smith-Waterman score: 6835;	86.9% identity in 1179 aa overlap				
(1-1177:1-1176)					
cryla-105.pe	MDNNPNINECIPTNCLSNPEVEVLGGERITGYTPIDISLSLTQFLSEFPVGA	10	20	30	40
	1176	1186	1196	1206	1216
X13535_1	MDNNPNINECIPTNCLSNPEVEVLGGERITGYTPIDISLSLTQFLSEFPVGA				
	10	20	30	40	50
cryla-105.pe	VDIINGIGPQSDAFVJQIOLINRIEFARNOAISREGLSNLYQIYAESPREWAD	70	80	90	100
	1176	1186	1196	1206	1216
X13535_1	VDIINGIGPQSDAFVJQIOLINRIEFARNOAISREGLSNLYQIYAESPREWAD				
	70	80	90	100	110
cryla-105.pe	PTNPALREEMRIQFNDMNSALTTAIPILAVONQVPILSVVQQAANLHLSVL	130	140	150	160
	1176	1186	1196	1206	1216
X13535_1	PTNPALREEMRIQFNDMNSALTTAIPILAVONQVPILSVVQQAANLHLSVL				
	130	140	150	160	170
cryla-105.pe	RWGFDAAATNSRYNDLTRIGNYTHDAVRWYNTGLERVWGPSRDMIRYNQFR	190	200	210	220
	1176	1186	1196	1206	1216
X13535_1	RWGFDAAATNSRYNDLTRIGNYTHDAVRWYNTGLERVWGPSRDMIRYNQFR				
	190	200	210	220	230
cryla-105.pe	LDIVSLFFPNYSRPTRTVSQLTRELYITNPVLENDGSPGAQIGESIRSPHLM	250	260	270	280
	1176	1186	1196	1206	1216
X13535_1	LDIVSLFFPNYSRPTRTVSQLTRELYITNPVLENDGSPGAQIGESIRSPHLM				
	250	260	270	280	290
cryla-105.pe	NSITIVTDHARGYEWGSHQIWASPVGSGFEEPTPLPYGTGNNAAPOQRIV	310	320	330	340
	1176	1186	1196	1206	1216
X13535_1	NSITIVTDHARGYEWGSHQIWASPVGSGFEEPTPLPYGTGNNAAPOQRIV				
	310	320	330	340	350
cryla-105.pe	TLSTSLYRRP-FNIGINQQQLSVLDGTETFAYGT-SSNLPASVYVCKSTVD	370	380	390	400
	1176	1186	1196	1206	1216
X13535_1	TLSTSLYRRP-FNIGINQQQLSVLDGTETFAYGT-SSNLPASVYVCKSTVD				
	370	380	390	400	410
cryla-105.pe	420	430	440	450	460
	470	480	490	500	510
X13535_1	420	430	440	450	460
	470	480	490	500	510

cryla-105.pe NVPPQGFHSHSGVMPFRSGFSSNSVSIIRAPMFSWHSARFNNIIASDSITQIPLVK
X13535_1 SVPPQGFHSHSGVMPFRSGFSSNSVSIIRAPMFSWHSARFNNIIASDSITQIPLVK
cryla-105.pe AHTQSGVTVVRGPETGDLIRRTSGFPAVTIVNGQLPQRYRARIYASTINLRIY
X13535_1 STNLGSGTSVVRGFTGQGLIRNAPGQISLRLNIITAPLSQRYRARIYASTINLRIY
cryla-105.pe VTVAGERIFAGQPNKIMDTQPNFQSFQATINAFTPNSQSSFTVQADTFSSGNEVY
X13535_1 TSIDGRPIQNGFNSATMSSGNLQSGSPFTVGFAPFPAHNGSSVFLSHARFNSGNEVY
cryla-105.pe IDRFELPVTATLEAEYNLEBAKAVNALFTSTNSLGNKNTVDYHIDQANLVTAASDA
X13535_1 IDRIEFVPAEVFEAEYDLERAQKAVNELFTSNQIGNKNTVDYHIDQANLVTAASDA
cryla-105.pe FCLDEKRESEKVKHAKLSDERNLLQDSNFXDINRQPERGWSGTGTTQSGSVFKEN
X13535_1 FCLDEKRESEKVKHAKLSDERNLLQDSNFXDINRQPERGWSGTGTTQSGSVFKEN
cryla-105.pe VYTLGTFDECPTLYLQKIDESKLAFTRYQIRGYIEDSDLEIYSRYNKAHETUNVP
X13535_1 VYTLGTFDECPTLYLQKIDESKLAFTRYQIRGYIEDSDLEIYSRYNKAHETUNVP
cryla-105.pe GTGSLWPLSAQSPIGKCGEPNRCAPHLWNPLDSCRDGKCAHSHHFLDIDVGCTD
X13535_1 GTGSLWPLSAQSPIGKCGEPNRCAPHLWNPLDSCRDGKCAHSHHFLDIDVGCTD
cryla-105.pe LNEDLGVWVIFKIKTDGCHABLGNLEFEKPLVGEALARKVRAEKWKDEKLEMETN
X13535_1 LNEDLGVWVIFKIKTDGCHABLGNLEFEKPLVGEALARKVRAEKWKDEKLEMETN
cryla-105.pe IVYKEAESVDALFVNSQYDQLOADTNIAHIAADKRVHSIREAYLPFELSVIPGVNAIF
X13535_1 IVYKEAESVDALFVNSQYDQLOADTNIAHIAADKRVHSIREAYLPFELSVIPGVNAIF
cryla-105.pe BELEGRIFTAFSLYDARNVIRKNGDFNNGLSQWVKGHVDVEEQNNQSRVLYVPEWEAEVS
X13535_1 BELEGRIFTAFSLYDARNVIRKNGDFNNGLSQWVKGHVDVEEQNNQSRVLYVPEWEAEVS
cryla-105.pe CEVRCVGRGYILRTAYKEGYGEGCVTTHEENNTDLKESNCVEEYLPNNVTGNDY
X13535_1 CEVRCVGRGYILRTAYKEGYGEGCVTTHEENNTDLKESNCVEEYLPNNVTGNDY
cryla-105.pe OEVAVCGRGYILRTAYKEGYGEGCVTTHEENNTDLKESNCVEEYLPNNVTGNDY
X13535_1 OEVAVCGRGYILRTAYKEGYGEGCVTTHEENNTDLKESNCVEEYLPNNVTGNDY

cryla-105.pe TVNQBEYGGAYTSRNGYNEAPSPADYASVYEKSYTDGRRENPCFENRGYRDYTPPLPV
X13535_1 TVNQBEYGGAYTSRNGYNEAPSPADYASVYEKSYTDGRRENPCFENRGYRDYTPPLPV
cryla-105.pe GYVTKLEVRPPTDKWIEIGTEGTFTIVDSVELLMEE
X13535_1 GYVTKLEVRPPTDKWIEIGTEGTFTIVDSVELLMEE
cryla-105.pe TXNS: CIAA_BACTK
X13535_1 TXNS: CIAA_BACTK
Description: P02965 bacillus thuringiensis (subsp. kurstaki), bacillus
thuringiensis (subsp.
Accession/ID: P02965
ID CIAA_BACTK STANDARD; PRT: 1176 AA.
AC P02965; P16478; P09664; Q9665; . . .
=====General comments=====

SCORES Initl: 4298 Initn: 6535 Opt: 6835 z-score: 7537.4 E(): 0
Initn: 6535 Initl: 4298 Opt: 6835 z-score: 7537.4 expect(): 0
Smith-Waterman score: 6835; 86.9% identity in 1179 aa overlap
(1-1177, 1-1176)

cryla-105.pe MONNINECIPYNCISNREVEVLGGRIETGTPIDISLSTQFLLSERVPGAGFVLGL
X13535_1 MONNINECIPYNCISNREVEVLGGRIETGTPIDISLSTQFLLSERVPGAGFVLGL
cryla-105.pe VLTGSIPEQMPFLVIEQINRIEFAFNQAIISRLGLESLNLYQIYAESFREWEAD
X13535_1 VLTGSIPEQMPFLVIEQINRIEFAFNQAIISRLGLESLNLYQIYAESFREWEAD
cryla-105.pe PTNPALREEMRIQNDNRNLSALTITVCLANQYQVNDLSVYVQAANLHLSVLRDVSFVQ
X13535_1 PTNPALREEMRIQNDNRNLSALTITVCLANQYQVNDLSVYVQAANLHLSVLRDVSFVQ
cryla-105.pe RWGFDAAATINSRYNDLTRIGNYNSHARWYNIGIRWGPDSRLNIRNOFRRELTIV
X13535_1 RWGFDAAATINSRYNDLTRIGNYNSHARWYNIGIRWGPDSRLNIRNOFRRELTIV
cryla-105.pe LDIVSLFVNDISRTYIRIVSOLTREITVPVLENTDGSRSAGIEGEGEGLTMDLIT
X13535_1 LDIVSLFVNDISRTYIRIVSOLTREITVPVLENTDGSRSAGIEGEGEGLTMDLIT
cryla-105.pe NSTIYTDVHGFYNSGHOITASVPVSGPEFAFLFNGNAGNAAPPV-LVSLTGLGIFR
X13535_1 NSTIYTDVHGFYNSGHOITASVPVSGPEFAFLFNGNAGNAAPPV-LVSLTGLGIFR

cry1a-105.pe TLSSLLYRRP-FNIGINNQSLVLDGTEFAYGT-SSNLPSAVYRSGTVDLSLDEIPQNN
CIAA_BACTK TLSSPLRRILSGNNGELFVLDGTEFASLTNLNSTIYQRGTVDSLVIPQDN
420 430 440 450 460 470
cry1a-105.pe NYPYRQGSRLSHVSMFRSGNSSVSIIRAPMFMIHRSFENNIADSIQTPLVK
CIAA_BACTK SVYPRAGSRLSHVMTLSQ--AAGAVVTLRAFTFSQWRHSFENNIIPSSQITPLTK
420 430 440 450 460 470
cry1a-105.pe AHTLQSGTIVRGPGFTGGDILRRTSQGFAYTIIVNINQQLPQRYEARIIYASTNLRIY
CIAA_BACTK SNLQSGTSVVKGPGFTGGDILRRTSQGFAYTIIVNINQQLPQRYEARIIYASTNLRIY
480 490 500 510 520 530
cry1a-105.pe VTVAGERIFACQFNKMTDGTDLTFQGSFVATINTAFTFPMQSGSFTVGADTFSSGNEVY
CIAA_BACTK TSIDGRPINQGNFSATMSSGSLQSGSFTVGTFTFNFSGSSVFTLSAHVNSGNEVY
540 550 560 570 580 590
cry1a-105.pe IDRFELIPVATLAEVNLERAQKAVNALFTSTNQLGKINVTVDYHIDQVSNLVTYLSDE
CIAA_BACTK IDRIEFVPAEVTFAEYDLERAQKAVNELFTSTNQLGKINVTVDYHIDQVSNLVTYLSDE
600 610 620 630 640 650
cry1a-105.pe FCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINQPERGKGGSTGTITQGGDDVFKEN
CIAA_BACTK FCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINQPERGKGGSTGTITQGGDDVFKEN
660 670 680 690 700 710
cry1a-105.pe YVTLGSGTDECYPTLYQKIDESKLAFTRYQLRGYIEDSQDLEYISIRYNAKHETVNPV
CIAA_BACTK YVTLGSGTDECYPTLYQKIDESKLAFTRYQLRGYIEDSQDLEYISIRYNAKHETVNPV
720 730 740 750 760 770
cry1a-105.pe GTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTD
CIAA_BACTK GTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTD
780 790 800 810 820 830
cry1a-105.pe LNEDLGVWVIFKINTQDGHARLGNLEFLEKPLVGGALARVRAEKWRDKREKLEWETN
CIAA_BACTK LNEDLGVWVIFKINTQDGHARLGNLEFLEKPLVGGALARVRAEKWRDKREKLEWETN
840 850 860 870 880 890
cry1a-105.pe IYVKEAKESVDALFVNSQVDQLQADTNIAITHAADKEVHSIREAYLPSELSPVGVNAATF
CIAA_BACTK IYVKEAKESVDALFVNSQVDQLQADTNIAITHAADKEVHSIREAYLPSELSPVGVNAATF
900 910 920 930 940 950
cry1a-105.pe EELEGRIFTAFSLYDARNVINKGDFNGLSCWNKYGHVDEEQNNQSRVLPVPEWAEVYS
CIAA_BACTK EELEGRIFTAFSLYDARNVINKGDFNGLSCWNKYGHVDEEQNNQSRVLPVPEWAEVYS
960 970 980 990 1000 1010
1020 1030 1040 1050 1060 1070

cry1a-105.pe QEVRCVPGRYILRVAYKEGEGCVTIHEIENNTDELKFSNCVEEEIYPNNTVTCDNY
CIAA_BACTK QEVRCVPGRYILRVAYKEGEGCVTIHEIENNTDELKFSNCVEEEIYPNNTVTCDNY
1020 1030 1040 1050 1060 1070
cry1a-105.pe TVNQEEYGAYTSNRNGYNAPSPADYASVVEKSYTDGRRNCPENRGRDYTLPLV
CIAA_BACTK TVNQEEYGAYTSNRNGYNAPSPADYASVVEKSYTDGRRNCPENRGRDYTLPLV
1080 1090 1100 1110 1120 1130
cry1a-105.pe GYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
CIAA_BACTK GYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140 1150 1160 1170
cry1a-105.pep
TXN5:Q45736
Description: Q45736 bacillus thuringiensis. insecticidal crystal protein.
6/2001
Accession/ID: Q45736
ID Q45736 PRELIMINARY; PRT; 1176 AA.
AC Q45736; . . .
=====General comments=====

SCORES Initl: 4287 Initn: 6533 Opt: 6833 z-score: 7535.2 E(): 0
>TXN5:Q45736
Initn: 6533 initl: 4287 opt: 6833 z-score: 7535.2 expect(): 0
Smith-Waterman score: 6833; 86.9% identity in 1179 aa overlap
(1-1177:1-1176)

cry1a-105.pe MDNPNINCEIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSFVPGAGFVLGL
Q45736 MDNPNINCEIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSFVPGAGFVLGL
10 20 30 40 50 60
cry1a-105.pe VDIIGIFGFSQWDAFLVQLEQLINQRIEFAFNQAISRLGSLNLYQIYAESFREWEAD
Q45736 VDIIGIFGFSQWDAFLVQLEQLINQRIEFAFNQAISRLGSLNLYQIYAESFREWEAD
70 80 90 100 110 120
cry1a-105.pe PTPNALREEMRIQFNDMNSALTTAIFLFAVQNYQVPLLSVYQAAANLHLSVLRDVSFVG
Q45736 PTPNALREEMRIQFNDMNSALTTAIFLFAVQNYQVPLLSVYQAAANLHLSVLRDVSFVG
130 140 150 160 170 180
cry1a-105.pe RWGFDATINSRYNDLTRELIGNYTDHAVYNTGLERWGPDSRDMIRYNQFRRELITV
Q45736 RWGFDATINSRYNDLTRELIGNYTDHAVYNTGLERWGPDSRDMIRYNQFRRELITV
190 200 210 220 230 240
cry1a-105.pe LDIVSFYNDSTRYPTIRTYTSQLTREIYTNPVLENFDSFGSAQIGSIRSPHLMIL
Q45736 LDIVSFYNDSTRYPTIRTYTSQLTREIYTNPVLENFDSFGSAQIGSIRSPHLMIL
250 260 270 280 290 300
1020 1030 1040 1050 1060 1070

Product Characterization Center

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cry1a-105.pe  ELEGRITATSLYDARNVTKGDFNGLSCWVYKGHVDFEENNRQSVLVVPEWEAEVS
960 970 980 990 1000 1010
Q45736
1020 1030 1040 1050 1060 1070
cry1a-105.pe  QEVVCPGGRGYILRVATAYKEGEGECVTHIEIENNTDELKFSNCVEEYIPNNTVTGNDY
Q45736  QEVVCPGGRGYILRVATAYKEGEGECVTHIEIENNTDELKFSNCVEEYIPNNTVTGNDY
1020 1030 1040 1050 1060 1070
1080 1090 1100 1110 1120 1130
cry1a-105.pe  TVNQEEYGAVTSRRNGYNAPSPADVASVVEKSYSDGRRNCPCFNRGRYDTPLPV
Q45736  TVNQEEYGAVTSRRNGYNAPSPADVASVVEKSYSDGRRNCPCFNRGRYDTPLPV
1080 1090 1100 1110 1120 1130
1140 1150 1160 1170
cry1a-105.pe  GYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
Q45736  GYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140 1150 1160 1170
=====
ID 09RC30 PRELIMINARY; PRT; 1176 AA.
AC 89C30
=====
SCORES Initl: 4276 Initn: 6508 Opt: 6803 z-score: 7502.1 E(): 0
>TXNS-09RC30
initn: 6508 initl: 4276 opt: 6803 z-score: 7502.1 expect(): 0
Smith-Waterman score: 6803; 88.5% identity in 1179 aa overlap
(1-1177:1-1176)
cry1a-105.pe  MDNNPNIHCIPYILNCLSNPEVYGGGRITNGYIDILSLTFLILSEFVPGAGFVLGL
Q9RC30  MDNNPNIHCIPYILNCLSNPEVYGGGRITNGYIDILSLTFLILSEFVPGAGFVLGL
10 20 30 40 50 60
10 20 30 40 50 60
cry1a-105.pe  VDIIWGIFGSPQMDAPLVQIEQLNORIEFPANQIISRLGELSNVONVARSFREWAD
Q9RC30  VDIIWGIFGSPQMDAPLVQIEQLNORIEFPANQIISRLGELSNVONVARSFREWAD
70 80 90 100 110 120
10 20 30 40 50 60
10 20 30 40 50 60
cry1a-105.pe  PTNFALREEMRIQFNDMNSALTTAIPLVAVONVQPLLSVVCANLHLVAVASVFGQ
Q9RC30  PTNFALREEMRIQFNDMNSALTTAIPLVAVONVQPLLSVVCANLHLVAVASVFGQ
130 140 150 160 170 180
130 140 150 160 170 180
cry1a-105.pe  RWGFDAATINSRYNDLTILIGNYTDHVAIRYNTGLGVWGPDSRDWRYNQFRRELTVA
Q9RC30  RWGFDAATINSRYNDLTILIGNYTDHVAIRYNTGLGVWGPDSRDWRYNQFRRELTVA
190 200 210 220 230 240
190 200 210 220 230 240

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cry1a-105.pe LDIVLFPNYSRTYPIRTVSQTLREIYNPVLENFDFSGRGAQIEGSIKSPHLMIL
Q9RC30 LDIVLFPNYSRTYPIRTVSQTLREIYNPVLENFDFSGRGAQIEGSIKSPHLMIL
310 260 270 280 290 300
cry1a-105.pe NSITITDARREYVWGHQIMASPVGSGPEFTPLVGTNGNAQQRIYVLAQLQGVYR
Q9RC30 NSITITDARREYVWGHQIMASPVGSGPEFTPLVGTNGNAQQRIYVLAQLQGVYR
310 320 330 340 350 360
cry1a-105.pe TISSTLYRRP-FNIGINNQQLSVLDTGETFAYGT-SSNLPASAVYAKSGTSDSLDIPQNN
Q9RC30 TISSTLYRRP-FNIGINNQQLSVLDTGETFAYGT-SSNLPASAVYAKSGTSDSLDIPQNN
370 380 390 400 410
cry1a-105.pe NVPPROGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWTHRSAPFNIIASDSITQIPLVK
Q9RC30 NVPPROGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWTHRSAPFNIIASDSITQIPLVK
420 430 440 450 460 470
cry1a-105.pe AHTLQSGTIVRGPGFTGDIILRTSGEPAYTIVNMQLPQRYRIRYASTTNLRIY
Q9RC30 AHTLQSGTIVRGPGFTGDIILRTSGEPAYTIVNMQLPQRYRIRYASTTNLRIY
480 490 500 510 520 530
cry1a-105.pe STNLGSGTVVKGPGFTGDIILRTSGEPAYTIVNMQLPQRYRIRYASTTNLRIY
Q9RC30 STNLGSGTVVKGPGFTGDIILRTSGEPAYTIVNMQLPQRYRIRYASTTNLRIY
540 550 560 570 580 590
cry1a-105.pe VIVAGERIFAGQNKMTGDTLTFQSFYATINTAFTPFMSQSFVTVGADTFSSGNEVY
Q9RC30 VIVAGERIFAGQNKMTGDTLTFQSFYATINTAFTPFMSQSFVTVGADTFSSGNEVY
600 610 620 630 640 650
cry1a-105.pe IDREFLIPVATIEAEYNLEAQAQAVNALFTSNOLGLTNVTVYHIDQVSNLVLSDE
Q9RC30 IDREFLIPVATIEAEYNLEAQAQAVNALFTSNOLGLTNVTVYHIDQVSNLVLSDE
660 670 680 690 700 710
cry1a-105.pe FCLDEKRELSEKVKHAKRLSDERNLLOQSNPKDINQPERGWSGSGTITIGQDDVFKEN
Q9RC30 FCLDEKRELSEKVKHAKRLSDERNLLOQSNPKDINQPERGWSGSGTITIGQDDVFKEN
720 730 740 750 760 770
cry1a-105.pe YVTLSTGFDCYPTLYVQKIDESKLAFTYQYRGVIEDSQDLETYSIRYNNAKHETVNP
Q9RC30 YVTLSTGFDCYPTLYVQKIDESKLAFTYQYRGVIEDSQDLETYSIRYNNAKHETVNP
780 790 800 810 820 830
cry1a-105.pe GTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGECAHSHHSFLSDIDVGCTD
Q9RC30 GTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGECAHSHHSFLSDIDVGCTD
840 850 860 870 880 890
cry1a-105.pe LNEDEGVWVIFKIQDQGHARLGNLEFLEKPLVGEALARYIAEKKWRDKREKLEWETN
Q9RC30 LNEDEGVWVIFKIQDQGHARLGNLEFLEKPLVGEALARYIAEKKWRDKREKLEWETN
900 910 920 930 940 950

cry1a-105.pe IVYKEAKESVDALFVNSQDQLQADTNIAHHAADKRVHSIREAYLPBLSVIRGVNAAIF
Q9RC30 IVYKEAKESVDALFVNSQDQLQADTNIAHHAADKRVHSIREAYLPBLSVIRGVNAAIF
900 910 920 930 940 950
cry1a-105.pe EELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEONNQRSLVLPWEAEVYS
Q9RC30 EELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEONNQRSLVLPWEAEVYS
960 970 980 990 1000 1010
cry1a-105.pe QEVYVCPGGRGIVLRTAYKEGEGECVTIHEIENNTDELKFSNCVEEIIYNNVTTCNDY
Q9RC30 QEVYVCPGGRGIVLRTAYKEGEGECVTIHEIENNTDELKFSNCVEEIIYNNVTTCNDY
1020 1030 1040 1050 1060 1070
cry1a-105.pe TVNOEYEGAYTSRNGCYNEAPSVADYASVYEKSYTDGRENCEFNRCGYRDTPLPV
Q9RC30 TVNOEYEGAYTSRNGCYNEAPSVADYASVYEKSYTDGRENCEFNRCGYRDTPLPV
1080 1090 1100 1110 1120 1130
cry1a-105.pe GYVTELEYFPETDKVWIEIGETGTFIVDSVELLMEE
Q9RC30 GYVTELEYFPETDKVWIEIGETGTFIVDSVELLMEE
1140 1150 1160 1170
cry1a-105.pep
TXN5:Q9S5V8
Description: Q9S5V8 bacillus thuringiensis. btt84al crystal protein. 6/2001
Accession/ID: Q9S5V8
ID Q9S5V8 PRELIMINARY; PRT: 1180 AA.
AC Q9S5V8;
DT 01-MAY-2000 (TRENBLrel. 13, Created) . . .
=====General comments=====

SCORES Initl: 3711 Initn: 6423 Opt: 6722 Z-score: 7412.7 E(): 0
>TXN5:Q9S5V8
Initn: 6423 Initl: 3711 Opt: 6722 Z-score: 7412.7 expect(): 0
Smith-Waterman score: 6722; 85.3% identity in 1183 aa overlap
(1-1177:1-1180)

cry1a-105.pe MDNPNINCEIPYCNCLSNPEVEVLGGERIETGTYTPIDISLSTQFLSEFVFGAGFVLGL
Q9S5V8 MDNPNINCEIPYCNCLSNPEVEVLGGERIETGTYTPIDISLSTQFLSEFVFGAGFVLGL
10 20 30 40 50 60
cry1a-105.pe VDIIMGIFGSPQMDAFVLQEQINQRIEIEFARNOAISRLGLSNLYQIYAESFWEAD
Q9S5V8 VDIIMGIFGSPQMDAFVLQEQINQRIEIEFARNOAISRLGLSNLYQIYAESFWEAD
70 80 90 100 110 120
cry1a-105.pe PTPALREEMRIQFNDNMSALTTPILFAVQNYQVPLLSVVOAANHLSLVLRDVSFVGO
Q9S5V8 PTPALREEMRIQFNDNMSALTTPILFAVQNYQVPLLSVVOAANHLSLVLRDVSFVGO
130 140 150 160 170 180
cry1a-105.pe PTPALREEMRIQFNDNMSALTTPILFAVQNYQVPLLSVVOAANHLSLVLRDVSFVGO
Q9S5V8 PTPALREEMRIQFNDNMSALTTPILFAVQNYQVPLLSVVOAANHLSLVLRDVSFVGO
190 200 210 220 230 240

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cryla-105.pe L N E D L G W V I F K I K T O D C H A R L G N L S F L B E E K P L G E A L A R V K E A E K K W D R K E K L E W E T H
840 850 860 870 880 890

cryla-105.pe I V Y K E A K E S V D A L F V N S Q Y D Q L A D T N I A M I H A A D K R V H S T R E A Y L P E L S V I P G N A A I F
900 910 920 930 940 950

cryla-105.pe I V Y K E A K E S V D A L F V N S Q Y D R L Q A D T N I A M I H A A D K R V H S T R E A Y L P E L S V I P G N A A I F
900 910 920 930 940 950

cryla-105.pe E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W N V K G H V D V E E Q N N H R S V L V V P E W E A E V S
960 970 980 990 1000 1010

cryla-105.pe E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W N V K G H V D V E E Q N N H R S V L V V P E W E A E V S
960 970 980 990 1000 1010

cryla-105.pe Q E V R V C F G R G Y I L R V T A Y K E G Y G E G C V T H E I E N N T D E L K F S N C V E E E Y P N N T V T C N D Y
1020 1030 1040 1050 1060 1070

cryla-105.pe Q E V R V C F G R G Y I L R V T A Y K E G Y G E G C V T H E I E N N T D E L K F S N C V E E E Y P N N T V T C N D Y
1020 1030 1040 1050 1060 1070

cryla-105.pe I V N O E E Y G G A N Y S R N R G Y N E A - - - - - P S V P A D Y A S V Y E K S Y T G C R E N P C E N R G Y R D Y T
1080 1090 1100 1110 1120 1130

cryla-105.pe T A T O E E Y G T Y S R N R G Y G A Y E S N S V P A D Y A S A E K A T I Q D R R D N P C E S N R G Y G D Y T
1080 1090 1100 1110 1120 1130

cryla-105.pe P L P A S V T Y K E L E Y F P E T D K V M I E I G E T G F T V D S V E L L M E E
1140 1150 1160 1170

cryla-105.pe P L P A S V T Y K E L E Y F P E T D K V M I E I G E T G F T V D S V E L L M E E
1140 1150 1160 1170

Description: Q9S514 bacillus thuringiensis, insecticidal crystal protein
Accession/ID: Q9S514 General comments:
ID Q9S514 PRELIMINARY
AC Q9S514

SCORES Initl: 4132 Inltrn: 6365 Opt: 6662 Score: 7346.5 E(): 0
>>XMS:Q9S514
Initl: 6365 Inltr: 4132 opt: 6662 Z-score: 7346.5 Expect(): 0
Smith-Waterman score: 6662; 85.0% identity in 116 aa overlap
(1-1177:1-1176)

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

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

cryla-105.pe V D I I W I G F G S Q W D A F L V I O E I Q L I N Q R I E F A R N O I S E L C L S N I V I A E S F R E W A D
70 80 90 100 110 120

cryla-105.pe V D I I W I G F G S Q W D A F L V I O E I Q L I N Q R I E F A R N O I S E L C L S N I V I A E S F R E W A D
70 80 90 100 110 120

cry1a-105.pe PTFPALREEMRIQFNDMNSALTAITPLFAVQNVQVPLLSVYVQAAHLHLSVLRDVSFVQO
Q9S514 PTFPALREEMRIQFNDMNSALTAITPLFAVQNVQVPLLSVYVQAAHLHLSVLRDVSFVQO
130 140 150 160 170 180
cry1a-105.pe RWGFDAAITNSRYNDLTLRLGNVTDHVRWNTGLERWCPDSRWIRYNFRRLTLTV
Q9S514 RWGFDAAITNSRYNDLTLRLGNVTDHVRWNTGLERWCPDSRWIRYNFRRLTLTV
190 200 210 220 230 240
cry1a-105.pe LDIVSLFNNYSRTYPIRTVSQLTREIYNPVLNFDGSPRGSQAQIEGSTRSPLMDIL
Q9S514 LDIVSLFNNYSRTYPIRTVSQLTREIYNPVLNFDGSPRGSQAQIEGSTRSPLMDIL
250 260 270 280 290 300
cry1a-105.pe NSITITDAHRGEYTWGHOIMASPVGSGPEFTFPLYGTMGNAAPQRIVAQLGQGVYR
Q9S514 NSITITDAHRGEYTWGHOIMASPVGSGPEFTFPLYGTMGNAAPQRIVAQLGQGVYR
310 320 330 340 350 360
cry1a-105.pe TSGSTLYRRP-FNIGINNQOLSVLDTGEFAYGT-SSNLPASAVYKSGTVDLSLDEIPQNN
Q9S514 TSGSTLYRRP-FNIGINNQOLSVLDTGEFAYGT-SSNLPASAVYKSGTVDLSLDEIPQNN
370 380 390 400 410
cry1a-105.pe NVPPRGFGRHLSHVMSFRSGFNSSVSIIRAPMSVHRSAGFNNIIASDSITQIPLVK
Q9S514 NVPPRGFGRHLSHVMSFRSGFNSSVSIIRAPMSVHRSAGFNNIIASDSITQIPLVK
420 430 440 450 460 470
cry1a-105.pe AHTLQSGTIVVGPFGTGGDILRTSGPFAVTIWNINGLPORVYRIRVASTINLRIY
Q9S514 AHTLQSGTIVVGPFGTGGDILRTSGPFAVTIWNINGLPORVYRIRVASTINLRIY
480 490 500 510 520 530
cry1a-105.pe VTVAGERIFAGQFNKMTDGLTFQSFYATINTAFTFPMSSOSTVGAUTFSGNEVY
Q9S514 VTVAGERIFAGQFNKMTDGLTFQSFYATINTAFTFPMSSOSTVGAUTFSGNEVY
540 550 560 570 580 590
cry1a-105.pe IDREFLIPVTATLEAYNLERAQKAVNALFTSTNGLKTNVTDYHIDOVSNLVTLSDE
Q9S514 IDREFLIPVTATLEAYNLERAQKAVNALFTSTNGLKTNVTDYHIDOVSNLVTLSDE
600 610 620 630 640 650
cry1a-105.pe FCLDKRELSEKVKHAKELSDERNLLQDSNFKDINRQPERGWGSGTGITIQGGDDVFKEN
Q9S514 FCLDKRELSEKVKHAKELSDERNLLQDSNFKDINRQPERGWGSGTGITIQGGDDVFKEN
660 670 680 690 700 710
cry1a-105.pe YVTLSGTFDECYPTLYLQKIDESKLAFTYQLRGVIEDSODLEISYINXAKHETVNP
Q9S514 YVTLSGTFDECYPTLYLQKIDESKLAFTYQLRGVIEDSODLEISYINXAKHETVNP
720 730 740 750 760 770
cry1a-105.pe YVTLGTFDECYPTLYLQKIDESKLAFTYQLRGVIEDSODLEISYINXAKHETVNP
Q9S514 YVTLGTFDECYPTLYLQKIDESKLAFTYQLRGVIEDSODLEISYINXAKHETVNP
780 790 800 810 820 830

cry1a-105.pe GTGSLWPLSAQSPICKCEPNRCAPHLEWNPDLDCSCDEKCAHSHSHFSLDIDVGCTD
Q9S514 GTGSLWPLSAQSPICKCEPNRCAPHLEWNPDLDCSCDEKCAHSHSHFSLDIDVGCTD
780 790 800 820 830
cry1a-105.pe LNEDELGVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARKAEKKWRDKREKLEMETN
Q9S514 LNEDELGVWVIFKIKTQDGHARLGNLEFLEKPLVGEALARKAEKKWRDKREKLEMETN
840 850 860 870 880 890
cry1a-105.pe IVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPESLVPVGNAAIF
Q9S514 IVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPESLVPVGNAAIF
900 910 920 930 940 950
cry1a-105.pe ELEGRIFTAFSLYDARNVKNKGNFNNGLSCMNKGVHVDVEEQNNQSVLVVPEWEAEVS
Q9S514 ELEGRIFTAFSLYDARNVKNKGNFNNGLSCMNKGVHVDVEEQNNQSVLVVPEWEAEVS
960 970 980 990 1000 1010
cry1a-105.pe QEVRCVCGRYILRTAYKEGSGCVTIEIENNTDELKFSNCVEEIIYNNVTTCNDY
Q9S514 QEVRCVCGRYILRTAYKEGSGCVTIEIENNTDELKFSNCVEEIIYNNVTTCNDY
1020 1030 1040 1050 1060 1070
cry1a-105.pe TVNQEEYGGYTSRNGYNEAPSPADYASVYEKSYTDGRENPCFENRGYRDYTPV
Q9S514 TVNQEEYGGYTSRNGYNEAPSPADYASVYEKSYTDGRENPCFENRGYRDYTPV
1080 1090 1100 1110 1120 1130
cry1a-105.pe GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
Q9S514 GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
1140 1150 1160 1170
cry1a-105.pe GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
Q9S514 GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
1180 1190 1200 1210 1220 1230
cry1a-105.pe GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
Q9S514 GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
1240 1250 1260 1270 1280 1290
cry1a-105.pe GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
Q9S514 GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
1300 1310 1320 1330 1340 1350
cry1a-105.pe GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
Q9S514 GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
1360 1370 1380 1390 1400 1410
cry1a-105.pe GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
Q9S514 GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
1420 1430 1440 1450 1460 1470
cry1a-105.pe GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
Q9S514 GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
1480 1490 1500 1510 1520 1530
cry1a-105.pe GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
Q9S514 GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
1540 1550 1560 1570 1580 1590
cry1a-105.pe GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
Q9S514 GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
1600 1610 1620 1630 1640 1650
cry1a-105.pe GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
Q9S514 GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
1660 1670 1680 1690 1700 1710
cry1a-105.pe GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
Q9S514 GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
1720 1730 1740 1750 1760 1770
cry1a-105.pe GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
Q9S514 GYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
1780 1790 1800 1810 1820 1830

Description: AF081248 Bacillus thuringiensis Bacillus thuringiensis
Accession/ID: AF081248
LOCUS AF081248.1 [AF081248]
DEFINITION Bacillus thuringiensis plasmid-encoded lepidoteran-specific toxin . . .
SCORES Initl: 3950 Initn: 6267 Opt: 6563 z-score: 7237.2 E(): 0
>>TXNS:AF081248.1
Initn: 6267 Initl: 3950 Opt: 6563 z-score: 7237.2 expect(): 0
Smith-Waterman score: 6563; 84.0% identity in 1183 aa overlap
(1-1177:1-1176)

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cry1a-105.pe VDIWIFGPNQNFELVIOEOLINORIEEFARNQASIRLEGLSNLYQIYAESFREWEAD
AF081248_1 VDIWIFGPNQNFELVIOEOLINORIEEFARNQASIRLEGLSNLYQIYAESFREWEAD
cry1a-105.pe PTPALREMRTOFAMASALTITAFENYQNYQVPLSVVQAAHLHSLVLDVSVFGQ
AF081248_1 PTPALREMRTOFAMASALTITAFENYQNYQVPLSVVQAAHLHSLVLDVSVFGQ
cry1a-105.pe RWGFDATINSRYNDLTRNGNDHVRVNTGLRWGPNQNRNIRYNQFRRLTLTV
AF081248_1 RWGFDATINSRYNDLTRNGNDHVRVNTGLRWGPNQNRNIRYNQFRRLTLTV
cry1a-105.pe LDIVLSFPNVDKRTPIRTVSQLTREIYNPVLENFQDSFGSNOGIEGRHSHPLMID
AF081248_1 LDIVLSFPNVDKRTPIRTVSQLTREIYNPVLENFQDSFGSNOGIEGRHSHPLMID
cry1a-105.pe NSIITYDARGHEYWMSGHQIMASPVGSGPEFTPLPYGTMGNAAPQRIWAGQGVYK
AF081248_1 NSIITYDARGHEYWMSGHQIMASPVGSGPEFTPLPYGTMGNAAPQRIWAGQGVYK
cry1a-105.pe TLSSLYRRP-FNIGINNOQLSVLDGTEFAYGT-SSNLPNAVYKSGTVDSDLEIPQNN
AF081248_1 TLSSLYRRP-FNIGINNOQLSVLDGTEFAYGT-SSNLPNAVYKSGTVDSDLEIPQNN
cry1a-105.pe NVPPRQGFQSHRLSHVMSRSGFNSSVSIIRAPMFSW----IHRSAFNIIASDIQI
AF081248_1 NVPPRQGFQSHRLSHVMSRSGFNSSVSIIRAPMFSW----IHRSAFNIIASDIQI
cry1a-105.pe PLVKAHTLOSQTIVRGPGFTGGDILRTSGGPFAYTIVNINQQLPQRYRIRASTTN
AF081248_1 PLVKAHTLOSQTIVRGPGFTGGDILRTSGGPFAYTIVNINQQLPQRYRIRASTTN
cry1a-105.pe LRIYVTVAGERIFAGQFNKMTDGLTFQSPFSYATINTAFTPMQSSFTVGADTFSSG
AF081248_1 LRIYVTVAGERIFAGQFNKMTDGLTFQSPFSYATINTAFTPMQSSFTVGADTFSSG
cry1a-105.pe NEVIDRFLIPVTAILEAEYNLERACKAVNALFTISVQGLKINVIDHIDQVSNLTVY
AF081248_1 NEVIDRFLIPVTAILEAEYNLERACKAVNALFTISVQGLKINVIDHIDQVSNLTVY
cry1a-105.pe LSDFCLDEKREISEKVKHAKLSDERNLLQDSNFKDINROPERGGSGTGLITIGQGDVV
AF081248_1 LSDFCLDEKREISEKVKHAKLSDERNLLQDSNFKDINROPERGGSGTGLITIGQGDVV

cry1a-105.pe FKENVTLSTGTEDECYPTVLYOKIDESKAKAFTRYOLRGYIEDSODLEIYSIRYNAKHET
AF081248_1 FKENVTLSTGTEDECYPTVLYOKIDESKAKAFTRYOLRGYIEDSODLEIYSIRYNAKHET
cry1a-105.pe VNVPTGTSIMPLSAQSPGKCGENRCAPHLEWNPDLDCSCRDGKCAHSHHFLSLDIDV
AF081248_1 VNVPTGTSIMPLSAQSPGKCGENRCAPHLEWNPDLDCSCRDGKCAHSHHFLSLDIDV
cry1a-105.pe GCTDUNEDLGVWIFIKTKIQDGHARLGNLEFLEEKPLVGEALARKVKAEEKWDRREKLE
AF081248_1 GCTDUNEDLGVWIFIKTKIQDGHARLGNLEFLEEKPLVGEALARKVKAEEKWDRREKLE
cry1a-105.pe WETNIVYKEAKESVDALFVNSOYDQLOADNIAHIAADKRVHSIREAYLPESLVPGVN
AF081248_1 WETNIVYKEAKESVDALFVNSOYDQLOADNIAHIAADKRVHSIREAYLPESLVPGVN
cry1a-105.pe AAIFEELEGRIFTAFSLXDARVINKGDFNNGLSQWNVKGVHDVEEQNNQSVLVVPEWE
AF081248_1 AAIFEELEGRIFTAFSLXDARVINKGDFNNGLSQWNVKGVHDVEEQNNQSVLVVPEWE
cry1a-105.pe AAVSEVNVCPGEGYFPRVTAYKEGYGCGVTIHEIENNTIDELAFSNCVEEIIYNNVT
AF081248_1 AAVSEVNVCPGEGYFPRVTAYKEGYGCGVTIHEIENNTIDELAFSNCVEEIIYNNVT
cry1a-105.pe CNVNVNNGGATSRNGYNEAPSVADYASVYVEEKSXTDGRRENPCFENRGYDYT
AF081248_1 CNVNVNNGGATSRNGYNEAPSVADYASVYVEEKSXTDGRRENPCFENRGYDYT
cry1a-105.pe PLFVGIVNLEKEPEPISQWYAKGEGEFLVSVLELLMEE
AF081248_1 PLFVGIVNLEKEPEPISQWYAKGEGEFLVSVLELLMEE
cry1a-105.pe TXNS:CIAG_BACTU
AF081248_1 TXNS:CIAG_BACTU
Description: Q9S515 bacillus thuringiensis, pesticidal crystal protein cryIag
(insecticidal)
Accession/ID: Q9S515
ID: CIAG_BACTU
AC: Q9S515
Scores: Init1: 3950 Initn: 6267 Opt: 6563 z-score: 7237.2 E(1) 0
>>TXNS:CIAG_BACTU (1176 aa)
initn: 6267 init1: 3950 opt: 6563 z-score: 7237.2 expect(1): 0
Smith-Waterman score: 6563.84.0% identity in 1183 aa overlap
(1-1177:1-1176)

Monsanto Company

cry1a-105.pe MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSITQFLISEFVPGAGFVLGL
CIAG_BACTU MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSITQFLISEFVPGAGFVLGL
70 80 90 100 110 120
cry1a-105.pe VDIIWGIFGQSOWDAFLVQIEQLINQRIEIEFARNQAISLEGLSNLQITIAESFREWAD
CIAG_BACTU VDIIWGIFGQSOWDAFLVQIEQLINQRIEIEFARNQAISLEGLSNLQITIAESFREWAD
70 80 90 100 110 120
cry1a-105.pe PTNPALREEMRIQFNDMNSALITAIPLFVQNYOVPLLSVYVQOANHLVSLRDSVFCQ
CIAG_BACTU PTNPALREEMRIQFNDMNSALITAIPLFVQNYOVPLLSVYVQOANHLVSLRDSVFCQ
130 140 150 160 170 180
cry1a-105.pe RKGFDAAATINSRYNDLTRIGNYTDHAVRWYNTGLERVWGPDSRDWRYNQFRRELTIV
CIAG_BACTU RKGFDAAATINSRYNDLTRIGNYTDHAVRWYNTGLERVWGPDSRDWRYNQFRRELTIV
190 200 210 220 230 240
cry1a-105.pe LDIVSLFNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGAGLEGSTRSPLHMDIL
CIAG_BACTU LDIVSLFNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGAGLEGSTRSPLHMDIL
250 260 270 280 290 300
cry1a-105.pe NSIITYTDHARGEYMSGHQIMASPVGSGPEFTFLYTGTMGAAPQRIVAQLGGGVYR
CIAG_BACTU NSIITYTDHARGEYMSGHQIMASPVGSGPEFTFLYTGTMGAAPQRIVAQLGGGVYR
310 320 330 340 350 360
cry1a-105.pe TLSSLYRRP-FNIGINNQLSLDCTEFAVGT-SSNLPSAYRKSCTVDSLEIPQNN
CIAG_BACTU TLSSLYRRP-FNIGINNQLSLDCTEFAVGT-SSNLPSAYRKSCTVDSLEIPQNN
370 380 390 400 410
cry1a-105.pe NVPPRQGSFHRSLSHVSMFRSGFSNSVSIIRAPMFSW---IHRGAEPNNIIASDSITQI
CIAG_BACTU NVPPRQGSFHRSLSHVSMFRSGFSNSVSIIRAPMFSW---IHRGAEPNNIIASDSITQI
420 430 440 450 460 470
cry1a-105.pe PLVKAHTIQSGTIVVRGPGFTGDIIRTSQGPAYITVININGQIPQYRARIKYSTIN
CIAG_BACTU PLVKAHTIQSGTIVVRGPGFTGDIIRTSQGPAYITVININGQIPQYRARIKYSTIN
480 490 500 510 520 530
cry1a-105.pe LRIYTVAGERIPAGQFNKMTDGTQSLTFQSFVSATINTAFTFPMQSSFTVGADTFSSG
CIAG_BACTU LRIYTVAGERIPAGQFNKMTDGTQSLTFQSFVSATINTAFTFPMQSSFTVGADTFSSG
540 550 560 570 580 590
cry1a-105.pe NEVYIDREFELIPVTATLEAEYNLERAKAVNALFTSTNQGLKTNVTDYHIDQVSNLVTY
CIAG_BACTU NEVYIDREFELIPVTATLEAEYNLERAKAVNALFTSTNQGLKTNVTDYHIDQVSNLVTY
600 610 620 630 640 650
cry1a-105.pe NEVYIDREFELIPVTATLEAEYNLERAKAVNALFTSTNQGLKTNVTDYHIDQVSNLVTY
CIAG_BACTU NEVYIDREFELIPVTATLEAEYNLERAKAVNALFTSTNQGLKTNVTDYHIDQVSNLVTY
660 670 680 690 700 710

cry1a-105.pe LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERMGSGSTGITIQGGDDV
CIAG_BACTU LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERMGSGSHDITITQGGDDV
660 670 680 690 700 710
cry1a-105.pe FKENYITLSCFDECYTYLYQKIDESKLKATRYQLRGYVIEDSODLEIYSIRYNAKHET
CIAG_BACTU FKENYITLSCFDECYTYLYQKIDESKLKATRYQLRGYVIEDSODLEIYSIRYNAKHET
720 730 740 750 760 770
cry1a-105.pe VNYVPGTSSLWPLSLAQSPGKPGKPNRCAPHLEWNPDLDCSCRDGEKCAHSHHSLDIDV
CIAG_BACTU VNYVPGTSSLWPLSLAQSPGKPGKPNRCAPHLEWNPDLDCSCRDGEKCAHSHHSLDIDV
780 790 800 810 820 830
cry1a-105.pe GCTDLNEDLGWVWIFPKITQDGHARLGNLEFLEKPLVGEALARYVGAEKWKRRKREKLE
CIAG_BACTU GCTDLNEDLGWVWIFPKITQDGHARLGNLEFLEKPLVGEALARYVGAEKWKRRKREKLE
840 850 860 870 880 890
cry1a-105.pe WETNIVYKAKESVDALFVNSQYDQLQADTNLMIHAADKRVHSIREAYLPELSVIRGVN
CIAG_BACTU WETNIVYKAKESVDALFVNSQYDQLQADTNLMIHAADKRVHSIREAYLPELSVIRGVN
900 910 920 930 940 950
cry1a-105.pe AAIFEELEGRIITAFSLYDARNVKNKGDFFNGLSCWNVKGVHVDVEEQNNQSVLVPWE
CIAG_BACTU AAIFEELEGRIITAFSLYDARNVKNKGDFFNGLSCWNVKGVHVDVEEQNNQSVLVPWE
960 970 980 990 1000 1010
cry1a-105.pe AEVSQEVRCPCRGYVILVATYKGYGEGCVTIHEIENNTDELKFSNCVEEIEYNNVT
CIAG_BACTU AEVSQEVRCPCRGYVILVATYKGYGEGCVTIHEIENNTDELKFSNCVEEIEYNNVT
1020 1030 1040 1050 1060 1070
cry1a-105.pe CNDYTVNQEEYGGAYTSNRNGYNEAPSVADYASVYEEKSYTDGRRNCFEFGYRKYDT
CIAG_BACTU CNDYTVNQEEYGGAYTSNRNGYNEAPSVADYASVYEEKSYTDGRRNCFEFGYRKYDT
1080 1090 1100 1110 1120 1130
cry1a-105.pe PLPVGYVTKLEIYFFETDKWIEIGETGTFIVDSVLELLMEE
CIAG_BACTU PLPVGYVTKLEIYFFETDKWIEIGETGTFIVDSVLELLMEE
1140 1150 1160 1170
cry1a-105.pep
TXN5:A27531_1
Description: A27531 Bacillus thuringiensis B.thuringiensis PS81RR1 endotoxin
Gene: 9/1995
Accession/ID: A27531
=====General comment s=====

©07

©07
MSG:A27561_1
IDLE: 5173 Init: 5636 GBT: 6507 Z-score: 7175.4 expect (1e-18)
Whaleman score: 6507; 82.0% identity in 1183 aa o
111775-1179).

a-105.pe MDNNNEICPQPSNPPEVVGGRTEGCTYPIDISLSTQF
331_1 MEIMNQNGSYPCNLANDKIEINIGERIEIYTYPIDISLSTQF
10 20 30 40
70 80 100
a-105.pe VDIINGIFGPSOWDAFLVQEQLNRIEFAFNQAISRLSLSLN
331_1 IDLIWGFVGPSOWDAFLVQEQLNRIEFAFNQAISRLSLSLN
70 80 90

20061017

©07
 MSG: A27561 1
 FROM: 41731 Initi 6636 GBT: 6507 Z-score: 7175.4 expect (1e-10)
 H: 100% identity in 1183 aa of 1183
 111775-11729)
 a-105.pe MDNNENIECPDIPGASNPPEVVLGGRTEGCTYPIDISLSLTQF
 10 20 30 40
 331_1 MEIMNNGQSYPCNLANDKIEINIGERIEYTYPIDISLSLTQF
 10 20 30 40
 a-105.pe VDIILWIGFGPSQDAFLVQEQINQRIEFARNQAIISKLSLSLS
 70 80 100
 331_1 IDLIWFGFGPSQDAFLVQIEQLINRFEERFARVIAISAGLSLN
 70 80 100

Description: M73250 *Bacillus thuringiensis* *Bacillus thuringiensis* (cryIA)(dn)
gene, complete C
Accession/ID: M73250

```
=====General comments=====
LOCUS      M73250.1 [BACCRVIAD]
DEFINITION Bacillus thuringiensis (cryIA(d)) gene, complete CDS. . . .

SCORES      Init1: 3610  Initn: 6147  Opt: 6481  Z-score: 7146.7  E(): 0
>>TXNS:M73250.1
Init1: 6147  Init1: 3610  Opt: 6481  Z-score: 7146.7  expect(): 0
Smith-Waterman score: 6481; 81.8% identity in 1183 aa overlap
(-1177..1-1179)
```

```
cryla-105.pe MNNPNNECIPNCLNSPEVEVIGGRIETGYPTIDISLSTOFLISEVPAGFVLGL  
| | : | | | | : | : | : | : | : | : | : | : | : | : | : |  
MEIMNQVCVPYNCLNDPTEILGERIETGYPTIDISLSTOFLISEVPAGFVLGL
```

```
crYla-105.pe VDIWGFGSQWDLVQIEOLINQRIEFARNQAISRLGSLNLYQIVAEFSREWAD      70    80    90   100   110   120
:|::|:IDIWGFSGSQWDLVQIEOLINQRIEFARNQAISRLGSLNLYQIVAEFSREWAD
M73250_1 IDIWGFSGSQWDLVQIEOLINQRIEFARNQAISRLGSLNLYQIVAEFSREWAD      70    80    90   100   110   120
```

```
cryla-105.pe PTNPALREEMRIOFNDMSALTTPAIFAVQNYQVPLLSVVYQAANUHLSLVRDVSVFQG
|||||
|||||
|||||
PTNPALTEEMRIOFNDMSALTTPAIFTQNYQVPLLSVVYQAANUHLSLVRDVSVFQG
M73250_1      |||||
|||||
```

	190	200	210	220	230	240
cr1yla-105.pe	RMGFDMATINSRNDTRIUGNYTHAVRWYNTGLERWVGPPSDRWRYNQFRREUTLIV					
	RMGFDMATINSRNDTRIUGNYTHAVRWYNTGLERWVGPPSDRWRYNQFRREUTLIV					
M73250_1	RMGFDMATINSRNDTRIUGTYDYAVRWYNTGLERWVGPPSDRWRYNQFRREUTLIV					
	RMGFDMATINSRNDTRIUGTYDYAVRWYNTGLERWVGPPSDRWRYNQFRREUTLIV					

```

cryla-105.pe LDIVLSPNDSTYPIRVTSQLTREITYTPVLENDFGSRCSAQEGIESRPSHMDLL 250 260 270 280 290 300
|||||
LDIVLSPNDSTYPIRVTSQLTREITYTPVLENDFGSRCSAQEGIESRPSHMDLL 250 260 270 280 290 300
|||||
M73250_1 LDIVLSPNDSTYPIRVTSQLTREITYTPVLENDFGSRCSAQEGIESRPSHMDLL 250 260 270 280 290 300
|||||

```

```

cryla-105.pe  NSITITDARGEVYNSGHMASVPGSPPEFTLYGTGMAAPQORIVAOQLGGY
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
M73250_1     NSITITDARGEVYNSGHQITASVPGFAGPEFTFYGTGMAAPV-IISTTGLGIFR
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

cryla-105.pe  TLSSLTRPP-FNIGINNQOLSVLDGTEFAVGT-SSNLPSAVYRKSVTGVDLDPPOQNN
               370   370   390   390   400   410
M73250_1     TLSSPVRRIILGSGNNOLFVLDGTEFAVGTGTSITVYRQRTGVDLDPPOQNN
               360   370   380   390   400   410

```

```
cryla-105.pe      nypPQGFShRLSHVMSFGSGNSVSITRAMFWSIHRGSAEFNIIASDITOPLPK  
                :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
M73250_1          SUPRAGSfHRLSHVTMLSQ--AGAGYTTATPRSWRHRSAEFSNIPQSITOPLPK
```

```
cryla-105.pe      480    490    500    510    520    530  
AHTLOSCTIVRGEGTGDIILRTSGPGPAVININQOLPORVARIYASTTNIRI  
: : : | : | : | : | : | : | : | : | : | : | : | : | :  
SINLGSTSVVKVGPGTGDIIILRTSPGISTURVTATPQSQRVRIYASTTNLQPH  
M73250_1          480    490    500    510    520    530
```

540 550 560 570 580 590

cryla-105.pe	VTVAGERIFAGQENKMTDQDPLTFQSPFSVATINTAFTFPMSSQSSFTVGADTFSSGNEVY	540	550	560	570	580	590
M73250_1	TSIDGRPIINGNFSATMSSGNGLOSGRFAGTFTPFNFNSGSSIFLTSAHVFNSGNEVY	600	610	620	630	640	650
cryla-105.pe	IDRFELIPVATIALEAYNIJERAQAKAVNALETSTNQLGKTNVTDYHIDQVSNLVTLSDE	660	670	680	690	700	710
M73250_1	IERIEFVPAEVTAEAYDLERAQAVNALETSTNQLGKTNVTDYHIDQVSNLVECLSGE	600	610	620	630	640	650
cryla-105.pe	FCLDREKLESEKVKHAKRLSDERNLLODSNFKDINRQPERGWSGSGTITQGGDQVFXEN	660	670	680	690	700	710
M73250_1	FCLDREKLESEKVKHANRLSDERNLLODPFRGNQPKDQGRWGSDTITQGGDQVFXEN	660	670	680	690	700	710
cryla-105.pe	VYVTLSGTFDECYPTLYIQKIDESKLKAFTRYQLRGVIEDSDLEIYSIRYNAKHETVNPV	720	730	740	750	760	770
M73250_1	VYVTLGTFNECYPTLYIQKIDESKLKATVTRYQLRGVIEDSOHLBIYLIRYNTKHETVNPV	720	730	740	750	760	770
cryla-105.pe	GTGSLWPLWSAQSPYIGKGPENPCAPHLEWAPDLDSCRDGEKCAHSHHESLIDIVGCTD	780	790	800	810	820	830
M73250_1	GTGSLWPLWSVFNPIGKGPENPCAPLEWAPDLDSCRDGEKCAHSHHESLIDIDGCTD	780	790	800	810	820	830
cryla-105.pe	LNEDLGVWVYFKIKTODGHARGNLNLEFLEEKPLVGLGEALARYKRAKKWRDKREKLEWETN	840	850	860	870	880	890
M73250_1	LNENLGVWVYFKIKMDDGHARGNLNLEFLEEKPLVGLGSLARYKRAKKWRDKREKLOVEIN	840	850	860	870	880	890
cryla-105.pe	IYVKEAKESVDALFVNSQYDQLQADTNIAHHAADKRVHSIREAYLPELSIVIEGVNAAIF	900	910	920	930	940	950
M73250_1	IYVKEAKESVDALFVNSQYDRQLQADTNIAHHAADKRVHIREAYLPELSIVIEGVNAGIF	900	910	920	930	940	950
cryla-105.pe	ESELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVDFVEQNNQRSLVLPWEMAEVYS	960	970	980	990	1000	1010
M73250_1	ESELEGRIFTAVSLYDARNVIKNGDFNGLSCWNVKGVDFVEQNNHRSVLVLPWEMAEVYS	960	970	980	990	1000	1010
cryla-105.pe	QEVRYVPCRGYIIRVATYAKEGYGEGCVTHIEINNTDELKSNCSVEEYIPNNVTVCNDY	1020	1030	1040	1050	1060	1070
M73250_1	QEVRYVPCRGYIIRVATYAKEGYGEGCVTHIEIDNTDELKSNCSVEEYIPNNVTVCNDY	1020	1030	1040	1050	1060	1070
cryla-105.pe	TVNQVEYGAFTSRNKGNYNEA- ---PSVPADYASVYEKSYTDCGRRENPCFNWRGYDVT	1080	1090	1100	1110	1120	1130
M73250_1	TANQEYGCATVSRNKGYESVSNSSIPAEVAPVVEE-AYTDCERKENPCESNREGYDVT	1080	1090	1100	1110	1120	1130
cryla-105.pe	PUPVGVTYKLEVFPETDKVWIEIGETEGTFTIVDSVELLLMEE	1140	1150	1160	1170		
M73250_1	PUPGAVTYKLEVFPETDKVWIEIGETEGTFTIVDSVELLLMEE	1140	1150	1160	1170		

007
 Description: 003744 *Beauveria thuringiensis* (subsp. aizawai). pesticidal
 crystal protease. City
 Accession/ID: 003744 General
 ID CIAD BACTA STANDARD; PRI; 11/79 RA.
 AC 003744;
 Scores Initial: 3610 Intra: 647 Opt: 6487 2-score: 1146.7 E(1): 0
 >>TXN5:CIAD BACTA
 Intra: 6447 Initial: 3610 Opt: 6481 2-score: 1147 expect(1): 0
 Smith-Waterman score: 6481; 81.8% identity to 112aa overlap
 (1-1177:1-1179)

cry1a-105.pe	MDNPNINCEIPYCNLSNPEVIGGERITETGYTNDLSLSLQFLSFPNAGAGFVGH	10	20	30	40	50	60
CIAD_BACTA	MEIMNQNCVPCYNCLNDPTIELEGERITETGYTPIDISLASLQFLSFPNAGAGFVGH	10	20	30	40	50	60
cry1a-105.pe	VDIITGIFGCSOWDAFLVQIETOLINORIEEFARNOAISRLLEGISLNYQIYIAEFSEWEV	70	80	90	100	110	120
CIAD_BACTA	IDLIWGFVGCSOWDAFLVQIETOLINORIEEFARNOAISRLLEGISLNYQIYIAEFSEWEV	70	80	90	100	110	120
cry1a-105.pe	PTNPALREMRIOFNDMNSALTTAIPLFAVQNYQVPLLSVYQAAMHLSVLRDVSVFQG	130	140	150	160	170	180
CIAD_BACTA	PTNPALTEMRIOFNDMNSALTTAIPLFTVQNYQVPLLSVYQAAMHLSVLRDVSVFQG	130	140	150	160	170	180
cry1a-105.pe	RWGFDATINSRYNDLTIELIGNYTDHAVMYNTGLERWVGPSDRMIRYNQFRELTLTV	190	200	210	220	230	240
CIAD_BACTA	RWGFDAVATINSRYNDLTIELIGTYDAVARYMYNTGLERWVGPSDRMIRYNQFRELTLTV	190	200	210	220	230	240
cry1a-105.pe	LDIVSLFPNYDSRTPIRTVSQLTREITYNPVLNFDGSGFSAQIEGSRSPHLMIL	250	260	270	280	290	300
CIAD_BACTA	LDIVSLFPNYDSRTPIRTVSQLTREITYNPVLNFDGSGFSAQIEQIRIQPHLMILL	250	260	270	280	290	300
cry1a-105.pe	NSITIYTDARGEYVWSHQIMASPVGFSGBEFTPLXTGMNAAQQRIVLAQOGGVYR	310	320	330	340	350	360
CIAD_BACTA	NSITIYTDVHRGNYWSGQHTASPVGAGPEFTFPRYTGTMNAAAPDV-LISTTGLGIFR	310	320	330	340	350	360
cry1a-105.pe	TLSSTLYRRP-FNIGINNQQSVLSDGTGEFAYGT-SNNLPSAVYRKSGTVDLSDEIPQNN	370	380	390	400	410	
CIAD_BACTA	TLSSTLYRRILIGSGFNQNLVLDGTGEFASLTADLIPSTIYRQRTGVDLSLDVIPQDN	370	380	390	400	410	
cry1a-105.pe	NYPYRQGFSHRLSHVSMFRSGFNSSVIRAPMFSWIRHSAEFNNIIASDSITQIPLVK	420	430	440	450	460	470
CIAD_BACTA	SVPARAGFSHRLSHVMTLSQ--AAGAVYTLRATFTSWRHSAEFNNLPSQSIQTQIPLTK	420	430	440	450	460	470

[illegible]

```
cryla-105.pe PLPVGYVTEKLEYPETDKYWIETGCTGTFIVDSVELLAMEE
CIAD_BACTA PLPAGVTEKLEYPETDKYWIETGCTGTFIVDSVELLAMEE
1140 1150 1160 1170

cryla-105.pep
TXN5: ClFA_BACTA

Description: Q03746 bacillus thuringiensis (subsp. aizawai). pesticidal
crystal protein cryI
Accession/ID: Q03746
=====General comments=====
ID ClFA_BACTA STANDARD; PRI: 1174 AA.
AC Q03746; . . .

SCORES Init1: 4184 Initn: 5748 Opt: 5915 z-score: 6522.1 E(): 0
>>TXN5: ClFA_BACTA
Initn: 5748 Opt: 5915 z-score: 6522.1 expect(): 0
Smith-Waterman score: 5915; 76.6% identity in 1184 aa overlap
(1-1177:1-1174)

cryla-105.pe MDNPNINCEIPNCLNPEVEVLGGERTGTYPIDISLSLQFLLESEFVPGAGFVLGL
10 20 30 40 50 60
cryla-105.pe MNNIQ-NQCVNCLNPEVEILNEER-STGRFLPDISLSLFLLESEFVPGVAFGL
10 20 30 40 50
ClFA_BACTA

cryla-105.pe VDIWGIFGSDWDLVQIEQLINQRIEFARNOAISRLGSLNLYQVIAESFREWAD
70 80 90 100 110 120
ClFA_BACTA

cryla-105.pe PTPALREEMRIQFNDMNSALTTPAIPFAVQNYQVPLLSYVQANLHLSVLRVSVFGQ
130 140 150 160 170 180
ClFA_BACTA

cryla-105.pe PNAQLREDVIRFANTDDALITAINNFTLSFELPLLSYVQANLHLSLRDAVSFGQ
120 130 140 150 160 170
ClFA_BACTA

cryla-105.pe RWGFDAATINSRYNDLTRLIGNVTDHAEVWNTGLERVMGPDSDRWIRYNQFRRLTLTV
190 200 210 220 230 240
ClFA_BACTA

cryla-105.pe LDIVLFPNYSRTYPIRTVTSQLTREIYNPVLEN--FDGSFRGSAQSIGESIRSPHLM
250 260 270 280 290
ClFA_BACTA

cryla-105.pe ILNLSITIVDHRGEYVWSGHOIMASVCFSPSEFTPLXGTGNAAQQRIQVQLQGVV
300 310 320 330 340 350
ClFA_BACTA

cryla-105.pe YRLTSLSYRRREFNIGINNQOLSV-LDGTETFAYGTSNMLPSAVYRKSGLVDSLDLIPPQN
360 370 380 390 400 410
ClFA_BACTA
```

```
cryla-105.pe NNVPPOGFSHRLSHVSMRSGFSNSSVSIIRAPMFSWIHBSAFNNIASDSITOIDLV
CIFA_BACTA NSGAFNDYSHVNLHVITFVRWPGEISGDSWRAPMFSWTHRSATPNTIDPERITOIDLV
420 430 440 450 460 470

cryla-105.pe KAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRI
CIFA_BACTA KAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTIVNINGQLPQRYRARIYASTTNLRI
480 490 500 510 520 530

cryla-105.pe YVTVAGERIFAGQFNKTMDTGDLTTFQSFYATINTATFFPMSOSSFTVGADTFSSGNEV
CIFA_BACTA YVTVAGERIFAGQFNKTMDTGDLTTFQSFYATINTATFFPMSOSSFTVGADTFSSGNEV
540 550 560 570 580 590

cryla-105.pe YIDRFELIPVTATLEAEYNLERAKAVNALFTSNQLGLKTNVDYHIDQVSNLYVLSL
CIFA_BACTA YIDRFELIPVTATLEAEYNLERAKAVNALFTSNQLGLKTNVDYHIDQVSNLYVLSL
600 610 620 630 640 650

cryla-105.pe EFCLDEKREUSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWCSTGTTIQGGDDVFKE
CIFA_BACTA EFCLDEKREUSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWCSTGTTIQGGDDVFKE
660 670 680 690 700 710

cryla-105.pe NYVTLSGTDFECYPTLVOKIDESKLAFTRYQLRGYIEDSODLEIYIRYNAKHETVNV
CIFA_BACTA NYVTLSGTDFECYPTLVOKIDESKLAFTRYQLRGYIEDSODLEIYIRYNAKHETVNV
720 730 740 750 760 770

cryla-105.pe PGTSLMPLSAQSPIGKCGENRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVCGT
CIFA_BACTA PGTSLMPLSAQSPIGKCGENRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVCGT
780 790 800 810 820 830

cryla-105.pe DLEDLGVWVIFKIKITQDGHARLGNLEFLEKPLVGEALARKAEKRWDRKREKLEWT
CIFA_BACTA DLEDLGVWVIFKIKITQDGHARLGNLEFLEKPLVGEALARKAEKRWDRKREKLEWT
840 850 860 870 880 890

cryla-105.pe NIVYKEAKESVDALFVNSQYQLQADTNIAIMIHAADKRVHSIREAYLPELSVPGVNAAI
CIFA_BACTA NIVYKEAKESVDALFVNSQYQLQADTNIAIMIHAADKRVHSIREAYLPELSVPGVNAAI
900 910 920 930 940 950

cryla-105.pe FEELGRIFTAFSLDARNVKNQDNFNGLSCKWVKGHVDVEEQNNORSVLYVVPWEAEV
CIFA_BACTA FEELGRIFTAFSLDARNVKNQDNFNGLSCKWVKGHVDVEEQNNORSVLYVVPWEAEV
960 970 980 990 1000 1010

cryla-105.pe SOEVKVCPRGYYILRVYAKGEGCGVTIHEIENNTDELKFSNCVEEYIPNNTVTCND
CIFA_BACTA SOEVKVCPRGYYILRVYAKGEGCGVTIHEIENNTDELKFSNCVEEYIPNNTVTCND
1020 1030 1040 1050 1060 1070

cryla-105.pe FEELGRIFTAFSLDARNVKNQDNFNGLSCKWVKGHVDVEEQNNORSVLYVVPWEAEV
CIFA_BACTA FEELGRIFTAFSLDARNVKNQDNFNGLSCKWVKGHVDVEEQNNORSVLYVVPWEAEV
1080 1090 1100 1110 1120 1130
```

cryla-105.pe	YRTLSTLRYRRPFMGINOQLSV-LDGTFFAYCTSNLPSAVYRKSQVLSLDEIPQON	420	430	440	450	460	470
M73254_1	YRTLSDPVVRG--GFGNPHYVLGRGVAFOQ-TGTN-HTRFRNSGFIHLSLDEIPQON	360	370	380	390	400	410
cryla-105.pe	NNVPPRQGSFHRSLKSHVSMFTSGFNSGSVGIKAPMFWSIHRSAEFNNIIASDSTQIPLV	420	430	440	450	460	470
M73254_1	NSGAPNDYSHVLNVHVTFTVRWPGCEISGDSWRAPMFWSIHRSAETPTNTIDPERITQIPLV	420	430	440	450	460	470
cryla-105.pe	KAHTLQSGTIVVRGPGFTGGDILRRTSQGPFAITVINQSLQPRVARIRVASTNLR	480	490	500	510	520	530
M73254_1	KAHTLQSGTIVVRGPGFTGGDILRRTSQGPFAITVINQSLQPRVARIRVASTNLR	480	490	500	510	520	530
cryla-105.pe	YVTVAGERIFAGQFNKMTDGTDLPTQSFYSYATINTAFTFPMQSSFTVGADTFSSGNEV	540	550	560	570	580	590
M73254_1	YVTVAGERIFAGQFNKMTDGTDLPTQSFYSYATINTAFTFPMQSSFTVGADTFSSGNEV	540	550	560	570	580	590
cryla-105.pe	YIDRFELIPVTATLEAEYNLERAKAVNALFTSTNQIGKINTVDHIDQVSNLVYLSL	600	610	620	630	640	650
M73254_1	YIDRFELIPVTATFEAYDLERAKAVNALFTSINQIGKINTVDHIDQVSNLVDCLSL	600	610	620	630	640	650

cryla-105.pe	650	670	680	690	700	710
M73254_1	650	670	680	690	700	710
cryla-105.pe	720	730	740	750	760	770
M73254_1	720	730	740	750	760	770
cryla-105.pe	780	790	800	810	820	830
M73254_1	780	790	800	810	820	830
cryla-105.pe	840	850	860	870	880	890
M73254_1	840	850	860	870	880	890
cryla-105.pe	900	910	920	930	940	950
M73254_1	900	910	920	930	940	950
cryla-105.pe	960	970	980	990	1000	1010
M73254_1	960	970	980	990	1000	1010
cryla-105.pe	1020	1030	1040	1050	1060	1070
M73254_1	1020	1030	1040	1050	1060	1070

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cryla-105.pe MDILNSITTYDHAHGEYWGSHQIMASPVGSGPEFTFLYGTMGNAAPQOORIVAQLOG
M73252_1 M73252_1 MDLNNLLITDILRGVHWAGHRVTSHTG-SSOVIITQYGITANAEPRTTASPFF
300 310 320 330 340 350
cryla-105.pe GV---VRTLSSTLYRRPNIGINNQQSLVDGTEFAYGTSNIPSAVYKSGTVDSDLEI
M73252_1 M73252_1 GLNFYRTLSNPFRRSENI-TPTGLINVQGVGIPQNNAEV---LYRSRGTVDLSNEL
360 370 380 390 400 410
cryla-105.pe PPNONVPPRQCFSHRLSHVMSFRSGNSSVSIIRAPMFSWTHRSAEFNNIASDSITQ
M73252_1 M73252_1 PIDGEN-SLVGYSGRHLSHWLTSLSYNTNITSL---PTFWTHRSATWNTINPDIITQ
420 430 440 450 460 470
cryla-105.pe IPVLKAKHTLOSQTIVRGPGFTGDIILRTSGGFAYTIVNINGQPQRYRARIRYASTT
M73252_1 M73252_1 IPLVKGFRIGGTSVINGPGFTGDIILRNTITGEFVSLQVNINSPIQRYRLRFRYASSR
470 480 490 500 510 520
cryla-105.pe NLRIYTVVAGERIPAGQENKMTGDPLTFQSFSAINTAFTFPMSQSFVTVGADFFSS
M73252_1 M73252_1 DARITVAIGQIRVMDTLKMEIGBSLTSRTSYTFNPSFPFRAMPDIIIRIAELPIR
530 540 550 560 570 580
cryla-105.pe GNEVYIDRFELIPVTATLEAYNLERAQKAVNALFTSNGLKTKTVDTHYDQVSNLVT
M73252_1 M73252_1 GGELYIDKIELLADATFESEYDLERAQKAVNALFTSNGLKTKTVDTHYDQVSNLVE
590 600 610 620 630 640
cryla-105.pe YLSDFCFLDKREJSEKYKAKRLSDERNLLQDNFKDINRQPERGWGGSTGIIQGGDD
M73252_1 M73252_1 CLSDFCLDKREJSEKYKAKRLSDERNLLQDNFNRGINRQPDRCMRGSTDITIIQGGDD
650 660 670 680 690 700
cryla-105.pe VFKENVTLSGTDFECYPTVLYOKIDESKLKATFYQIRGYIEDSODLEISIRYNAKHE
M73252_1 M73252_1 VFKENVTLPGFDFECYPTVLYOKIDESKLKATRYELRGYIEDSODLEISIRYNAKHE
710 720 730 740 750 760
cryla-105.pe TVNVPGTSLWPLSAQSPICKGCEPNRCAPHLEWNPDLDCSDRGKCAHSHHFSLDID
M73252_1 M73252_1 TVNVPGTSLWPLSAQSPICKGCEPNRCAPHLEWNPDLDCSDRGKCAHSHHFSLDID
770 780 790 800 810 820
cryla-105.pe VGTCDLNEDLGWVWIFIKTQDGHARPLGNLFLEKEKPLVGEALARKAEKKWADKREKL
M73252_1 M73252_1 VGTCDLNEDLGWVWIFIKTQDGYARPLGNLFLEKEKPLLEALARKAEKKWADKCKEL
830 840 850 860 870 880
cryla-105.pe EWTNITVYKEAKESVDALFVNSQYDQLQADNTNAMIHAADKRVHSIREAYLPESLVPVGV
M73252_1 M73252_1 EWTNITVYKEAKESVDALFVNSQYDQLQADNTNAMIHAADKRVHSIREAYLPESLVPVGV
890 900 910 920 930 940
cryla-105.pe EWTNITVYKEAKESVDALFVNSQYDQLQADNTNAMIHAADKRVHSIREAYLPESLVPVGV
M73252_1 M73252_1 EWTNITVYKEAKESVDALFVNSQYDQLQADNTNAMIHAADKRVHSIREAYLPESLVPVGV
950 960 970 980 990 1000 1010

```

cry1a-105.pe NAAIFEELEGRFTAFSLYDARVINKGDFNGLSQWVKGVDVVEQNNQSRVLYVPEW
M73252_1 NAAIFEELEGRFTAFSLYDARVINKGDFNGLSQWVKGVDVVEQNNQSRVLYVPEW
cry1a-105.pe EAPGQGVYTKLEVPETDKVMEIEGTEGTFVDSVEMLMEE
M73252_1 EAPGQGVYTKLEVPETDKVMEIEGTEGTFVDSVEMLMEE
cry1a-105.pe TCNDYTVNOEYGGAYTSRNGNEA-PSADYASVVEKSTDERNPCEVNGRDR
M73252_1 TCNDYTVNOEYGGAYTSRNGNEA-PSADYASVVEKSTDERNPCEVNGRDR
cry1a-105.pe YTPLPGYVTKLEVPETDKVMEIEGTEGTFVDSVEMLMEE
M73252_1 YTPLPGYVTKLEVPETDKVMEIEGTEGTFVDSVEMLMEE
cry1a-105.pe YTPLPGYVTKLEVPETDKVMEIEGTEGTFVDSVEMLMEE
TXN5:U94323_1 YTPLPGYVTKLEVPETDKVMEIEGTEGTFVDSVEMLMEE
Accession/ID: U94323
LOCUS U94323_1 [BTU94323]
DEFINITION Bacillus thuringiensis protoxin CryIEa4 (cryIEa4) gene, complete
(1-1177:1-1171)
=====
General comments=====

CRY1A-105.pe 3527 Initn: 4821 Opt: 5547 z-score: 6115.9 E(1): 0
>>TXN5:U94323_1
Initn: 4821 Initl: 3527 Opt: 5547 Z-score: 6115.9 expect(1): 0
Smith-Waterman score: 5593; 72.7% identity in 1185 aa overlap
(1-1177:1-1171)

cry1a-105.pe MDNNPNECIPYCNLSNPEVEVLGGERIEGTIPIDISLSITOFLLSEFVPCAGFVLGL
U94323_1 MDNNPNECIPYCNLSNPEVEVLGGERIEGTIPIDISLSITOFLLSEFVPCAGFVLGL
cry1a-105.pe VDIWIGFGSOWDAFLVOIEQLINORIEEFARNQAIISRLGSLNLYIYAESEFWEAD
U94323_1 VDIWIGFGSOWDAFLVOIEQLINORIEEFARNQAIISRLGSLNLYIYAESEFWEAD
cry1a-105.pe PTNPALREEMRIFQNDMNSALTAIPFAVONTQVPLLSVYVQAAHLHLSVLDSVFEQ
U94323_1 PTNPALREEMRIFQNDMNSALTAIPFAVONTQVPLLSVYVQAAHLHLSVLDSVFEQ
cry1a-105.pe RWGFDAAATNSRYNDLTRILGNYTDAVRWNTGLERVGPDS--RDWTRYNQFRRLT
U94323_1 RWGFDAAATNSRYNDLTRILGNYTDAVRWNTGLERVGPDS--RDWTRYNQFRRLT
cry1a-105.pe VGCCTDLNEDLGVVWVIFKIKTQDQGHARLGNLEFLEKPLVGEALARVRAEKWKREKL
U94323_1 VGCCTDLNEDLGVVWVIFKIKTQDQGHARLGNLEFLEKPLVGEALARVRAEKWKREKL

cry1a-105.pe LTVLDIVSLFPNYSKRTYPIRTVSQLTRELYTNPVLENFDSFRGSAQIGES-IRSPHL
U94323_1 LTVLDIVSLFPNYSKRTYPIRTVSQLTRELYTNPVLENFDSFRGSAQIGES-IRSPHL
cry1a-105.pe MDILNSTIYTDHAREYVWGHQIMASPVGSGPEFTFPLXGTMGNAPOQRIVAOLGQ
U94323_1 MDILNSTIYTDHAREYVWGHQIMASPVGSGPEFTFPLXGTMGNAPOQRIVAOLGQ
cry1a-105.pe GY--YRTLSSTLYRPPENIGNNQOLSVLDTGTFAYGTSNLPASVAVRKSQSTVSLDEI
U94323_1 GY--YRTLSSTLYRPPENIGNNQOLSVLDTGTFAYGTSNLPASVAVRKSQSTVSLDEI
cry1a-105.pe PPQNNVPPRQGFHSLKSVMSFRSGFSNSSLIIHAPMFWIHRSAEFNIIASDSITQ
U94323_1 PPQNNVPPRQGFHSLKSVMSFRSGFSNSSLIIHAPMFWIHRSAEFNIIASDSITQ
cry1a-105.pe IPIVKAHTLOSQTVVVRGPGFTGGDILRTSGGPFATVINGOLPORVARIYASTT
U94323_1 IPIVKAHTLOSQTVVVRGPGFTGGDILRTSGGPFATVINGOLPORVARIYASTT
cry1a-105.pe NLAVVTVVAGERIFAGQFNKMTDGTPLTFQSFYATINTATFPMQSQSTVAGADTFSS
U94323_1 NLAVVTVVAGERIFAGQFNKMTDGTPLTFQSFYATINTATFPMQSQSTVAGADTFSS
cry1a-105.pe GNLVLDIVSLFPNYSKRTYPIRTVSQLTRELYTNPVLENFDSFRGSAQIGES-IRSPHL
U94323_1 GNLVLDIVSLFPNYSKRTYPIRTVSQLTRELYTNPVLENFDSFRGSAQIGES-IRSPHL
cry1a-105.pe YLSDFECLDEKKEEGERKKAQKASLPEMLQDDNFGNROPDRGWRGSDITIQGDD
U94323_1 YLSDFECLDEKKEEGERKKAQKASLPEMLQDDNFGNROPDRGWRGSDITIQGDD
cry1a-105.pe VFKNVTLSGTTFDECPTTYLYONDESXKAPTRPOLRGYEDSDLYLSIRYNAKHE
U94323_1 VFKNVTLSGTTFDECPTTYLYONDESXKAPTRPOLRGYEDSDLYLSIRYNAKHE
cry1a-105.pe TVNVPCTGSLWPLSAQSPICKGCEPNRCAPHLEWNPDLSCCHGEKCAHLEHSLDID
U94323_1 TVNVPCTGSLWPLSAQSPICKGCEPNRCAPHLEWNPDLSCCHGEKCAHLEHSLDID
cry1a-105.pe VGCCTDLNEDLGVVWVIFKIKTQDQGHARLGNLEFLEKPLVGEALARVRAEKWKREKL
U94323_1 VGCCTDLNEDLGVVWVIFKIKTQDQGHARLGNLEFLEKPLVGEALARVRAEKWKREKL

Monsanto Company
Final Report

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MSL No. 20351
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cryla-105.pe EWEINIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPESLVPFVGV
U94323_1 EWEINIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPESLVPFVGV

cryla-105.pe NAAIFEELEGRIITAFSLYDARNVKNKGNDFNGLSCWNVKGHVDEVEQNNQKRSVLVPEW
U94323_1 NAAIFEELEGRIITAFSLYDARNVKNKGNDFNGLSCWNVKGHVDEVEQNNQKRSVLVPEW

cryla-105.pe EAEYSQEVRCPCRGYILRVYAYKEGEGCVTHIEIENNDELKFSNCVEEIEYNNIV
U94323_1 EAEYSQEVRCPCRGYILRVYAYKEGEGCVTHIEIENNDELKFSNCVEEIEYNNIV

cryla-105.pe TCNDYVNOQEYGGAYTSNRGYNEA-PSVPADYASVVEEKSYYTDGRRENPCFEFRGYRD
U94323_1 TCNDYVNOQEYGGAYTSNRGYNEA-PSVPADYASVVEEKSYYTDGRRENPCFEFRGYRD

cryla-105.pe YTPLPVGVTKLEYEPETDKVWIEIGETGTFFIVDSVELLIMEE
U94323_1 YTPLPVGVTKLEYEPETDKVWIEIGETGTFFIVDSVELLIMEE

cryla-105.pep
TXN5:006894
Description: 006894 bacillus thuringiensis. cryleat. 6/2001
Accession/ID: 006894
ID 006894
AC 006894
DT 01-JUL-1997 (Tremblrel. 04. Created) . . .

SCORES Initl: 3527 Initn: 4821 Opt: 5547 z-score: 6115.9 E(): 0
>TXN5:006894
Initn: 4821 Initl: 3527 Opt: 5547 z-score: 6115.9 expect(): 0
Smith-Waterman score: 5593; 72.7% identity in 1185 aa overlap
(1-1177:1-1171)

cryla-105.pe MDNNPNEICIPYCNLSHPEVEVLGGRIETGYTPIDISLSLTQFSLSEVPCAGFVGL
006894 MEIVNQNCQVPCYNCLNPFENEILLDIERSNSTVAT-NIALEISRLASA-TPIGGILLGL

cryla-105.pe VDIIWGIFGQSOMDAFLVQIOLINQRIEFAFNOAQLRGLSLNLYIYAESFREWEAD
006894 FDAIWGIFGQSOMDAFLVQIOLINQRIEFAFNOAQLRGLSLNLYIYAESFREWEAD

cryla-105.pe PTNPALKEEMRIQFNDMSALTAIPFAYQNVPLSVYQAAHLSVLSDVSVFGQ
006894 PTNPALKEEMRIQFNDMSALTAIPFAYQNVPLSVYQAAHLSVLSDVSVFGQ

cryla-105.pe RMGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERVMPDPS---RDWIRYNQFRRELT
006894 RMGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERVMPDPS---RDWIRYNQFRRELT

cryla-105.pe LTVLDIVSLFNPYSRTPYPIRTVQSOLTRITVNPVLENFDGFRGSAQIEGS-IRSPHL
006894 LTVLDIVSLFNPYSRTPYPIRTVQSOLTRITVNPVLENFDGFRGSAQIEGS-IRSPHL

cryla-105.pe MDLNLITIIYDHRGEYVMSGHQIMASFGVSGPEFTPELTGTMGNAAPQORIVAGLQ
006894 MDLNLITIIYDHRGEYVMSGHQIMASFGVSGPEFTPELTGTMGNAAPQORIVAGLQ

cryla-105.pe GV---YRTLSTLYRRFPNIGINNQOLSVDLGTETAYGTSSNLPSAVYKSGTVDSDEI
006894 GV---YRTLSTLYRRFPNIGINNQOLSVDLGTETAYGTSSNLPSAVYKSGTVDSDEI

cryla-105.pe PPONNNVPROGFSHRLSHVMSFRSGFSSVSIIRAPFMSHRSABFNNTIASDSITC
006894 PPONNNVPROGFSHRLSHVMSFRSGFSSVSIIRAPFMSHRSABFNNTIASDSITC

cryla-105.pe IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTVININGQLPQRYRARIYASIT
006894 IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYTVININGQLPQRYRARIYASIT

cryla-105.pe NLRIYTVAGERIFAGOFNKMTDGPITFQSFYATINTATFFPMSSOSTVGCADTFSS
006894 NLRIYTVAGERIFAGOFNKMTDGPITFQSFYATINTATFFPMSSOSTVGCADTFSS

cryla-105.pe GNEVYIDRFELIPVTATLEAEYNLRAQKAVNALFTSTNQLGKTNVTDYHIDQVSNLVT
006894 GNEVYIDRFELIPVTATLEAEYNLRAQKAVNALFTSTNQLGKTNVTDYHIDQVSNLVT

cryla-105.pe YLSDFCLDKRELSKVKHAKLSDERNLNLDQNSFKDINRQPERGWSGTGTTIQGGD
006894 YLSDFCLDKRELSKVKHAKLSDERNLNLDQNSFKDINRQPERGWSGTGTTIQGGD

cryla-105.pe VFENYVLTGTFDECPYTYLQKIDESKAKAFTRYOLRGYIEDSODLEIYSIRYNKHE
006894 VFENYVLTGTFDECPYTYLQKIDESKAKAFTRYOLRGYIEDSODLEIYSIRYNKHE

cryla-105.pe TVNVPQTSGLMPLSAQSPICKGEPNRCAPLHWNPDLCSCRDGKCAHSHHFSLDID
006894 TVNVPQTSGLMPLSAQSPICKGEPNRCAPLHWNPDLCSCRDGKCAHSHHFSLDID

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~~CXVLA-105.pe~~

cryla-105.pe EWEINIVKEAKESDADFINSOYDQCBNTIANIHAAKRVHSIREAYPELSVIPGV
006894 EWEINIVKEAKESVDALNSOYDRLQADNTIANIHAAKRVHSIREAYPELSVIPGV

```

      890      960      970      980      990      1000      1010
crr1a-105.pe NAAIFELGRIFTAFSLYDARNKINGNGKCNVKNVDYDQGNQORSILVLPW
NAAIFEELEGRIFTAFSLYDARNKINGNGKCNVKNVDYDQGNQORSILVLPW
NAAIFEELEGRIFTAFSLYDARNKINGNGKCNVKNVDYDQGNQORSILVLPW
NAAIFEELEGRIFTAFSLYDARNKINGNGKCNVKNVDYDQGNQORSILVLPW
      006894

```

[illegible][illegible]

	1140	1150	1160	1170
cryla-105.pe	YTPLPVGYVTKLEIFP	PEITDKWIEIGTEG	FIVDSV	ELLME
	YTPLPAGYVTKLEYFP	ETDKWIEIGTEG	FIVDSV	ELLME
O06894				
	1130	1140	1150	1160
	1170			

cryla-105.pap
TXN5:CIEA_BACTX
Description: O57458 bacillus thuringiensis (subsp. kenya) pesticidal

```

crystal protein clyle
Accession/ID: Q57458
=====General comments=====
ID C1EN_BACXY STANDARD; PRT: 1171 AA.
AC Q57458; Q03741; . . .

```

```

SCORES      Init1: 3521  Initn: 4817  Opt: 5543  z-score: 6111.5  E(): 0
>>>XMS:CIEA_BACTX
              Initn: 4817  Init1: 3521  opt: 5543  Z-score: 6111.5  expect(): 0
Smith-Waterman score: 5589;    72.7% identity in 1185 aa overlap
(1-1177:1-1171)

```

```
cryla-105.pe MDNNPNNECIPNCLSNPEVEVLGGRRITGVTPTDLSLSTOFLSEVPAGVGL  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
CLEA_BACTX MEIVNQOCVPNCINNENFELDIERNSTVAT-NIALESRLASA-TPIGGILLGL
```

```

cryla-105.pe 70 80 90 100 110 120
VDIWIGFGSMDALVIOELINQRIIEFARNQAIISLEGLSNLYVAESFREWAD
| | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | |
FOAINGSIGPMDLFIEQIELLDQKIEFARNQAIISLEGISYIGVITAEFREWAD
CIEA_BACTX 60 70 80 90 100 110

```

130 140 150 160 170 180

[illegible]

```

      190      200      210      220      230
CryIa-105.pe  RWGDAATINSRYNDLTRLIGNYTHAVRWNTGLERVMPQS---RDWIRYNFRRELT
               |||||
CIEA_BACTX    AWGFDIATNSRYNDLTRLIPYTDVAVRWNTGLDLR--PRTGGURWARFNQFRRELT
               |||||

```

[illegible]

```

300      310      320      330      340      350
MDILNSITYTDAHRGYWNSHQINASPVGSPETPLTGMNAPQORIVAQLGQ
CIEA  BACTX
MFENLLNTDIDLARGVHWHRVTSHTFG-SSQVITTPGYGITANAEPTATSPFF

```

~~CV01a-105.pe GV---VETLSSLYRRPFNIGINNOOLSVLDGTFAYGTSNIPSAVYRKGSTVDSDIEI
:
GLMLFVTILSNPFFERSENI--TTLGINVVQGVGFIPNNAEV--LYRSRGTTVDSLNEL~~

420 430 440 450 460 470
 428 430 440 450 460
 PIDGHN-ELVGYSHRUSHVLTFRSYNNTISL---PTFWVHHSATNTNTINPDITTO
 CLEA_BACTA

[illegible][illegible]

cryIa-105.pe

	600	610	620	630	640	650
GNEVYIDREFELIPVTATIEAEYNDFRACAKVAALFTSTNOLGKKNNTVS						
: :: :: :	:	:	:	:	:	:
GLGYIDKIELLIADATFEEDYLRAQRSVNAAFTSTNGGLGTVDTDNDISNVLVE						

CIEA_BACTX

```

cryla-105.pe  VLSDFCLDEKSEKVKHAKRUSDNRNLQDSNFKDINPQKRGASTDILQGGDD
                  660      670      680      690      700      710
C1EA_BACTX    CLSDFCLDEKSEKVKHAKRUSDNRNLQDSNFPNGINQKPGKSTDIILQGGDD
                  650      660      670      680      690      700

```

	720	730	740	750	760	770
cry1a-105.pe	VFKENYTLSTGTFDECPYYLQKIDSKLKATRYQLRGVIESQDLLEYSTRNAKE					
C1EA_BACTX	VFKENYTLSTGTFDECPYYLQKIDSKLKATRYQLRGVIESQDLLEYLYRYNAKE					
C1EA_						

	780	790	800	810	820	830
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cryla-105.pe TVNPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDID
CLEA_BACTX 770 780 790 800 810 820
      840 850 860 870 880 890
cryla-105.pe VGCTDNEGLGVWIFKIKTKODGHARLGNLFELEKPLVGEALARYKRAEKWRDKREKL
CLEA_BACTX 830 840 850 860 870 880
      890 900 910 920 930 940
cryla-105.pe EWEINIVYKEAKESVDALFVNSQYDQLQADTNIAHAAKRVHSIREAYLPESLVPVGV
CLEA_BACTX 890 900 910 920 930 940
      950 960 970 980 990 1000
cryla-105.pe NAAIFPELEGRIPTAFSLDARNVIRKNGDFNGLSCWNVKGVHVDVEEQNQRSLVVPVPEW
CLEA_BACTX 950 960 970 980 990 1000
      1020 1030 1040 1050 1060 1070
cryla-105.pe EAEVSOEVRVCPGRGYILRVTAKEGYGEGCVTHIEINNTDELKFSNCVEEIVPNNTV
CLEA_BACTX 1010 1020 1030 1040 1050 1060
      1070 1080 1090 1100 1110 1120
cryla-105.pe TCNDYTVNOEGYGGAYTSRNRGYNIA-PSVPADYASVYERKSTYDGRNCFENRGYRD
CLEA_BACTX 1070 1080 1090 1100 1110 1120
      1130 1140 1150 1160 1170 1180
cryla-105.pe YTPLPGVYVTELEVPETDKVMIEGEGTGFIVDSVELLMEE
CLEA_BACTX 1130 1140 1150 1160 1170
      1180 1190 1200 1210 1220 1230
cryla-105.pep
TXN5:Q45749
Description: Q45749 bacillus thuringiensis. crystal protein. 6/2001
Accession/ID: Q45749
ID Q45749 PRELIMINARY;
AC Q45749 PRT; 1174 AA.
DT 01-NOV-1996 (Tremblrel. 01, Created) . . .

=====
SCORES Init1: 2880 Initn: 5043 Opt: 5318 z-score: 5863.2 E(): 0
>>TXN5:Q45749
Initn: 5043 Init1: 2880 Opt: 5318 z-score: 5863.2 expect(): 0
Smith-Waterman score: 5318; 68.8% identity in 1187 aa overlap
(1-1177:1-1174)
```

```
cryla-105.pe VDIIMGIFGSPQMDAFLVQIEQLINQRIEIEFARNQAIISRLGLESLNLYQIYAESEFREWEAD
Q45749 60 70 80 90 100 110
      130 140 150 160 170 180
cryla-105.pe PTNPALREMRIOFNDMNSALITTAIPLFAVONYQVPLSVYVQAANLHLSVLSDVSVFGQ
Q45749 120 130 140 150 160 170
      180 190 200 210 220 230
cryla-105.pe RMGFDAATINSRYNDLTRIGNYTDHARVWNTGLERVWGPDSRDWIRYNQFRRELTIV
Q45749 180 190 200 210 220 230
      240 250 260 270 280 290
cryla-105.pe LDIVSLFPNDSTRYPIRTVSQLTREIYTNPVLEN--FDGFRGSAQIGSIRSPFLMD
Q45749 240 250 260 270 280 290
      300 310 320 330 340 350
cryla-105.pe ILNLSITYTDAHRGEYVWGHQIMASPVGSGPEFTFLYGTMGNAAPQORIVAQLGQGV
Q45749 300 310 320 330 340 350
      360 370 380 390 400 410
cryla-105.pe YRTLSSTLYRPPENIGINNQLSV-LDGTETFAYGTSNNLPSAVYRKSGTVDSLDSEIPON
Q45749 360 370 380 390 400 410
      420 430 440 450 460 470
cryla-105.pe NNVPFPGFGRHLSHVSMR--SGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQPL
Q45749 420 430 440 450 460 470
      480 490 500 510 520 530
cryla-105.pe VKAHTLOSITTVVRGPGFTGGDILRLRTSGGPFAYTIVNIGOLPQRYRARIYASTTNLR
Q45749 470 480 490 500 510 520
      530 540 550 560 570 580
cryla-105.pe IYVTVAGERIFACQKNKMTDGLPTFQSFSVATINTAFTPMQSSFTVGADTFSSQNE
Q45749 530 540 550 560 570 580
      590 600 610 620 630 640
cryla-105.pe VYIDRFELIPVTATLEAEVNLERAQKAVNALFTSTNQLGLKNTVDYHIDQVSNLTVLS
Q45749 590 600 610 620 630 640
      650 660 670 680 690 700
cryla-105.pe DEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGSGSTGTTIQQGDDVFK
Q45749 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
```

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cryla-105.pe ENVTLSGTPDECTYLYQKIDESKIKAFTRYQGVIEDSODLEIYSIRYNAKHETVN
Q45749 ENVTLSGTPDECTYLYQKIDESKIKAFTRYQGVIEDSODLEIYSIRYNAKHETVN
cryla-105.pe VPGGSAFELSAOSLGGGEPNCSAHLNNDLDCSCRGCEKCAHSHHFSLDIDVGC
Q45749 VPGGSAFELSAOSLGGGEPNCSAHLNNDLDCSCRGCEKCAHSHHFSLDIDVGC
cryla-105.pe TDLNEDLGVMVIFKIKTQDSHAGNLEFEEKRAVGEALNVAEKKVRDREKLEWE
Q45749 TDLNEDLGVMVIFKIKTQDSHAGNLEFEEKRAVGEALNVAEKKVRDREKLEWE
cryla-105.pe TNIVYKAKESVDALFVNSQYDRLOADNTIAMIAADKRAKRPHEAYDPFESPVADA
Q45749 TNIVYKAKESVDALFVNSQYDRLOADNTIAMIAADKRAKRPHEAYDPFESPVADA
cryla-105.pe IFEELEGRIFTAFSLYDARNVKNKGDFNGLSCWNVKGVHDVEEQNORSLVPEWEKE
Q45749 IFEELEGRIFTAFSLYDARNVKNKGDFNGLSCWNVKGVHDVEEQNORSLVPEWEKE
cryla-105.pe VSGEVRCFGYILIRVTAYKEGEGCVTHIEENTDELKFSVCVEEELIYFNVTCTN
Q45749 VSGEVRCFGYILIRVTAYKEGEGCVTHIEENTDELKFSVCVEEELIYFNVTCTN
cryla-105.pe DYTVNCE--EYGGATYRNRGYNEA---PSVPADYASVVEKSYTDGRRNCPENRGY
Q45749 DYTVNCE--EYGGATYRNRGYNEA---PSVPADYASVVEKSYTDGRRNCPENRGY
cryla-105.pe RDYTPLPVGYVTKLEYFPETDKWIEIGETEGTFIVDSVELLMEE
Q45749 RDYTPLPVGYVTKLEYFPETDKWIEIGETEGTFIVDSVELLMEE
cryla-105.pe
Q45749
Description: 066377 bacillus thuringiensis (subsp. morrisoni). pesticidal
crystal protein cr
Accession/ID: 066377
ID C1FB_BACTM STANDARD; PRT; 1169 AA.
AC 066377; Q9RC19; . . .
SCORES Initl: 3052 Initn: 4791 Opt: 5288 Z-score: 5830.1 E(): 0
>TXN5:C1FB_BACTM
Initn: 4791 Initl: 3052 Opt: 5288 Z-score: 5830.1 expect(): 0
Smith-Waterman score: 5288; 68.4% identity in 1186 aa overlap
(1-1177:1-1169)

cryla-105.pe MDNNPINECPYNCLNSPEVVLGGRIETGYPIDISLSTQFLLSSEFVPGAGFVLGL
C1FB_BACTM MDNNPINECPYNCLNSPEVVLGGRIETGYPIDISLSTQFLLSSEFVPGAGFVLGL
cryla-105.pe VDIIMGIFGSPQWDAFVQIQEOLINORIEEFARNOAISLEGSLNLYOYAESFREWEAD
C1FB_BACTM VDIIMGIFGSPQWDAFVQIQEOLINORIEEFARNOAISLEGSLNLYOYAESFREWEAD
cryla-105.pe PTPALREEMRIOFNDMSALTATPFAVQNYOVPLLSVYVQAANLHLSVLRDVSVFQO
C1FB_BACTM PTPALREEMRIOFNDMSALTATPFAVQNYOVPLLSVYVQAANLHLSVLRDVSVFQO
cryla-105.pe RWGFDAAATINSYNDLRLIGNYTDHVRWYNTGLERVWGFSDRMWIRYNOFRRELTIV
C1FB_BACTM RWGFDAAATINSYNDLRLIGNYTDHVRWYNTGLERVWGFSDRMWIRYNOFRRELTIV
cryla-105.pe LDIVSLFPYDSRTYPIRTYSOLTRTYVNPVLEN--FDGSEFGSAGQIEGSIIRSPHMD
C1FB_BACTM LDIVSLFPYDSRTYPIRTYSOLTRTYVNPVLEN--FDGSEFGSAGQIEGSIIRSPHMD
cryla-105.pe LNSITITYDAURGEYVMSGHQIMASPVGSGFEFFLYXTGMTNAAPOQRIVAQOGV
C1FB_BACTM LNSITITYDAURGEYVMSGHQIMASPVGSGFEFFLYXTGMTNAAPOQRIVAQOGV
cryla-105.pe VYVQSTYRPFNGINNOOLSV-LDGTEFAYGTSNLSAVYKRSYGVDSLEIPQON
C1FB_BACTM VYVQSTYRPFNGINNOOLSV-LDGTEFAYGTSNLSAVYKRSYGVDSLEIPQON
cryla-105.pe NVNPPRGSSHNLSHVSUR--SNFSSNSVILIRAPMFSWIRHSAEFNNIIASDSITQIPL
C1FB_BACTM NVNPPRGSSHNLSHVSUR--SNFSSNSVILIRAPMFSWIRHSAEFNNIIASDSITQIPL
cryla-105.pe VKAHTLOSQTIVVRGFGFTGDIIRTSGGPFAYTVININGOLPVRIRIIRASTTLNR
C1FB_BACTM VKAHTLOSQTIVVRGFGFTGDIIRTSGGPFAYTVININGOLPVRIRIIRASTTLNR
cryla-105.pe IYTVVAGERIFAGQFNKTMIDGDLPTQSFVSVAITNATPFPNSQSSFVAGLTSSGNE
C1FB_BACTM IYTVVAGERIFAGQFNKTMIDGDLPTQSFVSVAITNATPFPNSQSSFVAGLTSSGNE
cryla-105.pe VVIDREFELPVTATLEAEYNLERAKAVNALFTSNQGLKTNVTHVDQVSNVYVNS
C1FB_BACTM VVIDREFELPVTATLEAEYNLERAKAVNALFTSNQGLKTNVTHVDQVSNVYVNS
cryla-105.pe VVIDREFEPAETFEAESDLERAKAVNALFTSNQGLKTNVTHVDQVSNVYVNS
C1FB_BACTM VVIDREFEPAETFEAESDLERAKAVNALFTSNQGLKTNVTHVDQVSNVYVNS

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cryIa-105.pe DEFCLEKRELSEKVKHAKRLSDERNLLQDSNFKDINROPERGWSGGSTGITIQGGDVFVK
CLFB_BACTM DEFCLEKRELSEKVKHAKRLSDERNLLQDSNFKDINROPERGWSGGSTGITIQGGDVFVK
550 650 660 670 680 690 700

cryIa-105.pe ENVVTLSTGTFDECYTYLYQKIDESKLFKAFTRYQLRGYIEDSCDLEIYSIRYNAKHETVN
CLFB_BACTM ENVVTLSTGTFDECYTYLYQKIDESKLFKAFTRYQLRGYIEDSCDLEIYSIRYNAKHETVN
710 720 730 740 750 760

cryIa-105.pe VPGTGSLLWPLSAQSPGKGEENRCAPHLEWNPDLDCSCRDGCKCAHSHHFLDIDVGC
CLFB_BACTM VPGTGSLLWPLSAQSPGKGEENRCAPHLEWNPDLDCSCRDGCKCAHSHHFLDIDVGC
770 780 790 800 810 820

cryIa-105.pe TDINELDLGWVIFIKITQDGHARLGNLEFLEEKPLVGEALARKVKAERKWRDKREKLEWE
CLFB_BACTM TDINELDLGWVIFIKITQDGHARLGNLEFLEEKPLVGEALARKVKAERKWRDKREKLEWE
830 840 850 860 870 880

cryIa-105.pe TINVYKEAKESVDALFVNSQYDLQADTNIAMIHAAKRVHSIREAYLPELSVIPGVNAA
CLFB_BACTM TINVYKEAKESVDALFVNSQYDLQADTNIAMIHAAKRVHSIREAYLPELSVIPGVNAA
890 900 910 920 930 940

cryIa-105.pe IFEELGRIPTAFSLYDARNVKNKGFNNGLSQVNVKGVHVDVEEQNNORSVLYVPEWEAE
CLFB_BACTM IFEELGRIPTAFSLYDARNVKNKGFNNGLSQVNVKGVHVDVEEQNNORSVLYVPEWEAE
950 960 970 980 990 1000

cryIa-105.pe VSOEVRVCPGRGYILRTVATYKEGEGCVTHIEENNTDELKFS-NCVEEIRYNNVTVC
CLFB_BACTM VSOEVRVCPGRGYILRTVATYKEGEGCVTHIEENNTDELKFS-NCVEEIRYNNVTVC
1010 1020 1030 1040 1050 1060

cryIa-105.pe NDVTYNOEYGGAYTSNRGYNEA---PSVPADYASVYEKSYTDGRENPCFENRGYR
CLFB_BACTM NDY--NKNHGANACSSRNGGYDESYESNSIPADYAPVYEEAYTDGQRGNPCFENRGH-
1070 1080 1090 1100 1110 1120

cryIa-105.pe DYTEPLPVGVTKLEYFPETDKVWIEIGETEGTIVDSVLELLMEE
CLFB_BACTM --PPLPAGVVTAELEYFPETDVWVEIGETEGTIVDSVLELLMEE
1130 1140 1150 1160

cryIa-105.pep
TXN5:CLIEB_BACTA
Description: Q03745 bacillus thuringiensis (subsp. aizawai). pesticidal
crystal protein cryI
Accession/ID: Q03745
=====General comments=====
ID CLIEB_BACTA STANDARD; PRT; 1174 AA.
AC Q03745; . . .
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SCORES Initl: 2864 Initn: 4526 Opt: 5185 z-score: 5716.4 E(): 0

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>>TXN5:CLIEB_BACTA (1174 aa)
initn: 4526 opt: 2864 2-score: 5716.4 expect(): 0
Smith-Waterman score: 5244; 67.6% identity in 1188 aa overlap
(1-1177:1-1174)

cryIa-105.pe MDNPNINICIPYCNLSNPEVVEVGGERIETGYTIDISLSLTQFLSEFVPGAGVGLG
CLIEB_BACTA MENNIE-NOCIPYCNLSNPEVVEVGGERIETGYTIDISLSLTQFLSEFVPGAGVGLG
10 20 30 40 50

cryIa-105.pe VDIWIGFPGSOWDAFLVQIBOLINRIEFPARNOAISRLGSLNLYQIYAESPREWEAD
CLIEB_BACTA FDIWNGAIGPSOWDIFLEQIEELLIGRIEFPARNOAISRLGSLNLYQIYAFKNWEVD
60 70 80 90 100 110

cryIa-105.pe PTNPALREEMRIQFNDMNSALTATPLFAVQNYQVPLLSVYQAAHLHSLVLRDVSFVGQ
CLIEB_BACTA PTNPALREEMRIQFNDMNSALTATPLFAVQNYQVPLLSVYQAAHLHSLVLRDVSFVGQ
120 130 140 150 160 170

cryIa-105.pe RWGFDATINSRYNDLTQLIGNYTDHAVVYNTGLERV-WGPDSDRMVIRYNOFRELTLT
CLIEB_BACTA RWGFDVATINSRYNDLTQLIGEYTDHAVVYNTGLNRLPRNEGVRGWARFNRFRELTIS
180 190 200 210 220 230

cryIa-105.pe VLDIVSLFNPDSRTYPIRTVQSLTREIYNPNVLENFDGSPRGSAGQIEGS-IRSPHLM
CLIEB_BACTA VLDIISFPQYDSRLYPIPTIYQLTREVYTDVITDPIYVTPSFESISAIRSPHLM
240 250 260 270 280 290

cryIa-105.pe ILNSITIIDARGEYVHSGHQMNASPVGFSQPEFTPLIGTMGNAAPQORIVAGLQGVV
CLIEB_BACTA FLNNIIIDTLIRGVHVGWAGRVTSHTFTG-SSQVISSPQYGITANAEPSRTIAPSTFPGL
300 310 320 330 340 350

cryIa-105.pe ---YRTLSLTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASVYKSGTVDSLEIIPP
CLIEB_BACTA NLFYRTLSLDPFFRRSDNI-MPTLGINVVGQVGFQPNNGEV---LYRRGTVDLSLEIPI
360 370 380 390 400 410

cryIa-105.pe QNNVPPRQFHSRLHSHVSMRPSGFSNVSIIIRAPMSWIHRSAEFNIIIASDSITQIP
CLIEB_BACTA DGEN--SLVGYSRHLRSLVTLTRSLYNTNITSL---PTFWTHHSATDRNIYIPDVITQIP
420 430 440 450 460

cryIa-105.pe LVKAHTLQSGTTWVRGPGFTGCDILRRTSGGPFAYTVIWNQGLPORVBARIRYASTTNL
CLIEB_BACTA LVKFSLSLTSVTVRGPFTGCDIIRTVNNGVLSNLSNFNTSLQRYRVRYRYAASQTM
470 480 490 500 510 520

cryIa-105.pe RIYTVAGERIFAGQFNKMTMDTGDPLTFQSFYATINTAFTFPMSSQSTFVGADTFSSGN
CLIEB_BACTA VWRVNVGSGTTFDQGFPTMSANGSLTSQSFRAEFVGTSGSQTA-GISISNPNRQ
530 540 550 560 570 580

SCORES 600 610 620 630 640 650
```

[illegible]

cryIIa-105.pep
 TXN5:M73253_1
 Description: M73253 *Bacillus thuringiensis* (cryIE(b))
 gene, complete C
 Accession/ID: M73253

[illegible]

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cry1a-105.pe RIYTVAGERIFAGQFNKTMGTGDLPTFQSFYSYATINTAFTPFMSQSGFTVGADTFSSGN
M73253_1 VMRVNNGSTTFDQGFSTMSANGSLTSQSFRAFPVGVISGSGOTA-GISISNPGQR
530 540 550 560 570 580

cry1a-105.pe EVVIDRFELIPVATLEAEYNLERAKAVNALFTSTNQLGLKNTVDYHIDQVSNLVYL
M73253_1 TPLHDLRIEIPVDATFEAEYDLERAKAVNSLFTSSNQIELKNTVDYHIDQVSNLVCL
590 600 610 620 630 640

cry1a-105.pe SDFCLDEKELSEKVKHAKRLSDERNLLODSNPKDINROPERGCGSGTGITIOGGDDVF
M73253_1 SDFCLDEKELSEKVKHAKRLSDERNLLODPNFRGINRQPDGRGSGTGITIOGGDDVF
650 660 670 680 690 700

cry1a-105.pe KENVYVLSGTDFDECYPTLYQKIDESKLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
M73253_1 KENVYVLSGTDFDECYPTLYQKIDESKLKAYNRVQLRGYIEDSQDLEIYSIRYNAKHETV
710 720 730 740 750 760

cry1a-105.pe NVFGTSLWPLSAQSPFGKCGEPNRCAPHLEWNPDLDCSDRDEKCAHSHHFFSLDDIVG
M73253_1 NVFGTSLWPLSAQSPFGKCGEPNRCVPHLEWNPDLDCSDRDEKCAHSHHFFSLDDIVG
770 780 790 800 810 820

cry1a-105.pe CTDLNEDLGWVVFVKIKTOQBCHARLGNLEFLEKPLVGEALRKAERKAKRDRKREKLEW
M73253_1 CTDLQEDLGWVVFVKIKTOBQYARLGNLEFLEKPLVGEALRKAERKAKRDRKREKLOL
830 840 850 860 870 880

cry1a-105.pe ETNIVYKAKESVDALFVNSQYDQLQADNTNAMIHAADKRVHSIREAYLPELSVIPGNA
M73253_1 ETKRVYTEAKEAVDALFVDSQYDRQLQADNTNIGMIHAADRLVHQIHEAYLPELPFIPGINV
890 900 910 920 930 940

cry1a-105.pe AIFEELEGRIFFAFSLYDARNVTKNGDFNGLSCWVKGHVDEEKNQORSVLVVPWEA
M73253_1 VIFEELENRISTALSIDARNVTKNGDFNGLSCWVKGHVDEEKNQORSVLVVPWEA
950 960 970 980 990 1000

cry1a-105.pe EVSQEVRCPCGYILRTVAYKEGYGEGCVTHIEIENNTDELKNCVEEIEYNTVTC
M73253_1 EVSQITRVPCGYILRTVAYKEGYGEGCVTHIEIENNTDELKNCVEEIEYNTDGTGTC
1010 1020 1030 1040 1050 1060

cry1a-105.pe NDTVNOEEYGGAYT--SRNRGYNEA----PSVPADYASVVEKSTGGRNCEPNRG
M73253_1 NDTYAHQGTAGTSDSCSNRIRVEDAYENNTTASVNVKYPTVEERYTVDQGNCEYDRG
1070 1080 1090 1100 1110 1120

cry1a-105.pe YRDYVTLPLVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
M73253_1 YVNVPRPAGYVTKLEYFPETDKVWIEIGETEGKFIVDNVELLMEE
1130 1140 1150 1160 1170
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cry1a-105.pep
TXM5:A27529_1

Description: A27529 Bacillus thuringiensis B.thuringiensis PS81A2 endotoxin
Gene: 9/1995
Accession/ID: A27529
=====General comments=====
LOCUS A27529_1 [A27529]
DEFINITION B.thuringiensis PS81A2 endotoxin gene. . .
SMITH-WATERMAN SCORE: 5235; 67.5% identity in 1188 aa overlap
(1-1177:1-1174)

SCORES Initl: 2860 Initn: 4525 Opt: 5176 Z-score: 5706.5 E(): 0
>>TXM5:A27529_1
Initn: 4525 Initl: 2860 opt: 5176 Z-score: 5706.5 expect(): 0
Smith-Waterman score: 5235; 67.5% identity in 1188 aa overlap
(1-1177:1-1174)

cry1a-105.pe MDNPNNECIPYNCISNPVEVEVIGGERIETGTPIDISLSITQFLSEFVPGAGFVLGL
A27529_1 MENNIE-NOCIYPYNCINNPVEVEVIGGERIETGTPIDISLSITQFLSEFVPGAGFVLGL
10 20 30 40 50

cry1a-105.pe VDIWTFGSGQWDAFLVOIQBOLINQRIEFARNQAIISRLGSLNLYQIYAESFREWEAD
A27529_1 FDIWTFGSGQWDAFLVOIQBOLINQRIEFARNQAIISRLGSLNLYQIYAESFREWEAD
60 70 80 90 100 110 120

cry1a-105.pe PTNPALREEMRIQFNDMSALTATPLFAVONYOVPELLSVVYQAANHLSDVSVFGQ
A27529_1 PTNPALREEMRIQFNDMSALTATPLFVSVGVYVPELLSVVYQAANHLSDVSVFGQ
130 140 150 160 170 180

cry1a-105.pe RMGFDAATINSRYNDLTRIGNYTHAVRWYNTGLERV-WGPDSDRWIRYQFRRELTLT
A27529_1 RMGFDAATINSRYNDLTRIGNYTHAVRWYNTGLERV-WGPDSDRWIRYQFRRELTLT
190 200 210 220 230

cry1a-105.pe VLDIVSLFPNVDSRTYPTIYQTSQTLREIYTPVLENFDSFGSAGQIEGS-IRSPHLM
A27529_1 VLDIVSLFPNVDSRTYPTIYQTSQTLREIYTPVLENFDSFGSAGQIEGS-IRSPHLM
240 250 260 270 280 290

cry1a-105.pe ILNSTIYTHAHEGYMSGHQIMASPVGSGPEFTFFLYGTMGNAAPQORIVAQGGV
A27529_1 FLNNIITDLIRGVHAGHRVTSHTFTG-SSQVSSPOYGITANAEPSRTIAPSTFPL
300 310 320 330 340 350

cry1a-105.pe ---VETLSSTLYRPENGINNQQLSVLDGTEFAYCTSSNLPFSAYKSGTSDSDEIPE
A27529_1 NLFYETLSDDPFRRSNII-MPTLGINVVGQGTQPNNGEV---LYRRGTVDSDDELPI
360 370 380 390 400 410

cry1a-105.pe QNNVPPRQGFHRLSHVSMFSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIP
A27529_1 DGEN--SLVGVSHRLSHVSMFSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIP
420 430 440 450 460 470

480 490 500 510 520 530
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cry1a-105.pe LVKATVLOSSTVVRGPGFTGDLRTSGTGFAYTVININGQLPQRYRARIYASTNL
A27529_1 LVKSTSTGTSVVRGPGFTGDLRTSNVNGVLSNLSNLSQRYRARIYASTNL
cry1a-105.pe RLYTVASERIPAGNTMDTGDLRFQSTVATINTAFTFPMWSQSSFTVQADTFSSGN
A27529_1 RLYTVASERIPAGNTMDTGDLRFQSTVATINTAFTFPMWSQSSFTVQADTFSSGN
cry1a-105.pe EYIDRFELIPVATLEAFNLEKQVAKVLETSNQLGKNTVYHIDQVSLMTYL
A27529_1 EYIDRFELIPVATLEAFNLEKQVAKVLETSNQLGKNTVYHIDQVSLMTYL
cry1a-105.pe SDFECLDEKSELSEKVKHAKRLSDERNLLODSNPNINNOPEKMGSTLTITGGGCVF
A27529_1 SDFECLDEKSELSEKVKHAKRLSDERNLLODSNPNINNOPEKMGSTLTITGGGCVF
cry1a-105.pe KENYVTLASGTDFECYTYLYQKIDESKLAFTYQLRGVIEDSDLEIYSRTAKHETV
A27529_1 KENYVTLASGTDFECYTYLYQKIDESKLAFTYQLRGVIEDSDLEIYSRTAKHETV
cry1a-105.pe NYPGTSGLWPLSQAQSIGKCEPNKCAHLEWNPDLDCSDRGKCAHSHHESLIDVG
A27529_1 NYPGTSGLWPLSQAQSIGKCEPNKCAHLEWNPDLDCSDRGKCAHSHHESLIDVG
cry1a-105.pe CTDLNEDLGVMWVFKITQDGHARLGNLEFLEKPLVGEALARKVRAEKWKREKLEW
A27529_1 CTDLNEDLGVMWVFKITQDGHARLGNLEFLEKPLVGEALARKVRAEKWKREKLEW
cry1a-105.pe ETNIVYKESVDALFVNSQYDQLQADTNIAHAAKRVHSIKREAYLPESLVPQVNA
A27529_1 ETNIVYKESVDALFVNSQYDQLQADTNIAHAAKRVHSIKREAYLPESLVPQVNA
cry1a-105.pe AIFEELEGRIETAFSLYDARNVKNKGNDFNGLSCWNVKGVHVDVEQNNKRSVLVPEWEA
A27529_1 AIFEELEGRIETAFSLYDARNVKNKGNDFNGLSCWNVKGVHVDVEQNNKRSVLVPEWEA
cry1a-105.pe EYVQVRVCPGRGIVLRVAYKEGEGCVTIHEIENNTDELKFCNVEEETYPNNVTVC
A27529_1 EYVQVRVCPGRGIVLRVAYKEGEGCVTIHEIENNTDELKFCNVEEETYPNNVTVC
cry1a-105.pe NDYTVNOEYGGAT--SRNRGNEA---PSVPADVASVYEKSTVGRNPECFNRG
A27529_1 NDYTVNOEYGGAT--SRNRGNEA---PSVPADVASVYEKSTVGRNPECFNRG

cry1a-105.pe YRDYTPVGVVTKLEYFPETDKVWIEIGETGTFTIVDSVELLMEE
A27529_1 YNVRPVPAGVTVTKLEYFPETDKVWIEIGETGTFTIVDSVELLMEE
cry1a-105.pe
TXNS:CICB_BACTG
Description: P56953 bacillus thuringiensis (subsp. galleriae). pesticidal
crystal protein cr
Accession/ID: P56953
ID C1CB_BACTG STANDARD; PRI: 1176 AA.
AC P56953; General comment: s=====

SCORES Init1: 3092 Initn: 4578 Opt: 5094 z-score: 5616.0 E(): 0
>>TXNS:C1CB_BACTG
Initn: 4578 init1: 3092 opt: 5094 z-score: 5616.0 expect(): 0
Smith-Waterman score: 5288; 67.9% identity in 1195 aa overlap
(1-1177:1-1176)

cry1a-105.pe MDNPNINCEIPYNCLSNPEVVLGGERIETGTPIDISLSLTOFLSEFVPGAGFVLGL
C1CB_BACTG MENNIQ-NOCVPYNCLSNPEEILLDEERISTGSSIDISLSLVQLLVSNFVPGGFLVGL
cry1a-105.pe VDIKGFICPQMDAFVLEQLINQIEEFARNOAISRLGSLNLYOIAESPREWEAD
C1CB_BACTG LDFPYNISPSWDAFVLEQLINQIEEFARNOAISRLGSLNLYOIAESPREWEAD
cry1a-105.pe PTGALRSGRIQFNSNSALTTAFLFAVQNYQVPLLSVYQAAHLHLVLRDVSFVGQ
C1CB_BACTG PDPVTRTVVDFRFAILLDGERIDPSPRIAGFEVPLLSVYQAAHLHLVLRDVSFVGQ
cry1a-105.pe RWGFDAATNSERNDLRLKATIDHAVRNNTSERVWGPDSRDMIRVNOFRRELTLTV
C1CB_BACTG RWGLTTINVENYNLRLRIDEVANDASVYNGRLNLPKSTYQDWTIYNRRLDLTLTV
cry1a-105.pe LDIVSFPNYSRTVPIRTVQSQTNTNPNVLENGDSRGAQS---IEGS-IRSP
C1CB_BACTG LDIAAFPPSYDNRNRYPIQSVQLTREIYTDRLTFNPPQSVSAQLPTFNWESNARTIP
cry1a-105.pe HLMIDILNSTITVDADR-GE-YWWSGHQIMASVCFSGPNTNHYGTNMAVAPORIVA
C1CB_BACTG HLFEDVLNNTITFDWFSVGRNFWGGRHVRVNRIG--GGNITSPNIGRBNQOEPNAPFT
cry1a-105.pe QLGQGVRTLSTSLTVR---RPFNIGINNQLSVLDGTFAYGTSNLPASVYKRSSTVDS
C1CB_BACTG -FNGPVRILSNPTFRPLQQWPAPPPN--LAGVEGVF---STPLNSFTYRGRGTVDS

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cry1a-105.pe LDEIPKNNVPPQGFHSHLSVMP-RSGFNSNSVSIIRAPMFSWIHRSABFNIIAS
CICB_BACTG LLELPEDNSVFPREGYSHRLCHATFVORSG---TPFLITGTFVSWTHSATDRNIYIP
410 420 430 440 450 460
470 480 490 500 510 520
cry1a-105.pe DSIITQIPKVAHTLQSGTIVVRGPGFTGDIILRTSGGPFAYTIVNINGQIPQRYRARIR
CICB_BACTG DVINQLPLKAFNLTSVVRGPGFTGDIIRTNVNGSVLSNFSNTTLQRYVRVR
470 480 490 500 510 520
530 540 550 560 570 580
cry1a-105.pe YASTNLIYTVVAGERIFAGQFNMTGDTLTFQSFSAVINTAFTFPMNQ-SGFTVG
CICB_BACTG YAAQDMVMSVTVGGSTTGNQGFPMSTANGALTSQSFRAEFPPVGISASGQSASISIS
530 540 550 560 570 580
590 600 610 620 630 640
cry1a-105.pe ADTFSGNEVY-IDRFELIPVATLEAEYNLERAKAVNALFTSTNQLGLKNTVTDYHID
CICB_BACTG NNV--GRMFHLDRIEFLPVSTSTFEEDYDLERAQAVNALFTSTNQLGLKNTVTDYHID
590 600 610 620 630 640
650 660 670 680 690 700
cry1a-105.pe QVSNLYTSLDEFCLDEKRELSKVHAKRLSDERNLLQDSNFKDINQPERGWSGTGI
CICB_BACTG QVSNLVECLSDDEFCLDEKRELSKVHAKRLSDERNLLQDRNFRSINGQLDRGWRGSDTI
650 660 670 680 690 700
710 720 730 740 750 760
cry1a-105.pe TIQGGDVFKENYVTLTGTFDECYPTLYQKIDESKLKAPTRVQLRGVIEDSQDLETYSI
CICB_BACTG TIQGGDVFKENYVTLTGTFDECYPTLYQKIDESKLKSVTRYELRGVIEDSQDLETYLI
710 720 730 740 750 760
770 780 790 800 810 820
cry1a-105.pe RYNAKHETVNVPGTSLWPLSQAQSPIGKCGEPNRCAPHEWNPDLDCSRDGEKCAHSH
CICB_BACTG RYNAKHETVNVPGTSLWPLSQAQSPIGKCGEPNRCAPHEWNPDLDCSRDGEKCAHSH
770 780 790 800 810 820
830 840 850 860 870 880
cry1a-105.pe HFSLDIDVGCIDLNEDLGVMVIFKIKTODGHARLGNLEFLEEKPLVGEALARVRAEKKW
CICB_BACTG HFSLDIDVGCIDLNEDLGVMVIFKIKTODGHARLGNLEFLEEKPLVGEALARVRAEKKW
830 840 850 860 870 880
890 900 910 920 930 940
cry1a-105.pe RDKREKLEWETNIVYKAEKESVDALFVNSQYDQLQADNTAMIAHADKRVHSIREAYLPE
CICB_BACTG RDKREKLEWETNIVYKAEKESVDALFVNSQYDQLQADNTAMIAHADKRVHSIREAYLPE
890 900 910 920 930 940
950 960 970 980 990 1000
cry1a-105.pe LSVIPGWAAIFEELEGRIETFSLYDARNVKNKGNCLSCWNVKGVHVEEQNNQS
CICB_BACTG LSVIPGWAAIFEELEGRIETFSLYDARNVKNKGNCLSCWNVKGVHVEEQNNQS
950 960 970 980 990 1000
1010 1020 1030 1040 1050 1060
cry1a-105.pe VLVVPWEAEVSQEVRCVPCRGYILRVATYKEGYGEGCVTHIEINNTDELKFNCSVEEE
CICB_BACTG VLVVPWEAEVSQEVRCVPCRGYILRVATYKEGYGEGCVTHIEINNTDELKFNCSVEEE
1010 1020 1030 1040 1050 1060
1070 1080 1090 1100 1110 1120
```

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cry1a-105.pe IYPNNTVTCNDYVNOEYGGAYTSRNRGNEA---PSVPADYASVYEKSYTDGREN
CICB_BACTG VYPNNTVTCNDYVNOEYGGAYTSRNRGNEA---PSVPADYASVYEKSYTDGREN
1070 1080 1090 1100 1110 1120
1130 1140 1150 1160 1170
cry1a-105.pe PCFENRGYRDYPLPVGVVTKLEYFPETDKVMIEIGETGTFIVDSVELLMEE
CICB_BACTG HCESNRYGDTPLPAGVVTKELEYFPETDKVMIEIGETGTFIVDSVELLMEE
1130 1140 1150 1160 1170
cry1a-105.pep
TXN5:M13898_1
Description: M13898 Bacillus thuringiensis B.thuringiensis (berliner)
crystalline entomocidal
Accession/ID: M13898
=====General comments=====
LOCUS M13898_1 [BACCR8B]
DEFINITION B.thuringiensis (berliner) crystalline entomocidal protoxin gene.
SCORES Initl: 4688 Initn: 5153 Opt: 4702 Z-score: 5183.4 E(): 0
>>TXN3:M13898_1
Initl: 5153 Initn: 4688 Opt: 4702 Z-score: 5183.4 expect(): 0
Smith-Waterman score: 6896; 88.7% identity in 1181 aa overlap
(1-1177:1-1155)
cry1a-105.pe MDNPNNEICIPYNCLSNPEVEVLGGERIETGTPIDISLSLTQFLLSFVFGAGFVLGL
M13898_1 MDNPNNEICIPYNCLSNPEVEVLGGERIETGTPIDISLSLTQFLLSFVFGAGFVLGL
10 20 30 40 50 60
70 80 90 100 110 120
cry1a-105.pe VDIITWIFGFSQMDAFLVQIEQLINQRIEFARNQAIISRLKGLSNLYQIYAESFREWAD
M13898_1 VDIITWIFGFSQMDAFLVQIEQLINQRIEFARNQAIISRLKGLSNLYQIYAESFREWAD
130 140 150 160 170 180
cry1a-105.pe PTNPALREEMRIQFNDMNSALTTAIPLFAVQNVQVPLLSVYVQAANHLSLVLRDVSVEGQ
M13898_1 PTNPALREEMRIQFNDMNSALTTAIPLFAVQNVQVPLLSVYVQAANHLSLVLRDVSVEGQ
130 140 150 160 170 180
cry1a-105.pe RWGFDAAATINSRYNDLTLLIGNYTDHAWRYNTGLERVMGPDSDRMIRYNQFRRELTITV
M13898_1 RWGFDAAATINSRYNDLTLLIGNYTDHAWRYNTGLERVMGPDSDRMIRYNQFRRELTITV
190 200 210 220 230 240
cry1a-105.pe LDIIVSLFPNDYDSYETPIRVSQLTREIYTNPVLNFDGFSRGSAGQIEGSIIRSHPLMDIL
M13898_1 LDIIVSLFPNDYDSYETPIRVSQLTREIYTNPVLNFDGFSRGSAGQIEGSIIRSHPLMDIL
250 260 270 280 290 300
cry1a-105.pe NSIITYDHAHGEYVMSGHQIMASPVGSGPFTFPLVGTMGNAAPQORIVAQLGQGVYR
M13898_1 NSIITYDHAHGEYVMSGHQIMASPVGSGPFTFPLVGTMGNAAPQORIVAQLGQGVYR
310 320 330 340 350 360
370 380 390 400 410 420
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cryla-105.pe VRVCPGRGVILRVTAKEGEGECVTIHEINNTDELKFSNCVEEIEYNNITVTICNDYTV
MI13898_1 VRVCPGRGVILRVTAKEGEGECVTIHEINNTDELKFSNCVEEIEYNNITVTICNDYTV
1000 1010 1020 1030 1040 1050

cryla-105.pe NOBEYGGATVSNRNGYNEA---PSPADYASVVEEKSYYTDGRRNCPFNNGVADYTPL
MI13898_1 TQEEYECTVTSNRNGYDGAYESNSVPADYASAEKAYTDGRRDNPNCSENRGVDYTPL
1060 1070 1080 1090 1100 1110

cryla-105.pe PVGVYTKLEFEPEDTKVWIEGETGTCTFIVDSVELLMEE
MI13898_1 PAGVYTKLEFEPEDTKVWIEGETGTCTFIVDSVELLMEE
1120 1130 1140 1150

cryla-105.pe PVGVYTKLEFEPEDTKVWIEGETGTCTFIVDSVELLMEE
TXN5:CIAB_BACTK
Description: P06578 bacillus thuringiensis (subsp. kurstaki), bacillus
thuringiensis (subsp.
Accession/ID: P06578
ID CIAB_BACTK STANDARD; PRT: 1155 AA
AC P06578; P06577; P21257; P09663; P09666; P09667; . . .
GC 111741 (1155)
=====General comments=====
SCORES Initl: 4688 Initn: 5153 Opt: 4702 Z-score: 5183.4 E(): 0
XFN5:CIAB_BACTK
Initl: 5153 Initl: 4688 Opt: 4702 Z-score: 5183.4 expect(): 0
Smith-Waterman score: 6896; 88.7% identity in 1181 aa overlap
(1-11741 (1155))

cryla-105.pe MDMNPINCEIPNCLSPNEVEVLGGERTGTGTPIDISLTOFLSEVPGAGFVLGL
CIAB_BACTK MDMNPINCEIPNCLSPNEVEVLGGERTGTGTPIDISLTOFLSEVPGAGFVLGL
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

cryla-105.pe VDIWIGFGSOWDAFLQLEQLNLSNREFAFNOISNLEGLSNLYOYIAESFREWAD
CIAB_BACTK VDIWIGFGSOWDAFLQLEQLNLSNREFAFNOISNLEGLSNLYOYIAESFREWAD
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

cryla-105.pe PTNPALREENRQFNODMNSALTATPAIFAFONTQVLLSUYVQANLHILNVDIVSVFGO
CIAB_BACTK PTNPALREENRQFNODMNSALTATPAIFAFONTQVLLSUYVQANLHILNVDIVSVFGO
130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360

cryla-105.pe RWGFDAATINSRNDLTRLIGNYTHAVRWNTGLERVWGPDSRLIRNQFRELHILM
CIAB_BACTK RWGFDAATINSRNDLTRLIGNYTHAVRWNTGLERVWGPDSRLIRNQFRELHILM
190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360

cryla-105.pe LDIVSLFPNDYSRTYPIRTVSOLTREITVNPVLENTDGFSGAGOGIEGSIIRSPHMLDIT
CIAB_BACTK LDIVSLFPNDYSRTYPIRTVSOLTREITVNPVLENTDGFSGAGOGIEGSIIRSPHMLDIT
250 260 270 280 290 300 310 320 330 340 350 360

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[illegible]

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cryIa-105.pe NSITITDAHREYWSHQIMASPVGSGPEFTFPLPYGTMGNAAPQORIIVAGLQGVYR
CIAB_BACTK NSITITDAHREYWSHQIMASPVGSGPEFTFPLPYGTMGNAAPQORIIVAGLQGVYR
310 320 330 340 350 360 370 380 390 400 410 420
cryIa-105.pe TLSSTLYRPPNIGINNQQSLVDGTEFAYGTSNLPASVYRSGTGVSLDEIIPQNNV
CIAB_BACTK TLSSTLYRPPNIGINNQQSLVDGTEFAYGTSNLPASVYRSGTGVSLDEIIPQNNV
370 380 390 400 410 420
cryIa-105.pe PPRQGFSHLSHVSFMFSGFSNVSIIIRAPMFSWIHRSAEFNNIITASDITQPLVKAH
CIAB_BACTK PPRQGFSHLSHVSFMFSGFSNVSIIIRAPMFSWIHRSAEFNNIITASDITQPLVKAH
430 440 450 460 470 480
cryIa-105.pe TLOGSTTVKRGPGFTGGDILRTSGGPFAYITVININGQLPQVRARIRYASTTNLRIYVT
CIAB_BACTK TLOGSTTVKRGPGFTGGDILRTSGGPFAYITVININGQLPQVRARIRYASTTNLRIYVT
490 500 510 520 530 540
cryIa-105.pe VAGERIFACQFKMTMDGDLPTFQSPSVATINTAFTPMSSQSTVGADTFSSGNEVYID
CIAB_BACTK VAGERIFACQFKMTMDGDLPTFQSPSVATINTAFTPMSSQSTVGADTFSSGNEVYID
550 560 570 580 590 600
cryIa-105.pe IDGRPINQCNFSATMSGSLQSGSPFTVGTTFPNSGSSVFTLSAHVFNSGNEVYID
CIAB_BACTK IDGRPINQCNFSATMSGSLQSGSPFTVGTTFPNSGSSVFTLSAHVFNSGNEVYID
610 620 630 640 650 660
cryIa-105.pe RFLIPVTAILEAEYNLERAKAVNALFTSTNQLGKINTVDYHIDQVSNLVYLSDFEC
CIAB_BACTK RFLIPVTAILEAEYNLERAKAVNALFTSTNQLGKINTVDYHIDQVSNLVYLSDFEC
670 680 690 700 710 720
cryIa-105.pe LDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWSGTGTTGGDDVFKENYV
CIAB_BACTK LDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWSGTGTTGGDDVFKENYV
730 740 750 760 770 780
cryIa-105.pe TLOGTFDECYPTLYKIDESKILKAFTRYQLRGYIEDSOLEIYSIRYNAKHETVNVPGT
CIAB_BACTK TLOGTFDECYPTLYKIDESKILKAFTRYQLRGYIEDSOLEIYSIRYNAKHETVNVPGT
790 800 810 820 830 840
cryIa-105.pe GSLWPLSAGSPGKGEPNRCAPHLEWNPDLDCRGEKCAHSHHSLSLIDVGCCTDLN
CIAB_BACTK GSLWPLSAGSPGKGEPNRCAPHLEWNPDLDCRGEKCAHSHHSLSLIDVGCCTDLN
850 860 870 880 890 900
cryIa-105.pe EDLGVMVIFKIKTQDGHARLGNLFLEEKPLVGEALARVRAEKWRDREKLEWETNIV
CIAB_BACTK EDLGVMVIFKIKTQDGHARLGNLFLEEKPLVGEALARVRAEKWRDREKLEWETNIV
910 920 930 940 950 960
cryIa-105.pe YKEAKESVDALFVNSQYDLQADTNIAIHAADKRVHSIREAYLPBELSVFGVNAAFEE
CIAB_BACTK YKEAKESVDALFVNSQYDLQADTNIAIHAADKRVHSIREAYLPBELSVFGVNAAFEE
970 980 990 1000 1010 1020
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cryIa-105.pe LEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQSRVSVVPEWEAEVSQE
CIAB_BACTK LEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQSRVSVVPEWEAEVSQE
940 950 960 970 980 990
cryIa-105.pe VRVCEPGGYTLRTAYKSGYEGGCVTTHEENNTDELAFSCVCEEEIYFNNVTGNDYTV
CIAB_BACTK VRVCEPGGYTLRTAYKSGYEGGCVTTHEENNTDELAFSCVCEEEIYFNNVTGNDYTV
1000 1010 1020 1030 1040 1050
cryIa-105.pe NOEEYGGAYTSNRNGYNEA---PSPADYASVVEEKSVDGRRNCEPFRNGRYDYTPL
CIAB_BACTK NOEEYGGAYTSNRNGYNEA---PSPADYASVVEEKSVDGRRNCEPFRNGRYDYTPL
1060 1070 1080 1090 1100 1110
cryIa-105.pe TOEEVEGTYSRNRGYDGAYESNSSVPADYASAYEKAATDGRDNPCESNGYGYDTPL
CIAB_BACTK TOEEVEGTYSRNRGYDGAYESNSSVPADYASAYEKAATDGRDNPCESNGYGYDTPL
1120 1130 1140 1150
cryIa-105.pe PVGYVTKELYFFETDKVWIEIGETGTFIVDSVELLMEE
CIAB_BACTK PVGYVTKELYFFETDKVWIEIGETGTFIVDSVELLMEE
1160 1170
cryIa-105.pe
TXN5:D00117_1
Description: D00117 Bacillus thuringiensis Bacillus thuringiensis gene for
delta-endotoxin, c
Accession/ID: D00117
=====General comments=====
LOCUS D00117.1 (BACHDCRY)
DEFINITION Bacillus thuringiensis gene for delta-endotoxin, complete cds.
SCORES Initl: 4688 Initn: 5153 Opt: 4702 Z-score: 5183.4 E(1): 0
>>TXN5.D00117.1
Initn: 5153 Initl: 4688 opt: 4702 Z-score: 5183.4 expect(1): 0
Smith-Waterman score: 6896; 88.7% identity in 1181 aa overlap
(1-1177:1-1155)
cryIa-105.pe MDNPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSITQFLSEFVPGAGFVLGL
D00117_1 MDNPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSITQFLSEFVPGAGFVLGL
10 20 30 40 50 60
cryIa-105.pe VDIIWGIFGSDQDAFLVQIQQLINQRIEFAFNQAIISRLGSLNLYQIYAESFREWAD
D00117_1 VDIIWGIFGSDQDAFLVQIQQLINQRIEFAFNQAIISRLGSLNLYQIYAESFREWAD
70 80 90 100 110 120
cryIa-105.pe PTNPALREEMRIQFNDMSALTTAIPFAVONYQVPELLSVVYQAAHLHSLVDYSVFGQ
D00117_1 PTNPALREEMRIQFNDMSALTTAIPFAVONYQVPELLSVVYQAAHLHSLVDYSVFGQ
130 140 150 160 170 180
cryIa-105.pe RWGFDATINSRYNDLTRIGNYTHAVRWNTGLERWGPDSRDWIRYNQFRRELTIV
D00117_1 RWGFDATINSRYNDLTRIGNYTHAVRWNTGLERWGPDSRDWIRYNQFRRELTIV
190 200 210 220 230 240
cryIa-105.pe
TXN5:D00117_1
Initn: 5153 Initl: 4688 opt: 4702 Z-score: 5183.4 expect(1): 0
Smith-Waterman score: 6896; 88.7% identity in 1181 aa overlap
(1-1177:1-1155)
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cyla-105.pe YKEAVESVDALFVNSQDLOADNTAMTHAADKRVHSIREAYLPELSVPFGVNAAIPFE
D00117_1 YKEAVESVDALFVNSQDLOADNTAMTHAADKRVHSIREAYLPELSVPFGVNAAIPFE
880 980 990 910 920 930

cyla-105.pe LEGRIFTAFSLYDARNVIKNGDFNGLSCWNKYKGHVDEEQNNKSVLVWPEWEAEVSQE
D00117_1 LEGRIFTAFSLYDARNVIKNGDFNGLSCWNKYKGHVDEEQNNKSVLVWPEWEAEVSQE
970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080

cyla-105.pe VRVCGRGYILRTATKESYGEGCVTTHETENNDELKFSNCVEEIVPNNVTICNDYTV
D00117_1 VRVCGRGYILRTATKESYGEGCVTTHETENNDELKFSNCVEEIVPNNVTICNDYTA
1000 1010 1020 1030 1040 1050

cyla-105.pe NOBEYGGAYTSRRRGYNFA---PSVPADYASVYEKSYTDGSRNPCEFNRGVRYDTPL
D00117_1 TOBEYEGTYTSRRRGYDGAYESNSVPADYASVYEKAYTDGSRNDPCENRSGYGDYDTPL
1060 1070 1080 1090 1100 1110 1120 1130

cyla-105.pe PVCGYTKELVFPTDKVMIEGTCTGFIVDSVELLMEE
D00117_1 PAGVYTKELVFPTDKVMIEGTCTGFIVDSVELLMEE
1120 1130 1140 1150

cyla-105.pe PGVYTKELVFPTDKVMIEGTCTGFIVDSVELLMEE
D00117_1 PAGVYTKELVFPTDKVMIEGTCTGFIVDSVELLMEE
1120 1130 1140 1150

Description: A09398 Bacillus thuringiensis B.thuringiensis (var. Kurstaki HD1)
gene for delta
Accession/ID: A09398
LOCUS A09398.1 [A09398]
DEFINITION B.thuringiensis (var. Kurstaki HD1) gene for delta-endotoxin.
=====
General comments=====
SCORES Initl: 4688 Initn: 5153 Opt: 1705 z-score: 5183.4 E(): 0
>>TXNS:A09398.1
Initn: 5153 Initl: 4688 Opt: 4762 Z-score: 5183.4 expect(): 0
Smith-Waterman score: 6696. 98.7% identity in local aa overlap
(1-1177:1-1155)

cyla-105.pe MDNNPNINECTPYCNLSNREVEVGGERNTGTTFIDISLTOTLLSEFPVPGAGFVLGL
A09398_1 MDNNPNINECTPYCNLSNREVEVGGERNTGTTFIDISLTOTLLSEFPVPGAGFVLGL
10 20 30 40 50 60
MDNNPNINECTPYCNLSNREVEVGGERNTGTTFIDISLTOTLLSEFPVPGAGFVLGL
10 20 30 40 50 60
MDNNPNINECTPYCNLSNREVEVGGERNTGTTFIDISLTOTLLSEFPVPGAGFVLGL
70 80 90 100 110 120
MDNNPNINECTPYCNLSNREVEVGGERNTGTTFIDISLTOTLLSEFPVPGAGFVLGL
130 140 150 160 170 180
MDNNPNINECTPYCNLSNREVEVGGERNTGTTFIDISLTOTLLSEFPVPGAGFVLGL
190 200 210 220 230 240

cyla-105.pe VDIWGIFGSQDAFLVQIQLNQRIEFARNQAISRLEGSNLNYVAPAREWEAD
A09398_1 VDIWGIFGSQDAFLVQIQLNQRIEFARNQAISRLEGSNLNYVAPAREWEAD
70 80 90 100 110 120
VDIWGIFGSQDAFLVQIQLNQRIEFARNQAISRLEGSNLNYVAPAREWEAD
130 140 150 160 170 180
VDIWGIFGSQDAFLVQIQLNQRIEFARNQAISRLEGSNLNYVAPAREWEAD
190 200 210 220 230 240

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cry1a-105.pe RWGFDAAITNSRYNDLTRIGNYTDHVRWNTGLRVMGPDSDRWIRYNQFRRLTLTV
A09398_1 RWGFDAAITNSRYNDLTRIGNYTDHVRWNTGLRVMGPDSDRWIRYNQFRRLTLTV
250 260 270 280 290 300
cry1a-105.pe LDIVSLFNTDSRTPIRTVSQLTRREIYTNVLENFDPGRSGAQGIESIRSPHMDIL
A09398_1 LDIVSLFNTDSRTPIRTVSQLTRREIYTNVLENFDPGRSGAQGIESIRSPHMDIL
250 260 270 280 290 300
cry1a-105.pe NSITIIYDHRGEYVMSGHQIMASPVGSGPEFTPLXGTWGNAAPOORIVAQLGQGYR
A09398_1 NSITIIYDHRGEYVMSGHQIMASPVGSGPEFTPLXGTWGNAAPOORIVAQLGQGYR
310 320 330 340 350 360
cry1a-105.pe TLSSTLRRFPNIGINNQLSVLDGTEFAYGTSSNLPASVYRKSCTGVDLSDEIPPNQNV
A09398_1 TLSSTLRRFPNIGINNQLSVLDGTEFAYGTSSNLPASVYRKSCTGVDLSDEIPPNQNV
370 380 390 400 410 420
cry1a-105.pe PPROGFSHRLSHVMSRSGFNSSVSIIRAPMFSWIRHSAEFNNIIRASDSITQIPLVKAH
A09398_1 PPROGFSHRLSHVMSRSGFNSSVSIIRAPMFSWIRHSAEFNNIIRASDSITQIPLVKAH
430 440 450 460 470 480
cry1a-105.pe TLQSGTIVRGPGFTGGDILRRTSGPFAYTIIVNGLQIPORVIRVASTNRIYVT
A09398_1 NLGSGTIVRGPGFTGGDILRRTSGPFAYTIIVNGLQIPORVIRVASTNRIYVT
490 500 510 520 530 540
cry1a-105.pe VAGERIFAGOFNKMTDGLTDFOSFYATINTAFPMSCOSFTGADTFSSGNEVID
A09398_1 IDGRFINQGNFSATMSSGNSLQSGSFTTGTFTPFNFNGSSVFTLSAHVFNSGNEVID
550 560 570 580 590 600
cry1a-105.pe RFELIPVATLEAVNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDFEC
A09398_1 RIEFVPAEVTFAEYDLERAKAVNELFTSSNQLGLKTDVTDYHIDQVSNLVYLSDFEC
610 620 630 640 650 660
cry1a-105.pe LDEKRELSKVKHAKELSDERNLLQOSNEFKDINROPERGWSGTGTIGQDDVKEKNYV
A09398_1 LDEKRELSKVKHAKELSDERNLLQDPNFRGINRQDRGWRGSDTITIGQDDVKEKNYV
670 680 690 700 710 720
cry1a-105.pe TLTGTFDECYPTLYOKIDESKLAFTRYQLRGYIEDSDLEIYSIRYNAKHETVNVFGT
A09398_1 TLTGTFDECYPTLYOKIDESKLAFTRYQLRGYIEDSDLEIYLIRYNAKHETVNVFGT
730 740 750 760 770 780
cry1a-105.pe GSLWPLSAQSPGKCGEENRCAPHEWNPDLCSDCRDGEKCAHSHHFSLDIDVGCIDLN
A09398_1 GSLWPLSAQSPGKCGEENRCAPHEWNPDLCSDCRDGEKCAHSHHFSLDIDVGCIDLN
790 800 810 820 830 840
cry1a-105.pe GSLWPLSAQSPGKCGEENRCAPHEWNPDLCSDCRDGEKCAHSHHFSLDIDVGCIDLN
A09398_1 GSLWPLSAQSPGKCGEENRCAPHEWNPDLCSDCRDGEKCAHSHHFSLDIDVGCIDLN
790 800 810 820 830 840

cry1a-105.pe EDLGVWVIFKIKTODGHARLGNLEFLBEKPLVGEALARKRAEKKWRDKREKLEWETNIV
A09398_1 EDLGVWVIFKIKTODGHARLGNLEFLBEKPLVGEALARKRAEKKWRDKREKLEWETNIV
820 830 840 850 860 870
cry1a-105.pe YKEAKESVDALFVNSQYDRIQADTNIAHAAADKRVHSIREAYLPESLVPGVNAALFEE
A09398_1 YKEAKESVDALFVNSQYDRIQADTNIAHAAADKRVHSIREAYLPESLVPGVNAALFEE
880 890 900 910 920 930
cry1a-105.pe LEGRIFTAFSLYDARNVIKNGDFNNGLSQWNVGHVDVEEQNNQBSVLVPEWEAEVSQE
A09398_1 LEGRIFTAFSLYDARNVIKNGDFNNGLSQWNVGHVDVEEQNNQBSVLVPEWEAEVSQE
940 950 960 970 980 990
cry1a-105.pe VRVCPGRGYILRVTAAYKEGSGCVTITHEIENNTDELKFSNCEVEEYIPNNVTICNDYTV
A09398_1 VRVCPGRGYILRVTAAYKEGSGCVTITHEIENNTDELKFSNCEVEEYIPNNVTICNDYTV
1000 1010 1020 1030 1040 1050
cry1a-105.pe NOEEYCGATYSNRGYNEA----PSVPADYASVYEKSYTDGRRNCPENRGYRYTDL
A09398_1 IQEEHEGYITSRNGYDGAIVESNSVPADYASVYEKSYTDGRRNCPENRGYRYTDL
1060 1070 1080 1090 1100 1110
cry1a-105.pe PVGYVTKELFFPDTKRWIEIGETGTFIVDSVELLMEE
A09398_1 PVGYVTKELFFPDTKRWIEIGETGTFIVDSVELLMEE
1120 1130 1140 1150
cry1a-105.pe
TXNS:Q9F296
Description: Q9f296 bacillus thuringiensis. delta endotoxin. 6/2001
Accession/ID: Q9F296
ID Q9F296
AC Q9F296
DT 01-MAR-2001 (Tremblrel. 16, Created)
General comments:=====PRELIMINARY;PRT: 1155 AA.
=====
SCORES Init1: 4681 Initn: 5146 Opt: 4695 z-score: 5175.7 E(): 0
>>TXNS:Q9F296
Initn: 5146 Initl: 4681 opt: 4695 Z-score: 5175.7 expect(): 0
Smith-Waterman score: 6871; 88.4% identity in 1181 aa overlap
(1-1177:1-1155)
cry1a-105.pe MNMNNPINECIPYNCLSNPEVVLGGERIEGTPTIDISLSTQFLSEFPVPGAGVFLGL
Q9F296 MNMNNPINECIPYNCLSNPEVVLGGERIEGTPTIDISLSTQFLSEFPVPGAGVFLGL
10 20 30 40 50 60
cry1a-105.pe VDIINGIFGPSQMDAFIVIQEOLINQRIEEFARNQAIISRLGLSNLQIVAESFREWEAD
Q9F296 VDIINGIFGPSQMDAFIVIQEOLINQRIEEFARNQAIISRLGLSNLQIVAESFREWEAD
70 80 90 100 110 120
cry1a-105.pe
Q9F296
130 140 150 160 170 180

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cryla-105.pe	PTNPALREMRQFNDNSALTITAIPLFAVQNYQVPLSVYQAAMHLHSLVRDVSVFQG 170 180 190 200 210 220 230 240
Q9F296	PTNADREMRIOFNDSATTAIPLFAVQNYQVPLSVYQAAMHLHSLVRDVSVFQG 170 180 190 200 210 220 230 240
cryla-105.pe	RWGPDAATINSRYNTHIRLIGNVDHWZNTGLERWGPDSRDIRVNQFRRLTLTV 190 200 210 220 230 240
Q9F296	RWGPDAAINSDRLTHERGNVDHAWRYNGDERWGWGPDSDRDIRVNQFRRLTLTV 190 200 210 220 230 240
cryla-105.pe	LDIUSLPFNVDKRTPIRTVQSRIEYTYFLERPGDFSPRAQSGESIRSPHMDIL 250 260 270 280 290 300
Q9F296	LDIUSLPFNVDKRTPIRTVSOLTRATYNPVLRFDETRGSAQGSSTIRSPHMDIL 250 260 270 280 290 300
cryla-105.pe	NSITIYDAHRGEYYWSGHQIMASPVCFSGPEFTHTXWTGNMAAPOORVAQLGGYVR 310 320 330 340 350 360
Q9F296	NSITIYDAHRGEYYWSGHQIMASPVFGSGPEFTPLTGHNMAAPOOLRAAQGGYVR 310 320 330 340 350 360
cryla-105.pe	TLSSTLYRRFPNIGINNQOLSULDGTGFAYGTSNNLPAVYRKSGTVDSDETPONNVN 370 380 390 400 410 420
Q9F296	TLSSTLYRRFPNIGINNQOLSULDGTGFAYGTSNNLPAVYRKSGTVDSLEDEIPONNVN 370 380 390 400 410 420
cryla-105.pe	PPROGFSHRLSHVSMFRGFSNSSVSIIRAPMFSWIHSASFNNIIADSITOILPLVKAH 430 440 450 460 470 480
Q9F296	PPROGFSHRLSHVSMFRGFSNSSVSIIRAPMFSWIHSASFNNIIPSSOITOIPLTKST 430 440 450 460 470 480
cryla-105.pe	TLQSGTTVVRGPGFTGGDLARTSGGFAYTIIVNINGOLPORARIRYASTTNRIYVT 490 500 510 520 530 540
Q9F296	NLGSGTSVVRGPGFTGGDLARTSGPGISITLRVINIATPLOSORYRIRYASTTNLOFHTS 490 500 510 520 530 540
cryla-105.pe	VAGERIFAGOFNKMTDGPJLTFOFSVSATINTAFTPFMSSOSFTVGADTFSGNEVID 550 560 570 580 590 600
Q9F296	IDGRFINQHFSAITMSGNSLQSGSFYGVFTTFPNFNSGSSVTLNARVNSNGNEVID 550 560 570 580 590 600
cryla-105.pe	REFELIPVATLEAEYNLEBAQAVNAFLTSTNOGLKKTNTDYHDQVSNMLVTYLSDSEFC 610 620 630 640 650 660
Q9F296	RIEFVPAEVTFEAEYDLEBAQAVNELFTSSNQIGLKTDVTDHYDQVSNMLVECLSDSEFC 610 620 630 640 650 660
cryla-105.pe	LDEKEBLESEKVHKAKLSLERNLLQDNFKIDINORPEGCMWGSGTITIQGGDDVVFXENVU 670 680 690 700 710 720
Q9F296	LDEKEBLESEKVHKAKLSLERNLLQDPNLRGINQRQDRGWRSTDITIQGGDDVVFXENVU 670 680 690 700 710 720
cryla-105.pe	TLSGTFDBECPTYLYQKIDESKLKAFTYQURGYEDSOOLEIYSIRYNAKHETVPNVGPTG 730 740 750 760 770 780
Q9F296	TLGTFDBECPTYLYQKIDESKLKAYTAYQURGYEDSOOLEIYLIRYNAKHETVPNVGPTG 730 740 750 760 770 780

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cryla-105.pe GSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGECAHSHHSFLSDLDVGGCTDIN
Q9F296      790 -----AHSHHSFLSDLDVGGCTDIN
                        800      810
                        850      860      870      880      890      900
cryla-105.pe EDLGVMVIFKIKTODGHARLGNLEFUEEKPLVGELARVKRAEKKWRDKREKLWEWNIV
Q9F296      820      830      840      850      860      870
                        EELGVMVIFKIKTODGHARLGNLEFUEEKPLVGELARVKRAEKKWRDKREKLWEWNIV
                        880      890      900      910      920      930
cryla-105.pe YKEAKESVDALPWSOYDOLOADNTIAMIHAADKVHSIREAYLPELSVPICGVAAAFEE
Q9F296      940      950      960      970      980      990
                        YKEAKESVDALPWSOYDRLOADNTIAMIHAADKVHSIREAYLPELSVPICGVAAAFEE
                        1000      1010      1020      1030      1040      1050
cryla-105.pe LEGRIFTATSLYDAARNVIKNGDFNGLSCWNKYGHDVDEEONQRSVLVVPWEAEVSQE
Q9F296      1060      1070      1080      1090      1100      1110
                        LEGRISTATSLYDAARNVIKNGDFNGLSCWNKYGHDVDEEONHRSVLVVPWEAEVSQE
                        1120      1130      1140      1150
cryla-105.pe VRVCPGEGYILVTAYKEGCEGCVTTHIEENTTDLKFSNCVEEELYPNNTVTCNDYTV
Q9F296      1160      1170      1180      1190      1200
                        VRVCPGEGYILRTAYKEGCEGCVTTHIEENTTDLFKSNVCVEEELYPNNTVTCNDYTA
                        1210      1220      1230      1240      1250
cryla-105.pe NOERKGAVTSRNRGYNEA----PSVPADYASVYEKSYTDGRRNPCFNFRGYDYTPPL
Q9F296      1260      1270      1280      1290      1300
                        TOENRGAVTSRNRGYDGAVESNSVVPADYASAYEEKAYTDGRRDNPCSNRGYGDYTPPL
                        1310      1320      1330      1340      1350
cryla-105.pe PVWATVTSRPFPEKNIKEICTGTFFIVOSVELLMEE
Q9F296      1360      1370      1380      1390      1400
                        PASVVTRELYFPEDPKRWNTIGSEGTFFIVOSVELLMEE
                        1410      1420      1430      1440      1450
Description: U94191 Bacillus thuringiensis delta endotoxin gene, complete cds.
Accession/ID: U94191_1
LOCUS       U94191_1 [Btu94191]
DEFINITION  Bacillus thuringiensis delta endotoxin gene, complete cds.
SCORES      Initl: 4681   Inltnt: 5146   Opt: 4695   Z-score: 5175.7
>>XMS:U94191_1
Initn: 5146   Inltl: 4681   opt: 4695   Z-score: 5175.7   expect(0.01) = 0.0
Smith-Waterman score: 6871;    88.4% identity in 1181 aa overlap
(l-1177:l-1155)
cryla-105.pe MNNPNINECIPNCLSNFEVLGGERTGTPTDISLTOTFLLSFVPAGAGVNIV
U94191_1     10      20      30      40      50      60
              70      80      90      100      110      120

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cry1a-105.pe VDIWIFGSPQWDAFLVQIQLINORIEEFARNOAISRLGSLNLYQIYAESFREWEAD
U94191_1 VDIWIFGSPQWDAFLVQIQLINORIEEFARNOAISRLGSLNLYQIYAESFREWEAD
70 80 90 100 110 120
cry1a-105.pe PTFNPALEENRIRIQFNDMSALTTPALFVAVQNYQVPLLSVTVQAANLHSLVLRDVSVEFGQ
U94191_1 PTFNPALEENRIRIQFNDMSALTTPALFVAVQNYQVPLLSVTVQAANLHSLVLRDVSVEFGQ
130 140 150 160 170 180
cry1a-105.pe RWGFDAAATINSRVNDLTSLIGNYTHAVRWNTGLERWGPDSRDPWIRYNQFRRELITV
U94191_1 RWGFDAAATINSRVNDLTSLIGNYTHAVRWNTGLERWGPDSRDPWIRYNQFRRELITV
190 200 210 220 230 240
cry1a-105.pe LDIVSLFPNTDSRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQGGIEGSIIRSPHMLDIL
U94191_1 LDIVSLFPNTDSRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQGGIEGSIIRSPHMLDIL
250 260 270 280 290 300
cry1a-105.pe NSITIIYDARGEYVMSGHQIMASPVGSGPEFTPLFGTGTWGNAPQORIVAGLQGGYR
U94191_1 NSITIIYDARGEYVMSGHQIMASPVGSGPEFTPLFGTGTWGNAPQORIVAGLQGGYR
310 320 330 340 350 360
cry1a-105.pe TLSSTLVRRFNFIGNNQQLSVLDGTEFAYGTSSNLPAVYKSGTVDSLDEIPQNNNV
U94191_1 TLSSTLVRRFNFIGNNQQLSVLDGTEFAYGTSSNLPAVYKSGTVDSLDEIPQNNNV
370 380 390 400 410 420
cry1a-105.pe PPROGFSHRLSHVMSFRSGFNSSVSIIRAPMFSWHSRASFNNI IASGSIQIPLVKAH
U94191_1 PPROGFSHRLSHVMSFRSGFNSSVSIIRAPMFSWHSRASFNNI IASGSIQIPLVKAH
430 440 450 460 470 480
cry1a-105.pe TLQSGTIVVRGPGFTGGDILRRTSGPFAYTIWINGQLPQRYRIRVASTTNIRIYVT
U94191_1 TLQSGTIVVRGPGFTGGDILRRTSGPFAYTIWINGQLPQRYRIRVASTTNIRIYVT
490 500 510 520 530 540
cry1a-105.pe VAGERIFAGQFNKMTDGTPLTFOSFIATINTATFTFPMSOSSVTGADTFSSGNEVID
U94191_1 VAGERIFAGQFNKMTDGTPLTFOSFIATINTATFTFPMSOSSVTGADTFSSGNEVID
550 560 570 580 590 600
cry1a-105.pe RPELIPVATLEAEVNLERAQAVNALFTSNOLGLKTNVDYDHIQVSNLTYLSDEFC
U94191_1 RPELIPVATLEAEVNLERAQAVNALFTSNOLGLKTNVDYDHIQVSNLTYLSDEFC
610 620 630 640 650 660
cry1a-105.pe LDEKRELSKVKAHKLSDERNLLQDSNFKDINRQPERGWGGSGTITIOGGDDVFKENYV
U94191_1 LDEKRELSKVKAHKLSDERNLLQDSNFKDINRQPERGWGGSGTITIOGGDDVFKENYV
670 680 690 700 710 720
cry1a-105.pe LDEKRELSKVKAHKLSDERNLLQDSNFKDINRQPERGWGGSGTITIOGGDDVFKENYV
U94191_1 LDEKRELSKVKAHKLSDERNLLQDSNFKDINRQPERGWGGSGTITIOGGDDVFKENYV
730 740 750 760 770 780

cry1a-105.pe TLLSGTFDECYPTLYQKIDESKKAFTRYQLRGYIEDSDLEIYSIRYNAKHETVNPVPGT
U94191_1 TLLSGTFDECYPTLYQKIDESKKAFTRYQLRGYIEDSDLEIYSIRYNAKHETVNPVPGT
730 740 750 760 770 780
cry1a-105.pe GSWLPUSAQSPIGKGEPNRCAPHLEWNPDLDCSRDGEKCAHSHHFSLDIDVGCTDLN
U94191_1 GSWLPUSAQSPIGKGEPNRCAPHLEWNPDLDCSRDGEKCAHSHHFSLDIDVGCTDLN
790 800 810 820 830 840
cry1a-105.pe EDLGVWVIFKIKTODGHARLGNLEFLBEPKPLVGEALARYKRAKKWRDKREKLEWETNIV
U94191_1 EDLGVWVIFKIKTODGHARLGNLEFLBEPKPLVGEALARYKRAKKWRDKREKLEWETNIV
850 860 870 880 890 900
cry1a-105.pe YKEAKESVDALFVNSQVDQLQADTNIAHHAADKRVHSIREAYLPSELSVIFGVNAAIFEE
U94191_1 YKEAKESVDALFVNSQVDQLQADTNIAHHAADKRVHSIREAYLPSELSVIFGVNAAIFEE
910 920 930 940 950 960
cry1a-105.pe YKEAKESVDALFVNSQVDQLQADTNIAHHAADKRVHSIREAYLPSELSVIFGVNAAIFEE
U94191_1 YKEAKESVDALFVNSQVDQLQADTNIAHHAADKRVHSIREAYLPSELSVIFGVNAAIFEE
880 890 900 910 920 930
cry1a-105.pe LEGRIFTAFSLYDARNVIRKNGDFNNGLSCHWVKGHVDEEQQNQRSLVLPWEFAEVSQ
U94191_1 LEGRIFTAFSLYDARNVIRKNGDFNNGLSCHWVKGHVDEEQQNQRSLVLPWEFAEVSQ
970 980 990 1000 1010 1020
cry1a-105.pe VRVCPGRGVILLRTAYKEGEGCVTIIHEINNTDELKFSNCVEEIIYPNNVTICNDYTV
U94191_1 VRVCPGRGVILLRTAYKEGEGCVTIIHEINNTDELKFSNCVEEIIYPNNVTICNDYTV
1030 1040 1050 1060 1070 1080
cry1a-105.pe NQEEYGGAYTSRNGYNEA-----PSVPADYASVYEESKSYTDGRRNCPCFNRYDYTPL
U94191_1 NQEEYGGAYTSRNGYNEA-----PSVPADYASVYEESKSYTDGRRNCPCFNRYDYTPL
1090 1100 1110 1120 1130
cry1a-105.pe PVGYVTKELEVPETDKVWIEIGETEGTFIVDSVELLLMEE
U94191_1 PVGYVTKELEVPETDKVWIEIGETEGTFIVDSVELLLMEE
1140 1150 1160 1170
cry1a-105.pe PAGYVTKELEVPETDKVWIEIGETEGTFIVDSVELLLMEE
U94191_1 PAGYVTKELEVPETDKVWIEIGETEGTFIVDSVELLLMEE
1180 1190 1200 1210
cry1a-105.pe
U94191_1
TXNS:M37263_1
Description: M37263 Bacillus thuringiensis B.thuringiensis 5.3 class
delta-endotoxin gene, co
Accession/ID: M37263
=====General comments=====

LOCUS M37263.1 [BACENR12]
DEFINITION B.thuringiensis 5.3 class delta-endotoxin gene, complete cds; . . .
SCORES Init1: 4665 Initn: 5130 Opt: 4679 z-score: 5158.0 E(): 0
>>TXNS:M37263.1
Initn: 5130 Opt: 4679 z-score: 5158.0 expect(): 0
Smith-Waterman score: 6867; 88.4% identity in 1181 aa overlap
(1-1177:1-1155)

cry1a-105_pe	MDNNPNINCTAVNCLNPEVEVLGGERIETGYTPIDISLSLTOFLSLSEVPFGAGFVLGI	70	80	90	100	110	120
M37263_1	MDNNPNINCTAVNCLNPEVEVLGGERIETGYTPIDISLSLTOFLSLSEVPFGAGFVLGI	20	30	40	50		
cry1a-105_pe	VDIINGIPSPSOWDVLVGLFOLLINQPEESARNOASRLRLEGLSNLYQIYAESFREWAD	130	140	150	160	170	180
M37263_1	VDIINGIPSPSOWDVLVGLFOLLINQPEESARNOASRLRLEGLSNLYQIYAESFREWAD	70	80	90	100	110	120
cry1a-105_pe	PTNPALREEMRIQFNDMNSATITATPLFAQNYQVPLTSVYVQAMNLSLRDVSVPFGQ	190	200	210	220	230	240
M37263_1	PTNPALREEMRIQFNDMNSATITATPLFAQNYQVPLTSVYVQAMNLSLRDVSVPFGQ	130	140	150	160	170	180
cry1a-105_pe	RWGFDAAATNSRVDLTGLIGNYTDHAVRWYNTGLRVPDGRDMIRVYQFRRELITV	250	260	270	280	290	300
M37263_1	RWGFDAAATNSRVDLTGLIGNYTDHAVRWYNTGLRVPDGRDMIRVYQFRRELITV	190	200	210	220	230	240
cry1a-105_pe	LDIVSLFPNTDSRTPIRTVSQLTREIYTNVPLENFDGSPRGSQGIKESKSHLMDIL	310	320	330	340	350	360
M37263_1	LDIVSLFPNTDSRTPIRTVSQLTREIYTNVPLENFDGSPRGSQGIKESKSHLMDIL	250	260	270	280	290	300
cry1a-105_pe	NSITIYDARGEYVWSGHQIMASPVGSGPEFTPLVGTGMNAAPOORIVLAQLGGQYVR	370	380	390	400	410	420
M37263_1	NSITIYDARGEYVWSGHQIMASPVGSGPEFTPLVGTGMNAAPOORIVLAQLGGQYVR	310	320	330	340	350	360
cry1a-105_pe	TLSSLTLYRRFPNIGINNQOLSLVDGTGFAYGTSSNLPAAVYKSGTVDLSDEIPPNQNV	430	440	450	460	470	480
M37263_1	TLSSLTLYRRFPNIGINNQOLSLVDGTGFAYGTSSNLPAAVYKSGTVDLSDEIPPNQNV	370	380	390	400	410	420
cry1a-105_pe	PPRQGFSHRLSHVMSFRSGFNSSVSIIRAPMFSWTHRSAPFNIIADSDITQIPLVKAH	500	510	520	530	540	550
M37263_1	PPRQGFSHRLSHVMSFRSGFNSSVSIIRAPMFSWTHRSAPFNIIADSDITQIPLVKAH	440	450	460	470	480	490
cry1a-105_pe	TLQSGTTVVRGPGTGDDILRETSGPFAVTIVNGQLPQRYRARIYASTTNLRIVVT	560	570	580	590	600	610
M37263_1	TLQSGTTVVRGPGTGDDILRETSGPFAVTIVNGQLPQRYRARIYASTTNLRIVVT	500	510	520	530	540	550
cry1a-105_pe	VAGERIFAGQPKMTDGPDLTFQSFYSATINTAFTPFMSQSSFTVAGADTFSSNGEVID	620	630	640	650	660	670
M37263_1	VAGERIFAGQPKMTDGPDLTFQSFYSATINTAFTPFMSQSSFTVAGADTFSSNGEVID	560	570	580	590	600	610
cry1a-105_pe	RFELIPVTATLAEYNLERAQKAVNALPSTNQIGLKTNTVDYHDQVSNLVLYLSDSEFC	680	690	700	710	720	730
M37263_1	RFELIPVTATLAEYNLERAQKAVNALPSTNQIGLKTNTVDYHDQVSNLVLYLSDSEFC	620	630	640	650	660	670

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cyla-105.pe LDEKRELESEKVKVHKARLSDERNLLQDSHFKNQINQPERGHWGSGTGITITGGDDVFKENVY
M37263_1 LDEKELESEKVKVHANGLSDERNLLQDPNFRGINQDGRNGRSGTDITITGGDDVFKENVY
730 670 680 690 700 710 720
cyla-105.pe TLSGTEDECFPYLYQKIDESKLKAFTRYQURGVIEDSQLEIYSIRYNAKHETVNVPGT
M37263_1 TLTGTFDECFPYLYQKIDESKLKATTRYQURGVIEDSQLEIYLIRYNAKHETVNVPGT
730 740 750 760 770 780
cyla-105.pe GSWLPLSASQSPICKGCFENRCAPHLEWNPDLDCSCRDGECAHSHHSFLSDIDVGCGLDNL
M37263_1 GSWLPLSASPIGKC-----AAHSHHSFLSDIDVGCGLDNL
730 750 760 770 780 810
cyla-105.pe EDLGVWVIFKIKTQDGHARGLENLEFLEKPLVGEALARVRAKKWRDKREKLEWETNIV
M37263_1 EDLGVWVIFKIKTQDGHARGLILEFLEKPLVGEALARVRAKKWRDKREKLEWETNIV
790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960
cyla-105.pe YKEAKESVDALFVNSQYDQLQADNTAMTHAADKRVHSIREAYLPELSVPGVNAAFEE
M37263_1 YKEAKESVDALFVNSQYDRLOADNTAMTHAADKRVHSIREAYLPELSVPGVNAAFEE
790 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960
cyla-105.pe LEGSIFATSLSDARNVTKNGDFNGLSCWNVKGHVDVEEONQORSVLYVPPEWEAEVSQE
M37263_1 LEGSIFATSLSDARNVTKNGDFNGLSCWNVKGHVDVEEONQHRSVLYVPPEWEAEVSQE
970 980 990 1000 1010 1020
cyla-105.pe VRVGRGCLRVTKGSGEGCVTHIEHNTDELAFSCVEEELYPNNVTGNDYTV
M37263_1 VRVGRGCLRVTKGSGEGCVTHIEHNTDELAFSCVEEELYPNNVTGNDYTV
1030 1040 1050 1060 1070 1080
cyla-105.pe NOEEVGQKASRNGRYNARVSVPADPVSREKSVTQDRENNPCFNFGYDPTPL
M37263_1 TOEEYGGTYSRNRSDYDAYSNSASAPKASAYEKATQDRENNPCSNESGYDPTPL
1060 1070 1080 1090 1100 1110 1120 1130
cyla-105.pe PVGYVTKLEYPFETDKWIEIGSEGTCTVDSVLLMEE
M37263_1 PAGVYTKLEYPFETDKWIEIGTEGTCTVDSVLLMEE
1140 1150 1160 1170 1180 1190 1200
cyla-105.pe TXN5:X04698_1
M37263_1
Description: X04698 Bacillus thuringiensis Bacillus thuringiensis berliner 1715 bt2 gene for
Accession/ID: X04698
LOCUS X04698_1 [BTBT2TOX]
DEFINITION Bacillus thuringiensis berliner 1715 bt2 gene for delta endotoxin
=====General comments=====
SCORES Initl: 4661 Initn: 5126 Opt: 4675 z-score: 5153.6 E(): 0

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Description: X04698 Bacillus thuringiensis berliner 1715 bt2 gene for
 1715 bt2 gene for
 Accession/ID: X04698
 =====General comments=====
 LOCUS X04698_1 [B7B2T0X]
 DEFINITION Bacillus thuringiensis berliner 1715 bt2 gene for delta endotoxin

```
>>TXNS:X04698_1
initn: 5126 init1: 4661 opt: 4675 z-score: 5153.6 expect(1): 0
Smith-Waterman score: 6869; 88.6% identity in 1181 aa overlap
(1-1177:1-1155)

cry1a-105.pe MDNPNINECIPNCLSNPEVEVLGGERTETGTPIDISLSLQFLLSFVFGAGFVLGL 10 20 30 40 50 60
X04698_1 MDNPNINECIPNCLSNPEVEVLGGERTETGTPIDISLSLQFLLSFVFGAGFVLGL 10 20 30 40 50 60

cry1a-105.pe VDIWGIFGPSQWDAFLVQIEQLINQRIEFPARNOAISLEGLSNLQIYAESFREWAD 70 80 90 100 110 120
X04698_1 VDIWGIFGPSQWDAFLVQIEQLINQRIEFPARNOAISLEGLSNLQIYAESFREWAD 70 80 90 100 110 120

cry1a-105.pe PTPNPALEENRQFNDMNSALTTPAIPFAVQNYQVPLLSVYVQAANHLVSLRDSVFGQ 130 140 150 160 170 180
X04698_1 PTPNPALEENRQFNDMNSALTTPAIPFAVQNYQVPLLSVYVQAANHLVSLRDSVFGQ 130 140 150 160 170 180

cry1a-105.pe RWGFDAATINSRYNDLTLLIGNYTDHAWYNTGLERVWGPSRDMIRINQFRRELTLTV 190 200 210 220 230 240
X04698_1 RWGFDAATINSRYNDLTLLIGNYTDHAWYNTGLERVWGPSRDMIRINQFRRELTLTV 190 200 210 220 230 240

cry1a-105.pe LDIVSFPNYSRTYPIRTVSQLTREIYNPVLENFDSFGSAQIGESIRSPHMDIL 250 260 270 280 290 300
X04698_1 LDIVSFPNYSRTYPIRTVSQLTREIYNPVLENFDSFGSAQIGESIRSPHMDIL 250 260 270 280 290 300

cry1a-105.pe NSITITDHRGEYVWSGHQIMASPVGSGPEFTPELYGTWGNAAQQRIVAQLCGQYVR 310 320 330 340 350 360
X04698_1 NSITITDHRGEYVWSGHQIMASPVGSGPEFTPELYGTWGNAAQQRIVAQLCGQYVR 310 320 330 340 350 360

cry1a-105.pe TLSSTLYRRPFNIGINNQQSLVDGTEFAYGTSSNLPSAVYRKSQVDSLDLDEIPPQNNV 370 380 390 400 410 420
X04698_1 TLSSTLYRRPFNIGINNQQSLVDGTEFAYGTSSNLPSAVYRKSQVDSLDLDEIPPQNNV 370 380 390 400 410 420

cry1a-105.pe PPRQGSFSLHSHVMSFRSGFSNSVSIIRAPMFSWIRHSAFFNIITASDITQPLVKAH 430 440 450 460 470 480
X04698_1 PPRQGSFSLHSHVMSFRSGFSNSVSIIRAPMFSWIRHSAFFNIITASDITQPLVKAH 430 440 450 460 470 480

cry1a-105.pe TLOGSTYVRGFGFTGGDILRTSGGPFAYTTIVINQQLPQRVARIRVASTNLRIVYT 490 500 510 520 530 540
X04698_1 NLGSGTSVVKGFGFTGGDILRTSGGPFAYTTIVINQQLPQRVARIRVASTNLRIVYT 490 500 510 520 530 540

cry1a-105.pe VAGERIPAGQNKMTWDGDELTFQSFYSYATINTAFTPMSSQSFVAGDTFSSGNEVYID 550 560 570 580 590 600
X04698_1 IDGRPINQGNFSAATMSGNSLQSGSFRTVGTTPFNFSNGSSVFTLSAIVFNSGNEVYID 550 560 570 580 590 600

610 620 630 640 650 660
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cry1a-105.pe RFELIPVTATLEAEYNLERAKAVNALFTSTNOLGKTNVTDYHIDQVSNLVTLSDEPC 610 620 630 640 650 660
X04698_1 RIEFVPARVTEAEYDLERAQAVNELFTSNQIGLKTVDYHIDQVSNLVECLSDDEPC 610 620 630 640 650 660

cry1a-105.pe LDEKELSEKVKHAKSLRSLERNLQDSNFKDINQRPERGCMGGSTGITIQGGDDVFKENYV 670 680 690 700 710 720
X04698_1 LDEKELSEKVKHAKSLRSLERNLQDSNFKDINQRPERGCMGGSTGITIQGGDDVFKENYV 670 680 690 700 710 720

cry1a-105.pe TLLSGTFDECYTYLYOKIDESKLKAFYXOLRGYVIEDSODLEIYSIRYNAKHETVNPQT 730 740 750 760 770 780
X04698_1 TLLSGTFDECYTYLYOKIDESKLKAFYXOLRGYVIEDSODLEIYSIRYNAKHETVNPQT 730 740 750 760 770 780

cry1a-105.pe GSLMPLSAQSQSGKCGEPNRCAPHLEWNPDLDCRDKGEKCAHSHHFSLDIDVGCTDLN 790 800 810 820 830 840
X04698_1 GSLMPLSAQSQSGKCGEPNRCAPHLEWNPDLDCRDKGEKCAHSHHFSLDIDVGCTDLN 790 800 810 820 830 840

cry1a-105.pe EDLGVNVIKIKTQDGHARGLNLELBEKPLVGEALARKVRAEKKWRDKREKLEWETNIV 850 860 870 880 890 900
X04698_1 EDLGVNVIKIKTQDGHARGLNLELBEKPLVGEALARKVRAEKKWRDKREKLEWETNIV 850 860 870 880 890 900

cry1a-105.pe YKEAKESVDALFVNSQVLDQADTNIAHIAADKRVHSIREAYLPESLVIPGVNAAIFEE 910 920 930 940 950 960
X04698_1 YKEAKESVDALFVNSQVLDQADTNIAHIAADKRVHSIREAYLPESLVIPGVNAAIFEE 910 920 930 940 950 960

cry1a-105.pe LEGRIFAFSLYDARNVIIKNGDFNGLSCWNVKGHDVEEQNNQRSLVLPPEWAEVSQEE 970 980 990 1000 1010 1020
X04698_1 LEGRIFAFSLYDARNVIIKNGDFNGLSCWNVKGHDVEEQNNQRSLVLPPEWAEVSQEE 970 980 990 1000 1010 1020

cry1a-105.pe VRVCPGRGYILRVTAKEGYGEGCVTTHEENNTDELKFSNCVVEEIVPNNVTVCNDYTV 1030 1040 1050 1060 1070 1080
X04698_1 VRVCPGRGYILRVTAKEGYGEGCVTTHEENNTDELKFSNCVVEEIVPNNVTVCNDYTV 1030 1040 1050 1060 1070 1080

cry1a-105.pe NOEEYGGAYTSRRNGYNEA---PSVPADYASVYEKSYTDGRNCFEFGNRYDTPFL 1090 1100 1110 1120 1130
X04698_1 TOEEYEGTYSRRNGYDGAYESNSVPADYASAYEEKAYTDGRDNFCESNGYGYTFL 1090 1100 1110 1120 1130

cry1a-105.pe PVGYVTKELVFPETDKWIEGTETGTFIVDSVELLMEE 1140 1150 1160 1170
X04698_1 PVGYVTKELVFPETDKWIEGTETGTFIVDSVELLMEE 1140 1150 1160 1170

cry1a-105.pe TXNS:X13233_1
Description: X13233 Bacillus thuringiensis B. thuringiensis CryIC1 gene for
entomocidal delta
Accession/ID: X13233
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LOCUS X13233_1 (BTRC1C1)
DEFINITION B. thuringiensis cryIIA gene for entomocidal delta-endotoxin;

SCORES Initl: 4657 Inl: 22 Opt: 4671 z-score: 5149.2 E(): 0
>>TXNS: X13233_1
initl: 5122 inl: 4657 opt: 4671 z-score: 5149.2 expect(): 0
Smith-Waterman score: 4865 86.5% identity in 1181 aa overlap
(1-1177:1-1155)

cryIIa-105.pe MDNPNINECIPNCLSNPEVEVAGGERIAGVTGDISSNQPILSEFVPGAGFVLGL
X13233_1
MDNPNINECIPNCLSNPEVEVAGGERIAGVTGDISSNQPILSEFVPGAGFVLGL
X13233_1
cryIIa-105.pe VDIINGIFGQMDAFLVQIQLINRIEFAFNQIISNIEGLSNLYQIAESFREMID
X13233_1
VDIINGIFGQMDAFLVQIQLINRIEFAFNQIISNIEGLSNLYQIAESFREMID
X13233_1
cryIIa-105.pe PTNPALREEMRIQFNDWNSALTTAIPFAVQNYQVPLLSVYVQAAHLHLSRLDVSFQ
X13233_1
PTNPALREEMRIQFNDWNSALTTAIPFAVQNYQVPLLSVYVQAAHLHLSRLDVSFQ
X13233_1
cryIIa-105.pe RWGFDAAITNSRYNDLTRILIGNYTDHAVRWNTGLERVPDSDRWIRYQFRELTLTV
X13233_1
RWGFDAAITNSRYNDLTRILIGNYTDHAVRWNTGLERVPDSDRWIRYQFRELTLTV
X13233_1
cryIIa-105.pe LDIVSLFNFYDSRTYPIRTVQSOLTREIYTNVLENFGDPSRGSAGQIEGSRSPHLMIDL
X13233_1
LDIVSLFNFYDSRTYPIRTVQSOLTREIYTNVLENFGDPSRGSAGQIEGSRSPHLMIDL
X13233_1
cryIIa-105.pe NSITITDAHRGEIYWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQORIQAQGGQVYR
X13233_1
NSITITDAHRGEIYWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQORIQAQGGQVYR
X13233_1
cryIIa-105.pe TLSSTLYRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYKSGTVDLSLEIPQNNV
X13233_1
TLSSTLYRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYKSGTVDLSLEIPQNNV
X13233_1
cryIIa-105.pe PPRQGSRLSHLSVMFRSGFSNVSIIIRAPMFSWIRHSAEFNNIIASDSITQIPLVKAH
X13233_1
PPRQGSRLSHLSVMFRSGFSNVSIIIRAPMFSWIRHSAEFNNIIASDSITQIPLVKAH
X13233_1
cryIIa-105.pe TLOGSTTVVRGFGTGGDILRRITSGGPFAYITVINGQLQORVIRIRASTNLRIVT
X13233_1
TLOGSTTVVRGFGTGGDILRRITSGGPFAYITVINGQLQORVIRIRASTNLRIVT
X13233_1
NLGSGTGVKGFPGTGGDILRRITSGGPFAYITVINGQLQORVIRIRASTNLRIVT
X13233_1
NLGSGTGVKGFPGTGGDILRRITSGGPFAYITVINGQLQORVIRIRASTNLRIVT
X13233_1

cryIIa-105.pe VAGERIFAGQNKMTDGTGDLPTFQSFYATINTAFTFPMSSQSFVAGDFTSSGNEVYID
X13233_1
IDGRIINGNFSATMSGSGFNGVGTFTTFFNFSSGSSVFTLSAHVNGSNEVYID
X13233_1
cryIIa-105.pe RPELTPVATILEAEVNLERAQAVNALFTSNOLGLTKNTVTDYHIDQVSNLVTLSDEFC
X13233_1
RIEFVPAEVTTEAEYDLERAQAVNELTSSNQLGKTDVTDYHIDQVSNLVTLSDEFC
X13233_1
cryIIa-105.pe LDEKRELSKVKHAKRLSDERNLLODSNFKDINRQPERMGSGSTIITQGGDDVFFENYV
X13233_1
LDEKRELSKVKHAKRLSDERNLLODSNFKDINRQPERMGSGSTIITQGGDDVFFENYV
X13233_1
cryIIa-105.pe TLSGTDECEPTYLYOKIDESKLAFTRYQLRGVIEDSODLEIYSIRYNAKHETVNVPGT
X13233_1
TLGTFDECEPTYLYOKIDESKLAFTRYQLRGVIEDSODLEIYSIRYNAKHETVNVPGT
X13233_1
cryIIa-105.pe GSLWPLSAOSPIGKGFENRCAPHLEWNPDLDCSRDGEKCAHSHHFSLOLDVGCDDL
X13233_1
GSLWPLSAOSPIGKGFENRCAPHLEWNPDLDCSRDGEKCAHSHHFSLOLDVGCDDL
X13233_1
cryIIa-105.pe EDLWVVIKTIQDGHARLGNLEFLEKPLVGEALARVRAEKKWRDKREKLEWETNIV
X13233_1
EDLWVVIKTIQDGHARLGNLEFLEKPLVGEALARVRAEKKWRDKREKLEWETNIV
X13233_1
cryIIa-105.pe YKAKESVDALEFVNYQYDRUSADANIAMIAHADKRVHSIREAYLPSELSVPGVNAAFEE
X13233_1
YKAKESVDALEFVNYQYDRUSADANIAMIAHADKRVHSIREAYLPSELSVPGVNAAFEE
X13233_1
cryIIa-105.pe LEGRIFTAFSLDANVTNGDFNNGSGVYKGNVOTESONHRSVLPVPEWEAEVSQ
X13233_1
LEGRIFTAFSLDANVTNGDFNNGSGVYKGNVOTESONHRSVLPVPEWEAEVSQ
X13233_1
cryIIa-105.pe VRVCPGGRYILRTVAYKEGEGCVTHIENNTLEAFNSCVEEYNTVNTVNDYTV
X13233_1
VRVCPGGRYILRTVAYKEGEGCVTHIENNTLEAFNSCVEEYNTVNTVNDYTV
X13233_1
cryIIa-105.pe NOEYGGAYTSRNRGNEA---PSVPADYASVYEKSYKGCENPCENNDYTP
X13233_1
NOEYGGAYTSRNRGNEA---PSVPADYASVYEKSYKGCENPCENNDYTP
X13233_1
cryIIa-105.pe PVGVYKLEVEFETDKVWIEIGETGTFIVDSVLLMEE
X13233_1
PVGVYKLEVEFETDKVWIEIGETGTFIVDSVLLMEE
X13233_1

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Product Characterization Center

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cryla-105.pep
TXN5:Q9AM83

Description: Q9AM83 bacillus thuringiensis serovar kunthalarx24. insecticidal
crystal protein
Accession/ID: Q9AM83
=====General comments=====
ID Q9AM83 PRELIMINARY; PRT: 1118 AA.
AC Q9AM83; . . .

SCORES Init1: 4599 Initn: 4599 Opt: 4613 z-score: 5085.4 E(): 0
>>TXN5:Q9AM83
Initn: 4599 Opt: 4613 z-score: 5085.4 expect(): 0
Smith-Waterman score: 6228; 88.0% identity in 1075 aa overlap
(1-1075:1-1049)

cryla-105.pe MDNNPINECTPYNCLSNPEVEVLGERIETGYTPIDISLSLTOFLISEVPFGAGFVLGL
Q9AM83 MDNNLINIECTPYNCLSNPEVEVLGERIETGYTPIDISLSLTOFLISEVPFGAGFVLGL
10 20 30 40 50 60
10 20 30 40 50 60
70 80 90 100 110 120
cryla-105.pe VDIIWIGIFGSPQDAFVIQVEQLINQRIEERFARNQAIISLEGLSNLYQIYAESFREWAD
Q9AM83 VDIIWIGIFGSPQDAFVIQVEQLINQRIEERFARNQAIISLEGLSNLYQIYAESFREWAD
70 80 90 100 110 120
cryla-105.pe PTPNPALEEMRIQFNDMNSALTTAIPFAVQNVQVLLSVYQAAHLISVLRDVSFVGQ
Q9AM83 PTPNPALEEMRIQFNDMNSALTTAIPFAVQNVQVLLSVYQAAHLISVLRDVSFVGQ
130 140 150 160 170 180
130 140 150 160 170 180
190 200 210 220 230 240
cryla-105.pe RWGFDAAINISRYNDLTRLIGNYTHAVRWNTGLSERVWGPDSRDWIRYNQFRRELTIV
Q9AM83 RWGFDAAINISRYNDLTRLIGNYTHAVRWNTGLSERVWGPDSRDWIRYNQFRRELTIV
190 200 210 220 230 240
250 260 270 280 290 300
cryla-105.pe LDIVSLFNYDSRTYPIRTVSQLTREITYTPVLENDFSGRGAQIEGSIKPSHMDIL
Q9AM83 LDIVSLFNYDSRTYPIRTVSQLTREITYTPVLENDFSGRGAQIEGSIKPSHMDIL
250 260 270 280 290 300
310 320 330 340 350 360
cryla-105.pe NSITIYDAHRGEYWSGHQIMASPVGFSQPEFFPLXGTMGNAAPQORIVAQLGQGYR
Q9AM83 NSITIYDAHRGEYWSGHQIMASPVGFSQPEFFPLXGTMGNAAPQORIVAQLGQGYR
310 320 330 340 350 360
370 380 390 400 410 420
cryla-105.pe TLSSTLYRRPNIGINNQLSVLDGTBPAGTSSNLPAGVRKSGTVDLSDEIPQNNNV
Q9AM83 TLSSTLYRRPNIGINNQLSVLDGTBPAGTSSNLPAGVRKSGTVDLSDEIPQNNNV
370 380 390 400 410 420
430 440 450 460 470 480
cryla-105.pe PPRQGSFHLHSVMFSGFSSNSVYIIRAPMFESWIHRSFNNIINASDITQIPLVQKH
Q9AM83 PPRQGSFHLHSVMFSGFSSNSVYIIRAPMFESWIHRSFNNIINASDITQIPLVQKH
430 440 450 460 470 480
490 500 510 520 530 540

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[illegible]

Monsanto Company
Final Report
Product Characterization Center

cryla-105.pe
TXNS-CLGB_BACTZ
Description: Q92A26 bacillus thuringiensis (subsp. wuhanensis). pesticide
crystal protein C
Accession/ID: Q92A26
ID C1GB_BACTZ
AC Q92A26
General Comments: 1169 AA
STANDARD
=====

SCORES Initl: 3638 Initn: 5976 Opt: 3337 z-score: 5003.5 E(): 0
>TXNS-CLGB_BACTZ
Initn: 5076 initl: 3638 opt: 4539 z-score: 5003.5 expected: 0
Smith-Waterman score: 5229; 68.1% identity in 1763 aa overlap
(1-1177:1-1169)

cryla-105.pe
C1GB_BACTZ
MEIN-NOQCVPYCNLPNFESEILNVA-IFSSQVAEHNHITLLENFENFQSEAGL
10 20 30 40 50 60
70 80 90 100 110 120
130 140 150 160 170 180

cryla-105.pe
C1GB_BACTZ
VDIIMGIFGSQMDAFLVOIEOLINORIEEFARNOAISLEGSLNLYOINESREWEAD
10 20 30 40 50 60
70 80 90 100 110 120
130 140 150 160 170 180

cryla-105.pe
C1GB_BACTZ
PDPILGIFNEDQSAFLQVVEELINQRIETEFARGQAIQRLVGFGRSYDEVILAKSWND
10 20 30 40 50 60
70 80 90 100 110 120
130 140 150 160 170 180

cryla-105.pe
C1GB_BACTZ
PDPILGIFNEDQSAFLQVVEELINQRIETEFARGQAIQRLVGFGRSYDEVILAKSWND
10 20 30 40 50 60
70 80 90 100 110 120
130 140 150 160 170 180

cryla-105.pe
C1GB_BACTZ
PDPILGIFNEDQSAFLQVVEELINQRIETEFARGQAIQRLVGFGRSYDEVILAKSWND
10 20 30 40 50 60
70 80 90 100 110 120
130 140 150 160 170 180

cryla-105.pe
C1GB_BACTZ
PDPILGIFNEDQSAFLQVVEELINQRIETEFARGQAIQRLVGFGRSYDEVILAKSWND
10 20 30 40 50 60
70 80 90 100 110 120
130 140 150 160 170 180

cryla-105.pe
C1GB_BACTZ
PDPILGIFNEDQSAFLQVVEELINQRIETEFARGQAIQRLVGFGRSYDEVILAKSWND
10 20 30 40 50 60
70 80 90 100 110 120
130 140 150 160 170 180

cryla-105.pe
C1GB_BACTZ
PDPILGIFNEDQSAFLQVVEELINQRIETEFARGQAIQRLVGFGRSYDEVILAKSWND
10 20 30 40 50 60
70 80 90 100 110 120
130 140 150 160 170 180

cryla-105.pe
C1GB_BACTZ
PDPILGIFNEDQSAFLQVVEELINQRIETEFARGQAIQRLVGFGRSYDEVILAKSWND
10 20 30 40 50 60
70 80 90 100 110 120
130 140 150 160 170 180

cryla-105.pe
C1GB_BACTZ
PDPILGIFNEDQSAFLQVVEELINQRIETEFARGQAIQRLVGFGRSYDEVILAKSWND
10 20 30 40 50 60
70 80 90 100 110 120
130 140 150 160 170 180

cryla-105.pe
C1GB_BACTZ
PDPILGIFNEDQSAFLQVVEELINQRIETEFARGQAIQRLVGFGRSYDEVILAKSWND
10 20 30 40 50 60
70 80 90 100 110 120
130 140 150 160 170 180

cryla-105.pe
C1GB_BACTZ
PDPILGIFNEDQSAFLQVVEELINQRIETEFARGQAIQRLVGFGRSYDEVILAKSWND
10 20 30 40 50 60
70 80 90 100 110 120
130 140 150 160 170 180

cryla-105.pe
C1GB_BACTZ
PDPILGIFNEDQSAFLQVVEELINQRIETEFARGQAIQRLVGFGRSYDEVILAKSWND
10 20 30 40 50 60
70 80 90 100 110 120
130 140 150 160 170 180

cryla-105.pe
C1GB_BACTZ
VKAHTLOSQTIVVRGFGTGGDILRLRTSGGPFAYTIVNINCOLPQRYRARIYASTNLRL
470 480 490 500 510 520
530 540 550 560 570 580 590

cryla-105.pe
C1GB_BACTZ
IVTVVAGERIFACQFNKIMDGLITFQSPSATINTAFTFPMSSQSFVTGADTFSSGNE
540 550 560 570 580 590
600 610 620 630 640 650

cryla-105.pe
C1GB_BACTZ
FHTSINGRAINQANFPATWNGENLQSGSRVAGFTFTTFSDALSTFTIGAFSSSNE
530 540 550 560 570 580 590
600 610 620 630 640 650

cryla-105.pe
C1GB_BACTZ
VIDGIEFPAEVTATESQDRAOKAVNALFTSSNOIGLKTVDVTHIDOVSNLVECLIS
590 600 610 620 630 640 650
660 670 680 690 700 710

cryla-105.pe
C1GB_BACTZ
DEFCDKRELSERKVKAKELSDERNLLODSNFKINROPERGWSGTGTTIOGGDDVFK
660 670 680 690 700 710
720 730 740 750 760 770

cryla-105.pe
C1GB_BACTZ
ENVVTLSTGTFDECTVLYOKIDESKLAFTYQRLGYIEDSODLEIYSIRYNAKHTVN
720 730 740 750 760 770
780 790 800 810 820 830

cryla-105.pe
C1GB_BACTZ
ENVVTLSTGTFDECTVLYOKIDESKLAFTYQRLGYIEDSODLEIYSIRYNAKHTVN
720 730 740 750 760 770
780 790 800 810 820 830

cryla-105.pe
C1GB_BACTZ
ENVVTLSTGTFDECTVLYOKIDESKLAFTYQRLGYIEDSODLEIYSIRYNAKHTVN
720 730 740 750 760 770
780 790 800 810 820 830

cryla-105.pe
C1GB_BACTZ
ENVVTLSTGTFDECTVLYOKIDESKLAFTYQRLGYIEDSODLEIYSIRYNAKHTVN
720 730 740 750 760 770
780 790 800 810 820 830

cryla-105.pe
C1GB_BACTZ
ENVVTLSTGTFDECTVLYOKIDESKLAFTYQRLGYIEDSODLEIYSIRYNAKHTVN
720 730 740 750 760 770
780 790 800 810 820 830

cryla-105.pe
C1GB_BACTZ
ENVVTLSTGTFDECTVLYOKIDESKLAFTYQRLGYIEDSODLEIYSIRYNAKHTVN
720 730 740 750 760 770
780 790 800 810 820 830

cryla-105.pe
C1GB_BACTZ
ENVVTLSTGTFDECTVLYOKIDESKLAFTYQRLGYIEDSODLEIYSIRYNAKHTVN
720 730 740 750 760 770
780 790 800 810 820 830

cryla-105.pe
C1GB_BACTZ
ENVVTLSTGTFDECTVLYOKIDESKLAFTYQRLGYIEDSODLEIYSIRYNAKHTVN
720 730 740 750 760 770
780 790 800 810 820 830

cryla-105.pe
C1GB_BACTZ
ENVVTLSTGTFDECTVLYOKIDESKLAFTYQRLGYIEDSODLEIYSIRYNAKHTVN
720 730 740 750 760 770
780 790 800 810 820 830

cryla-105.pe
C1GB_BACTZ
ENVVTLSTGTFDECTVLYOKIDESKLAFTYQRLGYIEDSODLEIYSIRYNAKHTVN
720 730 740 750 760 770
780 790 800 810 820 830

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cryla-105.pe	480	490	500	510	520	530
C1GA_BACTU	410	420	430	440	450	
cryla-105.pe	480	490	500	510	520	530
C1GA_BACTU	460	470	480	490	500	510
cryla-105.pe	540	550	560	570	580	590
C1GA_BACTU	520	530	540	550	560	570
cryla-105.pe	600	610	620	630	640	650
C1GA_BACTU	580	590	600	610	620	630
cryla-105.pe	660	670	680	690	700	710
C1GA_BACTU	640	650	660	670	680	690
cryla-105.pe	720	730	740	750	760	770
C1GA_BACTU	700	710	720	730	740	750
cryla-105.pe	780	790	800	810	820	830
C1GA_BACTU	760	770	780	790	800	810
cryla-105.pe	840	850	860	870	880	890
C1GA_BACTU	820	830	840	850	860	870
cryla-105.pe	900	910	920	930	940	950
C1GA_BACTU	880	890	900	910	920	930
cryla-105.pe	960	970	980	990	1000	1010
C1GA_BACTU	940	950	960	970	980	990
cryla-105.pe	1020	1030	1040	1050	1060	1070
C1GA_BACTU	1000	1010	1020	1030	1040	1050
cryla-105.pe	1080	1090	1100	1110	1120	

©17
cryla-105.pe TNDYVNGEAGNTSRNGYNEA----PSVPADVASVYEKSVTDGRRENCEPNRG
CIGA_BACTU TNDYVNGEAGNTSRNGYNEA----PSVPADVASVYEKSVTDGRRENCEPNRG
cryla-105.pe YRDYDLPVWVLEKTEGTEFVDSVLLMEE
CIGA_BACTU YRDYDLPVWVLEKTEGTEFVDSVLLMEE
cryla-105.pe YGYDPLPASYVVELEYFETDNWIEIGENEGVIVESVLLMEE
CIGA_BACTU YGYDPLPASYVVELEYFETDNWIEIGENEGVIVESVLLMEE
cryla-105.pep
TXNS.CIHA_BACTU
Description: Q45748 bacillus thuringiensis, pest-killing crystal protein cryIa
(insecticidal)
Accession/ID: Q45748
ID TXNS.CIHA_BACTU STANDARD; PRT: 1172 AA.
AC Q45748;
Scores Initl: 3049 Initn: 4970 Opt: 4426 z-score: 4878.7
>TXNS.CIHA_BACTU
Initn: 4970 Initl: 3049 Opt: 4426 z-score: 4878.7 expect (0):
Smith-Waterman score: 5232; 67.6% identity in 1187 aa overlap
(1-1177:1-1172)

cryla-105.pe MDNPNINCEIPNCLSNPEVEIGERIEGTYP--IDLSLTQFLSEFVPGAGVL
CIHA_BACTU MDNPNINCEIPNCLSNPEVEIGERIEGTYP--IDLSLTQFLSEFVPGAGVL
cryla-105.pe GLVDILNGVGPQDNLFLAQIEQLIDQRIEAVHVRNQALISLEGLGSEVYIESLREWE
CIHA_BACTU GLVDILNGVGPQDNLFLAQIEQLIDQRIEAVHVRNQALISLEGLGSEVYIESLREWE
cryla-105.pe ADPTNPALREEMRIQFNDMNSALITAIPLFAVQVQVPLLSVYVQAAHLHLSVLDSVVF
CIHA_BACTU ADPTNPALREEMRIQFNDMNSALITAIPLFAVQVQVPLLSVYVQAAHLHLSVLDSVVF
cryla-105.pe GQRMGFDAATNSRYNDLRLIGNYVDHVRWNTGLERVMPGDSRWIRYNQFRRELT
CIHA_BACTU GQRMGFDAATNSRYNDLRLIGNYVDHVRWNTGLERVMPGDSRWIRYNQFRRELT
cryla-105.pe TVLDIVSLFPNYSRTPIRTVSQLTREIYNPVLENFNGSPRGAQIGESIRSLHMD
CIHA_BACTU TVLDIVSLFPNYSRTPIRTVSQLTREIYNPVLENFNGSPRGAQIGESIRSLHMD
cryla-105.pe ILMSITTYDAHRGEYVWGHQIMASPVFGSPFFPLGYGTMGNAAPQQRIVAQLGQV
CIHA_BACTU ILMSITTYDAHRGEYVWGHQIMASPVFGSPFFPLGYGTMGNAAPQQRIVAQLGQV

cryla-105.pe VRTLSSTLYRPPENIGINNOLSVLQGTGEFAYGTSSNLPSSA--VYRKSGTVDSLDIPPQ
CIHA_BACTU VRTLSSTLYRPPENIGINNOLSVLQGTGEFAYGTSSNLPSSA--VYRKSGTVDSLDIPPQ
cryla-105.pe NNNVPPRQGSHELHSHVSMFSGSSSVSIRAPMFNWHRSAEFNNIADSITQIPL
CIHA_BACTU NNNVPPRQGSHELHSHVSMFSGSSSVSIRAPMFNWHRSAEFNNIADSITQIPL
cryla-105.pe VZAHVLOSCTTVRGPFGTGGDILRRSG--GPFAYTVNNGOLPORVARIIVASTTN
CIHA_BACTU VZAHVLOSCTTVRGPFGTGGDILRRSG--GPFAYTVNNGOLPORVARIIVASTTN
cryla-105.pe LRIYTVVAGERIFAGQFNKMTDGDPLTFQSFYATINTAFTFPMSSOSTVGAUTFSG
CIHA_BACTU LRIYTVVAGERIFAGQFNKMTDGDPLTFQSFYATINTAFTFPMSSOSTVGAUTFSG
cryla-105.pe NEVYIDRELIPTATLEAEVYLNLEPAOKAVNALFTSTNOLGKTNVTDYHIDOVSNLTV
CIHA_BACTU NEVYIDRELIPTATLEAEVYLNLEPAOKAVNALFTSTNOLGKTNVTDYHIDOVSNLTV
cryla-105.pe LSPFCFLDEKRESEKVKHAKLSDERNLQDSNFKDINRQPERGWSGTITIQGDDV
CIHA_BACTU LSPFCFLDEKRESEKVKHAKLSDERNLQDSNFKDINRQPERGWSGTITIQGDDV
cryla-105.pe FKNSTYVDFDSEKPKYKQIKDESCLKAFTXOLRGYVIEDSODLEIYSIRYNAKHET
CIHA_BACTU FKNSTYVDFDSEKPKYKQIKDESCLKAFTXOLRGYVIEDSODLEIYSIRYNAKHET
cryla-105.pe VNVPGTGSWPLSAQSPKAPNRCAPHEMNDLDCSCRDGKCAHSHHFSLDIDV
CIHA_BACTU VNVPGTGSWPLSAQSPKAPNRCAPHEMNDLDCSCRDGKCAHSHHFSLDIDV
cryla-105.pe GCTDLNEDLGWVIFPKIKTQDGHANLGNLEKLVNENALRVEKAKWKRKREKLE
CIHA_BACTU GCTDLNEDLGWVIFPKIKTQDGHANLGNLEKLVNENALRVEKAKWKRKREKLE
cryla-105.pe WETNIVYKESVDALFVNSQVDQADTNAMHAADRVHREAYLPPALIPCVN
CIHA_BACTU WETNIVYKESVDALFVNSQVDQADTNAMHAADRVHREAYLPPALIPCVN
cryla-105.pe AAIFEELEGRITAFSLYDARNVTKGDFNGLSCWNVKGHVDEQNNQRSLVNEPE
CIHA_BACTU AAIFEELEGRITAFSLYDARNVTKGDFNGLSCWNVKGHVDEQNNQRSLVNEPE

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cry1a-105.pe  LNSITTYDHAARGEYSGHQIWASPVG-FSGPEFTTFLYGTGMAAQQRI-----VAQL
:::||||:::||||:::||||:::||||:::||||:::||||:::||||:::||||:::||||:::
IDRIYVINSRSTPVAGWEHVSRTTGOAGNEIRFLPYGTGVAANAEPFPIRTGTGTD
300 310 320 330 340 350
Y09326_1

```

```

360      370      380      390      400      410
cr1a-105.pe GCGVGTLSLTYRRPFGINNQQLSVLDGTAYGTSNLPFAVRKS-G-TVDSLDE
      |||      |||      |||      |||      |||      |||
Y09326_1 QRQWYRARS--LLSRFSSG--QDFSLDVAFLTFISA--VSIYRNGFGFNTDIDE
      360      370      380      390      400

```

```
cry1a_105.pe      420    430    440    450    460    470
:::|:::|SHRLSHVSMFSGESNSVSIIIPAPMFSWHSAEFNNTIASDIT
IPIEGTD--PFTGYSHRLCHVGFLASSFIQYAA--RAPIFSWTHSKSLNLTINAPDVII
```

[illegible]

cryIa-105.pe SG-NVYIDRFELIPVTATLAEVNLERAQKAVNALFTSNGLGKTNTVDYTHDVSNN
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
PKUTEVIDRIFFPAAVEAYEYDEKAQKAVNALFTSNGLGKTNTVDYTHDKVSNL
560

Y09326_1

```

cry1a-105.pe      VTVLSDEFCLDEKKESEKYKHAKRLSDERNLQDSNFDINRQPERGCGSGTITQQG      660   670   680   690   700   710
Y09326.1          VECLSPDFCLDEKKESEKYKHAKRLSDERNLQDSNFDINRQPERGCGSGTITQQG      660   670   680   690   700   710

```

```
cryla-105.pe DDVFKENVYTLGTFDCPYTYLYQKIDESKKAFTRYQLRGVIEDSODLEIYSIRNAK  
|||  
|||  
|||  
DDVFKENVYTLGTFDCPYTYLYQKIDESKKAFTRYQLRGVIEDSODLEIYSIRNAK  
|||  
|||  
|||  
DDVFKENVYTLGTFDCPYTYLYQKIDESKKAFTRYQLRGVIEDSODLEIYSIRNAK  
720 730 740 750 760 770
```

```

      780      790      800      810      820      830
cryla-105.pe  HETVNPVTGSLWPLSAQSIGKCGEPNRCAPHLEWNPOLDCSRDGSKCAHSHHSFSD
      760      770      780      790      800      810
Y09326_1      HETVNPVTGSLWPLSAQSIGKCGEPNRCAPHLEWNPOLDCSRDGSKCAHSHHSFSD

```

cry1a-105_pe IDVGCTDNLNEDLGGWVYFKTKTQDGHARLGNLFELEKPIVGFEALARVKAKEKKWDKKE
 840 850 860 870 880 890
 IDVGCTDNLNEDLGGWVYFKTKTQDGHARLGNLFELEKPIVGFEALARVKAKEKKWDKKE
 900 910 920
 Y09326_1

[illegible]

Year	1960	1970	1980	1990	2000	2010
Population (millions)	1.2	1.5	1.8	2.1	2.4	2.7
GDP (billions of dollars)	0.1	0.2	0.3	0.4	0.5	0.6
Life expectancy (years)	45	55	65	75	80	85
Urban population (%)	20	30	40	50	60	70
Female literacy (%)	10	20	30	40	50	60
Infant mortality (per 1,000 live births)	100	80	60	40	30	20
Renewable energy consumption (ktoe)	0.5	0.6	0.7	0.8	0.9	1.0
Forest area (million hectares)	1.0	1.1	1.2	1.3	1.4	1.5
Arable land (million hectares)	0.8	0.9	1.0	1.1	1.2	1.3
Water resources (km³)	1.0	1.1	1.2	1.3	1.4	1.5
CO2 emissions (million tonnes)	0.1	0.2	0.3	0.4	0.5	0.6
Electricity generation (TWh)	0.1	0.2	0.3	0.4	0.5	0.6
Healthcare expenditure (GDP %)	5	6	7	8	9	10
Government expenditure (GDP %)	10	11	12	13	14	15
Private sector contribution (GDP %)	40	45	50	55	60	65
Foreign aid (billion dollars)	0.1	0.2	0.3	0.4	0.5	0.6
Trade share (GDP %)	10	15	20	25	30	35
Research and development (GDP %)	0.5	0.6	0.7	0.8	0.9	1.0
Infrastructure investment (GDP %)	5	6	7	8	9	10
Environmental protection (GDP %)	0.5	0.6	0.7	0.8	0.9	1.0
Education expenditure (GDP %)	3	4	5	6	7	8
Healthcare expenditure (GDP %)	5	6	7	8	9	10
Government expenditure (GDP %)	10	11	12	13	14	15
Private sector contribution (GDP %)	40	45	50	55	60	65
Foreign aid (billion dollars)	0.1	0.2	0.3	0.4	0.5	0.6
Trade share (GDP %)	10	15	20	25	30	35
Research and development (GDP %)	0.5	0.6	0.7	0.8	0.9	1.0
Infrastructure investment (GDP %)	5	6	7	8	9	10
Environmental protection (GDP %)	0.5	0.6	0.7	0.8	0.9	1.0
Education expenditure (GDP %)	3	4	5	6	7	8
Healthcare expenditure (GDP %)	5	6	7	8	9	10
Government expenditure (GDP %)	10	11	12	13	14	15
Private sector contribution (GDP %)	40	45	50	55	60	65
Foreign aid (billion dollars)	0.1	0.2	0.3	0.4	0.5	0.6
Trade share (GDP %)	10	15	20	25	30	35
Research and development (GDP %)	0.5	0.6	0.7	0.8	0.9	1.0
Infrastructure investment (GDP %)	5	6	7	8	9	10
Environmental protection (GDP %)	0.5	0.6	0.7	0.8	0.9	1.0
Education expenditure (GDP %)	3	4	5	6	7	8
Healthcare expenditure (GDP %)	5	6	7	8	9	10
Government expenditure (GDP %)	10	11	12	13	14	15
Private sector contribution (GDP %)	40	45	50	55	60	65
Foreign aid (billion dollars)	0.1	0.2	0.3	0.4	0.5	0.6
Trade share (GDP %)	10	15	20	25	30	35
Research and development (GDP %)	0.5	0.6	0.7	0.8	0.9	1.0
Infrastructure investment (GDP %)	5	6	7	8	9	10
Environmental protection (GDP %)	0.5	0.6	0.7	0.8	0.9	1.0
Education expenditure (GDP %)	3	4	5	6	7	8
Healthcare expenditure (GDP %)	5	6	7	8	9	10
Government expenditure (GDP %)	10	11	12	13	14	15
Private sector contribution (GDP %)	40	45	50	55	60	65
Foreign aid (billion dollars)	0.1	0.2	0.3	0.4	0.5	0.6
Trade share (GDP %)	10	15	20	25	30	35
Research and development (GDP %)	0.5	0.6	0.7	0.8	0.9	1.0
Infrastructure investment (GDP %)	5	6	7	8	9	10
Environmental protection (GDP %)	0.5	0.6	0.7	0.8	0.9	1.0
Education expenditure (GDP %)	3	4	5	6	7	8
Healthcare expenditure (GDP %)	5	6	7	8	9	10
Government expenditure (GDP %)	10	11	12	13	14</	

cry1a-105.pe GVNAATFEELGRTIPAFSLYDARNVINKNGDFNGLSCWNVKGVHVDVEQNNQSRVULVP
Y09326_1 GVNAATFEELGRTIPAFSLYDARNVINKNGDFNGLSCWNVKGVHVDVEQNNQSRVULVP
Y09326_1 GVNAATFEELGRTIPAFSLYDARNVINKNGDFNGLSCWNVKGVHVDVEQNNQSRVULVP

cry1a-105.pe EWARNSONRVCPGGLRVTAYESGNGCVTIEIENNDLKFSCNVEEIEIYPNN
Y09326_1 EWARNSONRVCPGGLRVTAYESGNGCVTIEIENNDLKFSCNVEEIEIYPNN
Y09326_1 EWARNSONRVCPGGLRVTAYESGNGCVTIEIENNDLKFSCNVEEIEIYPNN

cry1a-105.pe TVTCNDYTNQEEYGGAYTSNRGNEA--PSWADYASVSESYDGRNCPGFN
Y09326_1 TVTCNDYTNQEEYGGAYTSNRGNEA--PSWADYASVSESYDGRNCPGFN
Y09326_1 TVTCNDYTNQEEYGGAYTSNRGNEA--PSWADYASVSESYDGRNCPGFN

cry1a-105.pe RGYRDYTPLVGVTKLEYFPETDKWIEIGETETSTNDVLELLME
Y09326_1 RGYRDYTPLVGVTKLEYFPETDKWIEIGETETSTNDVLELLME
Y09326_1 RGYRDYTPLVGVTKLEYFPETDKWIEIGETETSTNDVLELLME

cry1a-105.pep
TXN5:CIKA_BACTM

Description: Q45715 bacillus thuringiensis (subsp. morrisonii). pesticidal
crystal protein cr
Accession/ID: Q45715
ID CIKA_BACTM STANDARD; PRI; 1215 AA.
AC Q45715;

SCORES Initl: 3021 Initn: 4044 Opt: 4338 z-score: 4781.4 E(): 0
>>TXN5:CIKA_BACTM
Initn: 4044 Initl: 3021 Opt: 4338 Z-score: 4781.4 expect(): 0
Smith-Waterman score: 4666; 62.7% identity in 1181 aa overlap
(34-1177:54-1215)

cry1a-105.pe NPNINECIPYNCUSNEVEVLGGRIETGYTPIDISLSLTOTFLLSEF-VPGAGFVLGLVD
CIKA_BACTM SAQMDLSPDARIEDSLCVAEGNNIDPFVSASTVQTGISIAGRIILGVLPFAQGLASYS

cry1a-105.pe IIWGIFGFS--OWDAFLVQIEQLI-NORIEEFARNQAIISLEGLSLNLYQVIAESFREWE
CIKA_BACTM FLVGLWPSGSDPWELEFMEHVEQIVRQOQITDSVRDTALAEGLGLRGVRSYQQALETWL

cry1a-105.pe ADPTNPALREEMRIQNDNWSALTTAIPFAGVQVPLLSYVQAANHLHSLVLRDVSFV
CIKA_BACTM DNRNDAISRISIRYIALELDITTAIPFISIRNEEYVPLLYQAANHLHLLLRDLSLF

cry1a-105.pe GQWGFDAATNSRYNDLRLIGNVTHAVRWNTGLEWVCPDSRDWRVNFREELTL
CIKA_BACTM GSEWMSADVQNYQEQIRYITEEYSNHCVQWNTGLNLAGTTAETWRYNFRDLTL

cry1a-105.pe TVLIDVSLFENVDSRTYPIRTVSOLTREIVTNP--VLENFDGS-FRGSQAQ--GIEGSI-R
CIKA_BACTM GVLIDVSLFENVDSRTYPIRTVSOLTREIVTNP--VLENFDGS-FRGSQAQ--GIEGSI-R

cry1a-105.pe SPMLMDLNSITIID-AHRGEY--WSHQIMASPVGSPGPEFTPLIGMGNAAPQQ
CIKA_BACTM SPMLMDLNSITIID-AHRGEY--WSHQIMASPVGSPGPEFTPLIGMGNAAPQQ

cry1a-105.pe RIVAQLGQGVRTLSST-----LYREFNIGINNQQSLVLDGTEFAYGTSSNL
CIKA_BACTM RIVAQLGQGVRTLSST-----LYREFNIGINNQQSLVLDGTEFAYGTSSNL

cry1a-105.pe PSAVYKSGTVDSLDIIPQNNVPPRQGFSHLSHVSMSRSGNSVSIIIRAPMFWI
CIKA_BACTM PSAVYKSGTVDSLDIIPQNNVPPRQGFSHLSHVSMSRSGNSVSIIIRAPMFWI

cry1a-105.pe HRSAEFNITIASUSITQIPLVKAHTLOSQTIVRGPGFTGCDILRRTSGGPFAYTVIN
CIKA_BACTM HRSAEFNITIASUSITQIPLVKAHTLOSQTIVRGPGFTGCDILRRTSGGPFAYTVIN

cry1a-105.pe COLQRYEARIRYASTINRIYVTVAGERIFAGQFNKTMIDTGDPLTFQSFYSATINTAFT
CIKA_BACTM COLQRYEARIRYASTINRIYVTVAGERIFAGQFNKTMIDTGDPLTFQSFYSATINTAFT

cry1a-105.pe FPMSSSSNIGADTFSGNENVDNRFELIQVTATFAESDLEAFKAVNALFTSTNPRGL
CIKA_BACTM FPMSSSSNIGADTFSGNENVDNRFELIQVTATFAESDLEAFKAVNALFTSTNPRGL

cry1a-105.pe KTNVTDYHIDQVSNLVTYDSPEFIDEKRESEKAKVLSDERNLLQDSNFKDINROP
CIKA_BACTM KTNVTDYHIDQVSNLVTYDSPEFIDEKRESEKAKVLSDERNLLQDSNFKDINROP

cry1a-105.pe ERMGSGSTGITIGDGVFNENYVLSQFDECYPTLYQVDESKLANTROLRGYIE
CIKA_BACTM ERMGSGSTGITIGDGVFNENYVLSQFDECYPTLYQVDESKLANTROLRGYIE

cry1a-105.pe DSODLEIYSIRYNAKHETVNVPTCTSLMPLSAQSPGKCSNCAAPHLNAPVPCSCR
CIKA_BACTM DSODLEIYSIRYNAKHETVNVPTCTSLMPLSAQSPGKCSNCAAPHLNAPVPCSCR

cry1a-105.pe DGKCAHSHHFSLDIDVGCTDNLNEDLGWVWIFIKITQDGHARLGNLEFLEKPLGEL
CIKA_BACTM DGKCAHSHHFSLDIDVGCTDNLNEDLGWVWIFIKITQDGHARLGNLEFLEKPLGEL

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cryla-105.pe ADPTNPALREEMRIQFNOMNSALTATPLFAVONQVPELLSVYQAANHLHSLVRDSVSE
U28801_1      : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
DRNRDARSIIIRRYALELDTITPFIISNEEVLPMVAQAANHLHLLLRDASLF
150          160         170        180        190        200

```

```

cryla-105.pe QQRWGFDAATINSRYNDITRLIGNYTHAVRWYNTGLERWVGDFSDRWIRYNQPREUTL
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
GSEGMSSADVNQYQEQIRYTEYSNHCVQWYNTGLNRLTGTTAETWRYNQPRDUTL
U28801_1      210   215   220   225   230

```

```

cryla-105.pe      240    250    260    270    280    290
TLDIVSLFPNDSTYIRVTSOLTREITNP--VLENFDGS-FRGSQAQ--GIGSGI-R
|||:|||:|||:|||:|||:|||:::|||||:::|||||:::
U28801_1          270    280    290    300    310    320
GLVDLVALFSDYTDTIPTPTAOLTRVEYTDPNGVAGAPNNWFRNGSAFAISNAIR

```

```
cryla-105.pe SPHLMIDINSITVTD-AHRGEYV---WSGHQIMASPVGSGSEFFTPLYCTMGNAAPQQ
               300      310      320      330      340
U28801_1 QPHLYDFELTNLITYTRRSQGVCTTMMWAGHRTNFI--QGGSSEMIVGAITNPVSFVS
               330      340      350      360      370      380
```

```

350      360      370      380      390
cryla-105.pe RIVAAQGGVYTLST--LYRPFNIGINNQLSLDTEFYATSTNN
          : : : : : : : : : : : : : : : : : : : : : :
U28801_1 DI-PFVNRDVYTVSLAGGLGSLGRYGLTRVDFMTFNHP-DIVTGLFYHPG-HAGI
          390      400      410      420

```

```

400      410      420      430      440      450
cryla-105.pe PSAYRKSGTVSLDEIPQNNVPRQGFSHLSHVSFMFSGFSNYSIIRAFMSFI
U28801_1 ATQVK-----DSDLETPTTEQPNRAFSHLLSHISM--GPTQDVP-----PVYSWT
440      450      460      470      480

```

[illegible]

```

580      590      600      610      620      630
cry1a-105.pe  FPMQSFTVGADTSSGVEVYDRFLPVVATLEAYLEAKQAVNAFTSTNOLGL
                | : | : | : | : | : | : | : | : | : | : | : | : |
U28801_1      FPRSSSLTAGDATTSSGVEVYDRFLQVATFEASDLERAKVNAFTSTNPRGL
                | : | : | : | : | : | : | : | : | : | : | : | : |
610      620      630      640      650      660

```

640 650 660 670 680 690
 cry1a-105.pe KINVTYDHIDQVSNLVTYDSDFCLDEKRELSKVKHAKLSIDERNLLQDSNFKDINRQ
 U28801_1 KTDVTDHIDQVSNLVECLDSDFCLDEKRELSKVKHAKLSIDERNLLQDPTFTSISQGT
 670 680 690 700 710 720

```

700      710      720      730      740      750
cryla-105.pe  ERMGSGTGITTOGGDDVFKENVTLSGTFFDCEPTLYOKIDESKAFYQIRGVIE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
U38801_1      DRMGISGTSGISOGGDDIFKENVPLVGTVDCEPTLYOKIDESQLKSYTRQIRGVIE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
              760      770      780

```

810

©07

```
cry1a-105.pe DSQLEYSIRNANETVNVPGTGSINPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCR
U28801_1 DSQLEYSIRNANETVNVPGTGSINPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCR
790 800 810 820 830 840
cry1a-105.pe DGEKRAHSHSLADYDCTDLNEDGVNFKIKTODGHARGLNLEFLKPKLVGEAL
U28801_1 DGEKRAHSHSLADYDCTDLNEDGVNFKIKTODGHARGLNLEFLKPKLVGEAL
850 860 870
YGEKCVHSHSLADYDCTDLNEDGVNFKIKTODGHARGLNLEFLKPKLVGEAL
880 890 900
cry1a-105.pe ARVRAEKRWDRKREKLEWNSVYKAEKESVDASVNSQDSQVSTNIAMIHAADKRV
U28801_1 ARVRAEKRWDRKREKLEWNSVYKAEKESVDASVNSQDSQVSTNIAMIHAADKRV
910 920 930 940 950 960
SRVRAEKRWDRKREKLEWNSVYKAEKESVDASVNSQDSQVSTNIAMIHAADKRV
970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080
cry1a-105.pe HSIREAVLPESLVIPGVNAAIFEELEGRIPTAFSDADANVINKGDFNMVLSQWVYKSHV
U28801_1 HSIREAVLPESLVIPGVNAAIFEELEGRIPTAFSDADANVINKGDFNMVLSQWVYKSHV
1090 1100 1110 1120 1130 1140
cry1a-105.pe DVEQNNQSRVLVPEWEAEVSQVRVCPGRGYLRVYAYKEGYGECVTHETNNNTDE
U28801_1 DVEQNNQSRVLVPEWEAEVSQVRVCPGRGYLRVYAYKEGYGECVTHETNNNTDE
1060 1070 1080 1090
cry1a-105.pe LKFSNCEVEEYIPNNVTICNDYTVNOEYGG-AVTSNRGYNEA-----PSVPADY
U28801_1 LKFSNCEVEEYIPNNVTICNDYTVNOEYGG-AVTSNRGYNEA-----PSVPADY
1100 1110 1120 1130 1140
cry1a-105.pe ASVVEEKSYYDGRNCPENFGRYDTPLPVGYVTKLEYFPETDKVWIEGETEGTFI
U28801_1 ASVVEEKSYYDGRNCPENFGRYDTPLPVGYVTKLEYFPETDKVWIEGETEGTFI
1150 1160 1170 1180 1190 1200
cry1a-105.pe VDSVELLMEE
U28801_1 VDSVELLMEE
1210
cry1a-105.pep
TXN5:M12661_1
Description: M12661 Bacillus thuringiensis B.thuringiensis insecticidal
endotoxin gene, comp1
Accession/ID: M12661
=====General comments=====
LOCUS M12661_1 [BACWSQA]
DEFINITION B.thuringiensis insecticidal endotoxin gene, complete cds;
(1-1177:1-1156)
SCORES Initl: 2559 Initn: 4966 Opt: 4319 z-score: 4760.7 E(): 0
>TXN5:M12661_1
initn: 4966 Initl: 2559 Opt: 4319 z-score: 4760.7 expect(): 0
Smith-Waterman score: 6513; 84.7% identity in 1186 aa overlap
(1-1177:1-1156)
```

```
cry1a-105.pe MNNNTNINCEIPVNCLSNEVEVLGGRIETGTPIDISLSITOPLLSEFVPGAGFVLGL
M12661_1 MNNNTNINCEIPVNCLSNEVEVLGGRIETGTPIDISLSITOPLLSEFVPGAGFVLGL
10 20 30 40 50 60
cry1a-105.pe VDIWIFGFSQMDAFLVOIEQLINQRIEFAFNOAISLEGLSNLYQIYAEFREWED
M12661_1 VDIWIFGFSQMDAFLVOIEQLINQRIEFAFNOAISLEGLSNLYQIYAEFREWED
70 80 90 100 110 120
cry1a-105.pe PNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAAHLHLSVLRDVSFQO
M12661_1 PNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAAHLHLSVLRDVSFQO
130 140 150 160 170 180
cry1a-105.pe RWGFDAAATNSRYNDLTRILIGNVTDHAVRWYNTGLERVWGPDSRDWIRYNOFRRELTIV
M12661_1 RWGFDAAATNSRYNDLTRILIGNVTDHAVRWYNTGLERVWGPDSRDWIRYNOFRRELTIV
190 200 210 220 230 240
cry1a-105.pe LDIVSLIFPNYSRTYPIRTVYQSOLTRITNTVPLENFDGSRGSAQIEGSIIRSPHLMDL
M12661_1 LDIVSLIFPNYSRTYPIRTVYQSOLTRITNTVPLENFDGSRGSAQIEGSIIRSPHLMDL
250 260 270 280 290 300
cry1a-105.pe NSITVTAHGEYWGSHQIMASVPFGSGPEFTFPLGYTMGNAAPQORIVAOQGGVYR
M12661_1 NSITVTAHGEYWGSHQIMASVPFGSGPEFTFPLGYTMGNAAPQORIVAOQGGVYR
310 320 330 340 350 360
cry1a-105.pe TUSSTVYAFENIGNINNOQSVLDGTGTFAYTSSNLPNAVY RKSGTVDSLDELIPPNNN
M12661_1 TUSSTVYAFENIGNINNOQSVLDGTGTFAYTSSNLPNAVY RKSGTVDSLDELIPPNNN
370 380 390 400 410 420
cry1a-105.pe VPPROGFSHRCLATSNKSGFSMSQVIAEPAPNDSWAKCSAEFGDVIPSSQITQILPT
M12661_1 VPPROGFSHRCLATSNKSGFSMSQVIAEPAPNDSWAKCSAEFGDVIPSSQITQILPT
430 440 450 460 470 480
cry1a-105.pe KAHTLQSG--TTVVRGPGFTGGDTSRTSGGPFAYITVNIINGOLPRTYRIRYASTTNL
M12661_1 KAHTLQSG--TTVVRGPGFTGGDTSRTSGGPFAYITVNIINGOLPRTYRIRYASTTNL
490 500 510 520 530
cry1a-105.pe RIYTVAGERIFAGOFNKMTDGDPLTFQSPFSYATINTATPNSQSFVCAVDESSGN
M12661_1 RIYTVAGERIFAGOFNKMTDGDPLTFQSPFSYATINTATPNSQSFVCAVDESSGN
540 550 560 570 580 590
cry1a-105.pe EVVIDRFELIPVTLEAEYNLERAQKAVNALFTSTNQLGKTNVTDYHIDQVSNLVTTH
M12661_1 EVVIDRFELIPVTLEAEYNLERAQKAVNALFTSTNQLGKTNVTDYHIDQVSNLVTTH
600 610 620 630 640 650
cry1a-105.pe EVVIDRFELIPVTLEAEYNLERAQKAVNALFTSTNQLGKTNVTDYHIDQVSNLVTTH
M12661_1 EVVIDRFELIPVTLEAEYNLERAQKAVNALFTSTNQLGKTNVTDYHIDQVSNLVTTH
660 670 680 690 700 710
```

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Product Characterization Center

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MSL No. 20351
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```
cry1a-105.pe SDFCLDEKRELSKVKHAKELSDERNLLQDSNFKDINRQPERGWGSGTGIIOGGDDVF
M12661_1 SDFCLDEKRELSKVKHAKELSDERNLLQDPNFRGINRQRLDGRNGTNDITIOGGHDVF
660 670 680 690 700 710

cry1a-105.pe KENVTLTSGTFDECYPTLYOKIDESKLFKAFTRYOLGYIEDSODLEIYSIRYAKHETV
M12661_1 KENVTLTSGTFDECYPTLYOKIDESKLFKAFTRYOLGYIEDSODLEIYSIRYAKHETV
720 730 740 750 760 770

cry1a-105.pe NVPTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGEKCAHSHHFSLDIDVG
M12661_1 NVPTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGEKCAHSHHFSLDIDVG
780 790 800 810 820 830

cry1a-105.pe CTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKAEEKWDRKREKLEW
M12661_1 CTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKAEEKWDRKREKLEW
840 850 860 870 880 890

cry1a-105.pe ETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHADKRVHSIRREAYLPESLVIPGVNA
M12661_1 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHADKRVHSIRREAYLPESLVIPGVNA
900 910 920 930 940 950

cry1a-105.pe AIFEELEGRIFFAFSLYDARNVINKGDFNNGLSWNKVGKVDVEEQNNORSVLVVPWEA
M12661_1 AIFEELEGRIFFAFSLYDARNVINKGDFNNGLSWNKVGKVDVEEQNNORSVLVVPWEA
960 970 980 990 1000 1010

cry1a-105.pe EVSQEVVPCPGGYLLRVTAKEGYEGGCVTHIEENNTDELKFSNCVEEYFNNVTVC
M12661_1 EVSQEVVPCPGGYLLRVTAKEGYEGGCVTHIEENNTDELKFSNCVEEYFNNVTVC
1020 1030 1040 1050 1060 1070

cry1a-105.pe NDYTVNQEEYGGATSRNRNGYNEA---PSVPADYASYEEKSYTDGRRENPCFENRGYR
M12661_1 NDYTVNQEEYGGATSRNRNGYNEA---PSVPADYASYEEKSYTDGRRENPCFENRGYR
1080 1090 1100 1110 1120 1130

cry1a-105.pe DYTPLPVGYVTKLEYFPETDKWVIEIGETGTFLVDSVLLMEE
M12661_1 DYTPLPVGYVTKLEYFPETDKWVIEIGETGTFLVDSVLLMEE
1140 1150 1160 1170

cry1a-105.ppep
TXN5:ClAF_BACTU
Description: P96315 bacillus thuringiensis, pesticidal crystal protein cryIaf
(insecticidal)
Accession/ID: P96315
ID ClAF_BACTU STANDARD; PRT; 911 AA.
AC P96315;
```

SCORES Initl: 2986 Initn: 4785 Opt: 4198 Z-score: 4628.7 E(): 0

```
>>TXN5:ClAF_BACTU
initn: 4785 initl: 2986 opt: 4198 Z-score: 4628.7 expect(): 0
Smith-Waterman score: 4919; 81.6% identity in 942 aa overlap
(1-942:1-911)

cry1a-105.pe MNNPNNNECIPNCLSNPEVEVLGGRIETGTPIDISLSLTOFLISEFVPGAGFVLGL
ClAF_BACTU MNNPNNNECIPNCLSNPEVEVLGGRIETGTPIDISLSLTOFLISEFVPGAGFVLGL
10 20 30 40 50 60

cry1a-105.pe VDIWIGFQSDAFLVQIEQLINQRIEFPARNOAISLEGLSNLYQIYAESFREWAD
ClAF_BACTU VDIWIGFQSDAFLVQIEQLINQRIEFPARNOAISLEGLSNLYQIYAESFREWAD
70 80 90 100 110 120

cry1a-105.pe PTNPALREEMRIQFNDMSALTTAIPLFAVQNYQVPLLSVYVAANHLVSLDRDVSFQ
ClAF_BACTU PTNPALREEMRIQFNDMSALTTAIPLFAVQNYQVPLLSVYVAANHLVSLDRDVSFQ
130 140 150 160 170 180

cry1a-105.pe PTNPALREEMRIQFNDMSALTTAIPLFAVQNYQVPLLSVYVAANHLVSLDRDVSFQ
ClAF_BACTU PTNPALREEMRIQFNDMSALTTAIPLFAVQNYQVPLLSVYVAANHLVSLDRDVSFQ
190 200 210 220 230 240

cry1a-105.pe RMGFDAAITNSRYNDLTRILIGNYTDHVRVNTGLERVWGPDSRDWIRYNOQFRELLTV
ClAF_BACTU RMGFDAAITNSRYNDLTRILIGNYTDHVRVNTGLERVWGPDSRDWIRYNOQFRELLTV
250 260 270 280 290 300

cry1a-105.pe LDIVSLPNDSTRTYIRTVSOLTREIYTNPVLENDFGSRGSAQIEGSIKPSHPLMDIL
ClAF_BACTU LDIVSLPNDSTRTYIRTVSOLTREIYTNPVLENDFGSRGSAQIEGSIKPSHPLMDIL
310 320 330 340 350 360

cry1a-105.pe NSITITYDARGEYVWSGHQINASPVGSGPEFTFPLTGTMGNAAPQORIVAOLGQGVYR
ClAF_BACTU NSITITYDARGEYVWSGHQINASPVGSGPEFTFPLTGTMGNAAPQORIVAOLGQGVYR
370 380 390 400 410 420

cry1a-105.pe TLSSTLYRRPFPNIGINNQLSVLDGTEFAVGTSSNLPNAVYRKSGTVDSLDEIPPNNNV
ClAF_BACTU TLSSTLYRRPFPNIGINNQLSVLDGTEFAVGTSSNLPNAVYRKSGTVDSLDEIPPNNNV
430 440 450 460 470 480

cry1a-105.pe PPRQGFHRLSHVSMFRSGFNSSVSIIRAPMFMSWIHRSAEFNNIIASDSITQIPLVKAH
ClAF_BACTU PPRQGFHRLSHVSMFRSGFNSSVSIIRAPMFMSWIHRSAEFNNIIASDSITQIPLVKAH
490 500 510 520 530 540

cry1a-105.pe TLQSGTIVVRGPGFTGCDILRRTSGGPFAYTIWINGQLPORVYRIRYASTNRIYVT
ClAF_BACTU TLQSGTIVVRGPGFTGCDILRRTSGGPFAYTIWINGQLPORVYRIRYASTNRIYVT
550 560 570 580 590 600

cry1a-105.pe VAGERIFAGQFNKIMTDGDTLPQSFYATINTAFTFPMSSQSFVAGDFTSSGNEVID
ClAF_BACTU VAGERIFAGQFNKIMTDGDTLPQSFYATINTAFTFPMSSQSFVAGDFTSSGNEVID
610 620 630 640 650 660
```

~~Product Characterization Center~~

~~0018-105 pe RFELTPVATLAEANIERAKVAINALFTSTNQLGKTNVTDYHIDQVSNLVTLISDEF~~

~~0018-105 pe RFELTPVATLAEANIERAKVAINALFTSTNQLGKTNVTDYHIDQVSNLVTLISDEF~~

CLAF - BRCL0	600	610	620	630	640	650
KIERN PREL FFAEIDNROGNANELL IONGERADZ						

```
cryla-105.pe LDEKRELFSEKVKHARLDERNLLQDSNEYFDINRQPERGWGGSTGITIGGDDVFKENY  
|||||:|||||:  
|||::|||:  
|||::|||:  
|||::|||:
```

CLAF_BACTU
LDEKKELSSKVNIAKRLSSERNLQDPNFRGNRLDRGWRSTDIITQGGDDFFQENY
660 680 690 700 710

crv1a-105.pe TLGGTFDECPTYLYQKIDSKRAFTRYLQGVIEDSQDSEIYSIRYNAKHETVNVPGT
730 740 750 760 770 780

CI4F_BACTU	720	730	740	750	760	770
TLGLTL-MGFPS-IYIKKWWFEIKSLYPIPIRGWEDSLEIYLISNAHETHVNVPGT						

790 800 810 820 830 840
 GSIWPLSAQSPYIGKCGENRCAPHLEWNPDLDCSRDCEKCAHSHHSHHSDIDVGCSTDLN
 CFVLA-105.pe

CIAP_BACTU
VPYGRFPQVPIGKC
:: | | | | |
-----ANSHHSLEPID/GCTDLN
800

850	860	870	880	890	900
100	100	100	100	100	100
200	200	200	200	200	200
300	300	300	300	300	300
400	400	400	400	400	400
500	500	500	500	500	500
600	600	600	600	600	600
700	700	700	700	700	700
800	800	800	800	800	800
900	900	900	900	900	900
1000	1000	1000	1000	1000	1000

CLAF_BACTU EDLGMVIFIKITQDGHARLGNLEFLEEKPLVGEALARVKRAEKKKWRDREKLEKFNINLV
 CY1A-105.pe EDLGMVIFALNVDGHAAGNLEFLEEKFNLSPTARVAGKAKRWAKREKLEKFNINLV

810	820	830	840	850	860
910	920	930	940	950	960

cryla-105.pe yKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPELSVPVGWNAAFEE
:
c1ae bac11 yKEAKESVDALFVNSQYDRLQADTNIAIHAADKRVHSIREA

[illegible]

cryla-105.pe LEGRIFTAFSLYDARNVIKNGDFFNGLSCNVKGVHDVEEQNNQRSVLVVPPEWAEVSEQE

cryla-105.pap
TXNS:Q9AM82

Description: Q9am82 bacillus thuringiensis serovar kunthalarx28 insecticidal

	crystal protein	
Accession/ID:	Q9AM82	
		Comment

=====General Comments=====

AC Q9AM82; . . . PRT; 1118 AA.

ID Q9AM82 PRELIMINARY;

```
SCORES:  Initl: 4088  Initn: 4088  Opt: 4105  z-score: 4524.8  E(): 0
```

```
>>TXN5:Q9AM82
      (1118 aa)
      in1tn: 4088 in1tl: 4088 opt: 4105 Z-score: 4524.8 expect(): 0
      Smith-Waterman score: 5720: 82.3% identity in 1079 aa overlap
```

(1-1075:1-1049)

cry1a-105.pe MDNPNINCEIPYCNCLSNPEVEVLGGERIETGYTPIDISLSLTQLLSEFVPGAGFVLG 38

Q9AM82 MDNNPNINECIPYNCLSNPEVEVLGGRIETGYTPIDISLSLIQFLLESEFVFGAGFVLD

```

cryla-105.pe 70 80 90 100 110 120
VDIIWGIFGSPQWDAFLVQIEQLINQRIEERFARNQAIISKLEGLSNLYQIYAESFREWEA

```

Q9AM82
VDIIWGIFGPSQWDAFLVQIEQLNQRIIEFARNQAISKLEGLSNLIQIYAESPREWEAA

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720      730      740      750      760      770
cry1a-105.pe VPGTGLWPLSGSPGKGPNCAPHLWEPDLDCSCRCCKAHHSHHSLSLIDVGC
Q9AM82 VPGTGLWPLSGSPGKGPNCAPHLWEPDLDCSCRCCKAHHSHHSLSLIDVGC
780      790      800      810      820      830
cry1a-105.pe TDLNEDLGWVIFKIKTDGCHARLGNLEFLEKPLVGEALARKVRAEKWKRKLEWE
Q9AM82 TDLNEDLGWVIFKIKTDGCHARLGNLEFLEKPLVGEALARKVRAEKWKRKLEWE
840      850      860      870      880      890
cry1a-105.pe TDLNEDLGWVIFKIKTDGCHARLGNLEFLEKPLVGEALARKVRAEKWKRKLEWE
Q9AM82 TDLNEDLGWVIFKIKTDGCHARLGNLEFLEKPLVGEALARKVRAEKWKRKLEWE
900      910      920      930      940      950
cry1a-105.pe TIIYVKEKESVDALFVNSQYDQLQADTNIAHIAADKRVHSIREAYLPESLVIQVNA
Q9AM82 TIIYVKEKESVDALFVNSQYDQLQADTNIAHIAADKRVHSIREAYLPESLVIQVNA
960      970      980      990      1000      1010
cry1a-105.pe IFEELGRIFTAFSLYDARNVIKNGDFNGLSCWVKGHVDEEQNNQSRSLVVPWEAE
Q9AM82 IFEELGRIFTAFSLYDARNVIKNGDFNGLSCWVKGHVDEEQNNQSRSLVVPWEAE
1020      1030      1040      1050      1060      1070
cry1a-105.pe VSQVRVCPGRGVIIRVTAYKEGEGCVTHIENNTDELKFSNCVVEEYPPNNTVTCN
Q9AM82 VSQVRVCPGRGVIIRVTAYKEGEGCVTHIENNTDELKFSNCVVEEYPPNNTVTCN
1080      1090      1100      1110      1120      1130
cry1a-105.pe DYTQVQEGGAYTSRNRGYNAPSPADYASVYEKSYTDGRRENCFNCRGYDYTPL
Q9AM82 IILRLKNKVRVTLVIEDMTPEPKAILLYQLIMQPMKKKHQIMDEETILVNLTDGMI
1060      1070      1080      1090      1100      1110
cry1a-105.pe
TXN5:Q9S4B5
Description: Q9S4B5 bacillus thuringiensis, insecticidal protein cryIac
Accession/ID: Q9S4B5
ID Q9S4B5 PRELIMINARY; PRT; 723 AA.
AC Q9S4B5; . . .
=====
General comments:
=====
SCORES Initl: 3591 Initn: 3591 Opt: 4088 z-score: 4508.9 E(): 0
>TXN5:Q9S4B5
Initn: 3591 Initl: 3591 Opt: 4088 z-score: 4508.9 expect(): 0
Smith-Waterman score: 4088; 86.7% identity in 728 aa overlap
(1-723:1-723)

10      20      30      40      50      60
cry1a-105.pe MDNPNINICIPYCNCLSNPEVVLGGERTYETCTYDIDSLTQFLLSFVPGAGFVLGL
Q9S4B5 MDNPNINICIPYCNCLSNPEVVLGGERTYETCTYDIDSLTQFLLSFVPGAGFVLGL
10      20      30      40      50      60
cry1a-105.pe VDIIWGIFGSPQWDAFLVQIEQLINQRIEFPARNOAISRLGLESLNLYQIYAESFREWAD
Q9S4B5 VDIIWGIFGSPQWDAFLVQIEQLINQRIEFPARNOAISRLGLESLNLYQIYAESFREWAD
```

```

130      140      150      160      170      180
cry1a-105.pe PTNPALREMIQNDNMNSALTATPILFAVQNVQVPLLSVYVQAANHLSLVLRDVSFQ
Q9S4B5 PTNPALREMIQNDNMNSALTATPILFAVQNVQVPLLSVYVQAANHLSLVLRDVSFQ
190      200      210      220      230      240
cry1a-105.pe RWGFDAAATINSRYNDLTRIGNVTDHVRWNTGLERVGPDSDRWIRYNOFRRLTLTV
Q9S4B5 RWGFDAAATINSRYNDLTRIGNVTDHVRWNTGLERVGPDSDRWIRYNOFRRLTLTV
250      260      270      280      290      300
cry1a-105.pe LDIVSLFPNYSRTPIRTVTSQLTREIYTNPVLENDFGSGFRSAQIEGSIIRSPHLM
Q9S4B5 LDIVSLFPNYSRTPIRTVTSQLTREIYTNPVLENDFGSGFRSAQIEGSIIRSPHLM
310      320      330      340      350      360
cry1a-105.pe NSITTYDAHRGEYVWSGHQINASPVGSGPEFTFPLYGTMGNRAAPQRIVAOLGQVYR
Q9S4B5 NSITTYDAHRGEYVWSGHQINASPVGSGPEFTFPLYGTMGNRAAPQRIVAOLGQVYR
370      380      390      400      410      420
cry1a-105.pe TISSTLYRPPNIGINNQLSVLDGTEPAYGTSSNLPFSAVYKSGTVDSDLEIPPQNNV
Q9S4B5 TISSTLYRPPNIGINNQLSVLDGTEPAYGTSSNLPFSAVYKSGTVDSDLEIPPQNNV
430      440      450      460      470      480
cry1a-105.pe PRQGFSHRLSHVSMRSGFSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPVKAH
Q9S4B5 PRQGFSHRLSHVSMRSGFSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPVKAH
490      500      510      520      530      540
cry1a-105.pe TLQSGTIVVRGPGTGDILRRTSGGPFAYT--IVNINQLPQ--RYRARIYASTTNL
Q9S4B5 FLFNGS-VISGPGTGDILRRTSGGPFAYT--IVNINQLPQ--RYRARIYASTTNL
540      550      560      570      580      590
cry1a-105.pe RIYVYAGERIFAGQNKMTDGTDLTFQSFSTATINTAFTFPMSSQSSFTVGADTFSSGN
Q9S4B5 HLNWNWNGSSIFSNITVPATATSLDNLQSDFGYFESANAFSSLSGN---IVGVNFSGTA
600      610      620      630      640      650
cry1a-105.pe EYVIDRPELIPVTATLEAEYNLERAKAVNALFTSTNOLGKTNVTDYHIDQVSNLTVYL
Q9S4B5 GVIIDRPELIPVTATLEAEYNLERAKAVNALFTSTNOLGKTNVTDYHIDQVSNLTVYL
660      670      680      690      700      710
cry1a-105.pe SDEFLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF
Q9S4B5 SDEFLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF
720      730      740      750      760      770
cry1a-105.pe KENYVTLGTFDECYPTLYLOKIDESKLAFTYQLRGVIEDSQDLEIYIRNAXHETV
Q9S4B5 KENYVTLGTFDECYPTLYLOKIDESKLAFTYQLRGVIEDSQDLEIYIRNAXHETV
```

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cryla-105 rep
TXN5: C1HB_BACTM

Description: Q45718 bacillus thuringiensis (subsp. morrisoni), pesticidal crystal protein cr

Accession/ID: Q45718

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

ID C1HB_BACTM STANDARD PR: 1155 AA.

AC Q45718; . . .

SCORES Init1: 3030 Initn: 5096 Opt: 4083 Z-score: 4500.3 EN: 0
>>TXN5:C1HB_BACTM
Initn: 5096 Init1: 3030 Opt: 4083 Z-score: 4500.3 expect(): 0 (1155 aa)
Smith-Waterman score: 5110; 67.0% identity in 1155 aa overlap
(8-1155:7-1147)

```

      10      20      30      40      50      60
cryla-1.05.pe MDNPNINECTPYNCNLSPNEVULGRIETGYTP--IDISLSTUCLSEFPGGGSVL
CIHB_BACTM    MEVNHQEVCYPCNLKPKNIEMLDIGIERSREQVALESUGLTRFEESLPGRASETF
      10      20      30      40      50      60
cryla-1.05.pe GLVDIIWIGFGSQMDAFLVOIQEQLINORIEEFARQOASLRLEGLSLYLQIVAESFREME
CIHB_BACTM    GLFDIIWVGIPGDWSLFLOITEQLIDORI EAHVRQOASLRLEGLSGVEVYTESIREWE
      120     130     140     150     160     170
cryla-1.05.pe ADPTNPALRENRQIFNDMSALTATPLFAVONYVPILSYVORANHLHSRLDVSVF
CIHB_BACTM    ASPNSLOODVRNFSSNTONALTATPLIRREGQFELPILTYVORANHLHSRLDDAVYF
      180     190     200     210     220     230
cryla-1.05.pe GQRMGFDAATINRSYNOLTELGIGNYTHAVRWNYTGLERVMGPDSDMYNOYRRELTL
CIHB_BACTM    GQRGLDTATVNNHYNRLINLTYSDBCAQWFNRGLDN-FGVVT---ARYLDFPREVTI
      240     250     260     270     280     290
cryla-1.05.pe TVLDIVSLPVNDSTPEITVSOLTREIYMPVLNFNGSFRGSAGICEGSI RSPHLM
CIHB_BACTM    SVLDIALFPNDIDRTPIQTLSOLTREIYSVPAEP-GASLVNDLNI---LRFPHLMD
      300     310     320     330     340     350
cryla-1.05.pe IINSITIYDAHRGEYWSGHQIMASPVGFSQEFTFPPLYGTMGNAPOQRIVAQIOGVV
CIHB_BACTM    FLTRLVIYTGVOGGYHWAGHEISSRTGNLSSNIQPPLYGTSANADRPFNLAHYSETI
      360     370     380     390     400
cryla-1.05.pe YRTLSSLTRRRPNIGINNQQSLVLDGCTEFAYGTSNMLPSA--VYRKSGTVDSIDEIPPO
CIHB_BACTM    YRTLSADIYS--VSGGISPNRTAFVGEVFRFLTARDNNLNLFLFKREGSLDSFTLPEP
      420     430     440     450     460     470
cryla-1.05.pe NNNYPQPGQSURLSHGVSMFRSGSNSSVISIIRAPMFESMTWTHRSBFNNIASDIQTPL
CIHB_BACTM    DFNRPPIYGYSHELCHAPPARSSVLEEPSNFIAPVFSWTWHRSAGMTNVESSSRITQIOP

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410	420	430	440	450	460
cryla-105.pe	480	490	500	510	520
480	490	500	510	520	530
CIHB_BACTM	470	480	490	500	510
470	480	490	500	510	520
540	550	560	570	580	590
cryla-105.pe	540	550	560	570	580
540	550	560	570	580	590
CIHB_BACTM	530	540	550	560	570
530	540	550	560	570	580
600	610	620	630	640	650
cryla-105.pe	600	610	620	630	640
600	610	620	630	640	650
CIHB_BACTM	590	600	610	620	630
590	600	610	620	630	640
660	670	680	690	700	710
cryla-105.pe	660	670	680	690	700
660	670	680	690	700	710
CIHB_BACTM	650	660	670	680	690
650	660	670	680	690	700
720	730	740	750	760	770
cryla-105.pe	720	730	740	750	760
720	730	740	750	760	770
CIHB_BACTM	710	720	730	740	750
710	720	730	740	750	760
780	790	800	810	820	830
cryla-105.pe	780	790	800	810	820
780	790	800	810	820	830
CIHB_BACTM	770	780	790	800	810
770	780	790	800	810	820
840	850	860	870	880	890
cryla-105.pe	840	850	860	870	880
840	850	860	870	880	890
CIHB_BACTM	830	840	850	860	870
830	840	850	860	870	880
900	910	920	930	940	950
cryla-105.pe	900	910	920	930	940
900	910	920	930	940	950
CIHB_BACTM	890	900	910	920	930
890	900	910	920	930	940
960	970	980	990	1000	1010
cryla-105.pe	960	970	980	990	1000
960	970	980	990	1000	1010
CIHB_BACTM	950	960	970	980	990
950	960	970	980	990	1000
1020	1030	1040	1050	1060	1070
cryla-105.pe	1020	1030	1040	1050	1060
1020	1030	1040	1050	1060	1070
CIHB_BACTM	1010	1020	1030	1040	1050
1010	1020	1030	1040	1050	1060
1080	1090	1100	1110	1120	1130
cryla-105.pe	1080	1090	1100	1110	1120
1080	1090	1100	1110	1120	1130
CIHB_BACTM	1070	1080	1090	1100	1110
1070	1080	1090	1100	1110	1120

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cry1a-105_pe	360	370	380	390	400
U35780_1	410	420	430	440	450
U35780_1	460	470	480	490	500
U35780_1	510	520	530	540	550
U35780_1	560	570	580	590	600
U35780_1	610	620	630	640	650
U35780_1	660	670	680	690	700
U35780_1	710	720	730	740	750
U35780_1	760	770	780	790	800
U35780_1	810	820	830	840	850
U35780_1	860	870	880	890	900
U35780_1	910	920	930	940	950
U35780_1	960	970	980	990	1000
U35780_1	1010	1020	1030	1040	1050
U35780_1	1060	1070	1080	1090	1100
U35780_1	1110	1120	1130	1140	1150
U35780_1	1160	1170	1180	1190	1200
U35780_1	1210	1220	1230	1240	1250
U35780_1	1260	1270	1280	1290	1300
U35780_1	1310	1320	1330	1340	1350
U35780_1	1360	1370	1380	1390	1400
U35780_1	1410	1420	1430	1440	1450
U35780_1	1460	1470	1480	1490	1500
U35780_1	1510	1520	1530	1540	1550
U35780_1	1560	1570	1580	1590	1600
U35780_1	1610	1620	1630	1640	1650
U35780_1	1660	1670	1680	1690	1700
U35780_1	1710	1720	1730	1740	1750
U35780_1	1760	1770	1780	1790	1800
U35780_1	1810	1820	1830	1840	1850
U35780_1	1860	1870	1880	1890	1900
U35780_1	1910	1920	1930	1940	1950
U35780_1	1960	1970	1980	1990	2000
U35780_1	2010	2020	2030	2040	2050
U35780_1	2060	2070	2080	2090	2100
U35780_1	2110	2120	2130	2140	2150
U35780_1	2160	2170	2180	2190	2200
U35780_1	2210	2220	2230	2240	2250
U35780_1	2260	2270	2280	2290	2300
U35780_1	2310	2320	2330	2340	2350
U35780_1	2360	2370	2380	2390	2400
U35780_1	2410	2420	2430	2440	2450
U35780_1	2460	2470	2480	2490	2500
U35780_1	2510	2520	2530	2540	2550
U35780_1	2560	2570	2580	2590	2600
U35780_1	2610	2620	2630	2640	2650
U35780_1	2660	2670	2680	2690	2700
U35780_1	2710	2720	2730	2740	2750
U35780_1	2760	2770	2780	2790	2800
U35780_1	2810	2820	2830	2840	2850
U35780_1	2860	2870	2880	2890	2900
U35780_1	2910	2920	2930	2940	2950
U35780_1	2960	2970	2980	2990	3000
U35780_1	3010	3020	3030	3040	3050
U35780_1	3060	3070	3080	3090	3100
U35780_1	3110	3120	3130	3140	3150
U35780_1	3160	3170	3180	3190	3200
U35780_1	3210	3220	3230	3240	3250
U35780_1	3260	3270	3280	3290	3300
U35780_1	3310	3320	3330	3340	3350
U35780_1	3360	3370	3380	3390	3400
U35780_1	3410	3420	3430	3440	3450
U35780_1	3460	3470	3480	3490	3500
U35780_1	3510	3520	3530	3540	3550
U35780_1	3560	3570	3580	3590	3600

©01

1140 1150 1160 1170

U35780_1
YTPLPAGYETKELEYFPEITDITWPRNAYSVP
1130 1140 1150

Description: 09am81 bacillus thuringiensis serovar kunthalarx77. insecticidal

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=====General comments=====
TD 09AM81 PRELIMINARY: PRT: 1118 AA.
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AC 09AM81; . . .

cry1a-105.pe MDNPNINĖIPNCLSNPEVEVLGGERIETGYTPDISLSLTQFLLSFVPVGAQFVLGL
Q9AM81 MDNPNINĖFLIVEVTLEEKYC--GERIETGYTPDISLSLTQFLLSFVPVGAQFELGL

70 80 90 100 110 120
cyla-105.pe VDIWGFGPSQWDAFLVQIEQLNQIRIEEFARNOAISRLGLESLNLYQIYAESFREWAD
QPM81 VDIWGFGPSQWDAFLVQIEQLNQIRIEEFARNOAISRLGLESLNLYQIYVPFSREWAD

```

cryla-1.05.pe      130      140      150      160      170
PTNPALREENRIQFNDMSALTTAIPFAVQNYQVPLSLVSVYQAANJHLSVLR-DVSVF
PTNPALREENRIQFNDMSALTTAIPFAVQNYQVPLSLVSVYQAANJHLSVLR-DVSVF
Q9AM81             130      140      150      160      170
PTNPALREENRIQFNDMSALTTAIPFAVQNYQVPLSLVSVYQAANJHLSVLR-DVSVF
PTNPALREENRIQFNDMSALTTAIPFAVQNYQVPLSLVSVYQAANJHLSVLR-DVSVF

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180 190 200 210 220 230
cry1a-105.pe GQRGWFDAATINSYNDLTRLIGNVYTHDAVWVNTGLGVNGPDSRDWIRYNOFRELT
190 200 210 220 230
Q9AM81 SSR--FNALNRLHWTTLSRLIGNCTDHPGYVNTGLGVNGRSDRWIRYNOFRELT
180 190 200 210 220 230

```

	240	250	260	270	280	290
cryla-105.pe	TVLDIVLFPNYDSRTPIRTVSQLTREIYTNVPLENDFGFRGSAOGIEGSRISPHLMD					
Q9AM81	TVLDIVLFPNYDSRTPIRTVSQLTREIYTNVPLENDFGFRGSAOGIEGSRISPHLMD					

```

300      310      320      330      340      350
cry1a-105.pe  ILNSTIYDAHRGEYWSGHQIMASPVGSGPEFTFLYGTMGNAAPQQRIVVQLGGGV
               |||||
O9AM81        ILNSTIYDAHRGEYWSGHQIMASVVGSGPEFTFLYGTGLGNAAPQPPICAAQTGGGV
               |||||

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Q9AM81	360	370	380	390	400	410
Q9AM81	360	370	380	390	400	410
Q9AM81	360	370	380	390	400	410
Q9AM81	420	430	440	450	460	470
Q9AM81	420	430	440	450	460	470
Q9AM81	420	430	440	450	460	470
Q9AM81	480	490	500	510	520	530
Q9AM81	480	490	500	510	520	530
Q9AM81	540	550	560	570	580	590
Q9AM81	540	550	560	570	580	590
Q9AM81	600	610	620	630	640	650
Q9AM81	600	610	620	630	640	650
Q9AM81	660	670	680	690	700	710
Q9AM81	660	670	680	690	700	710
Q9AM81	720	730	740	750	760	770
Q9AM81	720	730	740	750	760	770
Q9AM81	780	790	800	810	820	830
Q9AM81	780	790	800	810	820	830
Q9AM81	840	850	860	870	880	890
Q9AM81	840	850	860	870	880	890
Q9AM81	900	910	920	930	940	950
Q9AM81	900	910	920	930	940	950
Q9AM81	960	970	980	990	1000	1010
Q9AM81	960	970	980	990	1000	1010

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          940   950   960   970   980   990
cry1a-105.pe VSGEVRVCPGGRGILRVITAYKEGYGEGCVTHIEINNTDELKPSNCVVEEIIYPMNTVTGN
          1020  1030  1040  1050  1060  1070
Q9AM81 VSGEVRVCPGGRGILRVITAYKEGYGEGCVTHIEINNTDELKPSNCVVEEIIYPMNTVTCK
          1000  1010  1020  1030  1040  1050
cry1a-105.pe DYTVNQEEYGGAYTSNRNGYNEAPSPADYASVVEEKSYYTDGRRENPECPNRGYRDYTPL
          1080  1090  1100  1110  1120  1130
Q9AM81 IILRLKNNRVTLVLVIEDTEPMKAILLYQLIMHQMKKHQWDEETILVLNLTEDMGI
          1060  1070  1080  1090  1100  1110
cry1a-105.pep
TXN5:CIDA_BACTA
Description: P19415 bacillus thuringiensis (subsp. aizawai). pesticidal
crystal protein cryI
Accession/ID: P19415
ID CIDA_BACTA STANDARD; PRT: 1165 AA.
AC P19415; . . . . .
=====General comments=====
SCORES Init1: 3102 Initn: 5514 Opt: 3954 z-score: 4357.8 E(): 0
>>TXN5:CIDA_BACTA
Initn: 5514 Init1: 3102 Opt: 3954 Z-score: 4357.8 expect(): 0
Smith-Waterman score: 5542; 71.8% identity in 1186 aa overlap
(1-1177:1-1165)
          10   20   30   40   50   60
cry1a-105.pe MNNPNNIECTPYNCLNSPEVEVLGGERIEGTYPIDISLSTOFLSEFPVAGFVLGL
          10  20  30  40  50  60
CIDA_BACTA MEIN-NQNOCPYINCLNSPREILGGELETGNTVDISLGLINFLINFLNFPVGGFIVGL
          10  20  30  40  50
cry1a-105.pe VDIIMGIFGPGQDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQVIAESFREMEAD
          70  80  90  100  110  120
CIDA_BACTA LELINGFIGPQMDIFLAQIEQLISQRIEEFARNQAISRLEGLSNLYQVYVAFSDWEKD
          60  70  80  90  100  110
cry1a-105.pe PTPPALREEMRIQFNDWNSALITTAIPFAVQNYOVLPLSYVQANLHSLVLRDVSFQG
          130  140  150  160  170  180
CIDA_BACTA PTPPALREEMRIQFNDWNSALITTAIPFRVQNYEVALLSVYVQANLHSLRDSVFGF
          120  130  140  150  160  170
cry1a-105.pe RWGFDAAATINSRVNDLRLIGNVTHAVRWYNTGLERVMGPDSDRWIRYNQFRELTLTV
          190  200  210  220  230  240
CIDA_BACTA RWGYDTATINRYSDLTSLIHVYTHCVDTYNOGLRLEGRFLSDWIVNFRFQLTISV
          180  190  200  210  220  230
cry1a-105.pe LDIVSLFPNDSRTYPIRTVSQLTREIYN-PVL-ENFD--GSFRGSAQGLEGSIRSPHL
          250  260  270  280  290
CIDA_BACTA LDIVAFPNNDIRTYPIQTATLTREVLDLPFINENLSPAASYPFTFAASAIIRSPHL
          240  250  260  270  280  290
cry1a-105.pe MDLINSITITDARGEYVNSGHQIMASPVGSGPEFTFPLCYTMGNAPQQRVAQLQG
          300  310  320  330  340  350
CIDA_BACTA VDFENSTIITDRLARYAYMGHVLNVSFRTGTTNLRSPLYRGEGNTERPVTITSPSV
```

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          300   310   320   330   340   350
cry1a-105.pe GYVITLSTLYRRPNIGNINNOQ--LSVLGDTGFAYGTSSNLPSSAVYKSGTVDSDLEIPP
          360  370  380  390  400  410
CIDA_BACTA PIFRILS-----VITGLDINSFVAGIEGVF-----QNTLSIYKSGPIDSFSELPF
          360  370  380  390  400
cry1a-105.pe QNNVVPQROGFHRLSHVSMFRSGNSVSIIRAPMFNSHRSFNFNIASDSITQIP
          420  430  440  450  460  470
CIDA_BACTA QDASVSPAIGYSHRLCHAT-FLERISGPRIA--GVFESWTHRSASFTNEVSPSRITQIP
          410  420  430  440  450  460
cry1a-105.pe LVKAITLQSGTTVVRGPGFTGGDILRTSGGPFAYTIIVNINGQLPQRYRARIYASITNL
          480  490  500  510  520  530
CIDA_BACTA WYKAITLASGASVIKPGFTGGDILRTSGMELGLTRVTFTGRLPQSYVIRFRYASVANR
          470  480  490  500  510  520
cry1a-105.pe RIYVTVAGERIFAGOPNKTMDTGDPLTFQSFYATINTAFTFPMSSQSSFTVGADTFSSGN
          540  550  560  570  580  590
CIDA_BACTA SGTFRYSQPPSGYIGSPKTMADAGEPLFSRFAHTILFTPTPSRAQEEFDL---YIQSG-
          530  540  550  560  570  580
cry1a-105.pe EYVIDRPELIPVTATLEAEYNLRAQKAVNALFTSTNGLKTNVDYHIDQVSNLVTYL
          600  610  620  630  640  650
CIDA_BACTA -VYIDRIEFPVTAITEAEYDLERAQKAVNALFTSTNGLKTNVDYHIDQVSNLVTYL
          590  600  610  620  630
cry1a-105.pe SDFCLDEKRELSEKVKAKLSDERNLQDSNFKDINRQPERGWGSGTIGTIQGGDDVF
          660  670  680  690  700  710
CIDA_BACTA SDFCLDEKRELSEKVKAKLSDERNLQDSNFKDINRQPERGWGSGTIGTIQGGDDVF
          640  650  660  670  680  690
cry1a-105.pe KENVVTLSGTDFDECYPTLYQKIDESKLKAFTRYQLRGYIEDSODLEIYSIRYNAKHETV
          720  730  740  750  760  770
CIDA_BACTA KENVVTLPSTDFDECYPTLYQKIDESKLKAFTRYQLRGYIEDSODLEIYSIRYNAKHETV
          700  710  720  730  740  750
cry1a-105.pe NVPGTSLWPLSAQSPGKCGEPNRCAPHLWNPDLCSCRDGKCAHSHHFSLDIDVG
          780  790  800  810  820  830
CIDA_BACTA NVPGTSLWPLSVENQIQGCGEPNRCAPHLWNPDLCSCRDGKCAHSHHFSLDIDVG
          760  770  780  790  800  810
cry1a-105.pe CTDLNEDLGVWYIFKIKTQDGHARLGNLRFLEKPLVGEALARYKRAEKKWRDKREKLEW
          840  850  860  870  880  890
CIDA_BACTA CTDLNEDLGVWYIFKIKTQDGHARLGNLRFLEKPLVGEALARYKRAEKKWRDKRETLQL
          820  830  840  850  860  870
cry1a-105.pe EETNIVYKEAKESVDALFVNSQDQLQADNTNIMIAHADKRVHSIREAYLPFELSVIPGVNA
          900  910  920  930  940  950
CIDA_BACTA EETIVYKEAKESVDALFVNSQDQLQADNTNIMIAHADKRVHSIREAYLPFELSVIPGVNA
          880  890  900  910  920  930
cry1a-105.pe AIFBEELSGRIFTAFSLYDARNVINGDFNNGLSNWNKVGHYDVEEQNNQNSYLVVPEWEA
          960  970  980  990  1000  1010
CIDA_BACTA AIFBEELSGRIFTAFSLYDARNVINGDFNNGLSNWNKVGHYDVEEQNNHRSVLVPEWEA
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240	250	260	270	280	290
cryla-105.pe	300	310	320	330	340
CIDB_BACTU	350	360	370	380	390
300	310	320	330	340	350
360	370	380	390	400	410
340	350	360	370	380	390
390	400	410	420	430	440
440	450	460	470	480	490
490	500	510	520	530	540
540	550	560	570	580	590
590	600	610	620	630	640
640	650	660	670	680	690
690	700	710	720	730	740
740	750	760	770	780	790
790	800	810	820	830	840
840	850	860	870	880	890
890	900	910	920	930	940
940	950	960	970	980	990

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cry1a-105.pe IFEELGRIETASLYDAARVTKNGDFNGLSCWVKGHVDFVEQNNQRSLVLPWEAEAE
C1DB_BACTU IFEELGRIETASLYDAARVTKNGDFNGLSCWVKGHVDFVEQNNQRSLVLPWEAEAE
950 960 970 980 990 1000
1020 1030 1040 1050 1060 1070
cry1a-105.pe VSQEVRCVPCRGVILRVATAYKEGEGCVTHIEINNTDELKFSNCVVEEIIYFNNTVCN
C1DB_BACTU VSQEVRCVPCRGVILRVATAYKEGEGCVTHIEINNTDELKFSNCVVEEIIYFNNTVCN
1010 1020 1030 1040 1050 1060
1080 1090 1100 1110 1120 1130
cry1a-105.pe DTVNQEEYGATISNRGNIEA---PSVPADYASVVEEKSYYTDGRRNCPCEFNRYRD
C1DB_BACTU DY--NKHGNGANSSNRGYDESNSISPADYAPVVEEAYTDGRRNCPCEFNRYRD
1070 1080 1090 1100 1110 1120
1140 1150 1160 1170
cry1a-105.pe YTPLPVGVTKLEYPPETDKWIEIGETGTIVDSVELLMEE
C1DB_BACTU -TLPVGVTKLEYPPETDKWIEIGETGTIVDSVELLMEE
1120 1130 1140 1150 1160
cry1a-105.pep
TXN5:AAK48937
Description: Aak48937 bacillus thuringiensis, insecticidal crystal protein.
6/2001
Accession/ID: 000000
====General comments====
ID AAK48937 PRELIMINARY; PRT: 1160 AA.
AC AAK48937; . . .
=====
SCORES Initl: 3058 Initn: 5369 Opt: 3854 z-score: 4247.5 E(): 0
>TXN5:AAK48937
Initn: 5369 Initl: 3058 Opt: 3854 z-score: 4247.5 expect(): 0
Smith-Waterman score: 5403; 70.5% identity in 1185 aa overlap
(1-1177:1-1160)
cry1a-105.pe MDNNPNINCEIPYCNLSNPEVEVLGGERIETGVTPTDLSLSLTOFLLSEFVPCGAGFVGL
AAK48937 MDINHQ-NQIPNPNCLSNPDAILLDAERLETGNTVADLSGLTINFLYSNFPVGGGFI VGL
10 20 30 40 50
70 80 90 100 110 120
cry1a-105.pe VDIWIFGFSQWDAFLVQIQLINQRIIEFARNQAIISRLGSLNLYQIYAESFREWAD
AAK48937 LELLWFGVPSQWEIFLAQIQLISQRIIEFARNQAIISRLGSLNLYQIYAESFREWAD
60 70 80 90 100 110
130 140 150 160 170 180
cry1a-105.pe PTNPALREWRIOFNDMNSALTTAIPLFAVQNYQVPLSVYVQAANHLHLSVDRDVSFGQ
AAK48937 PSNPALREWRIOFNDMNSALTTAIPLFAVQNYQVPLSVYVQAANHLHLSVDRDVSFGQ
120 130 140 150 160 170
190 200 210 220 230 240
cry1a-105.pe RWGFDPATVNSRYSNDLTRLIQNYTHAVRWYNTGLERWYGPDSRDWRVYQNFRELTITV
AAK48937 RWGFDPATVNSRYSNDLTRLIQNYTHAVRWYNTGLERWYGPDSRDWRVYQNFRELTITV
```

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180 190 200 210 220 230
cry1a-105.pe LDIVSLFNNYSRTPYRTVQSQTREIITN-P-VLENFD--GSFRGSAQIEGSIIRSPHL
AAK48937 LDIIIAEFNNYDIEAYPIQTASQTLREVVLDFPVNLTSPASYPPTFSAESAIIIRSPHL
240 250 260 270 280 290
300 310 320 330 340 350
cry1a-105.pe MDILNSITITIDAHURGEYVWSGHOIMASPGVSGFPEFTFLYGTMGNAAPQORIVAOLGQ
AAK48937 VDFLNSITITIDSLASVYAGHLYNSFRTGTITNLIRSELYGREGNTERTVPTISAPSV
300 310 320 330 340 350
360 370 380 390 400 410
cry1a-105.pe GVTRTLSTLIRRPFNIGINNQLSVLDGTGTFAYGTSSNLPFAVYKSGTVDLSDETPPQ
AAK48937 PIFRTLSTLIRRPFNIGINNQLSVLDGTGTFAYGTSSNLPFAVYKSGTVDLSDETPPQ
360 370 380 390 400 410
420 430 440 450 460 470
cry1a-105.pe NNNVPPROGFSHRLSHVSMFSGFSNSSVIRAPMFWSHRSABFNIIASDSITQPL
AAK48937 DVSVSPAIGYSHRLCHAT-FLERISGPRIA--GTVFSWTHRSASAPINEVSPSRITQIPW
410 420 430 440 450 460
480 490 500 510 520 530
cry1a-105.pe VKAHTLQSGTIVVRGPGTGGDILRTSGGPFAYTIIVNGLQLPQRYRARIYASTTNLR
AAK48937 VKAHTLQSGTIVVRGPGTGGDILRTSGGPFAYTIIVNGLQLPQRYRARIYASTTNLR
470 480 490 500 510 520
540 550 560 570 580 590
cry1a-105.pe IYTVAGEIEIFAGQNKMTDGTPLTFQSFYATINTAFTFPMSSQSSFTVGADTFSSGNE
AAK48937 GTFYRQPPSGISGIFPKINDAGEALTSRFAHTILFTPIIFSRAGEFDL---YIQSG--
530 540 550 560 570 580
600 610 620 630 640 650
cry1a-105.pe VYIDRFELIPVTATLEAEYNLRAQKAVNALFTSTNGLKTNVTDYHIDQVSNLVTYLS
AAK48937 VYIDRFELIPVTATLEAEYNLRAQKAVNALFTSTNGLKTNVTDYHIDQVSNLVTYLS
590 600 610 620 630 640
660 670 680 690 700 710
cry1a-105.pe DEFCLDEKRELSKVKAKLSDERNLLQDSNFKDINRQPERGWGGSTGIITIQGGDDVFK
AAK48937 DEFCLDEKRELSKVKAKLSDERNLLQDSNFKDINRQPERGWGGSTGIITIQGGDDVFK
650 660 670 680 690 700
720 730 740 750 760 770
cry1a-105.pe ENVVTLSGTFDECEPTYLYQKIDESKLAFTRYQYRGYIEDSODLEIYSIRYNAKHETVYV
AAK48937 ENVVTLSGTFDECEPTYLYQKIDESKLAFTRYQYRGYIEDSODLEIYSIRYNAKHETVYV
710 720 730 740 750 760
780 790 800 810 820 830
cry1a-105.pe VPGTGLWPLSAQSPICKCEPNRCAPHLWNPDLDSCRDSEKCAHSHHFLSDIDVGC
AAK48937 VPGTGLWPLSAQSPICKCEPNRCAPHLWNPDLDSCRDSEKCAHSHHFLSDIDVGC
770 780 790 800 810 820
840 850 860 870 880 890
cry1a-105.pe TDLNEDLGWVWIFKIKTDQGHARLGNLEFLEKPLVCGEALRVKRAEKKWRDKREKLEWE
AAK48937 TDLNEDLGWVWIFKIKTDQGHARLGNLEFLEKPLVCGEALRVKRAEKKWRDKREKLEWE
```

©01 Private Label Information

cr1ya-105.pe
AAK48937
900 830 840 850 860 870 880
900 910 920 930 940 950
cr1ya-105.pe
AAK48937
960 970 980 990 1000 1010
960 970 980 990 1000 1010
cr1ya-105.pe
AAK48937
1020 1030 1040 1050 1060 1070
1020 1030 1040 1050 1060 1070
cr1ya-105.pe
AAK48937
1080 1090 1100 1110 1120 1130
1080 1090 1100 1110 1120 1130
cr1ya-105.pe
AAK48937
1140 1150 1160 1170 1180 1190
1140 1150 1160 1170 1180 1190
cr1ya-105.pe
TXNS: CIJA_BACTU
Description: Q45738 bacillus thuringiensis, pesticidal crystal protein cr1ya
(Insecticidal)
Accession/ID: Q45738
ID ID CIJA_BACTU STANDARD; PRI: 1167 AA.
AC Q45738;
=====General comments=====

SCORES Initl: 2454 Initn: 4384 Opt: 3795 z-score: 4182.3 E(): 0
>>TXNS: CIJA_BACTU
Initn: 4384 Initl: 2454 Opt: 3795 z-score: 4182.3 expect(): 0
Smith-Waterman score: 5215; 67.5% identity in 1186 aa overlap
(1-1177:1-1167)

cr1ya-105.pe
CIJA_BACTU
10 20 30 40 50 60
10 20 30 40 50 60
cr1ya-105.pe
CIJA_BACTU
70 80 90 100 110 120
70 80 90 100 110 120
cr1ya-105.pe
CIJA_BACTU
130 140 150 160 170 180
130 140 150 160 170 180
cr1ya-105.pe
CIJA_BACTU
190 200 210 220 230 240
190 200 210 220 230 240

cr1ya-105.pe
CIJA_BACTU
120 130 140 150 160 170
120 130 140 150 160 170
cr1ya-105.pe
CIJA_BACTU
180 190 200 210 220 230
180 190 200 210 220 230
cr1ya-105.pe
CIJA_BACTU
240 250 260 270 280 290
240 250 260 270 280 290
cr1ya-105.pe
CIJA_BACTU
300 310 320 330 340 350
300 310 320 330 340 350
cr1ya-105.pe
CIJA_BACTU
360 370 380 390 400 410
360 370 380 390 400 410
cr1ya-105.pe
CIJA_BACTU
420 430 440 450 460 470
420 430 440 450 460 470
cr1ya-105.pe
CIJA_BACTU
480 490 500 510 520 530
480 490 500 510 520 530
cr1ya-105.pe
CIJA_BACTU
540 550 560 570 580 590
540 550 560 570 580 590
cr1ya-105.pe
CIJA_BACTU
600 610 620 630 640 650
600 610 620 630 640 650
cr1ya-105.pe
CIJA_BACTU
660 670 680 690 700 710
660 670 680 690 700 710
cr1ya-105.pe
CIJA_BACTU
720 730 740 750 760 770
720 730 740 750 760 770
cr1ya-105.pe
CIJA_BACTU
780 790 800 810 820 830
780 790 800 810 820 830

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	60	70	80	90	100	110
cry1a-105.pe	PTPALREEMRIQFNDSALTTAIPLFAVQNYQVPLSVVYQAANHLVSLRDSVFGQ	130	140	150	160	170
L32019_1	PDNEAAKSVRIDRFRILDLGLIEANIPSPRIIGFEVPLSVVYQAANHLALRDSVIFGE	120	130	140	150	160
	190	200	210	220	230	240
cry1a-105.pe	RWGFDAATINSYNDLITLLIGNTYDHAVERWYNTGLERWVPGDSRDMIRYNQPRELITLV	130	140	150	160	170
L32019_1	RWGLTTNNVDIYNRQIREIHEYSNCVDYNTYTELERGLGFSIAQWRIYNYNPRELITLV	180	190	200	210	220
	250	260	270	280	290	300
cry1a-105.pe	LDIVSLFPNYSRTYPIRTVSYQLTTRIYNPULENFPGSFR-GSAQG--IEGSIERSPHLM	130	140	150	160	170
L32019_1	LDIVALLFNDYSLRYPQTSQTRIEIVTSPVSEFYGVINSNGIIGTLUTEQIKRRPHLM	240	250	260	270	280
	310	320	330	340	350	360
cry1a-105.pe	DILNSIYITDAHGEYVWSGHOIMASPVGSGPEFTFPLYGTMGNAAPQORIVQAOLGOG	300	310	320	330	340
L32019_1	DFNSIMWITSNDRREHYWGLEMTAYFTGFAGQVSPFLAVGTREGESAPLT-VPSVNDG	300	310	320	330	340
	360	370	380	390	400	410
cry1a-105.pe	VYRILSTLYRRPNIGNNQQLSLVDGTEFAYGTSNLPFSAYVRKSGTVDSLOLPIPON	360	370	380	390	400
L32019_1	IYRILSAPFYSAPE-LGTIVLG-SRGEKDFALANNISPPSTIYRHPGTVDSLSVIPPQD	360	370	380	390	400
	420	430	440	450	460	470
cry1a-105.pe	NNVPPQGSFHRSLSHVSNFSGSNNSSVIRAPMFWIHRSEFNIIASDSITQPLV	420	430	440	450	460
L32019_1	NSVPPHSGSHRSLSHVTMRAS-----SPIFHWIHRSAITNTINPNAIQTPLV	420	430	440	450	460
	480	490	500	510	520	530
cry1a-105.pe	KAHTLQSGTIVVVRGPGTGDIILRTSGGPFAYTIVINQOLPQVRARIYASTTNLRI	480	490	500	510	520
L32019_1	KAPNLHSGATVVRGPGTGDIILRRINTGTADMRVNIITPLSORVVRARIYASTTDLQF	470	480	490	500	510
	540	550	560	570	580	590
cry1a-105.pe	YVTVAGERIFAGQFNKMTDGDPLTFQSFATINTATFTPMQSSFTVGADTFSSGNEV	540	550	560	570	580
L32019_1	FTIRNGTSVNOQNFORTMNRGDNLESGNFRTAGSTFPFSNAQSTFTLGTQAFSN-QEV	530	540	550	560	570
	600	610	620	630	640	650
cry1a-105.pe	YIDRFELIPVATLEAYNLERAKAVNALFTSTNQLGKINTYDHIQDVSNLVTYLSL	600	610	620	630	640
L32019_1	YIDRIEFVPAEVEASDSLERAQAVNALFTSTNQLGKLTVDYDQDVSNLVECLSL	590	600	610	620	630
	660	670	680	690	700	710
cry1a-105.pe	EFCLDEKRELSKVKHAKRLSDERNLLODSNFKDINRQPERGMSGSTGTTIQGGDVFKE	660	670	680	690	700
L32019_1	EFCLDEKRELSKVKHAKRLSDGNLLODPNFTSINQLDRGWRGSTDITIQGGDNVFE	650	660	670	680	690
	720	730	740	750	760	770
cry1a-105.pe	NYTLTSGTFDECYTYLYQKIDSKLAKATRYQLRGVIEDSODLEIYSRYNAKHTVNY	720	730	740	750	760
L32019_1	NYTLTSGTFDECYTYLYQKIDSKLAKATRYELRGVIEDSODLEIYSRYNAKHTVNY	720	730	740	750	760

	740	750	760	770	780	790	800	810	820
cy1a-105.pe	POCSLWPLSVSE	CGAGENR	CPILTNPD	LOCSRDEK	CAHSHHFLSD	TVGCT			
L32019_1	POCSLWPLSVSE	CGAGENR	CPILTNPD	LOCSRDEK	CAHSHHFLSD	TVGCT			
cy1a-105.pe	DNEDLGVWIF	KIKTGGH	AMLSIEKPL	VCENLNUK	AEKKWDEK	EKLEWET			
L32019_1	DNEDLGVWIF	KIKTGGH	AMLSIEKPL	VCENLNUK	AEKKWDEK	EKLEWET			

```

900 910 920 930 940 950
cryla-105.pe NITVYKAKESVDALFNSQYDLOADTNKAMHAAKDSVHS TREAYLPETSVIPGVNAAI
|||||
L32019 1 NITVYKAKESVDALFVDSHWNEQLDNTNIMHADRVMK TREAYLPETSVIPGVNAAI
|||||

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```
cryla-105.pe 960 970 980 990 1000 1010
FEELGRIFFATSLYDARNVINGDFNGLSCWNVKGVHDVEQNNVSULNPESVESE
FEELGRIFFATSLYDARNIIRNGDFNGLSCWNVKGVHDIO_QNDHRSVLNPESVESE
```

```

1020
1030
1040
1050
1060
1070
cry1a-105.pe  SQRVCFGRGYILRVATYKEGEGCVTIEIENNTDELKFSNCVEEIEIYNNVTTCN
1080
1090
1100
1110
1120
1130
1140
1150
1160
1170
1180
1190
1200
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crystal-105.pe YTVNQBEG--GAYTSNRGNWEA----PSPADVASVWEKSYTDTGRRENPCEFNNGYFV
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cr1a-105.pap
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=====
description: X07518 Bacillus thuringiensis
             delta-endotoxin; p
Accession/ID: X07518
=====General comments=====
LOCUS       X07518.1 [BTEOTOX]

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SCORES      Init1: 3103  Initn: 5072  Opt: 3784  z-score: 4170.1  E(): 0
>>TXN5:X07518.1  3103  5072  3784  z-score: 4170.1  expect(): 0
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(1-1177:1-1189)

F-016 / OV

[illegible]

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cry1a-105.pe      RMGFDAAITNSRNDLTGLIGNYTDHVRWNTGLERVGWGPDSRDWIYNQFRRLTIV          190    200    210    220    230    240
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cryl-a-105.pe LOJLSPNDSTYPIRVTSOLTREIYTVPUENDFSGFRSQG-----EGS-IRSP  
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[illegible][illegible]

cy1a-105.pe LGGPQQNNVPPPPVPPPHLSLSNNG RSGFSNSSVSIIRAFPMFSWTHRAENNIILAS

410 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 1191

470 480 490 500 510 520
 530 540 550 560 570 580
 CYLA-105.pe YASTNIRIYV-TVAGERIAGQ-----FNEQMDLPLTFQSPSMAINTATTFNUS

530 540 550 560 570 580
 590 600 610 620 630 640
 650 660 670 680 690 700
 710 720 730 740 750 760
 770 780 790 800 810 820
 830 840 850 860 870 880
 890 900 910 920 930 940
 950 960 970 980 990 1000
 1010 1020 1030 1040 1050 1060
 1070 1080 1090 1100 1110 1120
 1130 1140 1150 1160 1170 1180
 1190 1200 1210 1220 1230 1240
 1250 1260 1270 1280 1290 1300
 1310 1320 1330 1340 1350 1360
 1370 1380 1390 1400 1410 1420
 1430 1440 1450 1460 1470 1480
 1490 1500 1510 1520 1530 1540
 1550 1560 1570 1580 1590 1600
 1610 1620 1630 1640 1650 1660
 1670 1680 1690 1700 1710 1720
 1730 1740 1750 1760 1770 1780
 1790 1800 1810 1820 1830 1840
 1850 1860 1870 1880 1890 1900
 1910 1920 1930 1940 1950 1960
 1970 1980 1990 2000 2010 2020
 2030 2040 2050 2060 2070 2080
 2090 2100 2110 2120 2130 2140
 2150 2160 2170 2180 2190 2200
 2210 2220 2230 2240 2250 2260
 2270 2280 2290 2300 2310 2320
 2330 2340 2350 2360 2370 2380
 2390 2400 2410 2420 2430 2440
 2450 2460 2470 2480 2490 2500
 2510 2520 2530 2540 2550 2560
 2570 2580 2590 2600 2610 2620
 2630 2640 2650 2660 2670 2680
 2690 2700 2710 2720 2730 2740
 2750 2760 2770 2780 2790 2800
 2810 2820 2830 2840 2850 2860
 2870 2880 2890 2900 2910 2920
 2930 2940 2950 2960 2970 2980
 2990 3000 3010 3020 3030 3040
 3050 3060 3070 3080 3090 3100
 3110 3120 3130 3140 3150 3160
 3170 3180 3190 3200 3210 3220
 3230 3240 3250 3260 3270 3280
 3290 3300 3310 3320 3330 3340
 3350 3360 3370 3380 3390 3400
 3410 3420 3430 3440 3450 3460
 3470 3480 3490 3500 3510 3520
 3530 3540 3550 3560 3570 3580
 3590 3600 3610 3620 3630 3640
 3650 3660 3670 3680 3690 3700
 3710 3720 3730 3740 3750 3760
 3770 3780 3790 3800 3810 3820
 3830 3840 3850 3860 3870 3880
 3890 3900 3910 3920 3930 3940
 3950 3960 3970 3980 3990 4000
 4010 4020 4030 4040 4050 4060
 4070 4080 4090 4100 4110 4120
 4130 4140 4150 4160 4170 4180
 4190 4200 4210 4220 4230 4240
 4250 4260 4270 4280 4290 4300
 4310 4320 4330 4340 4350 4360
 4370 4380 4390 4400 4410 4420
 4430 4440 4450 4460 4470 4480
 4490 4500 4510 4520 4530 4540
 4550 4560 4570 4580 4590 4600
 4610 4620 4630 4640 4650 4660
 4670 4680 4690 4700 4710 4720
 4730 4740 4750 4760 4770 4780
 4790 4800 4810 4820 4830 4840
 4850 4860 4870 4880 4890 4900
 4910 4920 4930 4940 4950 4960
 4970 4980 4990 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
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 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

X07518_1
DILGISEQPFMGAGSISGG-ETIIGACATL.....600 610 620 630 640

X07518_1_LXTDVTDYHIDQVSNLVDCLSDFTCLDERKUSEATNGHAKKUSDEKATZQAMKATKAT

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MSL No. 20351
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650      700      710      720      730      740      680      690      700
cry1a-105.pe PERGEGSTGTTGGDDVFNKYNVILSGTFDECPYLYOKIDSKLKATRYQLRGYI
X07518_1 PDGMRGSDITIGGDDVFNKYNVILSGTFDECPYLYOKIDSKLKATRYQLRGYI
710      720      730      740      750      760
cry1a-105.pe EDSDLEIYSIRYNAKHETVNVPGTGLMPLSAQSPGKCGENRCAPHLWNPDDDCSC
X07518_1 EDSDLEIYSIRYNAKHETVNVPGTGLMPLSAQSPGKCGENRCAPHLWNPDDDCSC
770      780      790      800      810      820
cry1a-105.pe RDGEKCAHSHHSFLDIDVCGTDLNEDLGWVWIFKIKTQDGHARLGNLEFLERPLVGEA
X07518_1 RDGEKCAHSHHSFLDIDVCGTDLNEDLGWVWIFKIKTQDGHARLGNLEFLERPLVGEA
830      840      850      860      870      880
cry1a-105.pe RDGEKCAHSHHSFLDIDVCGTDLNEDLGWVWIFKIKTQDGHARLGNLEFLERPLVGEA
X07518_1 RDGEKCAHSHHSFLDIDVCGTDLNEDLGWVWIFKIKTQDGHARLGNLEFLERPLVGEA
890      900      910      920      930
cry1a-105.pe LARVKAEEKWDRKLEKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAHIAADKR
X07518_1 LARVKAEEKWDRKLEKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAHIAADKR
940      950      960      970      980      990
cry1a-105.pe VHSIREAYLPESLVIPGVNAAIFEELEGRIFTAFSLYDARNVTKNGDFNGLSCNVKGH
X07518_1 VHSIREAYLPESLVIPGVNAAIFEELEGRIFTAFSLYDARNVTKNGDFNGLSCNVKGH
1000     1010     1020     1030     1040     1050
cry1a-105.pe VDVEEQNNORSVLVPEWEAEVQEVRCVGRGYLIRVTAKEGYGEGCVTIHEIENNTD
X07518_1 VDVEEQNNORSVLVPEWEAEVQEVRCVGRGYLIRVTAKEGYGEGCVTIHEIENNTD
1060     1070     1080     1090     1100     1110
cry1a-105.pe ELKFSNCVEEYIPNNVTCTNDYVNOEYGGAYTSNRNGNEA---PSVPADYASVYE
X07518_1 ELKFSNCVEEYIPNNVTCTNDYVNOEYGGAYTSNRNGNEA---PSVPADYASVYE
1120     1130     1140     1150     1160     1170
cry1a-105.pe EKSYTGRRNCFENRGYRDTPLPGVYVTKLEYRPTDKWIEIGETGTFIVDSVE
X07518_1 EKSYTGRRNCFENRGYRDTPLPGVYVTKLEYRPTDKWIEIGETGTFIVDSVE
1180     1190     1200     1210     1220     1230
cry1a-105.pe LLLMEE
X07518_1 LLLMEE

Description: P05518 bacillus thuringiensis (subsp. entomocidus), and bacillus
thuringiensis (
Accession/ID: P05518
ID C1CA_BACTE STANDARD; PRT; 1189 AA.
AC P05518; P10327; Q045725;

=====
General comments=====
=====
```

```

SCORES Initl: 3103 Initn: 5089 Opt: 3783 Z-score: 4169.0 E(): 0
>TXNS:C1CA_BACTE
Initn: 5089 Initl: 3103 Opt: 3783 Z-score: 4169.0 expect(): 0
Smith-Waterman score: 5406; 69.1% identity in 1206 aa overlap
(1-1177:1-1189)

cry1a-105.pe MDNPNINCEIPNCLSPPEVEVLGGERTGTGTIDISLSLTQFLLSRFPVPGAGFVLGL
C1CA_BACTE MEEN-NQONCIPNCLSPPEVEVLGGERTGTGTIDISLSLTQFLLSRFPVPGAGFVLGL
10 20 30 40 50 60

cry1a-105.pe VDIIWIGFQSDMDAFLVQIQLINORIEFARNQAIISRLSGLSNLYIVAESFREWEAD
C1CA_BACTE IDFMVIGVGSQMDAFLVQIQLINORIEFARNQAIISRLSGLSNLYIVAESFREWEAD
70 80 90 100 110 120

cry1a-105.pe PTNPALREEMRIQFNDMSALTAIPLFAVQNVQVPLLSVTVQAANHLVLRDVSFVGQ
C1CA_BACTE PNPATRIVIDRFRILDLGLDERDIPSRISGFEVPLLSVTVQAANHLVLRDVSFVGQ
130 140 150 160 170 180

cry1a-105.pe PKGFDATINRSYNDLTRIGNYTDHARVNTGLERVGPDSRDWIRYNQPRRLTIV
C1CA_BACTE RWGLTINVENRNLRIHIDEYADHCANTYNGLNLPKSTYQDWITYNELRDLTIV
190 200 210 220 230 240

cry1a-105.pe LDIVLFPNDTSRTYRTVSQLTREIYTNPVLNPDGDFRGSAGQ----IEGS-IRSP
C1CA_BACTE LDIAAFPNDNRRTYRTVSQLTREIYTNPVLNPDGDFRGSAGQ----IEGS-IRSP
250 260 270 280 290 300

cry1a-105.pe HLMDFILNSITITDARH-CE-YVWSGHQIMASPVGSGPEFTFLYCTMGNAAPQRIYA
C1CA_BACTE HLMDFILNSITITDARH-CE-YVWSGHQIMASPVGSGPEFTFLYCTMGNAAPQRIYA
310 320 330 340 350 360

cry1a-105.pe QLGQGVYRTLSSTLYR---RPFNIGINNQQLSVLDGTGTFAYGTSSNLPSPVYKSGTVDS
C1CA_BACTE -FNGVPFRTLSNPTLLQOPWAPPFN--LRGVEGVFES--TPTN--SFTYGRGTVDS
370 380 390 400 410 420

cry1a-105.pe LDEIPQNNVPPRQGFSHRLSHVSMF-RGQFSNNSVSIIRAPMFSWIHRSARFNIIAS
C1CA_BACTE LDEIPQNNVPPRQGFSHRLSHVSMF-RGQFSNNSVSIIRAPMFSWIHRSARFNIIAS
430 440 450 460 470 480

cry1a-105.pe DSITQIPLVKAHTLQSGTTVVRGPGTGGDILRRTSQGPFAFYTVININGQLPQRYRIR
C1CA_BACTE ERINGQIPLVKAHTLQSGTTVVRGPGTGGDILRRTSQGPFAFYTVININGQLPQRYRIR
490 500 510 520 530 540

cry1a-105.pe YASTNLRIRYV-TVAGERIFAGQ-----FNKTMQDGLPDTQSFYSATINIAFTFPMQ
C1CA_BACTE YASTNLRIRYV-TVAGERIFAGQ-----FNKTMQDGLPDTQSFYSATINIAFTFPMQ
550 560 570 580 590 600

cry1a-105.pe YASSRDARVILVTGAATGVGGQSVNMPLOKMEIGENLTSTRTFRYTFDFSNPFRANP
C1CA_BACTE YASSRDARVILVTGAATGVGGQSVNMPLOKMEIGENLTSTRTFRYTFDFSNPFRANP
610 620 630 640 650 660
```

©01
530 540 550 560 570

CICA_BACTE
 DLIIGSEQPLFCAOSTSG-ELYDKNIILADTFAESDLEAQAQKAVNALFFUSNQIC
 590 600 610 620 630 640 650 660 670 680 690

CICA_BACTE
LKTDVTYHIDQVSNLWLESDF CLMSNBSA VNTNRUSGONVNDENTL NGRAT
650 660 670 680 690 700
700 710 720 730 740 750

760 770 780 790 800 810

crv1a-105.pe RDEKCAHHHFSDIDVGCTDNLNEDLGVMWIFKIKTQDCHARLGNLEFLEKPLVSEA

880 890 900 910 920 930
cry1a-105.pe LARYKRAEKKWRDREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAAADKR

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

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1000      1010      1020      1030      1040      1050
cry1a-105.pe VDVEQNQRSLVVPWEAEVSQEVRCRGYILRVYAYEGYGECCVTIHIEINNTD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

cryla-105.pe ELKFSNCVEEIIYPNNVTTCNDYTVNOEYGGAYTSNRNGYNEA---PSVPADYASVVE 1110

```

cry1a-105.pe      1120 1130 1140 1150 1160 1170
E KSYTDGRRENCFEFGNGRYDTPLPGVGVTKLEYFPPTDKWIEIGETEGTTFIVDSVF
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
F KSYTDGRRENCFESNGYGDYTPLPAGVYTKOLEYFPPTDKWIEIGETEGTTFIVDSVF
C1CA RACTE

```

cryla-105.pe LLMEE
|||||
ClCA BACTE LLMEE

```

Description: Q91877 bacillus thuringiensis. toxin cryIa6. 6/2001
Accession/ID: Q91877
=====General comments=====

```

SCORES Initl: 3100 Initn: 5080 Opt: 3776 z-score: 4161.2 E(): 0
"NAME: 001.977 (1189 aa)

(1-1177:1-1189)

```

cry18-105 pe VDIIWGIFGPSOWDAFLVQIEQLINQRIEEFARNQAIISRLEGISLNLYQIYAESPWEAD
70 80 90 100 110 120

```

[illegible]

cryla-105.pe RCGFSAATNSRYDRLIGNYTDVAVWYNTGLERVWCPDSRDWIRYNQFRRELTIV

```

cry1a-105.pe LDIVSLPNYDSRTYPRIVSOLTREIVNPNVLENFDSFGSAQG-----IEGS-IRSP
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
LDIAA::FNNRRYPIOPVGSITREIVYD::LITNAPQLOQSAQDRTFNVMESSAIRNP

```

cryla-105.pe HLMILNSTIYTDHR-GE-YVWGHQIMASPVSGPFTFPLVWGNAPQODIVA
|||:|||:||| : |||::||| : |||:
HLFDILNUTIFTDFWSVGNFYGGHVRVSSLIG-GGNTSPICREAWOEPRSST-

```

cry1a-105.pe  QLGCGVYRTLSSTLYR---RPFNIGINNQQLSVLDGTEFAVGTSSNDPSAVYKKSVDLCC
               ::  |||||:  |  ::|  ::|||:  -  ::|||:  -  ::|||:  -  ::|||:  -  ::|||:  -
               -FNGVFRTLSNPTLRLQGPWPAPPFN--LRGVEGVFFS--TPTN--SFYVAGRGVTVDS
Q91877         320  330  340  350  360  370  380  390  400

```

```
cryla-105.pe LDEIPPQNNVPPRCQGFSHRLSHVSNF-RSGFNSSSYSIIKAPMF SNIHRSAEFNMLIA  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
|TELFPEDNSVPREGYSHRLCHATFQRSGTFLITGVW----FSWTHRSATLNTLTIIDP
```

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cryIa-105.pe DSITQPLVKAHTLQSGTIVVRGPGFTGDIILRTSGSPFAYTVVINGQLPQRYRARIR
Q9L877 ERINQPLVKGFRVWGTSVITGPGFTGDIILRWNTGDFVSLQVINSPIQYRLRFR
cryIa-105.pe YASTTNRLIYV-TVAGERIFAGQ-----FNKWTGDTGDLTFOFSYATINTATFFPMQ
Q9L877 YASRDARVILVTGAAGTGGVGVSVNMPLOKMEIGENLTSTFRYDFNPFSPFRANP
cryIa-105.pe SSFTV-----GADTFSSGNEVVIDRFEFLIPVTATLEAEYNLERAKAVNALFTSTNOLG
Q9L877 DIIGISERPLFGAGSISG-ELYIDKIEIILADAIPEAESDLERAKAVNALFTSSNQIG
cryIa-105.pe LKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVHAKRLSDERNLLQDNFKNQ
Q9L877 LKTDVTDYHIDQVSNLVCLDEFCLDEKRELSKVHAKRLSDERNLLQDPNFRGINRQ
cryIa-105.pe PERGMSGTITIOGGDDVFNKYNVTLSTGTEGYPYLYOKIDESKLAFTRIQLRGYI
Q9L877 PDGRWGSTDTITIOGGDDVFNKYNVTLPGTVDECPYLYOKIDESKLAFTRIQLRGYI
cryIa-105.pe EDSDLEIYIRYNAKHETVNVFGTSLWPLSAQSPGKKGEPNRCAPHLEWNPDLDCSC
Q9L877 EDSDLEIYIRYNAKHETVNVFGTSLWPLSAQSPGKKGEPNRCAPHLEWNPDLDCSC
cryIa-105.pe RDGKCAHSHHFTLDDIVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEA
Q9L877 RDGKCAHSHHFTLDDIVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEA
cryIa-105.pe LARVKAKKWRDKREKLEMETNIVVKEAKESVDALFVNSQYDQLQADTNIAMTHAADKR
Q9L877 LARVKAKKWRDKREKLEMETNIVVKEAKESVDALFVNSQYDQLQADTNIAMTHAADKR
cryIa-105.pe VHSIRAVILPELSVPGVNAAIPEELRIGRIITAFSLVDARNVKNKGDPNGLSCWNVKGH
Q9L877 VHSIRAVILPELSVPGVNAAIPEELRIGRIITAFSLVDARNVKNKGDPNGLSCWNVKGH
cryIa-105.pe VDVEENONRVSIVVPEWEAESQVVRVCPGRGYILRVATYKESGECVTHIEINNTD
Q9L877 VDVEENONRVSIVVPEWEAESQVVRVCPGRGYILRVATYKESGECVTHIEINNTD
cryIa-105.pe ELKFSNCVEEIVPNTVTCNDYTNQEEYGGAYTSNRNGYEA----PSVPADYASVYE
Q9L877 ELKFSNCVEEIVPNTVTCNDYTNQEEYGGAYTSNRNGYEA----PSVPADYASVYE

cryIa-105.pe EKSYTDCRRNCPENRGYRDYTLPGVYVTKELXFFETDKWIEIGTEGTFIVDSVE
Q9L877 EKSYTDCRRNCPENRGYRDYTLPGVYVTKELXFFETDKWIEIGTEGTFIVDSVE
cryIa-105.pe LLLMEE
Q9L877 LVLMEE
cryIa-105.pe
TXNS:AF215647_1
Description: AF215647 Bacillus thuringiensis Bacillus thuringiensis toxin
CryIa6 (cryIa6) g
Accession/ID: AF215647
=====General comments=====

LOCUS AF215647.1 [AF215647]
DEFINITION Bacillus thuringiensis toxin CryIa6 (cryIa6) gene, complete cds; . . .

SCORES Initl: 3100 Initn: 5080 Opt: 3776 Z-score: 4161.2 E(): 0
>TXNS:AF215647_1
Initl: 5080 Initn: 3100 Opt: 3776 Z-score: 4161.2 expect(): 0
Smith-Waterman score: 5397; 68.9% identity in 1206 aa overlap
(1-1177:1-1189)

cryIa-105.pe MDNPNNECIPNCLSPNEVEVLGGERITGVTPIDISLSLTQFLSFEVPGAGFVLGL
AF215647_1 MEEN-NQNCIPNCLSPNEVEVLGGERITGVTPIDISLSLTQFLSFEVPGAGFVLGL
cryIa-105.pe VDIWIGFQSDAFVQIQLINQRIEFARNOAISRLSGLSNLYQIYAESFREWEAD
AF215647_1 IDVWIGFQSDAFVQIQLINQRIEFARNOAISRLSGLSNLYQIYAESFREWEAD
cryIa-105.pe PTNPALREEMRIQFNDMSALTATPLFAVQYQVPLSVYVQAAHLISLVLDVSVFQ
AF215647_1 PNPATRVIRVDFRILQGLDERIDFSGFVPLSVYVQAAHLISLVLDVSVFQ
cryIa-105.pe RWGFDAAINRSYNDLRLIGNYTDHARVWNTGLERVWGPDSRDMIRYNQFRRLTLTV
AF215647_1 RWGVTINNVNENYRLSHIDEVADHCAVNTYRGLNLPKTYQDMITYNRLRDLTLTV
cryIa-105.pe LDIVSLFPNDRTPIKTVSQTLRELYTNPVLENFDFSGFSGAQG-----IEGS-IRSP
AF215647_1 LDIAAFPNFNNRRYPIQFQVQLTREYTDPLI-NFNPLQSQVQLFTFNVMESAIRNP
cryIa-105.pe HLMIDILNLSITIVDAHR-GE-YWWSGHQIMAGFVGSGFPEPTPLPYGTMGNAAPQORIVA
AF215647_1 HLFILNLNLTITDFWFSYGRNFWGGRHVRVSSLIIG--GQNTSPYIGREANQEPFRSFT-

[illegible]

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950      950      960      970      980      990      1000
1000      1010      1020      1030      1040      1050
cyla-105.pe VDEEENQNRSVLIVPEWEAEVSOEVRVCPGRGVILLRTATKEGYSGGCVTHIEENNTD
AF215647_1 VDEEENQNRHSVLIVPEWEAEVSOEVRVCPGRGVILLRTATKEGYSGGCVTHIEDNTD
1010      1020      1030      1040      1050      1060
1060      1070      1080      1090      1100      1110
cyla-105.pe ELKFSNCVEEELYPNNTVTICNDYTNQOEYGGAYTSRNGYNEA-----PSVPADYASVYE
AF215647_1 ELKFSNCVEEELYPNNTVTICNNYTGQIEYEGTYSSRNGQYDEAFGNNPSVPADYASVYE
1070      1080      1090      1100      1110      1120
1120      1130      1140      1150      1160      1170
cyla-105.pe EKSYTGRRNCPNCFNGYRDYTPLPVGKVTKELEYFPPDKVWIEGTEGTFIVDSVE
AF215647_1 EKSYTGRRNCPNCFNGYRDYTPLPAGVTKDLEFFDKVWIEGTEGTFIVDSVE
1130      1140      1150      1160      1170      1180
1180      1190      1200      1210      1220      1230
cyla-105.pe LLMSEE
AF215647_1 LVLNSEE

cyla-105.pep
>>>XNS:M73251_1
Accession: M73251_1
Gene complete
Accession: M73251_1
Description: M73251 Bacillus thuringiensis (cryIC(b)) gene, complete CDS.
Accession: M73251_1
Definition: Bacillus thuringiensis (cryIC(b)) gene, complete CDS.
Accession: M73251_1
General comments=====
LOCUS M73251_1 [BACCHICES]
DEFINITION Bacillus thuringiensis (cryIC(b)) gene, complete CDS.
SCORES Init: 5085 Initn: 5071 Opt: 3766 2-score: 4150.2 E(): 0
>>>XNS:M73251_1
Initn: 5071 Init: 3085 Opt: 3766 2-score: 4150.2 expect(): 0
Smith-Waterman score: 5342; 687% identity in 1206 aa overlap
(1-1177:1-1189)
10 20 30 40 50 60
cyla-105.pe MNNPNINECIPNCLSPNEVFLGGRNRYTPTIDLSLSPFLLEFVPGAGFVLGL
M73251_1 MEEN-NNQNCIPNCLSPNEVFLGGRNRYTPTIDLSLSPFLLEFVPGAGFVLGL
10 20 30 40 50 60
cyla-105.pe VDIWIGFPGSOWDAFLVQIEQLINRIEFARMOASRLGLSLNLYVAESTFEWERD
M73251_1 IDFVWIGVPGSOWDAFLVQIEQLINRIEFARMOASRLGLSLNLYVAESTFEWERD
60 70 80 90 100 110 120
cyla-105.pe PTNPALREEMRIQFNDMSALTTAIPFAVQNYQVPLISVYQANLHLSVARDVSLK
M73251_1 PNPATPRVTRIDFRILDGLGLRDIPEFRISGVEPLLSVTAQANLHLSVARDVSLK
120 130 140 150 160 170 180
cyla-105.pe RWGFDAAATINRSYNDLTRILIGNYTHDAVRWYNTGLERVWGPSRDMIRYNQFRRLTIV
M73251_1 RWGLTINNVNENYRLRIHIDEYADHCANTYNGRLNLPKSTYQDMITYNRLRLRLTIV
190 200 210 220 230 240
cyla-105.pe
M73251_1

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830      840      850      860      870      880
cry1a-105.pe      880      890      900      910      920      930
LARVKRAEKKWRDKREKLEWETNIVYKAEKESVDALFVNSQYDQLQADNTIAMTAAADKR
MT73251_1      890      900      910      920      930      940
LARVKRAEKKWRDKREKLEQLENTIVYKAEKESVDALFVNSQYDRLQVNTIAMTAAADKR

940      950      960      970      980      990
cry1a-105.pe      940      950      960      970      980      990
VHSIREAYLPESLVIPGVNNAIPELEEGRIFTAFSLYDARNVTKNGDFNGLSCWNVKGH
MT73251_1      950      960      970      980      990      1000
VHSIREAYLPESLVIPGVNNAIPELEEGRIFTAFSLYDARNVTKNGDFNGLSCWNVKGH

1000      1010      1020      1030      1040      1050
cry1a-105.pe      1000      1010      1020      1030      1040      1050
VDVEQNQRNSVLIVPEWEAEVSEVPCRGVYLIRVTAYKSGYEGECVTHIEIENNTD
MT73251_1      1010      1020      1030      1040      1050      1060
VDVEQNQRNSVLIVPEWEAEVSEVPCRGVYLIRVTAYKSGYEGECVTHIEIENNTD

1060      1070      1080      1090      1100      1110
cry1a-105.pe      1060      1070      1080      1090      1100      1110
ELKFSNCVVEEIEYPNNTVTCDYTNQEEYGGAYTSRNRGYNEA----PSVPADYASVYE
MT73251_1      1070      1080      1090      1110      1120
ELKFSNCVEEIEYPNNTVTCCNYTGTOEEYEGTYTSRNGQVDAYGNWPSVPADYASVYE

1120      1130      1140      1150      1160      1170
cry1a-105.pe      1120      1130      1140      1150      1160      1170
EKSYTDGRRENPCFNRGDRYDPLPGVYVTKELIEYFPETDKVMIEIGTSGTIVDSVE
MT73251_1      1130      1140      1150      1160      1170      1180
EKSYTDGRRENPCESNRGYDGYDPLPGVYVTKDELYFPETDKVMIEIGTSGTIVDSVE

1180      1190      1200      1210      1220      1230
cry1a-105.pe      1180      1190      1200      1210      1220      1230
LLLMEE
MT73251_1      1180      1190      1200      1210      1220      1230
LLLMEE

cry1a-105.pep
TXN5:U31527_1
Description: U31527 Bacillus thuringiensis Bacillus thuringiensis
delta-endotoxin (cryEtl) ge
Accession/ID: U31527
=====General comments=====
LOCUS      U31527_1 (BTU31527)
DEFINITION Bacillus thuringiensis delta-endotoxin (cryEtl) gene, complete cds;

SCORES      Initl: 2622      Inltn: 4047      Opt: 3490      Z-score: 3845.7 E(): 2.7e-208
>>TXN5:U31527_1
      Inltn: 4047      Inltn: 2622      Opt: 3490      Z-score: 3845.7 expect(): 2.7e-208
Smith-Waterman score: 4915;      64.4% identity in 1191 aa overlap
      (1-1177:1-1170)

cry1a-105.pe      10      20      30      40      50      60
MNNPNINCEIPYCNLSNPEVEVLGGRIETGYTPIDLSLSLQTFLLSEFVPGAGFVLGL
U31527_1      MEIN-NQOQCIIPYCNLSNPEEVLDDGERILPDIDPLEVSNLSLQFLNNFVPGGFIISGL

10      20      30      40      50      60
cry1a-105.pe      70      80      90      100      110      120
VDIINGIFGSPQMDAFLVQIQLINQRIEFAFNQAIISRLLEGSLNLYQIYAESFREWEAD
U31527_1      VDIINGIFGSPQMDAFLVQIQLINQRIEFAFNQAIISRLLEGSLNLYQIYAESFREWEAD

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U31527_1 FDKINGALRESNELFLAQIBOLIDQRIEATVRAKAIAELEGIGRSFQLYVEAFKMEBEET
60 70 80 90 100 110
cry1a-105.pe PNDALRESNRNDMSALNTRILFAVQNYQVPLISVYVOAANHLISLVRDVSVEGO
120 130 140 150 160 170 180
U31527_1 PNDNARSRYTEFEADIAQIEANIPSRNGFEVPLISVYVAQAANHLALURDSVIPGE
120 130 140 150 160 170 180
cry1a-105.pe RMGPDATINRSVNLTRIGNYTDNINWNTGLENGWQDSR-DMIRYNOFRRELITLT
190 200 210 220 230
U31527_1 RMGLTTINVDIINRQVKELHEISDHCVDKXTPREL-GEFSRAWKIYNQFRRELITLT
180 190 200 210 220 230
cry1a-105.pe VLDIVSLFPNVDRTYPIRIVTSQLTREIYNTPLENFDGSHSSAQ-GI--BASINSPLH
240 250 260 270 280 290
U31527_1 VLDIVAVPNVDGKLYFIQTKSELTRITYTSPVSEYRIGARINNNYONGITQERQINPRL
240 250 260 270 280 290
cry1a-105.pe MDLANSITIVDARGEYVMSCHOIMASPVGFSPEFTPLYGTHQVNAFQORFIAQOLPS
300 310 320 330 340 350
U31527_1 MOFFNIMTMTSINRREYVWSGLENTAYFTGFGAGPQVSPPLACTGDAALFENVJESVND
300 310 320 330 340 350
cry1a-105.pe GYVRLTSLLYRFPNIGINNQOLSVD--GTEFAYGTS--SNLDSAVKSGTVDLSLDE
360 370 380 390 400 410
U31527_1 GYVRLSAPFFYSAPF-LGT-----SVLGRGEFEMFALANNISPPFSARYRNPGTVDLSVS
360 370 380 390 400 410
cry1a-105.pe IPPQNNVPPQGFHSRSHLSVMSFRSGFSNSSVSIIRAPMFSWIRSAEFNNIIADSIT
420 430 440 450 460 470
U31527_1 IPPQNSVPPHRSRSHLSVMT-----RNS-----PIFHWTHRSATTNIRNSDVIIT
420 430 440 450 460 470
cry1a-105.pe QIPLVKAHTLQSGTIVVRGFTGGDILRRTSQGPFAITTVININGOLPQRYRARIYAST
480 490 500 510 520 530
U31527_1 QIPMWKYNLHAGATVVRGFTGGDILRRTSNGVMVTLRVDSASAVRNQRYRIRFYAAT
470 480 490 500 510 520
cry1a-105.pe TNLRIYTVAGERIFAGQNKMTMDGDLPTFQSFYSATINTAFTPMSSQSFYVGDITFS
540 550 560 570 580 590
U31527_1 SNFIVVRGNGLVNGREIMKMSIGELKKSASVFLGEFITTFNFENQVPLQIEQSLS
530 540 550 560 570 580 590
cry1a-105.pe SGMEVYIDRFELIPVTAILEAYNLERAKAVNALFTSTNQGLKNTVTDYHIDQVSNLV
600 610 620 630 640 650
U31527_1 PGGEVYLDKIEFIPADITFEAYDLERAKAVNALFTSTNQGLKNTVTDYHIDQVSNLV
590 600 610 620 630 640 650
cry1a-105.pe TYLSDFCFLDEKRELSEKVKHAKRSDERNLLQDSNFKDINRQPEBGSGSTGTIGGGD
660 670 680 690 700 710
U31527_1 ECLSDFCFLDEKRELSEKVKHAKRSDERNLLQDPNFTSINGOLDGRWGSDITIIIOGNN
650 660 670 680 690 700 710
cry1a-105.pe DVFKENVTLSGTDFECYPTLYQKIDESKLKAFTRYOLRGYTEDSODLEIYSRYNAKH
720 730 740 750 760 770

U31527_1 DVFKENVTLSGTDFECYPTLYQKIDESKLKAYTRYELRGYIEDSODLEIYLRINAKH
710 720 730 740 750 760
cry1a-105.pe ETVNVPGTGLWPLSASQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHHSHHFLSDI
780 790 800 810 820 830
U31527_1 ETLANVPGTGLSRLTSLVESQNGRCGELNCPHMKWNPDLDCSCRDGKCAHHSHHFLSDI
770 780 790 800 810 820
cry1a-105.pe DVGCTDLAEDLGVMWVFKIKTQEGHARLGNLEFLEEKPLVGEALARYRAEKWRDKREK
840 850 860 870 880 890
U31527_1 DVGCTDLAEDLGVMWVFKIKTQEGHARLGNLEFLEEKPLVGEALARYRAEKWRDKREK
830 840 850 860 870 880
cry1a-105.pe LEWETNIVYKAKESVDALFVNSOYDQADINIAMIHAAKRVHSIREAYLPELSVIPG
900 910 920 930 940 950
U31527_1 LELETXRVYTEKAEAVDALVDSQYDRQADTNIGMIHAADKLVRHICETYLPELPFIPG
890 900 910 920 930 940
cry1a-105.pe VNAAFEEELGRIFTAFSLYDARNVKNKGDFNGLSCWNVKGVHDVDEQNNQORSVLVPE
960 970 980 990 1000 1010
U31527_1 INALIFEELNRISTAFPLYEARNVINGDFNGLTCWNVKGVHDVQ-QSHRSVLVIPE
950 960 970 980 990
cry1a-105.pe WEAEVSOVRVCPGSGYLLRVATYKSGYGGCVTHIEINNTDELKFSNCVEEIIYPNNT
1020 1030 1040 1050 1060 1070
U31527_1 WEAEVSOVRVCPGSGYLLRVATYKSGYGGCVTHIEINNTDELKFSNCVEEIIYPNNT
1010 1020 1030 1040 1050 1060
cry1a-105.pe VTCDNATGVEEYICAYT--SRNGYNEA---PSVPADYASVYEKSYTDGRRNCFEF
1080 1090 1100 1110 1120
U31527_1 GTNAPFGAAGADVDNSRNVGYKDAYETNTSASVNYKPTYEEETVDVREDNHCEY
1070 1080 1090 1100 1110
cry1a-105.pe NRGKRDTPLPVQVYKAEYFPEKSNVIEIGETGTFIVDSVELLMEE
1130 1140 1150 1160 1170
U31527_1 DRGVNTPPLPASTVTKETSEFFETDVTWVLEIGETGTFIVDSVELLMEE
1120 1130 1140 1150 1160 1170
cry1a-105.pe TXN5: CLUB_BACTU
TXN5: CLUB_BACTU
Description: Q45716 bacillus thuringiensis, pest-dial crystal protein cryIjb
(insecticidal)
Accession/ID: Q45716
ID CLUB_BACTU STANDARD; PRT; 1170 AA.
AC Q45716;
Scores Initl: 2622 Initln: 4047 Opt: 3490 z-score: 3845.7 E: 2.7e-208
>>TXN5: CLUB_BACTU
Initl: 4047 Initln: 2622 Opt: 3490 z-score: 3845.7 expect (): 2.7e-208
Smith-Waterman score: 4915; 64.4% identity in 1191 aa overlap
(1-1177:1-1170)
cry1a-105.pe MDNNPNNECIPNCLSNPEVEVJGGRIETGYTPIDISLSTOFLLSRFVAGVGL
10 20 30 40 50 60

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Final Report

Product Characterization Center

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CLJB_BACTU MEIN-NQOQIPYNCLSNPEVLLDGERILPDIDPLEVSNLSLQFLNNFVPGGGFISGL
10 20 30 40 50
70 80 90 100 110 120
cry1a-105.pe VDLINGIGPQWDALFVQIEQLINQRIEERFARNQALREGLSNLYOTIAESFRWEAD
130 140 150 160 170 180
CLJB_BACTU FDKINGALRPDSEWELFLAQIEQLIDQRIEATVRAKAELEGLGSLFSGFVYFAKFEWEET
60 70 80 90 100 110
130 140 150 160 170 180
cry1a-105.pe PTPNALREEMRIQFNDMNSALTTAIPLEAVONQVPLLSVYQAAANLHLSVLKRVDSVFQO
130 140 150 160 170 180
CLJB_BACTU PONTAARSRVTEREIRIDAQIEANIPSPRIGFEVPLLSVYQAAANLHLLALRDSVIFGE
120 130 140 150 160 170
190 200 210 220 230
cry1a-105.pe RWGFAATINSRYNDLTRLIGNYTHAVRWYNTGLEKRVGPPDSR-DWIRYNQFRRELTLT
190 200 210 220 230
CLJB_BACTU RWGLTITNVNDIYNRQVKRIHEYSDHVDYTKLELRL-GFTSRAQWRIYNQFRRELTLT
180 190 200 210 220 230
240 250 260 270 280 290
cry1a-105.pe VLDIVSLNDSRTYPIRTVQSLTRELITVNPVLENDSGRSAQ-GI--EGSIRSPHL
240 250 260 270 280 290
CLJB_BACTU VLDIVAFNPDGKLYPIQKSELREIYTSFVSEYYGAINNQNQGIQTERQIROPHL
240 250 260 270 280 290
300 310 320 330 340 350
cry1a-105.pe MDILANSITYIDAHGEYVMSHQIMASFGVSGFETFPFLYGTGMGAAPQQRIVAQLGQ
300 310 320 330 340 350
CLJB_BACTU MDPFNITMTYTSYNNREYVMSGLEMTAYFTGFAQPQVSPFLACTRGDAAPFN-VRSVND
300 310 320 330 340 350
360 370 380 390 400 410
cry1a-105.pe GYVTRLSLTYRRFNFIGNNQSLVLD--GTBPAYGTS--SNLSAYVRKSGTVDLSDE
360 370 380 390 400 410
CLJB_BACTU GYTRILSAPFYSAPF-LGT-----SVLGSRGEEFPMFALNISPSPSAPRNPFTVDSLV
360 370 380 390 400 410
420 430 440 450 460 470
cry1a-105.pe IPPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSMIHRSAEFNIIASDSIT
420 430 440 450 460 470
CLJB_BACTU IPPQDMSVPPHRGSSHRLSHVTM-----RNSS-----PIEHTHRSATTTNRINSVDIT
420 430 440 450 460 470
480 490 500 510 520 530
cry1a-105.pe QIPLVKAMTLQSGTIVVRGPGFTGGDILRRTSGGPFAYITVINGQLQRYRIRVAST
480 490 500 510 520 530
CLJB_BACTU QIPMWKAYNLHAGATVVRGPGFTGGDILRRTSGGPFAYITVINGQLQRYRIRVAST
470 480 490 500 510 520
540 550 560 570 580 590
cry1a-105.pe TNLRIYTVVAGERIFAGQFNKMTMDTGLPITFQSPSYATINTAFTFPMQSSFTVGADTFS
540 550 560 570 580 590
CLJB_BACTU SNFYFVRGNGLVNGREIMKMTSGTEELKKSASFVLGFEITFPNFENQVPLQIEIQSL
530 540 550 560 570 580
600 610 620 630 640 650
cry1a-105.pe SGNEVVIDREFELIPVTATLEAYNLERAKAVNALFTSTNQLGKINYDHYHDQVSNLV
600 610 620 630 640 650
CLJB_BACTU PGGEVYLDKIEFIADTFAEYDLERAKAVNALFTSTNORGLKIDYDHYHDQVSNLV
590 600 610 620 630 640
660 670 680 690 700 710
cry1a-105.pe TYLSDEFCLDEKRELSKVKHAKLSDERNLLQDNFTSINGQLDRGWRGSTDITIOGNG
660 670 680 690 700 710
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CLJB_BACTU ECLSDFECLDEKRELSKVKHAKLSDERNLLQDNFTSINGQLDRGWRGSTDITIOGNG
650 660 670 680 690 700
720 730 740 750 760 770
cry1a-105.pe DVFKENVTLSSTFDECPTVLYQKIDSKLKAFTRQQLRGYIEDQDLIYSHYRAKH
720 730 740 750 760 770
CLJB_BACTU DVFKENVTLPDGTDECPTVLYQKIDSKLKAFTRQQLRGYIEDQDLIYSHYRAKH
710 720 730 740 750 760
780 790 800 810 820 830
cry1a-105.pe ETNVNPTGSLWPLSAQSPGKGCENRCAPHLNWPDLDCSCRDGKCAHSHHFLSLDI
780 790 800 810 820 830
CLJB_BACTU ETNVNPTGSLWPLSAQSPGKGCENRCAPHLNWPDLDCSCRDGKCAHSHHFLSLDI
770 780 790 800 810 820
840 850 860 870 880 890
cry1a-105.pe DVGCTDINEDLGVWVIFKIKTQGHARLGNLSEFLEKPLVGEALARKAEKKWDRKREK
840 850 860 870 880 890
CLJB_BACTU DVGCTDINEDLGVWVIFKIKTQGHARLGNLSEFLEKPLVGEALARKAEKKWDRKREK
830 840 850 860 870 880
900 910 920 930 940 950
cry1a-105.pe LEWETINIVYKEAKESVDALFVNSOYDQLOADTNIAHIAADKRVHSIREAYLPVLPFG
900 910 920 930 940 950
CLJB_BACTU LELEIKSVYTEAKEAVDALFVDSOYDQLOADTNIAHIAADKRVHSIREAYLPVLPFG
890 900 910 920 930 940
960 970 980 990 1000 1010
cry1a-105.pe VNAAIFELEGRIFTAFSLYDARNVKNKGFNNGLSCWNVKGVHDVEEQNNQSRVLYVPE
960 970 980 990 1000 1010
CLJB_BACTU INAIIFEELENRISTAFLEYEARVNNKGFNNGLTGNVKGHVDVQ-QSHHRSVLVPE
950 960 970 980 990
1020 1030 1040 1050 1060 1070
cry1a-105.pe WEAEVSGEVRVCPGRGYILRVYATKEGYEGCVTHIEENNTDELKFSNCVVEEYFPNT
1020 1030 1040 1050 1060 1070
CLJB_BACTU WEAEVSGEVRVCPGRGYILRVYATKEGYEGCVTHIEENNTDELKFSNCVVEEYFPNT
1000 1010 1020 1030 1040 1050
1080 1090 1100 1110 1120
cry1a-105.pe VTCNDYTVNOEEYGGAYT--SRNRGVNEA---PSVPADYASVVEEKSVDGRRNPCEF
1080 1090 1100 1110 1120
CLJB_BACTU GTCNNDYPSAGAGACADVCNERNVGVKADYETNTSASVNYKPYEETVTDVREDNHCEY
1060 1070 1080 1090 1100 1110
1130 1140 1150 1160 1170
cry1a-105.pe ARGVRYDPLPVGVTYKLEYFPEPTDKWIEGETEGTFIVDSVELLMEE
1130 1140 1150 1160 1170
CLJB_BACTU DRGVNYNPLPAGVYKLEYFPEPTDKWIEGETEGTFIVDSVELLMEE
1120 1130 1140 1150 1160 1170
cry1a-105.pep
TXN5:032306
Description: 032306 bacillus thuringiensis. delta-endotoxin. 6/2001
Accession/ID: 032306
ID 032306 PRELIMINARY; PRI; 618 AA.
AC 032306
DT 01-JAN-1998 (TREMBLrel. 05, Created)
SCORES Initl: 3203 Initn: 3464 Opt: 3475 Z-score: 3833.3 E(): 1.3e-207
>TXN5:032306 (618 aa)
initn: 3464 initl: 3203 opt: 3475 Z-score: 3833.3 expect(): 1.3e-207
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Smith-Waterman score: 3475; 86.0% identity in 622 aa overlap
(1-617:1-618)

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cry1a-105.pe MDNNPINEICIPYNCLSNPEVEVLGGERIEGTPTIDISLSLTQFLSEFVPGAGFVLGL
O32306          10 20 30 40 50 60
              20 30 40 50 60
cry1a-105.pe VDIIMGIFGSPQMDAFLVQLEQINQRIEFAFNQALSRLEGLSNLYQIYAESFREWAD
O32306          70 80 90 100 110 120
              80 90 100 110 120
cry1a-105.pe PTPALREERNRQFNDMNSALTITAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ
O32306          130 140 150 160 170 180
              140 150 160 170 180
cry1a-105.pe PTPALREERNRQFNDMNSALTITAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ
O32306          190 200 210 220 230 240
              200 210 220 230 240
cry1a-105.pe RWGFDAAITNSRYNDLTRLIGNYTDHVRWNTGLERVMGPDSDRWIRYNQFRRELTIV
O32306          250 260 270 280 290 300
              260 270 280 290 300
cry1a-105.pe LDIVSLFPNDSTRTYPIRTVSQLTREITNPVLENDGSGFGSAQGGIEGIRSPHLMIDL
O32306          310 320 330 340 350 360
              320 330 340 350 360
cry1a-105.pe NSITIIYDHRGEYVWSGHQIMASPVGSGPEFTFLYGTMGNAAPQRIVAQLGGQYR
O32306          370 380 390 400 410 420
              380 390 400 410 420
cry1a-105.pe TLSSLTLYRRPFIINNOQLSVLDGTEFAYGTSSNLPASVYKSGTSDSLDEIPPNNNV
O32306          430 440 450 460 470 480
              440 450 460 470 480
cry1a-105.pe PPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWHRSAEFNNIIASDSITQIPLVKAH
O32306          490 500 510 520 530 540
              500 510 520 530 540
cry1a-105.pe TLOSGFTVVRGPGFTGDLIRLRTSGFPAYT--IVNINQLQFQ---RYRARIYASTNML
O32306          550 560 570 580 590 600
              560 570 580 590 600
cry1a-105.pe FLVNGS-VISGPGFTGDLVRLNLSGNNIQRGYIEVPIHFPTSTRTYRVRVYASVTPI
O32306          610 620 630 640 650 660
              620 630 640 650 660
cry1a-105.pe EVVIDRFLIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVDYHIDQVSNLVTYL
O32306          670 680 690 700 710 720
              680 690 700 710 720
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O32306          GVIIIDREFIPVTATLEAEYNL
              600 610
cry1a-105.pe
TXN5:Y09787_1
Description: Y09787 Bacillus thuringiensis B.thuringiensis cryIA(c) gene;
insecticidal crysta
Accession/ID: Y09787
=====General comments=====
LOCUS Y09787_1 [BTCRYDE]
DEFINITION B.thuringiensis cryIA(c) gene;
=====
SCORES Initl: 3203 Initn: 3464 Opt: 3475 z-score: 3833.3 E(): 1.3e-207
>TXN5:Y09787_1
Initn: 3464 Initl: 3203 Opt: 3475 z-score: 3833.3 expect(): 1.3e-207
Smith-Waterman score: 3475; 86.0% identity in 622 aa overlap
(1-617:1-618)
cry1a-105.pe MDNNPINEICIPYNCLSNPEVEVLGGERIEGTPTIDISLSLTQFLSEFVPGAGFVLGL
O32306          10 20 30 40 50 60
              20 30 40 50 60
cry1a-105.pe VDIIMGIFGSPQMDAFLVQLEQINQRIEFAFNQALSRLEGLSNLYQIYAESFREWAD
O32306          70 80 90 100 110 120
              80 90 100 110 120
cry1a-105.pe PTPALREERNRQFNDMNSALTITAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ
O32306          130 140 150 160 170 180
              140 150 160 170 180
cry1a-105.pe PTPALREERNRQFNDMNSALTITAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQ
O32306          190 200 210 220 230 240
              200 210 220 230 240
cry1a-105.pe RWGFDAAITNSRYNDLTRLIGNYTDHVRWNTGLERVMGPDSDRWIRYNQFRRELTIV
O32306          250 260 270 280 290 300
              260 270 280 290 300
cry1a-105.pe LDIVSLFPNDSTRTYPIRTVSQLTREITNPVLENDGSGFGSAQGGIEGIRSPHLMIDL
O32306          310 320 330 340 350 360
              320 330 340 350 360
cry1a-105.pe NSITIIYDHRGEYVWSGHQIMASPVGSGPEFTFLYGTMGNAAPQRIVAQLGGQYR
O32306          370 380 390 400 410 420
              380 390 400 410 420
cry1a-105.pe TLSSLTLYRRPFIINNOQLSVLDGTEFAYGTSSNLPASVYKSGTSDSLDEIPPNNNV
O32306          430 440 450 460 470 480
              440 450 460 470 480
cry1a-105.pe PPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWHRSAEFNNIIASDSITQIPLVKAH
O32306          490 500 510 520 530 540
              500 510 520 530 540
```

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Y09787_1  PPROGFSHRLSHVMSFRSGFSNSSVSIIRAPMFMSWHRSAEFNNIIASDSITQIPAVKGN
          430 440 450 460 470 480
          490 500 510 520 530
cry1a-105.pe  TLOSGTTVVRGPGFTGGDLIRRTSGPFAYT--IVNINGQLPQ---RYRARIYASTTNL
          1 11 21 31 41 51 61 71 81 91 101 111 121 131 141 151 161 171 181 191 201 211 221 231 241 251 261 271 281 291 301 311 321 331 341 351 361 371 381 391 401 411 421 431 441 451 461 471 481 491 501 511 521 531
Y09787_1  FLNFGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPESTSTRYRVRYASVTPI
          490 500 510 520 530
cry1a-105.pe  RLYVTVAGERIFAGOFNKMTDGLTFQSFYSYATINTAFTPMSSQSFVGDFTSSGN
          540 550 560 570 580 590
Y09787_1  HLNWNKSSIFSNTVPATATSLDNLOSDFGYFESANAFSSLGN---IVGVNFSGTA
          540 550 560 570 580 590
cry1a-105.pe  EYVIDRFEIPVATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
          600 610 620 630 640 650
Y09787_1  GVIIDRFEFIPVATLEAEYNL
          600 610
cry1a-105.pep
TXN5:U63372_1
Description: U63372 synthetic construct Synthetic, truncated cry1Ac gene from
Bacillus thurin
Accession/ID: U63372
LOCUS U63372.1 [XXU63372]
DEFINITION Synthetic, truncated cry1Ac gene from Bacillus thuringiensis; ...
=====General comments=====
SCORES Init1: 3165 Initn: 3395 Opt: 3406 Z-score: 3757.2 E(): 2.3e-203
>TXN5:U63372_1
Initn: 3395 Init1: 3165 opt: 3406 Z-score: 3757.2 expect(): 2.3e-203
Smith-Waterman score: 3406; 84.9% identity in 617 aa overlap
(1-612:1-613)
cry1a-105.pe  MDNPNINECIPYCNLSNPEVEVLGGERIETGTPIDISLSLTQFLSEFVPGAGFVLGL
          10 20 30 40 50 60
U63372_1  MDNPNINECIPYCNLSNPEVEVLGGERIETGTPIDISLSLTQFLSEFVPGAGFVLGL
          10 20 30 40 50 60
cry1a-105.pe  VDIINGIFGSPQMDAFVLQIEQLINQRIEFARNQAIISRLBGLSLNLYQIYAESFREWAD
          70 80 90 100 110 120
U63372_1  VDIINGIFGSPQMDAFVLQIEQLINQRIEFARNQAIISRLBGLSLNLYQIYAESFREWAD
          70 80 90 100 110 120
cry1a-105.pe  PTPNPALEENRIQFNDMNSALTITAIPLFAVQYQVPLLSVYVQANHLVLRDVSFVGQ
          130 140 150 160 170 180
U63372_1  PTPNPALEENRIQFNDMNSALTITAIPLFAVQYQVPLLSVYVQANHLVLRDVSFVGQ
          130 140 150 160 170 180
cry1a-105.pe  RWGFDAAATNSRYNDLTGLIGNYTDHAWRYNTGLERVWGPDSRDWRVYNQFRRELTIV
          190 200 210 220 230 240
U63372_1  RWGFDAAATNSRYNDLTGLIGNYTDHAWRYNTGLERVWGPDSRDWRVYNQFRRELTIV
          190 200 210 220 230 240
cry1a-105.pe  LDIVISFPYDSRTYPIETVSQLTREIYNPVLNFDGSRGSGNOGIESIRSPHLMIDL
          250 260 270 280 290 300
```

```
U63372_1  LDIVALFPYDSRRYPIRTVSQLTREIYNPVLNFDGSRGSGNOGIESIRSPHLMIDL
          250 260 270 280 290 300
cry1a-105.pe  NSITITDAHRGEYMGQIMASPVGSGPEFTFLYGTMGNAAPQORIVAQLGGQVYR
          310 320 330 340 350 360
U63372_1  NSITITDAHRGEYMGQIMASPVGSGPEFTFLYGTMGNAAPQORIVAQLGGQVYR
          310 320 330 340 350 360
cry1a-105.pe  TLLSSTLYRRPNIGINNQQLSVLDTGTEPAYGTSSNLPSSAVYRKSGTVDLSDEIPQNNV
          370 380 390 400 410 420
U63372_1  TLLSSTLYRRPNIGINNQQLSVLDTGTEPAYGTSSNLPSSAVYRKSGTVDLSDEIPQNNV
          370 380 390 400 410 420
cry1a-105.pe  PPRQGFSHRLSHVMSFRSGFSNSSVSIIRAPMFMSWHRSAEFNNIIASDSITQIPAVKGN
          430 440 450 460 470 480
U63372_1  PPRQGFSHRLSHVMSFRSGFSNSSVSIIRAPMFMSWHRSAEFNNIIASDSITQIPAVKGN
          430 440 450 460 470 480
cry1a-105.pe  TLOSGTTVVRGPGFTGGDLIRRTSGPFAYT--IVNINGQLPQ---RYRARIYASTTNL
          490 500 510 520 530
U63372_1  FLNFGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPESTSTRYRVRYASVTPI
          490 500 510 520 530
cry1a-105.pe  RLYVTVAGERIFAGOFNKMTDGLTFQSFYSYATINTAFTPMSSQSFVGDFTSSGN
          540 550 560 570 580 590
U63372_1  HLNWNKSSIFSNTVPATATSLDNLOSDFGYFESANAFSSLGN---IVGVNFSGTA
          540 550 560 570 580 590
cry1a-105.pe  EYVIDRFEIPVATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
          600 610 620 630 640 650
U63372_1  GVIIDRFEFIPVATLEAEYNL
          600 610
Description: Q45737 bacillus thuringiensis. cry1a(c) insecticidal crystal
protein (lepidopter
Accession/ID: Q45737
ID Q45737 PRELIMINARY; PRT; 618 AA.
AC Q45737;
=====General comments=====
SCORES Init1: 2909 Initn: 2909 Opt: 3406 Z-score: 3757.2 E(): 2.3e-203
>TXN5:Q45737
Initn: 2909 Init1: 2909 opt: 3406 Z-score: 3757.2 expect(): 2.3e-203
Smith-Waterman score: 3406; 84.4% identity in 623 aa overlap
(1-618:1-618)
cry1a-105.pe  MDNPNINECIPYCNLSNPEVEVLGGERIETGTPIDISLSLTQFLSEFVPGAGFVLGL
          10 20 30 40 50 60
Q45737  MDNPNINECIPYCNLSNPEVEVLGGERIETGTPIDISLSLTQFLSEFVPGAGFVLGL
          10 20 30 40 50 60
cry1a-105.pe  VDIINGIFGSPQMDAFVLQIEQLINQRIEFARNQAIISRLBGLSLNLYQIYAESFREWAD
          70 80 90 100 110 120
```

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VDIIMGTFGSPSMDATFVQIEQLINORIEEFARNQAIISLEGLSNLQIVIAESFREWAD
Q45737 170 80 90 100 110 120

PTPALREMRONDMNSALFATALFAVQYVPLLSVYQAAHLSLVLRDVSFVQ
cryla-105.pe 170 140 150 160 170 180

PTPALREMRONDMNSALFATALFAVQYVPLLSVYQAAHLSLVLRDVSFVQ
Q45737 170 140 150 160 170 180

RWGFDAAATINSYNDLRLTGNITDIAKWWATGLNKGSRRDWIEYVQFRELTLTV
cryla-105.pe 190 200 210 220 230 240

RWGFDAAATINSYNDLRLTGNITDIAKWWATGLNKGSRRDWIEYVQFRELTLTV
Q45737 190 200 210 220 230 240

LDIVSLFPYVDSRTPIRTYSQLTREIYTNVLENFQSGFSAQOIEGFSIRSPHNDIL
cryla-105.pe 250 260 270 280 290 300

LDIVSLFPYVDSRTPIRTYSQLTREIYTNVLENFQSGFSAQOIEGFSIRSPHNDIL
Q45737 250 260 270 280 290 300

NSIITYTDAHRGEYVWSGHQIMASPVGSGPEFTPLPGTNGNAACQINVAQICQVTV
cryla-105.pe 310 320 330 340 350 360

NSIITYTDAHRGEYVWSGHQIMASPVGSGPEFTPLPGTNGNAACQINVAQICQVTV
Q45737 310 320 330 340 350 360

TLSSLTLYRRPFGNIGINNQLSVLDGTEFAYGTSNLPASAVRVKSGTVDSLDEIPQNNNY
cryla-105.pe 370 380 390 400 410 420

TLSSLTLYRRPFGNIGINNQLSVLDGTEFAYGTSNLPASAVRVKSGTVDSLDEIPQNNNY
Q45737 370 380 390 400 410 420

PPROQGFHRLSHVSMFRSGSNSVSIIRAPMFSMIHRSAEFNNIIASDSITQIPLVKAH
cryla-105.pe 430 440 450 460 470 480

PPROQGFHRLSHVSMFRSGSNSVSIIRAPMFSMIHRSAEFNNIIASDSITQIPLVKAH
Q45737 430 440 450 460 470 480

FLFNGS-VISGPGFTGCDILVNLNSGNNTQNGYIEVPIHFPSTSTRVAVRVYASVTPI
cryla-105.pe 490 500 510 520 530 540

FLFNGS-VISGPGFTGCDILVNLNSGNNTQNGYIEVPIHFPSTSTRVAVRVYASVTPI
Q45737 490 500 510 520 530 540

RIYVYAGERIFAGQFNKMTDGPLOTFQSFSTATINATFTPMWSQSFVAGDFTSSGN
cryla-105.pe 550 560 570 580 590 600

RIYVYAGERIFAGQFNKMTDGPLOTFQSFSTATINATFTPMWSQSFVAGDFTSSGN
Q45737 550 560 570 580 590 600

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

EYVIDRFEIIPVATLAEYVNLRAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLTVLTY
Q45737 610 620 630 640 650 660

GWIDRFEIIPVATLAEYVNLRAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLTVLTY
cryla-105.pe 670 680 690 700 710 720

GWIDRFEIIPVATLAEYVNLRAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLTVLTY
Q45737 670 680 690 700 710 720

Description: Q45721 bacillus thuringiensis. cryia(c) (fragment). 6/2001
Accession/ID: Q45721
ID Q45721 PRELIMINARY; PRT: 607 AA.
AC Q45721

DT 01-NOV-1996 (TrEMBLrel. 01. Created)
 SCORES Init1: 2906 Initn: 3047 Opt: 3343 z-score: 3687.8 E(): 1.7e-199
 >TXN5:Q45721
 Initn: 3047 init1: 2906 opt: 3343 z-score: 3687.8 expect(): 1.7e-199
 Smith-Waterman score: 3343; 84.2% identity in 612 aa overlap
 (1-607:1-607)
 cry1a-105.pe MDNNPNIIECTIPNCLSNSEVEVLGGERIETGTPIDISLSLTOPLLSEFVPGAGFVLGL
 10 20 30 40 50 60
 Q45721 MDNNPNIIECTIPNCLSNSEVEVLGGERIETGTPIDISLSLTOPLLSEFVPGAGFVLGL
 10 20 30 40 50 60
 cry1a-105.pe VDIWIIFGSPQDAFVQIQEQLINQRIETEFAPNAQIRLEGLSNLYQIYASFPREAF
 70 80 90 100 110 120
 Q45721 VDIWIIFGSPQDAFVQIQEQLINQRIETEFAPNAQIRLEGLSNLYQIYASFPREAF
 70 80 90 100 110 120
 cry1a-105.pe PTNPALREEMRIQFNDWNSALITAPLFAVQNVQPLSVVQAAHLHLSVLRDVSFVG
 130 140 150 160 170 180
 Q45721 PTNPALREEMRIQFNDWNSALITAPLFAVQNVQPLSVVQAAHLHLSVLRDVSFVG
 130 140 150 160 170 180
 cry1a-105.pe RWGFDAATINSRYNDLTRLLGNVTHAVRWNTGLERVWGPDSRWIRINQFRRLTIV
 190 200 210 220 230 240
 Q45721 RWGFDAATINSRYNDLTRLLGNVTHAVRWNTGLERVWGPDSRWIRINQFRRLTIV
 190 200 210 220 230 240
 cry1a-105.pe LDIVSLFPPNRRPPIRTYVTSQLTREITVNPVLENDGSGFRGSAQIGESIRSPHMLDIL
 250 260 270 280 290 300
 Q45721 LDIVSLFPPNRRPPIRTYVTSQLTREITVNPVLENDGSGFRGSAQIGESIRSPHMLDIL
 250 260 270 280 290 300
 cry1a-105.pe NSIITYTDARHGSEYVSNQIMASVPGSGSEFTFPLPYGTMGNAAPQRIVAOLGGQVVR
 310 320 330 340 350 360
 Q45721 NSIITYTDARHGSEYVSNQIMASVPGSGSEFTFPLPYGTMGNAAPQRIVAOLGGQVVR
 310 320 330 340 350 360
 cry1a-105.pe TLISSTLVRRPPIGNINQOQSVLQGTPEFGVSNLPSAVRKSNTVDSLDEIPPONNV
 370 380 390 400 410 420
 Q45721 TLISSTLVRRPPIGNINQOQSVLQGTPEFGVSNLPSAVRKSNTVDSLDEIPPONNV
 370 380 390 400 410 420
 cry1a-105.pe PPRQGFSHRLSHVSMFRGFSNGSVLIIIRAPMFSNHRSEFFNIIRASDITQIPVRK
 430 440 450 460 470 480
 Q45721 PPRQGFSHRLSHVSMFRGFSNGSVLIIIRAPMFSNHRSEFFNIIRASDITQIPVRK
 430 440 450 460 470 480
 cry1a-105.pe TLOSGTIVRRGPGFTGGILARTSGGPVAT--IWNIGOLPO--RYRRAIRASVTN
 490 500 510 520 530
 Q45721 TLOSGTIVRRGPGFTGGILARTSGGPVAT--IWNIGOLPO--RYRRAIRASVTN
 490 500 510 520 530
 cry1a-105.pe RYVTVAGERIFAQGNKMTDGPLTOSFSYATINFTAFFMSSQSSFTVGADTSSGN
 540 550 560 570 580 590
 Q45721 RYVTVAGERIFAQGNKMTDGPLTOSFSYATINFTAFFMSSQSSFTVGADTSSGN
 540 550 560 570 580 590

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Q45721 HLNVNMGNSIFSNTVPATATSLDNLQSDFGYFESANAFSTSLGN--IVGVRNFSGTA
540 550 560 570 580 590
cryIa-105.pe EVYIDRFELIPVATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
600 610 620 630 640 650
Q45721 GVIIDRFEFIPV
600
cryIa-105.pe
TXN5:U43606_1
Description: U43606 Bacillus thuringiensis Bacillus thuringiensis cryIA(c)
gene, partial cds.
Accession/ID: U43606
=====General comments=====
LOCUS U43606_1 [BTU43606]
DEFINITION Bacillus thuringiensis cryIA(c) gene, partial cds; . . .
SCORES Init1: 2906 Initn: 3047 Opt: 3343 z-score: 3687.8 E(): 1.7e-199
>>TXN5:U43606_1
Initn: 3047 Init1: 2906 Opt: 3343 z-score: 3687.8 expect(): 1.7e-199
Smith-Waterman score: 3343, 84.2% identity in 612 aa overlap
(1-607:1-607)
cryIa-105.pe MDNPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLQFLSEFVPGAGFVLGL
10 20 30 40 50 60
U43606_1 MDNPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLQFLSEFVPGAGFVLGL
10 20 30 40 50 60
cryIa-105.pe VDIWIGFGPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGSLNLYQIYAESFREWEAD
70 80 90 100 110 120
U43606_1 VDIWIGFGPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGSLNLYQIYAESFREWEAD
70 80 90 100 110 120
cryIa-105.pe PTPNALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANHLSLVLRDVSFVGQ
130 140 150 160 170 180
U43606_1 PTPNALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANHLSLVLRDVSFVGQ
130 140 150 160 170 180
cryIa-105.pe RMGFDAAATINSRYNDLTRELIGNYTDHAVRWNTGLERVWGSPDRDWIRYNQFRRELTLY
190 200 210 220 230 240
U43606_1 RMGFDAAATINSRYNDLTRELIGNYTDHAVRWNTGLERVWGSPDRDWIRYNQFRRELTLY
190 200 210 220 230 240
cryIa-105.pe LDIVSLFPNYSRTPYPIRTVSQLTRITNPNVLENFPGSPRGAQIEGSIIRSPHLMIDL
250 260 270 280 290 300
U43606_1 LDIVSLFPNYSRTPYPIRTVSQLTRITNPNVLENFPGSPRGAQIEGSIIRSPHLMIDL
250 260 270 280 290 300
cryIa-105.pe NSITITDAHRGEYVWGHQIMASPVGSGPEFTFPIYGTMGNAAPQRIVAQLGQGVYR
310 320 330 340 350 360
U43606_1 NSITITDAHRGEYVWGHQIMASPVGSGPEFTFPIYGTMGNAAPQRIVAQLGQGVYR
310 320 330 340 350 360
cryIa-105.pe TLSSTLYRRPPNIGINNQLSVLDGTGFAYGTSNLPASVYRKSGTVDSLSLEIPPQNNVY
370 380 390 400 410 420

U43606_1 TLSSTLYRRPPNIGINNQLSVLDGTGFAYGTSNLPASVYRKSGTVDSLSLEIPPQNNVY
370 380 390 400 410 420
cryIa-105.pe PPROGFSHRLSHVSMFRSG-SSSSVSIIRAPMFSWIHRSAFNNIIASDSITQIPLVKAH
430 440 450 460 470 480
U43606_1 PPROGFSHRLSHVSMFRSG-SSSSVSIIRAPMFSWIHRSAFNNIIASDSITQIPLVKAH
430 440 450 460 470 480
cryIa-105.pe TLQSGTTVVRGPGFTGGDILRTTSGGPFAYT--IVNINGLPQ---RYRARIYASTTNL
490 500 510 520 530
U43606_1 FLFNGS-VISGPGFTGGDILRTTSGGPFAYT--IVNINGLPQ---RYRARIYASTTNL
490 500 510 520 530
cryIa-105.pe RIYVTVAGERIPAGQNKMTDGTPLTFQSFYATINTAFTFPMSQSSFTVGADTFSSGN
540 550 560 570 580 590
U43606_1 HLNVNMGNSIFSNTVPATATSLDNLQSDFGYFESANAFSTSLGN--IVGVRNFSGTA
540 550 560 570 580 590
cryIa-105.pe EVYIDRFELIPVATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
600 610 620 630 640 650
U43606_1 GVIIDRFEFIPV
600
cryIa-105.pep
TXN5:AF177675_1
Description: AF177675 synthetic construct Synthetic construct Cry Iac
insecticidal toxin gene
Accession/ID: AF177675
=====General comments=====
LOCUS AF177675_1 [AF177675]
DEFINITION Synthetic construct Cry Iac insecticidal toxin gene, complete cds; . . .
SCORES Init1: 2951 Initn: 3181 Opt: 3192 z-score: 3521.3 E(): 3.1e-190
>>TXN5:AF177675_1
Initn: 3181 Init1: 2951 Opt: 3192 z-score: 3521.3 expect(): 3.1e-190
Smith-Waterman score: 3192, 84.0% identity in 589 aa overlap
(29-612:3-587)
cryIa-105.pe MDNPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLQFLSEFVPGAGFVLGL
10 20 30 40 50 60
AF177675_1 MAIETGYTPIDISLSLQFLSEFVPGAGFVLGL
10 20 30
cryIa-105.pe VDIWIGFGPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGSLNLYQIYAESFREWEAD
70 80 90 100 110 120
AF177675_1 VDIWIGFGPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGSLNLYQIYAESFREWEAD
70 80 90 100 110 120
cryIa-105.pe PTPNALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANHLSLVLRDVSFVGQ
130 140 150 160 170 180
AF177675_1 PTPNALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANHLSLVLRDVSFVGQ
130 140 150 160 170 180
cryIa-105.pe RMGFDAAATINSRYNDLTRELIGNYTDHAVRWNTGLERVWGSPDRDWIRYNQFRRELTLY
190 200 210 220 230 240

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AF177675_1  RMGFDARTINSYNDATRLIGNYDYAVRWNTGLERVWGDSRDWRVYNQFRRLTLTV
160 170 180 190 200 210
cry1a-105.pe  LDNSLFFNDSONPIRTVSQTLREIYTNVLENFDFGFRSGAGIERSIRSPHMDIL
250 260 270 280 290 300
AF177675_1  LDNALFNVDSRYEIRTVSQTREITNVLENFDFGFRSGAGIERSIRSPHMDIL
220 230 240 250 260 270
cry1a-105.pe  NSITITDAHGEYVNSGQIMASPVKSGFFTFPKNGKNAAPQRIYVAQGGQVVR
310 320 330 340 350 360
AF177675_1  NSITITDAHGEYVNSGQIMASPVKSGFFTFPKNGKNAAPQRIYVAQGGQVVR
280 290 300 310 320 330
cry1a-105.pe  TLSTLYRPPFNIGINNQQLSVLDTGTEFAVTSNLPASVAVTSGTVDSLDLIPPNNVV
370 380 390 400 410 420
AF177675_1  TLSTLYRPPFNIGINNQQLSVLDTGTEFAVTSNLPASVAVTSGTVDSLDLIPPNNVV
340 350 360 370 380 390
cry1a-105.pe  PPRQGFSHLSHVMSFRSGSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIRKPM
430 440 450 460 470 480
AF177675_1  PPRQGFSHLSHVMSFRSGSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIRKPM
400 410 420 430 440 450
cry1a-105.pe  TLOSGTVVRGPGFTGGDILRRTSGGPFAYT--IWNINGOLPO--RYRARIYASTNL
490 500 510 520 530
AF177675_1  FLNFGS--VLSGGPGFTGGDILRRNSGNNIQNGYIEVPIHFPSTRYRVRVASTPI
460 470 480 490 500 510
cry1a-105.pe  RIYVTVAGERIFAGQFNKMTDGLTFQSFYATINTAFTPMSQSSSTVAGDTSSGN
540 550 560 570 580 590
AF177675_1  HLANWNGNSIIFNTVPATATSLDNLQSSDFGYFESANAFSTSLGN--IVGVNFSGTA
520 530 540 550 560 570
cry1a-105.pe  EYIDRPELIPVTATLEAYNLEAQAQVAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
600 610 620 630 640 650
AF177675_1  GVIIDRPELIPVTATLE
580
cry1a-105.pep
TXN5:U43605_1
Description: U43605 Bacillus thuringiensis Bacillus thuringiensis cry1A(a)
Gene, partial cds;
Accession/ID: U43605
=====General comments=====
LOCUS U43605_1 [BTU43605]
DEFINITION Bacillus thuringiensis cry1A(a) gene, partial cds; . . .
SCORES Initl: 2251 Initn: 3103 Opt: 3192 Z-score: 3521.0 E(): 3.3e-190
>>TXN5:U43605_1
Initn: 3103 Initl: 2251 Opt: 3192 Z-score: 3521.0 expect(): 3.3e-190
Smith-Waterman score: 3192; 78.0% identity in 623 aa overlap
(1-621:1-620)
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U43605_1  MDNPNINECIPYNCLSNPEVVLGGERIETGTYPIDISLSLTQFLLSSEFVPGAGFVLGL
10 20 30 40 50 60
cry1a-105.pe  VDIWIFGFSOWDAFLVQIQLINRIEFEPARNOAISREGLSNLYQIYAESPREWAD
70 80 90 100 110 120
U43605_1  VDIWIFGFSOWDAFLVQIQLINRIEFEPARNOAISREGLSNLYQIYAESPREWAD
70 80 90 100 110 120
cry1a-105.pe  PTNPALREERNIQQNDMSALTATPILFAVQNYQVPLLSVYVQAANLHLSVLDRVSVFGQ
130 140 150 160 170 180
U43605_1  PTNPALREERNIQQNDMSALTATPILFAVQNYQVPLLSVYVQAANLHLSVLDRVSVFGQ
130 140 150 160 170 180
cry1a-105.pe  RMGFDAAATINSRINDLTLIGNYTDHARVAVNTGLERVWGPDSRDWRVYNQFRRLTLTV
190 200 210 220 230 240
U43605_1  RMGFDAAATINSRINDLTLIGNYTDHARVAVNTGLERVWGPDSRDWRVYNQFRRLTLTV
190 200 210 220 230 240
cry1a-105.pe  LDIVSLPNDVDSRTYRIVTSQTLREIYTNVLENFDFGFRSGAGIERSIRSPHMDIL
250 260 270 280 290 300
U43605_1  LDIVSLPNDVDSRTYRIVTSQTLREIYTNVLENFDFGFRSGAGIERSIRSPHMDIL
250 260 270 280 290 300
cry1a-105.pe  NSITITDAHGEYVNSGQIMASPVKSGFFTFPKNGKNAAPQRIYVAQGGQVVR
310 320 330 340 350 360
U43605_1  NSITITDAHGEYVNSGQIMASPVKSGFFTFPKNGKNAAPQRIYVAQGGQVVR
310 320 330 340 350 360
cry1a-105.pe  TLSTLYRPPFNIGINNQQLSVLDTGTEFAVTSNLPASVAVTSGTVDSLDLIPPNNVV
370 380 390 400 410
U43605_1  TLSTLYRPPFNIGINNQQLSVLDTGTEFAVTSNLPASVAVTSGTVDSLDLIPPNNVV
370 380 390 400 410
cry1a-105.pe  NYPFRQGFSHLSHVMSFRSGSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIRKPM
420 430 440 450 460 470
U43605_1  NYPFRQGFSHLSHVMSFRSGSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIRKPM
420 430 440 450 460 470
cry1a-105.pe  AHTLOSQTTVVRGPGFTGGDILRRTSGGPFAYT--IWNINGOLPO--RYRARIYASTNLRY
480 490 500 510 520 530
U43605_1  AHTLOSQTTVVRGPGFTGGDILRRTSGGPFAYT--IWNINGOLPO--RYRARIYASTNLRY
480 490 500 510 520 530
cry1a-105.pe  VTVAGERIFAGQFNKMTDGLTFQSFYATINTAFTPMSQSSSTVAGDTSSGN
540 550 560 570 580 590
U43605_1  VTVAGERIFAGQFNKMTDGLTFQSFYATINTAFTPMSQSSSTVAGDTSSGN
540 550 560 570 580 590
cry1a-105.pe  IDRFELIPVTATLEAYNLEAQAQVAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSD
600 610 620 630 640 650
U43605_1  IDRFELIPVTATLEAYNLEAQAQVAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSD
600 610 620 630 640 650
cry1a-105.pep
TXN5:Q45720
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