(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
30 June 2016 (30.06.2016)

WIPO | PCT

(10) International Publication Number
WO 2016/106066 A2

(51) International Patent Classification:
C07K 14/325 (2006.01) *C12N 15/82* (2006.01)

(21) International Application Number:
PCT/US2015/066314

(22) International Filing Date:
17 December 2015 (17.12.2015)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
62/095,524 22 December 2014 (22.12.2014) US

(71) Applicant: **AGBIOME, INC.** [US/US]; 104 T.W. Alexander Drive, Research Triangle Park, NC 27709 (US).

(72) Inventors: **PARKS, Jessica**; 5433 Wade Park Boulevard, Apt. 2201, Raleigh, NC 27607 (US). **ROBERTS, Kira, Bulazel**; 7810 Roxboro Road, Bahama, NC 27503 (US). **THAYER, Rebecca, E.**; 100 Hammond Wood Place, Morrisville, NC 27560 (US).

(74) Agents: **ROTHSCHILD, Cynthia, B.** et al.; Kilpatrick Townsend & Stockton LLP, 1001 West Fourth St., Winston-Salem, NC 27101 (US).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:

— *of inventorship (Rule 4.17(iv))*

Published:

— *without international search report and to be republished upon receipt of that report (Rule 48.2(g))*

— *with sequence listing part of description (Rule 5.2(a))*

WO 2016/106066 A2

(54) Title: PESTICIDAL GENES AND METHODS OF USE

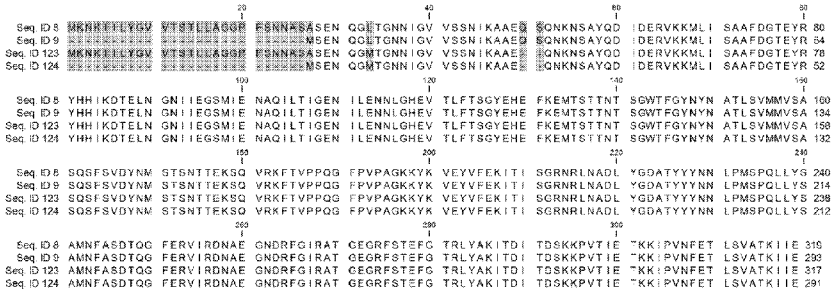


Figure 1

(57) Abstract: Compositions having pesticidal activity and methods for their use are provided. Compositions include isolated and recombinant polypeptides having pesticidal activity, recombinant and synthetic nucleic acid molecules encoding the polypeptides, DNA constructs and vectors comprising the nucleic acid molecules, host cells comprising the vectors, and antibodies to the polypeptides. Polynucleotide sequences encoding the polypeptides can be used in DNA constructs or expression cassettes for transformation and expression in organisms of interest. The compositions and methods provided are useful for producing organisms with enhanced pest resistance or tolerance. Transgenic plants and seeds comprising a nucleotide sequence that encodes a pesticidal protein of the invention are also provided. Such plants are resistant to insects and other pests. Methods are provided for producing the various polypeptides disclosed herein, and for using those polypeptides for controlling or killing a pest. Methods and kits for detecting polypeptides of the invention in a sample are also included.

PESTICIDAL GENES AND METHODS OF USE

CROSS REFERENCE TO RELATED APPLICATION

[0001] This application claims the benefit of U.S. Provisional Application Serial No. 62/095,524, filed December 22, 2014, the contents of this application is herein incorporated by reference in their entirety.

FIELD OF THE INVENTION

[0002] The invention is drawn to methods and compositions for controlling pests, particularly plant pests.

REFERENCE TO A SEQUENCE LISTING SUBMITTED AS A TEXT FILE VIA EFS-WEB

[0003] The official copy of the sequence listing is submitted electronically via EFS-Web as an ASCII formatted sequence listing with a file named AgB006.PCT_SEQLIST.txt, created on December 14, 2015 and having a size of 956 KB and is filed concurrently with the specification. The sequence listing contained in this ASCII formatted document is part of the specification and is herein incorporated by reference in its entirety.

BACKGROUND

[0004] Pests, plant diseases, and weeds can be serious threats to crops. Losses due to pests and diseases have been estimated at 37% of the agricultural production worldwide, with 13% due to insects, bacteria and other organisms.

[0005] Toxins are virulence determinants that play an important role in microbial pathogenicity and/or evasion of the host immune response. Toxins from the gram-positive bacterium Bacillus, particularly *Bacillus thuringensis*, have been used as insecticidal proteins (commonly referred to as Bt toxins). Current strategies use the genes expressing these toxins to produce transgenic crops. Transgenic crops expressing insecticidal protein toxins are used to combat crop damage from insects.

[0006] While the use of Bacillus toxins has been successful in controlling insects, resistance to Bt toxins has developed in some target pests in many parts of the world where such toxins have been used intensively. One way of solving this problem is sowing Bt crops

with alternating rows of regular non Bt crops (refuge). An alternative method to avoid or slow down development of insect resistance is stacking insecticidal genes with different modes of action against insects in transgenic plants. The current strategy of using transgenic crops expressing insecticidal protein toxins is placing increasing emphasis on the discovery of novel toxins, beyond those already derived from the bacterium *B. thuringiensis*. Novel toxins may prove useful as alternatives to those derived from *B. thuringiensis* for deployment in insect- and pest-resistant transgenic plants. Thus, new toxin proteins are needed.

BRIEF DESCRIPTION OF THE FIGURES

[0007] Figure 1 provides an amino acid alignment of SEQ ID NOs: 8, 9, 123, and 124. Highlighted regions denote regions where the amino acids are different between the four polypeptides.

[0008] Figure 2 provides an amino acid alignment of SEQ ID NOs: 25, 26, 125 and 126. Highlighted regions denote regions where the amino acids are different between the four polypeptides.

[0009] Figure 3 provides an amino acid alignment of SEQ ID NOs: 72, 94, 127, and 128. Highlighted regions denote regions where the amino acids are different between the four polypeptides.

[0010] Figure 4 provides an amino acid alignment of SEQ ID NOs: 70, 71, 129, 130 and 131. Highlighted regions denote regions where the amino acids are different between the five polypeptides.

[0011] Figures 5A-5H provide an amino acid alignment of SEQ ID NOs: 6, 7, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and 159. Highlighted regions denote regions conserved in each of the polypeptides. Conserved regions present in this alignment are set forth in Table 4.

[0012] Figure 6 provides the percent sequence identity relationship of each of SEQ ID NOs: 6 and 132-159.

[0013] Figure 7 provides the assay scoring guidelines (size x mortality matrix) employed in the western corn rootworm bioassay.

SUMMARY

[0014] Compositions having pesticidal activity and methods for their use are provided. Compositions include isolated and recombinant polypeptide sequences having pesticidal activity, recombinant and synthetic nucleic acid molecules encoding the pesticidal polypeptides, DNA constructs comprising the nucleic acid molecules, vectors comprising the nucleic acid molecules, host cells comprising the vectors, and antibodies to the pesticidal polypeptides. Nucleotide sequences encoding the polypeptides provided herein can be used in DNA constructs or expression cassettes for transformation and expression in organisms of interest, including microorganisms and plants.

[0015] The compositions and methods provided herein are useful for the production of organisms with enhanced pest resistance or tolerance. These organisms and compositions comprising the organisms are desirable for agricultural purposes. Transgenic plants and seeds comprising a nucleotide sequence that encodes a pesticidal protein of the invention are also provided. Such plants are resistant to insects and other pests.

[0016] Methods are provided for producing the various polypeptides disclosed herein, and for using those polypeptides for controlling or killing a pest. Methods and kits for detecting polypeptides of the invention in a sample are also included.

DETAILED DESCRIPTION

[0017] The present inventions now will be described more fully hereinafter with reference to the accompanying drawings, in which some, but not all embodiments of the inventions are shown. Indeed, these inventions may be embodied in many different forms and should not be construed as limited to the embodiments set forth herein; rather, these embodiments are provided so that this disclosure will satisfy applicable legal requirements. Like numbers refer to like elements throughout.

[0018] Many modifications and other embodiments of the inventions set forth herein will come to mind to one skilled in the art to which these inventions pertain having the benefit of the teachings presented in the foregoing descriptions and the associated drawings. Therefore, it is to be understood that the inventions are not to be limited to the specific embodiments disclosed and that modifications and other embodiments are intended to be included within the scope of the appended claims. Although specific terms are employed herein, they are used in a generic and descriptive sense only and not for purposes of limitation.

I. Polynucleotides and Polypeptides

[0019] Compositions and method for conferring pesticidal activity to an organism are provided. The modified organism exhibits resistance or tolerance to pests. Recombinant pesticidal proteins, or polypeptides and fragments and variants thereof that retain pesticidal activity, are provided and include those set forth in SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159. The pesticidal proteins are biologically active (for example, are pesticidal) against pests including insects, fungi, nematodes, and the like. Polynucleotides encoding the pesticidal polypeptides, including for example, SEQ ID NOS: 1-159 or active fragments or variants thereof, can be used to produce transgenic organisms, such as plants and microorganisms. The transformed organisms are characterized by genomes that comprise at least one stably incorporated DNA construct comprising a coding sequence for a pesticidal protein disclosed herein. In some embodiments, the coding sequence is operably linked to a promoter that drives expression of the encoded pesticidal polypeptide. Accordingly, transformed microorganisms, plant cells, plant tissues, plants, seeds, and plant parts are provided. A summary of various polypeptides, active variants and fragments thereof, and polynucleotides encoding the same are set forth below in Table 1. As noted in Table 1, various forms of polypeptides are provided. Full length pesticidal polypeptides, as well as, modified versions of the original full-length sequence (referred to as variants) are provided. Table 1 further denotes "CryBP1" sequences. Such sequences (SEQ ID NOs: 24, 67 and 73) comprise accessory polypeptides that can be associated with some of the toxin genes. In such instances, the CryBP1 sequences can be used alone or in combination with any of the pesticidal polypeptides provided herein. Table 1 further provides Split-Cry C'-terminus polypeptides (SEQ ID NOs: 3, 74, 77, 80 and 91). Such sequences comprise the sequence of a downstream protein that has homology to the C'-terminal end of the Cry class of toxin genes and are usually found after a Cry gene that is not full-length and is missing the expected C'-terminal region.

Table 1. Summary of SEQ ID NOs, Gene Class, and Variants Thereof

Gene Name	Full-length SEQ ID No.	Variant SEQID No.(s)	CryBP1 SEQ ID No.	Split-Cry C-terminus SEQ ID No.	Homologs	Gene Class	Polypeptides of the invention (and polynucleotides encoding the same) include those having the % sequence identity listed below	Polypeptides of the invention (and polynucleotides encoding the same) include those having the similarity set forth below
APG00002	1	2, 95, 96		3	APG00034 (60.3% identity, 70.6% similarity)	Cry	40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					APG00101 (46.6% identity, 61.8% similarity)			
					APG00048 (41.5% identity, 56.6% similarity)			
					Cry13Aa1 (35.6% identity, 51.6% similarity)			
					US_7923602_B2-12 (34.2% identity, 49.8% similarity)			
APG00005	4	5			US_8461415_B2-28 (29.5% identity, 44.0% similarity)	Cry	30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					US_8318900_B2-83 (28.8% identity, 44.6% similarity)			
					Cry54Aa2 (28.7% identity, 44.4% similarity)			
					US_8318900_B2-80 (28.2% identity, 43.4% similarity)			
					WP_016099738.1 (27.8% identity, 45.7% similarity)			
APG00008	6	7, 132-159			WP_002169786.1 (95.1% identity, 97.3% similarity)	Cry22B	96, 97, 98, 99	98, 99
					US_7208656_B2-8 (94.8% identity, 97.5% similarity)			
					Cry22Ba1 (94.6% identity, 97.5% similarity)			
					US_8461421_B2-109 (94.1% identity, 96.8% similarity)			
					Cry22Bb1 (94.0% identity, 96.8% similarity)			
APG00010	8	9, 123, 124			Sip1A-Ls (81.2% identity, 89.3% similarity)	Sip1A	85, 90, 95, 96, 97, 98, 99	90, 95, 96, 97, 98, 99
					US_8318900_B2-74 (61.1% identity, 73.4% similarity)			

Gene Name	Full-length SEQ ID No.	Variant SEQID No.(s)	CryBP1 SEQ ID No.	Split-Cry C-terminus SEQ ID No.	Homologs	Gene Class	Polypeptides of the invention (and polynucleotides encoding the same) include those having the % sequence identity listed below	Polypeptides of the invention (and polynucleotides encoding the same) include those having the similarity set forth below
					US_8440882_B2-21 (59.6% identity, 75.5% similarity)			
					Sip1A-BtMC28 (59.3% identity, 75.2% similarity)			
					US_8461415_B2-31 (26.4% identity, 43.3% similarity)			
APG00027	10	11, 12, 13			WP_016093954.1 (58.4% identity, 72.0% similarity)	Cry70	60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	75, 80, 85, 90, 95, 96, 97, 98, 99
					WP_002147758.1 (58.1% identity, 72.0% similarity)			
					Cry70Bb1 (57.7% identity, 71.4% similarity)			
					ETT82181.1 (57.7% identity, 71.2% similarity)			
					WP_016095385.1 (57.6% identity, 71.4% similarity)			
APG00034	14	15			APG00101 (61.3% identity, 73.7% similarity)	Cry	40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					APG00002 (60.3% identity, 70.6% similarity)			
					APG00048 (50.4% identity, 64.5% similarity)			
					Cry13Aa1 (38.4% identity, 55.0% similarity)			
					APG00097 (37.0% identity, 54.3% similarity)			
APG00039	16	17, 18, 19			US_20130227743_A1-26 (53.8% identity, 64.4% similarity)	Cry	55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					APG00046 (37.1% identity, 53.2% similarity)			
					YP_006815593.1 (35.6% identity, 47.3% similarity)			
					ACP43734.1 (35.5% identity, 47.2% similarity)			
					Cry53Aa1 (34.4% identity,			

Gene Name	Full-length SEQ ID No.	Variant SEQID No.(s)	CryBP1 SEQ ID No.	Split-Cry C-terminus SEQ ID No.	Homologs	Gene Class	Polypeptides of the invention (and polynucleotides encoding the same) include those having the % sequence identity listed below	Polypeptides of the invention (and polynucleotides encoding the same) include those having the similarity set forth below
					45.8% similarity)			
APG00046	20	21, 97, 98			EXY04476.1 (47.9% identity, 62.6% similarity)	Cry	50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					US_8686124_B2-22 (46.9% identity, 60.0% similarity)			
					US_8686124_B2-23 (46.7% identity, 59.8% similarity)			
					APG00039 (37.1% identity, 53.2% similarity)			
					Cry9Aa4 (34.1% identity, 45.1% similarity)			
APG00048	22	23, 99, 100	24		APG00101 (52.1% identity, 64.0% similarity)	Cry	40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					APG00034 (50.4% identity, 64.5% similarity)			
					APG00097 (42.3% identity, 54.0% similarity)			
					APG00002 (41.6% identity, 56.7% similarity)			
					Cry13Aa1 (39.8% identity, 53.5% similarity)			
APG00052	25	26, 125, 126			US_8147856_B2-2 (89.5% identity, 95.4% similarity)	Cry14A	90, 95, 96, 97, 98, 99	96, 97, 98, 99
					Cry14Ab1 (89.5% identity, 95.4% similarity)			
					US_8147856_B2-33 (89.2% identity, 95.0% similarity)			
					US_7923602_B2-38 (87.0% identity, 92.8% similarity)			
					Cry14Aa1 (84.0% identity, 90.4% similarity)			
APG00059	27	28, 101, 102			US_7919272_B2-13 (66.9% identity, 77.8% similarity)	Cry69	70, 75, 80, 85, 90, 95, 96, 97, 98, 99	80, 85, 90, 95, 96, 97, 98, 99
					WP_016084446.1 (65.1% identity, 74.2% similarity)			

Gene Name	Full-length SEQ ID No.	Variant SEQID No.(s)	CryBP1 SEQ ID No.	Split-Cry C-terminus SEQ ID No.	Homologs	Gene Class	Polypeptides of the invention (and polynucleotides encoding the same) include those having the % sequence identity listed below	Polypeptides of the invention (and polynucleotides encoding the same) include those having the similarity set forth below
					WP_016085042.1 (63.5% identity, 73.9% similarity)			
					WP_016084057.1 (63.4% identity, 73.8% similarity)			
					APG00079 (63.3% identity, 73.0% similarity)			
					Cry69Aa1 (57.0% identity, 68.3% similarity)			
APG00062	29	30			APG00094 (57.7% identity, 70.8% similarity)	Cry	35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					WP_002187556.1 (33.1% identity, 47.7% similarity)			
					US_20130227743_A1-32 (32.1% identity, 49.9% similarity)			
					APG00130 (32.1% identity, 49.4% similarity)			
					Cry73Aa (30.4% identity, 45.1% similarity)			
APG00065	31	32			WP_000839920.1 (71.3% identity, 80.0% similarity)	Bin	75, 80, 85, 90, 95, 96, 97, 98, 99	85, 90, 95, 96, 97, 98, 99
					WP_002166959.1 (71.2% identity, 80.5% similarity)			
					WP_002191947.1 (71.0% identity, 80.5% similarity)			
					US_8318900_B2-72 (68.3% identity, 76.8% similarity)			
					US_20130227743_A1-146 (68.1% identity, 76.6% similarity)			
APG00066	33	34, 103			US_6063597_A-51.1 (29.3% identity, 46.8% similarity)	Cry	30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					Cry29Aa1 (29.3% identity, 44.4% similarity)			
					US7521235B2_2 (27.6% identity, 43.5% similarity)			

Gene Name	Full-length SEQ ID No.	Variant SEQID No.(s)	CryBP1 SEQ ID No.	Split-Cry C-terminus SEQ ID No.	Homologs	Gene Class	Polypeptides of the invention (and polynucleotides encoding the same) include those having the % sequence identity listed below	Polypeptides of the invention (and polynucleotides encoding the same) include those having the similarity set forth below
					WP_016098322.1 (27.3% identity, 43.6% similarity)			
					AGV55018.1 (26.0% identity, 40.6% similarity)			
APG00068	35	36			US_8318900_B2-82 (63.5% identity, 74.6% similarity)	Cry32	65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	75, 80, 85, 90, 95, 96, 97, 98, 99
					Cry32Ea1 (63.2% identity, 74.2% similarity)			
					US_8461421_B2-91 (62.1% identity, 72.8% similarity)			
					US_8461421_B2-99 (61.9% identity, 74.4% similarity)			
					AGU13868.1 (60.4% identity, 72.5% similarity)			
APG00070	37	38			US_8147856_B2-6 (31.8% identity, 47.3% similarity)	Cry	35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					Cry21Ga1 (31.4% identity, 48.1% similarity)			
					US_8147856_B2-35 (31.1% identity, 46.1% similarity)			
					Cry21Ca1 (30.5% identity, 45.9% similarity)			
					Cry21Da1 (30.0% identity, 44.0% similarity)			
APG00072	39				ABW89739.1 (25.5% identity, 37.4% similarity)	Cry	30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					Cry11Aa1 (25.2% identity, 37.3% similarity)			
					APG00124 (9.7% identity, 17.4% similarity)			
					APG00079 (7.8% identity, 14.0% similarity)			
					US_8461415_B2-69 (4.2% identity, 6.1% similarity)			
APG00075	40	104			US_8299323_B2-2 (41.7% identity, 56.3% similarity)	Bin	45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99

Gene Name	Full-length SEQ ID No.	Variant SEQID No.(s)	CryBP1 SEQ ID No.	Split-Cry C-terminus SEQ ID No.	Homologs	Gene Class	Polypeptides of the invention (and polynucleotides encoding the same) include those having the % sequence identity listed below	Polypeptides of the invention (and polynucleotides encoding the same) include those having the similarity set forth below
					Cry49Ab1 (36.9% identity, 51.1% similarity)			
					Cry49Aa1 (36.4% identity, 50.9% similarity)			
					Cry36Aa1 (36.2% identity, 49.1% similarity)			
					WP_016099737.1 (33.0% identity, 48.3% similarity)			
APG00076	41	42, 92, 93			US_20130227743_A1-74 (34.3% identity, 50.4% similarity)	Cry	35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					BAE79727.1 (33.8% identity, 49.2% similarity)			
					US_7803993_B2-2 (29.2% identity, 43.8% similarity)			
					US_7491536_B2-2 (28.0% identity, 42.1% similarity)			
					APG00039 (23.1% identity, 37.3% similarity)			
					CAJ86549.1 (22.2% identity, 32.3% similarity)			
					Cry4Aa2 (22.0% identity, 31.8% similarity)			
APG00079	43	44			US_7919272_B2-13 (72.3% identity, 80.0% similarity)	Cry69	75, 80, 85, 90, 95, 96, 97, 98, 99	85, 90, 95, 96, 97, 98, 99
					APG00059 (63.3% identity, 73.0% similarity)			
					WP_016085042.1 (61.6% identity, 72.8% similarity)			
					WP_016084057.1 (61.6% identity, 72.8% similarity)			
					YP_006815453.1 (61.4% identity, 73.2% similarity)			
					Cry69Aa1 (58.3% identity, 70.1% similarity)			
APG000	45	46, 105, 106			US_8461415_B2-47 (35.3%	Cry	40, 45, 50, 55, 60, 65, 70, 75, 80, 85,	50, 55, 60, 65, 70, 75, 80, 85, 90,

Gene Name	Full-length SEQ ID No.	Variant SEQID No.(s)	CryBP1 SEQ ID No.	Split-Cry C-terminus SEQ ID No.	Homologs	Gene Class	Polypeptides of the invention (and polynucleotides encoding the same) include those having the % sequence identity listed below	Polypeptides of the invention (and polynucleotides encoding the same) include those having the similarity set forth below
85					identity, 48.1% similarity)		90, 95, 96, 97, 98, 99	95, 96, 97, 98, 99
					US_8461415_B2-49 (35.1% identity, 48.4% similarity)			
					US_8461415_B2-62 (35.0% identity, 47.5% similarity)			
					APG00039 (33.2% identity, 48.7% similarity)			
					ABV55105.1 (31.9% identity, 45.4% similarity)			
					US_7329736_B2-2 (30.9% identity, 44.7% similarity)			
APG00087	47	48, 107			ADB02881.1 (29.3% identity, 44.3% similarity)	Cry	30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					US_6063605_A-4 (29.0% identity, 44.3% similarity)			
					US_8563808_B2-4 (27.0% identity, 40.5% similarity)			
					Cry1If1 (26.9% identity, 41.2% similarity)			
					Cry1Ib1 (26.7% identity, 40.7% similarity)			
APG00090	49	108			WP_017154552.1 (61.6% identity, 76.7% similarity)	Bin	65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	80, 85, 90, 95, 96, 97, 98, 99
					US_20130227743_A1-50 (47.3% identity, 63.0% similarity)			
					US_20130227743_A1-154, (41.6% identity, 53.7% similarity)			
					US_20130227743_A1-156 (41.6% identity, 51.0% similarity)			
					WP_000143308.1 (27.9% identity, 44.4% similarity)			
APG00094	50	51, 109, 110			APG00062 (57.7% identity, 70.8% similarity)	Cry	35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99

Gene Name	Full-length SEQ ID No.	Variant SEQID No.(s)	CryBP1 SEQ ID No.	Split-Cry C-terminus SEQ ID No.	Homologs	Gene Class	Polypeptides of the invention (and polynucleotides encoding the same) include those having the % sequence identity listed below	Polypeptides of the invention (and polynucleotides encoding the same) include those having the similarity set forth below
					APG00130 (33.2% identity, 51.3% similarity)			
					WP_002187556.1 (32.2% identity, 46.4% similarity)			
					AHN52957.1 (30.7% identity, 41.9% similarity)			
					US_8461421_B2-84 (30.3% identity, 44.5% similarity)			
					Cry73Aa (30.0% identity, 44.1% similarity)			
APG00095	52				Cry49Ab1 (29.3% identity, 41.0% similarity)	Cry	30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					Cry49Aa1 (28.9% identity, 40.5% similarity)			
					APG00075 (27.7% identity, 41.3% similarity)			
					US_8299323_B2-2 (24.6% identity, 38.8% similarity)			
					CAA73756.1 (24.5% identity, 36.9% similarity)			
APG00097	53	54, 111, 112			APG00048 (42.3% identity, 54.0% similarity)	Cry	35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					APG00101 (37.9% identity, 52.9% similarity)			
					APG00034 (37.7% identity, 54.5% similarity)			
					APG00002 (34.2% identity, 49.4% similarity)			
					US_7923602_B2-29 (33.2% identity, 47.4% similarity)			
					US_8147856_B2-12 (32.5% identity, 46.3% similarity)			
					Cry13Aa1 (32.0% identity, 46.7% similarity)			
APG00099	55	56			Cry13Aa1 (30.8% identity, 45.6% similarity)	Cry	35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99

Gene Name	Full-length SEQ ID No.	Variant SEQID No.(s)	CryBP1 SEQ ID No.	Split-Cry C-terminus SEQ ID No.	Homologs	Gene Class	Polypeptides of the invention (and polynucleotides encoding the same) include those having the % sequence identity listed below	Polypeptides of the invention (and polynucleotides encoding the same) include those having the similarity set forth below
					APG00048 (30.0% identity, 44.3% similarity)			
					APG00101 (28.5% identity, 43.3% similarity)			
					US_8461415_B2-35 (28.0% identity, 40.2% similarity)			
					APG00034 (27.7% identity, 41.6% similarity)			
APG00101	57	58			APG00034 (61.3% identity, 73.7% similarity)	Cry	40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					APG00048 (52.1% identity, 64.0% similarity)			
					APG00002 (46.6% identity, 61.8% similarity)			
					APG00097 (37.9% identity, 52.9% similarity)			
					Cry13Aa1 (37.0% identity, 53.9% similarity)			
APG00104	59	113			Vip3Ad2 (23.8% identity, 40.4% similarity)	Vip	25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					US_8237021_B2-6 (23.8% identity, 40.4% similarity)			
					CAI43276.1 (23.8% identity, 40.4% similarity)			
					Vip3Aa4 (23.7% identity, 41.0% similarity)			
					Vip3Aa42 (23.2% identity, 40.2% similarity)			
APG00110	60	61, 62, 63, 114			US_8318900_B2-205 (62.0% identity, 74.4% similarity)	Cry	65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	75, 80, 85, 90, 95, 96, 97, 98, 99
					US_8318900_B2-69 (55.8% identity, 68.1% similarity)			
					WP_016110336.1 (48.7% identity, 62.6% similarity)			
					US_8461421_B2-100 (32.1% identity, 48.1% similarity)			

Gene Name	Full-length SEQ ID No.	Variant SEQID No.(s)	CryBP1 SEQ ID No.	Split-Cry C-terminus SEQ ID No.	Homologs	Gene Class	Polypeptides of the invention (and polynucleotides encoding the same) include those having the % sequence identity listed below	Polypeptides of the invention (and polynucleotides encoding the same) include those having the similarity set forth below
					WP_016109534.1 (29.9% identity, 42.8% similarity)			
					APG00027 (24.4% identity, 38.4% similarity)			
					US_8318900_B2-89 (23.5% identity, 37.5% similarity)			
					YP_002774176.1 (22.7% identity, 37.9% similarity)			
					WP_016742208.1 (22.4% identity, 39.1% similarity)			
					Cry70Bb1 (22.1% identity, 35.8% similarity)			
APG00114	64				US_8461415_B2-42 (66.3% identity, 81.7% similarity)	Cry	70, 75, 80, 85, 90, 95, 96, 97, 98, 99	85, 90, 95, 96, 97, 98, 99
					US_8461415_B2-43 (54.1% identity, 66.4% similarity)			
					US_20130227743_A1-194 (35.6% identity, 43.8% similarity)			
					US_20130227743_A1-90 (21.3% identity, 26.3% similarity)			
					APG00140 (20.6% identity, 34.8% similarity)			
					APG00027 (19.1% identity, 32.8% similarity)			
					US_8318900_B2-69 (18.9% identity, 31.9% similarity)			
					US_8318900_B2-205 (18.9% identity, 31.5% similarity)			
					WP_002147758.1 (18.8% identity, 31.5% similarity)			
					WP_002069902.1 (18.7% identity, 31.3% similarity)			
APG00115	65	66, 115, 116	67		WP_002205004.1 (56.7% identity, 67.4% similarity)	Cry	60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	70, 75, 80, 85, 90, 95, 96, 97, 98, 99

Gene Name	Full-length SEQ ID No.	Variant SEQID No.(s)	CryBP1 SEQ ID No.	Split-Cry C-terminus SEQ ID No.	Homologs	Gene Class	Polypeptides of the invention (and polynucleotides encoding the same) include those having the % sequence identity listed below	Polypeptides of the invention (and polynucleotides encoding the same) include those having the similarity set forth below
					US_8461421_B2-83 (54.8% identity, 64.1% similarity)			
					US_8461421_B2-75 (53.2% identity, 62.4% similarity)			
					US_8461421_B2-104 (45.1% identity, 56.5% similarity)			
					WP_002187573.1 (45.0% identity, 53.2% similarity)			
					US_8318900_B2-61 (42.5% identity, 56.5% similarity)			
					US_8461421_B2-92 (40.4% identity, 53.7% similarity)			
					APG00068 (35.5% identity, 48.1% similarity)			
					WP_002187555.1 (34.2% identity, 37.2% similarity)			
					WP_002187592.1 (33.7% identity, 37.8% similarity)			
APG00120	68	69, 117, 118			Cry41Ba2 (44.1% identity, 58.6% similarity)	Cry	45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					Cry41Aa1 (39.5% identity, 54.4% similarity)			
					Cry41Ab1 (37.0% identity, 52.7% similarity)			
					US_8461421_B2-94 (36.7% identity, 51.7% similarity)			
					WP_002169796.1 (35.3% identity, 49.3% similarity)			
APG00124	70	71, 129, 130, 131,			US_8461421_B2-99 (43.9% identity, 54.4% similarity)	Cry	45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					Cry32Ea1 (43.2% identity, 53.9% similarity)			
					AGU13868.1 (43.1% identity, 53.7% similarity)			
					APG00068 (42.4% identity, 53.1% similarity)			

Gene Name	Full-length SEQ ID No.	Variant SEQID No.(s)	CryBP1 SEQ ID No.	Split-Cry C-terminus SEQ ID No.	Homologs	Gene Class	Polypeptides of the invention (and polynucleotides encoding the same) include those having the % sequence identity listed below	Polypeptides of the invention (and polynucleotides encoding the same) include those having the similarity set forth below
					Cry32Ab1 (41.8% identity, 52.0% similarity)			
APG00130	72	127, 128, 94	73	74	WP_002187593.1 (63.8% identity, 69.4% similarity)	Cry73	65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					US_8461421_B2-84 (61.2% identity, 67.1% similarity)			
					Cry73Aa (60.6% identity, 66.5% similarity)			
					APG00140 (47.7% identity, 57.4% similarity)			
					AHN52957.1 (46.8% identity, 57.4% similarity)			
APG00136	75	76		77	Cry65Aa2 (52.6% identity, 61.0% similarity)	Cry65	55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					US_8461421_B2-94 (24.8% identity, 38.3% similarity)			
					APG00120 (23.9% identity, 35.8% similarity)			
					Cry41Ba2 (23.4% identity, 35.0% similarity)			
					BAD35163.1 (21.7% identity, 34.6% similarity)			
APG00140	78	79		80	AHN52957.1 (67.3% identity, 77.2% similarity)	Cry73	70, 75, 80, 85, 90, 95, 96, 97, 98, 99	80, 85, 90, 95, 96, 97, 98, 99
					Cry73Aa (54.6% identity, 67.4% similarity)			
					WP_002187593.1 (54.6% identity, 66.8% similarity)			
					US_8461421_B2-84 (54.3% identity, 67.0% similarity)			
					APG00130 (47.7% identity, 57.4% similarity)			
APG00144	81				Cry35Ca1 (28.0% identity, 44.7% similarity)	Cry	30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99

Gene Name	Full-length SEQ ID No.	Variant SEQID No.(s)	CryBP1 SEQ ID No.	Split-Cry C-terminus SEQ ID No.	Homologs	Gene Class	Polypeptides of the invention (and polynucleotides encoding the same) include those having the % sequence identity listed below	Polypeptides of the invention (and polynucleotides encoding the same) include those having the similarity set forth below
					Cry35Ac1 (25.7% identity, 41.3% similarity)			
					WP_002016877.1 (25.6% identity, 42.8% similarity)			
					WP_016097060.1 (25.2% identity, 42.5% similarity)			
					Cry35Ac2 (25.1% identity, 41.5% similarity)			
APG00162	82	83, 119, 120			Cry4Cc1 (39.7% identity, 55.9% similarity)	Cry	40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					Cry4Aa2 (39.6% identity, 56.1% similarity)			
					ABM97547.1 (39.5% identity, 56.6% similarity)			
					ABR12214.1 (39.4% identity, 56.2% similarity)			
					Cry4Aa1 (39.4% identity, 55.9% similarity)			
APG00183	84				WP_016093722.1 (28.9% identity, 51.3% similarity)	Bin	30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					WP_002167240.1 (28.5% identity, 50.3% similarity)			
					WP_002016877.1 (28.0% identity, 50.1% similarity)			
					US_20130227743_A1-146 (26.6% identity, 40.9% similarity)			
					US_20130227743_A1-6 (26.1% identity, 46.0% similarity)			
APG00195	85	86, 87, 88			APG00110 (19.4% identity, 32.0% similarity)	Cry	20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99	35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99
					US_8318900_B2-205 (19.3% identity, 32.5% similarity)			
					US_8461421_B2-100 (17.5% identity, 31.0% similarity)			

Gene Name	Full-length SEQ ID No.	Variant SEQID No.(s)	CryBP1 SEQ ID No.	Split-Cry C-terminus SEQ ID No.	Homologs	Gene Class	Polypeptides of the invention (and polynucleotides encoding the same) include those having the % sequence identity listed below	Polypeptides of the invention (and polynucleotides encoding the same) include those having the similarity set forth below
					US_8318900_B2-69 (16.7% identity, 29.2% similarity)			
					Cry5Ba3 (13.4% identity, 20.8% similarity)			
APG00204	89	90, 121, 122		91	Cry40Da1 (65.9% identity, 77.3% similarity)	Cry40	70, 75, 80, 85, 90, 95, 96, 97, 98, 99	80, 85, 90, 95, 96, 97, 98, 99
					Cry40Ca1 (57.9% identity, 68.7% similarity)			
					BAB72018.1 (57.7% identity, 71.2% similarity)			
					Cry40Ba1 (51.4% identity, 62.8% similarity)			
					US_8133858_B2-3 (51.0% identity, 65.2% similarity)			

i. Classes of Pesticidal proteins

[0020] The pesticidal proteins provided herein and the nucleotide sequences encoding them are useful in methods for impacting pests. That is, the compositions and methods of the invention find use in agriculture for controlling or killing pests, including pests of many crop plants. The pesticidal proteins provided herein are toxin proteins from bacteria and exhibit activity against certain pests. The pesticidal proteins are from several classes of toxins including Cry, Cyt, BIN, Mtx toxins. See, for example, Table 1 for the specific protein classifications of the various SEQ ID NOs provided herein. In addition, reference is made throughout this disclosure to Pfam database entries. The Pfam database is a database of protein families, each represented by multiple sequence alignments and a profile hidden Markov model. Finn *et al.* (2014) *Nucl. Acid Res.* Database Issue 42:D222-D230.

[0021] *Bacillus thuringiensis* (Bt) is a gram-positive bacterium that produces insecticidal proteins as crystal inclusions during its sporulation phase of growth. The proteinaceous inclusions of Bt are called crystal proteins or δ-endotoxins (or Cry proteins), which are toxic to members of the class Insecta and other invertebrates. Similarly, Cyt proteins are parasporal inclusion proteins from Bt that exhibits hemolytic (Cytolitic) activity or has obvious sequence similarity to a known Cyt protein. These toxins are highly specific to their target organism, are innocuous to humans, vertebrates, and plants.

[0022] The structure of the Cry toxins reveals five conserved amino acid blocks, concentrated mainly in the center of the domain or at the junction between the domains. The Cry toxin consists of three domains, each with a specific function. Domain I is a seven α-helix bundle in which a central helix is completely surrounded by six outer helices. This domain is implicated in channel formation in the membrane. Domain II appears as a triangular column of three anti-parallel β–sheets, which are similar to antigen–binding regions of immunoglobulins. Domain III contains anti-parallel β–strands in a β sandwich form. The N-terminal part of the toxin protein is responsible for its toxicity and specificity and contains five conserved regions. The C-terminal part is usually highly conserved and probably responsible for crystal formation. See, for example, U.S. Patent No. 8,878,007.

[0023] Strains of *B. thuringiensis* show a wide range of specificity against different insect orders (Lepidoptera, Diptera, Coleoptera, Hymenoptera, Homoptera, Phthiraptera or Mallophaga,

and Acari) and other invertebrates (Nemathelminthes, Platyhelminthes, and Sarocomastebrates). The Cry proteins have been classified into groups based on toxicity to various insect and invertebrate groups. Generally, Cry I proteins demonstrate toxicity to lepidopterans, Cry II proteins demonstrate to lepidopterans and dipterans, CryIII proteins demonstrate to coleopterans, Cry IV proteins demonstrate to dipterans, and Cry V and Cry VI proteins demonstrate to nematodes. New Cry proteins can be identified and assigned to a Cry group based on amino acid identity. See, for example, Bravo, A. (1997) *J. of Bacteriol.* 179:2793-2801; Bravo *et al.* (2013) *Microb. Biotechnol.* 6:17-26, herein incorporated by reference.

[0024] Over 750 different *cry* gene sequences have been classified into 73 groups (Cry1–Cry73), with new members of this gene family continuing to be discovered (Crickmore *et al.* (2014) www.btnomenclature.info/). The *cry* gene family consists of several phylogentically non-related protein families that may have different modes of action: the family of three-domain Cry toxins, the family of mosquitocidal Cry toxins, the family of the binary-like toxins, and the Cyt family of toxins (Bravo et al., 2005). Some Bt strains produce additional insecticidal toxins called VIP toxins. See, also, Cohen *et al.* (2011) *J. Mol. Biol.* 413:4-814; Crickmore *et al.* (2014) *Bacillus thuringiensis* toxin nomenclature, found on the World Wide Web at lifesci.sussex.ac.uk/home/Neil_Crickmore/Bt/; Crickmore *et al.* (1988) *Microbiol. Mol. Biol. Rev.* 62: 807-813; Gill *et al.* (1992) *Ann. Rev. Entomol.* 37: 807-636; Goldbert *et al.* (1997) *Appl. Environ. Microbiol.* 63:2716-2712; Knowles *et al.* (1992) *Proc. R. Soc. Ser. B.* 248: 1-7; Koni *et al.* (1994) *Microbiology* 140: 1869-1880; Lailak *et al.* (2013) *Biochem. Biophys. Res. Commun.* 435: 216-221; Lopez-Diaz *et al.* (2013) *Environ. Microbiol.* 15: 3030-3039; Perez *et al. (*2007) *Cell. Microbiol.* 9: 2931-2937; Promdonkoy *et al.* (2003) *Biochem. J.* 374: 255-259;Rigden (2009) *FEBS Lett.* 583: 1555-1560; Schnepf *et al.* (1998) *Microbiol. Mol. Biol. Rev.* 62: 775-806; Soberon *et al.* (2013) *Peptides* 41: 87-93; Thiery *et al.* (1998) *J. Am. Mosq. Control Assoc.* 14: 472-476; Thomas *et al.* (1983) FEBS Lett. 154: 362-368; Wirth *et al.* (1997) *Proc. Natl. Acad. Sci.* U.S.A. 94: 10536-10540; Wirth *et al* (2005) *Appl. Environ. Microbiol.* 71: 185-189; and, Zhang *et al.* (2006) *Biosci. Biotechnol. Biochem.* 70: 2199-2204; each of which is herein incorporated by reference in their entirety.

[0025] Cyt designates a parasporal crystal inclusion protein from *Bacillus thuringiensis* with cytolytic activity, or a protein with sequence similarity to a known Cyt protein. (Crickmore *et al.*

(1998) *Microbiol. Mol. Biol. Rev.* 62: 807-813). The gene is denoted by *cyt*. These proteins are different in structure and activity from Cry proteins (Gill *et al.* (1992) *Annu. Rev. Entomol.* 37: 615-636). The Cyt toxins were first discovered in *B. thuringiensis* subspecies *israelensis* (Goldberg *et al.* (1977) *Mosq. News.* 37: 355-358). There are 3 Cyt toxin families including 11 holotype toxins in the current nomenclature (Crickmore *et al.* (2014) *Bacillus thuringiensis* toxin nomenclature found on the World Wide Web at lifesci.sussex.ac.uk/home/Neil_Crickmore/Bt/). The majority of the *B. thuringiensis* isolates with *cyt* genes show activity against dipteran insects (particularly mosquitoes and black flies), but there are also *cyt* genes that have been described in *B. thuringiensis* strains targeting lepidopteran or coleopteran insects (Guerchicoff *et al.* (1997) *Appl. Environ. Microbiol.* 63: 2716-2721).

[0026] The structure of Cyt2A, solved by X-ray crystallography, shows a single domain where two outer layers of α-helix wrap around a mixed β-sheet. Further available crystal structures of Cyt toxins support a conserved α-β structural model with two α-helix hairpins flanking a β-sheet core containing seven to eight β-strands. (Cohen *et al.* (2011) *J. Mol. Biol.* 413: 80 4-814) Mutagenic studies identified β-sheet residues as critical for toxicity, while mutations in the helical domains did not affect toxicity (Adang *et al.*; Diversity of *Bacillus thuringiensis* Crystal Toxins and Mechanism of Action. In: T. S. Dhadialla and S. S. Gill, eds, *Advances in Insect Physiology, Vol. 47*, Oxford: Academic Press, 2014, pp. 39-87.) The representative domain of the Cyt toxin is a δ-endotoxin, Bac_thur_toxin (Pfam PF01338).

[0027] There are multiple proposed models for the mode of action of Cyt toxins, and it is still an area of active investigation. Some Cyt proteins (Cyt1A) have been shown to require the presence of accessory proteins for crystallization. Cyt1A and Cyt2A protoxins are processed by digestive proteases at the same sites in the N- and C-termini to a stable toxin core. Cyt toxins then interact with non-saturated membrane lipids, such as phosphatidylcholine, phosphatidylethanolamine, and sphingomyelin. For Cyt toxins, pore-formation and detergent-like membrane disruption have been proposed as non-exclusive mechanisms; and it is generally accepted that both may occur depending on toxin concentration, with lower concentrations favoring oligomeric pores and higher concentrations leading to membrane breaks. (Butko (2003) *Appl. Environ. Microbiol.* 69: 2415-2422) In the pore-formation model, the Cyt toxin binds to the cell membrane, inducing the formation of cation-selective channels in the membrane vesicles

leading to colloid-osmotic lysis of the cell. (Knowles *et al.* (1989) FEBS Lett. 244: 259-262; Knowles *et al.* (1992) *Proc. R. Soc. Ser. B.* 248: 1-7 and Promdonkoy *et al.* (2003) *Biochem. J.* 374: 255-259). In the detergent model, there is a nonspecific aggregation of the toxin on the surface of the lipid bilayer leading to membrane disassembly and cell death. (Butko (2003) *supra*; Manceva *et al.* (2005) *Biochem.* 44: 589-597).

[0028] Multiple studies have shown synergistic activity between Cyt toxins and other *B. thuringiensis* toxins, particularly the Cry, Bin, and Mtx toxins. This synergism has even been shown to overcome an insect's resistance to the other toxin. (Wirth 1997, Wirth 2005, Thiery 1998, Zhang 2006) The Cyt synergistic effect for Cry toxins is proposed to involve Cyt1A binding to domain II of Cry toxins in solution or on the membrane plane to promote formation of a Cry toxin pre-pore oligomer. Formation of this oligomer is independent of the Cyt oligomerization, binding or insertion. (Lailak 2013, Perez 2007, Lopez-Diaz 2013)

[0029] A number of pesticidal proteins unrelated to the Cry proteins are produced by some strains of *B. thuringiensis* and *B. cereus* during vegetative growth (Estruch *et al.* (1996) *Proc Natl Acad Sci USA* 93:5389–5394; Warren *et al.* (1994) WO 94/21795). These vegetative insecticidal proteins, or Vips, do not form parasporal crystal proteins and are apparently secreted from the cell. The Vips are presently excluded from the Cry protein nomenclature because they are not crystal-forming proteins. The term VIP is a misnomer in the sense that some *B. thuringiensis* Cry proteins are also produced during vegetative growth as well as during the stationary and sporulation phases, most notably Cry3Aa. The location of the Vip genes in the *B. thuringiensis* genome has been reported to reside on large plasmids that also encode cry genes (Mesrati *et al.* (2005) *FEMS Microbiol. Lett.* 244(2):353-8). A web-site for the nomenclature of Bt toxins can be found on the World Wide Web at lifesci.sussex.ac.uk with the path "/home/Neil_Crickmore/Bt/" and at: "btnomenclature.info/". See also, Schnepf *et al.* (1998) *Microbiol. Mol. Biol. Rev.* 62(3):775-806. Such references are herein incorporated by reference.

[0030] To date four categories of Vips have been identified. Some Vip genes form binary two-component protein complexes; an "A" component is usually the "active" portion, and a "B" component is usually the "binding" portion. (Pfam _pfam.xfam.org/family/PF03495.) The Vip1 and Vip4 proteins generally contain binary toxin B protein domains. Vip2 proteins generally contain binary toxin A protein domains.

[0031] The Vip1 and Vip2 proteins are the two components of a binary toxin that exhibits toxicity to coleopterans. Vip1Aa1 and Vip2Aa1 are very active against corn rootworms, particularly *Diabrotica virgifera* and *Diabrotica longicornis* (Han *et al.* (1999) *Nat. Struct. Biol.* 6:932–936; Warren GW (1997) "Vegetative insecticidal proteins: novel proteins for control of corn pests" In: Carozzi NB, Koziel M (eds) *Advances in insect control, the role of transgenic plants*; Taylor & Francis Ltd, London, pp 109–21). The membrane-binding 95 kDa Vip1 multimer provides a pathway for the 52 kDa Vip2 ADP-ribosylase to enter the cytoplasm of target western corn rootworm cells (Warren (1997) *supra*). The NAD-dependent ADP-ribosyltransferase Vip2 likely modifies monomeric actin at Arg177 to block polymerization, leading to loss of the actin cytoskeleton and eventual cell death due to the rapid subunit exchange within actin filaments *in vivo* (Carlier M.F. (1990) *Adv. Biophys.* 26:51-73).

[0032] Like Cry toxins, activated Vip3A toxins are pore-forming proteins capable of making stable ion channels in the membrane (Lee *et al.* (2003) *Appl. Environ. Microbiol.* 69:4648–4657). Vip3 proteins are active against several major lepidopteran pests (Rang *et al.* (2005) *Appl. Environ. Microbiol.* 71(10):6276-6281; Bhalla *et al.* (2005) *FEMS Microbiol. Lett.* 243:467–472; Estruch *et al.* (1998) WO 9844137; Estruch *et al.* (1996) *Proc Natl Acad Sci USA* 93:5389–5394; Selvapandiyan *et al.* (2001) *Appl. Environ Microbiol.* 67:5855–5858; Yu *et al.* (1997) *Appl. Environ Microbiol.* 63:532–536). V ip3A is active against *Agrotis ipsilon, Spodoptera frugiperda, Spodoptera exigua, Heliothis virescens*, and *Helicoverpa zea* (Warren *et al.* (1996) WO 96/10083; Estruch *et al.* (1996) *Proc Natl Acad Sci USA* 93:5389–5394). Like Cry toxins, Vip3A proteins must be activated by proteases prior to recognition at the surface of the midgut epithelium of specific membrane proteins different from those recognized by Cry toxins.

[0033] The MTX family of toxin proteins is characterized by the presence of a conserved domain, ETX_MTX2 (pfam 03318). Members of this family share sequence homology with the mosquitocidal toxins Mtx2 and Mtx3 from *Bacillus sphaericus,* as well as with the epsilon toxin ETX from *Clostridium perfringens* (Cole *et al.* (2004) *Nat. Struct. Mol. Biol.* 11: 797-8; Thanabalu *et al.* (1996) *Gene* 170:85-9). The MTX-like proteins are structurally distinct from the three-domain Cry toxins, as they have an elongated and predominately β-sheet-based structure. However, similar to the three-domain toxins, the MTX-like proteins are thought to

form pores in the membranes of target cells (Adang *et al.* (2014) *supra*). Unlike the three-domain Cry proteins, the MTX-like proteins are much smaller in length, ranging from 267 amino acids (Cry23) to 340 amino acids (Cry15A).

[0034] To date, only 15 proteins belonging to the family of MTX-like toxins have been assigned Cry names, making this a relatively small class compared to the three-domain Cry family (Crickmore *et al.* (2014) *supra*; Adang *et al.* (2014) *supra*). The members of the MTX-like toxin family include Cry15, Cry23, Cry33, Cry38, Cry45, Cry46, Cry51, Cry60A, Cry60B, and Cry64. This family exhibits a range of insecticidal activity, including activity against insect pests of the Lepidopteran and Coleopteran orders. Some members of this family may form binary partnerships with other proteins, which may or may not be required for insecticidal activity.

[0035] Cry15 is a 34 kDA protein that was identified in *B. thuringiensis* serovar thompsoni HD542. Cry15 occurs naturally in a crystal together with an unrelated protein of approximately 40 kDa. The gene encoding Cry15 and its partner protein are arranged together in an operon. Cry15 alone has been shown to have activity against lepidopteran insect pests including *Manduca sexta*, *Cydia pomonella*, and *Pieris rapae,* with the presence of the 40 kDA protein having been shown to increase activity of Cry15 only against *C. pomonella* (Brown K. and Whiteley H. (1992) *J. Bacteriol.* 174:549-557; Naimov *et al.* (2008) *Appl. Environ. Microbiol.* 74:7145–7151). Further studies are needed to elucidate the function of the partner protein of Cry15. Similarly, Cry23 is a 29 kDA protein that has been shown to have activity against the coleopteran pests *Tribolium castaneum* and *Popillia japonica* together with its partner protein Cry37 (Donovan *et al.* (2000) U.S.Patent No. 6,063,756).

[0036] New members of the MTX-like family are continuing to be identified. An ETX_MTX toxin gene was recently identified in the genome of *Bacillus thuringiensis* serovar tolworthi strain Na205-3. This strain was found to be toxic against the lepidpoteran pest *Helicoverpa armigera*, and it also contained homologs of Cry1, Cry11, Vip1, Vip2, and Vip3 (Palma *et al.* (2014) *Genome Announc.* 2(2): e00187-14. Published online Mar 13, 2014 at doi: 10.1128/genomeA.00187-14; PMCID: PMC3953196). Because the MTX-like proteins have a unique domain structure relative to the three-domain Cry proteins, they are believed to possess a

unique mode of action, thereby making them a valuable tool in insect control and the fight against insect resistance.

[0037] Bacterial cells produce large numbers of toxins with diverse specificity against host and non-host organisms. Large families of binary toxins have been identified in numerous bacterial families, including toxins that have activity against insect pests. (Poopathi and Abidha (2010) *J. Physiol. Path.* 1(3): 22-38). *Lysinibacillus sphaericus* (*Ls*), formerly *Bacillus sphaericus*, (Ahmed *et al.* (2007) *Int. J. Syst. Evol. Microbiol.* 57:1117-1125) is well-known as an insect biocontrol strain. *Ls* produces several insecticidal proteins, including the highly potent binary complex BinA/BinB. This binary complex forms a parasporal crystal in *Ls* cells and has strong and specific activity against dipteran insects, specifically mosquitos. In some areas, insect resistance to existing *Ls* mosquitocidal strains has been reported. The discovery of new binary toxins with different target specificity or the ability to overcome insect resistance is of significant interest.

[0038] The *Ls* binary insecticidal protein complex contains two major polypeptides, a 42 kDa polypeptide and a 51 kDa polypeptide, designated BinA and BinB, respectively (Ahmed *et al.* (2007), *supra*). The two polypeptides act synergistically to confer toxicity to their targets. Mode of action involves binding of the proteins to receptors in the larval midgut. In some cases, the proteins are modified by protease digestion in the larval gut to produce activated forms. The BinB component is thought to be involved in binding, while the BinA component confers toxicity (Nielsen-LeRoux *et al.* (2001) *Appl. Environ. Microbiol.* 67(11):5049–5054). When cloned and expressed separately, the BinA component is toxic to mosquito larvae, while the BinB component is not. However, co-administration of the proteins markedly increases toxicity (Nielsen-LeRoux *et al.* (2001) *supra*).

[0039] A small number of Bin protein homologs have been described from bacterial sources. Priest *et al.* (1997) *Appl. Environ. Microbiol.* 63(4):1195-1198 describe a hybridization effort to identify new *Ls* strains, although most of the genes they identified encoded proteins identical to the known BinA/BinB proteins. The BinA protein contains a defined conserved domain known as the Toxin 10 superfamily domain. This toxin domain was originally defined by its presence in BinA and BinB. The two proteins both have the domain, although the sequence similarity

between BinA and BinB is limited in this region (<40%). The Cry49Aa protein, which also has insecticidal activity, also has this domain (described below).

[0040] The Cry48Aa/Cry49Aa binary toxin of Ls has the ability to kill *Culex quinquefasciatus* mosquito larvae. These proteins are in a protein structural class that has some similarity to the *B. thuringiensis* (Bt) Cry protein complex. The Cry34/Cry35 binary toxin of Bt is also known to kill insects, including Western corn rootworm, a significant pest of corn. Cry34, of which several variants have been identified, is a small (14 kDa) polypeptide, while Cry35 (also encoded by several variants) is a 44 kDa polypeptide. These proteins have some sequence homology with the BinA/BinB protein group and are thought to be evolutionarily related (Ellis *et a*l. (2002) *Appl. Environ. Microbiol.* 68(3):1137-1145).

[0041] Provided herein are pesticidal proteins from these classes of toxins. The pesticidal proteins are classified by their structure, homology to known toxins and/or their pesticidal specificity.

ii. Variants and Fragments of Pesticidal Proteins and Polynucleotides Encoding the Same

[0042] Pesticidal proteins or polypeptides of the invention include those set forth in SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159 and fragments and variants thereof. By "pesticidal toxin" or "pesticidal protein" or "pesticidal polypeptide" is intended a toxin or protein or polypeptide that has activity against one or more pests, including, insects, fungi, nematodes, and the like such that the pest is killed or controlled.

[0043] An "isolated" or "purified" polypeptide or protein, or biologically active portion thereof, is substantially or essentially free from components that normally accompany or interact with the polypeptide or protein as found in its naturally occurring environment. Thus, an isolated or purified polypeptide or protein is substantially free of other cellular material, or

culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. A protein that is substantially free of cellular material includes preparations of protein having less than about 30%, 20%, 10%, 5%, or 1% (by dry weight) of contaminating protein. When the protein of the invention or biologically active portion thereof is recombinantly produced, optimally culture medium represents less than about 30%, 20%, 10%, 5%, or 1% (by dry weight) of chemical precursors or non-protein-of-interest chemicals.

[0044] The term "fragment" refers to a portion of a polypeptide sequence of the invention. "Fragments" or "biologically active portions" include polypeptides comprising a sufficient number of contiguous amino acid residues to retain the biological activity (have pesticidal activity). Fragments of the pesticidal proteins include those that are shorter than the full-length sequences, either due to the use of an alternate downstream start site, or due to processing that produces a shorter protein having pesticidal activity. Processing may occur in the organism the protein is expressed in, or in the pest after ingestion of the protein. Examples of fragments of the proteins can be found in Table 1. A biologically active portion of a pesticidal protein can be a polypeptide that is, for example, 10, 25, 50, 100, 150, 200, 250 or more amino acids in length of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159. Such biologically active portions can be prepared by recombinant techniques and evaluated for pesticidal activity. As used here, a fragment comprises at least 8 contiguous amino acids of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135,

136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159.

[0045] Bacterial genes, including those encoding the pesticidal proteins disclosed herein, quite often possess multiple methionine initiation codons in proximity to the start of the open reading frame. Often, translation initiation at one or more of these start codons will lead to generation of a functional protein. These start codons can include ATG codons. However, bacteria such as *Bacillus sp.* also recognize the codon GTG as a start codon, and proteins that initiate translation at GTG codons contain a methionine at the first amino acid. On rare occasions, translation in bacterial systems can initiate at a TTG codon, though in this event the TTG encodes a methionine. Furthermore, it is not often determined *a priori* which of these codons are used naturally in the bacterium. Thus, it is understood that use of one of the alternate methionine codons may also lead to generation of pesticidal proteins. These pesticidal proteins are encompassed in the present invention and may be used in the methods disclosed herein. It will be understood that, when expressed in plants, it will be necessary to alter the alternate start codon to ATG for proper translation.

[0046] In various embodiments the pesticidal proteins provided herein include amino acid sequences deduced from the full-length nucleotide sequences and amino acid sequences that are shorter than the full-length sequences due to the use of an alternate downstream start site. Thus, the nucleotide sequence of the invention and/or vectors, host cells, and plants comprising the nucleotide sequence of the invention (and methods of making and using the nucleotide sequence of the invention) may comprise a nucleotide sequence encoding an alternate start site.

[0047] It is recognized that modifications may be made to the pesticidal polypeptides provided herein creating variant proteins. Changes designed by man may be introduced through the application of site-directed mutagenesis techniques. Alternatively, native, as yet-unknown or as yet unidentified polynucleotides and/or polypeptides structurally and/or functionally-related to the sequences disclosed herein may also be identified that fall within the scope of the present invention. Conservative amino acid substitutions may be made in non-conserved regions that do not alter the function of the pesticidal proteins. Alternatively, modifications may be made that improve the activity of the toxin. For example, various Cry protein variants are contemplated. Modification of Cry toxins by domain III swapping has resulted in some cases in hybrid toxins

with improved toxicities against certain insect species. Thus, domain III swapping could be an effective strategy to improve toxicity of Cry toxins or to create novel hybrid toxins with toxicity against pests that show no susceptibility to the parental Cry toxins. Site-directed mutagenesis of domain II loop sequences may result in new toxins with increased insecticidal activity. Domain II loop regions are key binding regions of initial Cry toxins that are suitable targets for the mutagenesis and selection of Cry toxins with improved insecticidal properties. Domain I of the Cry toxin may be modified to introduce protease cleavage sites to improve activity against certain pests. Strategies for shuffling the three different domains among large numbers of *cry* genes and high through output bioassay screening methods may provide novel Cry toxins with improved or novel toxicities.

[0048] As indicated, fragments and variants of the polypeptides disclosed herein will retain pesticidal activity Pesticidal activity comprises the ability of the composition to achieve an observable effect diminishing the occurrence or an activity of the target pest, including for example, bringing about death of at least one pest, or a noticeable reduction in pest growth, feeding, or normal physiological development. Such decreases in numbers, pest growth, feeding or normal development can comprise any statistically significant decrease, including, for example a decrease of about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 85%, 90%, 95% or greater. The pesticidal activity against one or more of the various pests provided herein, including, for example, pesticidal activity against *Coleoptera, Diptera, Hymenoptera, Lepidoptera, Mallophaga, Homoptera, Hemiptera, Orthroptera, Nematodes, Thysanoptera, Dermaptera, Isoptera, Anoplura, Siphonaptera, Trichoptera,* etc., or any other pest described herein. It is recognized that the pesticidal activity may be different or improved relative to the activity of the native protein, or it may be unchanged, so long as pesticidal activity is retained. Methods for measuring pesticidal activity are provide elsewhere herein. See also, Czapla and Lang (1990) *J. Econ. Entomol.* 83:2480-2485; Andrews *et al.* (1988) *Biochem. J.* 252:199-206; Marrone *et al.* (1985) *J. of Economic Entomology* 78:290-293; and U.S. Pat. No. 5,743,477, all of which are herein incorporated by reference in their entirety.

[0049] Variants of this disclosure include polypeptides having an amino acid sequence that is at least about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about

95%, about 96%, about 97%, about 98% or about 99% identical to the amino acid sequence of any of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159 and retain pesticidal activity. Table 1 provides non-limiting examples of variant polypeptides (and polynucleotide encoding the same) for each of SEQ ID NOS: 1-159. A biologically active variant of a pesticidal polypeptide provided herein may differ by as few as about 1-15 amino acid residues, as few as about 1-10, such as about 6-10, as few as 5, as few as 4, as few as 3, as few as 2, or as few as 1 amino acid residue. In specific embodiments, the polypeptides can comprise an N'-terminal or a C'-terminal truncation, which can comprise at least a deletion of 10, 15, 20, 25, 30, 35, 40, 45, 50 amino acids or more from either the N' or C' terminal end of the polypeptide.

[0050] Table 2 provides protein domains found in SEQ ID NOs: 1-159 based on PFAM data. Both the domain description and the positions within a given SEQ ID NO are provided in Table 2. In specific embodiments, the active variant comprising any one of SEQ ID NOs: 1-159 can comprise at least 70%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to any one of SEQ ID NOs: 1-159 and further comprises at least one of the conserved domain set forth in Table 2. For example, in one embodiment, the active variant will comprise at least 70%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NO:15, and further comprises the native amino acids at positions 78-329, the native amino acids at positions 554-708, or the native amino acids at positions 78-329 and positions 554-708.

Table 2. Summary of PFAM domains in each of SEQ ID NOs: 1-159

APG ID	SEQ ID NO	Modification Type	PFAM domain	Domain Description	Domain positions	
					Start	Stop

APG ID	SEQ ID NO	Modification Type	PFAM domain	Domain Description	Domain positions	
					Start	Stop
APG00002	SEQ ID NO:1		PF03945	Endotoxin N	141	398
			PF03944	Endotoxin C	623	778
APG00002 modified	SEQ ID NO:2	3' Truncation	PF03945	Endotoxin N	141	398
			PF03944	Endotoxin C	623	777
APG00005	SEQ ID NO:4		PF03945	Endotoxin N	69	297
			PF03944	Endotoxin C	515	657
APG00005 modified	SEQ ID NO:5	3' Truncation	PF03945	Endotoxin N	69	297
			PF03944	Endotoxin C	515	657
APG00010	SEQ ID NO:8		PF03318	ETX MTX2	33	300
APG00010 modified	SEQ ID NO:9	Signal Peptide removed	PF03318	ETX MTX2	15	274
APG00027	SEQ ID NO:10		PF03945	Endotoxin N	96	347
			PF03944	Endotoxin C	527	662
APG00027 modified	SEQ ID NO:11	Signal Peptide removed	PF03945	Endotoxin N	66	317
			PF03944	Endotoxin C	497	632
APG00027 modified	SEQ ID NO:12	3' Truncation	PF03945	Endotoxin N	96	347
			PF03944	Endotoxin C	527	661
APG00027 modified	SEQ ID NO:13	Signal Peptide removed and 3' Truncation	PF03945	Endotoxin N	65	317
			PF03944	Endotoxin C	497	631
APG00034	SEQ ID NO:14		PF03945	Endotoxin N	78	329
			PF03944	Endotoxin C	554	709
APG00034 modified	SEQ ID NO:15	3' Truncation	PF03945	Endotoxin N	78	329
			PF03944	Endotoxin C	554	708
APG00039	SEQ ID NO:16		PF03945	Endotoxin N	82	305
			PF00555	Endotoxin M	310	516
			PF03944	Endotoxin C	526	659
			PF14200	Ricin B Lectin 2	694	794
APG00039 modified	SEQ ID NO:17	Alternate start	PF03945	Endotoxin N	79	302
			PF00555	Endotoxin M	307	513
			PF03944	Endotoxin C	523	656
			PF14200	Ricin B Lectin 2	691	791
APG00039 modified	SEQ ID NO:18	3' Truncation	PF03945	Endotoxin N	82	305
			PF00555	Endotoxin M	310	516
			PF03944	Endotoxin C	526	658
APG00039 modified	SEQ ID NO:19	Alternate start and 3' Truncation	PF03945	Endotoxin N	79	302
			PF00555	Endotoxin M	307	513
			PF03944	Endotoxin C	523	655
APG00046	SEQ ID NO:20		PF03945	Endotoxin N	59	292
			PF00555	Endotoxin M	297	508
			PF03944	Endotoxin C	518	648

APG ID	SEQ ID NO	Modification Type	PFAM domain	Domain Description	Domain positions	
					Start	Stop
			PF14200	Ricin B Lectin 2	686	788
APG00046 modified	SEQ ID NO:21	3' Truncation	PF03945	Endotoxin N	59	292
			PF00555	Endotoxin M	297	508
			PF03944	Endotoxin C	518	647
APG00048	SEQ ID NO:22		PF03945	Endotoxin N	93	343
			PF00555	Endotoxin M	348	546
			PF03944	Endotoxin C	559	711
APG00048 modified	SEQ ID NO:23	3' Truncation	PF03945	Endotoxin N	93	343
			PF00555	Endotoxin M	348	546
			PF03944	Endotoxin C	559	710
APG00048 CryBP1	SEQ ID NO:24		PF07029	CryBP1	49	209
APG00052	SEQ ID NO:25		PF03945	Endotoxin N	62	315
			PF00555	Endotoxin M	320	520
			PF03944	Endotoxin C	533	677
APG00052 modified	SEQ ID NO:26	3' Truncation	PF03945	Endotoxin N	62	315
			PF00555	Endotoxin M	320	520
			PF03944	Endotoxin C	533	676
APG00059	SEQ ID NO:27		PF03945	Endotoxin N	67	288
			PF00555	Endotoxin M	293	502
			PF03944	Endotoxin C	512	652
APG00059 modified	SEQ ID NO:28	3' Truncation	PF03945	Endotoxin N	67	288
			PF00555	Endotoxin M	293	502
			PF03944	Endotoxin C	512	651
APG00062	SEQ ID NO:29		PF03945	Endotoxin N	60	310
			PF03944	Endotoxin C	516	650
APG00062 modified	SEQ ID NO:30	3' Truncation	PF03945	Endotoxin N	60	310
			PF03944	Endotoxin C	516	649
APG00065	SEQ ID NO:31		PF05431	Toxin 10	209	402
APG00065 modified	SEQ ID NO:32	Signal Peptide removed	PF05431	Toxin 10	171	364
APG00066	SEQ ID NO:33		PF03945	Endotoxin N	91	325
			PF00555	Endotoxin M	333	532
			PF03944	Endotoxin C	552	715
APG00066 modified	SEQ ID NO:34	3' Truncation	PF03945	Endotoxin N	91	325
			PF00555	Endotoxin M	333	532
			PF03944	Endotoxin C	552	714
APG00068	SEQ ID NO:35		PF03945	Endotoxin N	63	302
			PF00555	Endotoxin M	307	518
			PF03944	Endotoxin C	528	668
APG00068	SEQ ID	3' Truncation	PF03945	Endotoxin N	63	302

APG ID	SEQ ID NO	Modification Type	PFAM domain	Domain Description	Domain positions	
					Start	Stop
modified	NO:36		PF00555	Endotoxin M	307	518
			PF03944	Endotoxin C	528	667
APG00070	SEQ ID NO:37		PF03945	Endotoxin N	63	286
			PF03944	Endotoxin C	460	597
APG00070 modified	SEQ ID NO:38	3' Truncation	PF03945	Endotoxin N	63	286
			PF03944	Endotoxin C	460	596
APG00072	SEQ ID NO:39		PF03945	Endotoxin N	1	111
APG00075	SEQ ID NO:40		PF05431	Toxin 10	279	474
APG00076	SEQ ID NO:41		PF03945	Endotoxin N	78	335
			PF00555	Endotoxin M	340	532
			PF03944	Endotoxin C	542	682
APG00076 modified	SEQ ID NO:42	3' Truncation	PF03945	Endotoxin N	78	335
			PF00555	Endotoxin M	340	532
			PF03944	Endotoxin C	542	681
APG00079	SEQ ID NO:43		PF03945	Endotoxin N	61	284
			PF00555	Endotoxin M	289	495
			PF03944	Endotoxin C	505	633
APG00079 modified	SEQ ID NO:44	3' Truncation	PF03945	Endotoxin N	61	284
			PF00555	Endotoxin M	289	495
			PF03944	Endotoxin C	505	632
APG00085	SEQ ID NO:45		PF03945	Endotoxin N	90	312
			PF00555	Endotoxin M	317	528
			PF03944	Endotoxin C	538	676
			PF14200	Ricin B Lectin 2	715	823
APG00085 modified	SEQ ID NO:46	3' Truncation	PF03945	Endotoxin N	90	312
			PF00555	Endotoxin M	317	528
			PF03944	Endotoxin C	538	675
APG00087	SEQ ID NO:47		PF03945	Endotoxin N	40	276
			PF00555	Endotoxin M	281	472
			PF03944	Endotoxin C	482	619
APG00087 modified	SEQ ID NO:48	3' Truncation	PF03945	Endotoxin N	40	276
			PF00555	Endotoxin M	281	472
			PF03944	Endotoxin C	482	618
APG00090	SEQ ID NO:49		PF00652	Ricin B Lectin	38	165
			PF05431	Toxin 10	175	373
APG00094	SEQ ID NO:50		PF03945	Endotoxin N	68	318
			PF00555	Endotoxin M	325	432
			PF03944	Endotoxin C	524	660
APG00094 modified	SEQ ID NO:51	3' Truncation	PF03945	Endotoxin N	68	318
			PF00555	Endotoxin M	325	432

APG ID	SEQ ID NO	Modification Type	PFAM domain	Domain Description	Domain positions	
					Start	Stop
			PF03944	Endotoxin C	524	659
APG00095	SEQ ID NO:52		PF05431	Toxin 10	192	383
APG00097	SEQ ID NO:53		PF03945	Endotoxin N	87	345
			PF03944	Endotoxin C	576	736
APG00097 modified	SEQ ID NO:54	3' Truncation	PF03945	Endotoxin N	87	345
			PF03944	Endotoxin C	576	735
APG00099	SEQ ID NO:55		PF03945	Endotoxin N	67	318
			PF03944	Endotoxin C	529	671
APG00099 modified	SEQ ID NO:56	3' Truncation	PF03945	Endotoxin N	67	318
			PF03944	Endotoxin C	529	670
APG00101	SEQ ID NO:57		PF03945	Endotoxin N	78	329
			PF03944	Endotoxin C	557	701
APG00101 modified	SEQ ID NO:58	3' Truncation	PF03945	Endotoxin N	78	329
			PF03944	Endotoxin C	557	700
APG00104	SEQ ID NO:59		PF12495	Vip3A N	16	188
			PF02018	CBM 4 9	544	669
APG00110	SEQ ID NO:60		PF03945	Endotoxin N	90	325
			PF03944	Endotoxin C	512	645
			PF01473	CW binding 1	723	740
			PF01473	CW binding 1	752	769
			PF01473	CW binding 1	802	816
APG00110 modified	SEQ ID NO:61	Signal Peptide removed	PF03945	Endotoxin N	60	295
			PF03944	Endotoxin C	482	615
			PF01473	CW binding 1	693	710
			PF01473	CW binding 1	722	739
			PF01473	CW binding 1	772	786
APG00110 modified	SEQ ID NO:62	3' Truncation	PF03945	Endotoxin N	90	325
			PF03944	Endotoxin C	512	642
APG00110 modified	SEQ ID NO:63	Signal Peptide removed and 3' Truncation	PF03945	Endotoxin N	60	295
			PF03944	Endotoxin C	482	612
APG00114	SEQ ID NO:64		PF03945	Endotoxin N	54	301
			PF00030	Crystall	730	810
APG00115	SEQ ID NO:65		PF03945	Endotoxin N	71	283
			PF03945	Endotoxin N	301	361
			PF00555	Endotoxin M	366	584
			PF03944	Endotoxin C	594	726
APG00115 modified	SEQ ID NO:66	3' Truncation	PF03945	Endotoxin N	71	283
			PF03945	Endotoxin N	299	361
			PF00555	Endotoxin M	366	584
			PF03944	Endotoxin C	594	725

APG ID	SEQ ID NO	Modification Type	PFAM domain	Domain Description	Domain positions	
					Start	Stop
APG00115 CryBP1	SEQ ID NO:67		PF07029	CryBP1	74	129
APG00120	SEQ ID NO:68		PF03945	Endotoxin N	72	281
			PF03945	Endotoxin N	311	351
			PF00555	Endotoxin M	358	564
			PF03944	Endotoxin C	574	713
APG00120 modified	SEQ ID NO:69	3' Truncation	PF03945	Endotoxin N	72	281
			PF03945	Endotoxin N	311	351
			PF00555	Endotoxin M	358	564
			PF03944	Endotoxin C	574	712
APG00124	SEQ ID NO:70		PF03945	Endotoxin N	61	289
			PF00555	Endotoxin M	294	523
			PF03944	Endotoxin C	533	670
APG00124 modified	SEQ ID NO:71	3' Truncation	PF03945	Endotoxin N	61	289
			PF00555	Endotoxin M	294	523
			PF03944	Endotoxin C	533	669
APG00130	SEQ ID NO:72		PF03945	Endotoxin N	68	320
			PF00555	Endotoxin M	327	512
			PF03944	Endotoxin C	522	662
APG00130 CryBP1	SEQ ID NO:73		PF07029	CryBP1	39	196
APG00130 Split-Cry C-term	SEQ ID NO:74		-			
APG00136	SEQ ID NO:75		PF03945	Endotoxin N	37	270
			PF03945	Endotoxin N	299	346
			PF03944	Endotoxin C	592	729
APG00136 modified	SEQ ID NO:76	3' Truncation	PF03945	Endotoxin N	37	270
			PF03945	Endotoxin N	299	346
			PF03944	Endotoxin C	592	728
APG00136 Split-Cry C-term	SEQ ID NO:77		*no PFAM domains*			
APG00140	SEQ ID NO:78		PF03945	Endotoxin N	63	313
			PF00555	Endotoxin M	320	510
			PF03944	Endotoxin C	520	657
			PF14200	Ricin B Lectin 2	703	802
APG00140 modified	SEQ ID NO:79	3' Truncation	PF03945	Endotoxin N	63	313
			PF00555	Endotoxin M	320	510
			PF03944	Endotoxin C	520	656

APG ID	SEQ ID NO	Modification Type	PFAM domain	Domain Description	Domain positions	
					Start	Stop
APG00140 Split-Cry C-term	SEQ ID NO:80		*no PFAM domains*			
APG00144	SEQ ID NO:81		PF05431	Toxin 10	139	345
APG00162	SEQ ID NO:82		PF03945	Endotoxin N	87	330
			PF00555	Endotoxin M	335	533
			PF03944	Endotoxin C	543	689
APG00162 modified	SEQ ID NO:83	3' Truncation	PF03945	Endotoxin N	87	330
			PF00555	Endotoxin M	335	533
			PF03944	Endotoxin C	543	688
APG00183	SEQ ID NO:84		PF05431	Toxin 10	159	357
APG00195	SEQ ID NO:85		PF03945	Endotoxin N	207	368
			PF03944	Endotoxin C	577	719
APG00195 modified	SEQ ID NO:86	Signal Peptide removed	PF03945	Endotoxin N	166	331
			PF03944	Endotoxin C	540	682
APG00195 modified	SEQ ID NO:87	3' Truncation	PF03945	Endotoxin N	210	368
			PF03944	Endotoxin C	577	718
APG00195 modified	SEQ ID NO:88	Signal Peptide removed and 3' Truncation	PF03945	Endotoxin N	174	331
			PF03944	Endotoxin C	540	681
APG00204	SEQ ID NO:89		PF03945	Endotoxin N	57	289
			PF00555	Endotoxin M	294	493
			PF03944	Endotoxin C	503	632
APG00204 modified	SEQ ID NO:90	3' Truncation	PF03945	Endotoxin N	57	289
			PF00555	Endotoxin M	294	493
			PF03944	Endotoxin C	503	631
APG00204 Split-Cry C-term	SEQ ID NO:91		*no PFAM domains*			
APG00076 modified	SEQ ID NO:92	Alternate start	PF03945	Endotoxin N	69	326
			PF00555	Endotoxin M	331	523
			PF03944	Endotoxin C	533	673
APG00076 modified	SEQ ID NO:93	Alternate start and 3' Truncation	PF03945	Endotoxin N	69	326
			PF00555	Endotoxin M	331	523
			PF03944	Endotoxin C	533	672
APG00130 modified	SEQ ID NO:94	Alternate start	PF03945	Endotoxin N	63	315
			PF00555	Endotoxin M	322	507
			PF03944	Endotoxin C	517	657
APG00002 modified	SEQ ID NO:95	Alternate start	PF03945	Endotoxin N	76	333
			PF03944	Endotoxin C	558	713

APG ID	SEQ ID NO	Modification Type	PFAM domain	Domain Description	Domain positions	
					Start	Stop
APG00002 modified	SEQ ID NO:96	Alternate start and 3' Truncation	PF03945	Endotoxin N	76	333
			PF03944	Endotoxin C	558	712
APG00046 modified	SEQ ID NO:97	Alternate start	PF03945	Endotoxin N	56	289
			PF00555	Endotoxin M	294	505
			PF03944	Endotoxin C	515	645
			PF14200	Ricin B Lectin 2	683	785
APG00046 modified	SEQ ID NO:98	Alternate start and 3' Truncation	PF03945	Endotoxin N	56	289
			PF00555	Endotoxin M	294	505
			PF03944	Endotoxin C	515	644
APG00048 modified	SEQ ID NO:99	Alternate start	PF03945	Endotoxin N	78	328
			PF00555	Endotoxin M	333	531
			PF03944	Endotoxin C	544	696
APG00048 modified	SEQ ID NO:100	Alternate start and 3' Truncation	PF03945	Endotoxin N	78	328
			PF00555	Endotoxin M	333	531
			PF03944	Endotoxin C	544	696
APG00059 modified	SEQ ID NO:101	Alternate start	PF03945	Endotoxin N	61	282
			PF00555	Endotoxin M	287	496
			PF03944	Endotoxin C	506	646
APG00059 modified	SEQ ID NO:102	Alternate start and 3' Truncation	PF03945	Endotoxin N	61	282
			PF00555	Endotoxin M	287	496
			PF03944	Endotoxin C	506	645
APG00066 modified	SEQ ID NO:103	Alternate start	PF03945	Endotoxin N	74	308
			PF00555	Endotoxin M	316	515
			PF03944	Endotoxin C	535	698
APG00075 modified	SEQ ID NO:104	Alternate start	PF05431	Toxin 10	276	471
APG00085 modified	SEQ ID NO:105	Alternate start	PF03945	Endotoxin N	71	293
			PF00555	Endotoxin M	298	509
			PF03944	Endotoxin C	519	657
			PF14200	Ricin B Lectin 2	696	804
APG00085 modified	SEQ ID NO:106	Alternate start and 3' Truncation	PF03945	Endotoxin N	71	293
			PF00555	Endotoxin M	298	509
			PF03944	Endotoxin C	519	656
APG00087 modified	SEQ ID NO:107	Alternate start	PF03945	Endotoxin N	29	265
			PF00555	Endotoxin M	270	461
			PF03944	Endotoxin C	471	608
APG00090 modified	SEQ ID NO:108	Alternate start	PF00652	Ricin B Lectin	37	164
			PF05431	Toxin 10	174	372
APG00094 modified	SEQ ID NO:109	Alternate start	PF03945	Endotoxin N	44	294
			PF00555	Endotoxin M	301	408
			PF03944	Endotoxin C	500	636

APG ID	SEQ ID NO	Modification Type	PFAM domain	Domain Description	Domain positions	
					Start	Stop
APG00094 modified	SEQ ID NO:110	Alternate start and 3' Truncation	PF03945	Endotoxin N	44	294
			PF00555	Endotoxin M	301	408
			PF03944	Endotoxin C	500	635
APG00097 modified	SEQ ID NO:111	Alternate start	PF03945	Endotoxin N	72	330
			PF03944	Endotoxin C	561	721
APG00097 modified	SEQ ID NO:112	Alternate start and 3' Truncation	PF03945	Endotoxin N	72	330
			PF03944	Endotoxin C	561	720
APG00104 modified	SEQ ID NO:113	Alternate start	PF12495	Vip3A N	14	186
			PF02018	CBM 4 9	542	667
APG00114 modified	SEQ ID NO:114	Alternate start	PF03945	Endotoxin N	51	298
			PF00030	Crystall	727	807
APG00115 modified	SEQ ID NO:115	Alternate start	PF03945	Endotoxin N	66	278
			PF03945	Endotoxin N	296	356
			PF00555	Endotoxin M	361	579
			PF03944	Endotoxin C	589	721
APG00115 modified	SEQ ID NO:116	Alternate start and 3' Truncation	PF03945	Endotoxin N	66	278
			PF03945	Endotoxin N	294	356
			PF00555	Endotoxin M	361	579
			PF03944	Endotoxin C	589	720
APG00120 modified	SEQ ID NO:117	Alternate start	PF03945	Endotoxin N	61	270
			PF03945	Endotoxin N	300	340
			PF00555	Endotoxin M	347	553
			PF03944	Endotoxin C	563	702
APG00120 modified	SEQ ID NO:118	Alternate start and 3' Truncation	PF03945	Endotoxin N	61	270
			PF03945	Endotoxin N	300	340
			PF00555	Endotoxin M	347	553
			PF03944	Endotoxin C	563	701
APG00162 modified	SEQ ID NO:119	Alternate start	PF03945	Endotoxin N	73	316
			PF00555	Endotoxin M	321	519
			PF03944	Endotoxin C	529	675
APG00162 modified	SEQ ID NO:120	Alternate start and 3' Truncation	PF03945	Endotoxin N	73	316
			PF00555	Endotoxin M	321	519
			PF03944	Endotoxin C	529	674
APG00204 modified	SEQ ID NO:121	Alternate start	PF03945	Endotoxin N	54	286
			PF00555	Endotoxin M	291	490
			PF03944	Endotoxin C	500	629
APG00204 modified	SEQ ID NO:122	Alternate start and 3' Truncation	PF03945	Endotoxin N	54	286
			PF00555	Endotoxin M	291	490
			PF03944	Endotoxin C	500	628
APG00489	SEQ ID NO:123		PF03318	ETX MTX2	33	298

APG ID	SEQ ID NO	Modification Type	PFAM domain	Domain Description	Domain positions	
					Start	Stop
APG00489 modified	SEQ ID NO:124	Signal Peptide removed	PF03318	ETX MTX2	16	272
APG00497	SEQ ID NO:125		PF03945	Endotoxin N	62	315
			PF00555	Endotoxin M	320	520
			PF03944	Endotoxin C	533	677
APG00497 modified	SEQ ID NO:126	3' Truncation	PF03945	Endotoxin N	62	315
			PF00555	Endotoxin M	320	520
			PF03944	Endotoxin C	533	676
APG00511	SEQ ID NO:127		PF03945	Endotoxin N	68	320
			PF00555	Endotoxin M	327	512
			PF03944	Endotoxin C	522	662
APG00511 modified	SEQ ID NO:128	Alternate start	PF03945	Endotoxin N	63	315
			PF00555	Endotoxin M	322	507
			PF03944	Endotoxin C	517	657
APG00520	SEQ ID NO:129		PF03945	Endotoxin N	61	289
			PF00555	Endotoxin M	294	523
			PF03944	Endotoxin C	533	670
APG00520 modified	SEQ ID NO:130	3' Truncation	PF03945	Endotoxin N	61	289
			PF00555	Endotoxin M	294	523
			PF03944	Endotoxin C	533	669
APG00544	SEQ ID NO:131		PF03945	Endotoxin N	61	289
			PF00555	Endotoxin M	294	523
			PF03944	Endotoxin C	533	670

[0051] Variants of SEQ ID NO: 8 comprise SEQ ID NOs: 9, 123 and 124. Figure 1 provides an amino acid sequence alignment of SEQ ID NOS: 8, 9, 123 and 124, and Table 3 provides a summary of the type of modification and percent sequence identity SEQ ID NOs: 9, 123 and 124 share with SEQ ID NO: 8.

[0052] Variants of SEQ ID NO: 25 comprise SEQ ID NOs: 26, 125 and 126. Figure 2 provides an amino acid sequence alignment of SEQ ID NOs: 25, 26, 125 and 126, and Table 3 provides a summary of the type of modification and percent sequence identity SEQ ID NOs: 26, 125 and 126 share with SEQ ID NO: 25.

[0053] Variants of SEQ ID NO: 72 comprise SEQ ID NOs: 94, 127 and 128. Figure 3 provides an amino acid sequence alignment of SEQ ID NOs: 72, 94, 127 and 128, and Table 3 provides a summary of the type of modification and percent sequence identity SEQ ID NOs: 94, 127 and 128 share with SEQ ID NO: 72.

[0054] Variants of SEQ ID NO: 70 comprise SEQ ID NOs: 71, 129, 130, and 131. Figure 4 provides an amino acid sequence alignment of SEQ ID NOs: 70, 71, 129, 130, and 131. Table 3 provides a summary of the type of modification and percent sequence identity SEQ ID NOs: 71, 129, 130, and 131 share with SEQ ID NO: 70.

Table 3. Summary of Variants for SEQ ID NOs: 8, 25, 72, and 70

Related Gene Family		**Gene Name**	**SEQ ID No.**	**Modification Type**	**% identity to SEQ ID NOs: 8, 25 and 72**
Gene Name	**SEQ ID No.**				
APG00010	8	APG00489	123		99.06
		APG00489 modified	124	Removed Signal Peptide	99.31
APG00052	25	APG00497	125		99.33
		APG00497 modified	126	3' Truncation	99.85
APG00130	72	APG00511	127		99.70
		APG00511 modified	128	Alternate start	99.70
APG00124	70	APG00520	129		99.90
		APG00520 modified	130	3' Truncation	99.85
		APG00544	131		99.80
APG00008	6	APG00573	132		86.71
		APG00573 modified	133	Alternate start	86.71
		APG00605	134		98.73
		APG00605 modified	135	Alternate start	98.58
		APG00620	136		98.58
		APG00620 modified	137	Alternate start	98.42
		APG00640	138		88.13
		APG00725	139		98.26
		APG00725 modified	140	Alternate start	98.10
		APG00730	141		99.68
		APG00730 modified	142	Alternate start	99.53

		APG00490	143		94.07
		APG00490 modified	144	Alternate start	93.86
		APG00512	145		94.30
		APG00512 modified	146	Alternate start	94.15
		APG00525	147		98.10
		APG00525 modified	148	Alternate start	97.94
		APG00539	149		86.87
		APG00539 modified	150	Alternate start	86.87
		APG00554	151		93.51
		APG00554 modified	152	Alternate start	93.35
		APG00567	153		99.84
		APG00567 modified	154	Alternate start	99.68
		APG00575	155		87.66
		APG00604	156		94.15
		APG00604 modified	157	Alternate start	93.99
		APG00621	158		95.09
		APG00621 modified	159	Alternate start	94.94

[0055] As noted in Figures 5A-5H, each of SEQ ID NOs: 6, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and 159 share common motifs as denoted below in Table 4. Figures 5A-5H indicate where each of the conserved sequences is found in each of SEQ ID NOs: 6 and 132-159.

Table 4. Conserved regions in SEQ ID NOs: 6 and 132-159

Conserved Sequence	SEQ ID NO:
ICSINGSAKFDPNTN	161
NSQAGAIAGKTA	162
IGSATGAANN	163
PLNYEPIGLKATD	164
VPVIDDGWENGDP	165
EDEENALNGKWVF	166
DKHVAIYKQVE	167

[0056] In specific embodiments, the active variant comprising SEQ ID NOs: 6 or 132-159 can comprise at least 70%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to any one of SEQ ID NOs: 6 and 132-159 and further comprises at least one of the conserved domains set forth in Table 4. For example, in one embodiment, the active variant will comprise at least 70%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NOs: 6 or 132-159, and further comprise one or more amino acid domains set forth in Table 4 (that is at least one of SEQ ID NOS: 161, 162, 163, 164, 165, 166, and/or 167). In a non-limiting embodiment, the active variant comprises at least 70%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NOs: 6 or 132-159, and further comprises SEQ ID NO: 166. In another embodiment, an active variant of SEQ ID NOs: 6 or 132-159 comprises a sequence having at least 70%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to SEQ ID NOs: 6 or 132-159, wherein the active variant is not SEQ ID NO: 160.

[0057] Figure 6 provides the percent sequence identity relationship between SEQ ID NOs: 6, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and 159.

[0058] Recombinant or synthetic nucleic acids encoding the pesticidal polypeptides disclosed herein are also provided. Of particular interest are nucleic acid sequences that have been designed for expression in a plant of interest. For example, the nucleic acid sequence can be optimized for increased expression in a host plant. A pesticidal protein as provided herein may be back-translated to produce a nucleic acid comprising codons optimized for expression in a particular host, for example, a crop plant.In another embodiment, the polynucleotides encoding the polypeptides provided herein may be optimized for increased expression in the transformed plant. For example, the polynucleotides can be synthesized using plant-preferred codons for improved expression. See, for example, Campbell and Gowri (1990) *Plant Physiol.* 92:1-11 for a discussion of host-preferred codon usage. Methods are available in the art for synthesizing plant-preferred genes. See, for example, U.S. Patent Nos. 5,380,831 and 5,436,391, and Murray

et al. (1989) *Nucleic Acids Res.* 17:477-498, each of which is herein incorporated by reference. Expression of such a coding sequence by the transformed plant (for example, dicot or monocot) will result in the production of a pesticidal polypeptide and confer increased resistance in the plant to a pest. Recombinant and synthetic nucleic acid molecules encoding the pesticidal proteins of the invention do not include the naturally occurring bacterial sequence encoding the protein.

[0059] A "recombinant polynucleotide" or "recombinant nucleic acid" comprises a combination of two or more chemically linked nucleic acid segments which are not found directly joined in nature. By "directly joined" is intended the two nucleic acid segments are immediately adjacent and joined to one another by a chemical linkage. In specific embodiments, the recombinant polynucleotide comprises a polynucleotide of interest or a variant or fragment thereof such that an additional chemically linked nucleic acid segment is located either 5', 3' or internal to the polynucleotide of interest. Alternatively, the chemically-linked nucleic acid segment of the recombinant polynucleotide can be formed by deletion of a sequence. The additional chemically linked nucleic acid segment, or the sequence deleted to join the linked nucleic acid segments, can be of any length, including for example, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20 nucleotides or more. Various methods for making such recombinant polynucleotides include chemical synthesis, and the manipulation of isolated segments of polynucleotides by genetic engineering techniques. In specific embodiments, the recombinant polynucleotide can comprise a recombinant DNA sequence or a recombinant RNA sequence. A "fragment of a recombinant polynucleotide or nucleic acid" comprises at least one of a combination of two or more chemically linked amino acid segments that are not found directly joined in nature.

[0060] Fragments of a polynucleotide (RNA or DNA) may encode protein fragments that retain activity. In specific embodiments, a fragment of a recombinant polynucleotide or a recombinant polynucleotide construct comprises at least one junction of the two or more chemically linked or operably linked nucleic acid segments which are not found directly joined in nature. A fragment of a polynucleotide that encodes a biologically active portion of a polypeptide that retains pesticidal activity will encode at least 25, 30, 40, 50, 60, 70, 75, 80, 90, 100, 110, 120, 125, 130, 140, 150, 160, 170, 175, or 180 contiguous amino acids, or up to the total number of amino acids present in a full-length polypeptide as set forth in SEQ ID NOs: 1, 2,

3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159. In specific embodiments, such polypeptide fragments are active fragments. In some embodiments, the polypeptide fragment comprises a recombinant polypeptide fragment. As used herein, a fragment of a recombinant polypeptide comprises at least one of a combination of two or more chemically linked amino acid segments which are not found directly joined in nature.

[0061] The term "variants" as used herein is intended to mean substantially similar sequences. For polynucleotides, a variant comprises a deletion and/or addition of one or more nucleotides at one or more internal sites within the native polynucleotide and/or a substitution of one or more nucleotides at one or more sites in the native polynucleotide. As used herein, a "native" polynucleotide or polypeptide comprises a naturally occurring nucleotide sequence or amino acid sequence, respectively.

[0062] Variants of a particular polynucleotide of the invention (i.e., the reference polynucleotide) can also be evaluated by comparison of the polypeptide encoded by a variant polynucleotide and the polypeptide encoded by the reference polynucleotide to determine the percent sequence identity between the two. Thus, for example, an isolated polynucleotide that encodes a polypeptide with a given percent sequence identity to the polypeptide of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159 are disclosed. Percent sequence identity between any two polypeptides can be calculated using

sequence alignment programs and parameters described elsewhere herein. Where any given pair of polynucleotides of the invention is evaluated by comparison of the percent sequence identity shared by the two polypeptides they encode, the percent sequence identity between the two encoded polypeptides is at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159. In other embodiments, the variant of the polynucleotide provided herein differs from the native sequence by at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more nucleotides.

iii. Sequence Comparisons

[0063] As used herein, the term "identity" or "percent identity" when used with respect to a particular pair of aligned amino acid sequences, refers to the percent amino acid sequence identity that is obtained by counting the number of identical matches in the alignment and dividing such number of identical matches by the length of the aligned sequences. As used herein, the term "similarity" or "percent similarity" when used with respect to a particular pair of aligned amino acid sequences, refers to the sum of the scores that are obtained from a scoring matrix for each amino acid pair in the alignment divided by the length of the aligned sequences.

[0064] Unless otherwise stated, identity and similarity is calculated by the Needleman-Wunsch global alignment and scoring algorithms (Needleman and Wunsch (1970) *J. Mol. Biol.* 48(3):443-453) as implemented by the "needle" program, distributed as part of the EMBOSS software package (Rice, P. Longden, I. and Bleasby, A., EMBOSS: The European Molecular Biology Open Software Suite, 2000, *Trends in Genetics* 16, (6) pp. 276-277, versions 6.3.1 available from EMBnet at embnet.org/resource/emboss and emboss.sourceforge.net, among other sources) using default gap penalties and scoring matrices (EBLOSUM62 for protein and EDNAFULL for DNA). Equivalent programs may also be used. By "equivalent program" is

intended any sequence comparison program that, for any two sequences in question, generates an alignment having identical nucleotide residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by needle from EMBOSS version 6.3.1.

[0065] Additional mathematical algorithms are known in the art and can be utilized for the comparison of two sequences. See, for example, the algorithm of Karlin and Altschul (1990) Proc. Natl. Acad. Sci. USA 87:2264, modified as in Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5877. Such an algorithm is incorporated into the BLAST programs of Altschul et al. (1990) J. Mol. Biol. 215:403. BLAST nucleotide searches can be performed with the BLASTN program, to obtain nucleotide sequences homologous to pesticidal-like nucleic acid molecules of the invention. BLAST protein searches can be performed with the BLASTP program to obtain amino acid sequences homologous to pesticidal protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389. Alternatively, PSI-Blast can be used to perform an iterated search that detects distant relationships between molecules. See Altschul *et al.* (1997) *supra.* When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., BLASTX and BLASTN) can be used. Alignment may also be performed manually by inspection.

[0066] Two sequences are "optimally aligned" when they are aligned for similarity scoring using a defined amino acid substitution matrix (for example, BLOSUM62), gap existence penalty and gap extension penalty so as to arrive at the highest score possible for that pair of sequences. Amino acid substitution matrices and their use in quantifying the similarity between two sequences are well-known in the art and described, for example, in Dayhoff et al. (1978) "A model of evolutionary change in proteins." In "Atlas of Protein Sequence and Structure," Vol. 5, Suppl. 3 (ed. M. O. Dayhoff), pp. 345-352. Natl. Biomed. Res. Found., Washington, D.C. and Henikoff et al. (1992) Proc. Natl. Acad. Sci. USA 89:10915-10919. The BLOSUM62 matrix is often used as a default scoring substitution matrix in sequence alignment protocols. The gap existence penalty is imposed for the introduction of a single amino acid gap in one of the aligned sequences, and the gap extension penalty is imposed for each additional empty amino acid

position inserted into an already opened gap. The alignment is defined by the amino acids positions of each sequence at which the alignment begins and ends and, optionally, by the insertion of a gap or multiple gaps in one or both sequences, so as to arrive at the highest possible score. While optimal alignment and scoring can be accomplished manually, the process is facilitated by the use of a computer-implemented alignment algorithm, such as, for example, gapped BLAST 2.0, described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402, and made available to the public at the National Center for Biotechnology Information Website (www.ncbi.nlm.nih.gov). Optimal alignments, including multiple alignments, can be prepared using, for example, PSI-BLAST, available through www.ncbi.nlm.nih.gov and described by Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402.

[0067] With respect to an amino acid sequence that is optimally aligned with a reference sequence, an amino acid residue "corresponds to" the position in the reference sequence with which the residue is paired in the alignment. The "position" is denoted by a number that sequentially identifies each amino acid in the reference sequence based on its position relative to the N-terminus. For example, in SEQ ID NO: 1, position 1 is M, position 2 is A, position 3 is N, etc. When a test sequence is optimally aligned with SEQ ID NO: 1, a residue in the test sequence that aligns with the N at position 3 is said to "correspond to position 3" of SEQ ID NO: 1. Owing to deletions, insertion, truncations, fusions, etc., that must be taken into account when determining an optimal alignment, in general the amino acid residue number in a test sequence as determined by simply counting from the N-terminal will not necessarily be the same as the number of its corresponding position in the reference sequence. For example, in a case where there is a deletion in an aligned test sequence, there will be no amino acid that corresponds to a position in the reference sequence at the site of deletion. Where there is an insertion in an aligned reference sequence, that insertion will not correspond to any amino acid position in the reference sequence. In the case of truncations or fusions there can be stretches of amino acids in either the reference or aligned sequence that do not correspond to any amino acid in the corresponding sequence.

iv. Antibodies

[0068] Antibodies to the polypeptides of the present invention, or to variants or fragments thereof, are also encompassed. Methods for producing antibodies are well known in the art (see,

for example, Harlow and Lane (1988) Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.; and U.S. Pat. No. 4,196,265). These antibodies can be used in kits for the detection and isolation of toxin polypeptides. Thus, this disclosure provides kits comprising antibodies that specifically bind to the polypeptides described herein, including, for example, polypeptides having the sequence of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159.

II. Pests

[0069] The compositions and methods provided herein are useful against a variety of pests. "Pests" includes but is not limited to, insects, fungi, bacteria, nematodes, acarids, protozoan pathogens, animal-parasitic liver flukes, and the like. Pests of particular interest are insect pests, particularly insect pests that cause significant damage to agricultural plants. Insect pests include insects selected from the orders Coleoptera, Diptera, Hymenoptera, Lepidoptera, Mallophaga, Homoptera, Hemiptera, Orthroptera, Thysanoptera, Dermaptera, Isoptera, Anoplura, Siphonaptera, Trichoptera, or nematodes. In non-limiting embodiments, the insect pest comprises Western corn rootworm, *Diabrotica virgifera virgifera*; Fall armyworm, *Spodoptera frugiperda;* Colorado potato beetle, *Leptinotarsa decemlineata*; Corn earworm, *Helicoverpa zea* (in North America same species attacks cotton and called cotton bollworm); European corn borer, *Ostrinia nubilalis*; Black cutworm, *Agrotis ipsilon*; Diamondback moth, *Plutella xylostella*; Velvetbean caterpillar, *Anticarsia gemmatalis*; Southwestern corn borer, *Diatraea grandiosella;* Cotton bollworm, *Helicoverpa armigera* (found other than USA in rest of the world); Southern green stinkbug, *Nezara viridula*; Green stinkbug, *Chinavia halaris*; Brown marmorated stinkbug, *Halyomorpha halys*; and Brown stinbug, *Euschistus servus*. In other embodiments, the pest comprises a nematode including, but not limited to, *Meloidogyne hapla* (Northern root-knot nematode); *Meloidogyne enterolobii, Meloidogyne arenaria* (peanut root-knot nematode); and *Meloidogyne javanica.*

[0070] The term "insect pests" as used herein refers to insects and other similar pests such as, for example, those of the order Acari including, but not limited to, mites and ticks. Insect pests of the present invention include, but are not limited to, insects of the order Lepidoptera, e.g. *Achoroia grisella*, *Acleris gloverana*, *Acleris variana*, *Adoxophyes orana*, *Agrotis ipsilon*, *Alabama argillacea*, *Alsophila pometaria*, *Amyelois transitella*, *Anagasta kuehniella*, *Anarsia lineatella*, *Anisota senatoria*, *Antheraea pernyi*, *Anticarsia gemmatalis*, Archips sp., Argyrotaenia sp., *Athetis mindara*, *Bombyx mori*, *Bucculatrix thurberiella*, *Cadra cautella*, Choristoneura sp., *Cochylls hospes*, *Colias eurytheme*, *Corcyra cephalonica*, *Cydia latiferreanus*, *Cydia pomonella*, *Datana integerrima*, *Dendrolimus sibericus*, Desmiafeneralis, *Diaphania hyalinata*, *Diaphania nitidalis*, *Diatraea grandiosella*, *Diatraea saccharalis*, *Ennomos subsignaria*, *Eoreuma loftini*, *Esphestia elutella*, *Erannis tilaria*, *Estigmene acrea*, *Eulia salubricola*, *Eupocoellia ambiguella*, *Eupoecilia ambiguella*, *Euproctis chrysorrhoea*, *Euxoa messoria*, *Galleria mellonella*, *Grapholita molesta*, *Harrisina americana*, *Helicoverpa subflexa*, *Helicoverpa zea*, *Heliothis virescens*, *Hemileuca oliviae*, *Homoeosoma electellum*, *Hyphantia cunea*, *Keiferia lycopersicella*, *Lambdina fiscellaria fiscellaria*, *Lambdina fiscellaria lugubrosa*, *Leucoma salicis*, *Lobesia botrana*, *Loxostege sticticalis*, *Lymantria dispar*, *Macalla thyrisalis*, Malacosoma sp., *Mamestra brassicae*, *Mamestra configurata*, *Manduca quinquemaculata*, *Manduca sexta*, *Maruca testulalis*, *Melanchra picta*, *Operophtera brumata*, Orgyia sp., *Ostrinia nubilalis*, *Paleacrita vernata*, *Papilio cresphontes*, *Pectinophora gossypiella*, *Phryganidia californica*, *Phyllonorycter blancardella*, *Pieris napi*, *Pieris rapae*, *Plathypena scabra*, *Platynota flouendana*, *Platynota stultana*, *Platyptilia carduidactyla*, *Plodia interpunctella*, *Plutella xylostella*, *Pontia protodice*, *Pseudaletia unipuncta*, *Pseudoplasia includens*, *Sabulodes aegrotata*, *Schizura concinna*, *Sitotroga cerealella*, *Spilonta ocellana*, Spodoptera sp., *Thaurnstopoea pityocampa*, *Tinsola bisselliella*, *Trichoplusia hi*, *Udea rubigalis*, *Xylomyges curiails*, and *Yponomeuta padella*.

[0071] Insect pests also include insects selected from the orders Diptera, Hymenoptera, Lepidoptera, Mallophaga, Homoptera, Hemiptera, Orthroptera, Thysanoptera, Dermaptera, Isoptera, Anoplura, Siphonaptera, Trichoptera, Coleoptera.

[0072] Insect pests for the major crops include, but are not limited to: Maize: *Ostrinia nubilalis*, European corn borer; *Agrotis ipsilon*, black cutworm; *Helicoverpa zeae*, corn earworm;

Spodoptera frugiperda, fall armyworm; *Diatraea grandiosella*, southwestern corn borer; *Elasmopalpus lignosellus*, lesser cornstalk borer; *Diatraea saccharalis*, surgarcane borer; western corn rootworm, e.g., *Diabrotica virgifera virgifera*; northern corn rootworm, e.g., *Diabrotica longicornis barberi*; southern corn rootworm, e.g., *Diabrotica undecimpunctata howardi*; Melanotus spp., wireworms; *Cyclocephala borealis*, northern masked chafer (white grub); *Cyclocephala immaculata*, southern masked chafer (white grub); *Popillia japonica*, Japanese beetle; *Chaetocnema pulicaria*, corn flea beetle; *Sphenophorus maidis*, maize billbug; *Rhopalosiphum maidis*, corn leaf aphid; *Anuraphis maidiradicis*, corn root aphid; *Blissus leucopterus leucopterus*, chinch bug; *Melanoplus femurrubrum*, redlegged grasshopper; *Melanoplus sanguinipes*, migratory grasshopper; *Hylemya platura*, seedcorn maggot; *Agromyza parvicornis*, corn blotch leafminer; *Anaphothrips obscrurus*, grass thrips; *Solenopsis milesta*, thief ant; *Tetranychus urticae*, two spotted spider mite; Sorghum: *Chilo partellus*, sorghum borer; *Spodoptera frugiperda*, fall armyworm; *Helicoverpa zea*, corn earworm; *Elasmopalpus lignosellus*, leser cornstalk borer; *Feltia subterranea*, granulate cutworm; *Phyllophaga crinita*, white grub; *Eleodes, Conoderus*, and Aeolus spp., wireworms; *Oulema melanopus*, cereal leaf beetle; *Chaetocnema pulicaria*, corn flea beetle; *Sphenophorus maidis*, maize billbug; *Rhopalosiphum maidis*; corn leaf aphid; *Sipha flava*, yellow sugarcane aphid; chinch bug, e.g., *Blissus leucopterus leucopterus*; *Contarinia sorghicola*, sorghum midge; *Tetranychus cinnabarinus*, carmine spider mite; *Tetranychus urticae*, two-spotted spider mite; Wheat: *Pseudaletia unipunctata*, army worm; *Spodoptera frugiperda*, fall armyworm; *Elasmopalpus lignosellus*, lesser cornstalk borer; *Agrotis orthogonia*, pale western cutworm; *Elasmopalpus lignosellus*, lesser cornstalk borer; *Oulema melanopus*, cereal leaf beetle; *Hypera punctata*, clover leaf weevil; southern corn rootworm, e.g., *Diabrotica undecimpunctata howardi*; Russian wheat aphid; *Schizaphis graminum*, greenbug; *Macrosiphum avenae*, English grain aphid; *Melanoplus femurrubrum*, redlegged grasshopper; *Melanoplus differentialis*, differential grasshopper; *Melanoplus sanguinipes*, migratory grasshopper; *Mayetiola destructor*, Hessian fly; *Sitodiplosis mosellana*, wheat midge; *Meromyza americana*, wheat stem maggot; *Hylemya coarctata*, wheat bulb fly; *Frankliniella fusca*, tobacco thrips; *Cephus cinctus*, wheat stem sawfly; *Aceria tulipae*, wheat curl mite; Sunflower: *Cylindrocupturus adspersus*, sunflower stem weevil; *Smicronyx fulus*, red sunflower seed weevil; *Smicronyx sordidus*, gray sunflower seed weevil; *Suleima helianthana*, sunflower bud moth; *Homoeosoma electellum*, sunflower

moth; *Zygogramma exclamationis*, sunflower beetle; *Bothyrus gibbosus*, carrot beetle; *Neolasioptera murtfeldtiana*, sunflower seed midge; Cotton: *Heliothis virescens*, tobacco budworm; *Helicoverpa zea*, cotton bollworm; *Spodoptera exigua*, beet armyworm; *Pectinophora gossypiella*, pink bollworm; boll weevil, e.g., *Anthonomus grandis*; *Aphis gossypii*, cotton aphid; *Pseudatomoscelis seriatus*, cotton fleahopper; *Trialeurodes abutilonea*, bandedwinged whitefly; *Lygus lineolaris*, tarnished plant bug; *Melanoplus femurrubrum*, redlegged grasshopper; *Melanoplus differentialis*, differential grasshopper; *Thrips tabaci*, onion thrips; *Franklinkiella fusca*, tobacco thrips; *Tetranychus cinnabarinus*, carmine spider mite; *Tetranychus urticae*, two-spotted spider mite; Rice: *Diatraea saccharalis*, sugarcane borer; *Spodoptera frugiperda*, fall armyworm; *Helicoverpa zea*, corn earworm; *Colaspis brunnea*, grape colaspis; *Lissorhoptrus oryzophilus*, rice water weevil; *Sitophilus oryzae*, rice weevil; *Nephotettix nigropictus*, rice leafhoper; chinch bug, e.g., *Blissus leucopterus leucopterus*; *Acrosternum hilare*, green stink bug; Soybean: *Pseudoplusia includens*, soybean looper; *Anticarsia gemmatalis*, velvetbean caterpillar; *Plathypena scabra*, green cloverworm; *Ostrinia nubilalis*, European corn borer; *Agrotis ipsilon*, black cutworm; *Spodoptera exigua*, beet armyworm; *Heliothis virescens*, tobacco budworm; *Helicoverpa zea*, cotton bollworm; *Epilachna varivestis*, Mexican bean beetle; *Myzus persicae*, green peach aphid; *Empoasca fabae*, potato leafhopper; *Acrosternum hilare*, green stink bug; *Melanoplus femurrubrum*, redlegged grasshopper; *Melanoplus differentialis*, differential grasshopper; *Hylemya platura*, seedcorn maggot; *Sericothrips variabilis*, soybean thrips; *Thrips tabaci*, onion thrips; *Tetranychus turkestani*, strawberry spider mite; *Tetranychus urticae*, two-spotted spider mite; Barley: *Ostrinia nubilalis*, European corn borer; *Agrotis ipsilon*, black cutworm; *Schizaphis graminum*, greenbug; chinch bug, e.g., *Blissus leucopterus leucopterus*; *Acrosternum hilare*, green stink bug; *Euschistus servus*, brown stink bug; *Jylemya platura*, seedcorn maggot; *Mayetiola destructor*, Hessian fly; *Petrobia latens*, brown wheat mite; Oil Seed Rape: *Vrevicoryne brassicae*, cabbage aphid; *Phyllotreta cruciferae*, crucifer flea beetle; *Phyllotreta striolata*, striped flea beetle; *Phyllotreta nemorum*, striped turnip flea beetle; *Meligethes aeneus*, rapeseed beetle; and the pollen beetles *Meligethes rufimanus*, *Meligethes nigrescens*, *Meligethes canadianus*, and *Meligethes viridescens*; Potato: *Leptinotarsa decemlineata*, Colorado potato beetle.

[0073] The methods and compositions provided herein may be effective against Hemiptera such as Lygus hesperus, Lygus lineolaris, Lygus pratensis, Lygus rugulipennis Popp, Lygus

pabulinus, Calocoris norvegicus, Orthops compestris, Plesiocoris rugicollis, Cyrtopeltis modestus, Cyrtopeltis notatus, Spanagonicus albofasciatus, Diaphnocoris chlorinonis, Labopidicola allii, Pseudatomoscelis seriatus, Adelphocoris rapidus, Poecilocapsus lineatus, Blissus leucopterus, Nysius ericae, Nysius raphanus, Euschistus servus, Nezara viridula, Eurygaster, Coreidae, Pyrrhocoridae, Tinidae, Blostomatidae, Reduviidae, and Cimicidae. Pests of interest also include Araecerus fasciculatus, coffee bean weevil; Acanthoscelides obtectus, bean weevil; Bruchus rufmanus, broadbean weevil; Bruchus pisorum, pea weevil; Zabrotes subfasciatus, Mexican bean weevil; Diabrotica balteata, banded cucumber beetle; Cerotoma trifurcata, bean leaf beetle; Diabrotica virgifera, Mexican corn rootworm; Epitrix cucumeris, potato flea beetle; Chaetocnema confinis, sweet potato flea beetle; Hypera postica, alfalfa weevil; Anthonomus quadrigibbus, apple curculio; Sternechus paludatus, bean stalk weevil; Hypera brunnipennis, Egyptian alfalfa weevil; Sitophilus granaries, granary weevil; Craponius inaequalis, grape curculio; Sitophilus zeamais, maize weevil; Conotrachelus nenuphar, plum curculio; Euscepes postfaciatus, West Indian sweet potato weevil; Maladera castanea, Asiatic garden beetle; Rhizotrogus majalis, European chafer; Macrodactylus subspinosus, rose chafer; Tribolium confusum, confused flour beetle; Tenebrio obscurus, dark mealworm; Tribolium castaneum, red flour beetle; Tenebrio molitor, yellow mealworm.

[0074] Nematodes include parasitic nematodes such as root-knot, cyst, and lesion nematodes, including Heterodera spp., Meloidogyne spp., and Globodera spp.; particularly members of the cyst nematodes, including, but not limited to, *Heterodera glycines* (soybean cyst nematode); *Heterodera schachtii* (beet cyst nematode); *Heterodera avenae* (cereal cyst nematode); and *Globodera rostochiensis* and *Globodera pailida* (potato cyst nematodes). Lesion nematodes include Pratylenchus spp.

[0075] Insect pests may be tested for pesticidal activity of compositions of the invention in early developmental stages, e.g., as larvae or other immature forms. The insects may be reared in total darkness at from about 20°C to about 30°C and from about 30% to about 70% relative humidity. Bioassays may be performed as described in Czapla and Lang (1990) *J. Econ. Entomol.* 83 (6): 2480-2485. See, also the experimental section herein.

III. Expression Cassettes

[0076] Polynucleotides encoding the pesticidal proteins provided herein can be provided in expression cassettes for expression in an organism of interest. The cassette will include 5' and 3' regulatory sequences operably linked to a polynucleotide encoding a pesticidal polypeptide provided herein that allows for expression of the polynucleotide. The cassette may additionally contain at least one additional gene or genetic element to be cotransformed into the organism. Where additional genes or elements are included, the components are operably linked. Alternatively, the additional gene(s) or element(s) can be provided on multiple expression cassettes. Such an expression cassette is provided with a plurality of restriction sites and/or recombination sites for insertion of the polynucleotides to be under the transcriptional regulation of the regulatory regions. The expression cassette may additionally contain a selectable marker gene.

[0077] The expression cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region (i.e., a promoter), a pesticidal polynucleotide of the invention, and a transcriptional and translational termination region (i.e., termination region) functional in the organism of interest, i.e., a plant or bacteria. The promoters of the invention are capable of directing or driving expression of a coding sequence in a host cell. The regulatory regions (i.e., promoters, transcriptional regulatory regions, and translational termination regions) may be endogenous or heterologous to the host cell or to each other. As used herein, "heterologous" in reference to a sequence is a sequence that originates from a foreign species, or, if from the same species, is substantially modified from its native form in composition and/or genomic locus by deliberate human intervention. As used herein, a chimeric gene comprises a coding sequence operably linked to a transcription initiation region that is heterologous to the coding sequence.

[0078] Convenient termination regions are available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also Guerineau *et al.* (1991) *Mol. Gen. Genet.* 262:141-144; Proudfoot (1991) *Cell* 64:671-674; Sanfacon *et al.* (1991) *Genes Dev.* 5:141-149; Mogen *et al.* (1990) *Plant Cell* 2:1261-1272; Munroe *et al.* (1990) *Gene* 91:151-158; Ballas *et al.* (1989) *Nucleic Acids Res.* 17:7891-7903; and Joshi *et al.* (1987) *Nucleic Acids Res.* 15:9627-9639.

[0079] Additional regulatory signals include, but are not limited to, transcriptional initiation start sites, operators, activators, enhancers, other regulatory elements, ribosomal binding sites, an initiation codon, termination signals, and the like. See, for example, U.S. Patent Nos. 5,039,523 and 4,853,331; EPO 0480762A2; Sambrook et al. (1992) Molecular Cloning: A Laboratory Manual, ed. Maniatis et al. (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.) (hereinafter "Sambrook 11"); Davis et al., eds. (1980) Advanced Bacterial Genetics (Cold Spring Harbor Laboratory Press), Cold Spring Harbor, N.Y., and the references cited therein.

[0080] In preparing the expression cassette, the various DNA fragments may be manipulated, so as to provide for the DNA sequences in the proper orientation and, as appropriate, in the proper reading frame. Toward this end, adapters or linkers may be employed to join the DNA fragments or other manipulations may be involved to provide for convenient restriction sites, removal of superfluous DNA, removal of restriction sites, or the like. For this purpose, *in vitro* mutagenesis, primer repair, restriction, annealing, resubstitutions, e.g., transitions and transversions, may be involved.

[0081] A number of promoters can be used in the practice of the invention. The promoters can be selected based on the desired outcome. The nucleic acids can be combined with constitutive, inducible, tissue-preferred, or other promoters for expression in the organism of interest. See, for example, promoters set forth in WO 99/43838 and in U.S. Patent Nos: 8,575,425; 7,790,846; 8,147,856; 8,586832; 7,772,369; 7,534,939; 6,072,050; 5,659,026; 5,608,149; 5,608,144; 5,604,121; 5,569,597; 5,466,785; 5,399,680; 5,268,463; 5,608,142; and 6,177,611; herein incorporated by reference.

[0082] For expression in plants, constitutive promoters also include CaMV 35S promoter (Odell *et al.* (1985) *Nature* 313:810-812); rice actin (McElroy *et al.* (1990) *Plant Cell* 2:163-171); ubiquitin (Christensen *et al.* (1989) *Plant Mol. Biol.* 12:619-632 and Christensen *et al.* (1992) *Plant Mol. Biol.* 18:675-689); pEMU (Last *et al.* (1991) *Theor. Appl. Genet.* 81:581-588); MAS (Velten *et al.* (1984) *EMBO J.* 3:2723-2730). Inducible promoters include those that drive expression of pathogenesis-related proteins (PR proteins), which are induced following infection by a pathogen. See, for example, Redolfi *et al.* (1983) *Neth. J. Plant Pathol.* 89:245-254; Uknes *et al.* (1992) *Plant Cell* 4:645-656; and Van Loon (1985) *Plant Mol. Virol.* 4:111-116; and WO 99/43819, each herein incorporated by reference. Promoters that are expressed locally at or near

the site of pathogen infection may also be used (Marineau *et al.* (1987) *Plant Mol. Biol.* 9:335-342; Matton *et al.* (1989) *Molecular Plant-Microbe Interactions* 2:325-331; Somsisch *et al.* (1986) *Proc. Natl. Acad. Sci. USA* 83:2427-2430; Somsisch *et al.* (1988) *Mol. Gen. Genet.* 2:93-98; and Yang (1996) *Proc. Natl. Acad. Sci. USA* 93:14972-14977; Chen *et al.* (1996) *Plant J.* 10:955-966; Zhang *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:2507-2511; Warner *et al.* (1993) *Plant J.* 3:191-201; Siebertz *et al.* (1989) *Plant Cell* 1:961-968; Cordero *et al.* (1992) *Physiol. Mol. Plant Path.* 41:189-200; U.S. Patent No. 5,750,386 (nematode-inducible); and the references cited therein).

[0083] Wound-inducible promoters may be used in the constructions of the invention. Such wound-inducible promoters include pin II promoter (Ryan (1990) *Ann. Rev. Phytopath.* 28:425-449; Duan *et al.* (1996) *Nature Biotechnology* 14:494-498); wun1 and wun2 (U.S. Patent No. 5,428,148); win1 and win2 (Stanford *et al.* (1989) *Mol. Gen. Genet.* 215:200-208); systemin (McGurl *et al.* (1992) *Science* 225:1570-1573); WIP1 (Rohmeier *et al.* (1993) *Plant Mol. Biol.* 22:783-792; Eckelkamp *et al.* (1993) *FEBS Letters* 323:73-76); MPI gene (Corderok *et al.* (1994) *Plant J.* 6(2):141-150); and the like, herein incorporated by reference.

[0084] Tissue-preferred promoters for use in the invention include those set forth in Yamamoto *et al.* (1997) *Plant J.* 12(2):255-265; Kawamata *et al.* (1997) *Plant Cell Physiol.* 38(7):792-803; Hansen *et al.* (1997) *Mol. Gen Genet.* 254(3):337-343; Russell *et al.* (1997) *Transgenic Res.* 6(2):157-168; Rinehart *et al.* (1996) *Plant Physiol.* 112(3):1331-1341; Van Camp *et al.* (1996) *Plant Physiol.* 112(2):525-535; Canevascini *et al.* (1996) *Plant Physiol.* 112(2):513-524; Yamamoto *et al.* (1994) *Plant Cell Physiol.* 35(5):773-778; Lam (1994) *Results Probl. Cell Differ.* 20:181-196; Orozco *et al.* (1993) *Plant Mol Biol.* 23(6):1129-1138; Matsuoka *et al.* (1993) *Proc Natl. Acad. Sci. USA* 90(20):9586-9590; and Guevara-Garcia *et al.* (1993) *Plant J.* 4(3):495-505.

[0085] Leaf-preferred promoters include those set forth in Yamamoto *et al.* (1997) *Plant J.* 12(2):255-265; Kwon *et al.* (1994) *Plant Physiol.* 105:357-67; Yamamoto *et al.* (1994) *Plant Cell Physiol.* 35(5):773-778; Gotor *et al.* (1993) *Plant J.* 3:509-18; Orozco *et al.* (1993) *Plant Mol. Biol.* 23(6):1129-1138; and Matsuoka *et al.* (1993) *Proc. Natl. Acad. Sci. USA* 90(20):9586-9590.

[0086] Root-preferred promoters are known and include those in Hire *et al.* (1992) *Plant Mol. Biol.* 20(2):207-218 (soybean root-specific glutamine synthetase gene); Keller and Baumgartner (1991) *Plant Cell* 3(10):1051-1061 (root-specific control element); Sanger *et al.* (1990) *Plant Mol. Biol.* 14(3):433-443 (mannopine synthase (MAS) gene of *Agrobacterium tumefaciens*); and Miao *et al.* (1991) *Plant Cell* 3(1):11-22 (cytosolic glutamine synthetase (GS)); Bogusz *et al.* (1990) *Plant Cell* 2(7):633-641; Leach and Aoyagi (1991) *Plant Science* (Limerick) 79(1):69-76 (rolC and rolD); Teeri *et al.* (1989) *EMBO J.* 8(2):343-350; Kuster *et al.* (1995) *Plant Mol. Biol.* 29(4):759-772 (the VfENOD-GRP3 gene promoter); and Capana *et al.* (1994) *Plant Mol. Biol.* 25(4):681-691 (rolB promoter). See also U.S. Patent Nos. 5,837,876; 5,750,386; 5,633,363; 5,459,252; 5,401,836; 5,110,732; and 5,023,179.

[0087] "Seed-preferred" promoters include both "seed-specific" promoters (those promoters active during seed development such as promoters of seed storage proteins) as well as "seed-germinating" promoters (those promoters active during seed germination). See Thompson *et al.* (1989) *BioEssays* 10:108. Seed-preferred promoters include, but are not limited to, Cim1 (cytokinin-induced message); cZ19B1 (maize 19 kDa zein); milps (myo-inositol-1-phosphate synthase) (see WO 00/11177 and U.S. Patent No. 6,225,529). Gamma-zein is an endosperm-specific promoter. Globulin 1 (Glb-1) is a representative embryo-specific promoter. For dicots, seed-specific promoters include, but are not limited to, bean β-phaseolin, napin, β-conglycinin, soybean lectin, cruciferin, and the like. For monocots, seed-specific promoters include, but are not limited to, maize 15 kDa zein, 22 kDa zein, 27 kDa zein, gamma-zein, waxy, shrunken 1, shrunken 2, Globulin 1, etc. See also WO 00/12733, where seed-preferred promoters from *end1* and *end2* genes are disclosed.

[0088] For expression in a bacterial host, promoters that function in bacteria are well-known in the art. Such promoters include any of the known crystal protein gene promoters, including the promoters of any of the pesticidal proteins of the invention, and promoters specific for *B. thuringiensis* sigma factors. Alternatively, mutagenized or recombinant crystal protein-encoding gene promoters may be recombinantly engineered and used to promote expression of the novel gene segments disclosed herein.

[0089] The expression cassette can also comprise a selectable marker gene for the selection of transformed cells. Selectable marker genes are utilized for the selection of transformed cells or

tissues. Marker genes include genes encoding antibiotic resistance, such as those encoding neomycin phosphotransferase II (NEO) and hygromycin phosphotransferase (HPT), as well as genes conferring resistance to herbicidal compounds, such as glufosinate ammonium, bromoxynil, imidazolinones, and 2,4-dichlorophenoxyacetate (2,4-D). Additional selectable markers are known and any can be used. See, for example, U.S.Provisional application 62/094,697, filed on December 19, 2014, herein incorporated by reference in its entirety, which discloses glufosinate resistance sequences that can be employed as selectable markers.

IV. Methods, Host Cells and Plant Cells

[0090] As indicated, DNA constructs comprising nucleotide sequences encoding the pesticidal proteins or active variants or fragment thereof can be used to transform plants of interest or other organisms of interest. Methods for transformation involve introducing a nucleotide construct into a plant. By "introducing" is intended to introduce the nucleotide construct to the plant or other host cell in such a manner that the construct gains access to the interior of a cell of the plant or host cell. The methods of the invention do not require a particular method for introducing a nucleotide construct to a plant or host cell, only that the nucleotide construct gains access to the interior of at least one cell of the plant or the host organism. Methods for introducing nucleotide constructs into plants and other host cells are known in the art including, but not limited to, stable transformation methods, transient transformation methods, and virus-mediated methods.

[0091] The methods result in a transformed organisms, such as a plant, including whole plants, as well as plant organs (e.g., leaves, stems, roots, etc.), seeds, plant cells, propagules, embryos and progeny of the same. Plant cells can be differentiated or undifferentiated (e.g. callus, suspension culture cells, protoplasts, leaf cells, root cells, phloem cells, pollen).

[0092] "Transgenic plants" or "transformed plants" or "stably transformed" plants or cells or tissues refers to plants that have incorporated or integrated a polynucleotide encoding at least one pesticidal polypeptide of the invention. It is recognized that other exogenous or endogenous nucleic acid sequences or DNA fragments may also be incorporated into the plant cell. *Agrobacterium*-and biolistic-mediated transformation remain the two predominantly employed approaches. However, transformation may be performed by infection, transfection, microinjection, electroporation, microprojection, biolistics or particle bombardment, electroporation, silica/carbon fibers, ultrasound mediated, PEG mediated, calcium phosphate co-

precipitation, polycation DMSO technique, DEAE dextran procedure, Agro and viral mediated (Caulimoriviruses, Geminiviruses, RNA plant viruses), liposome mediated and the like.

[0093] Transformation protocols as well as protocols for introducing polypeptides or polynucleotide sequences into plants may vary depending on the type of plant or plant cell, i.e., monocot or dicot, targeted for transformation. Methods for transformation are known in the art and include those set forth in U.S. Patent Nos: 8,575,425; 7,692,068; 8,802,934; and 7,541,517; each of which is herein incorporated by reference. See, also, Rakoczy-Trojanowska, M. (2002) *Cell Mol Biol Lett.* 7:849-858; Jones *et al.* (2005) *Plant Methods* 1:5; Rivera *et al.* (2012) *Physics of Life Reviews* 9:308-345; Bartlett *et al.* (2008) *Plant Methods* 4:1-12; Bates, G.W. (1999) *Methods in Molecular Biology* 111:359-366; Binns and Thomashow (1988) *Annual Reviews in Microbiology* 42:575-606; Christou, P. (1992) *The Plant Journal* 2:275-281; Christou, P. (1995) *Euphytica* 85:13-27; Tzfira *et al.* (2004) *TRENDS in Genetics* 20:375-383; Yao *et al.* (2006) *Journal of Experimental Botany* 57:3737-3746; Zupan and Zambryski (1995) *Plant Physiology* 107:1041-1047; and Jones *et al.* (2005) *Plant Methods* 1:5.

[0094] Transformation may result in stable or transient incorporation of the nucleic acid into the cell. "Stable transformation" is intended to mean that the nucleotide construct introduced into a host cell integrates into the genome of the host cell and is capable of being inherited by the progeny thereof. "Transient transformation" is intended to mean that a polynucleotide is introduced into the host cell and does not integrate into the genome of the host cell.

[0095] Methods for transformation of chloroplasts are known in the art. See, for example, Svab et al. (1990) Proc. Natl. Acad. Sci. USA 87:8526-8530; Svab and Maliga (1993) Proc. Natl. Acad. Sci. USA 90:913-917; Svab and Maliga (1993) EMBO J. 12:601-606. The method relies on particle gun delivery of DNA containing a selectable marker and targeting of the DNA to the plastid genome through homologous recombination. Additionally, plastid transformation can be accomplished by transactivation of a silent plastid-borne transgene by tissue-preferred expression of a nuclear-encoded and plastid-directed RNA polymerase. Such a system has been reported in McBride et al. (1994) Proc. Natl. Acad. Sci. USA 91:7301-7305.

[0096] The cells that have been transformed may be grown into plants in accordance with conventional ways. See, for example, McCormick et al. (1986) Plant Cell Reports 5:81-84. These plants may then be grown, and either pollinated with the same transformed strain or

different strains, and the resulting hybrid having constitutive expression of the desired phenotypic characteristic identified. Two or more generations may be grown to ensure that expression of the desired phenotypic characteristic is stably maintained and inherited and then seeds harvested to ensure expression of the desired phenotypic characteristic has been achieved. In this manner, the present invention provides transformed seed (also referred to as "transgenic seed") having a nucleotide construct of the invention, for example, an expression cassette of the invention, stably incorporated into their genome.

[0097] In specific embodiments, the sequences provide herein can be targeted to a specific site within the genome of the host cell or plant cell. Such methods include, but are not limited to, meganucleases designed against the plant genomic sequence of interest (D'Halluin *et al.* 2013 *Plant Biotechnol J*); CRISPR-Cas9, TALENs, and other technologies for precise editing of genomes (Feng, *et al.* Cell Research 23:1229-1232, 2013, Podevin, *et al. Trends Biotechnology*, online publication, 2013, Wei *et al.*, *J Gen Genomics*, 2013, Zhang *et al* (2013) WO 2013/026740); Cre-lox site-specific recombination (Dale *et al.* (1995) *Plant J* 7:649-659; Lyznik, *et al.* (2007) *Transgenic Plant J* 1:1-9; FLP-FRT recombination (Li *et al.* (2009) *Plant Physiol* 151:1087-1095); Bxb1-mediated integration (Yau *et al. Plant J* (2011) 701:147-166); zinc-finger mediated integration (Wright *et al.* (2005) *Plant J* 44:693-705); Cai *et al.* (2009) *Plant Mol Biol* 69:699-709); and homologous recombination (Lieberman-Lazarovich and Levy (2011) *Methods Mol Biol* 701: 51-65); Puchta (2002) *Plant Mol Biol* 48:173-182).

[0098] The sequence provided herein may be used for transformation of any plant species, including, but not limited to, monocots and dicots. Examples of plants of interest include, but are not limited to, corn (maize), sorghum, wheat, sunflower, tomato, crucifers, peppers, potato, cotton, rice, soybean, sugarbeet, sugarcane, tobacco, barley, and oilseed rape, Brassica sp., alfalfa, rye, millet, safflower, peanuts, sweet potato, cassaya, coffee, coconut, pineapple, citrus trees, cocoa, tea, banana, avocado, fig, guava, mango, olive, papaya, cashew, macadamia, almond, oats, vegetables, ornamentals, and conifers.

[0099] Vegetables include, but are not limited to, tomatoes, lettuce, green beans, lima beans, peas, and members of the genus Curcumis such as cucumber, cantaloupe, and musk melon. Ornamentals include, but are not limited to, azalea, hydrangea, hibiscus, roses, tulips, daffodils, petunias, carnation, poinsettia, and chrysanthemum. Preferably, plants of the present invention

are crop plants (for example, maize, sorghum, wheat, sunflower, tomato, crucifers, peppers, potato, cotton, rice, soybean, sugarbeet, sugarcane, tobacco, barley, oilseed rape, etc.).

[0100] As used herein, the term plant includes plant cells, plant protoplasts, plant cell tissue cultures from which plants can be regenerated, plant calli, plant clumps, and plant cells that are intact in plants or parts of plants such as embryos, pollen, ovules, seeds, leaves, flowers, branches, fruit, kernels, ears, cobs, husks, stalks, roots, root tips, anthers, and the like. Grain is intended to mean the mature seed produced by commercial growers for purposes other than growing or reproducing the species. Progeny, variants, and mutants of the regenerated plants are also included within the scope of the invention, provided that these parts comprise the introduced polynucleotides. Further provided is a processed plant product or byproduct that retains the sequences disclosed herein, including for example, soymeal.

[0101] In another embodiment, the genes encoding the pesticidal proteins can be used to transform insect pathogenic organisms. Such organisms include baculoviruses, fungi, protozoa, bacteria, and nematodes. Microorganism hosts that are known to occupy the "phytosphere" (phylloplane, phyllosphere, rhizosphere, and/or rhizoplana) of one or more crops of interest may be selected. These microorganisms are selected so as to be capable of successfully competing in the particular environment with the wild-type microorganisms, provide for stable maintenance and expression of the gene expressing the pesticidal protein, and desirably, provide for improved protection of the pesticide from environmental degradation and inactivation.

[0102] Such microorganisms include archaea, bacteria, algae, and fungi. Of particular interest are microorganisms such as bacteria, e.g., Bacillus, Pseudomonas, Erwinia, Serratia, Klebsiella, Xanthomonas, Streptomyces, Rhizobium, Rhodopseudomonas, Methylius, Agrobacterium, Acetobacter, Lactobacillus, Arthrobacter, Azotobacter, Leuconostoc, and Alcaligenes. Fungi include yeast, e.g., Saccharomyces, Cryptococcus, Kluyveromyces, Sporobolomyces, Rhodotorula, and Aureobasidium. Of particular interest are such phytosphere bacterial species as *Pseudomonas syringae*, *Pseudomonas aeruginosa, Pseudomonas fluorescens*, *Serratia marcescens*, *Acetobacter xylinum*, Agrobacteria, *Rhodopseudomonas spheroides*, *Xanthomonas campestris*, *Rhizobium melioti*, *Alcaligenes entrophus*, *Clavibacter xyli* and *Azotobacter vinlandir* and phytosphere yeast species such as *Rhodotorula rubra*, *R. glutinis*, *R. marina*, *R. aurantiaca*, *Cryptococcus albidus*, *C. diffluens*, *C. laurentii*, *Saccharomyces rosei*, *S.*

pretoriensis, *S. cerevisiae*, *Sporobolomyces rosues*, *S. odorus*, *Kluyveromyces veronae*, *Aureobasidium pollulans*, *Bacillus thuringiensis*, *Escherichia coli*, *Bacillus subtilis*, and the like.

[0103] Illustrative prokaryotes, both Gram-negative and gram-positive, include Enterobacteriaceae, such as Escherichia, Erwinia, Shigella, Salmonella, and Proteus; Bacillaceae; Rhizobiceae, such as Rhizobium; Spirillaceae, such as photobacterium, Zymomonas, Serratia, Aeromonas, Vibrio, Desulfovibrio, Spirillum; Lactobacillaceae; Pseudomonadaceae, such as Pseudomonas and Acetobacter; Azotobacteraceae and Nitrobacteraceae. Fungi include Phycomycetes and Ascomycetes, e.g., yeast, such as Saccharomyces and Schizosaccharomyces; and Basidiomycetes yeast, such as Rhodotorula, Aureobasidium, Sporobolomyces, and the like.

[0104] Genes encoding pesticidal proteins can be introduced by means of electrotransformation, PEG induced transformation, heat shock, transduction, conjugation, and the like. Specifically, genes encoding the pesticidal proteins can be cloned into a shuttle vector. An exemplary shuttle vector is pHT3101 (Lerecius *et al.* (1989) *FEMS Microbiol. Letts.* 60: 211-218). The shuttle vector pHT3101 containing the coding sequence for the particular pesticidal protein gene can, for example, be transformed into the root-colonizing Bacillus by means of electroporation (Lerecius *et al.* (1989) *FEMS Microbiol. Letts.* 60: 211-218).

[0105] Expression systems can be designed so that pesticidal proteins are secreted outside the cytoplasm of gram-negative bacteria by fusing an appropriate signal peptide to the amino-terminal end of the pesticidal protein. Signal peptides recognized by *E. coli* include the OmpA protein (Ghrayeb *et al.* (1984) *EMBO J*, 3: 2437-2442).

[0106] Pesticidal proteins and active variants thereof can be fermented in a bacterial host and the resulting bacteria processed and used as a microbial spray in the same manner that *Bacillus thuringiensis* strains have been used as insecticidal sprays. In the case of a pesticidal protein(s) that is secreted from Bacillus, the secretion signal is removed or mutated using procedures known in the art. Such mutations and/or deletions prevent secretion of the pesticidal protein(s) into the growth medium during the fermentation process. The pesticidal proteins are retained within the cell, and the cells are then processed to yield the encapsulated pesticidal proteins.

[0107] Alternatively, the pesticidal proteins are produced by introducing heterologous genes into a cellular host. Expression of the heterologous gene results, directly or indirectly, in the

intracellular production and maintenance of the pesticide. These cells are then treated under conditions that prolong the activity of the toxin produced in the cell when the cell is applied to the environment of target pest(s). The resulting product retains the toxicity of the toxin. These naturally encapsulated pesticidal proteins may then be formulated in accordance with conventional techniques for application to the environment hosting a target pest, e.g., soil, water, and foliage of plants. See, for example U.S. Patent No. 6,468,523 and U.S. Publication No. 20050138685, and the references cited therein. In the present invention, a transformed microorganism (which includes whole organisms, cells, spore(s), pesticidal protein(s), pesticidal component(s), pest-impacting component(s), mutant(s), living or dead cells and cell components, including mixtures of living and dead cells and cell components, and including broken cells and cell components) or an isolated pesticidal protein can be formulated with an acceptable carrier into a pesticidal or agricultural composition(s) that is, for example, a suspension, a solution, an emulsion, a dusting powder, a dispersible granule, a wettable powder, and an emulsifiable concentrate, an aerosol, an impregnated granule, an adjuvant, a coatable paste, and also encapsulations in, for example, polymer substances.

[0108] Agricultural compositions may comprise a polypeptide, a recombinogenic polypeptide or a variant or fragment thereof, as disclosed herein. The agricultural composition disclosed herein may be applied to the environment of a plant or an area of cultivation, or applied to the plant, plant part, plant cell, or seed.

[0109] Such compositions disclosed above may be obtained by the addition of a surface-active agent, an inert carrier, a preservative, a humectant, a feeding stimulant, an attractant, an encapsulating agent, a binder, an emulsifier, a dye, a UV protectant, a buffer, a flow agent or fertilizers, micronutrient donors, or other preparations that influence plant growth. One or more agrochemicals including, but not limited to, herbicides, insecticides, fungicides, bactericides, nematicides, molluscicides, acaracides, plant growth regulators, harvest aids, and fertilizers, can be combined with carriers, surfactants or adjuvants customarily employed in the art of formulation or other components to facilitate product handling and application for particular target pests. Suitable carriers and adjuvants can be solid or liquid and correspond to the substances ordinarily employed in formulation technology, e.g., natural or regenerated mineral substances, solvents, dispersants, wetting agents, tackifiers, binders, or fertilizers. The active

ingredients of the present invention are normally applied in the form of compositions and can be applied to the crop area, plant, or seed to be treated. For example, the compositions of the present invention may be applied to grain in preparation for or during storage in a grain bin or silo, etc. The compositions of the present invention may be applied simultaneously or in succession with other compounds. Methods of applying an active ingredient of the present invention or an agrochemical composition of the present invention that contains at least one of the pesticidal proteins produced by the bacterial strains of the present invention include, but are not limited to, foliar application, seed coating, and soil application. The number of applications and the rate of application depend on the intensity of infestation by the corresponding pest.

[0110] Suitable surface-active agents include, but are not limited to, anionic compounds such as a carboxylate of, for example, a metal; a carboxylate of a long chain fatty acid; an N-acylsarcosinate; mono or di-esters of phosphoric acid with fatty alcohol ethoxylates or salts of such esters; fatty alcohol sulfates such as sodium dodecyl sulfate, sodium octadecyl sulfate or sodium cetyl sulfate; ethoxylated fatty alcohol sulfates; ethoxylated alkylphenol sulfates; lignin sulfonates; petroleum sulfonates; alkyl aryl sulfonates such as alkyl-benzene sulfonates or lower alkylnaphtalene sulfonates, e.g., butyl-naphthalene sulfonate; salts of sulfonated naphthalene-formaldehyde condensates; salts of sulfonated phenol-formaldehyde condensates; more complex sulfonates such as the amide sulfonates, e.g., the sulfonated condensation product of oleic acid and N-methyl taurine; or the dialkyl sulfosuccinates, e.g., the sodium sulfonate of dioctyl succinate. Non-ionic agents include condensation products of fatty acid esters, fatty alcohols, fatty acid amides or fatty-alkyl- or alkenyl-substituted phenols with ethylene oxide, fatty esters of polyhydric alcohol ethers, e.g., sorbitan fatty acid esters, condensation products of such esters with ethylene oxide, e.g., polyoxyethylene sorbitar fatty acid esters, block copolymers of ethylene oxide and propylene oxide, acetylenic glycols such as 2,4,7,9-tetraethyl-5-decyn-4,7-diol, or ethoxylated acetylenic glycols. Examples of a cationic surface-active agent include, for instance, an aliphatic mono-, di-, or polyamine such as an acetate, naphthenate or oleate; or oxygen-containing amine such as an amine oxide of polyoxyethylene alkylamine; an amide-linked amine prepared by the condensation of a carboxylic acid with a di- or polyamine; or a quaternary ammonium salt.

[0111] Examples of inert materials include but are not limited to inorganic minerals such as kaolin, phyllosilicates, carbonates, sulfates, phosphates, or botanical materials such as cork, powdered corncobs, peanut hulls, rice hulls, and walnut shells.

[0112] The compositions of the present invention can be in a suitable form for direct application or as a concentrate of primary composition that requires dilution with a suitable quantity of water or other diluant before application. The pesticidal concentration will vary depending upon the nature of the particular formulation, specifically, whether it is a concentrate or to be used directly. The composition contains 1 to 98% of a solid or liquid inert carrier, and 0 to 50% or 0.1 to 50% of a surfactant (w/w, v/v, or w/v, as appropriate or desired). These compositions will be administered at the labeled rate for the commercial product, for example, about 0.01 lb-5.0 lb. per acre when in dry form and at about 0.01 pts-10 pts per acre when in liquid form.

[0113] In a further embodiment, the compositions, as well as the transformed microorganisms and pesticidal proteins, provided herein can be treated prior to formulation to prolong the pesticidal activity when applied to the environment of a target pest as long as the pretreatment is not deleterious to the pesticidal activity. Such treatment can be by chemical means, physical means, or both, as long as the treatment does not deleteriously affect the properties of the composition(s). Examples of chemical reagents include but are not limited to halogenating agents; aldehydes such as formaldehyde and glutaraldehyde; anti-infectives, such as zephiran chloride; alcohols, such as isopropanol and ethanol; and histological fixatives, such as Bouin's fixative and Helly's fixative (see, for example, Humason (1967) *Animal Tissue Techniques* (W.H. Freeman and Co.).

[0114] In one aspect, pests may be killed or reduced in numbers in a given area by application of the pesticidal proteins provided herein to the area. Alternatively, the pesticidal proteins may be prophylactically applied to an environmental area to prevent infestation by a susceptible pest. Preferably the pest ingests, or is contacted with, a pesticidally-effective amount of the polypeptide. By "pesticidally-effective amount" is intended an amount of the pesticide that is able to bring about death to at least one pest, or to noticeably reduce pest growth, feeding, or normal physiological development. This amount will vary depending on such factors as, for example, the specific target pests to be controlled, the specific environment, location, plant, crop,

or agricultural site to be treated, the environmental conditions, and the method, rate, concentration, stability, and quantity of application of the pesticidally-effective polypeptide composition. The formulations or compositions may also vary with respect to climatic conditions, environmental considerations, and/or frequency of application and/or severity of pest infestation.

[0115] The active ingredients are normally applied in the form of compositions and can be applied to the crop area, plant, or seed to be treated. Methods are therefore provided for providing to a plant, plant cell, seed, plant part or an area of cultivation, an effective amount of the agricultural composition comprising the polypeptide, recombinogenic polypeptide or an active variant or fragment thereof. By "effective amount" is intended an amount of a protein or composition has pesticidal activity that is sufficient to kill or control the pest or result in a noticeable reduction in pest growth, feeding, or normal physiological development. Such decreases in pest numbers, pest growth, pest feeding or pest normal development can comprise any statistically significant decrease, including, for example a decrease of about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 85%, 90%, 95% or greater. For example, the compositions may be applied to grain in preparation for or during storage in a grain bin or silo, etc. The compositions may be applied simultaneously or in succession with other compounds. Methods of applying an active ingredient or an agrochemical composition comprising at least one of the polypeptides, recombinogenic polypeptides, or variants or fragments thereof, as disclosed herein include, but are not limited to, foliar application, seed coating, and soil application.

[0116] Methods for increasing plant yield are provided. The methods comprise providing a plant or plant cell expressing a polynucleotide encoding the pesticidal polypeptide sequence disclosed herein and growing the plant or a seed thereof in a field infested with (or susceptible to infestation by) a pest against which said polypeptide has pesticidal activity. In some embodiments, the polypeptide has pesticidal activity against a lepidopteran, coleopteran, dipteran, hemipteran, or nematode pest, and said field is infested with a lepidopteran, hemipteran, coleopteran, dipteran, or nematode pest. As defined herein, the "yield" of the plant refers to the quality and/or quantity of biomass produced by the plant. By "biomass" is intended any measured plant product. An increase in biomass production is any improvement in the yield

of the measured plant product. Increasing plant yield has several commercial applications. For example, increasing plant leaf biomass may increase the yield of leafy vegetables for human or animal consumption. Additionally, increasing leaf biomass can be used to increase production of plant-derived pharmaceutical or industrial products. An increase in yield can comprise any statistically significant increase including, but not limited to, at least a 1% increase, at least a 3% increase, at least a 5% increase, at least a 10% increase, at least a 20% increase, at least a 30%, at least a 50%, at least a 70%, at least a 100% or a greater increase in yield compared to a plant not expressing the pesticidal sequence. In specific methods, plant yield is increased as a result of improved pest resistance of a plant expressing a pesticidal protein disclosed herein. Expression of the pesticidal protein results in a reduced ability of a pest to infest or feed.

[0117] The plants can also be treated with one or more chemical compositions, including one or more herbicide, insecticide, or fungicide, or combination of two or more thereof.

[0118] Non-limiting embodiments include:

[0119] 1. An isolated polypeptide having pesticidal activity, comprising

(a) a polypeptide comprising an amino acid sequence selected from the group consisting of sequences set forth in SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159; or

(b) a polypeptide comprising an amino acid sequence having at least the percent sequence identity set forth in Table 1 to an amino acid sequence selected from the group consisting of sequences set forth in SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114,

115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159.

[0120] 2. The polypeptide of embodiment 1, wherein said polypeptide comprises the amino acid sequence set forth in SEQ ID NOs. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159.

[0121] 3. A composition comprising the polypeptide of embodiments 1 or 2.

[0122] 4. The polypeptide of embodiment 2, further comprising heterologous amino acid sequences.

[0123] 5. A recombinant nucleic acid molecule that encodes the polypeptide of embodiment 1, wherein said recombinant nucleic acid molecule is not the naturally occurring sequence encoding said polypeptide.

[0124] 6. The recombinant nucleic acid of embodiment 5, wherein said nucleic acid molecule is a synthetic sequence that has been designed for expression in a plant.

[0125] 7. The recombinant nucleic acid molecule of embodiment 6, wherein said nucleic acid molecule is operably linked to a promoter capable of directing expression in a plant cell.

[0126] 8. The recombinant nucleic acid molecule of embodiment 5, wherein said nucleic acid molecule is operably linked to a promoter capable of directing expression in a bacteria.

[0127] 9. A host cell that contains the recombinant nucleic acid molecule of embodiment 8.

[0128] 10. The host cell of embodiment 9, wherein said host cell is a bacterial host cell.

[0129] 11. A DNA construct comprising a promoter that drives expression in a plant cell operably linked to a recombinant nucleic acid molecule comprising

(a) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159; or,

(b) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence having at least the percent sequence identity set forth in Table 1 to an amino acid sequence selected from the group consisting of sequences set forth in SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159.

[0130] 12. The DNA construct of embodiment 11, wherein said nucleotide sequence is a synthetic DNA sequence that has been designed for expression in a plant.

[0131] 13. A vector comprising the DNA construct of embodiment 11.

[0132] 14. A host cell that contains the DNA construct of any one of embodiments 11-13.

[0133] 15. The host cell of embodiment 14, wherein the host cell is a plant cell.

[0134] 16. A transgenic plant comprising the host cell of embodiment 15.

[0135] 17. A composition comprising the host cell of embodiment 10.

[0136] 18. The composition of embodiment 17, wherein said composition is selected from the group consisting of a powder, dust, pellet, granule, spray, emulsion, colloid, and solution.

[0137] 19. The composition of embodiment 17, wherein said composition comprises from about 1% to about 99% by weight of said polypeptide.

[0138] 20. A method for controlling a pest population comprising contacting said population with a pesticidal-effective amount of the composition of embodiment 3 or 17.

[0139] 21. A method for killing a pest population comprising contacting said population with a pesticidal-effective amount of the composition of embodiment 3 or 17.

[0140] 22. A method for producing a polypeptide with pesticidal activity, comprising culturing the host cell of embodiment 9 under conditions in which the nucleic acid molecule encoding the polypeptide is expressed.

[0141] 23. A plant having stably incorporated into its genome a DNA construct comprising a nucleotide sequence that encodes a protein having pesticidal activity, wherein said nucleotide sequence comprise

(a) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159; or,

(b) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence having at least the percent sequence identity set forth in Table 1 to an amino acid sequence selected from the group consisting of sequences set forth in SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84,

85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159.

[0142] 24. A transgenic seed of the plant of embodiment 23.

[0143] 25. A method for protecting a plant from an insect pest, comprising expressing in a plant or cell thereof a nucleotide sequence that encodes a pesticidal polypeptide, wherein said nucleotide sequence comprising.

(a) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159; or,

(b) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence having at least the percent sequence identity set forth in Table 1 to an amino acid sequence selected from the group consisting of sequences set forth in SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159.

[0144] 26. The method of embodiment 25, wherein said plant produces a pesticidal polypeptide having pesticidal against a lepidopteran or coleopteran pest or a Hemipteran pest.

[0145] 27. A method for increasing yield in a plant comprising growing in a field a plant or seed thereof having stably incorporated into its genome a DNA construct comprising a promoter that drives expression in a plant operably linked to a nucleotide sequence that encodes a pesticidal polypeptide, wherein said nucleotide sequence comprises.

(a) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159; or,

(b) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence having at least the percent sequence identity set forth in Table 1 to an amino acid sequence selected from the group consisting of sequences set forth in SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, and/or 159.

[0146] The following examples are offered by way of illustration and not by way of limitation.

EXAMPLES

Example 1: Discovery of Novel Genes by Sequencing and DNA Analysis

[0147] Microbial cultures were grown in liquid culture in standard laboratory media. Cultures were grown to saturation (16 to 24 hours) before DNA preparation. DNA was extracted from bacterial cells by detergent lysis, followed by binding to a silica matrix and washing with an

ethanol buffer. Purified DNA was eluted from the silica matrix with a mildly alkaline aqueous buffer.

[0148] DNA for sequencing was tested for purity and concentration by spectrophotometry. Sequencing libraries were prepared using the Nextera XT library preparation kit according to the manufacturer's protocol. Sequence data was generated on a HiSeq 2000 according to the Illumina HiSeq 2000 System User Guide protocol.

[0149] Sequencing reads were assembled into draft genomes using the CLC Bio Assembly Cell software package. Following assembly, gene calls were made by several methods and resulting gene sequences were interrogated to identify novel homologs of pesticidal genes. Novel genes were identified by BLAST, by domain composition, and by pairwise alignment versus a target set of pesticidal genes. A summary of such sequences is set forth in Table 1.

[0150] Genes identified in the homology search were amplified from bacterial DNA by PCR and cloned into bacterial expression vectors containing fused in-frame purification tags. Cloned genes were expressed in *E. coli* and purified by column chromatography. Purified proteins were assessed in insect diet bioassay studies to identify active proteins.

[0151] Insect diet bioassays were performed using a wheat germ and agar artificial diet to which purified protein were applied as a surface treatment. Insect larvae were applied to treated diet and monitored for mortality.

[0152] Insect diet bioassays were performed using a sucrose liquid diet contained in a membrane sachet to which purified protein was added. Insect nymphs were allowed to feed on the diet sachet and were monitored for mortality. Insects tested in bioassays included the Brown Stink Bug (BSB), *Euschistus servus*, and the Southern Green Stink Bug (SGSB), *Nezara viridula*. Data is listed in the below in Table 5.

Table 5. Bioassay Results

Gene	**Expression Level**	**Test 1**	**Test 2**	**Test 3**
APG00059	Very Low (<10 ppm)	+ BSB	+ SGSB	+ SGSB
APG00046	High (>500ppm)	+ BSB	+ BSB	
APG00002	Low (50 ppm)	+ SGSB	+ SGSB	+ SGSB

BSB = Brown Stink Bug, SGSB = Southern Green Stink Bug

Example 2. Heterologous Expression in *E. coli*

[0153] Each open reading frame set forth in Tables 6 and 7 was cloned into an *E. coli* expression vector containing a maltose binding protein (pMBP). The expression vector was transformed into BL21*RIPL. An LB culture supplemented with carbenicillin was inoculated with a single colony and grown overnight at 37°C using 0.5% of the overnight culture, a fresh culture was inoculated and grown to logarithmic phase at 37°C. The culture was induced using 250 mM IPTG for 18 hours at 16°C. The cells were pelleted and resuspended in 10mM Tris pH7.4 and 150 mM NaCl supplemented with protease inhibitors. The protein expression was evaluated by SDS-PAGE.

Example 3. Pesticidal Activity against Coleopteran and Lepidoptera

[0154] *Protein Expression:* Each sequence set forth in Table 6 was expressed in *E. coli* as described in Example 2. 400 mL of LB was inoculated and grown to an OD600 of 0.6. The culture was induced with 0.25mM IPTG overnight at 16°C. The cells were spun down and the cell pellet was resuspend in 5 mL of buffer. The resuspension was sonicated for 2 min on ice.

[0155] *Bioassay:* Fall army worm (FAW), corn ear worm (CEW), European corn borer (ECB) southwestern corn borer (SWCB) and diamond backed moth (DBM) eggs were purchased from a commercial insectary (Benzon Research Inc., Carlisle, PA). The FAW, CEW, ECB and BCW eggs were incubated to the point that eclosion would occur within 12 hrs of the assay setup. SWCB and DBM were introduced to the assay as neonate larvae. Assays were carried out in 24-well trays containing multispecies lepidopteran diet (Southland Products Inc., Lake Village, AR). Samples of the sonicated lysate were applied to the surface of the diet (diet overlay) and allowed to evaporate and soak into the diet. For CEW, FAW, BCW, ECB and SWCB, a 125 µl of sonicated lysate was added to the diet surface and dried. For DBM, 50 µl of a 1:2 dilution of sonicated lysate was added to the diet surface. The bioassay plates were sealed with a plate sealing film vented with pin holes. The plates were incubated at 26°C at 65% relative humidity (RH) on a 16:8 day:night cycle in a Percival for 5 days. The assays were assessed for level of mortality, growth inhibition and feeding inhibition.

[0156] For the western corn rootworm bioassay, the protein construct/lysate was evaluated in an insect bioassay by dispensing 60 µl volume on the top surface of diet in well/s of 24-well plate (Cellstar, 24-well, Greiner Bio One) and allowed to dry. Each well contained 500 µl diet

(Marrone et al., 1985). Fifteen to twenty neonate larvae were introduced in each well using a fine tip paint brush and the plate was covered with membrane (Viewseal, Greiner Bio One). The bioassay was stored at ambient temperature and scored for mortality, and/or growth/feeding inhibition at day 4. Figure 7 provides the assay scoring guidelines for the corn root worm bioassay.

[0157] For Colorado Potato Beetle (CPB) a cork bore size No. 8 leaf disk was excised from potato leaf and was dipped in the protein construct/lysate until thoroughly wet and placed on top of filter disk (Millipore, glass fiber filter, 13 mm). 60 µl dH_2O was added to each filter disk and placed in each well of 24-well plate (Cellstar, 24-well, Greiner Bio One). The leaf disk was allowed to dry and five to seven first instar larvae were introduced in each well using a fine tip paint brush. The plate was covered with membrane (Viewseal, Greiner Bio One) and small hole was punctured in each well of the membrane. The construct was evaluated with four replicates, and scored for mortality and leaf damage on day 3.

[0158] Table 6 provides a summary of pesticidal activity against coleopteran and lepidoptera of the various sequences. Table code: "-" indicates no activity seen; "NT" indicates not tested; "S" indicates stunt; "SS" indicates slight stunt; "LF" indicates low feeding.

Table 6. Summary of Pesticidal Activity against Coleopteran and Lepidoptera.

			Tested Against:							
AgB Ref. No.	SEQ ID NO	# of variants	FAW	CEW	BCW	ECB	SWCB	CPB	Px	CRW
APG00010	9	1	NT	-	-	-	-	NT	NT	>80% mortality
APG00034	15	1	-	-	-	-	-	-	-	>80% mortality
APG00076	93	2	-	-	-	-	-	-	-	50-80% mortality
APG00039	17	2	-	SS	-	-	-	-	-	-
APG00008	7	1	SS	-	-	SS	-	-	-	>80% mortality
APG00052	25	2	S, LF	-	-	-	SS	-	-	50-80% mortality

APG00065	32	1	NT	SS	-	-	NT	-	-	NT
APG00124	71	2	NT	S	-	-	NT	NT	NT	-
APG00130	94	1	-	-	-	-	-	NT	NT	>80% mortality

Example 4. Pesticidal Activity against Hemipteran

[0159] *Protein Expression:* Each of the sequences set forth in Table 7 was expressed in *E. coli* as described in Example 2. 400 mL of LB was inoculated and grown to an OD600 of 0.6. The culture was induced with 0.25mM IPTG overnight at 16°C. The cells were spun down and the cell pellet was re-suspend in 5 mL of buffer. The resuspension was sonicated for 2 min on ice.

[0160] Second instar SGSB were obtained from a commercial insectary (Benzon Research Inc., Carlisle, PA). A 50% v/v ratio of sonicated lysate sample to 20% sucrose was employed in the bioassay. Stretched parafilm was used as a feeding membrane to expose the SGSB to the diet/sample mixture. The plates were incubated at 25°C:21°C, 16:8 day:night cycle at 65%RH for 5 days.

[0161] Mortality was scored for each sample. The results are set forth in Table 7. A dashed line indicates no mortality was detected. The protein (APG00034) showed 25% mortality against southern green stinkbug (1 stinkbug out of 4 died). The negative controls (empty vector expressed binding domain and buffer only) both showed no mortality (0 stinkbugs out of 4).

Table 7.Summary of Pesticidal Activity against Hemipteran

AgB Ref. No.	SEQ ID NO	Tested against SGSB
APG00034	15	25% mortality
APG00010	9	---
APG00076	93	---
APG00039	17	----
APG00008	7	---
APG00052	25	---
APG00065	32	---

AgB Ref. No.	SEQ ID NO	Tested against SGSB
APG00124	71	---
APG00130	94	---

Example 5. Transformation of Soybean

[0162] DNA constructs comprising each of SEQ ID NOs: 1-159 or active variants or fragments thereof operably linked to a promoter active in a plant are cloned into transformation vectors and introduced into Agrobacterium as described in U.S. Provisional Application No. 62/094,782, filed December 19, 2015, herein incorporated by reference in its entirety.

[0163] Four days prior to inoculation, several loops of Agrobacterium are streaked to a fresh plate of YEP* medium supplemented with the appropriate antibiotics** (spectinomycin, chloramphenicol and kanamycin). Bacteria are grown for two days in the dark at 28°C. After two days, several loops of bacteria are transferred to 3 ml of YEP liquid medium with antibiotics in a 125 ml Erlenmeyer flask. Flasks are placed on a rotary shaker at 250 RPM at 28°C overnight. One day before inoculation, 2-3 ml of the overnight culture were transferred to 125 ml of YEP with antibiotics in a 500 ml Erlenmeyer flask. Flasks are placed on a rotary shaker at 250 RPM at 28°C overnight.

[0164] Prior to inoculation, the OD of the bacterial culture is checked at OD 620. An OD of 0.8-1.0 indicates that the culture is in log phase. The culture is centrifuged at 4000 RPM for 10 minutes in Oakridge tubes. The supernatant is discarded and the pellet is re-suspended in a volume of Soybean Infection Medium (SI) to achieve the desired OD. The cultures are held with periodic mixing until needed for inoculation.

[0165] Two or three days prior to inoculation, soybean seeds are surface sterilized using chlorine gas. In a fume hood, a petri dish with seeds is place in a bell jar with the lid off. 1.75 ml of 12 N HCl is slowly added to 100 ml of bleach in a 250 ml Erlenmeyer flask inside the bell jar. The lid is immediately placed on top of the bell jar. Seeds are allowed to sterilize for 14-16 hours (overnight). The top is removed from the bell jar and the lid of the petri dish is replaced. The petri dish with the surface sterilized is then opened in a laminar flow for around 30 minutes to disperse any remaining chlorine gas.

[0166] Seeds are imbibed with either sterile DI water or soybean infection medium (SI) for 1-2 days. Twenty to 30 seeds are covered with liquid in a 100x25 mm petri dish and incubated in the dark at 24°C. After imbibition, non-germinating seeds are discarded.

[0167] Cotyledonary explants are processed on a sterile paper plate with sterile filter paper dampened using SI medium employing the methods of U.S. Patent No. 7,473,822, herein incorporated by reference.

[0168] Typically, 16-20 cotyledons are inoculated per treatment. The SI medium used for holding the explants is discarded and replaced with 25 ml of Agrobacterium culture (OD 620=0.8-20). After all explants are submerged, the inoculation is carried out for 30 minutes with periodic swirling of the dish. After 30 minutes, the Agrobacterium culture is removed.

[0169] Co-cultivation plates is prepared by overlaying one piece of sterile paper onto Soybean Co-cultivation Medium (SCC). Without blotting, the inoculated cotyledons is cultured adaxial side down on the filter paper. Around 20 explants can be cultured on each plate. The plates are sealed with Parafilm and cultured at 24°C and around 120 µmoles $m^{-2}s^{-1}$ (in a Percival incubator) for 4-5 days.

[0170] After co-cultivation, the cotyledons are washed 3 times in 25 ml of Soybean Wash Medium with 200 mg/l of cefotaxime and timentin. The cotyledons are blotted on sterile filter paper and then transferred to Soybean Shoot Induction Medium (SSI). The nodal end of the explant is depressed slightly into the medium with distal end kept above the surface at about 45deg. No more than 10 explants are cultured on each plate. The plates are wrapped with Micropore tape and cultured in the Percival at 24°C and around 120 µmoles $m^{-2}s^{-1}$.

[0171] The explants are transferred to fresh SSI medium after 14 days. Emerging shoots from the shoot apex and cotyledonary node are discarded. Shoot induction is continued for another 14 days under the same conditions.

[0172] After 4 weeks of shoot induction, the cotyledon is separated from the nodal end and a parallel cut is made underneath the area of shoot induction (shoot pad). The area of the parallel cut is placed on Soybean Shoot Elongation Medium (SSE) and the explants cultured in the Percival at 24°C and around 120 µmoles $m^{-2}s^{-1}$. This step is repeated every two weeks for up to 8 weeks as long as shoots continue to elongate.

[0173] When shoots reach a length of 2-3 cm, they are transferred to Soybean Rooting Medium (SR) in a Plantcon vessel and incubated under the same conditions for 2 weeks or until roots reach a length of around 3-4 cm. After this, plants are transferred to soil.

[0174] Note, all media mentioned for soybean transformation are found in Paz et al. (2010) Agrobacterium-mediated transformation of soybean and recovery of transgenic soybean plants; Plant Transformation Facility of Iowa State University, which is herein incorporated by reference in its entirety. (See, agron-www.agron.iastate.edu/ptf/protocol/Soybean.pdf.)

Example 6. Transformation of Maize

[0175] Maize ears are best collected 8-12 days after pollination. Embryos are isolated from the ears, and those embryos 0.8-1.5 mm in size are preferred for use in transformation. Embryos are plated scutellum side-up on a suitable incubation media, such as DN62A5S media (3.98 g/L N6 Salts; 1 mL/L (of 1000X Stock) N6 Vitamins; 800 mg/L L-Asparagine; 100 mg/L Myo-inositol; 1.4 g/L L-Proline; 100 mg/L Casamino acids; 50 g/L sucrose; 1 mL/L (of 1 mg/mL Stock) 2,4-D). However, media and salts other than DN62A5S are suitable and are known in the art. Embryos are incubated overnight at 25°C in the dark. However, it is not necessary per se to incubate the embryos overnight.

[0176] The resulting explants are transferred to mesh squares (30-40 per plate), transferred onto osmotic media for about 30-45 minutes, and then transferred to a beaming plate (see, for example, PCT Publication No. WO/0138514 and U.S. Patent No. 5,240,842). DNA constructs designed to express the GRG proteins of the present invention in plant cells are accelerated into plant tissue using an aerosol beam accelerator, using conditions essentially as described in PCT Publication No. WO/0138514. After beaming, embryos are incubated for about 30 min on osmotic media, and placed onto incubation media overnight at 25°C in the dark. To avoid unduly damaging beamed explants, they are incubated for at least 24 hours prior to transfer to recovery media. Embryos are then spread onto recovery period media, for about 5 days, 25°C in the dark, and then transferred to a selection media. Explants are incubated in selection media for up to eight weeks, depending on the nature and characteristics of the particular selection utilized. After the selection period, the resulting callus is transferred to embryo maturation media, until the formation of mature somatic embryos is observed. The resulting mature somatic embryos are then placed under low light, and the process of regeneration is initiated by methods known in the

art. The resulting shoots are allowed to root on rooting media, and the resulting plants are transferred to nursery pots and propagated as transgenic plants.

Example 7. Pesticidal activity against Nematodes

Heterodera glycine's (Soybean Cyst Nematode) *in vitro* assay

[0177] Soybean Cyst Nematodes are dispensed into a 96 well assay plate with a total volume of 100uls and 100 J2 per well. The protein of interest as set forth in any one of SEQ ID NOs: 1-159 is dispensed into the wells and held at room temperature for assessment. Finally, the 96 well plate containing the SCN J2 is analyzed for motility. Data is reported as % inhibition as compared to the controls. Hits are defined as greater or equal to 70% inhibition.

Heterodera glycine's (Soybean Cyst Nematode) on-plant assay

[0178] Soybean plants expressing one or more of SEQ ID NOs: 1-159 are generated as described elsewhere herein. A 3-week-old soybean cutting is inoculated with 5000 SCN eggs per plant. This infection is held for 70days and then harvested for counting of SCN cyst that has developed on the plant. Data is reported as % inhibition as compared to the controls. Hits are defined as greater or equal to 90% inhibition.

Meloidogyne incognita (Root-Knot Nematode) *in vitro* assay

[0179] Root-Knot Nematodes are dispensed into a 96 well assay plate with a total volume of 100uls and 100 J2 per well. The protein of interest comprising any one of SEQ ID NOs: 1-159 is dispensed into the wells and held at room temperature for assessment. Finally the 96 well plate containing the RKN J2 is analyzed for motility. Data is reported as % inhibition as compared to the controls. Hits are defined as greater or equal to 70% inhibition.

Meloidogyne incognita (Root-Knot Nematode) on-plant assay

[0180] Soybean plants expressing one or more of SEQ ID NOs: 1-159 are generated as described elsewhere herein. A 3-week-old soybean is inoculated with 5000 RKN eggs per plant. This infection is held for 70days and then harvested for counting of RKN eggs that have developed in the plant. Data is reported as % inhibition as compared to the controls. Hits are defined as greater or equal to 90% inhibition.

Example 8. Additional Assays for Pesticidal Activity

[0181] The various polypeptides set forth in SEQ ID NOs: 1-159 can be tested to act as a pesticide upon a pest in a number of ways. One such method is to perform a feeding assay. In such a feeding assay, one exposes the pest to a sample containing either compounds to be tested or control samples. Often this is performed by placing the material to be tested, or a suitable dilution of such material, onto a material that the pest will ingest, such as an artificial diet. The material to be tested may be composed of a liquid, solid, or slurry. The material to be tested may be placed upon the surface and then allowed to dry. Alternatively, the material to be tested may be mixed with a molten artificial diet, and then dispensed into the assay chamber. The assay chamber may be, for example, a cup, a dish, or a well of a microtiter plate.

[0182] Assays for sucking pests (for example aphids) may involve separating the test material from the insect by a partition, ideally a portion that can be pierced by the sucking mouth parts of the sucking insect, to allow ingestion of the test material. Often the test material is mixed with a feeding stimulant, such as sucrose, to promote ingestion of the test compound.

[0183] Other types of assays can include microinjection of the test material into the mouth, or gut of the pest, as well as development of transgenic plants, followed by test of the ability of the pest to feed upon the transgenic plant. Plant testing may involve isolation of the plant parts normally consumed, for example, small cages attached to a leaf, or isolation of entire plants in cages containing insects.

[0184] Other methods and approaches to assay pests are known in the art, and can be found, for example in Robertson and Preisler, eds. (1992) Pesticide bioassays with arthropods, CRC, Boca Raton, Fla. Alternatively, assays are commonly described in the journals Arthropod Management Tests and Journal of Economic Entomology or by discussion with members of the Entomological Society of America (ESA). Any one of SEQ ID NOS: 1-159 can be expressed and employed in an assay as set forth in Examples 3 and 4, herein.

[0185] All publications and patent applications mentioned in the specification are indicative of the level of skill of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

[0186] Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims.

THAT WHICH IS CLAIMED IS:

1. A recombinant polypeptide having pesticidal activity, comprising

(a) a polypeptide comprising an amino acid sequence having at least 90% percent sequence identity to an amino acid sequence selected from the group consisting of sequences set forth in SEQ ID NOs: 15, 9, 93, 17, 7, 25, 32, 71, or 94; or,

(b) a polypeptide comprises the amino acid sequence set forth in SEQ ID NOs: 15, 9, 93, 17, 7, 25, 32, 71, or 94.

2. The polypeptide of claim 1, further comprising a heterologous amino acid sequence.

3. A composition comprising the polypeptide of claims 1 or 2.

4. A recombinant nucleic acid molecule encoding an amino acid sequence comprising

(a) at least 90% percent sequence identity to an amino acid sequence selected from the group consisting of sequences set forth in SEQ ID NOs: 15, 9, 93, 17, 7, 25, 32, 71, or 94; or

(b) the amino acid sequence set forth in SEQ ID NOs: 15, 9, 93, 17, 7, 25, 32, 71, or 94;

wherein said recombinant nucleic acid molecule is not the naturally occurring sequence encoding said polypeptide.

5. The recombinant nucleic acid of claim 4, wherein said nucleic acid molecule is a synthetic sequence designed for expression in a plant.

6. The recombinant nucleic acid molecule of claims 4 or 5, wherein said nucleic acid molecule is operably linked to a promoter capable of directing expression in a plant cell.

7. The recombinant nucleic acid molecule of any one of claims 4 to 6, wherein said nucleic acid molecule is operably linked to a promoter capable of directing expression in a bacteria.

8. A host cell comprising the recombinant nucleic acid molecule of any one of claims 4 to 7.

9. The host cell of claim 8, wherein said host cell is a bacterial host cell.

10. A DNA construct comprising a promoter that drives expression in a plant cell operably linked to a recombinant nucleic acid molecule comprising a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence having at least 90% percent sequence identity to an amino acid sequence selected from the group consisting of sequences set forth in SEQ ID NOs: 15, 9, 93, 17, 7, 25, 32, 71, or 94.

11. The DNA construct of claim 10, wherein said nucleotide sequence is a synthetic DNA sequence designed for expression in a plant.

12. A vector comprising the DNA construct of claim 10.

13. A host cell comprising the DNA construct of claims 12 or 13.

14. A composition comprising the host cell of claim 13.

15. The composition of claim 14, wherein said composition is selected from the group consisting of a powder, dust, pellet, granule, spray, emulsion, colloid, and solution.

16. The composition of claim 15, wherein said composition comprises from about 1% to about 99% by weight of said polypeptide.

17. A method for controlling a pest population comprising contacting said pest population with a pesticidal-effective amount of the composition of claims 3 or 14.

18. A method for producing a polypeptide with pesticidal activity comprising culturing the host cell of claims 8 or 13 under conditions in which the nucleic acid molecule encoding the polypeptide is expressed.

19. A plant having stably incorporated into its genome a DNA construct comprising a nucleotide sequence that encodes a protein having pesticidal activity, wherein said nucleotide sequence comprise

(a) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 15, 9, 93, 17, 7, 25, 32, 71, or 94; or

(b) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence having at least 90% percent sequence identity to an amino acid sequence selected from the group consisting of sequences set forth in SEQ ID NOs: 15, 9, 93, 17, 7, 25, 32, 71, or 94.

20. A transgenic seed of the plant of claim 19.

21. A method for protecting a plant from an insect pest, comprising expressing in a plant or cell thereof a nucleotide sequence that encodes a pesticidal polypeptide, wherein said nucleotide sequence comprising

(a) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 15, 9, 93, 17, 7, 25, 32, 71, or 94; or

(b) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence having at least 90% percent sequence identity to an amino acid sequence selected from the group consisting of sequences set forth in SEQ ID NOs: 15, 9, 93, 17, 7, 25, 32, 71, or 94.

22. The method of claim 21, wherein said plant produces a pesticidal polypeptide having pesticidal against a lepidopteran or coleopteran pest or a Hemipteran pest.

23. A method for increasing yield in a plant comprising growing in a field a plant or seed thereof having stably incorporated into its genome a DNA construct comprising a promoter that drives expression in a plant operably linked to a nucleotide sequence that encodes a pesticidal polypeptide, wherein said nucleotide sequence comprises

(a) a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence of any one of SEQ ID NOs: 15, 9, 93, 17, 7, 25, 32, 71, or 94; or

(b) a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence having at least 90% percent sequence identity to an amino acid sequence selected from the group consisting of sequences set forth in SEQ ID NOs: 15, 9, 93, 17, 7, 25, 32, 71, or 94.

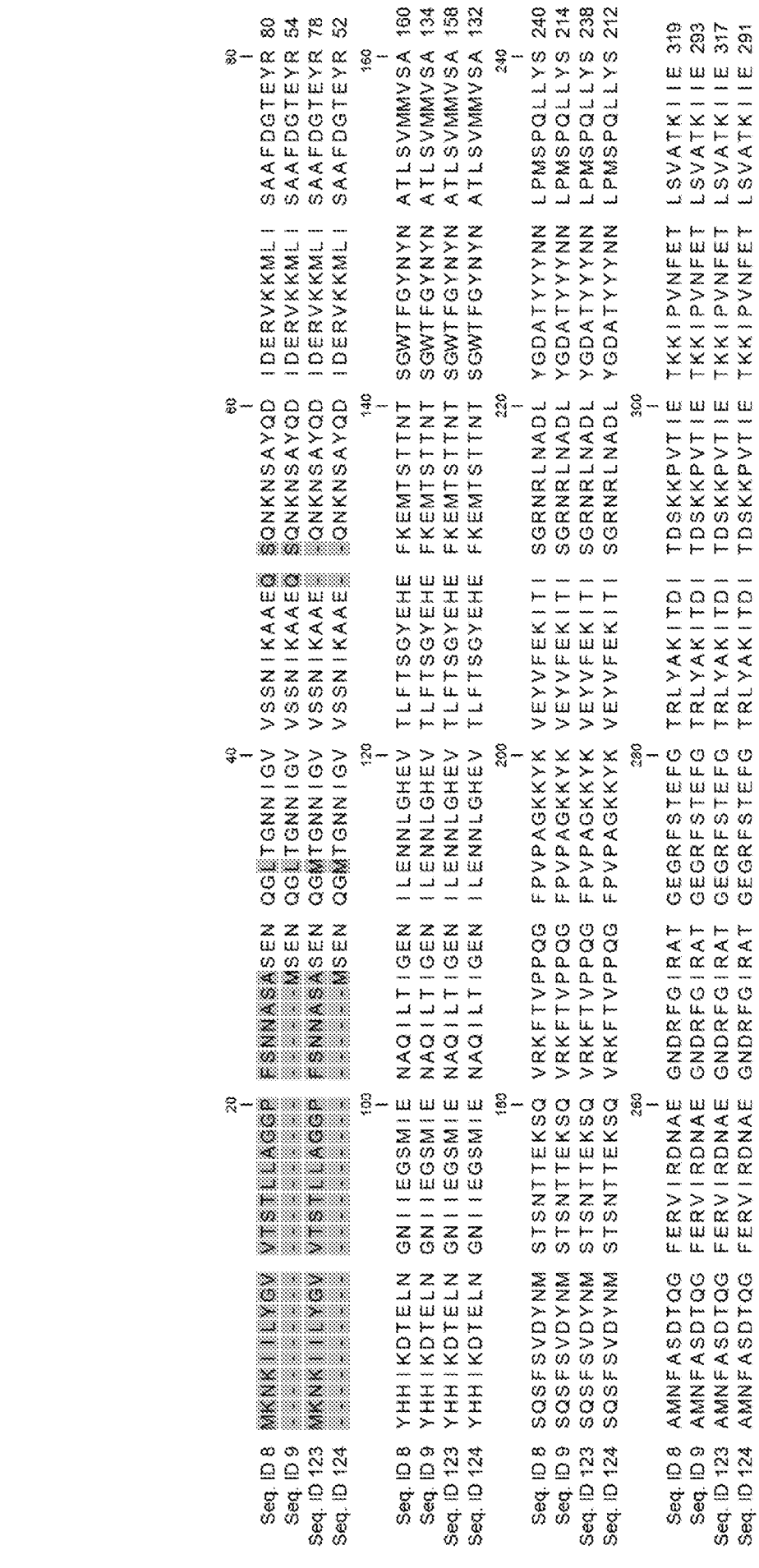

Seq. ID 8 MKNKIILYGV VTSTLLAGGP FSNNASASEN QGLTGNNIGV VSSNIKAAEQ SQNKNSAYQD IDERVKKMLI SAAFDGTEYR 80
Seq. ID 9 ---------- ---------- ------MSEN QGLTGNNIGV VSSNIKAAEQ SQNKNSAYQD IDERVKKMLI SAAFDGTEYR 54
Seq. ID 123 MKNKIILYGV VTSTLLAGGP FSNNASASEN QGMTGNNIGV VSSNIKAAEI QQNKNSAYQD IDERVKKMLI SAAFDGTEYR 78
Seq. ID 124 ---------- ---------- ------MSEN QGMTGNNIGV VSSNIKAAEI QQNKNSAYQD IDERVKKMLI SAAFDGTEYR 52
Seq. ID 8 YHHIKDTELN GNIIEGSMIE NAQILTIGEN ILENNLGHEV TLFTSGYEHE FKEMTSTTNT SGWTFGYNYN ATLSVMMVSA 160
Seq. ID 9 YHHIKDTELN GNIIEGSMIE NAQILTIGEN ILENNLGHEV TLFTSGYEHE FKEMTSTTNT SGWTFGYNYN ATLSVMMVSA 134
Seq. ID 123 YHHIKDTELN GNIIEGSMIE NAQILTIGEN ILENNLGHEV TLFTSGYEHE FKEMTSTTNT SGWTFGYNYN ATLSVMMVSA 158
Seq. ID 124 YHHIKDTELN GNIIEGSMIE NAQILTIGEN ILENNLGHEV TLFTSGYEHE FKEMTSTTNT SGWTFGYNYN ATLSVMMVSA 132
Seq. ID 8 SQSFSVDYNM STSNTTEKSQ VRKFTVPPQG FPVPAGKKYK VEYVFEKITI SGRNRLNADL YGDATYYYNN LPMSPQLLYS 240
Seq. ID 9 SQSFSVDYNM STSNTTEKSQ VRKFTVPPQG FPVPAGKKYK VEYVFEKITI SGRNRLNADL YGDATYYYNN LPMSPQLLYS 214
Seq. ID 123 SQSFSVDYNM STSNTTEKSQ VRKFTVPPQG FPVPAGKKYK VEYVFEKITI SGRNRLNADL YGDATYYYNN LPMSPQLLYS 238
Seq. ID 124 SQSFSVDYNM STSNTTEKSQ VRKFTVPPQG FPVPAGKKYK VEYVFEKITI SGRNRLNADL YGDATYYYNN LPMSPQLLYS 212
Seq. ID 8 AMNFASDTQG FERVIRDNAE GNDRFGIRAT GEGRFSTEFG TRLYAKITDI TDSKKPVTIE TKKIPVNFET LSVATKIIE 319
Seq. ID 9 AMNFASDTQG FERVIRDNAE GNDRFGIRAT GEGRFSTEFG TRLYAKITDI TDSKKPVTIE TKKIPVNFET LSVATKIIE 293
Seq. ID 123 AMNFASDTQG FERVIRDNAE GNDRFGIRAT GEGRFSTEFG TRLYAKITDI TDSKKPVTIE TKKIPVNFET LSVATKIIE 317
Seq. ID 124 AMNFASDTQG FERVIRDNAE GNDRFGIRAT GEGRFSTEFG TRLYAKITDI TDSKKPVTIE TKKIPVNFET LSVATKIIE 291

Figure 1

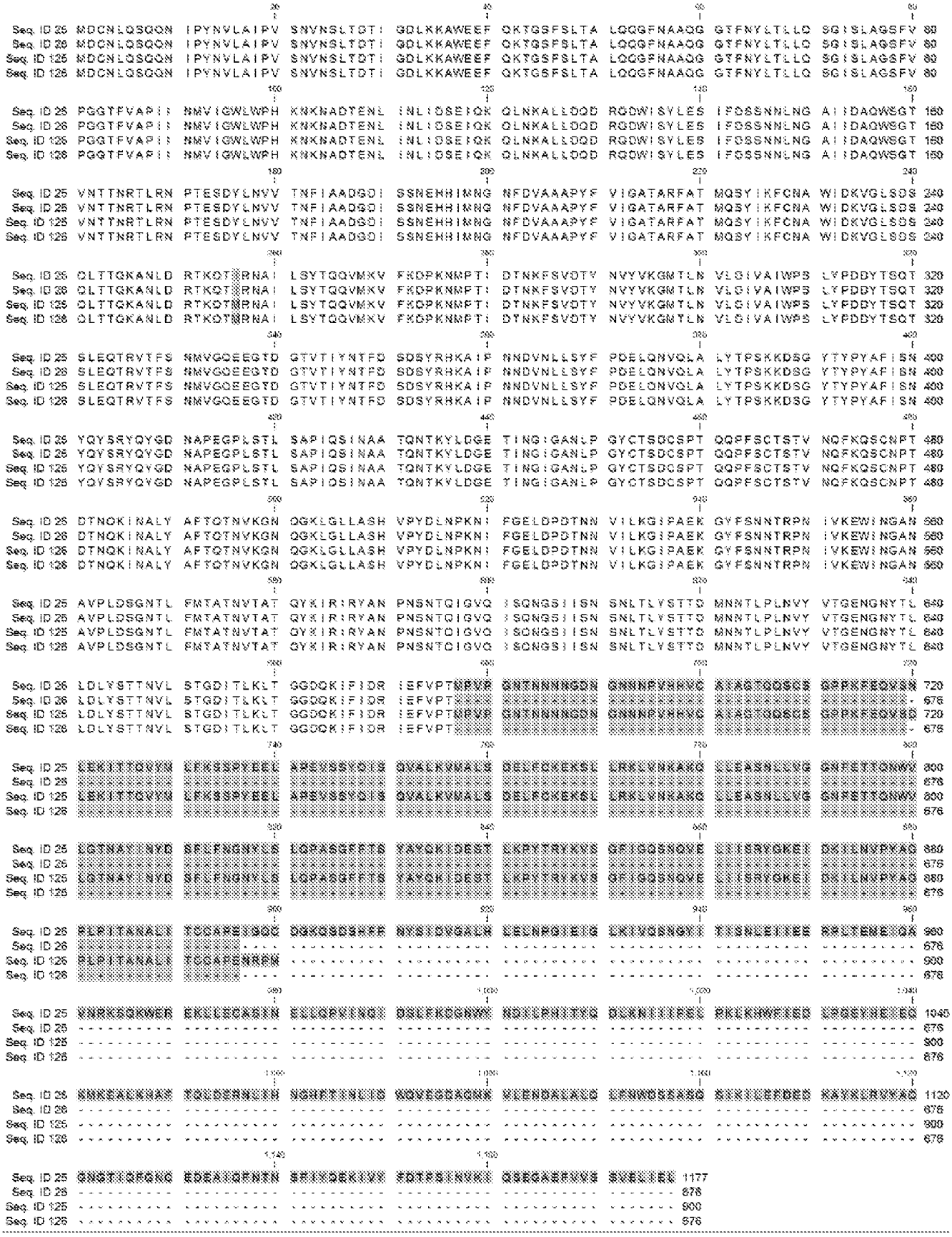


Figure 2

Seq. ID 72 MGGLEMMQYY NMNEYEILDN GVQCCSPRYP LAQAPGSEWQ NMNYQDVMNT SVGREYQAVQ QVNVGEAVGA ALGILTTILK 80
Seq. ID 94 MNQYY NMNEYEILDN GVQCCSPRYP LAQAPGSEWQ NMNYQDVMNT SVGREYQAVQ QVNVGEAVGA ALGILTTILK 75
Seq. ID 127 MGGLEMMQYY NMNEYEILDN GVQCCSPRYP LAQAPGSEWQ NMNYQDVMNT SVGREYQAVQ QVNVGEAVGA ALGILTTILK 80
Seq. ID 128 MMQYY NMNEYEILDN GVQCCSPRYP LAQAPGSEWQ NMNYQDVMNT SVGREYQAVQ QVNVGEAVGA ALGILTTILK 75
Seq. ID 72 AVNPTLGTAA GVISSIFGFL WKRFGTDPQA QWKQFMEAVE YLVSQKITDA VRSKAVSELE GVQRAVELYQ EAANAWNMMP 160
Seq. ID 94 AVNPTLGTAA GVISSIFGFL WKRFGTDPQA QWKQFMEAVE YLVSQKITDA VRSKAVSELE GVQRAVELYQ EAANAWNMMP 155
Seq. ID 127 AVNPTLGTAA GVISSIFGFL WKRFGTDPQA QWKQFMEAVE YLVSQKITDA VRSKAVSELE GVQRAVELYQ EAANAWNMMP 160
Seq. ID 128 AVNPTLGTAA GVISSIFGFL WKRFGTDPQA QWKQFMEAVE YLVSQKITDA VRSKAVSELE GVQRAVELYQ EAANAWNMMP 155
Seq. ID 72 DMAAAKERIR RQYTSTNTVI EYAMPSFRVG SFEVPLLTVY AQAANLHLLL LRDAVKFGAG WGFSPTEVED NYTRLQARTA 240
Seq. ID 94 DMAAAKERIR RQYTSTNTVI EYAMPSFRVG SFEVPLLTVY AQAANLHLLL LRDAVKFGAG WGFSPTEVED NYTRLQARTA 235
Seq. ID 127 DMAAAKERIR RQYTSTNTVI EYAMPSFRVG SFEVPLLTVY AQAANLHLLL LRDAVKFGAG WGFSPTEVED NYTRLQARTA 240
Seq. ID 128 DMAAAKERIR RQYTSTNTVI EYAMPSFRVG SFEVPLLTVY AQAANLHLLL LRDAVKFGAG WGFSPTEVED NYTRLQARTA 235
Seq. ID 72 EYTNHCTNTY DKGLKQAYDL APNPTQYNKY PYLNPYSKQP IYGKYYTAPV QWNLFNDFRR DMTLMVLDIV AVWPTYNPRL 320
Seq. ID 94 EYTNHCTNTY DKGLKQAYDL APNPTQYNKY PYLNPYSKQP IYGKYYTAPV QWNLFNDFRR DMTLMVLDIV AVWPTYNPRL 315
Seq. ID 127 EYTNHCTNTY DKGLKQAYDL APNPTQYNKY PYLNPYSKQP IYGKYYTAPV QWNLFNDFRR DMTLMVLDIV AVWPTYNPRL 320
Seq. ID 128 EYTNHCTNTY DKGLKQAYDL APNPTQYNKY PYLNPYSKQP IYGKYYTAPV QWNLFNDFRR DMTLMVLDIV AVWPTYNPRL 315
Seq. ID 72 YNNPNGVQIQ LSREVYSTVY GRGWSNNSTV DAIESTLVRP PHLVTELTKL TFDERNLYEA ETVPVAFRKV TNTLHYYGSS 400
Seq. ID 94 YNNPNGVQIQ LSREVYSTVY GRGWSNNSTV DAIESTLVRP PHLVTELTKL TFDERNLYEA ETVPVAFRKV TNTLHYYGSS 395
Seq. ID 127 YNNPNGVQIQ LSREVYSTVY GRGWSNNSTV DAIESTLVRP PHLVTELTKL TFDERNLYEA ETVPVAFRKV TNTLHYYGSS 400
Seq. ID 128 YNNPNGVQIQ LSREVYSTVY GRGWSNNSTV DAIESTLVRP PHLVTELTKL TFDERNLYEA ETVPVAFRKV TNTLHYYGSS 395
Seq. ID 72 TTWEQSFSAT PVGSLKAVHN VLATDIGNLA LSLGAVPLGF SFYNKNDQHI TTVGYSGGWW NGIPKDEGSN QNSHHLSYVA 480
Seq. ID 94 TTWEQSFSAT PVGSLKAVHN VLATDIGNLA LSLGAVPLGF SFYNKMDQHI TTVGYSGGWW NGIPKDEGSN QNSHHLSYVA 475
Seq. ID 127 TTWEQSFSAT PVGSLKAVHN VLATDIGNLA LSLGAVPLGF SFYNKMDQHI TTVGYSGGWW NGIPKDEGSN QNSHHLSYVA 480
Seq. ID 128 TTWEQSFSAT PVGSLKAVHN VLATDIGNLA LSLGAVPLGF SFYNKNDQHI TTVGYSGGWW NGIPKDEGSN QNSHHLSYVA 475
Seq. ID 72 ALETQTTAGW FPTYPVPLLG EWGFGMQHNS LKYTNRLVTN QINQLPAVKA SALVNHARVS KGTTGTGGNI IELVNPNCGF 560
Seq. ID 94 ALETQTTAGW FPTYPVPLLG EWGFGMQHNS LKYTNRLVTN QINQLPAVKA SALVNHARVS KGTTGTGGNI IELVNPNCGF 555
Seq. ID 127 ALETQTTAGW FPTYPVPLLG EWGFGMQHNS LKYTNRLVTN QINQLPAVKA SALVNHARVS KGTTGTGGNI IELVNPNCGF 560
Seq. ID 128 ALETQTTAGW FPTYPVPLLG EWGFGMQHNS LKYTNRLVTN QINQLPAVKA SALVNHARVS KGTTGTGGNI IELVNPNCGF 555
Seq. ID 72 IFNFYAEPEN PQCQAFNIRI RYSATVPGKL NIRHLESGKE FMNTPRDFKG TTTGTMWIPK FQEYQYLDLG PIVLRTGMNY 640
Seq. ID 94 IFNFYAEPEN PQCQAFNIRI RYSATVPGKL NIRHLESGKE FMNTPRDFKG TTTGTMWIPK FQEYQYLDLG PIVLRTGMNY 635
Seq. ID 127 IFNFYAEPEN PQCQAFNIRI RYSATVPGKL NIRHLESGKE FMNTPRDFKG TTTGTMWIPK FQEYQYLDLG PIVLRTGMNY 640
Seq. ID 128 IFNFYAEPEN PQCQAFNIRI RYSATVPGKL NIRHLESGKE FMNTPRDFKG TTTGTMWIPK FQEYQYLDLG PIVLRTGMNY 635
Seq. ID 72 GFKIELASGQ LVSIDKIEFL PF 662
Seq. ID 94 GFKIELASGQ LVSIDKIEFL PF 657
Seq. ID 127 GFKIELASGQ LVSIDKIEFL PF 662
Seq. ID 128 GFKIELASGQ LVSIDKIEFL PF 657

Figure 3

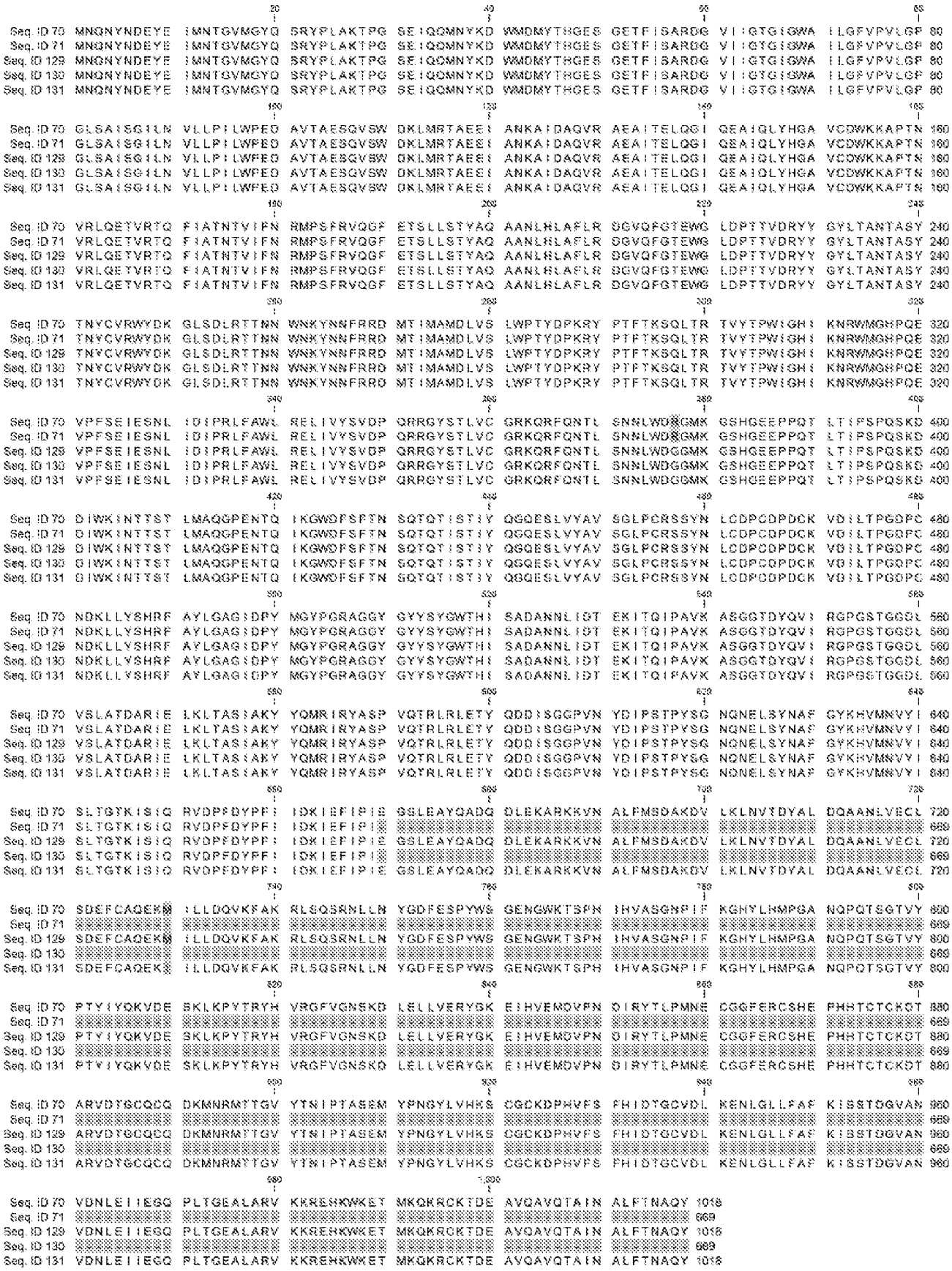


Figure 4

20 40 60 80
Seq. ID 8 ----------L NSKSIIENEV QENQYIDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 7 ----------M NSKSIIENEV QENQYIDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 132 MKGRRPMGNM DSKSVMEKKE QKSQYLDIRD ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTAFDMRH DFTLVADIYL 80
Seq. ID 133 ----------M DSKSVMEKKE QKSQYLDIRD ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTAFDMRH DFTLVADIYL 71
Seq. ID 134 ----------L NSKSIIENEV QENQYIDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 135 ----------M NSKSIIENEV QENQYIDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 136 ----------L NSKSIIENEV QENQYIDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 137 ----------M NSKSIIENEV QENQYIDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 138 ----------M NSKSTIEKEV QKSQYLDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTALDMRH DFTLVADIYL 71
Seq. ID 139 ----------L NSKSIIENEV QENQYIDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 140 ----------M NSKSIIENEV QENQYIDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 141 ----------L NSKSIIENEV QENQYIDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 142 ----------M NSKSIIENEV QENQYIDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 143 ----------L NSKSITEKEI QENQYIDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTALDMKR DFTLVADIYL 71
Seq. ID 144 ----------M NSKSITEKEI QENQYIDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTALDMKR DFTLVADIYL 71
Seq. ID 145 ----------L NSKSIIEKGV QENQYIDIRN ICSINGSAKF DPNTNVTTLT EAINSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 146 ----------M NSKSIIEKGV QENQYIDIRN ICSINGSAKF DPNTNVTTLT EAINSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 147 ----------L NSKSIIENEV QENQYIDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 148 ----------M NSKSIIENEV QENQYIDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTAFDMRH DFTLVADIYL 71
Seq. ID 149 MKGRRPMGNM DSKSVMEKKE QKSQYLDIRD ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTAFDMRH DFTLVADIYL 80
Seq. ID 150 ----------M DSKSVMEKKE QKSQYLDIRD ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTAFDMRH DFTLVADIYL 71
Seq. ID 151 ----------L NSKSIIEKEV QESQYIDIRN ICSINGSAKF DPNTNITTLT EAKNSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 152 ----------M NSKSIIEKEV QESQYIDIRN ICSINGSAKF DPNTNITTLT EAKNSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 153 ----------L NSKSIIENEV QENQYIDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 154 ----------M NSKSIIENEV QENQYIDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 155 ----------M NSKSTIEKEV QKSQYLDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTALDMRH DFTLVADIFL 71
Seq. ID 156 ----------L NSKSIIEKGV QENQYIDIRN ICSINGSAKF DPNTNVTTLT EAINSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 157 ----------M NSKSIIEKGV QENQYIDIRN ICSINGSAKF DPNTNVTTLT EAINSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 158 ----------L NSKSIIEKGV QENQYIDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTALDMRR DFTLVADIYL 71
Seq. ID 159 ----------M NSKSIIEKGV QENQYIDIRN ICSINGSAKF DPNTNITTLT EAINSQAGAI AGKTALDMRR DFTLVADIYL 71

Figure 5A

100
1
120
1
140
1
160
1
Seq. ID 6 GSKSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STNRNASYLT 151
Seq. ID 7 GSKSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STNRNASYLT 151
Seq. ID 132 GSKSSGADGI AIAFHRGSIG FIGQMGGGLG ILGAPNGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STNRNTSYLT 160
Seq. ID 133 GSKSSGADGI AIAFHRGSIG FIGQMGGGLG ILGAPNGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STNRNTSYLT 151
Seq. ID 134 GSKSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STNRNASYLT 151
Seq. ID 135 GSKSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STNRNASYLT 151
Seq. ID 136 GSKSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPSGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STNRNASYLT 151
Seq. ID 137 GSKSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPSGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STNRNASYLT 151
Seq. ID 138 GSKSSGADGI AIAFHRGSIG FIGNMGGGLG ILGAPNGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STNRNASYLT 151
Seq. ID 139 GSKSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STDRKASYLT 151
Seq. ID 140 GSKSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STDRKASYLT 151
Seq. ID 141 GSKSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STNRNASYLT 151
Seq. ID 142 GSKSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STNRNASYLT 151
Seq. ID 143 GSKSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKATS DETGDSFGHG QMNGAHAGFV STNRNASYLT 151
Seq. ID 144 GSKSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKATS DETGDSFGHG QMNGAHAGFV STNRNASYLT 151
Seq. ID 145 GSNSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKATS DETGDSFGHS QMNGAHAGFV STNRNASYLT 151
Seq. ID 146 GSNSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKATS DETGDSFGHS QMNGAHAGFV STNRNASYLT 151
Seq. ID 147 GSKSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STDRKASYLT 151
Seq. ID 148 GSKSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STDRKASYLT 151
Seq. ID 149 GSKSSGADGI AIAFHRGSIG FIGQMGGGLG ILGAPNGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STNRNTSYLT 160
Seq. ID 150 GSKSSGADGI AIAFHRGSIG FIGQMGGGLG ILGAPNGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STNRNTSYLT 151
Seq. ID 151 GSNSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKATS DETGDSFGHG QMNGAHAGFV STNRNASYLT 151
Seq. ID 152 GSNSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKATS DETGDSFGHG QMNGAHAGFV STNRNASYLT 151
Seq. ID 153 GSKSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STNRNASYLT 151
Seq. ID 154 GSKSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STNRNASYLT 151
Seq. ID 155 GSKSSGADGI AITFHRGSIG FIGNMGGGLG ILGAPNGIGF EIDTYWKASS DETGDSFGHG QMNGPHAGFV STNRNASYLT 151
Seq. ID 156 GSNSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKATS DETGDSFGHG QMNGAHAGFV STNRNASYLT 151
Seq. ID 157 GSNSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKATS DETGDSFGHG QMNGAHAGFV STNRNASYLT 151
Seq. ID 158 GSKSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKATS DETGDSFGHG QMNGAHAGFV STNQNASYLT 151
Seq. ID 159 GSKSSGADGI AIAFHRGSIG FIGTMGGGLG ILGAPNGIGF EIDTYWKATS DETGDSFGHG QMNGAHAGFV STNQNASYLT 151

Figure 5B

180
200
220
240
Seq. ID 6 ALAPMQRIPA PNDKWRVLTI NWDARNNKLT ASLQEKNNDA STRSATPRYQ AWELLNPAFD LNQKYTFVIG SATGAANKH 231
Seq. ID 7 ALAPMQRIPA PNDKWRVLTI NWDARNNKLT ASLQEKNNDA STRSATPRYQ AWELLNPAFD LNQKYTFVIG SATGAANKH 231
Seq. ID 132 ALAPMQRIPA PNSKWRILTI NWDARNNKLT ARLQEKNNDD TTRSASPRYQ TWELLNPAFD LNQKYTFVIG SATGAANKH 240
Seq. ID 133 ALAPMQRIPA PNSKWRILTI NWDARNNKLT ARLQEKNNDD TTRSASPRYQ TWELLNPAFD LNQKYTFVIG SATGAANKH 231
Seq. ID 134 ALAPMQRIAP PNGQWRVLTI KWDARDNKLT ASLQEKNNDA STRSATPRYQ TWELLNPAFD LNQKYTFVIG SATGAANKH 231
Seq. ID 135 ALAPMQRIAP PNGQWRVLTI KWDARDNKLT ASLQEKNNDA STRSATPRYQ TWELLNPAFD LNQKYTFVIG SATGAANKH 231
Seq. ID 136 ALAPMQRIAP PNGQWRVLTI KWDARDNKLT ASLQEKNNDA STRSATPRYQ TWELLNPAFD LNQKYTFVIG SATGAANKH 231
Seq. ID 137 ALAPMQRIAP PNGQWRVLTI KWDARDNKLT ASLQEKNNDA STRSATPRYQ TWELLNPAFD LNQKYTFVIG SATGAANKH 231
Seq. ID 138 ALAPMQRIST PNGKWRVLTI NWDARNNKLT ARLQEKNNDA STSSASPRYQ TWELLNPAFD LNQKYTFVIG SATGAANKH 231
Seq. ID 139 ALAPMQRIAP PNGQWRVLTI KWDARDNKLT ASLQEKNNDA STRSATPRYQ TWELLNPAFD LNQKYTFVIG SATGAANKH 231
Seq. ID 140 ALAPMQRIAP PNGQWRVLTI KWDARDNKLT ASLQEKNNDA STRSATPRYQ TWELLNPAFD LNQKYTFVIG SATGAANKH 231
Seq. ID 141 ALAPMQRIPA PNDKWRVLTI NWDARNNKLT ASLQEKNNDA STRSATPRYQ AWELLNPAFD LNQKYTFVIG SATGAANKH 231
Seq. ID 142 ALAPMQRIPA PNDKWRVLTI NWDARNNKLT ASLQEKNNDA STRSATPRYQ AWELLNPAFD LNQKYTFVIG SATGAANKH 231
Seq. ID 143 ALAPMQKIPE PNNKWRVLTI NWDARNNKLT ARLQEKSNDA STSTPSPRYQ TWELLNPAFD LNQKYTFIIG SATGAANEH 231
Seq. ID 144 ALAPMQKIPE PNNKWRVLTI NWDARNNKLT ARLQEKSNDA STSTPSPRYQ TWELLNPAFD LNQKYTFIIG SATGAANEH 231
Seq. ID 145 ALAPMQKIPA PNNKWRVLTI NWDARNNKLT ARLQEKSNDA STSTPSPRYQ TWELLNPSFD LNQKYTFIIG SATGAANKH 231
Seq. ID 146 ALAPMQKIPA PNNKWRVLTI NWDARNNKLT ARLQEKSNDA STSTPSPRYQ TWELLNPSFD LNQKYTFIIG SATGAANKH 231
Seq. ID 147 ALAPMQRIAP PNGQWRVLTI KWDARDNKLT ASLQEKNNDA STRSATPRYQ TWELLNPAFD LNQKYTFVIG SATGAANKH 231
Seq. ID 148 ALAPMQRIAP PNGQWRVLTI KWDARDNKLT ASLQEKNNDA STRSATPRYQ TWELLNPAFD LNQKYTFVIG SATGAANKH 231
Seq. ID 149 ALAPMQRIPA PNSKWRILTI NWDARNNKLT ARLQEKNNDD TTRSASPRYQ TWELLNPAFD LNQKYTFVIG SATGAANKH 240
Seq. ID 150 ALAPMQRIPA PNSKWRILTI NWDARNNKLT ARLQEKNNDD TTRSASPRYQ TWELLNPAFD LNQKYTFIIG SATGAANKH 231
Seq. ID 151 ALAPMQKIPA PNNKWRVLTI NWDARNNKLI ASLQEKNNDA STRSATPRYQ TWELLNPAFD LKQKYTFIIG SATGAANKH 231
Seq. ID 152 ALAPMQKIPA PNNKWRVLTI NWDARNNKLI ASLQEKNNDA STRSATPRYQ TWELLNPAFD LKQKYTFIIG SATGAANKH 231
Seq. ID 153 ALAPMQRIPA PNDKWRVLTI NWDARNNKLT ASLQEKNNDA STRSATPRYQ AWELLNPAFD LNQKYTFVIG SATGAANKH 231
Seq. ID 154 ALAPMQRIPA PNDKWRVLTI NWDARNNKLT ASLQEKNNDA STRSATPRYQ AWELLNPAFD LNQKYTFVIG SATGAANKH 231
Seq. ID 155 ALAPMQRIPA PNGKWRVLTI NWDARNNKLT ARLQEKSNDA STSSPSPRYQ TWELLNPAFD LNQKYTFVIG SATGAANKH 231
Seq. ID 156 ALAPMQKIPA PNNKWRVLTI NWDARNNKLT ARLQEKSNDA STSTPSPSYQ TWELLNPAFD LNQKYTFIIG SATGAANKH 231
Seq. ID 157 ALAPMQKIPA PNNKWRVLTI NWDARNNKLT ARLQEKSNDA STSTPSPSYQ TWELLNPAFD LNQKYTFIIG SATGAANKH 231
Seq. ID 158 ALAPMQKIPA PNNKWRVLTI NWDARNNKLT ARLQEKSNDA STRTPSPRYQ TWELLNPAFD LNQKYTFIIG SATGAANKH 231
Seq. ID 159 ALAPMQKIPA PNNKWRVLTI NWDARNNKLT ARLQEKSNDA STRTPSPRYQ TWELLNPAFD LNQKYTFIIG SATGAANKH 231

Figure 5C

		260		280		300		320	
Seq. ID 6	QIGVTLFEAY	FTKPTIVANP	VDIEIGTAFD	PLNYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	TYKVVNSYGE	311
Seq. ID 7	QIGVTLFEAY	FTKPTIVANP	VDIEIGTAFD	PLNYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	TYKVVNSYGE	311
Seq. ID 132	QIGVTLFEAY	FTKPTIEANP	VDIEIGTAFD	PLKYELIGLK	ATDEIDGDIT	DKITVEFNNV	DTSKPGAYRV	TYKVLNSYEE	320
Seq. ID 133	QIGVTLFEAY	FTKPTIEANP	VDIEIGTAFD	PLKYELIGLK	ATDEIDGDIT	DKITVEFNNV	DTSKPGAYRV	TYKVLNSYEE	311
Seq. ID 134	QIGVTLFEAY	FTKPTIVANP	VDIEIGTAFD	PLNYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	TYKVVNSYGE	311
Seq. ID 135	QIGVTLFEAY	FTKPTIVANP	VDIEIGTAFD	PLNYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	TYKVVNSYGE	311
Seq. ID 136	QIGVTLFEAY	FTKPTIVANP	VDIEIGTAFD	PLNYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	TYKVVNSYGE	311
Seq. ID 137	QIGVTLFEAY	FTKPTIVANP	VDIEIGTAFD	PLNYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	TYKVVNSYGE	311
Seq. ID 138	QIGVTLFEAY	FTKPTIEANP	VDIEAGTAFD	PLNYEPIGLK	ATDEIDGDIT	DKITVEFNDV	DTSKPGAYRV	TYKVVNSYEE	311
Seq. ID 139	QIGVTLFEAY	FTKPTIVANP	VDIEIGTAFD	PLNYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	TYKVVNSYGE	311
Seq. ID 140	QIGVTLFEAY	FTKPTIVANP	VDIEIGTAFD	PLNYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	TYKVVNSYGE	311
Seq. ID 141	QIGVTLFEAY	FTKPTIVANP	VDIEIGTAFD	PLKYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	TYKVVNSYGE	311
Seq. ID 142	QIGVTLFEAY	FTKPTIVANP	VDIEIGTAFD	PLKYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	TYKVVNSYGE	311
Seq. ID 143	QIGVTLFEAY	FTKPTIEANP	VDIELGTAFD	....	....	....	....	....	281
Seq. ID 144	QIGVTLFEAY	FTKPTIEANP	VDIELGTAFD	....	....	....	....	....	281
Seq. ID 145	QIGVTLFEAY	FTKPTIEANP	VDIELGTAFD	PLNYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	TYKVVNSYGE	311
Seq. ID 146	QIGVTLFEAY	FTKPTIEANP	VDIELGTAFD	PLNYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	TYKVVNSYGE	311
Seq. ID 147	QIGVTLFEAY	FTKPTIVANP	VDIEIGTAFD	PLNYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	TYKVVNSYGE	311
Seq. ID 148	QIGVTLFEAY	FTKPTIVANP	VDIEIGTAFD	PLNYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	TYKVVNSYGE	311
Seq. ID 149	QIGVTLFEAY	FTKPTIEANP	VDIEIGTAFD	PLKYELIGLK	ATDEIDGDIT	DKITVEFNNV	DTSKPGAYRV	TYKVLNSYEE	320
Seq. ID 150	QIGVTLFEAY	FTKPTIEANP	VDIEIGTAFD	PLKYELIGLK	ATDEIDGDIT	DKITVEFNNV	DTSKPGAYRV	TYKVLNSYEE	311
Seq. ID 151	QIGVTLFEAY	FTKPTIVANP	VDIELGTAFD	PLNYQPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGPYRV	TYKVVNSYGE	311
Seq. ID 152	QIGVTLFEAY	FTKPTIVANP	VDIELGTAFD	PLNYQPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGPYRV	TYKVVNSYGE	311
Seq. ID 153	QIGVTLFEAY	FTKPTIVANP	VDIEIGTAFD	PLNYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	TYKVVNSYGE	311
Seq. ID 154	QIGVTLFEAY	FTKPTIVANP	VDIEIGTAFD	PLNYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	TYKVVNSYGE	311
Seq. ID 155	QIGITLFEAY	FTKPTIEANP	VDIEIGTAFD	PLNYEPIGLK	ATDEIDGDIT	DKITVGFNDV	DTSKPGAYRV	TYKVVNSYEE	311
Seq. ID 156	QIGVTLFEAY	FTKPTIEANP	VDIELGTAFD	PLNYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	IYKVVNSYGE	311
Seq. ID 157	QIGVTLFEAY	FTKPTIEANP	VDIELGTAFD	PLNYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	IYKVVNSYGE	311
Seq. ID 158	QIGVTLFEAY	FTKPTIEANP	VDIELGTAFD	PLNYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	TYKVVNSYGE	311
Seq. ID 159	QIGVTLFEAY	FTKPTIEANP	VDIELGTAFD	PLNYEPIGLK	ATDEVDGDIT	KDITVEFNDV	DTSKPGAYRV	TYKVVNSYGE	311

Figure 5D

		340		360		380		400	
Seq. ID 6	SDEKTIEVVV	YTKPTITAHD	VAIKKGLAFD	PLNYEPIGLK	ATDPIDGDIT	DKITVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 7	SDEKTIEVVV	YTKPTITAHD	VAIKKGLAFD	PLNYEPIGLK	ATDPIDGDIT	DKITVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 132	SDEKIIEVVV	YTKPTIAAHD	VAIKKDLAFD	PLDYEPIELK	ATDPIDGDIT	DKITIESNNA	DTSKPGKYHV	TYKVLNSYEK	400
Seq. ID 133	SDEKIIEVVV	YTKPTIAAHD	VAIKKDLAFD	PLDYEPIELK	ATDPIDGDIT	DKITIESNNA	DTSKPGKYHV	TYKVLNSYEK	391
Seq. ID 134	SDEKTIEVVV	YTKPTITAHD	VAIKKGLAFD	PLNYEPIGLK	ATDPIDGDIT	DKITVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 135	SDEKTIEVVV	YTKPTITAHD	VAIKKGLAFD	PLNYEPIGLK	ATDPIDGDIT	DKITVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 136	SDEKTIEVVV	YTKPTITAHD	VAIKKGLAFD	PLNYEPIGLK	ATDPIDGDIT	DKITVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 137	SDEKTIEVVV	YTKPTITAHD	VAIKKGLAFD	PLNYEPIGLK	ATDPIDGDIT	DKITVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 138	SDEKTIEVIV	YTKPTITAHD	VIIKKDLAFD	PLNYEPIGLK	ATDPIDGDIT	DKVTVESNNV	DTSKPGKYHV	AYKVVNSYEK	391
Seq. ID 139	SDEKTIEVVV	YTKPTITAHD	VAIKKGLAFD	PLNYEPIGLK	ATDPIDGDIT	DKITVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 140	SDEKTIEVVV	YTKPTITAHD	VAIKKGLAFD	PLNYEPIGLK	ATDPIDGDIT	DKITVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 141	SDEKTIEVVV	YTKPTITAHD	VAIKKGLAFD	PLNYEPIGLK	ATDPIDGDIT	DKITVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 142	SDEKTIEVVV	YTKPTITAHD	VAIKKGLAFD	PLNYEPIGLK	ATDPIDGDIT	DKITVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 143	----------	----------	----------	----------	----------	----------	----------	----------	261
Seq. ID 144	----------	----------	----------	----------	----------	----------	----------	----------	261
Seq. ID 145	SDEKTIEVVV	YTKPTITAHD	IAIKKDLAFD	PLNYEPIGLK	ATDPIDGDIT	DKIAVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 146	SDEKTIEVVV	YTKPTITAHD	IAIKKDLAFD	PLNYEPIGLK	ATDPIDGDIT	DKIAVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 147	SDEKTIEVVV	YTKPTITAHD	VAIKKGLAFD	PLNYEPIGLK	ATDPIDGDIT	DKITVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 148	SDEKTIEVVV	YTKPTITAHD	VAIKKGLAFD	PLNYEPIGLK	ATDPIDGDIT	DKITVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 149	SDEKTIEVVV	YTKPTIAAHD	VAIKKDLAFD	PLDYEPIELK	ATDPIDGDIT	DKITIESNNA	DTSKPGKYHV	TYKVLNSYEK	400
Seq. ID 150	SDEKTIEVVV	YTKPTIAAHD	VAIKKDLAFD	PLDYEPIELK	ATDPIDGDIT	DKITIESNNA	DTSKPGKYHV	TYKVLNSYEK	391
Seq. ID 151	SDEKTIEVVV	YTKPTITAHD	IAIKKDLAFD	PLNYEPIGLK	ATDPIDGDIT	DKIAVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 152	SDEKTIEVVV	YTKPTITAHD	IAIKKDLAFD	PLNYEPIGLK	ATDPIDGDIT	DKIAVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 153	SDEKTIEVVV	YTKPTITAHD	VAIKKGLAFD	PLNYEPIGLK	ATDPIDGDIT	DKITVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 154	SDEKTIEVVV	YTKPTITAHD	VAIKKGLAFD	PLNYEPIGLK	ATDPIDGDIT	DKITVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 155	SDEKTIEVIV	YTKPTITAHD	VVIKKDLAFD	PLNYEPIGLK	AIDPIDGDIT	DKVTVESNNV	DTSKPGKYHV	AYKVVNSYEK	391
Seq. ID 156	SDEKTIEVVV	YTKPTITAHD	IAIKKDLAFD	PLNYEPIGLK	ATDPIDGDIT	DKIAVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 157	SDEKTIEVVV	YTKPTITAHD	IAIKKDLAFD	PLNYEPIGLK	ATDPIDGDIT	DKIAVKFNNV	DTSKPGKYHV	TYKVINSYEK	391
Seq. ID 158	SDEKTIEVVV	YTKPTITAHD	IAIKKDLTFD	PLNYEPIGLK	ATDPIDGDIT	DKITVKFNNV	DTSKPGKYHI	TYKVVNSYEK	391
Seq. ID 159	SDEKTIEVVV	YTKPTITAHD	IAIKKDLTFD	PLNYEPIGLK	ATDPIDGDIT	DKITVKFNNV	DTSKPGKYHI	TYKVVNSYEK	391

Figure 5E

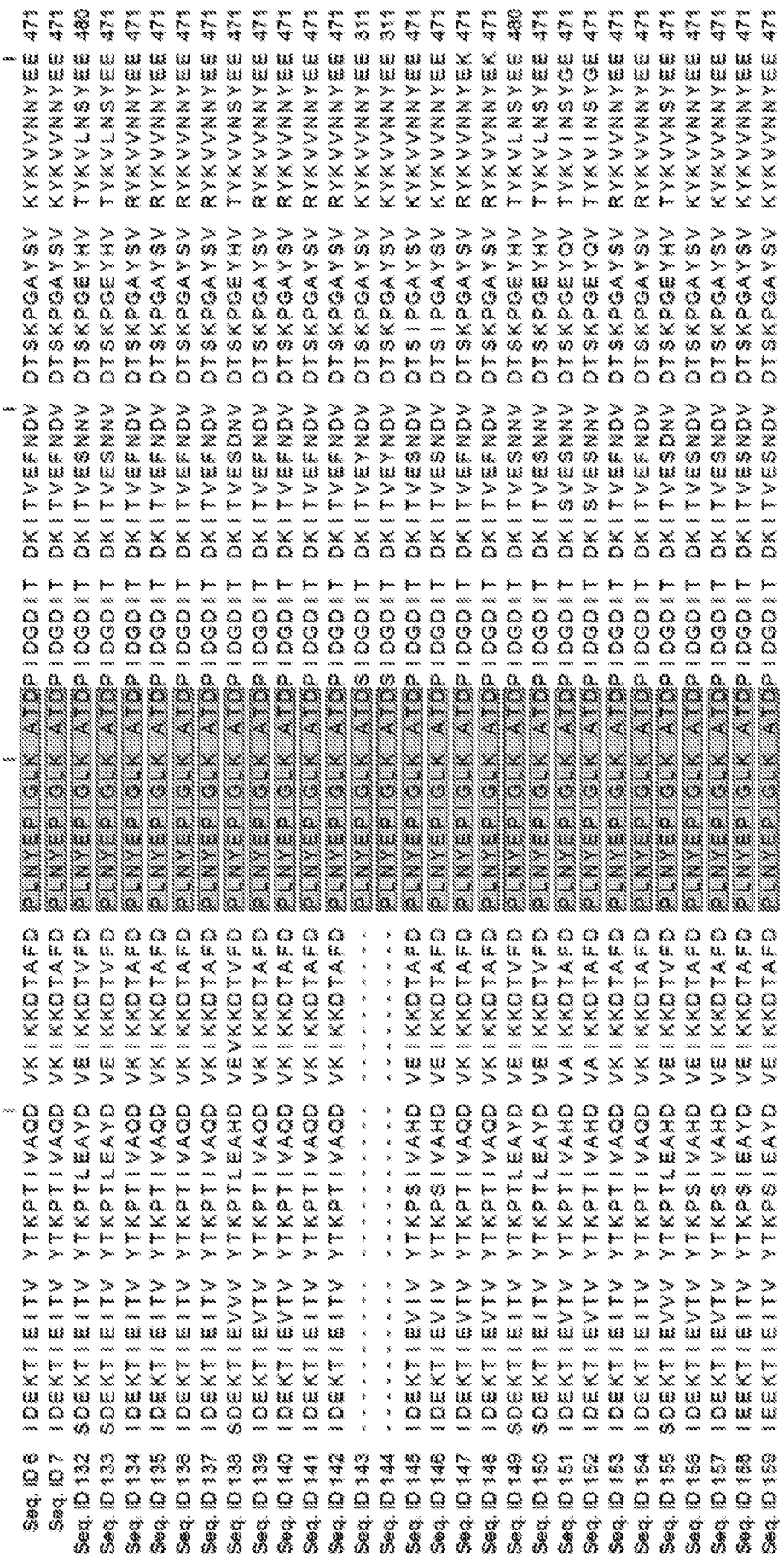

420
1
440
1
460
1
480
1
Seq. ID 6 IDEKTIEITV YTKPTIVAQD VKIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVEFNDV DTSKPGAYSV KYKVVNNYEE 471
Seq. ID 7 IDEKTIEITV YTKPTIVAQD VKIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVEFNDV DTSKPGAYSV KYKVVNNYEE 471
Seq. ID 132 SDEKTIEITV YTKPTLEAYD VEIKKDTVFD PLNYEPIGLK ATDPIDGDIT DKITVESNNV DTSKPGEYHV TYKVLNSYEE 480
Seq. ID 133 SDEKTIEITV YTKPTLEAYD VEIKKDTVFD PLNYEPIGLK ATDPIDGDIT DKITVESNNV DTSKPGEYHV TYKVLNSYEE 471
Seq. ID 134 IDEKTIEITV YTKPTIVAQD VKIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVEFNDV DTSKPGAYSV RYKVVNNYEE 471
Seq. ID 135 IDEKTIEITV YTKPTIVAQD VKIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVEFNDV DTSKPGAYSV RYKVVNNYEE 471
Seq. ID 136 IDEKTIEITV YTKPTIVAQD VKIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVEFNDV DTSKPGAYSV RYKVVNNYEE 471
Seq. ID 137 IDEKTIEITV YTKPTIVAQD VKIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVEFNDV DTSKPGAYSV RYKVVNNYEE 471
Seq. ID 138 SDEKTIEVVV YTKPTLEAHD VEVKKDTVFD PLNYEPIGLK ATDPIDGDIT DKITVESDNV DTSKPGEYHV TYKVVNSYEE 471
Seq. ID 139 IDEKTIEVTV YTKPTIVAQD VKIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVEFNDV DTSKPGAYSV RYKVVNNYEE 471
Seq. ID 140 IDEKTIEVTV YTKPTIVAQD VKIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVEFNDV DTSKPGAYSV RYKVVNNYEE 471
Seq. ID 141 IDEKTIEITV YTKPTIVAQD VKIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVEFNDV DTSKPGAYSV RYKVVNNYEE 471
Seq. ID 142 IDEKTIEITV YTKPTIVAQD VKIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVEFNDV DTSKPGAYSV RYKVVNNYEE 471
Seq. ID 143 ---------- ---------- ---------- PLNYEPIGLK ATDSIDGDIT DKITVEYNDV DTSKPGAYSV KYKVVNNYEE 311
Seq. ID 144 ---------- ---------- ---------- PLNYEPIGLK ATDSIDGDIT DKITVEYNDV DTSKPGAYSV KYKVVNNYEE 311
Seq. ID 145 IDEKTIEVIV YTKPSIVAHD VEIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVESNDV DTSIPGAYSV KYKVVNNYEE 471
Seq. ID 146 IDEKTIEVIV YTKPSIVAHD VEIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVESNDV DTSIPGAYSV KYKVVNNYEE 471
Seq. ID 147 IDEKTIEVTV YTKPTIVAQD VKIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVEFNDV DTSKPGAYSV RYKVVNNYEK 471
Seq. ID 148 IDEKTIEVTV YTKPTIVAQD VKIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVEFNDV DTSKPGAYSV RYKVVNNYEK 471
Seq. ID 149 SDEKTIEITV YTKPTLEAYD VEIKKDTVFD PLNYEPIGLK ATDPIDGDIT DKITVESNNV DTSKPGEYHV TYKVLNSYEE 480
Seq. ID 150 SDEKTIEITV YTKPTLEAYD VEIKKDTVFD PLNYEPIGLK ATDPIDGDIT DKITVESNNV DTSKPGEYHV TYKVLNSYEE 471
Seq. ID 151 IDEKTIEVTV YTKPTIVAHD VAIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKISVESNNV DTSKPGEYQV TYKVINSYGE 471
Seq. ID 152 IDEKTIEVTV YTKPTIVAHD VAIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKISVESNNV DTSKPGEYQV TYKVINSYGE 471
Seq. ID 153 IDEKTIEITV YTKPTIVAQD VKIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVEFNDV DTSKPGAYSV RYKVVNNYEE 471
Seq. ID 154 IDEKTIEITV YTKPTIVAQD VKIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVEFNDV DTSKPGAYSV RYKVVNNYEE 471
Seq. ID 155 SDEKTIEVVV YTKPTLEAHD VEIKKDTVFD PLNYEPIGLK ATDPIDGDIT DKITVESDNV DTSKPGEYHV TYKVVNSYEE 471
Seq. ID 156 IDEKTIEVTV YTKPSIVAHD VEIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVESNDV DTSKPGAYSV KYKVVNNYEE 471
Seq. ID 157 IDEKTIEVTV YTKPSIVAHD VEIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVESNDV DTSKPGAYSV KYKVVNNYEE 471
Seq. ID 158 IEEKTIEITV YTKPSIEAYD VEIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVESNDV DTSKPGAYSV KYKVVNNYEE 471
Seq. ID 159 IEEKTIEITV YTKPSIEAYD VEIKKDTAFD PLNYEPIGLK ATDPIDGDIT DKITVESNDV DTSKPGAYSV KYKVVNNYEE 471

Figure 5F

500
1
520
1
540
1
560
1
Seq. ID 6 SDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNTPYQITVYVKPEDE 551
Seq. ID 7 SDEKTIAVTVPVIDDGMENGDPTGWKFFSQETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNTPYQITVYVKPEDE 551
Seq. ID 132 SDEKTITVMVPVIDDGMENGDPNGWKFFSGESITLEEDEENALNGKWVFY SDKHVAIYKQVELENNISYQITVYVKPEDE 560
Seq. ID 133 SDEKTITVMVPVIDDGMENGDPNGWKFFSGETITLEEDEENALNGKWVFY SDKHVAIYKQVELENNISYQITVYVKPEDE 551
Seq. ID 134 SDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNTPYQITVYVKPEDE 551
Seq. ID 135 SDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNTPYQITVYVKPEDE 551
Seq. ID 136 SDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNTPYQITVYVKPEDE 551
Seq. ID 137 SDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNTPYQITVYVKPEDE 551
Seq. ID 138 SDEKSILVTVPVIDDGMENGDPKGWKFFSGESITLDEDEENALNGKWVFY SDKHVAIYKQVELENNTTYQITVYVKPEDE 551
Seq. ID 139 SDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNTPYQITVYVKPEDE 551
Seq. ID 140 SDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNTPYQITVYVKPEDE 551
Seq. ID 141 SDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNTPYQITVYVKPEDE 551
Seq. ID 142 SDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNTPYQITVYVKPEDE 551
Seq. ID 143 SDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNIPYQITVYVKPEDE 391
Seq. ID 144 SDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNIPYQITVYVKPEDE 391
Seq. ID 145 SDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNIPYQITVYVKPEDE 551
Seq. ID 146 SDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNIPYQITVYVKPEDE 551
Seq. ID 147 SDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHIAIYKQVELKNNTPYQITVYVKPEDE 551
Seq. ID 148 SDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHIAIYKQVELKNNTPYQITVYVKPEDE 551
Seq. ID 149 SDEKTIAVTVPVIDDGMENGDPNGWKFFSGESITLEEDEENALNGKWVFY SDKHIAIYKQVELENNISYQITVYVKPEDE 560
Seq. ID 150 SDEKTITVMVPVIDDGMENGDPNGWKFFSGESITLEEDEENALNGKWVFY SDKHVAIYKQVELENNISYQITVYVKPEDE 551
Seq. ID 151 FDDKTITITVPVIDDGMENGDPDGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVEFKNNTPYQITVYIKPEDE 551
Seq. ID 152 FDDKTITITVPVIDDGMENGDPDGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVEFKNNTPYQITVYIKPEDE 551
Seq. ID 153 SDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNTPYQITVYVKPEDE 551
Seq. ID 154 SDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNTPYQITVYVKPEDE 551
Seq. ID 155 SDEKSLVTVPVIDDGMENGDPKGWKFFSGESITLDEDEENALNGKWVFS SDKHVAIYKQVELENNTTYQITVYVKPEDE 551
Seq. ID 156 CDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNIPYQITVYVKPEDE 551
Seq. ID 157 CDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNIPYQITVYVKPEDE 551
Seq. ID 158 SDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNTPYQITVYVKPEDE 551
Seq. ID 159 SDEKTIAVTVPVIDDGMENGDPTGWKFFSGETITLEEDEENALNGKWVFY ADKHVAIYKQVELKNNTPYQITVYVKPEDE 551

Figure 5G

	580			600			620			640		
	1			1			1			1		
Seq. ID 6	ETVAHHIVKV	SFKSDSAGQE	SEEIINERLI	DAEQIQKGYR	KLTSIPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIVEPT	631
Seq. ID 7	ETVAHHIVKV	SFKSDSAGQE	SEEIINERLI	DAEQIQKGYR	KLTSIPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIVEPT	631
Seq. ID 132	GTVANHIVKV	SLKPDPASGE	SQEILNTRLL	GAEQIQKGYR	KLTSNPFIPT	TIEPYKKPII	VIENFLVGWI	GGIKIIVEPT	640
Seq. ID 133	GTVANHIVKV	SLKPDPASGE	SQEILNTRLL	GAEQIQKGYR	KLTSNPFIPT	TIEPYKKPII	VIENFLVGWI	GGIKIIVEPT	631
Seq. ID 134	ETVAHHIVKV	SFKSDSAGQE	SEEIINERLI	DAEQIQKGYR	KLTSIPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIVEPT	631
Seq. ID 135	ETVAHHIVKV	SFKSDSAGQE	SEEIINERLI	DAEQIQKGYR	KLTSIPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIVEPI	631
Seq. ID 136	ETVAHHIVKV	SFKSDSAGQE	SEEIINERLI	DAEQIQKGYR	KLTSIPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIVEPT	631
Seq. ID 137	ETVAHHIVKV	SFKSDSAGQE	SEEIINERLI	DAEQIQKGYR	KLTSIPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIVEPT	631
Seq. ID 138	GTVAHHIVKA	SLKPNPSGPD	SEELLNERLI	NGEQIQKGYR	KLTSIPFTPT	TIEPYKKPLI	VIENYLAGWI	GGIKIIVEPT	631
Seq. ID 139	ETVAHHIVKV	SFKSDSAGQE	SEEIINERLI	DAEQIQKGYR	KLTSIPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIVEPT	631
Seq. ID 140	ETVAHHIVKV	SFKSDSAGQE	SEEIINERLI	DAEQIQKGYR	KLTSIPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIVEPT	631
Seq. ID 141	ETVAHHIVKV	SFKSDSAGQE	SEEIINERLI	DAEQIQKGYR	KLTSIPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIVEPT	631
Seq. ID 142	ETVAHHIVKV	SFKSDSAGQE	SEEIINERLI	DAEQIQKGYR	KLTSIPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIVEPI	631
Seq. ID 143	GTVAHHIVKV	SFKSDSAGPE	NEEVINERLI	DAEQIQKGYR	KLTSMPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIVEPT	471
Seq. ID 144	GTVAHHIVKV	SFKSDSAGPE	NEEVINERLI	DAEQIQKGYR	KLTSMPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIVEPT	471
Seq. ID 145	GTVAHHIVKV	SFKSDSAGPE	NEEVINERLI	DAEQIQKGYR	KLTSMPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIVEPT	631
Seq. ID 146	GTVAHHIVKV	SFKSDSAGPE	NEEVINERLI	DAEQIQKGYR	KLTSMPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIVEPT	631
Seq. ID 147	ETVAHHIVKV	SFKSDSAGQE	SEEIINERLI	DAEQIQKGYR	KLTSIPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIVEPT	631
Seq. ID 148	ETVAHHIVKV	SFKSDSAGQE	SEEIINERLI	DAEQIQKGYR	KLTSIPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIVEPT	631
Seq. ID 149	GTVANHIVKV	SLKPDPASGE	SQEILNTRLL	GAEQIQKGYR	KLTSNPFIPT	TIEPYKKPII	VIENFLAGWI	GGIKIIVEPT	640
Seq. ID 150	GTVANHIVKV	SLKPDPASGE	SQEILNTRLL	GAEQIQKGYR	KLTSNPFIPT	TIEPYKKPII	VIENFLAGWI	GGIKIIVEPT	631
Seq. ID 151	ETVAHHNVKV	SFKSDSASQE	SEELNERLI	DAEQIQKGYR	KLTSIPFTPT	TIAPNKKPVI	IVENFLPGWI	GGVRIIVEPT	631
Seq. ID 152	ETVAHHNVKV	SFKSDSASQE	SEELNERLI	DAEQIQKGYR	KLTSIPFTPT	TIAPNKKPVI	IVENFLPGWI	GGVRIIVEPT	631
Seq. ID 153	ETVAHHIVKV	SFKSDSAGQE	SEEIINERLI	DAEQIQKGYR	KLTSIPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIVEPI	631
Seq. ID 154	ETVAHHIVKV	SFKSDSAGQE	SEEIINERLI	DAEQIQKGYR	KLTSIPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIVEPT	631
Seq. ID 155	GTVAHHIVKA	SLKPDPSGPD	SEELLNERLI	NGEQIQKGYR	KLTSIPFTPT	TIEPYKKPLI	VIENYLAGWI	GGIKIIVEPT	631
Seq. ID 156	GTVAHHIVKV	SFKSDSASPE	SEEVINERLI	DAEQIRKGYR	QLTSIPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIEPT	631
Seq. ID 157	GTVAHHIVKV	SFKSDSASPE	SEEVINERLI	DAEQIRKGYR	QLTSIPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRIIEPT	631
Seq. ID 158	GTVAHHIVKV	SFKSDSAGQE	SEEIINKRLI	DAEQIQKGYR	KLASIPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRVIVEPT	631
Seq. ID 159	GTVAHHIVKV	SFKSDSAGQE	SEEIINKRLI	DAEQIQKGYR	KLASIPFTPT	TIVPNKKPVI	IVENFLPGWI	GGVRVIVEPT	631

Figure 5H

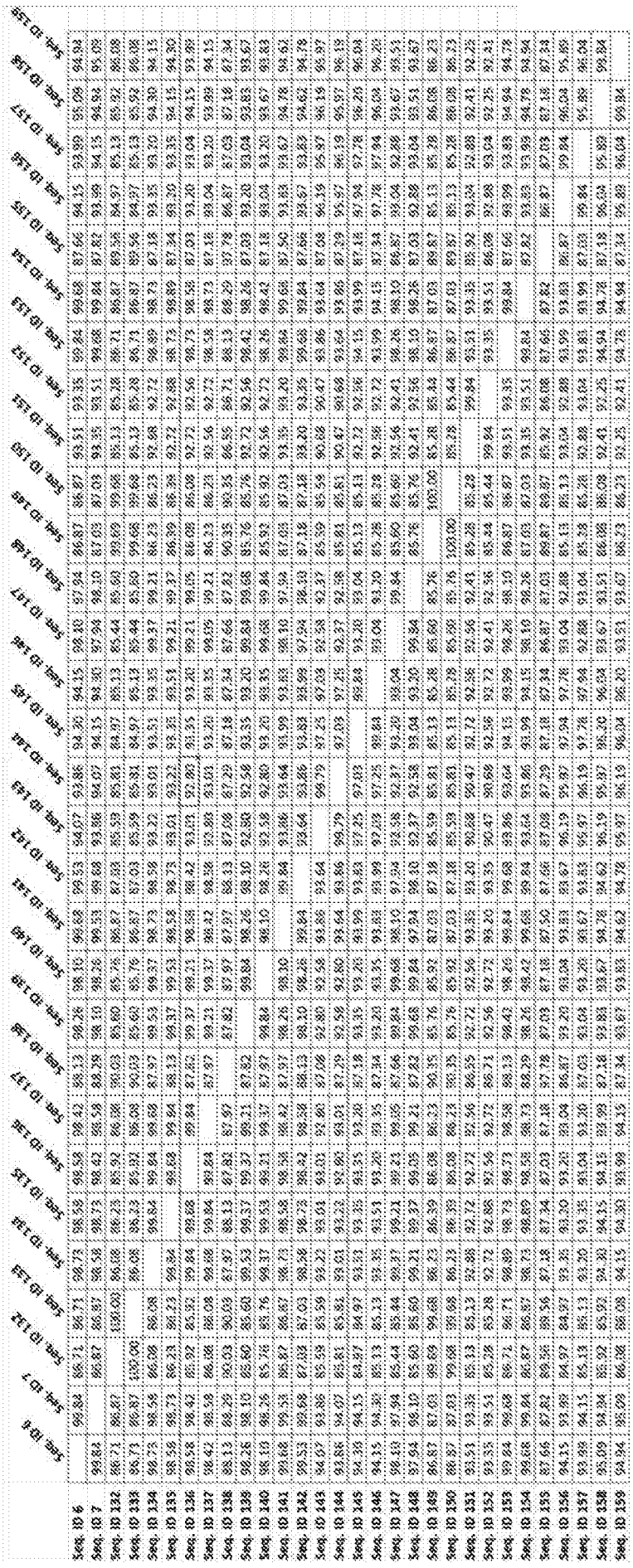


Figure 6

Increasing size phenotype

Increasing mortality

	b	m,b	s,b	s,m,b	s,m	s
0-50%	-	-	-	-	+/-	+/-
50-80%	-	-	-	+/-	+/-	+/-
80-100%	+/-	+/-	+/-	+/-	+	+

Figure 7