06 84256

Industria y Comercio

SUPERINTENDENCIA

Delegatura de propiedad Industrial

División de Nuevas Creaciones

BF

PCT

SOLICITUD

PATENTE DE INVENCIÓN

21 **EXPEDIENTE No** 06-84256

54 **TÍTULO** NUEVOS POLIPEPTIDOS CRISTALINOS Y POLINUCLEOTIDOS DE BACILLUS THURINGIENSIS Y COMPOSICIONES CON LOS MISMOS

51 **CLASIFICACIÓN INTERNACIONAL**

71 **SOLICITANTE** PIONEER HI-BRED INTERNATIONAL, INC

DOMICILIO 7100 NW 62nd Avenue, P.O.Box 1014, Johnston, IA 50131-1014, ESTADOS UNIDOS DE AMERICA

74 **APODERADO** DRA MARGARITA CASTELLANOS ABONDANO

22 **BOGOTÁ, D C,** 25 AGOSTO 2006

FORMA P 10)

PETITORIO

Industria y Comercio
SUPERINTENDENCIA

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO
Rad: 06-084256- -00000-0000
Fec: 2006-08-25 15:08:40 Dep: 2020 NUECREACIONES
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Eve: 378 FASENACIONALI
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FORMULARIO UNICO DE SOLICITUD DE PATENTE
PCT
ENTRADA EN FASE NACIONAL

25/09/06

SOLICITUD DE:

① [X] Patente de Invención. [ ] Patente de Modelo de Utilidad.

[X] Capítulo I [ ] Capítulo II

② **SOLICITANTE (71)**

Nombre: PIONEEER HI-BRED INTERNATIONAL, INC.
Dirección: 7100 NW 62nd Avenue, P.O.BOX 1014, Johnston, IA 50131-1014, ESTADOS UNIDOS DE AMERICA
Nacionalidad o Domicilio: Johnston, IA, ESTADOS UNIDOS DE AMERICA
Lugar de Constitución:
Teléfono: Fax:
E-mail:

IDENTIFICACIÓN
C.C. [ ] NIT [ ]
C.E. [ ] Otro [ ] Cual ____
Número ____

③ **REPRESENTANTE O APODERADO (74)**

Nombre: MARGARITA CASTELLANOS A.
Dirección: CALLE 94A No. 7A-09
Teléfono: 610 7420 Fax: 610 0706
E-mail: info@castellanosyco.com

IDENTIFICACIÓN
C.C. [X] NIT [ ]
C.E. [ ] Otro [ ] Cual ____
Número 39'778.654 TPA 70.819

④ **INVENTOR (ES) (72)**

Nombre: ERICKA BERMUDEZ, ROBIN EMIG, KEVIN MCBRIDE, TAKASHI YAMAMOTO
Dirección: 734 Clubhouse Drive, Aptos, CA 95003, ESTADOS UNIDOS DE AMERICA; 1405 Marshall St. # 715, Redwood City, CA 94063, ESTADOS UNIDOS DE AMERICA; 1309 Marina Circle, Davis, CA 95616, ESTADOS UNIDOS DE AMERICA; 3760 Tivoli Garden Terrace, Fremont, CA 94536, ESTADOS UNIDOS DE AMERICA.
Nacionalidad o Domicilio ESTADOUNIDENSES

⑤ **PCT (86)**

Solicitud Internacional No. PCT/US2005/006238 Fecha 25/02/2005
Publicación Internacional No. WO 2005/082077 Fecha 09/09/2005

⑥ **Título (54):** NUEVOS POLIPEPTIDOS CRISTALINOS Y POLINUCLEOTIDOS DE BACILLUS THURINGIENSIS Y COMPOSICIONES CON LOS MISMOS

⑦ **Clasificación Internacional (51)** C12N 15/32 ; C07K 14/325 ; C12P 21/02. A01H 5/00

⑧ **Prioridad** SI [X] NO [ ]

(33) País de Origen	(32) Fecha	(31) Número de Solicitud
US	25/02/2004	60/547,664

⑨ **Comprobante de pago No.** 06- **Fecha** Agosto 25 de 2006

Instrucciones para el diligenciamiento del presente formulario, ver reverso de esta página.

(10) Anexos

- [X] Comprobante de pago de la tasa de presentación de la solicitud.
- [ ] Documento que acredita la existencia y representación legal cuando el solicitante sea persona jurídica.
- [ ] Poderes, si fuere el caso, junto con la sustitución del mismo a mi favor
- [ ] Documento de cesión del inventor al solicitante o a su causante.
- [ ] Declaraciones.
- [X] Copia de la solicitud internacional (Resumen, descripción, reivindicaciones, dibujos).
- [X] Traducción de la solicitud internacional al castellano (Resumen, descripción, reivindicaciones, dibujos).
- [ ] Copia del examen preliminar internacional efectuado por la Autoridad Internacional de Examen Preliminar (IPEA).
- [ ] Traducción del examen preliminar internacional efectuado por la IPEA.
- [ ] De ser el caso, copia del contrato de acceso.
- [ ] De ser el caso, documento que acredite la licencia o autorización de uso de conocimientos tradicionales de las comunidades indígenas.
- [ ] De ser el caso, certificado de depósito del material biológico.
- [X] Arte final 12x12
- [ ] De ser el caso, información sobre otras solicitudes de patente o títulos obtenidos en el extranjero por el mismo titular o su causante, relacionadas parcial o totalmente con la invención de esta solicitud.
- [ ] De ser el caso, modificaciones efectuadas a la solicitud internacional.
- [X] Otros **Tarjeta Propietario, Tarjeta Temática y Extracto para la Publicación**

(11) FIGURA CARACTERÍSTICA:

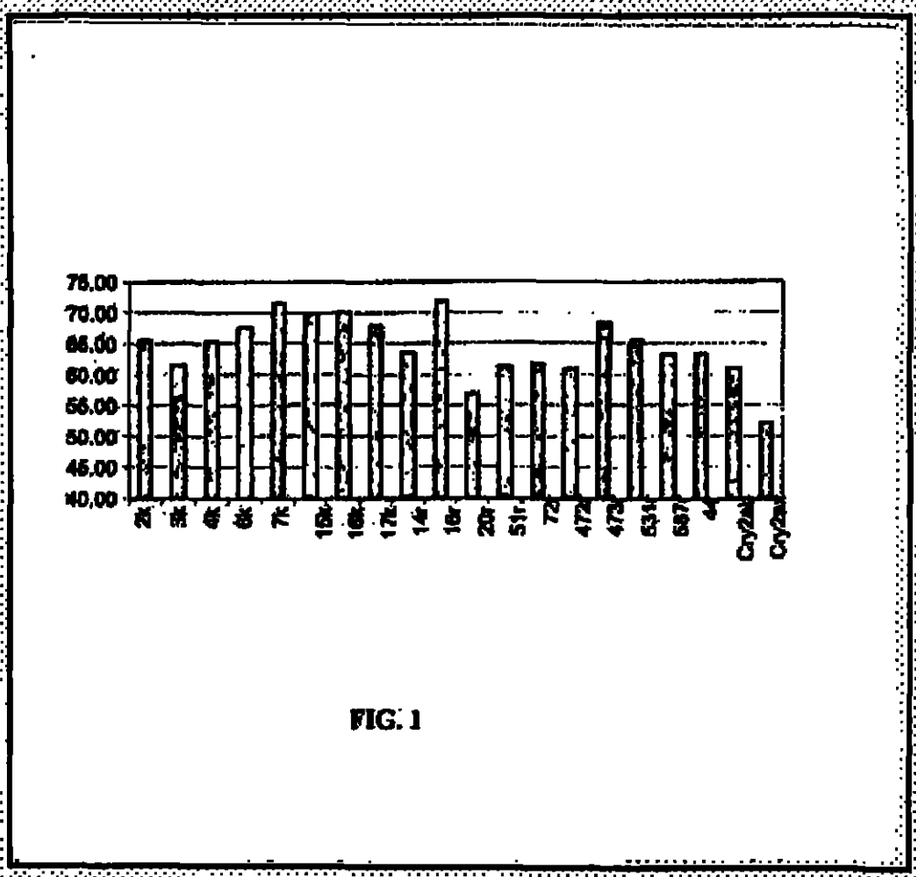


FIG. 1

(12) Solicito la concesión de la patente.

NOMBRE: MARGARITA CASTELLANOS ABONDANO

FIRMA:

C.C. No. 39.679.854 Usaquén - TPA 70.819 C.S.J.

25 AGO. 2006

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO
Rad: 06-064256- -00000-0000
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SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO

NIT : 800176089-2

RECIBO OFICIAL DE CAJA : 06 - 65,544
FECHA : AGOSTO 25 DE 2006

C O N S I G N A C I O N

DEPOSITANTE	TIPO PAGO	BANCO	CUENTA	No. PAGO	FECHA PGO	Vr. PAGO
ALVARO CASTELLANOS	CONSIGNACION	BANCO POPULAR	050-00110-6	48145651	25/08/2006	2,233,000.00

C O N C E P T O

CANT.	RENTISTICO	CONCEPTO	TOTAL CONCEPTO
1	50005-01-01 SOLICITUDES	1 TRAMITES DE SOL. DE PATENTE DE IN	463,000.00
		TOTAL : $	463,000.

SON: CUATROCIENTOS SESENTA Y TRES MIL PESOS

RESPONSABLE : _____

RECIBO DE CAJA APLICADO AL EXPEDIENTE No._____

Industria y Comercio
SUPERINTENDENCIA

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO
DIVISION DE NUEVAS CREACIONES
TARJETA ARCHIVO TEMATICO

PATENTE DE INVENCION ___ PCT X MODELO DE UTILIDAD ___ DISEÑO INDUSTRIAL ___

(21) Nº de solicitud: 06-84256 (22) Fecha de solicitud: 20/08/06
(51) Clasificación Internacional : No clasificado

(71) Solicitante(s) PIONEER HI-BRED INTERNATIONAL, INC.

(72) Inventor(es) ERICKA BERMUDEZ, ROBIN EMIG, KEVIN MCBRIDE, TAKASHI YAMAMOTO

(74) Apoderado: DRA. MARGARITA CASTELLANOS ABONDANO

(30) Prioridad	(31) Nº Prioridad	32) Fecha	(33) País
	60/547.664	25/02/2004	US

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(86) Datos relativos a la presentación de la solic. PCT
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Nº de solicitud PCT/US2005/006238

(87) Publicación Internacional:
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FIG. 1

(54) Título: NUEVOS POLIPEPTIDOS CRISTALINOS Y POLINUCLEOTIDOS DE BACILLUS THURINGIENSIS Y COMPOSICIONES CON LOS MISMOS

(57) Resumen:
Una molécula de ácido nucleico aislada que comprende cualquiera de SEQ ID Nº 1, 3, 5, 7, 9, 11. 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83. 85, 87. 89, 91, 93, 95, 97. 99. 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129. 131, 133, 135, 137, 139, 141, 143, 145, 147. 149, 151. 153. 155. 157. 159. 161, 163, 165, 167. 169, 171, 173, 175, 177. 179, 181, 183, 185. 187, 189, 191, 193, 195, 197, 199. 201, 203, 205, 207, 209, 211, 213. 215. 217. 219, 221. 223, 225. 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247. 249, 251, 253, 255, 257, 259, o un complemento de ésta.

CONTINUA AL RESPALDO ...

Industria y Comercio
SUPERINTENDENCIA

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO
DIVISION DE NUEVAS CREACIONES
TARJETA ARCHIVO PROPIETARIOS

PATENTE DE INVENCION ___ PCT X MODELO DE UTILIDAD ___ DISEÑO INDUSTRIAL ___

(21) Nº de solicitud: 06-84256 (22) Fecha de solicitud: 25/09/06
(51) Clasificación Internacional : No Clasificado

(71) Solicitante(s) PIONEER HI-BRED INTERNATIONAL, INC.

(72) Inventor(es) ERICKA BERMUDEZ, ROBIN EMIG, KEVIN MCBRIDE, TAKASHI YAMAMOTO

(74) Apoderado: DRA. MARGARITA CASTELLANOS ABONDANO

(30) Prioridad	(31) Nº Prioridad	32) Fecha	(33) País
	60/547.664	25/02/2004	US

(85) Fecha inicio fase nacional: 25/09/06
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Fecha: 09/09/2005
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(54) Título: NUEVOS POLIPEPTIDOS CRISTALINOS Y POLINUCLEOTIDOS DE BACILLUS THURINGIENSIS Y COMPOSICIONES CON LOS MISMOS

Industria y Comercio
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SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO
DIVISION DE NUEVAS CREACIONES
EXTRACTO PARA PUBLICACIÓN
SOLICITUD DE PATENTE DE INVENCIÓN PCT

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60/547.664 25/02/2004 US

(51) Int. Cl.: C1ZN 15/32 AC, C7K 14/325 AC C12P 21/2 AC, A1H 3/10 AC.

(71) Solicitante(s) PIONEER HI-BRED INTERNATIONAL, INC.

(72) Inventor(es) ERICKA BERMUDEZ, ROBIN EMIG, KEVIN MCBRIDE, TAKASHI YAMAMOTO

(74) Apoderado: DRA. MARGARITA CASTELLANOS A.

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(54) Título: **NUEVOS POLIPEPTIDOS CRISTALINOS Y POLINUCLEOTIDOS DE BACILLUS THURINGIENSIS Y COMPOSICIONES CON LOS MISMOS**

Reivindicación(es):

Una molécula de ácido nucleico aislada que comprende cualquiera de SEQ ID Nº 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, o un complemento de ésta.

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60/547,664 25 February 2004 (25.02.2004) US

(71) Applicant (*for all designated States except US*): PIONEER HI-BRED INTERNATIONAL, INC. [US/US]; 7100 NW 62nd Avenue, P.O. Box 1014, Johnston, IA 50131-1014 (US).

(72) Inventors; and
(75) Inventors/Applicants (*for US only*): BERMUDEZ, Ericka [ES/US]; 734 Clubhouse Drive, Aptos, CA 95003 (US). EMIG, Robin [US/US]; 1405 Marshall St. #715, Redwood City, CA 94063 (US). MCBRIDE, Kevin [US/US]; 1309 Marina Circle, Davis, CA 95616 (US). YAMAMOTO, Takashi [US/US]; 3780 Tivoli Garden Terrace, Fremont, CA 94538 (US).

(74) Agent: WENK, Melissa; Morgan & Finnegan LLP, 3 World Financial Center, New York, NY 10281-2101 (US).

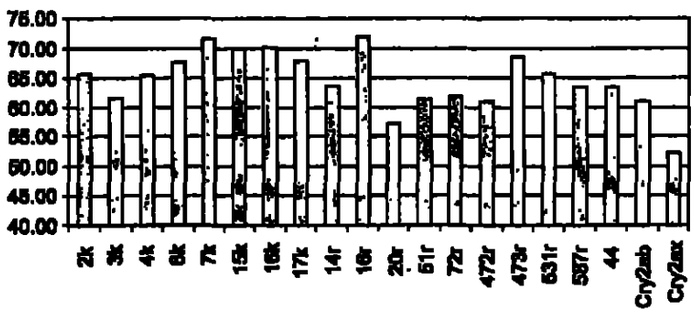
(81) Designated States (*unless otherwise indicated, for every kind of national protection available*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,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

(84) Designated States (*unless otherwise indicated, for every kind of regional protection available*): ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: NOVEL BACILLUS THURINGIENSIS CRYSTAL POLYPEPTIDES, POLYNUCLEOTIDES, AND COMPOSITIONS THEREOF



(57) Abstract: The present invention provides insecticidal polypeptides related to *Bacillus* Cry2 polypeptides. Nucleic acids encoding the polypeptides of the invention are also provided. Methods for using the polypeptides and nucleic acids of the invention to enhance resistance of plants to insect predation are encompassed.

WO 2005/082077 A2

Novel Bacillus Thuringiensis Crystal Polypeptides, Polynucleotides, and Compositions Thereof

1. FIELD OF THE INVENTION

[0001] The present invention relates generally to the field of pest control and provides insecticidal polypeptides related to *Bacillus* Cry2 polypeptides and the polynucleotides that encode them. The present invention also relates to methods and compositions for altering resistance of plants to insect predation including, but not limited to, transgenic plant production.

2. BACKGROUND OF THE INVENTION

[0002] Numerous commercially valuable plants, including common agricultural crops, are susceptible to attack by insect and nematode pests. These pests can cause substantial reductions in crop yield and quality. Traditionally, farmers have relied heavily on chemical pesticides to combat pest damage. However, the use of chemical pesticides raises its own set of problems, including the cost and inconvenience of applying the pesticides. Furthermore, chemical residues raise environmental and health concerns. For these and other reasons there is a demand for alternative insecticidal agents.

[0003] An environmentally friendly approach to controlling pests is the use of pesticidal crystal proteins derived from the soil bacterium *Bacillus thuringiensis* ("Bt"), commonly referred to as "Cry proteins." Many of these proteins are quite toxic to specific target insects, but harmless to plants and other non-targeted organisms. Some Cry proteins have been recombinantly expressed in crop plants to provide pest-resistant transgenic plants. Among those, Bt-transgenic cotton and corn have been widely cultivated.

[0004] A large number of Cry proteins have been isolated, characterized and classified based on amino acid sequence homology (Crickmore *et al.*, 1998, *Microbiol. Mol. Biol. Rev.*, 62: 807-813). This classification scheme provides a systematic mechanism for naming and categorizing newly discovered Cry proteins.

[0005] It has generally been found that individual Cry proteins possess relatively narrow activity spectra with the exception of Cry2A. Cry2A is unusual in that this subset of Cry proteins possesses a broader effective range that includes toxicity to both the *Lepidoptera* and

Diptera orders of insects. The Cry2A protein was discovered to be a toxin showing a dual activity against *Trichoplusia ni* (cabbage looper) and *Aedes taeniorhynchus* (mosquito) (Yamamoto and McLaughlin ,1982, *Biochem. Biophys. Res. Comm.* 130: 414-421). The nucleic acid molecule encoding the Cry2A protein (termed Cry2Aa) was cloned and expressed in *B. megaterium* and found to be active against both *Lepidoptera* and *Diptera* insects (Donovan *et al.* 1988, *J. Bacteriol.* 170: 4732-4738). An additional coding sequence homologous to Cry2Aa was cloned (termed Cry2Ab) and was found to be active only against *Lepidoptera* larvae (Widner and Whiteley, 1989, *J Bacteriol* 171:2).

[0006] Second generation transgenic crops could be more resistant to insects if they are able to express multiple and/or novel Bt genes. Accordingly, new insecticidal proteins having broad activity spectra would be highly desirable.

3. SUMMARY OF THE INVENTION

[0007] The present invention relates to a novel Cry2 polypeptide, Cry2Ax (SEQ ID NO:2), isolated from *Bacillus thuringiensis*. Also encompassed by the present invention are Cry2Ax-derived polypeptides (SEQ ID NOS:4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260). In addition to the polypeptide sequence of Cry2Ax and Cry2Ax-derived polypeptides, it will be appreciated that polypeptides of the invention also encompass variants thereof, including, but not limited to, any fragment, analog, homolog, naturally occurring allele, or mutant thereof. Polypeptides of the invention also encompass those polypeptides that are encoded by any Cry2Ax or Cry2Ax-derived nucleic acid of the invention. In one embodiment, polypeptides that have at least one Cry2Ax functional activity (e.g., insecticidal activity) and are at least 85%, 90%, 95%, 97%, 98%, or 99% identical to the polypeptide sequence of any of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134,

136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, or variants thereof. In another embodiment, polypeptides are encompassed that have at least one Cry2Ax functional activity (e.g., insecticidal activity), are at least 25, 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600, or 625 contiguous amino acids in length, and are encoded by a polynucleotide that hybridizes under stringent conditions to the nucleic acid that encodes any of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, or a variant thereof. Methods of production of the polypeptides of the invention, e.g., by recombinant means, are also provided. Compositions comprising one or more polypeptides of the invention are also encompassed.

[0005] The present invention also relates to the nucleic acid molecules of Cry2Ax (SEQ ID NO:1) and Cry2Ax-derived nucleic acid molecules (SEQ ID NOS:3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259). Also encompassed by the present invention are fragments and analogs which encode polypeptides that are at least partially functionally active, *i.e.*, they are capable of displaying one or more known functional activities associated with a wild type Cry2Ax polypeptide. In one embodiment, the invention encompasses an isolated nucleic acid molecule that comprises a nucleotide sequence i) which is at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identical to the nucleotide sequence of any of SEQ ID NOS:1,

3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259; ii) that hybridizes with a nucleic acid probe consisting of the nucleotide sequence of any of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, or a complement thereof under stringent conditions; and/or iii) that comprises a nucleic acid molecule that encodes a polypeptide comprising the amino acid sequence of any of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260. Vectors comprising nucleic acids of the invention are also encompassed. Cells or plants comprising the vectors of the invention are also encompassed.

[0006] The present invention also relates to transgenic plants expressing a nucleic acid and/or polypeptide of the invention. The transgenic plants can express the transgene in any way known in the art including, but not limited to, constitutive expression, developmentally regulated expression, tissue specific expression, etc. Seed obtained from a transgenic plant of the invention is also encompassed.

4. BRIEF DESCRIPTION OF THE FIGURES

[0007] FIG. 1 shows insecticidal activity of DNA clones from the second round of shuffling. Each clone was expressed in *N. benthamiana* leaves using forced infiltration. Each leaf disk was fed to a single 3rd instar *H. zea* larvae. Following a 24-hour incubation period, the feeding activity was determined by visual observation and expressed as an approximate fraction of leaf area remaining. The y-axis is the percent of the leaf disk remaining after exposure to the insect. The x-axis is the clone expressed in the leaf disk. Several clones shoed increased insecticidal activity such as 7K (D_S01000779) (SEQ ID NO:10), 15K (D_S00999080) (SEQ ID NO:12), 16K (D_S01000269) (SEQ ID NO:14), 16R (D_S01037143) (SEQ ID NO:16), and 473R (D_S01037677) (SEQ ID NO:18).

[0008] FIG. 2 shows insecticidal activity of first round shuffled clone 44 (D_S00503970) and third round shuffled clone D_S01764701. Each clone was expressed in *N. benthamiana* leaves using forced infiltration. Each leaf disk was fed to a single 3rd instar *H. zea* larva. Following a 24-hour incubation period, the feeding activity was determined by video capture of the leaf disk. The y-axis is the number of pixels present in the captured leaf disk image. The x-axis is the clone expressed in the leaf disk. Results are shown for the average of three experiments. For each experiment at least eight leaf disks were tested for each clone.

[0009] FIGS. 3A-3B show efficacy results for transgenic tobacco plants expressing first round shuffled clone 44 in the plastid compartment (left panels) or in the cytoplasm (right panels). The efficacy of (A) *H. zea* or (B) *S. exigua* inhibition was determined after incubation of the leaves with the worms for 24 hours. The amount of leaf remaining was observed with video capture equipment for actual calculation of relative leaf area remaining (number of pixels). Each transgenic plant had six leaf disks taken for analysis. Because twenty five transgenic plants were made using each transgene construct, the numbers distinguish different plants using a particular construct.

[0010] FIGS. 4A-4B show transgene expression levels in the first round shuffled clone 44-expressing transgenic plants. This shuffled Cry2-derived polypeptide was expressed in (A) the plastidic or (B) cytoplasmic subcellular compartments by transformation with pMAXY5469 or pMAXY5471, respectively. Western blot analysis was performed on transgenic plant extracts using a polyclonal antibody directed to the toxin region of the first round shuffled clone 44 polypeptide. Negative controls were extracts taken from an untransformed plant. Positive controls were either 20 ng or 40 ng of purified Cry2Ax toxin.

The molecular weight of the positive control Cry2Ax differs from that of the Cry2Ax-derived polypeptide in the plant extracts because the former is trypsin activated and the latter is pro-toxin.

5. DETAILED DESCRIPTION

[0011] The present invention provides insecticidal polypeptides related to *Bacillus* Cry2 polypeptides. Nucleic acid molecules encoding the polypeptides of the invention are also provided. Methods for using the polypeptides and nucleic acids of the invention to enhance resistance of plants to insect predation are encompassed.

5.1 Polypeptides of the Invention

[0012] The present invention relates to a novel Cry2 polypeptide, Cry2Ax (SEQ ID NO:2), isolated from *Bacillus thuringiensis*. Also encompassed by the present invention are Cry2Ax-derived polypeptides (SEQ ID NOS: 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260). Polypeptides of the invention also encompass those polypeptides that are encoded by any Cry2Ax or Cry2Ax-derived nucleic acid of the invention (see Section 5.2).

[0013] In addition to the polypeptide sequence of Cry2Ax and Cry2Ax-derived polypeptides, it will be appreciated that polypeptides of the invention also encompass variants thereof, including, but not limited to, any substantially similar sequence, any fragment, analog, homolog, naturally occurring allele, or mutant thereof. Variants encompassed by the invention are polypeptides that are at least partially functionally active, *i.e.*, they are capable of displaying one or more known functional activities associated with a wild type Cry2Ax polypeptide. Such functional activities include, but are not limited to, biological activities, such as insecticidal activity; antigenicity, *i.e.*, an ability to bind or compete with Cry2Ax for binding to an anti-Cry2Ax antibody; immunogenicity, *i.e.*, an ability to generate antibody which binds to a Cry2Ax polypeptide. In some embodiments, the

variants have at least one functional activity that is substantially similar to its parent polypeptide (*e.g.*, a variant of Cry2Ax will have at least one functional activity that is substantially similar to Cry2Ax). As used herein, the functional activity of the variant will be considered "substantially similar" to its parent polypeptide if it is within one standard deviation of the parent.

[0014] In one embodiment, polypeptides that have at least one Cry2Ax functional activity (*e.g.*, insecticidal activity) and are at least 85%, 90%, 95%, 97%, 98%, or 99% identical to the polypeptide sequence of any of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260 are encompassed by the invention. Such polypeptides of the invention contain at least 1, at least 5, at least 10, at least 20, at least 30, or all 40 amino acid residues from the group consisting of H_2, S_7, Q_{27}, Q_{35}, E_{36}, K_{43}, D_{44}, N_{45}, D_{51}, A_{58}, V_{69}, R_{78}, N_{79}, K_{99}, T_{118}, V_{124}, E_{125}, R_{129}, N_{138}, R_{139}, A_{141}, T_{162}, Q_{165}, M_{166}, L_{183}, I_{192}, H_{211}, R_{213}, R_{217}, D_{218}, V_{324}, I_{386}, T_{399}, S_{405}, Q_{445}, I_{551}, S_{587}, I_{591}, L_{610}, and L_{631}. The subscript indicates the amino acid residue position corresponding to the position in SEQ ID NO:2 upon optimal alignment of the polypeptide sequence with SEQ ID NO:2. With respect to an amino acid sequence that is optimally aligned with a reference sequence, an amino acid "corresponds" to the position in the reference sequence with which the residue is paired in the alignment.

[0015] As used herein, where a sequence is defined as being "at least X% identical" to a reference sequence, *e.g.*, "a polypeptide at least 95% identical to SEQ ID NO:2," it is to be understood that "X% identical" refers to absolute percent identity, unless otherwise indicated. The term "absolute percent identity" refers to a percentage of sequence identity determined by scoring identical amino acids or nucleic acids as one and any substitution as zero, regardless of the similarity of mismatched amino acids or nucleic acids. In a typical sequence alignment the "absolute percent identity" of two sequences is presented as a percentage of amino acid or nucleic acid "identities." In cases where an optimal alignment of two sequences requires the insertion of a gap in one or both of the sequences, an amino acid

residue in one sequence that aligns with a gap in the other sequence is counted as a mismatch for purposes of determining percent identity. Gaps can be internal or external, *i.e.*, a truncation. Absolute percent identity can be readily determined using, for example, the Clustal W program, version 1.8, June 1999, using default parameters (Thompson *et al.*, 1994, *Nucleic Acids Research* 22: 4673-4680).

[0016] In another embodiment, fragments of Cry2Ax and Cry2Ax-derived polypeptides are encompassed by the invention. Polypeptides are encompassed that have at least one Cry2Ax functional activity (*e.g.*, insecticidal activity), are at least 25, 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600, or 625 contiguous amino acids in length of any of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, and are encoded by a polynucleotide that hybridizes under stringent conditions to the nucleic acid that encodes any of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260. In embodiments where the fragment of the invention encompasses any of the amino acid residues that correspond to amino acid residues 2, 7, 27, 35, 36, 43, 44, 45, 51, 58, 69, 78, 79, 99, 118, 124, 125, 129, 138, 139, 141, 161, 165, 166, 183, 192, 211, 213, 217, 218, 324, 386, 399, 405, 445, 551, 587, 591, 610, 631 of SEQ ID NO:2, such polypeptides of the invention contain at least 1, at least 5, at least 10, at least 20, at least 30, or all 40 amino acid residues from the group consisting of H_2, S_7, Q_{27}, Q_{35}, E_{36}, K_{43}, D_{44}, N_{45}, D_{51}, A_{58}, V_{69}, R_{78}, N_{79}, K_{99}, T_{118}, V_{124}, E_{125}, R_{129}, N_{138}, R_{139}, A_{141}, T_{162}, Q_{165}, M_{166}, L_{183}, I_{192}, H_{211}, R_{213}, R_{217}, D_{218}, V_{324}, I_{386}, T_{399}, S_{405}, Q_{445}, I_{551}, S_{587}, I_{591}, L_{610}, and L_{631}.

[0017] In a specific embodiment, a fragment of the invention corresponds to the length of the processed pro-toxin. There is a 5-6 kDa difference in molecular weight between full length pro-toxin Cry2 and the processed Cry2 toxin. This is the result of ~40 amino acids being cleaved from the pro-toxin Cry2 polypeptide (Rukmini *et al.*, 2000, *Biochimie* 82:109-116; Aronson *et al.*, 1993, *Mol. Microbiol.* 7:489-496; Morse *et al.*, 2001, *Structure* 9:409-17). Polypeptides that correspond to this processed Cry2 fragment can be provided in the methods of the present invention directly to circumvent the need for pro-toxin processing.

[0018] In another specific embodiment, a fragment of the invention corresponds to a Cry2 domain. Cry2 polypeptides have three domains including i) domain I which is involved in insertion into the insect apical midgut membrane and affects ion channel function, ii) domain II which is involved in receptor binding on the insect midgut epithelial cell membrane, and iii) domain III which is involved in ion channel function, receptor binding, and insertion into the membrane (Dean *et al.*, 1996, *Gene* 179:111-117; Schnepf *et al.*, 1998, *Microbiol. Molec. Biol. Rev.* 62:775-806).

[0019] In another embodiment, analog polypeptides are encompassed by the invention. Analog polypeptides may possess residues that have been modified, *i.e.*, by the covalent attachment of any type of molecule to the Cry2Ax or Cry2Ax-derived polypeptides. For example, but not by way of limitation, an analog polypeptide of the invention may be modified, *e.g.*, by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein, etc. An analog polypeptide of the invention may be modified by chemical modifications using techniques known to those of skill in the art, including, but not limited to specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, etc. Furthermore, an analog of a polypeptide of the invention may contain one or more non-classical amino acids.

[0020] Methods of production of the polypeptides of the invention, *e.g.*, by recombinant means, are also provided (see Section 5.6).

[0021] Compositions comprising one or more polypeptides of the invention are also encompassed. The compositions of the invention can further comprise additional agents including, but not limited to, spreader-sticker adjuvants, stabilizing agents, other insecticidal additives, diluents, agents that optimize the rheological properties or stability of the composition, such as, for example, surfactants, emulsifiers, dispersants, and/or polymers.

5.2 Nucleic Acids of the Invention

[0022] The present invention also relates to the nucleic acid molecules of Cry2Ax (SEQ ID NO:1) and Cry2Ax-derived nucleic acid molecules (SEQ ID NOS:3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259). Nucleic acid molecules of the invention also encompass those nucleic acid molecules that encode any Cry2Ax or Cry2Ax-derived polypeptide of the invention (see Section 5.1).

[0023] In addition to the nucleic acid molecule of Cry2Ax and Cry2Ax-derived nucleic acid molecules, it will be appreciated that nucleic acids of the invention also encompass variants thereof, including, but not limited to any substantially similar sequence, any fragment, homolog, naturally occurring allele, or mutant thereof. Variant nucleic acid molecules encompassed by the present invention encode polypeptides that are at least partially functionally active, *i.e.*, they are capable of displaying one or more known functional activities associated with a wild type Cry2Ax polypeptide. Such functional activities include, but are not limited to, biological activities, such as insecticidal activity; antigenicity, *i.e.*, an ability to bind or compete with Cry2Ax for binding to an anti-Cry2Ax antibody; immunogenicity, *i.e.*, an ability to generate antibody which binds to a Cry2Ax polypeptide. In some embodiments, the variants have at least one functional activity that is substantially similar to its parent nucleic acid molecule (*e.g.*, a variant of a Cry2Ax nucleic acid molecule will encode a polypeptide that has at least one functional activity that is substantially similar to the polypeptide encoded for by the Cry2Ax nucleic acids molecule). As used herein, the functional activity of the variant will be considered "substantially similar" to its parent polypeptide if it is within one standard deviation of the parent.

[0024] In one embodiment, nucleic acid molecules that are at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identical to any of the nucleic acid molecules of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49,

51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259 are encompassed by the invention. Such nucleic acid molecules of the invention encode polypeptides that contain at least one, at least 5, at least 10, at least 20, at least 30, or all 40 amino acid residues from the group consisting of H_2, S_7, Q_{27}, Q_{35}, E_{36}, K_{43}, D_{44}, N_{45}, D_{51}, A_{58}, V_{69}, R_{78}, N_{79}, K_{99}, T_{118}, V_{124}, E_{125}, R_{129}, N_{138}, R_{139}, A_{141}, T_{162}, Q_{165}, M_{166}, L_{183}, I_{192}, H_{211}, R_{213}, R_{217}, D_{218}, V_{324}, I_{386}, T_{399}, S_{405}, Q_{445}, I_{551}, S_{587}, I_{591}, L_{610}, and L_{691}.

[0025] To determine the percent identity of two nucleic acid molecules, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first nucleic acid molecule for optimal alignment with a second or nucleic acid molecule). The nucleotides at corresponding nucleotide positions are then compared. When a position in the first sequence is occupied by the same nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = number of identical overlapping positions/total number of positions x 100%). In one embodiment, the two sequences are the same length.

[0026] The determination of percent identity between two sequences can also be accomplished using a mathematical algorithm. A non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci.* 87:2264-2268, modified as in Karlin and Altschul, 1993, *Proc. Natl. Acad. Sci.* 90:5873-5877). Such an algorithm is incorporated into the NBLAST and XBLAST programs (Altschul *et al.*, 1990, *J. Mol. Biol.* 215:403 and Altschul *et al.*, 1997, *Nucleic Acid Res.* 25:3389-3402). Software for performing BLAST analyses is publicly available, *e.g.*, through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score

threshold (Altschul *et al., supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M = 5, N = -4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, 1989, PNAS, 89:10915).

[0027] The Clustal V method of alignment can also be used to determine percent identity (Higgins and Sharp, 1989, *CABIOS. 5*:151-153) and found in the Megalign program of the LASERGENE bioinformatics computing suite (DNASTAR Inc., Madison, WI). The "default parameters" are the parameters pre-set by the manufacturer of the program and for multiple alignments they correspond to GAP PENALTY=10 and GAP LENGTH PENALTY=10, while for pairwise alignments they are KTUPLE 1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5. After alignment of the sequences, using the Clustal V program, it is possible to obtain a "percent identity" by viewing the "sequence distances" table on the same program.

[0028] The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, typically only exact matches are counted.

[0029] In another embodiment, fragments of Cry2Ax and Cry2Ax-derived nucleic acid molecules are encompassed by the invention. Nucleic acid molecules are encompassed that have at least one Cry2Ax functional activity (*e.g.*, insecticidal activity), are at least 100, 250, 500, 750, 1000, 1500, or 1800 contiguous nucleotides in length of any of SEQ ID NOS: 1, 3,

5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, and/or hybridize under stringent conditions to the nucleic acid molecule that encodes any of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260. In embodiments where the nucleic acid fragment of the invention encodes a polypeptide that encompasses any of the amino acid residues that correspond to amino acid residues 2, 7, 27, 35, 36, 43, 44, 45, 51, 58, 69, 78, 79, 99, 118, 124, 125, 129, 138, 139, 141, 161, 165, 166, 183, 192, 211, 213, 217, 218, 324, 386, 399, 405, 445, 551, 587, 591, 610, 631 of SEQ ID NO:2, such nucleic acids molecules of the invention contain coding sequences for at least 1, at least 5, at least 10, at least 20, at least 30, or all 40 amino acid residues from the group consisting of H_2, S_7, Q_{27}, Q_{35}, E_{36}, K_{43}, D_{44}, N_{45}, D_{51}, A_{58}, V_{69}, R_{78}, N_{79}, K_{99}, T_{118}, V_{124}, E_{125}, R_{129}, N_{138}, R_{139}, A_{141}, T_{162}, Q_{165}, M_{166}, L_{183}, I_{192}, H_{211}, R_{213}, R_{217}, D_{218}, V_{324}, I_{386}, T_{399}, S_{405}, Q_{445}, I_{551}, S_{587}, I_{591}, L_{610}, and L_{631}.

[0030] In a specific embodiment, a fragment of the invention corresponds to the length of nucleic acid that encodes the processed pro-toxin. There is a 5-6 kDa difference in molecular weight between full length pro-toxin Cry2 and the processed Cry2 toxin. This is the result of ~40 amino acids being cleaved from the pro-toxin Cry2 polypeptide (Rukmini *et al.*, 2000, *Biochimie* 82:109-116; Aronson *et al.*, 1993, *Mol. Microbiol.* 7:489-496; Morse *et al.*, 2001, *Structure* 9:409-17).

[0031] In another specific embodiment, a fragment of the invention encodes a polypeptide that corresponds to a Cry2 domain.

[0032] In another embodiment, a nucleic acid molecule that hybridizes under stringent conditions to any one of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259 is encompassed by the invention. Such nucleic acid molecules of the invention encode polypeptides that contain at least 1, at least 5, at least 10, at least 20, at least 30, or all 40 amino acid residues from the group consisting of H_2, S_7, Q_{27}, Q_{35}, E_{36}, K_{43}, D_{44}, N_{45}, D_{51}, A_{58}, V_{69}, R_{78}, N_{79}, K_{99}, T_{118}, V_{124}, E_{125}, R_{129}, N_{138}, R_{139}, A_{141}, T_{162}, Q_{165}, M_{166}, L_{183}, I_{192}, H_{211}, R_{213}, R_{217}, D_{218}, V_{324}, I_{386}, T_{399}, S_{405}, Q_{445}, I_{551}, S_{587}, I_{591}, L_{610}, and L_{631}.

[0033] The phrase "stringent conditions" refers to hybridization conditions under which a nucleic acid will hybridize to its target nucleic acid, typically in a complex mixture of nucleic acid, but to essentially no other nucleic acids. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer nucleic acids hybridize specifically at higher temperatures. Extensive guides to the hybridization of nucleic acids can be found in the art (*e.g.*, Tijssen, Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993)). Generally, highly stringent conditions are selected to be about 5-10 °C lower than the thermal melting point (T_m) for the specific nucleic acid at a defined ionic strength pH. Low stringency conditions are generally selected to be about 15-30 °C below the T_m. The T_m is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which 50% of the probes complementary to the target hybridize to the target nucleic acid at equilibrium (as the target nucleic acids are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Hybridization conditions are typically those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30 °C for short probes (e.g., 10 to 50 nucleotides) and at least about 60 °C for long probes (*e.g.*, greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a

positive signal is at least two times background, and preferably 10 times background hybridization. In one embodiment, stringent conditions include at least one wash (usually 2) in 0.2X SSC at a temperature of at least about 50° C, usually about 55° C, or sometimes 60° C or 65° C, for 20 minutes, or substantially equivalent conditions. In a specific embodiment, the nucleic acid molecule of the invention specifically hybridizes following at least one wash in 0.2X SSC at 55 °C for 20 minutes to a polynucleotide encoding the polypeptide of any of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260. In another embodiment, stringent conditions include hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45° C followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65° C.

[0034] The phrase "specifically hybridizes" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (*e.g.*, total cellular or library DNA or RNA).

[0035] Vectors comprising nucleic acids of the invention are also encompassed. Cells or plants comprising the vectors of the invention are also encompassed.

[0036] The term "nucleic acid" or "nucleic acid molecule" herein refer to a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases read from the 5' to the 3' end. It includes chromosomal DNA, self-replicating plasmids and DNA or RNA that performs a primarily structural role. The term "encoding" refers to a polynucleotide sequence encoding one or more amino acids. The term does not require a start or stop codon. An amino acid sequence can be encoded in any one of six different reading frames provided by a polynucleotide sequence and its complement.

[0037] Table 1 discloses Cry2Ax and Cry2Ax-derived sequences and the corresponding sequence identity number.

5.3 Cry2Ax-Derived Sequences

[0038] Cry2Ax-derived polypeptides and nucleic acids of the invention can be created by introducing one or more nucleotide substitutions, additions and/or deletions into the nucleotide sequence of Cry2Ax or related nucleic acids, such that one or more amino acid substitutions, additions and/or deletions are introduced into the encoded protein. Generally, Cry2Ax-derived sequences are created in order to accentuate a desirable characteristic or reduce an undesirable characteristic of a Cry2Ax polypeptide. In one embodiment, Cry2Ax-derived polypeptides have improved insecticidal activity over Cry2Ax including, but not limited to, greater potency and/or increased insect pest range. In another embodiment, Cry2Ax-derived polypeptides are expressed better than Cry2Ax including, but not limited to, increased half life, less susceptible to degradation, and/or more efficient transcription or translation.

[0039] In one embodiment, a Cry2Ax (SEQ ID NO:1) nucleic acid molecule is used as a template to create Cry2Ax-derived nucleotides. In another embodiment, a Cry2Ax related nucleic acid is used as a template to create Cry2Ax-derived nucleotides. In a specific embodiment, Cry2Ab* is used as a template. Cry2Ab* has two amino acid changes relative to wild type Cry2Ab (K to R at position 36 and M to T at position 241 of GenBank Accession No. M23724). In another specific embodiment, clones isolated from one round of alteration can be used as template for further rounds of alteration (*e.g.*, clones 38, 44, and 473R; see Sections 6.2 and 6.4).

[0040] Sequence alterations can be introduced by standard techniques such as directed molecular evolution techniques *e.g.*, DNA shuffling methods (see *e.g.*, Christians *et al.*, 1999, *Nature Biotechnology* 17:259-264; Crameri *et al.*, 1998, *Nature*, 391:288-291; Crameri, *et al.*, 1997, *Nature Biotechnology* 15:436-438; Crameri *et al.*, 1996, *Nature Biotechnology* 14:315-319; Stemmer, 1994, *Nature* 370:389-391; Stemmer *et al.*, 1994, *Proc. Natl. Acad. Sci.*, 91:10747-10751; United States Patent Nos. 5,605,793; 6,117,679; 6,132,970; 5,939,250; 5,965,408; 6,171,820; International Publication Nos. WO 95/22625; WO 97/0078; WO 97/35966; WO 98/27230; WO 00/42651; and WO 01/75767); site directed mutagenesis (see *e.g.*, Kunkel, 1985, *Proc. Natl. Acad. Sci.*, 82:488-492; Oliphant *et al.*, 1986, *Gene* 44:177-183); oligonucleotide-directed mutagenesis (see *e.g.*, Reidhaar-Olson *et al.*, 1988, *Science* 241:53-57); chemical mutagenesis (see *e.g.*, Eckert *et al.*, 1987, *Mutat. Res.* 178:1-10); error prone PCR (see *e.g.*, Caldwell & Joyce, 1992, *PCR Methods Applic.* 2:28-33); and cassette

mutagenesis (see *e.g.*, Arkin *et al.*, *Proc. Natl. Acad. Sci.*, 1992, 89:7871-7815); (see generally, *e.g.*, Arnold, 1993, *Curr. Opinion Biotechnol.* 4:450-455; Ling *et al.*, 1997, *Anal. Biochem.*, 254(2):157-78; Dale *et al.*, 1996, *Methods Mol. Biol.* 57:369-74; Smith, 1985, *Ann. Rev. Genet.* 19:423-462; Botstein *et al.*, 1985, *Science*, 229:1193-1201; Carter, 1986, *Biochem. J.* 237:1-7; Kramer *et al.*, 1984, *Cell* 38:879-887; Wells *et al.*, 1985, *Gene* 34:315-323; Minshull *et al.*, 1999, *Current Opinion in Chemical Biology* 3:284-290).

[0041] In one embodiment, DNA shuffling is used to create Cry2Ax-derived nucleotides. DNA shuffling can be accomplished *in vitro*, *in vivo*, *in silico*, or a combination thereof. In silico methods of recombination can be effected in which genetic algorithms are used in a computer to recombine sequence strings which correspond to homologous (or even non-homologous) nucleic acids. The resulting recombined sequence strings are optionally converted into nucleic acids by synthesis of nucleic acids which correspond to the recombined sequences, *e.g.*, in concert with oligonucleotide synthesis gene reassembly techniques. This approach can generate random, partially random or designed alterations. Many details regarding in silico recombination, including the use of genetic algorithms, genetic operators and the like in computer systems, combined with generation of corresponding nucleic acids as well as combinations of designed nucleic acids (*e.g.*, based on cross-over site selection) as well as designed, pseudo-random or random recombination methods are described in the art (see *e.g.*, International Publication Nos. WO 00/42560 and WO 00/42559).

[0042] In another embodiment, targeted mutagenesis is used to create Cry2Ax-derived nucleotides by choosing particular nucleotide sequences or positions of the Cry2Ax or related nucleic acid for alteration. Such targeted mutations can be introduced at any position in the nucleic acid. For example, one can make nucleotide substitutions leading to amino acid substitutions at "non-essential" or "essential" amino acid residues. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence without altering the biological activity, whereas an "essential" amino acid residue is required for at least one biological activity of the polypeptide. For example, amino acid residues that are not conserved or only semi-conserved among homologs of various species may be non-essential for activity. Alternatively, amino acid residues that are conserved among the homologs of various species may be essential for activity.

[0043] Such targeted mutations can be conservative or non-conservative. A "non-conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a dissimilar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid, asparagine, glutamine), uncharged polar side chains (*e.g.*, glycine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), β-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine).

[0044] Alternatively or in addition to non-conservative amino acid residue substitutions, such targeted mutations can be conservative. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Following mutagenesis, the encoded protein can be expressed recombinantly and the activity of the protein can be determined.

[0045] In another embodiment, random mutagenesis is used to create Cry2Ax-derived nucleotides. Mutations can be introduced randomly along all or part of the coding sequence (*e.g.*, by saturation mutagenesis). In certain embodiments, nucleotide sequences encoding other related polypeptides that have similar domains, structural motifs, active sites, or that align with a portion of the Cry2Ax of the invention with mismatches or imperfect matches, can be used in the mutagenesis process to generate diversity of sequences.

[0046] It should be understood that for each mutagenesis step in some of the techniques mentioned above, a number of iterative cycles of any or all of the steps may be performed to optimize the diversity of sequences. The above-described methods can be used in combination in any desired order. In many instances, the methods result in a pool of altered nucleic acid sequences or a pool of recombinant host cells comprising altered nucleic acid sequences. The altered nucleic acid sequences or host cells expressing an altered nucleic acid sequence with the desired characteristics can be identified by screening with one or more assays known in the art. The assays may be carried out under conditions that select for polypeptides possessing the desired physical or chemical characteristics. The alterations in the nucleic acid sequence can be determined by sequencing the nucleic acid molecule encoding the altered polypeptide in the clones.

[0047] Additionally, Cry2Ax and Cry2Ax-derived nucleic acid molecules can be codon optimized, either wholly or in part. Because any one amino acid (except for methionine) is encoded by a number of codons (Table 2), the sequence of the nucleic acid molecule may be changed without changing the encoded amino acid. Codon optimization is when one or more codons are altered at the nucleic acid level such that the amino acids are not changed but expression in a particular host organism is increased. Those having ordinary skill in the art will recognize that tables and other references providing preference information for a wide range of organisms are available in the art.

5.4 Methods Of Assaying Insecticidal Activity

[0048] As used herein, the term "insecticidal activity" refers to the ability of a polypeptide to decrease or inhibit insect feeding and/or to increase insect mortality upon ingestion of the polypeptide. Although any insect may be effected, preferably insects of the *Lepidoptera* and *Diptera* orders of insects are affected.

[0049] A variety of assays can be used to determine whether a particular polypeptide of the invention has insecticidal activity and, if so, to what degree. Generally, an insect pest is provided a polypeptide of the invention in any form that can be ingested. The reaction of the insect pest to ingestion of the polypeptide of the invention is observed (*e.g.*, for about one to three days). A decrease or inhibition of feeding and/or an increase in insect pest mortality after ingestion of the polypeptide of the invention are indicators of insecticidal activity. A polypeptide of the invention with unknown insecticidal activity should be compared to a positive and/or negative control to assess more accurately the outcome of the assay.

[0050] In one embodiment, a polypeptide of the invention is purified (either in soluble form or in crystal form) and added to the insect diet.

[0051] In another embodiment, a polypeptide of the invention is expressed in a recombinant microbe (*e.g.*, *E. coli*). The recombinant microbe is fed directly to the insect pests (see Moellenbeck *et al.*, 2001, *Nat. Biotechnol.* 19:668).

[0052] In another embodiment, the polypeptide of the invention is expressed in a plant and the plant is fed to the insect pest. Following the incubation period, the feeding activity of the insect pest can be determined by visual observation (*e.g.*, of approximate fraction of leaf area remaining) or video capture (*e.g.*, number of pixels in a leaf area remaining) of the plant parts that would normally have been eaten by the insect pest. In a specific embodiment,

expression of the polypeptide of the invention in the plant is transient. In such embodiments, a nucleic acid encoding a polypeptide of the invention is cloned into a plant expression vector and transfected into *Agrobacterium tumefaciens*. The transformed bacteria is co-cultivated with a leaf from *N. benthamiana* and, using forced infiltration, the leaf expresses the polypeptide of the invention. However, expression of the polypeptide is variable between leaf co-cultures. In another specific embodiment, expression of the polypeptide of the invention in the plant is stable. In such embodiments, a transgenic plant is made that expresses a polypeptide of the invention.

[0053] In another embodiment, insecticidal activity of a polypeptide of the invention can be assayed by measuring cell death and/or cell growth using cultured cells. Such assays typically involve the use of cultured insect cells that are susceptible to the particular toxin being screened, or cells that express a receptor for the particular toxin, either naturally or as a result of expression of a heterologous gene. Thus, in addition to insect cells, mammalian, bacterial, and yeast cells are among those cells useful in the *in vitro* assays. *In vitro* bioassays which measure toxicity against cultured cells are described in the art (*e.g.*, Johnson, 1994, *J. Invertebr. Pathol.* 63:123-129).

[0054] In another embodiment, insecticidal activity of a polypeptide of the invention can be assayed by measuring pore formation in target insect-derived midgut epithelial membrane vesicles (Juttner and Ebel, 1998, *Biochim. Biophys. Acta* 1370:51-63.; English *et al.*, 1991, *Insect Biochem.* 21:177-184). Such an assay may constitute toxin conditional release of a ligand activated substrate from the lumen of the membrane vesicles. This requires that the ligand be on the outside of the vesicle. Alternatively the reverse scenario may be utilized whereby the ligand is in the vesicle lumen and the ready to be activated substrate is located on the outside of the vesicle. The higher the toxin activity the greater the number or size of pores formed.

5.5 Methods of Enhancing Insect Resistance in Plants

[0055] The present invention provides methods of enhancing plant resistance to insect pests including, but not limited to, members of the *Helicoverpa ssp.(e.g., Helicoverpa Zea)* and/or *Spodoptera ssp. (e.g., Spodopter exigua)* through the use of Cry2 related insecticidal polypeptides. Any method known in the art can be used to cause the insect pests to ingest one or more polypeptides of the invention during the course of feeding on the plant. As such,

the insect pest will ingest insecticidal amounts of the one or more polypeptides of the invention and may discontinue feeding on the plant. In some embodiments, the insect pest is killed by ingestion of the one or more polypeptides of the invention. In other embodiments, the insect pests are inhibited or discouraged from feeding on the plant without being killed.

[0056] In one embodiment, transgenic plants can be made to express one or more polypeptides of the invention (see generally Section 5.7 for methods of transgenic plant production). The transgenic plant may express the one or more polypeptides of the invention in all tissues (*e.g.*, global expression). Alternatively, the one or more polypeptides of the invention may be expressed in only a subset of tissues (*e.g.*, tissue specific expression), preferably those tissues consumed by the insect pest. Polypeptides of the invention can be expressed constitutively in the plant or be under the control of an inducible promoter.

[0057] In another embodiment, a composition comprising one or more polypeptides of the invention can be applied externally to a plant susceptible to the insect pests. External application of the composition includes direct application to the plant, either in whole or in part, and/or indirect application, *e.g.*, to the environment surrounding the plant such as the soil. The composition can be applied by any method known in the art including, but not limited to, spraying, dusting, sprinkling, or the like. In general, the composition can be applied at any time during plant growth. One skilled in the art can use methods known in the art to determine empirically the optimal time for administration of the composition. Factors that affect optimal administration time include, but are not limited to, the type of susceptible plant, the type of insect pest, which one or more polypeptides of the invention are administered in the composition.

[0058] The composition comprising one or more polypeptides of the invention may be *substantially purified polypeptides*, a *cell suspension*, a *cell pellet*, a cell supernatant, a cell extract, or a spore-crystal complex of *Bacillus thuringiensis* cells (see generally Section 5.6 for recombinant polypeptide synthesis techniques). The composition comprising one or more polypeptides of the invention may be in the form of a solution, an emulsion, a suspension, or a powder. Liquid formulations may be aqueous or non-aqueous based and may be provided as foams, gels, suspensions, emulsifiable concentrates, or the like. The formulations may include agents in addition to the one or more polypeptides of the invention. For example, compositions may further comprise spreader-sticker adjuvants, stabilizing agents, other

insecticidal additives, diluents, agents that optimize the rheological properties or stability of the composition, such as, for example, surfactants, emulsifiers, dispersants, or polymers.

[0059] In another embodiment, recombinant hosts that express one or more polypeptides of the invention are applied on or near a plant susceptible to attack by an insect pest. The recombinant hosts include, but are not limited to, microbial hosts and insect viruses that have been transformed with and express one or more nucleic acid molecules (and thus polypeptides) of the invention. In some embodiments, the recombinant host secretes the polypeptide of the invention into its surrounding environment so as to contact an insect pest. In other embodiments, the recombinant hosts colonize one or more plant tissues susceptible to insect infestation.

5.6 Recombinant Expression

[0060] Nucleic acid molecules and polypeptides of the invention can be expressed recombinantly using standard recombinant DNA and molecular cloning techniques that are well known in the art (*e.g.*, Sambrook, Fritsch, and Maniatis, Molecular Cloning: A Laboratory Manual; Cold Spring Harbor Laboratory Press: Cold Spring Harbor, 1989). Additionally, recombinant DNA techniques may be used to create nucleic acid constructs suitable for use in making transgenic plants (see Section 5.7).

[0061] Accordingly, an aspect of the invention pertains to vectors, preferably expression vectors, comprising a nucleic acid molecule of the invention, or a variant thereof. As used herein, the term "vector" refers to a polynucleotide capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be introduced. Another type of vector is a viral vector, wherein additional DNA segments can be introduced into the viral genome.

[0062] Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal vectors). Other vectors (*e.g.*, non-episomal vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids (vectors). However, the invention is intended to include such

other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses).

[0063] The recombinant expression vectors of the invention comprise a nucleic acid molecule of the invention in a form suitable for expression of the nucleic acid molecule in a host cell. This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably associated with the polynucleotide to be expressed. Within a recombinant expression vector, "operably associated" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described in the art (*e.g.*, Goeddel, Gene Expression Technology: Methods in Enzymology, 1990, Academic Press, San Diego, CA). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cells and those which direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, the area of the organism in which expression is desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids molecules as described herein.

[0064] In some embodiments, isolated nucleic acids which serve as promoter or enhancer elements can be introduced in the appropriate position (generally upstream) of a non-heterologous form of a polynucleotide of the present invention so as to up or down regulate expression of a polynucleotide of the present invention. For example, endogenous promoters can be altered *in vivo* by mutation, deletion, and/or substitution (see, U.S. Patent No. 5,565,350; International Patent Application No. PCT/US93/03868), or isolated promoters can be introduced into a plant cell in the proper orientation and distance from a cognate gene of a polynucleotide of the present invention so as to control the expression of the gene. Gene expression can be modulated under conditions suitable for plant growth so as to alter the total concentration and/or alter the composition of the polypeptides of the present invention in

plant cell. Thus, the present invention provides compositions, and methods for making heterologous promoters and/or enhancers operably linked to a native, endogenous (*i.e.*, non-heterologous) form of a polynucleotide of the present invention.

[0065] If polypeptide expression is desired, it is generally desirable to include a polyadenylation region at the 3'-end of a polynucleotide coding region. The polyadenylation region can be derived from the natural gene, from a variety of other plant genes, or from T-DNA. The 3' end sequence to be added can be derived from, for example, the nopaline synthase or octopine synthase genes, or alternatively from another plant gene, or less preferably from any other eukaryotic gene.

[0066] The recombinant expression vectors of the invention can be designed for expression of a polypeptide of the invention in prokaryotic (*e.g.*, *Enterobacteriaceae*, such as *Escherichia*; *Bacillaceae*; *Rhizoboceae*, such as *Rhizobium* and *Rhizobacter*; *Spirillaceae*, such as photobacterium; *Zymomonas*; *Serratia*; *Aeromonas*; *Vibrio*; *Desulfovibrio*; *Spirillum*; *Lactobacillaceae*; *Pseudomonadaceae*, such as *Pseudomonas* and *Acetobacter*; *Azotobacteraceae* and *Nitrobacteraceae*) or eukaryotic cells (*e.g.*, insect cells using baculovirus expression vectors, yeast cells, plant cells, or mammalian cells) (see Goeddel, *supra*. For a discussion on suitable host cells). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

[0067] Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors comprising constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve at least three purposes: 1) to increase expression of the recombinant protein; 2) to increase the solubility of the recombinant protein; and/or 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988, Gene 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia,

Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

[0068] In another embodiment, the expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari *et al.*, 1987, *EMBO J.* 6:229-234), pMFa (Kurjan and Herskowitz, 1982, *Cell* 30:933-943), pJRY88 (Schultz *et al.*, 1987, *Gene* 54:113-123), pYES2 (Invitrogen Corp., San Diego, CA), and pPicZ (Invitrogen Corp., San Diego, CA).

[0069] Alternatively, the expression vector is a baculovirus expression vector. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf9 cells) include the pAc series (Smith *et al.*, 1983, *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers, 1989, *Virology* 170:31-39).

[0070] In yet another embodiment, a nucleic acid of the invention is expressed in plant cells using a plant expression vector including, but not limited to, tobacco mosaic virus and potato virus expression vectors.

[0071] Other suitable expression systems for both prokaryotic and eukaryotic cells are known in the art (see, *e.g.*, chapters 16 and 17 of Sambrook *et al.* 1990, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY).

[0072] 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, tissue-specific, inducible, or other promoters for expression in the host organism.

[0073] A "tissue-specific promoter" may direct expression of nucleic acids of the present invention in a specific tissue, organ or cell type. Tissue-specific promoters can be inducible. Similarly, tissue-specific promoters may only promote transcription within a certain time frame or developmental stage within that tissue. Other tissue specific promoters may be active throughout the life cycle of a particular tissue. One of ordinary skill in the art will recognize that a tissue-specific promoter may drive expression of operably linked sequences in tissues other than the target tissue. Thus, as used herein, a tissue-specific promoter is one that drives expression preferentially in the target tissue or cell type, but may also lead to some expression in other tissues as well. A number of tissue-specific promoters can be used in the present invention. With the appropriate promoter, any organ can be targeted, such as shoot vegetative organs/structures (*e.g.* leaves, stems and tubers), roots, flowers and floral

organs/structures (*e.g.* bracts, sepals, petals, stamens, carpels, anthers and ovules), seed (including embryo, endosperm, and seed coat) and fruit. For instance, promoters that direct expression of nucleic acids in leaves, roots or flowers are useful for enhancing resistance to pests that infect those organs. For expression of a polynucleotide of the present invention in the aerial vegetative organs of a plant, photosynthetic organ-specific promoters, such as the *RBCS* promoter (Khoudi *et al.*, *Gene* 197:343, 1997), can be used. Root-specific expression of polynucleotides of the present invention can be achieved under the control of a root-specific promoter, such as, for example, the promoter from the *ANR1* gene (Zhang and Forde, *Science*, 279:407, 1998). Other exemplary promoters include the root-specific glutamine synthetase gene from soybean (Hirel *et al.*, 1992, *Plant Molecular Biology* 20:207-218) and the root-specific control element in the GRP 1.8 gene of French bean (Keller *et al.*, 1991, *The Plant Cell* 3:1051-1061).

[0074] A "constitutive promoter" is defined as a promoter which will direct expression of a gene in all tissues and are active under most environmental conditions and states of development or cell differentiation. Examples of constitutive promoters include the cauliflower mosaic virus (CaMV) 35S transcription initiation region, the 1'- or 2'- promoter derived from T-DNA of *Agrobacterium tumafaciens*, and other transcription initiation regions from various plant genes known to those of ordinary skill in the art. Such genes include for example, *ACT11* from *Arabidopsis* (Huang *et al.* 1996, *Plant Mol. Biol.* 33:125-139), *Cat3* from *Arabidopsis* (GenBank Accession No. U43147, Zhong *et al.*, 1996, *Mol. Gen. Genet.* 251:196-203), the gene encoding stearoyl-acyl carrier protein desaturase from *Brassica napus* (Genbank Accession No. X74782, Solocombe *et al.* 1994, *Plant Physiol.* 104:1167-1176), GPc1 from maize (GenBank Accession No. X15596, Martinez *et al.*, 1989, *J. Mol. Biol.* 208:551-565), and Gpc2 from maize (GenBank Accession No. U45855, Manjunath *et al.*, 1997, *Plant Mol. Biol.* 33:97-112). Any strong, constitutive promoter, such as the CaMV 35S promoter, can be used for the expression of polynucleotides of the present invention throughout the plant.

[0075] The term "inducible promoter" refers to a promoter that is under precise environmental or developmental control. Examples of environmental conditions that may effect transcription by inducible promoters include anaerobic conditions, elevated temperature, the presence of light, or spraying with chemicals/hormones.

[0076] Suitable constitutive promoters for use in a plant host cell include, for example, the core promoter of the Rsyn7 promoter and other related constitutive promoters (International Publication No. WO 99/43838 and U.S. Patent No. 6,072,050); the core 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); ALS promoter (U.S. Patent No. 5,659,026), and the like (*e.g.*, U.S. Patent Nos. 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).

[0077] Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

[0078] Accordingly, the present invention provides a host cell having an expression vector comprising a nucleic acid of the invention, or a variant thereof. A host cell can be any prokaryotic (*e.g.*, *E. coli, Bacillus thuringiensis*) or eukaryotic cell (*e.g.*, insect cells, yeast or plant cells). The invention also provides a method for expressing a nucleic acid of the invention thus making the encoded polypeptide comprising the steps of i) culturing a cell comprising a nucleic acid molecule of the invention under conditions that allow production of the encoded polypeptide; and ii) isolating the expressed polypeptide.

[0079] Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid molecules into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in the art (*e.g.*, Sambrook, *et al. supra*.).

5.7 Production of Transgenic Plants

[0080] Any method known in the art can be used for transforming a plant or plant cell with a nucleic acid molecule of the present invention. Nucleic acid molecules can be incorporated into plant DNA (*e.g.*, genomic DNA or chloroplast DNA) or be maintained without insertion into the plant DNA (*e.g.*, through the use of artificial chromosomes). Suitable methods of introducing nucleic acid molecules into plant cells include microinjection (Crossway *et al.*, 1986, *Biotechniques* 4:320-334); electroporation (Riggs *et al.*, 1986, *Proc. Natl. Acad. Sci.* 83:5602-5606; D'Halluin *et al.*, 1992, *Plant Cell* 4:1495-1505); Agrobacterium-mediated transformation (U.S. Patent Nos. 5,563,055 and 5,981,840, Osjoda *et al.*, 1996, *Nature Biotechnology* 14:745-750; Horsch *et al.*, 1984, *Science* 233:496-498, Fraley *et al.*, 1983, *Proc. Natl. Acad. Sci.* 80:4803, and *Gene Transfer to Plants*, Potrykus, ed., Springer-Verlag, Berlin 1995); direct gene transfer (Paszkowski *et al.*, 1984, *EMBO J.* 3:2717-2722); ballistic particle acceleration (U.S. Patent Nos. 4,945,050; 5,879,918; 5,886,244; 5,932,782; Tomes *et al.*, 1995, "Direct DNA Transfer into Intact Plant Cells via Microprojectile Bombardment, in Plant Cell, Tissue, and Organ Culture: Fundamental Methods, ed. Gamborg and Phillips, Springer-Verlag, Berlin; and McCabe *et al.*, 1988, *Biotechnology* 6:923-926); virus-mediated transformation (U.S. Patent Nos. 5,889,191, 5,889,190, 5,866,785, 5,589,367 and 5,316,931); pollen transformation (De Wet *et al.*, 1985, in The Experimental Manipulation of Ovule Tissues, ed. Chapman *et al.*, Longman, New York, pp. 197-209); Lec 1 transformation (U.S. Patent Application Ser. No. 09/435,054; International Publication No. WO 00/28058); whisker-mediated transformation (Kaeppler *et al.*, 1990, *Plant Cell Reports* 9:415-418; Kaeppler *et al.*, 1992, *Theor. Appl. Genet.* 84:560-566); and chloroplast transformation technology (Bogorad, 2000, *Trends in Biotechnology* 18: 257-263; Ramesh *et al.*, 2004, *Methods Mol Biol.* 274:301-7; Hou *et al.*, 2003, *Transgenic Res.* 12:111-4; Kindle *et al.*, 1991, *Proc. Natl. Acad. Sci.* 88:1721-5; Bateman and Purton, 2000, *Mol Gen Genet.* 263:404-10; Sidorov *et al.*, 1999, *Plant J.* 19:209-216).

[0081] The choice of transformation protocols used for generating transgenic plants and plant cells can vary depending on the type of plant or plant cell, *i.e.*, monocot or dicot, targeted for transformation. Examples of transformation protocols particularly suited for a particular plant type include those for : potato (Tu *et al.*, 1998, *Plant Molecular Biology* 37:829-838; Chong *et al.*, 2000, *Transgenic Research* 9:71-78); soybean (Christou *et al.*,

1988, *Plant Physiol.* 87:671-674; McCabe *et al.*, 1988, *BioTechnology* 6:923-926; Finer and McMullen, 1991, *In Vitro Cell Dev. Biol.* 27P:175-182; Singh *et al.*, 1998, *Theor. Appl. Genet.* 96:319-324); maize (Klein *et al.*, 1988, *Proc. Natl. Acad. Sci.* 85:4305-4309; Klein *et al.*, 1988, *Biotechnology* 6:559-563; Klein *et al.*, 1988, *Plant Physiol.* 91:440-444; Fromm *et al.*, 1990, *Biotechnology* 8:833-839; Tomes *et al.*, 1995, "Direct DNA Transfer into Intact Plant Cells via Microprojectile Bombardment," in Plant Cell, Tissue, and Organ Culture; Fundamental Methods, ed. Gamborg (Springer-Verlag, Berlin)); cereals (Hooykaas-Van Slogteren *et al.*, 1984, *Nature* 311:763-764; U.S. Patent No. 5,736,369).

[0082] In some embodiments, more than one construct is used for transformation in the generation of transgenic plants and plant cells. Multiple constructs may be included in cis or trans positions. In preferred embodiments, each construct has a promoter and other regulatory sequences.

[0083] Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype and thus the desired phenotype. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium, typically relying on a biocide and/or herbicide marker that has been introduced together with the desired nucleotide sequences. Plant regeneration from cultured protoplasts is described in the art (*e.g.*, Evans *et al.*, Protoplasts Isolation and Culture, Handbook of Plant Cell Culture, pp. 124-176, MacMillilan Publishing Company, New York, 1983; and Binding, Regeneration of Plants, Plant Protoplasts, pp. 21-73, CRC Press, Boca Raton, 1985). Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are also described in the art (e.g., Klee et al. 1987, Ann. Rev. of Plant Phys. 38:467-486).

[0084] The term "plant" includes whole plants, shoot vegetative organs/structures (*e.g.* leaves, stems and tubers), roots, flowers and floral organs/structures (*e.g.* bracts, sepals, petals, stamens, carpels, anthers and ovules), seed (including embryo, endosperm, and seed coat) and fruit (the mature ovary), plant tissue (*e.g.* vascular tissue, ground tissue, and the like) and cells (*e.g.* guard cells, egg cells, trichomes and the like), and progeny of same. The class of plants that can be used in methods of the present invention includes the class of higher and lower plants amenable to transformation techniques, including angiosperms (monocotyledonous and dicotyledonous plants), gymnosperms, ferns, and multicellular algae.

Plants of a variety of ploidy levels, including aneuploid, polyploid, diploid, haploid and hemizygous plants are also included.

[0085] The nucleic acid molecules of the invention can be used to confer desired traits on essentially any plant. Thus, the invention has use over a broad range of plants, including species from the genera *Agrotis, Allium, Ananas, Anacardium, Apium, Arachis, Asparagus, Athamantha, Atropa, Avena, Bambusa, Beta, Brassica, Bromus, Browaalia, Camellia, Cannabis, Carica, Ceratonia. Cicer, Chenopodium, Chicorium, Citrus, Citrullus, Capsicum, Carthamus, Cocos, Coffea, Coix, Cucumis, Cucurbita, Cynodon, Dactylis, Datura, Daucus, Dianthus, Digitalis, Dioscorea, Elaeis, Eliusine, Euphorbia, Festuca, Ficus, Fragaria, Geranium, Glycine, Graminae, Gossypium, Helianthus, Heterocallis, Hevea, Hibiscus, Hordeum, Hyoscyamus, Ipomoea, Lactuca, Lathyrus, Lens, Lilium, Linum, Lolium, Lotus, Lupinus, Lycopersicon, Macadamia, Macrophylla, Malus, Mangifera, Manihot, Majorana, Medicago, Musa, Narcissus, Nemesia, Nicotiana, Onobrychis, Olea, Olyreae, Oryza, Panicum, Panicum, Panieum, Pannisetum, Pennisetum, Petunia, Pelargonium, Persea, Pharoideae, Phaseolus, Phleum, Picea, Poa, Pinus, Pistachia, Pisum, Populus, Pseudotsuga, Pyrus, Prunus, Pseudotsuga, Psidium, Quercus, Ramunculus, Raphanus, Ribes, Ricinus, Rhododendron, Rosa, Saccharum, Salpiglossis, Secale, Senecio, Setaria, Sequoia, Sinapis, Solanum, Sorghum, Stenotaphrum, Theobromus, Trigonella, Trifolium, Trigonella, Triticum, Tsuga, Tulipa, Vicia, Vitis, Vigna,* and *Zea.*

[0086] In specific embodiments, transgenic plants are maize, potato, rice, soybean or cotton plants.

[0087] Transgenic plants may be grown and pollinated with either the same transformed strain or different strains. Two or more generations of the plants may be grown to ensure that expression of the desired nucleic acid molecule, polypeptide and/or phenotypic characteristic is stably maintained and inherited. One of ordinary skill in the art will recognize that after the nucleic acid molecule of the present invention is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed.

5.8 Determination Of Expression in Transgenic Plants

[0091] Any method known in the art can be used for determining the level of expression in a plant of a nucleic acid molecule of the invention or polypeptide encoded therefrom. For example, the expression level in a plant of a polypeptide encoded by a nucleic acid molecule of the invention can be determined by immunoassay, quantitative gel electrophoresis, etc. Additionally, the expression level in a plant of a polypeptide encoded by a nucleic acid molecule of the invention can be determined by the degree to which the plant phenotype is altered. In a specific embodiment, enhanced insect resistance is the phenotype to be assayed.

[0092] As used herein, "enhanced insect resistance" refers to increased resistance of a transgenic plant expressing a polypeptide of the invention to consumption and/or infestation by an insect pest as compared to a plant not expressing a polypeptide of the invention. Enhanced resistance can be measured in a number of ways. In one embodiment, enhanced resistance is measured by decreased damage to a plant expressing a polypeptide of the invention as compared to a plant not expressing a polypeptide of the invention after the same period of insect incubation. Insect damage can be assessed visually. For example in cotton plants, damage after infestation can be measured by looking directly at cotton plant bolls for signs of consumption by insects. In another embodiment, enhanced resistance is measured by increased crop yield from a plant expressing a polypeptide of the invention as compared to a plant not expressing a polypeptide of the invention after the same period of insect incubation. In particular embodiments, the insect pest are from the orders *Lepidoptera* and/or *Diptera*.

[0093] Determinations can be made using whole plants, tissues thereof, or plant cell culture.

[0094] The Sequence Listing (named 21194286PC.TXT) that is 0.97 MB and was created on February 24, 2005 on the compact disk submitted concurrently is incorporated by reference in its entirety.

[0095] The contents of all published articles, books, reference manuals and abstracts cited herein, are hereby incorporated by reference in their entirety to more fully describe the state of the art to which the invention pertains.

[0096] As various changes can be made in the above-described subject matter without departing from the scope and spirit of the present invention, it is intended that all subject matter contained in the above description, and/or defined in the appended claims, be

interpreted as descriptive and illustrative of the present invention. Modifications and variations of the present invention are possible in light of the above teachings.

6. EXAMPLES

6.1 Example 1: Primary insect screening

[0094] Primary insect screening identified Bt cultures from a biodiversity collection having activity against *Helicoverpa* spp. The screening was conducted with spore-crystal complex samples at one high dose against *Helicoverpa zea* neonate larvae.

[0095] Spore-crystal complex samples were prepared in deep-well production plates containing 1 ml CYS sporulation medium (Yamamoto, 1990, Analytical Chemistry of *Bacillus thuringiensis* 432:46-60). The production plates were inoculated with 10 µl seed cultures that had been kept frozen at -80 °C and incubated at 30 °C, 350 rpm for 3 days until most cultures sporulated and released free spores and crystals. The plates were centrifuged at 4000 rpm, for 40 min to precipitate spores, crystals and unlysed cells. The precipitated spore-crystal complex was suspended in 1.2 ml 15 mM potassium acetate containing 100 µg lysozyme and incubated at 30 °C, 250 rpm for 16 h to ensure full sporulation and cell lysis. After the 16-hr incubation, the spore-crystal complex was collected by centrifugation and suspended in 15 mM potassium acetate. This potassium acetate step was repeated once. The final spore-crystal suspension was made in 1 ml 15 mM potassium acetate and used to screen for *H. zea* activity.

[0096] Insect screening was done in shallow 96-well plates containing 150 µl artificial insect diet in each well. 20 µl of spore-crystal suspension was placed on the insect diet. About 5 neonate larvae were placed in each well. The insect assay plates were incubated at 29 °C for 3 days. Insect responses to Bt crystals included feeding inhibition and mortality. About 400 cultures showed substantial mortality and were therefore identified as positive. Cry2Ax was among the positives.

6.2 Example 2: DNA shuffling to isolate Cry2Ax-derived polypeptides

[0097] Starting with the Cry2Ax polypeptide (SEQ ID NO:2) and the Cry2Ab* polypeptide (Cry2Ab* has 2 amino acid changes relative to wild type Cry2Ab; K to R at position 36 and M to T at position 241 of GenBank Accession No. M23724), synthetic DNA templates were created for DNA shuffling. Using a phylogenetic comparison of Cry2Ab

(Gen Bank Accession No. M23724) and Cry2Ax (SEQ ID NO:2) a library was created that varied the 40 amino acid positions (see Section 5.1) that were different between these two polypeptide sequences. Shuffled DNA libraries were created using oligonucleotide directed shuffling with the synthetic gene encoding Cry2Ax acting as the parental DNA template. The PCR DNA libraries were cloned into pMAXY3219 by replacing the Cry2Ab* gene. The toxin clones were built such that they are expressed as a fusion to the *E. coli* maltose binding protein (MBP). Primary insect screening identified cultures active against *Helicoverpa* spp. The screening was conducted by incorporating a small amount of *E. coli* culture expressing the MBP::Cry2Ax-derived polypeptide fusion at one low dose in artificial diet followed by infestation with *H. zea* larvae. Screening was done in shallow 96-well plates containing 150 µl artificial insect diet in each well. ~0.5 µl of MBP::Cry2Ax-derived polypeptide fusion expressing culture was incorporated into the insect diet. About 5 *H. zea* neonate larvae were placed in each well. The insect assay plates were incubated at 29 °C for 4 days. Insect responses to the *E. coli* samples included feeding inhibition and mortality. Those samples causing severe stunting or death to the larvae were re-arrayed for further analysis.

[0098] Screening of this first round library led to the discovery of several clones improved insecticidal activity relative to Cry2Ax and Cry2Ab*. In particular, clones 38 (D_S00503480) (SEQ ID NO:4) and 44 (D_S00503970) (SEQ ID NO:6) were found to be highly active when expressed (data not shown). These clones were therefore chosen for a successive round of DNA shuffling.

[0099] For the second round of shuffling, parent DNA templates from clones 38 (D_S00503480) (SEQ ID NO:4) and 44 (D_S00503970) (SEQ ID NO:6) were PCR amplified in the presence of uracil and then fragmented with uracil N-glycosylase. The fragmented templates were then mixed, reassembled before recombinant templates were amplified by PCR. A library of these shuffled templates was created in pMAXY3219 as described above. The sequence of some of the clones isolated from the first and second rounds of shuffling is shown in Table 3 indicating the amino acid residues that were changed.

[00100] In order to further diversify one of the top performing 2nd Round hits, clone 473R (D_S01037677) (SEQ ID NO:18), the first 46 amino acid residues at the amino terminal region of the polypeptide were modified to contain residues found in eight different Cry2 polypeptide sequences (*i.e.*, Cry2Aa, Cry2Ab, Cry2Ac, Cry2Ad, Cry2Ae, Cry2Af, Cry2Ag, and Cry2Ax). In addition, two residues, I13 and D15, were substituted with conservative

residues valine and glutamate, respectively (see Table 4). The modified clone was termed clone 473N (SEQ ID NO:8).

6.3 Example 3: Activity of Cry2Ax-derived polypeptides

[00101] Screening of the activities of the shuffled clones was carried out in several stages. Initially the clones were screened for high insecticidal activity by providing a small amount of *E. coli* expressing a clone fusion protein into artificial diet for first instar *H. zea* larvae. Clones causing either complete death or complete stunting of the larvae were chosen for further study. Those clones that demonstrated high insecticidal activity were then used to create a new library in a plant expression vector in *Agrobacterium tumefaciens*. The library was screened by co-cultivating each clone in four replicates with *N. benthamiana* leaves (using forced infiltration of each respective culture), and then feeding each corresponding disk to a single 3rd instar *H. zea* larvae. Following a 24-hour incubation period, the feeding activity was determined by visual observation and expressed as an approximate fraction of leaf area remaining.

[00102] The clones passing further repetition of the *E. coli* expression / diet incorporation assays were re-cloned individually into plant expression vector pMAXY4384 and tested for efficacy *in planta* as described above. A final *in planta* activity assessment of the best hits from the *E. coli* expression multi-tiered assay and the plant library approach is shown in FIG. 1. From this analysis several clones appeared to have increased insecticidal activity including 7K (D_S01000779) (SEQ ID NO:10), 15K (D_S00999080) (SEQ ID NO:12), 16K (D_S01000269) (SEQ ID NO:14), 16R (D_S01037143) (SEQ ID NO:16), and 473R (D_S01037677) (SEQ ID NO:18).

6.4 Example 4: DNA shuffling to isolate additional Cry2Ax-derived polypeptides

[00103] Clones 44 (D_S00503970) (SEQ ID NO:6), 473R (D_S01037677) (SEQ ID NO: 18) which were 1st and 2nd round shuffling hits as described Section 6.2 and Cry2Ab* were used as templates for further shuffling. Using these templates and oligonucleotide directed shuffling, derived polypeptides were created having amino acid diversity from wild type Cry2 polypeptides (*i.e.*, Cry2Ae and Cry2Ag) as well as computer generated random conservative amino acid substitutions and random substitutions within segments of certain structural loop regions. The shuffled DNA libraries were cloned into pMAXY3219 by

replacing the Cry2Ab* gene. The toxin clones were built such that they were expressed as a fusion to the *E. coli* maltose binding protein (MBP). A summary of the isolated sequences is shown in Tables 5-7.

6.5 Example 5: Activity of additional Cry2Ax-derived polypeptides

[00104] In order to assess the activity of the shuffled derived polypeptides against the cotton pest *Helicoverpa zea*, high throughput screening using artificial diet containing whole *E. coli* cells expressing a clone fusion protein was performed as described *supra*. Clones having a high level of activity were further tested for *in planta* activity to confirm that the changes made to each derived polypeptide did not negatively impact gene expression or protein accumulation in plant cells. To initiate this process, each Cry2Ax-derived polypeptide was cloned into an *Agrobacterium tumefaciens* based plant expression vector, transformed into the host *Agrobacterium* strain and then arrayed into microtiter dishes. The hits were then screened by co-cultivating each in four replicates with *N. benthamiana* leaves (using forced infiltration of each respective culture), followed by feeding each corresponding disk to a single 3rd instar *H. zea* larvae. Following a 24-hour incubation period the feeding activity on each disc was determined by the visual capture and analysis method as described *supra*. Some derived polypeptides from this process were improved compared to the parental clones. One such clone is D_S01764701 (SEQ ID NO:134) that showed improved activity over clone 44. Feeding assay results are shown for three experiments in FIG. 2.

6.6 Example 6: Transgenic plants expressing clone 44

[00105] Transgenic tobacco plants expressing clone 44 (D_S00503970) were generated by *Agrobacterium*-mediated transformation with glyphosate selection using binary vectors pMAXY5469 and pMAXY5471. These vectors contain a dSVBV driven GAT gene and a dMMV driven clone 44 nucleic acid molecule clone 44 (SEQ ID NO:5). pMAXY5469 differs from pMAXY5471 in that it contains plastid targeting signal fused to the coding region of clone 44 such that this toxin variant will accumulate in the plastid compartment. Approximately 25 transformants were generated for each construct. Leaf disks expressing clone 44 were placed on a bed of agar in a 48-well titer tray and then infested with either 3rd instar *Helicoverpa zea* larvae or 4th instar *Spodoptera exigua* larvae. The leaves were incubated 24 hrs with the worms and then the larvae which were then removed and the leaf

remaining was observed with video capture equipment for actual calculation of relative leaf area remaining (number of pixels). Results using the top transformants for each vector are shown in FIG. 3A for the *H. zea* and FIG. 3B for the *S. exigua*. Each transgenic plant has 6 leaf disks taken for analysis as shown.

[00106] Expression of then clone 44 polypeptide in the transgenic tobacco plants in the plastid (FIG. 4A) or in the cytoplasmic compartment (FIG. 4B) was assayed by western blot using a polyclonal antibody directed to clone 44 polypeptide. Lane numbers in FIG. 4 correspond to plant numbers in FIG. 3.

[00107] The polyclonal antibody used in the western blot was prepared by immunizing chickens with purified trypsin truncated clone 44 polypeptide and then purifying Cry2 specific antibodies using an affinity column made with trypsin truncated clone 44 polypeptide as the substrate.

[00108] The most obvious difference between the two types of transgenic plants is that inhibition of *S. exigua* is much greater for the plastid-accumulated toxin (comparing right and left panels of FIG. 3B). These data in conjunction with the expression data (FIG. 4) showing that plants harboring the T-DNA derived from 5469 (FIG. 4A) are capable of producing far more toxin than those of 5471 (FIG. 4B).

Table 1: Cry2Ax and Cry2Ax-derived sequences

Clone name	Type	SEQ ID NO
Cry2Ax	nucleic acid	1
Cry2Ax	polypeptide	2
38 (D_S00503480)	nucleic acid	3
38 (D_S00503480)	polypeptide	4
44 (D_S00503970)	nucleic acid	5
44 (D_S00503970)	polypeptide	6
473N	nucleic acid	7
473N	polypeptide	8
7K (D_S01000779)	nucleic acid	9
7K (D_S01000779)	polypeptide	10
15K (D_S00999080)	nucleic acid	11
15K (D_S00999080)	polypeptide	12
16K (D_S01000269)	nucleic acid	13
16K (D_S01000269)	polypeptide	14
16R (D_S01037143)	nucleic acid	15
16R (D_S01037143)	polypeptide	16
473R (D_S01037677)	nucleic acid	17
473R (D_S01037677)	polypeptide	18
D_S01466681	nucleic acid	19
D_S01466681	polypeptide	20
D_S01466770	nucleic acid	21
D_S01466770	polypeptide	22
D_S01467219	nucleic acid	23
D_S01467219	polypeptide	24
D_S01466712	nucleic acid	25
D_S01466712	polypeptide	26
D_S01467003	nucleic acid	27
D_S01467003	polypeptide	28
D_S01460229	nucleic acid	29
D_S01460229	polypeptide	30
D_S01459398	nucleic acid	31
D_S01459398	polypeptide	32
D_S01464856	nucleic acid	33
D_S01464856	polypeptide	34
D_S0146578G2	nucleic acid	35
D_S0146578G2	polypeptide	36
D_S01458733	nucleic acid	37
D_S01458733	polypeptide	38
D_S01457892	nucleic acid	39
D_S01457892	polypeptide	40
D_S01442158	nucleic acid	41
D_S01442158	polypeptide	42
D_S01443366	nucleic acid	43
D_S01443366	polypeptide	44
D_S01442132	nucleic acid	45
D_S01442132	polypeptide	46
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D_S01532041	nucleic acid	49
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D_S01611723	nucleic acid	51
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D_S01561330	polypeptide	58
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D_S01570568	polypeptide	64
D_S01572168	nucleic acid	65
D_S01572168	polypeptide	66
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D_S01572374	nucleic acid	71
D_S01572374	polypeptide	72
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D_S01561856	nucleic acid	77
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D_S01571529	nucleic acid	81
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D_S01599948	nucleic acid	83
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D_S01601459	nucleic acid	85
D_S01601459	polypeptide	86
D_S01602925	nucleic acid	87
D_S01602925	polypeptide	88
D_S01613034	nucleic acid	89
D_S01613034	polypeptide	90
D_S01614407	nucleic acid	91
D_S01614407	polypeptide	92
D_S01631557	nucleic acid	93
D_S01631557	polypeptide	94
D_S01633080	nucleic acid	95
D_S01633080	polypeptide	96
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D_S01632237	polypeptide	98
D_S01633031	nucleic acid	99
D_S01633031	polypeptide	100
D_S01632121	nucleic acid	101
D_S01632121	polypeptide	102

Clone name	Type	SEQ ID NO
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D_S01764502	nucleic acid	105
D_S01764502	polypeptide	106
D_S01764505	nucleic acid	107
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D_S01764533	nucleic acid	109
D_S01764533	polypeptide	110
D_S01764543	nucleic acid	111
D_S01764543	polypeptide	112
D_S01764546	nucleic acid	113
D_S01764546	polypeptide	114
D_S01764554	nucleic acid	115
D_S01764554	polypeptide	116
D_S01764568	nucleic acid	117
D_S01764568	polypeptide	118
D_S01764569	nucleic acid	119
D_S01764569	polypeptide	120
D_S01764577	nucleic acid	121
D_S01764577	polypeptide	122
D_S01764642	nucleic acid	123
D_S01764642	polypeptide	124
D_S01764643	nucleic acid	125
D_S01764643	polypeptide	126
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D_S01764680	polypeptide	128
D_S01764685	nucleic acid	129
D_S01764685	polypeptide	130
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D_S01764701	nucleic acid	133
D_S01764701	polypeptide	134
D_S01764706	nucleic acid	135
D_S01764706	polypeptide	136
D_S01764723	nucleic acid	137
D_S01764723	polypeptide	138
D_S02847715	nucleic acid	139
D_S02847715	polypeptide	140
D_S01765051	nucleic acid	141
D_S01765051	polypeptide	142
D_S01765068	nucleic acid	143
D_S01765068	polypeptide	144
D_S01765100	nucleic acid	145
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D_S01765063	nucleic acid	147
D_S01765063	polypeptide	148
D_S01765119	nucleic acid	149
D_S01765119	polypeptide	150
D_S01765104	nucleic acid	151
D_S01765104	polypeptide	152

Clone name	Type	SEQ ID NO
D_S01765112	nucleic acid	153
D_S01765112	polypeptide	154
D_S01765174	nucleic acid	155
D_S01765174	polypeptide	156
D_S01765242	nucleic acid	157
D_S01765242	polypeptide	158
D_S01765308	nucleic acid	159
D_S01765308	polypeptide	160
D_S01765221	nucleic acid	161
D_S01765221	polypeptide	162
D_S01765254	nucleic acid	163
D_S01765254	polypeptide	164
D_S01765231	nucleic acid	165
D_S01765231	polypeptide	166
D_S01765255	nucleic acid	167
D_S01765255	polypeptide	168
D_S01765377	nucleic acid	169
D_S01765377	polypeptide	170
D_S01765430	nucleic acid	171
D_S01765430	polypeptide	172
D_S01765446	nucleic acid	173
D_S01765446	polypeptide	174
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D_S01764642	polypeptide	178
D_S01766041	nucleic acid	179
D_S01766041	polypeptide	180
D_S01764706	nucleic acid	181
D_S01764706	polypeptide	182
D_S01766073	nucleic acid	183
D_S01766073	polypeptide	184
D_S01764643	nucleic acid	185
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D_S01764758	polypeptide	198
D_S01764768	nucleic acid	199
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D_S01764860	nucleic acid	201
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Clone name	Type	SEQ ID NO
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D_S01765018	polypeptide	204
D_S01764947	nucleic acid	205
D_S01764947	polypeptide	206
D_S01764934	nucleic acid	207
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D_S01765693	nucleic acid	223
D_S01765693	polypeptide	224
D_S01765687	nucleic acid	225
D_S01765687	polypeptide	226
D_S01765765	nucleic acid	227
D_S01765765	polypeptide	228
D_S01765932	nucleic acid	229
D_S01765932	polypeptide	230
D_S01766010	nucleic acid	231
D_S01766010	polypeptide	232

Clone name	Type	SEQ ID NO
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D_S01766026	polypeptide	234
D_S02838294	nucleic acid	235
D_S02838294	polypeptide	236
D_S02838310	nucleic acid	237
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D_S02838327	nucleic acid	239
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D_S02838328	nucleic acid	241
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D_S02838330	nucleic acid	243
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D_S02838454	polypeptide	246
D_S02838470	nucleic acid	247
D_S02838470	polypeptide	248
D_S02838478	nucleic acid	249
D_S02838478	polypeptide	250
D_S02838434	nucleic acid	251
D_S02838434	polypeptide	252
D_S02838549	nucleic acid	253
D_S02838549	polypeptide	254
D_S02838632	nucleic acid	255
D_S02838632	polypeptide	256
D_S02838640	nucleic acid	257
D_S02838640	polypeptide	258
D_S02838648	nucleic acid	259
D_S02838648	polypeptide	260
Cry2Ab	polypeptide	261

Table 2: Codon Table

Amino acids			Codon					
Alanine	Ala	A	GCA	GCC	GCG	GCU		
Cysteine	Cys	C	UGC	UGU				
Aspartic acid	Asp	D	GAC	GAU				
Glutamic acid	Glu	E	GAA	GAG				
Phenylalanine	Phe	F	UUC	UUU				
Glycine	Gly	G	GGA	GGC	GGG	GGU		
Histidine	His	H	CAC	CAU				
Isoleucine	Ile	I	AUA	AUC	AUU			
Lysine	Lys	K	AAA	AAG				
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU
Methionine	Met	M	AUG					
Asparagine	Asn	N	AAC	AAU				
Proline	Pro	P	CCA	CCC	CCG	CCU		
Glutamine	Gln	Q	CAA	CAG				
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU
Threonine	Thr	T	ACA	ACC	ACG	ACU		
Valine	Val	V	GUA	GUC	GUG	GUU		
Tryptophan	Trp	W	UGG					
Tyrosine	Tyr	Y	UAC	UAU				

Table 3: Sequence of clones of interest isolated from DNA shuffling

	Parents		1st Rd		2nd Rd					
Amino acid position	2Ab	2Ax	38	44	7K	15K	16K	16R	473R	Amino Acid Sequence
3	N	H	H	H	H	H	H	H	H	
4	S	N	N	N	N	N	N	N	N	
20	A	V	A	A	A	A	A	A	A	
25	V	I	V	V	V	V	V	V	V	
37	K	E	E	E	E	E	E	E	E	
40	T	M	M	M	M	M	M	M	M	
42	W	W	W	W	W	W	R	W	W	
45	N	D	D	D	D	D	D	D	D	
51	L	V	V	V	V	L	L	V	V	
89	N	N	S	N	S	S	S	S	S	
163	P	T	T	P	P	P	P	P	P	
210	R	Q	R	Q	R	R	Q	R	R	
211	D	N	N	N	N	N	N	N	N	
212	Y	H	H	H	H	H	H	H	H	
214	K	R	R	R	R	R	R	R	R	
230	S	T	S	T	S	S	S	S	T	
233	K	R	R	R	R	R	R	R	R	
243	M	M	M	M	V	M	M	M	M	
318	S	T	S	S	S	S	S	S	S	
319	N	Q	Q	Q	Q	Q	Q	Q	Q	
330	S	T	T	T	T	T	T	T	T	
347	I	V	V	V	V	V	V	V	V	

	Parents		1st Rd		2nd Rd					
Amino acid position	2Ab	2Ax	38	44	7K	15K	16K	16R	473R	Amino Acid Sequence
355	S	-	S	S	S	S	S	S	S	
395	P	V	P	P	P	P	P	P	P	
398	N	N	T	N	T	T	T	N	N	
402	N	S	S	S	S	S	S	S	S	
406	E	G	G	G	G	G	G	G	G	
408	V	I	V	V	V	V	V	V	V	
409	A	N	A	N	A	N	N	A	N	
447	E	Q	Q	Q	Q	Q	Q	Q	Q	
452	A	E	E	A	E	A	A	A	E	
461	A	L	A	L	A	L	L	A	A	
477	H	Y	Y	Y	Y	Y	Y	Y	Y	
484	S	T	T	S	T	S	T	T	T	
490	N	E	E	E	E	E	E	E	E	
529	N	S	S	S	S	S	S	S	S	
570	T	S	S	T	T	S	S	S	T	
600	S	D	D	S	S	S	S	S	D	
602	S	T	S	S	S	S	S	S	S	
603	D	N	N	D	D	D	D	D	N	
619	D	E	E	D	D	E	E	D	D	
625	L	F	F	F	F	F	F	F	F	
630	I	L	L	L	L	L	L	L	L	
631	S	F	S	F	P	S	S	F	F	

Table 4: Sequence comparison of wild type Cry2 polypeptides with clone 473N

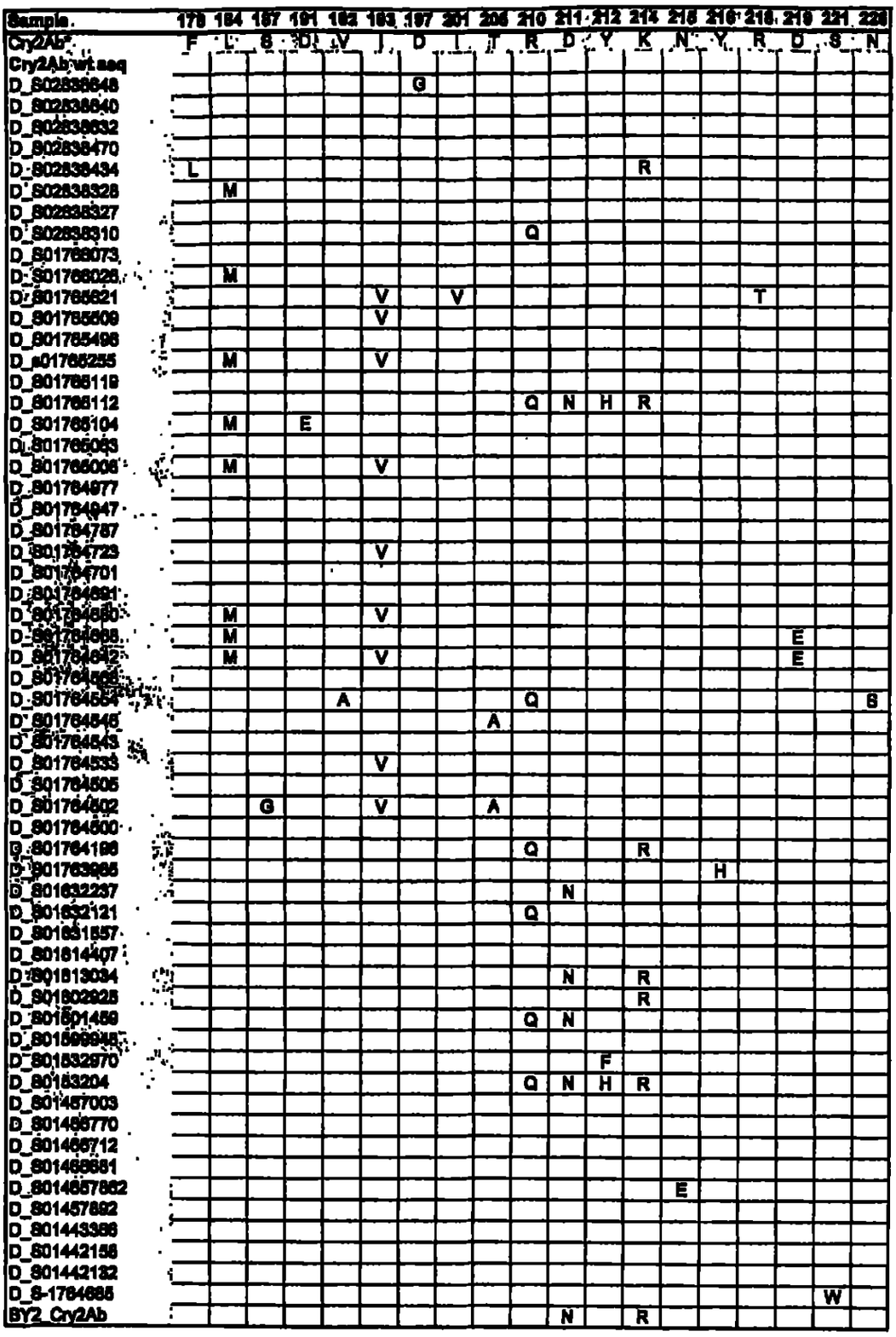
	Parents									Modified Clone	Amino Acid Sequence
Amino acid position	Cry2Aa	Cry2Ab	Cry2Ac	Cry2Ad	Cry2Ae	Cry2Af	Cry2Ag	Cry2Ax	473R	473N	
8	S	S	N	S	N	S	S	S	S	N	
9	S	G	G	G	G	G	E	G	G	E	
11	S	T	N	N	T	T	T	T	T	N	
13	S	I	T	I	I	I	K	I	I	V	
15	S	D	H	D	D	D	G	D	D	E	
17	S	Y	H	Y	Y	Y	Y	Y	Y	H	
21	S	A	A	V	A	A	A	A	A	V	
22	S	H	H	H	H	H	H	H	H	R	
28	S	Q	E	Q	E	Q	E	Q	Q	E	
36	S	Q	E	D	E	Q	Q	Q	Q	E	
37	S	K	K	N	K	E	K	E	E	K	
40	S	T	K	M	M	M	M	M	M	T	
44	S	K	R	K	R	K	R	K	K	R	
45	S	N	T	D	T	D	T	D	D	N	
46	S	N	D	N	D	N	D	N	N	D	

using Cry2Ab as probe

Sample	1	3	4	7	8	10	11	12	13	14	20	25	26	27	28	29	31	34	36	37	42	46	48	49
Cry2Ab*	M	N	S	N	G	R	T	T	I	C	A	F	S	F	Q	H	S	T	Q	R	W	N	S	L
Cry2Ab wt seq																				K				
D_802838648				D													P			R	R			
D_802838640																				R				
D_802838632																			R	R				P
D_802838470																				R				
D_802838434																				R				
D_802838328																				R				
D_802838327																				R				
D_802838310																				R				
D_801766073																				R				
D_801766026																				R		D		
D_801765821																				R				
D_801765509																				R				
D_801765496															R					R				
D_801765255															R					R				
D_801765119																				R				
D_801765112									T	R										R				
D_801765104						H														R				
D_801765069																				R				
D_801765008																				R				
D_801764977																				R				
D_801764947													L							R				
D_801764767																				R				
D_801764723													L							R				
D_801764701																				R				
D_801764691																				R				
D_801764680												S						S		R				
D_801764668																				R				
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D_801764554																				R				
D_801764548																				R				
D_801764543																				R				
D_801764533																				R				
D_801764505		H	N								V									R				
D_801764502								A												R				
D_801764500																				R				
D_801764196					S															R				
D_801763985																				R				
D_801632237																				R				
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D_801631657																				R				
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D_801466661		H																						
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D_801442158																				R			L	
D_801442132																				R				
D_8-1764666																				R				
BY2_Cry2Ab																				R				

Sample	51	54	56	64	70	76	78	80	88	93	96	97	100	101	107	111	116	119	122	123	124	126
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D_802836632																						
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D_802836434								S														
D_802836328																						
D_802836327								S					E									
D_802836310																						
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BY2_Cry2Ab								S										E				

Sample	126	130	135	137	138	140	141	142	144	155	164	160	162	164	166	167	168	169	172
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BY2_Cry2Ab																			



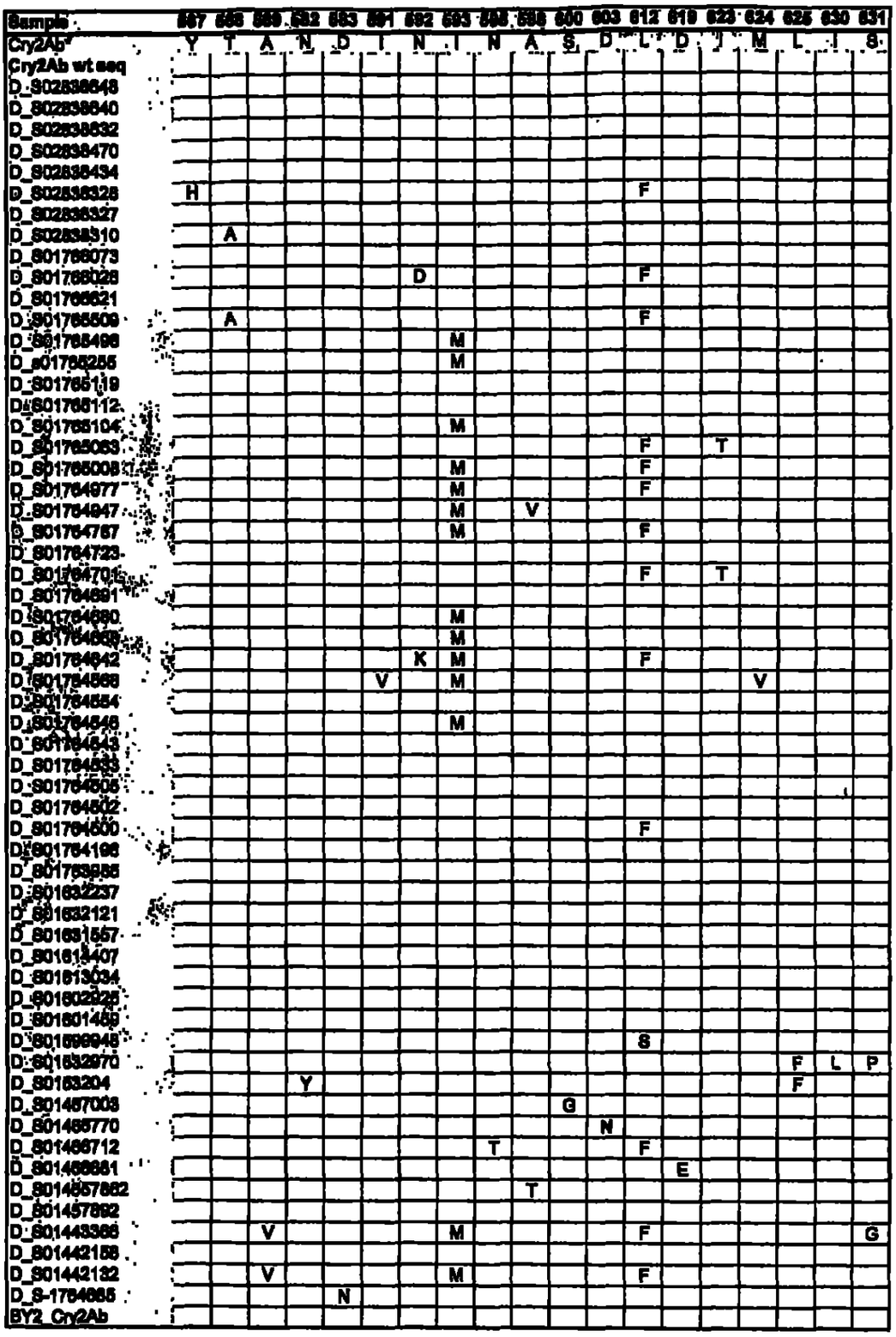
Sample	178	184	187	191	192	193	197	201	206	210	211	212	214	215	216	218	219	221	226
Cry2Ab	F	L	S	D	V	I	D	I	T	R	D	Y	K	N	Y	R	D	S	N
Cry2Ab wt seq																			
D_802838648							G												
D_802838640																			
D_802838632																			
D_802838470																			
D_802838434	L												R						
D_802838328		M																	
D_802838327																			
D_802838310										Q									
D_801766073																			
D_801766026		M																	
D_801765621						V		V								T			
D_801765509						V													
D_801765496																			
D_801765235		M				V													
D_801765119																			
D_801765112										Q	N	H	R						
D_801765104		M		E															
D_801765093																			
D_801765006		M				V													
D_801764977																			
D_801764947																			
D_801764787																			
D_801764723						V													
D_801764701																			
D_801764691																			
D_801764680		M				V													
D_801764668		M															E		
D_801764642		M				V											E		
D_801764568																			
D_801764564					A					Q									S
D_801764546									A										
D_801764543																			
D_801764533						V													
D_801764505																			
D_801764502			G			V			A										
D_801764500																			
D_801764196										Q			R						
D_801763965															H				
D_801632237											N								
D_801632121										Q									
D_801631557																			
D_801614407																			
D_801613094											N		R						
D_801602925													R						
D_801601469										Q	N								
D_801599948																			
D_801532970												F							
D_80153204										Q	N	H	R						
D_801467003																			
D_801466770																			
D_801466712																			
D_801466681																			
D_801457862														E					
D_801457692																			
D_801443386																			
D_801442156																			
D_801442132																			
D_8-1764665																		W	
BY2_Cry2Ab											N		R						

Sample	229	230	233	234	237	238	240	241	242	244	273	276	279	283	284	285	286	288	291
Cry2Ab*	Q	S	K	G	T	R	H	D	T	E	G	A	S	P	Q	Q	T	S	S
Cry2Ab wt seq									M										
D_802838648									T										
D_802838640		T							T										G
D_802838632									T										
D_802838470									T										
D_802838494									T										
D_802838326									T										
D_802838327									T										
D_802838310		T							T										
D_801766073																	A		
D_801766026									T										
D_801765821									T										
D_801765509									T										
D_801765498									T									L	
D_801765255									T										
D_801765119									T										
D_801765112		T	R																
D_801765104									T										
D_801765093								G	T										
D_801765006									T										
D_801764977									T	K									
D_801764947									T										
D_801764787					A				T										
D_801764723									T		S								
D_801764701								G	T										
D_801764691									T										
D_801764660							R		T										
D_801764658									T										
D_801764642									T										
D_801764598									T										
D_801764564									T										
D_801764548									T										
D_801764543		T							T				C						
D_801764533									T										
D_801764505									T										
D_801764502								G	T										
D_801764500				A					T			T					A		
D_801764198						G			T										
D_801763665		T							T					V	T	N			
D_801632237		T							T										
D_801632121		T							T										
D_801631557	R								T										
D_801614407		T							T										
D_801616034		T							T					V	T	N			
D_801602025		T							T										
D_801601489		T							T								R		
D_801599048		T							T										
D_801532970																			
D_80153204		T	R						T										
D_801467003									T										
D_801466770									T										
D_801466712									T				R						
D_801466661									T										
D_801457662									T										
D_801457692									T										
D_801443366									T										
D_801442158									T										
D_801442132									T										
D_S-1764685																R			
BY2_Cry2Ab		T							T										

Sample	295	302	306	307	310	311	317	318	321	323	328	330	331	344	347	358	362	367	383
Cry2Ab*	Y	Q	S	Y	N	Q	L	N	F	N	V	S	T	S	I	N	N	L	S
Cry2Ab wt seq																			
D_802838648																			
D_802838640																			
D_802838632																			
D_802838470	H																		
D_802838434																			
D_802838328											G								
D_802838327																			
D_802838310																			
D_801766073																		T	
D_801766026																			
D_801765621											G								
D_801765609											G								
D_801765496																			
D_801765255											G				V				
D_801765119																			
D_801765112								Q	L										
D_801765104											G								
D_801765063											G								
D_801765008											G								
D_801764977																			
D_801764947																			
D_801764787											G								
D_801764723							S												
D_801764701											G								
D_801764691																			
D_801764690				H							G								
D_801764668											G			P					
D_801764642						S													
D_801764588																			
D_801764554													A						
D_801764546																			
D_801764543																			
D_801764539											G								
D_801764506		Q									G								
D_801764502					S														
D_801764500																			
D_801764198																			
D_801763986																			
D_801632237					S														
D_801632121					H														
D_801631557																			
D_801614407										S									
D_801613034																			
D_801602925																			
D_801601459												N							
D_801599948																			
D_801532970												T			V		S		
D_80153204								Q				T							
D_801467003																			
D_801466770																			
D_801466712																			
D_801466681																			
D_8014667892					D														
D_801457892																			
D_801443366																			
D_801442168																			
D_801442132																			
D_8-1764666		R														S		T	R
BY2_Cry2Ab																			

Sample	386	389	391	399	401	403	405	407	408	413	420	436	438	444	445	447	448	459	461
Cry2Ab*	E	A	V	F	T	L	L	S	Q	R	P	R	N	H	Y	E	I	G	A
Cry2Ab wt seq																			
D_802838648																			
D_802838640																			
D_802838632																			
D_802838470																			
D_802838434																			
D_802838328																			
D_802838327																			
D_802838310																			
D_801766073																			
D_801766029																			
D_801765621																			
D_801765609																			
D_801765498																			
D_s01765255																			
D_801765119																			
D_801765112	G	N																	L
D_801765104					S	I	I		R										
D_801765093																			
D_801765008					S	I	I	C											
D_801764917																			
D_801764857																			
D_801764787																			
D_801764723												K							
D_801764701																			
D_801764691																			
D_801764690																			
D_801764668					S	I	I												
D_801764642																			
D_801764568																			
D_801764554																			
D_801764548																	T		
D_801764543																		S	
D_801764533																			
D_801764505														Y	F				
D_801764502																			
D_801764500																			
D_801764196																			
D_801763986																			
D_801632237																			
D_801632131																			
D_801631557																			
D_801614407																			
D_801613034																			
D_801602925																			
D_801601489																			
D_801599948										K									
D_801532070			L													Q			L
D_80153204	G	N																	
D_801467003											S		D						
D_801466770													D						
D_801466712																			
D_801466681																			
D_801457662				L															
D_801457692																			
D_801443366																			
D_801442158																			
D_801442132																			
D_S-1764685																			
BY2_Cry2Ab																			

Sample	478	480	481	482	487	488	500	508	513	517	526	530	537	538	543	548	553	560	566
Cry2Ab*	H	N	D	Y	I	S	I	Q	I	F	N	N	L	R	S	N	I	V	V
Cry2Ab wt seq																			
D_S02838648														K					
D_S02838640									V										
D_S02838632																			
D_S02838470																			
D_S02838434																			
D_S02838328																			
D_S02838327																			
D_S02838310						G													
D_S01766073																			
D_S01766026																			
D_S01765821							V												
D_S01765509																			
D_S01765496																			
D_S01765255																			
D_S01765119																			
D_S01765112	Y	E									S								
D_S01765104			G					-											
D_S01765063																			
D_S01765008														G					
D_S01764977															P				
D_S01764947																			
D_S01764787																		A	
D_S01764723																			
D_S01764701																			
D_S01764691																			
D_S01764660																			
D_S01764658																			
D_S01764642														W					
D_S01764588																			
D_S01764554																			
D_S01764548																			
D_S01764547																			
D_S01764533																			
D_S01764505																			
D_S01764502																			
D_S01764500																	T		
D_S01764196																			A
D_S01763965																			
D_S01632237																			
D_S01632121																			
D_S01631557																			
D_S01614407								R											
D_S01613034																			
D_S01602926																			
D_S01601459																			
D_S01599948																D			
D_S01592970		E																	
D_S0163204															P	D		A	
D_S01467003													F				L		
D_S01466770										L	T		F				L		
D_S01466712											T						L		
D_S01466681																			
D_S01465662																	·		
D_S01457892		G											F						
D_S01443366				M							T						L		
D_S01442158											A		F						
D_S01442132											T								
D_S-1764665				H								Y							
BY2_Cry2Ab																			



Sample	587	588	589	592	593	601	602	603	604	606	608	609	612	619	623	624	625	630	631
Cry2Ab*	Y	T	A	N	D	I	N	I	N	A	S	D	L	D	T	M	L	I	S
Cry2Ab wt seq																			
D_902838648																			
D_902838640																			
D_902838632																			
D_902838470																			
D_902838434																			
D_902838328	H												F						
D_902838327																			
D_902838310		A																	
D_901766073																			
D_901766026							D						F						
D_901766021																			
D_901766009		A											F						
D_901766496								M											
D_s01766256								M											
D_901765119																			
D_901765112																			
D_901765104								M											
D_901765083													F		T				
D_901765081								M					F						
D_901764977								M					F						
D_901764947								M		V									
D_901764767								M					F						
D_901764723																			
D_901764701													F		T				
D_901764691																			
D_901764680								M											
D_901764668								M											
D_901764642							K	M					F						
D_901764568						V		M								V			
D_901764554																			
D_901764545								M											
D_901764543																			
D_901764533																			
D_901764505																			
D_901764502																			
D_901764500													F						
D_901764196																			
D_901763986																			
D_901632237																			
D_901632121																			
D_901631557																			
D_901613407																			
D_901613034																			
D_901602926																			
D_901601469																			
D_901599946													S						
D_901592970																	F	L	P
D_901583204				Y													F		
D_901467003											G								
D_901466770												N							
D_901466712									T				F						
D_901466681														E					
D_901457882										T									
D_901457862																			
D_901443366			V					M					F						G
D_901442158																			
D_901442132			V					M					F						
D_S-1764665					N														
BY2_Cry2Ab																			

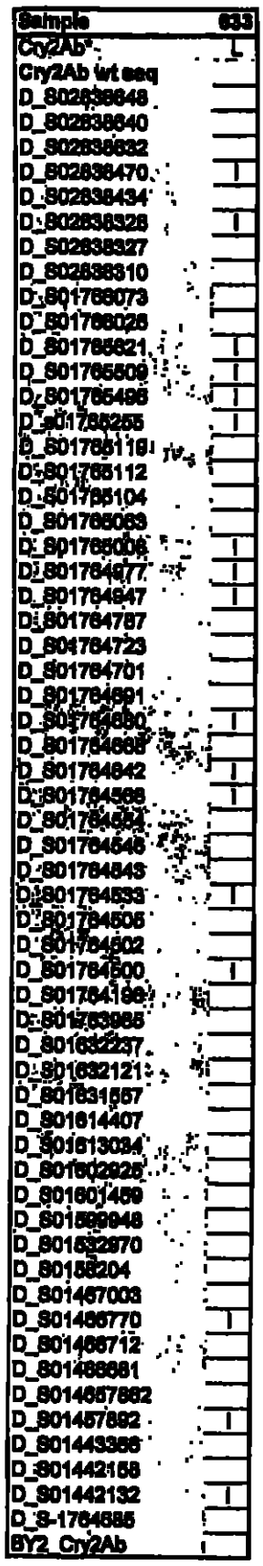

Sample 633
Cry2Ab*
Cry2Ab wt seq
D_S02838648
D_S02838640
D_S02838632
D_S02838470
D_S02838434
D_S02838328
D_S02838327
D_S02838310
D_S01766073
D_S01766026
D_S01765821
D_S01765509
D_S01765496
D_S01765255
D_S01765119
D_S01765112
D_S01765104
D_S01765063
D_S01765006
D_S01764977
D_S01764947
D_S01764787
D_S01764723
D_S01764701
D_S01764691
D_S01764680
D_S01764668
D_S01764642
D_S01764568
D_S01764554
D_S01764548
D_S01764543
D_S01764533
D_S01764505
D_S01764502
D_S01764500
D_S01764196
D_S01763985
D_S01632237
D_S01632121
D_S01631557
D_S01614407
D_S01613034
D_S01602926
D_S01601459
D_S01599948
D_S01592970
D_S01588204
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D_S01466681
D_S01465862
D_S01457892
D_S01443366
D_S01442158
D_S01442132
D_S-1764686
BY2_Cry2Ab

Table 6: Amino acid sequence changes of clones of interest isolated from DNA shuffling using clone 44 as parent



Table 7: Amino acid sequence changes of clones of interest isolated from DNA shuffling using clone 473R as parent

Sample	4	12	17	29	31	32	34	38	51	93	96	108	124	137	139	140	141	142	143	144	147	163	167	168	169	170	177	189	195
D_S01037677 (parental clone 473)	N	T	Y	H	S	L	T	E	V	D	R	T	N	N	N	R	N	A	V	P	I	T	M	Q	G	Y	L	I	N
D_S01765231																													
D_S01764643						P																							
D_S01572374																													
D_S01571875																													S
D_S01766010															H	P	T	I	S	H							V		
D_S01572168					P										T	Q	T		T	R			L	H		R			
D_S01765242										G													L	N	N	R			
D_S01764953			H	R				G					S								V		L	R		H			
D_S01764728									I			A										M	L	R	D	P			
D_S01764758																							L	G	E				
D_S01571529		S					A																V	E	R				
D_S01571315											C												V	G		F			
D_S01570809														D															
D_S01570568																												V	
D_S01570511		A																											

Sample	223	228	250	266	296	306	315	323	324	350	355	356	357	358	362	372	378	384	390	425	434	446	447	451	455	474	479	482
D_S01037677 (parental clone 473)	Y	N	F	Q	F	N	A	N	I	G	S	P	F	N	S	T	W	D	T	R	V	N	Q	I	S	N	H	Y
D_S01765231								S																			R	
D_S01764643																												
D_S01572374		S								S																		
D_S01571875																				Q								H
D_S01766010	H		S			S											R								P			
D_S01572168																			A									
D_S01765242																		G										
D_S01764953																												
D_S01764728									V																	D		
D_S01764758					S		V				R	T	A	G	N	S					A							
D_S01571529						D								D														
D_S01571315																								T				
D_S01570809																						S						
D_S01570568				R																			H					
D_S01570511																												

Sample	504	505	527	553	555	556	570	599	611	616	623
D_S01037677 (parental clone 473)	Q	V	E	I	N	R	T	S	T	T	I
D_S01765231											
D_S01764643			G								
D_S01572374											
D_S01571875								R			
D_S01768010	R						A				
D_S01572168											
D_S01765242											
D_S01764953		A									
D_S01764728									A	V	
D_S01764758										I	
D_S01571529	R					Q					
D_S01571315											
D_S01570809											
D_S01570568				V							
D_S01570511					S						

WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule comprising any of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, or a compliment thereof.

2. An isolated nucleic acid molecule selected from the group consisting of:

a) a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the nucleotide sequence of any of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, or a complement thereof;

b) a nucleic acid molecule that encodes a polypeptide comprising the amino acid sequence of any of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260;

c) a nucleic acid molecule that hybridizes with a nucleic acid probe consisting of the nucleotide sequence of any of SEQ ID NOS: 1, 3, 5,

7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, or a complement thereof following at least one wash in 0.2X SSC at 55 °C for 20 minutes; and

d) a fragment comprising at least 600 consecutive nucleotides of any of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259.

3. The isolated nucleic acid molecule of claim 2, wherein the nucleic acid molecule encodes a polypeptide comprising at least one amino acid selected from the group consisting of H_2, S_7, Q_{27}, Q_{35}, E_{36}, K_{43}, D_{44}, N_{45}, D_{51}, A_{58}, V_{69}, R_{78}, N_{79}, K_{99}, T_{118}, V_{124}, E_{125}, R_{129}, N_{138}, R_{139}, A_{141}, T_{162}, Q_{165}, M_{166}, L_{183}, I_{192}, H_{211}, R_{213}, R_{217}, D_{218}, V_{324}, I_{386}, T_{399}, S_{405}, Q_{445}, I_{551}, S_{587}, I_{591}, L_{610}, and L_{631}.

4. The isolated nucleic acid molecule of claim 1 or 2, wherein the nucleic acid molecule encodes a polypeptide with insecticidal activity.

5. The isolated nucleic acid molecule of claim 4, wherein *Diptera* or *Lepidoptera* are susceptible to the insecticidal activity of the polypeptide.

6. A vector comprising a nucleic acid molecule of claim 1 or 2.

7. The vector of claim 6 that is an expression vector.

8. A host cell which comprises the vector of claim 6.

9. The host cell of claim 8, wherein the cell is selected from the group consisting of plant cell, bacterial cell, fungal cell.

10. An isolated polypeptide comprising any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260.

11. An isolated polypeptide selected from the group consisting of:

a) a polypeptide that is at least 95% identical to the amino acid sequence of any of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260;

b) a polypeptide that is encoded by a nucleic acid molecule comprising a nucleotide sequence that is at least 95% identical to any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193,

195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, or a complement thereof;

c) a polypeptide that is encoded by a nucleic acid molecule that hybridizes with a nucleic acid probe consisting of the nucleotide sequence of any of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, or a complement thereof following at least one wash in 0.2X SSC at 55 °C for 20 minutes;

d)' a fragment comprising at least 200 consecutive amino acids of any of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260.

12. The isolated polypeptide of claim 11, wherein the polypeptide comprises at least one amino acid selected from the group consisting of H_2, S_7, Q_{27}, Q_{35}, E_{36}, K_{43}, D_{44}, N_{45}, D_{51}, A_{58}, V_{69}, R_{78}, N_{79}, K_{99}, T_{118}, V_{124}, E_{125}, R_{129}, N_{138}, R_{139}, A_{141}, T_{162}, Q_{165}, M_{166}, L_{183}, I_{192}, H_{211}, R_{213}, R_{217}, D_{218}, V_{324}, I_{386}, T_{399}, S_{405}, Q_{445}, I_{551}, S_{587}, I_{591}, L_{610}, and L_{631}.

13. The isolated polypeptide of claim 10 or 11, wherein the polypeptide has an insecticidal activity.

14. The isolated polypeptide of claim 13, wherein *Diptera* or *Lepidoptera* are susceptible to the insecticidal activity of the polypeptide.

15. A transgenic plant comprising a transgene that expresses

(a) a polypeptide of any of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260; or

(b) a nucleic acid molecule of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259.

16. The transgenic plant of claim 15, wherein the plant is selected from the group consisting of maize, soybean, potato, and cotton.

17. The transgenic plant of claim 15, wherein the transgenic plant has increased resistance to an insect pest as compared to a plant that is not transgenic.

18. The transgenic plant of claim 17, wherein *Diptera* or *Lepidoptera* is the insect pest.

19. A transgenic plant comprising a transgene that expresses

(a) a polypeptide of claim 11, or

(b) a nucleic acid molecule of claim 2.

20. The transgenic plant of claim 19, wherein the plant is selected from the group consisting of maize, soybean, potato, and cotton.

21. The transgenic plant of claim 19, wherein the transgenic plant has increased resistance to an insect pest as compared to a plant that is not transgenic.

22. The transgenic plant of claim 21, wherein *Diptera* or *Lepidoptera* is the insect pest.

23. A composition comprising one or more polypeptides of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260 and an agent, wherein the agent is selected from the group consisting of spreader-sticker adjuvants, stabilizing agents, insecticidal agents, diluents, surfactants, emulsifiers, and dispersants.

24. The composition of claim 23, wherein the composition further comprises cells.

25. The composition of claim 24, wherein the cells are whole or lysed.

26. The composition of claim 25, wherein the cells are in suspension or are pelted.

27. The composition of claim 23, wherein the composition further comprises a spore-crystal complex of *Bacillus thuringiensis*.

28. The composition of claim 23, wherein the polypeptide is purified.

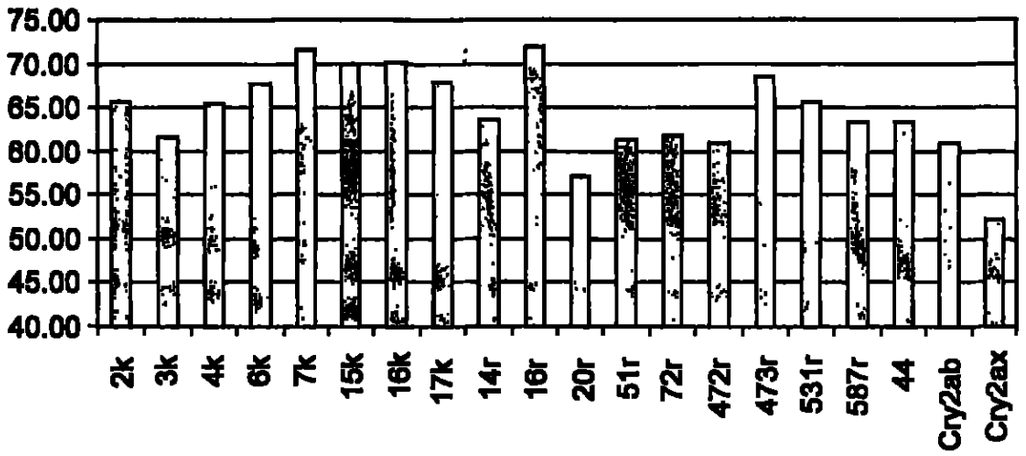

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587r
44
Cry2ab
Cry2ax

FIG. 1

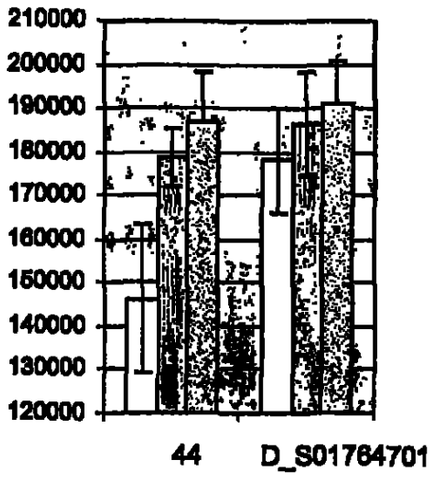

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FIG. 2

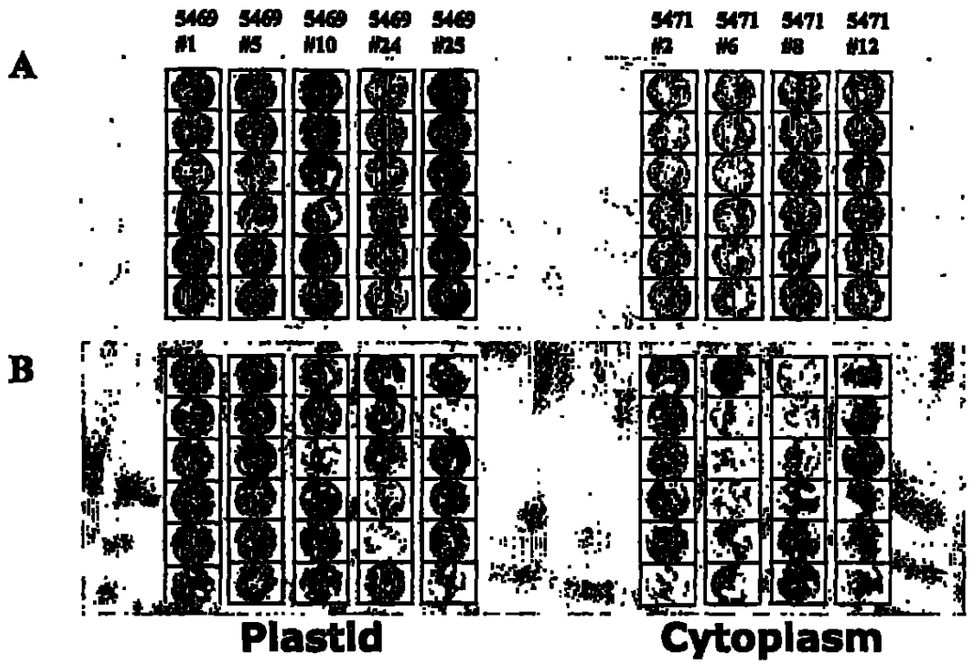

A
B
5469 #1
5469 #5
5469 #10
5469 #24
5469 #25
5471 #2
5471 #6
5471 #8
5471 #12
Plastid
Cytoplasm

FIG. 3

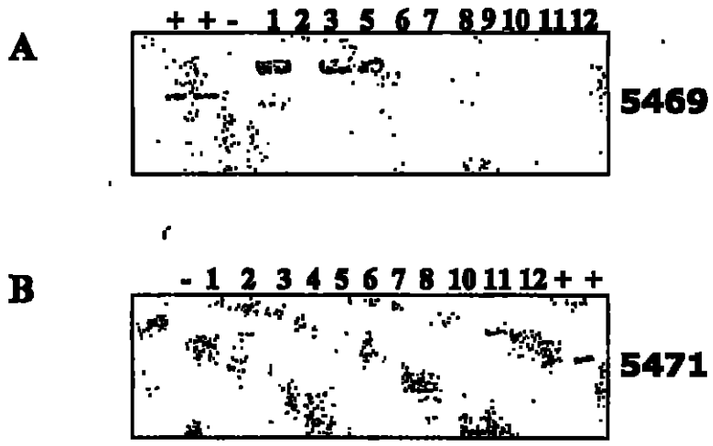


FIG. 4

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C12N 15/82 (2006.01) *C12P 21/02* (2006.01)

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(30) Priority Data:
60/547,664 25 February 2004 (25.02.2004) US

(71) Applicant *(for all designated States except US)*: PIONEER HI-BRED INTERNATIONAL, INC. [US/US]; 7100 NW 62nd Avenue, P.O. Box 1014, Johnston, IA 50131-1014 (US).

(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: HERMUDEZ, Ericka [ES/US]; 734 Clubhouse Drive, Aptos, CA 95003 (US). EMIG, Robin [US/US]; 1405 Marshall St. #715, Redwood City, CA 94063 (US). MCBRIDE, Kevin [US/US]; 1309 Marina Circle, Davis, CA 95616 (US). YAMAMOTO, Takashi [US/US]; 3780 Tivoli Garden Terrace, Fremont, CA 94538 (US).

(74) Agent: WENK, Melissa; Morgan & Finnegan LLP, 3 World Financial Center, New York, NY 10281-2101 (US).

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

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report*
— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments*
— *with sequence listing part of description published separately in electronic form and available upon request from the International Bureau*

(88) Date of publication of the international search report:
6 July 2006

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: NOVEL BACILLUS THURINGIENSIS CRYSTAL POLYPEPTIDES, POLYNUCLEOTIDES, AND COMPOSITIONS THEREOF

(57) Abstract: The present invention provides insecticidal polypeptides related to *Bacillus* Cry2 polypeptides. Nucleic acids encoding the polypeptides of the invention are also provided. Methods for using the polypeptides and nucleic acids of the invention to enhance resistance of plants to insect predation are encompassed.

WO 2005/082077 A3

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US05/06238

A. CLASSIFICATION OF SUBJECT MATTER
IPC: C12N 15/32(2006.01),15/63(2006.01),15/82(2006.01);A01H 5/00(2006.01);C07K 14/325(2006.01)
C12P 21/02(2006.01)

USPC: 536/23.71;530/350;800/302;424/93.2;435/320.1
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 536/23.71; 530/350; 800/302; 424/93.2; 435/320.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
sequence databases

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X — A	WO 00/26371 (MONSANTO CO.) 11 May 2000 (11.05.2000), SEQ ID NOs:2, 12, 18, claims 1, 14-15.	2-9, 11-14, 19-22 — 1, 10, 15-18, 23-28
X — A	WO 2002/57664A (BAYER CROPSCIENCE N.V.) 25 July 2002 (25.07.2002), see SEQ ID NO:3, claims 2, 4-5, 8, 10-22.	2-9, 11-14, 19-22 — 1, 10, 15-18, 23-28

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
05 April 2006 (05.04.2006)	09 MAY 2006
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US Commissioner for Patents P.O. Box 1450 Alexandria, Virginia 22313-1450 Facsimile No. (571) 273-3201	Authorized officer Anne R. Knight Telephone No. (571) 272-0547

Form PCT/ISA/210 (second sheet) (April 2005)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US05/06238

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of any additional fees.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.: drawn to SEQ ID NOs: 7, 8, 133 and 134

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest
- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US05/06238

BOX III. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions that are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

The inventions listed as Groups 1-260 do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: They fail to share a special technical feature.

The technical feature linking the groups is pesticidal proteins that differ from Cry2Ab by one or a few amino acids, and nucleic acids encoding them. This technicala feature is taught by Arnaut et al (US 20030167517 A1, 4 September 2003). Arnaut et al teach a nucleic acid that is 99.7% identical to SEQ ID NO:1 and the protein encoded by it, which is 99.4% identical to SEQ ID NO:2. Thus, claims 2 and 11, among others, are not novel, and the technical feature linking the claims is not special.

06-84256 78

NUEVOS POLIPÉPTIDOS CRISTALINOS Y POLINUCLEÓTIDOS DE *BACILLUS THURINGIENSIS* Y COMPOSICIONES CON LOS MISMOS

1. CAMPO DE LA INVENCIÓN

La presente invención se relaciona en general con el campo del control de plagas y provee polipéptidos insecticidas relacionados con polipéptidos Cry2 de *Bacillus*, y los polinucleótidos que los codifican. La presente invención también se relaciona con métodos y composiciones para alterar la resistencia de las plantas a la predación por insectos, incluyendo, sin limitaciones, la producción de plantas transgénicas.

2. ANTECEDENTES DE LA INVENCIÓN

Numerosas plantas de valor comercial, incluyendo cultivos agrícolas comunes, son susceptibles de ser atacadas por plagas de insectos y nematodes. Estas plagas pueden causar reducciones sustanciales en el rendimiento y la calidad de los cultivos. Tradicionalmente, los granjeros han empleado plaguicidas químicos para combatir el daño causado por las plagas. Sin embargo, el uso de plaguicidas químicos genera su propio conjunto de problemas, incluyendo el costo y la inconveniencia de aplicar los plaguicidas. Además, los residuos químicos provocan preocupaciones ambientales y de salud. Por estas y otras razones, existe una demanda de agentes insecticidas alternativos.

Un abordaje para el control de plagas beneficioso para el ambiente es el uso de las proteínas cristalinas plaguicidas derivadas de la bacteria habitante de la tierra *Bacillus thuringiensis* ("Bt"), conocidas comúnmente como "proteínas Cry". Muchas de estas proteínas son bastante tóxicas para insectos blanco específicos, pero son inofensivas para las plantas y otros organismos distintos del blanco. Se han expresado algunas proteínas Cry en forma recombinante en plantas de cultivo para proporcionar plantas transgénicas resistentes a plagas. Entre éstas, se ha cultivado ampliamente algodón y maíz transgénico-Bt.

Se ha aislado, caracterizado y clasificado una gran cantidad de proteínas Cry sobre la base de la homología de sus secuencias de aminoácidos (Crickmore et al., 1998, Microbiol. Mol. Biol. Rev., 62: 807-813). Este esquema de clasificación provee un mecanismo sistemático para nombrar y categorizar proteínas Cry recién descubiertas.

Generalmente se ha establecido que las proteínas Cry individuales poseen espectros de actividad relativamente estrechos, con la excepción de Cry2A. Cry2A es inusual, ya que constituye un subconjunto de proteínas Cry que poseen un rango efectivo más amplio, que incluye toxicidad a los órdenes de insectos Lepidoptera y Diptera. Se ha descubierto que la proteína Cry2A es una toxina que presenta actividad doble contra *Trichoplusia ni* (rizador del repollo) y *Aedes taeniorhynchus* (mosquito) (Yamamoto y McLaughlin,1982, Biochem. Biophys. Res. Comm. 130: 414-421). La molécula de ácido nucleico que codifica la proteína Cry2A (denominada Cry2Aa) fue clonada y expresada en *B. Megaterium*, y se estableció que era activa contra insectos lepidópteros y dípteros (Donovan et al. 1988, J. Bacteriol. 170: 4732-4738). Se clonó una secuencia codificante adicional homóloga a Cry2Aa (denominada Cry2Ab), y se descubrió que era activa solamente contra larvas de lepidópteros (Widner y Whiteley, 1989, J Bacteriol 171:2).

Los cultivos transgénicos de segunda generación podrían ser más resistentes a los insectos si fueran capaces de expresar múltiples y/o nuevos genes Bt. Por consiguiente, se desean nuevas proteínas insecticidas con espectros de actividad más amplios.

3. RESUMEN DE LA INVENCIÓN

La presente invención se relaciona con un nuevo polipéptido Cry2, Cry2Ax (SEQ ID Nº 2), aislado de *Bacillus thuringiensis*. La presente invención también comprende los polipéptidos derivados de Cry2Ax (SEQ ID Nº 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260). Además de la secuencia del polipéptido Cry2Ax y los polipéptidos derivados de Cry2Ax, se apreciará que los polipéptidos de la invención también abarcan variantes de polipéptidos, incluyendo, sin limitaciones, cualquier fragmento, análogo, homólogo, alelo

de ocurrencia natural o mutante de éstos. Los polipéptidos de la invención también comprenden aquellos polipéptidos que son codificados por cualquier ácido nucleico Cry2Ax o derivado de Cry2Ax de la invención. En una realización, los polipéptidos tienen al menos una actividad funcional de Cry2Ax (por ejemplo, actividad insecticida) y al menos 85%, 90%, 95%, 97%, 98% o 99% idénticos a la secuencia del polipéptido de cualquiera de SEQ ID Nº 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, o variantes de éstos. En otra realización, se incluyen los polipéptidos que tienen al menos una actividad funcional de Cry2Ax (por ejemplo, actividad insecticida), que tienen al menos 25, 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600 ó 625 aminoácidos contiguos de largo, y que están codificados por un polinucleótido que hibridiza bajo condiciones severas con el ácido nucleico que codifica cualquiera de SEQ ID Nº 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, o una variante de éstas. También se proporcionan métodos para producir los polipéptidos de la invención, por ejemplo, por medios recombinantes. También se incluyen las composiciones que comprenden uno o más polipéptidos de la invención.

La presente invención también se relaciona con las moléculas de ácidos nucleicos de Cry2Ax (SEQ ID Nº 1) y las moléculas de ácidos nucleicos derivadas de Cry2Ax (SEQ

ID Nº 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259). La presente invención también comprende los fragmentos y los análogos que codifican polipéptidos que presentan una actividad funcional al menos parcial, es decir, que son capaces de presentar una o más actividades funcionales asociadas con un polipéptido Cry2Ax tipo salvaje. En una realización, la invención comprende una molécula de ácido nucleico aislada que comprende una secuencia de nucleótidos i) que es al menos 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% o 99% idéntica a la secuencia de nucleótidos de cualquiera de SEQ ID Nº 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259; ii) que hibridiza con una sonda de ácido nucleico que consiste en la secuencia de nucleótidos de cualquiera de SEQ ID Nº 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, o un complemento de ésta, bajo condiciones severas; y/o iii) que comprende una molécula de ácido nucleico que codifica un polipéptido que comprende la secuencia

de aminoácidos de cualquiera de SEQ ID Nº 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260. También se incluyen los vectores que comprenden los ácidos nucleicos de la invención. También se incluyen las células o las plantas que comprenden los vectores de la invención.

La presente invención también se relaciona con plantas transgénicas que expresan un ácido nucleico y/o un polipéptido de la invención. Las plantas transgénicas pueden expresar el transgen de cualquier forma conocida en la técnica, incluyendo, sin limitaciones, la expresión constitutiva, la expresión regulada por el desarrollo, la expresión específica por tejido, etcétera. También están comprendidas las semillas obtenidas de una planta transgénica de la invención.

4. BREVE DESCRIPCIÓN DE LAS FIGURAS

La FIG. 1 muestra la actividad insecticida de los clones de ADN del segundo experimento de barajado. Cada clon se expresó en hojas de *N. benthamiana* usando infiltración forzada. Se alimentó cada disco de hoja a una única larva de *H. zea* de 3er estadío. Después de un período de incubación de 24 horas, se determinó la actividad de alimentación por observación visual, y se la expresó como una fracción aproximada del área foliar remanente. El eje y es el porcentaje de disco foliar remanente después de exponerlo al insecto. El eje x es el clon expresado en el disco de hoja. Varios clones presentaron una actividad insecticida incrementada, tales como (D_S01000779) (SEQ ID Nº 10), 15K (D_S00999080) (SEQ ID Nº 12), 16K (D_S01000269) (SEQ ID Nº 14), 16R (D_S01037143) (SEQ ID Nº 16) y 473R (D_S01037677) (SEQ ID Nº 18)

FIG. 2 muestra la actividad insecticida del clon resultante del primer barajado 44 (D_S00503970) y el clon resultante del tercer barajado D_S01764701. Cada clon se

expresó en hojas de *N. benthamiana* usando infiltración forzada. Se alimentó cada disco de hoja a una única larva de *H. zea* de 3er estadío. Después de un período de incubación de 24 horas, se determinó la actividad de alimentación por captura en video del disco de hoja. El eje y es la cantidad de píxeles presentes en la imagen capturada del disco de hoja. El eje x es el clon expresado en el disco de hoja. Se presentan los resultados del promedio de tres experimentos. Para cada experimento, se evaluaron al menos ocho discos de hojas para cada clon.

Las FIGS. 3A-3B muestran los resultados de eficacia para tres plantas de tabaco transgénicas que expresan el clon resultante del primer barajado 44 en el compartimiento del plástido (paneles de la izquierda) o en el citoplasma (paneles de la derecha). Se determinó la eficacia de inhibición de (A) *H. zea* o (B) *S. exigua* después de incubar las hojas con larvas por 24 horas. Se observó la cantidad de hoja remanente con equipo de captura de video para realizar el cálculo real del área foliar relativa remanente (cantidad de píxeles). Se tomaron seis discos de hojas para analizar en cada planta transgénica. Como se prepararon veinticinco plantas transgénicas usando cada construcción transgénica, las cantidades distinguen distintas plantas que usan una construcción particular.

Las FIGS. 4A-4B muestran los niveles de expresión de transgenes en las plantas transgénicas que expresan el clon resultante del primer barajado 44. Este polipéptido derivado de Cry2 se expresó en los compartimientos celulares (A) plastídico y (B) citoplasmático, vía transformación con pMAXY5469 o pMAXY5471, respectivamente. Se realizó un análisis de Western blot en extractos de plantas transgénicas usando un anticuerpo policlonal dirigido contra la región de la toxina del polipéptido del clon resultante del primer barajado 44. Los controles negativos fueron extractos tomados de planta sin transformar. Los controles positivos fueron 20 ng o 40 ng de toxina Cry2Ax purificada. El peso molecular del control positivo Cry2Ax difiere de aquél del polipéptido derivado de Cry2Ax en los extractos de plantas debido a que el primero está activado por tripsina y el segundo es la pro-toxina.

5. DESCRIPCIÓN DETALLADA

La presente invención provee polipéptidos insecticidas relacionados con polipéptidos Cry2 de *Bacillus*. También se proporcionan moléculas de ácidos nucleicos que codifican los polipéptidos de la invención. También se abarcan los métodos para usar los polipéptidos y los ácidos nucleicos de la invención para mejorar la resistencia de las plantas a la predación por insectos.

5.1 Polipéptidos de la Invención

La presente invención se relaciona con un nuevo polipéptido Cry2, Cry2Ax (SEQ ID N° 2), aislado de *Bacillus thuringiensis*. La presente invención también comprende los polipéptidos derivados de Cry2Ax (SEQ ID N° 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260). Los polipéptidos de la invención también abarcan aquellos polipéptidos codificados por cualquier ácido nucleico Cry2Ax o derivado de Cry2Ax de la invención (véase la sección 5.2).

Además de las secuencias de los polipéptidos Cry2Ax y derivados de Cry2Ax, se apreciará que los polipéptidos de la invención también comprenden variantes de éstos, incluyendo, sin limitaciones, cualquier secuencia sustancialmente similar, cualquier fragmento, análogo, homólogo, alelo de ocurrencia natural o mutante de éstos. Las variantes comprendidas por la invención son polipéptidos que presentan una actividad funcional al menos parcial, es decir, son capaces de presentar una o más actividades funcionales conocidas asociadas con un polipéptido Cry2Ax tipo salvaje. Estas actividades funcionales incluyen, sin limitaciones, actividades biológicas, tales como actividad insecticida; antigenicidad, es decir, la capacidad de unirse o competir con la unión de Cry2Ax a un anticuerpo anti-Cry2Ax; inmunogenicidad, es decir, la capacidad de generar un anticuerpo que se una a un polipéptido Cry2Ax. En algunas realizaciones, las

variantes tienen al menos una actividad funcional que es sustancialmente similar a aquella del polipéptido original (por ejemplo, una variante de Cry2Ax tendrá al menos una actividad funcional que es sustancialmente similar a aquella de Cry2Ax). Como se lo usa en la presente documentación, se considerará la actividad funcional de la variante como "sustancialmente similar" a aquella del polipéptido progenitor si está dentro de una desviación estándar de la original.

En una realización, los polipéptidos que tienen al menos una actividad funcional de Cry2Ax (por ejemplo, actividad insecticida) y son al menos 85%, 90%, 95%, 97%, 98% o 99% idénticos a la secuencia del polipéptido de cualquiera de SEQ ID Nº 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260 están abarcados por la invención. Estos polipéptidos de la invención contienen al menos 1, al menos 5, al menos 10, al menos 20, al menos 30 o todos los 40 residuos de aminoácidos del grupo que consiste en H_2, S_7, Q_{27}, Q_{35}, E_{36}, K_{43}, D_{44}, N_{48}, D_{61}, A_{68}, V_{69}, R_{78}, N_{79}, K_{99}, T_{119}, V_{124}, E_{125}, R_{129}, N_{138}, R_{139}, A_{141}, T_{162}, Q_{165}, M_{166}, L_{183}, I_{192}, H_{211}, R_{213}, R_{217}, D_{218}, V_{324}, I_{388}, T_{399}, S_{405}, Q_{445}, I_{551}, S_{587}, I_{591}, L_{610} y L_{631}. El subíndice indica la posición del residuo de aminoácido correspondiente en la posición en SEQ ID Nº 2, al completarse el alineamiento óptimo de la secuencia del polipéptido con SEQ ID Nº 2. Respecto de una secuencia de aminoácidos que se alinea en forma óptima con una secuencia de referencia, un aminoácido "corresponde" a la posición en la secuencia de referencia con la cual está apareado el residuo en el alineamiento.

Como se lo usa en la presente documentación, cuando se define una secuencia como "al menos X% idéntica" a una secuencia de referencia, por ejemplo, "un polipéptido al menos 95% idéntico a SEQ ID Nº 2", debe interpretarse que "X% idéntico" hace referencia al porcentaje de identidad absoluta, a menos que se indique lo contrario. El

término "porcentaje de identidad absoluta" hace referencia a un porcentaje de identidad de secuencia, que se determina asignando a los aminoácidos y los ácidos nucleicos idénticos un valor de uno, y cero para cualquier sustitución, sin importar la similitud de los aminoácidos o los ácidos nucleicos no coincidentes. En un alineamiento de secuencia típico, el "porcentaje de identidad absoluta" de dos secuencias se presenta como un porcentaje de "identidades" de aminoácidos o ácidos nucleicos. En los casos en que el alineamiento óptimo de dos secuencias requiere la inserción de una extensión vacía en una o ambas secuencias, un residuo de aminoácido en una secuencia alineado con parte de la sección vacía en la otra secuencia se cuenta como una falta de coincidencia, para los propósitos de la determinación del porcentaje de identidad. Las extensiones vacías pueden ser internas o externas, es decir, un corte. Puede determinarse fácilmente el porcentaje de identidad absoluta usando, por ejemplo, el programa Clustal W, versión 1.8, Junio 1999, con los parámetros por omisión (Thompson et al., 1994, Nucleic Acids Research 22: 4673-4680).

En otra realización, la invención abarca los fragmentos de polipéptidos Cry2Ax y derivados de Cry2Ax. Se abarcan polipéptidos que tienen al menos una actividad funcional de Cry2Ax (por ejemplo, actividad insecticida), que tienen al menos 25, 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600 ó 625 aminoácidos contiguos de largo de cualquiera de SEQ ID Nº 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, y que están codificados por un polinucleótido que hibridiza bajo condiciones severas con el ácido nucleico que codifica cualquiera de SEQ ID Nº 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96,

98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260. En las realizaciones donde el fragmento de la invención comprende cualquiera de los residuos de aminoácidos que corresponden a los residuos de aminoácidos 2, 7, 27, 35, 36, 43, 44, 45, 51, 58, 69, 78, 79, 99, 118, 124, 125, 129, 138, 139, 141, 161, 165, 166, 183, 192, 211, 213, 217, 218, 324, 386, 399, 405, 445, 551, 587, 591, 610, 631 de SEQ ID Nº 2, estos polipéptidos de la invención contienen al menos 1, al menos 5, al menos 10, al menos 20, al menos 30 o todos los 40 residuos de aminoácidos del grupo que consiste en H_2, S_7, Q_{27}, Q_{35}, E_{36}, K_{43}, D_{44}, N_{45}, D_{51}, A_{58}, V_{69}, R_{78}, N_{79}, K_{99}, T_{118}, V_{124}, E_{125}, R_{129}, N_{138}, R_{139}, A_{141}, T_{162}, Q_{165}, M_{166}, L_{183}, I_{192}, H_{211}, R_{213}, R_{217}, D_{218}, V_{324}, I_{386}, T_{399}, S_{405}, Q_{445}, I_{551}, S_{587}, I_{591}, L_{610} y L_{631}.

En una realización específica, un fragmento de la invención corresponde a la longitud de la pro-toxina procesada. Existe una diferencia de 5-6 kDa en el peso molecular entre la pro-toxina Cry2 completa y la toxina Cry2 procesada. Esto es el resultado del corte de aproximadamente 40 aminoácidos del polipéptido de la pro-toxina de Cry2 (Rukmini et al., 2000, Biochimie 82:109-116; Aronson et al., 1993, Mol. Microbiol. 7:489-496; Morse et al., 2001, Structure, 9:409-17). Los polipéptidos que corresponden a este fragmento Cry2 procesado pueden obtenerse en forma directa en los métodos de la presente invención, para evitar la necesidad de procesamiento de la pro-toxina.

En otra realización específica, un fragmento de la invención corresponde a un dominio Cry2. Los polipéptidos Cry2 tienen tres dominios, incluyendo i) el dominio I, que participa en la inserción en la membrana apical del mesenterón del insecto y afecta la función de los canales de iones, ii) el dominio II, que participa en la unión con el receptor en la membrana de las células epiteliales del mesenterón del insecto, y iii) el dominio III, que participa en la función de los canales de iones, la unión de los receptores y la inserción en la membrana (Dean et al., 1996, Gene 179:111-117; Schnepf et al., 1998, Microbiol. Molec. Biol. Rev. 62:775-806).

En otra realización, la invención comprende polipéptidos análogos. Los polipéptidos análogos pueden poseer residuos que hayan sido modificados, es decir, por la unión covalente de cualquier tipo de molécula a los polipéptidos Cry2Ax o derivados de Cry2Ax. Por ejemplo, pero sin limitaciones, puede modificarse un polipéptido análogo de la invención, por ejemplo, por glicosilación, acetilación, pegilación, fosforilación, amidación, derivatización por grupos protectores/bloqueadores conocidos, corte proteolítico, unión con un ligando u otra proteína celular, etcétera. Puede modificarse un polipéptido análogo de la invención a través de modificaciones químicas, usando procedimientos conocidos por aquellos entrenados en la técnica, incluyendo, sin limitaciones, corte químico específico, acetilación, formilación, síntesis metabólica de tunicamicina, etcétera. Además, un análogo de un polipéptido de la invención puede contener uno o más aminoácidos no clásicos.

También se proporcionan métodos para producir los polipéptidos de la invención, por ejemplo, por medios recombinantes (véase la sección 5.6).

También se comprenden composiciones que comprenden uno o más polipéptidos de la invención. Además, las composiciones de la invención pueden comprender agentes adicionales, incluyendo, sin limitaciones, coadyuvantes dispersantes-adhesivos, agentes estabilizadores, otros aditivos insecticidas, diluyentes, agentes que optimizan las propiedades reológicas o la estabilidad de la composición, tales como, por ejemplo, agentes tensioactivos, emulsificantes, dispersantes y/o polímeros.

5.2 <u>Ácidos nucleicos de la invención</u>

La presente invención también se relaciona con las moléculas de ácidos nucleicos de Cry2Ax (SEQ ID Nº 1) y las moléculas de ácidos nucleicos derivadas de Cry2Ax (SEQ ID Nº 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241,

243, 245, 247, 249, 251, 253, 255, 257, 259). Las moléculas de ácidos nucleicos de la invención también comprenden aquellas moléculas de ácidos nucleicos que codifican cualquier polipéptido Cry2Ax o derivado de Cry2Ax de la invención (véase la sección 5.1).

Además de las moléculas de ácidos nucleicos de Cry2Ax y las moléculas de ácidos nucleicos derivadas de Cry2Ax, se apreciará que los ácidos nucleicos de la invención también abarcan variantes de ácidos nucleicos, incluyendo, sin limitaciones, cualquier secuencia sustancialmente similar, cualquier fragmento, homólogo, alelo de ocurrencia natural, o mutante de éstos. Las variantes de las moléculas de ácidos nucleicos comprendidas por la presente invención codifican polipéptidos que presentan una actividad funcional al menos parcial, es decir, que son capaces de presentar una o más actividades funcionales conocidas asociadas con un polipéptido Cry2Ax tipo salvaje. Estas actividades funcionales incluyen, sin limitaciones, actividades biológicas, tales como actividad insecticida; antigenicidad, es decir, la capacidad de unirse o competir con la unión de Cry2Ax a un anticuerpo anti-Cry2Ax; inmunogenicidad, es decir, la capacidad de generar un anticuerpo que se una a un polipéptido Cry2Ax. En algunas realizaciones, las variantes tienen al menos una actividad funcional que es sustancialmente similar a aquella de la molécula de ácido nucleico original (por ejemplo, una variante de una molécula de ácido nucleico de Cry2Ax codificará un polipéptido que tendrá al menos una actividad funcional que es sustancialmente similar a aquella del polipéptido codificado por la molécula de ácido nucleico de Cry2Ax). Como se lo usa en la presente documentación, se considerará la actividad funcional de la variante como "sustancialmente similar" a aquella del polipéptido progenitor si está dentro de una desviación estándar de la original.

En una realización, las moléculas de ácidos nucleicos que son al menos 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% o 99% idénticas a cualquiera de las moléculas de ácidos nucleicos de SEQ ID Nº 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193,

195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259 están abarcadas por la invención. Estas moléculas de ácidos nucleicos de la invención codifican polipéptidos que contienen al menos uno, al menos 5, al menos 10, al menos 20, al menos 30 o todos los 40 residuos de aminoácidos del grupo que consiste en H_2, S_7, Q_{27}, Q_{35}, E_{36}, K_{43}, D_{44}, N_{45}, D_{51}, A_{58}, V_{69}, R_{78}, N_{79}, K_{90}, T_{118}, V_{124}, E_{125}, R_{129}, N_{138}, R_{139}, A_{141}, T_{162}, Q_{165}, M_{166}, L_{183}, I_{192}, H_{211}, R_{213}, R_{217}, D_{218}, V_{324}, I_{366}, T_{369}, S_{405}, Q_{445}, I_{531}, S_{587}, I_{591}, L_{610} y L_{631}.

Para determinar el porcentaje de identidad de dos moléculas de ácidos nucleicos, se alinean las secuencias con el propósito de realizar una comparación óptima (por ejemplo, pueden introducirse extensiones vacías en la secuencia de una primera molécula de ácido nucleico, de modo de alinearla en forma óptima con una segunda molécula de ácido nucleico). Luego se comparan los nucleótidos en las posiciones correspondientes. Cuando una posición en la primera secuencia está ocupada por el mismo nucleótido en la posición correspondiente en la segunda secuencia, luego las moléculas son idénticas en esta posición. El porcentaje de identidad entre las dos secuencias es una función de la cantidad de posiciones idénticas compartidas por las secuencias (es decir, % de identidad = cantidad de posiciones idénticas superpuestas/cantidad total de posiciones x 100%). En una realización, las dos secuencias tienen la misma longitud.

La determinación del porcentaje de identidad entre dos secuencias también puede realizarse usando un algoritmo matemático. Un ejemplo no limitante de un algoritmo matemático utilizado para comparar las dos secuencias es el algoritmo de Karlin y Altschul (Karlin y Altschul, 1990, *Proc. Natl. Acad. Sci.* 87:2264-2268, modificado como se indica en Karlin y Altschul, 1993, *Proc. Natl. Acad. Sci.* 90:5873-5877). Este algoritmo está incorporado en los programas NBLAST y XBLAST (Altschul et al., 1990, *J. Mol. Biol.* 215:403 y Altschul et al., 1997, *Nucleic Acid Res.* 25:3389-3402). El software para realizar análisis BLAST está disponible para el público, por ejemplo, en el Centro Nacional de Información Biotecnológica. Este algoritmo comprende primero la identificación de los pares de secuencia con mayor puntuación (HSP), mediante la identificación de palabras cortas con longitud W en la secuencia de búsqueda, que coinciden o satisfacen un valor

umbral positivo T cuando se alinean con una palabra de la misma longitud en la secuencia de la base de datos. T se conoce como el valor umbral de vecindad de palabra (Altschul et al., *supra*). Estos aciertos iniciales de vecindad de palabras actúan como semillas para iniciar búsquedas para hallar HSP que las contienen. Luego se extienden los aciertos de palabras en ambas direcciones dentro de cada secuencia en la medida en que pueda extenderse el valor de alineamiento acumulativo. Los valores acumulativos se calculan usando, para secuencias de nucleótidos, los parámetros M (valor de recompensa para un par de residuos coincidentes; siempre > 0) y N (valor de penalidad para residuos no coincidentes; siempre < 0). Para las secuencias de aminoácidos, se usa una matriz de puntuación para calcular el valor acumulativo. Se detiene la extensión de los aciertos de palabras cuando el valor de alineamiento acumulativo cae debajo en una cantidad X respecto del valor máximo alcanzado; cuando el valor acumulativo disminuye hasta cero o menos, debido a la acumulación de uno o más alineamientos de residuos de valor negativo; o cuando se alcanza el final de cualquiera de las secuencias. Los parámetros del algoritmo BLAST W, T y X determinan la sensibilidad y la velocidad del alineamiento. El programa BLASTN (para secuencias de nucleótidos) usa como parámetros por omisión una longitud de palabra (W) de 11, una expectativa (E) de 10, un corte de 100, M = 5, N = -4 para la comparación de ambas cadenas. Para las secuencias de aminoácidos, el programa BLASTP usa como parámetros por omisión una longitud de palabra (W) de 3, una expectativa (E) de 10 y la matriz de puntuación BLOSUM62 (véase Henikoff & Henikoff, 1989, PNAS, 89:10915).

También puede usarse el método de alineamiento Clustal V para determinar el porcentaje de identidad (Higgins y Sharp,1989, CABIOS. 5:151-153), hallado en el programa Megalign del conjunto bioinformático de computación LASERGENE (DNASTAR Inc., Madison, WI). Los "parámetros por omisión" son los parámetros prefijados por el fabricante del programa y, para alineamientos múltiples, corresponden una penalidad de falta de coincidencia = 10 y penalidad de longitud de falta de coincidencia = 10, al tiempo que, para los alineamientos por pares, son ktuple 1, penalidad de falta de coincidencia = 3, ventana = 5 y diagonales guardadas = 5. Después de alinear las secuencias usando el

programa Clustal V, es posible obtener un "porcentaje de identidad" observando la tabla de "distancias de secuencia" en el mismo programa.

Puede determinarse el porcentaje de identidad entre dos secuencias usando procedimientos similares a aquellos descriptos previamente, permitiendo o no la existencia de faltas de coincidencia. Para calcular el porcentaje de identidad, típicamente se cuentan sólo las coincidencias exactas.

En otra realización, los fragmentos de Cry2Ax y las moléculas de ácidos nucleicos derivadas de Cry2Ax están abarcadas por la invención. Se incluyen moléculas de ácidos nucleicos que tienen al menos una actividad funcional de Cry2Ax (por ejemplo, actividad insecticida), que comprenden al menos 100, 250, 500, 750, 1000, 1500 ó 1800 nucleótidos contiguos de largo de cualquiera de SEQ ID Nº 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, y/o hibridizan bajo condiciones severas con las moléculas de ácidos nucleicos que codifican cualquiera de SEQ ID Nº 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260. En realizaciones donde el fragmento de ácido nucleico de la invención codifica un polipéptido que comprende cualquiera de los residuos de aminoácidos que corresponden a los residuos de aminoácidos 2, 7, 27, 35, 36, 43, 44, 45, 51, 58, 69, 78, 79, 99, 118, 124, 125, 129, 138, 139, 141, 161, 165, 166, 183, 192, 211, 213, 217, 218, 324, 386, 399, 405, 445,

551, 587, 591, 610, 631 de SEQ ID Nº 2, estas moléculas de ácidos nucleicos de la invención contienen secuencias codificantes de al menos 1, al menos 5, al menos 10, al menos 20, al menos 30 o todos los 40 residuos de aminoácidos del grupo que consiste en H_2, S_7, Q_{27}, Q_{35}, E_{36}, K_{43}, D_{44}, N_{46}, D_{61}, A_{68}, V_{69}, R_{76}, N_{78}, K_{99}, T_{118}, V_{124}, E_{125}, R_{129}, N_{136}, R_{139}, A_{141}, T_{162}, Q_{165}, M_{166}, L_{183}, I_{192}, H_{211}, R_{213}, R_{217}, D_{218}, V_{324}, I_{386}, T_{399}, S_{405}, Q_{445}, I_{551}, S_{587}, I_{591}, L_{610} y L_{631}.

En una realización específica, un fragmento de la invención corresponde a la longitud del ácido nucleico que codifica la pro-toxina procesada. Existe una diferencia de 5-6 kDa en el peso molecular entre la pro-toxina Cry2 completa y la toxina Cry2 procesada. Esto es el resultado del corte de aproximadamente 40 aminoácidos en el extremo C-terminal del polipéptido de la pro-toxina de Cry2 (Rukmini et al., 2000, Biochimie 82:109-116; Aronson et al., 1993, Mol. Microbiol. 7:489-496; Morse et al., 2001, Structure, 9:409-17).

En otra realización específica, un fragmento de la invención codifica un polipéptido que corresponde a un dominio Cry2.

En otra realización, una molécula de ácido nucleico que hibridiza bajo condiciones severas con cualquiera de SEQ ID Nº 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259 está abarcada por la invención. Estas moléculas de ácidos nucleicos de la invención codifican polipéptidos que codifican al menos 1, al menos 5, al menos 10, al menos 20, al menos 30 o todos los 40 residuos de aminoácidos del grupo que consiste en H_2, S_7, Q_{27}, Q_{35}, E_{36}, K_{43}, D_{44}, N_{46}, D_{61}, A_{68}, V_{69}, R_{76}, N_{78}, K_{99}, T_{118}, V_{124}, E_{125}, R_{129}, N_{136}, R_{139}, A_{141}, T_{162}, Q_{165}, M_{166}, L_{183}, I_{192}, H_{211}, R_{213}, R_{217}, D_{218}, V_{324}, I_{386}, T_{399}, S_{405}, Q_{445}, I_{551}, S_{587}, I_{591}, L_{610} y L_{631}.

La frase "condiciones severas" hace referencia a las condiciones de hibridización bajo las cuales un ácido nucleico hibridiza con el ácido nucleico blanco, típicamente en una mezcla compleja de ácidos nucleicos, pero esencialmente sin otros ácidos nucleicos. Las condiciones severas dependen de la secuencia y serán diferentes bajo distintas circunstancias. Los ácidos nucleicos más largos hibridizan específicamente a mayores temperaturas. Pueden hallarse guías extensas sobre la hibridización de ácidos nucleicos en la literatura técnica (por ejemplo, Tijssen, *Techniques in Biochemistry and Molecular Biology – Hybridization with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993)). En general, las condiciones muy severas se seleccionan con temperaturas aproximadamente 5-10°C menores que el punto de fusión térmica (T_m) del ácido nucleico específico a un pH de fuerza iónica definida. Las condiciones de baja severidad generalmente se seleccionan con temperaturas aproximadamente 15-30°C menores que el T_m. El T_m es la temperatura (bajo una fuerza iónica, un pH y una concentración de ácidos nucleicos definida) a la cual 50% de las sondas complementarias con el blanco hibridizan con el ácido nucleico blanco en equilibrio (cuando los ácidos nucleicos están presentes en exceso en el T_m, 50% de la sondas están ocupadas en equilibrio). Las condiciones de hibridización típicamente son aquellas donde la concentración de sal es menor que iones sodio aproximadamente 1,0 M, típicamente una concentración de iones sodio (u otras sales) de entre aproximadamente 0,01 y 1,0 M, a un pH de entre 7,0 y 8,3, y a una temperatura de al menos aproximadamente 30°C para las sondas cortas (por ejemplo, de entre 10 y 50 nucleótidos) y al menos aproximadamente 60°C para las sondas largas (por ejemplo, de más de 50 nucleótidos). También pueden obtenerse condiciones severas con la adición de agentes desestabilizadores, tales como formamida. Para realizar una hibridización selectiva o específica, una señal positiva es al menos el doble de la hibridización de fondo, y preferiblemente 10 veces la hibridización de fondo. En una realización, las condiciones severas incluyen al menos un lavado (usualmente 2) en SSC 0,2X a una temperatura de al menos aproximadamente 50°C, usualmente aproximadamente 55°C, o algunas veces 60°C o 65°C, por 20 minutos, o condiciones sustancialmente equivalentes.

En una realización específica, la molécula de ácido nucleico de la invención hibridiza específicamente después de al menos un lavado en SSC 0,2X a 55°C por 20 minutos, con un polinucleótido que codifica el polipéptido de cualquiera de SEQ ID Nº 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260. En otra realización, las condiciones severas incluyen una hibridización en cloruro de sodio/citrato 6X (SSC) a aproximadamente 45°C, seguida por uno o más lavados en SSC 0,2X, 0,1% de SDS a 50-65°C.

La frase "hibridiza específicamente" hace referencia a la unión, la duplicación o la hibridización de una molécula solamente con una secuencia de nucleótidos particular, bajo condiciones de hibridización severas, cuando dicha secuencia está presente en una mezcla compleja (por ejemplo, una biblioteca de ADN o ARN celular total).

También se incluyen los vectores que comprenden los ácidos nucleicos de la invención. También se incluyen las células o las plantas que comprenden los vectores de la invención.

El término "ácido nucleico" o "molécula de ácido nucleico", como se lo usa en la presente documentación, hace referencia a un polímero de bases de desoxirribonucleótidos o ribonucleótidos de cadena simple o doble, que se lee desde el extremo 5' hacia el extremo 3'. Incluye ADN cromosómico, plásmidos de replicación autónoma y ADN o ARN que tiene una función estructural primaria. El término "codificante" hace referencia a una secuencia de polinucleótidos que codifica uno o más aminoácidos. El término no requiere un codón de inicio o terminación. Una secuencia de aminoácidos puede estar codificada en cualquiera de los seis marcos abiertos de lectura diferentes proporcionados por una secuencia de polinucleótidos y su complemento.

La Tabla 1 describe secuencias Cry2Ax y derivadas de Cry2Ax, y el número de identidad de secuencia correspondiente.

6.3 Secuencias derivadas de Cry2Ax

Los polipéptidos y los ácidos nucleicos derivados de Cry2Ax de la invención pueden crearse introduciendo una o más sustituciones, adiciones y/o deleciones de nucleótidos en la secuencia de nucleótidos de Cry2Ax, o en ácidos nucleicos relacionados, de modo o tal que se introduzcan sustituciones, adiciones y/o deleciones de aminoácidos en la proteína codificada. Generalmente, se crean derivados de las secuencias Cry2Ax para acentuar una característica deseable o reducir una característica indeseable de un polipéptido Cry2Ax. En una realización, los polipéptidos derivados de Cry2Ax tienen una mayor actividad insecticida respecto de los polipéptidos Cry2Ax, incluyendo, sin limitaciones, mayor potencia y/o mayor rango de insectos plaga. En otra realización, los polipéptidos derivados de Cry2Ax se expresan mejor que los polipéptidos Cry2Ax, incluyendo, sin limitaciones, mayor vida media, menor susceptibilidad a la degradación y/o transcripción o traducción más eficiente.

En una realización, se usa una molécula de ácido nucleico de polipéptidos como molde para crear nucleótidos derivados de Cry2Ax. En otra realización, se usa un ácido nucleico relacionado con Cry2Ax como molde para crear nucleótidos derivados de Cry2Ax. En una realización específica, se usa Cry2Ab* como molde. Cry2Ab* tiene dos cambios de aminoácidos respecto de Cry2Ab tipo salvaje (K por R en la posición 36 y M por T en la posición 241 del Nº de acceso GenBank M23724). En otra realización específica, pueden usarse los clones aislados de un experimento de alteración como moldes para realizar otros experimentos de alteración (por ejemplo, los clones 38, 44, y 473R; véanse las secciones 6.2 y 6.4).

Pueden introducirse alteraciones de secuencia empleando procedimientos comunes, tales como procedimientos de evolución molecular dirigida, por ejemplo, métodos de barajado de ADN (véanse, por ejemplo, Christians et al., 1999, Nature Biotechnology 17:259-264; Crameri et al., 1998, Nature, 391:288-291; Crameri, et al., 1997, Nature Biotechnology 15:436-438; Crameri et al., 1996, Nature Biotechnology

14:315-319; Stemmer, 1994, Nature 370:389-391; Stemmer et al., 1994, *Proc. Natl. Acad. Sci.*, 91:10747-10751; Patentes de los EEUU Nº 5605793; 6117679; 6132970; 5939250; 5965408; 6171820; Publicaciones Internacionales Nº WO 95/22625; WO 97/0078; WO 97/35966; WO 98/27230; WO 00/42651; y WO 01/75767); mutagénesis dirigidas a sitios específicos (véanse, por ejemplo, Kunkel, 1985, *Proc. Natl. Acad. Sci.*, 82:488-492; Oliphant et al., 1986, Gene 44:177-183); mutagenesis dirigida a oligonucleótidos (véase, por ejemplo, Reidhaar-Olson et al., 1988, Science 241:53-57); mutagénesis química (véase, por ejemplo, Eckert et al., 1987, Mutat. Res. 178:1-10); PCR con susceptibilidad a errores (véase, por ejemplo, Caldwell & Joyce, 1992, PCR Methods Applic. 2:28-33); y mutagénesis de cassettes (véase, por ejemplo, Arkin et al., *Proc. Natl. Acad. Sci.*, 1992, 89:7871-7815); (véanse en general, por ejemplo, Arnold, 1993, Curr. Opinion Biotechnol. 4:450-455; Ling et al., 1997, Anal. Biochem., 254:157-78; Dale et al., 1996, Methods Mol. Biol. 57:369-74; Smith, 1985, Ann. Rev. Genet. 19:423-462; Botstein et al., 1985, Science, 229:1193-1201; Carter, 1986, Biochem. J. 237:1-7; Kramer et al., 1984, Cell 38:879-887; Wells et al., 1985, Gene 34:315-323; Minshull et al., 1999, Current Opinion in Chemical Biology 3:284-290).

En una realización, se usa barajado0 de ADN para crear nucleótidos derivados de Cry2Ax. El barajado de ADN puede realizarse *in vitro*, *in vivo*, *in silico* o en una combinación de estos ambientes. Pueden ponerse en práctica métodos de recombinación in silico donde se usen algoritmos genéticos para recombinar extensiones de secuencia que correspondan a ácidos nucleicos homólogos (o aún no homólogos). Las extensiones de secuencias recombinadas resultantes se convierten opcionalmente en ácidos nucleicos sintetizando ácidos nucleicos que corresponden a las secuencias recombinadas, por ejemplo, en combinación con procedimientos de síntesis de oligonucleótidos por re-ensamblaje. Este abordaje permite generar alteraciones al azar, parcialmente al azar o determinadas. En la técnica se describen muchos detalles respecto de la recombinación in silico, incluyendo el uso de algoritmos genéticos, operadores genéticos y semejantes en sistemas informáticos, combinados con la generación de los ácidos nucleicos correspondientes, así como combinaciones de ácidos nucleicos designados (por ejemplo,

basadas en la selección de sitios de cruzamiento), y métodos de recombinación determinada, pseudo-azarosa o al azar (véanse, por ejemplo, las Publicaciones Internacionales de Patente Nº WO 00/42560 y WO 00/42559).

En otra realización, se usa mutagénesis dirigida para crear nucleótidos derivados de Cry2Ax, seleccionando secuencias de nucleótidos o posiciones particulares del ácido nucleico Cry2Ax o relacionado con Cry2Ax que se desea alterar. Estas mutaciones dirigidas pueden introducirse en cualquier posición del ácido nucleico. Por ejemplo, pueden realizarse sustituciones de nucleótidos que conducen a sustituciones de aminoácidos en residuos de aminoácidos "no esenciales" o "esenciales". Un residuo de aminoácido "no esencial" es un residuo que puede alterarse en la secuencia tipo salvaje sin alterar la actividad biológica, al tiempo que un residuo de aminoácido "esencial" es necesario para al menos una actividad biológica del polipéptido. Por ejemplo, los residuos de aminoácidos que no están conservados o que solamente están semi-conservados entre homólogos de varias especies pueden no ser esenciales para la actividad. Como alternativa, los residuos de aminoácidos que están conservados entre los homólogos de varias especies pueden ser esenciales para la actividad.

Estas mutaciones dirigidas pueden ser conservativas o no conservativas. Una "sustitución de aminoácidos no conservativa" es una donde se reemplaza el residuo de aminoácido por un residuo de aminoácido que tiene una cadena lateral disímil. Las familias de residuos de aminoácidos con cadenas laterales similares han sido definidas en la técnica. Estas familias incluyen aminoácidos con cadenas laterales básicas (por ejemplo, lisina, arginina, histidina), cadenas laterales ácidas (por ejemplo, ácido aspártico, ácido glutámico, asparragina, glutamina), cadenas laterales polares sin carga (por ejemplo, glicina, serina, treonina, tirosina, cisteina), cadenas laterales no polares (por ejemplo, alanina, valina, leucina, isoleucina, prolina, fenilalanina, metionina, triptofano), cadenas laterales con ramificaciones β (por ejemplo, treonina, valina, isoleucina) y cadenas laterales aromáticas (por ejemplo, tirosina, fenilalanina, triptofano, histidina).

Como alternativa o además de las sustituciones de residuos de aminoácidos no conservativas, estas mutaciones dirigidas pueden ser conservativas. Una "sustitución de

aminoácidos conservativa" es una donde se reemplaza el residuo de aminoácido por un residuo de aminoácido que tiene una cadena lateral similar. Después de la mutagénesis, puede expresarse la proteína codificada en forma recombinante y puede determinarse la actividad de la proteína.

En otra realización, se usa mutagénesis al azar para crear nucleótidos derivados de Cry2Ax. Pueden introducirse mutaciones al azar en toda o parte de la secuencia codificante (por ejemplo, por mutagénesis de saturación). En determinadas realizaciones, pueden usarse secuencias de nucleótidos que codifican otros polipéptidos relacionados con *dominios, motivos estructurales o sitios activos similares*, o que se alinean con una porción de las secuencias de Cry2Ax de la invención con faltas de coincidencia o coincidencias imperfectas, en el proceso de mutagénesis, para generar una diversidad de secuencias.

Deberá comprenderse que, para cada paso de mutagénesis en *algunos* de los procedimientos mencionados previamente, puede ser necesario realizar una cantidad de ciclos de iteración de algunos o todos los pasos, con el fin de optimizar la diversidad de las secuencias. Los métodos descriptos previamente pueden usarse en combinación y en cualquier orden deseado. En muchos casos, los métodos resultan en una reserva de secuencias de ácidos nucleicos alteradas o una reserva de células huésped recombinantes que comprenden secuencias de ácidos nucleicos alteradas. Las secuencias de ácidos nucleicos alteradas, o las células huésped que expresan una secuencia de ácido nucleico alterada con las características deseadas, pueden identificarse realizando búsquedas con uno o más ensayos conocidos en la técnica. Los ensayos pueden efectuarse bajo condiciones que permitan seleccionar polipéptidos con características físicas o químicas deseadas. Pueden determinarse las alteraciones en la secuencia de ácido nucleico secuenciando la molécula de ácido nucleico que codifica el polipéptido alterado en los clones.

Adicionalmente, las moléculas de ácidos nucleicos de Cry2Ax y derivadas de Cry2Ax pueden tener codones optimizados por completo o en parte. Como todos los aminoácidos (excepto la metionina) son codificados por una cantidad de codones (Tabla

2), puede cambiarse la secuencia de la molécula de ácido nucleico sin cambiar el aminoácido codificado. La optimización de codones es el procedimiento de alteración de uno o más codones a nivel de los ácidos nucleicos, de modo que no se alteran los aminoácidos, sino que se incrementa la expresión en un organismo huésped particular. Aquellos entrenados en la técnica reconocerán que existen tablas y otras referencias que proporcionan información preferencia para un amplio rango de organismos disponibles en la técnica.

5.4 Métodos para evaluar la actividad insecticida

Como se lo usa en la presente documentación, el término "actividad insecticida" hace referencia a la capacidad de un polipéptido de disminuir o inhibir la alimentación del insecto y/o incrementar la mortalidad del insecto una vez ingerido el polipéptido. Aunque puede afectarse cualquier insecto, preferiblemente se ven afectados los insectos de los órdenes Lepidoptera y Diptera.

Puede usarse una variedad de ensayos para determinar si un polipéptido particular de la invención tiene actividad insecticida y, de tenerla, en qué grado se presenta dicha actividad. En general, se le proporciona un polipéptido de la invención a un insecto plaga de cualquier forma que pueda ser ingerida. Se observa la reacción del insecto plaga a la ingestión del polipéptido de la invención (por ejemplo, por entre aproximadamente uno y tres días). Una disminución o una inhibición de la alimentación, y/o un incremento en la mortalidad del insecto plaga después de ingerir el polipéptido de la invención son indicadores de actividad insecticida. Un polipéptido de la invención con actividad insecticida desconocida debería compararse con un control positivo y/o negativo para evaluar el resultado del ensayo con mayor precisión.

En una realización, se purifica un polipéptido de la invención (ya sea en forma soluble o en forma cristalina) y se lo agrega a la dieta del insecto.

En otra realización, se expresa un polipéptido de la invención en un microbio recombinante (por ejemplo, *E. coli*). Las plagas de insectos se alimentan directamente con el microbio recombinante (véase Moellenbeck et al., 2001, Nat. Biotechnol. 19:668).

En otra realización, se expresa el polipéptido de la invención en una planta, y se alimenta el insecto plaga con la planta. Después del período de incubación, puede determinarse la actividad de alimentación del insecto plaga por observación visual (por ejemplo, de una fracción aproximada de área foliar remanente) o captura en video (por ejemplo, cantidad de pixeles en el área foliar remanente) de las partes de la planta que normalmente habrían sido comida por los insectos plaga. En una realización específica, la expresión del polipéptido de la invención en la planta es transitoria. En dichas realizaciones, se clona un ácido nucleico que codifica un polipéptido de la invención en un vector de expresión en plantas, y se lo transfecta en *Agrobacterium tumefaciens*. Las bacterias transformadas se co-cultivan con una hoja de *N. Benthamiana*, y, usando infiltración forzada, la hoja expresa el polipéptido de la invención. Sin embargo, la expresión del polipéptido es variable entre los co-cultivos de hojas. En otra realización específica, la expresión del polipéptido de la invención en la planta es estable. En estas realizaciones, se prepara una planta transgénica que expresa un polipéptido de la invención.

En otra realización, puede evaluarse la actividad insecticida de un polipéptido de la invención midiendo la muerte celular y/o el crecimiento celular mediante el uso de células en cultivo. Estos ensayos típicamente comprenden el uso de células de insecto en cultivo que son susceptibles a la toxina particular usada, o células que expresan un receptor para la toxina particular, ya sea en forma natural o como resultado de la expresión de un gen heterólogo. Por consiguiente, además de las células de insectos, las células de mamíferos, bacterias y levaduras están entre aquellas células que son útiles para los ensayos *in vitro*. En la técnica se describen ensayos biológicos *in vitro* que miden la toxicidad contra células cultivadas (por ejemplo, Johnson, 1994, J. Invertebr. Pathol. 63:123-129).

5.5 Métodos para mejorar la resistencia a insectos en plantas

La presente invención provee métodos para mejorar la resistencia de las plantas a insectos plaga, incluyendo, sin limitaciones, miembros de *Helicoverpa ssp.* (por ejemplo, *Helicoverpa Zea*) y/o *Spodoptera ssp.* (por ejemplo, *Spodoptera exigua*) mediante el uso

de polipéptidos insecticidas relacionados con Cry2. Puede usarse cualquier método conocido en la técnica para provocar que estos insectos plaga ingieran uno o más polipéptidos de la invención durante el curso de la alimentación de la planta. De este modo, los insectos plaga ingerirán cantidades insecticidas de uno o más polipéptidos de la invención, y dejarán de alimentarse con la planta. En algunas realizaciones, los insectos plaga son eliminados por la ingestión de uno o más polipéptidos de la invención. En otras realizaciones, puede inhibirse o repelerse la alimentación de los insectos plaga sobre la planta, sin eliminarlos.

En una realización, pueden prepararse plantas transgénicas que expresen uno o más polipéptidos de la invención (véase en general la sección 5.7 para hallar métodos para producir plantas transgénicas). La planta transgénica puede expresar uno o más polipéptidos de la invención en todos los tejidos (por ejemplo, expresión global). Como alternativa, puede expresarse uno o más polipéptidos de la invención solamente en un subconjunto de tejidos (por ejemplo, expresión con especificidad tisular), preferiblemente aquellos tejidos consumidos por el insecto plaga. Los polipéptidos de la invención pueden expresarse en forma constitutiva en la planta, o pueden estar bajo el control de un promotor inducible.

En otra realización, puede aplicarse una composición que comprende uno o más polipéptidos de la invención en forma externa a una planta susceptible a plagas de insectos. La aplicación externa de la composición incluye la aplicación directa sobre la planta, completa o en parte, y/o la aplicación indirecta, por ejemplo, al ambiente que rodea la planta, tal como la tierra. Puede aplicarse la composición empleando cualquier método conocido en la técnica, incluyendo, sin limitaciones, rocío, espolvoreado, riego o semejantes. En general, puede aplicarse la composición en cualquier momento durante el crecimiento de la planta. Aquellos entrenados en la técnica pueden usar métodos conocidos en la técnica para determinar en forma empírica el momento óptimo para administrar la composición. Los factores que afectan el momento óptimo para la administración incluyen, sin limitaciones, el tipo de planta susceptible, el tipo de insecto plaga, y cuál o cuáles polipéptidos de la invención se administran en la composición.

La composición que comprende uno o más polipéptidos de la invención puede comprender polipéptidos sustancialmente purificados, una suspensión celular, un precipitado celular, un extracto celular o un complejo de esporas-cristales de células de *Bacillus thuringiensis* (véase en general la sección 5.7 para hallar procedimientos para sintetizar polipéptidos recombinantes). La composición que comprende uno o más polipéptidos de la invención puede tomar la forma de una solución, una emulsión, una suspensión o un polvo. Las formulaciones líquidas pueden ser acuosas o no acuosas, y pueden proporcionarse como espumas, geles, suspensiones, concentrados emulsificables o semejantes. Las formulaciones pueden incluir agentes adicionales, además de uno o más polipéptidos de la invención. Por ejemplo, las composiciones pueden comprender adicionalmente coadyuvantes dispersantes-adhesivos, agentes estabilizadores, otros aditivos insecticidas, diluyentes, agentes que optimizan las propiedades reológicas o la estabilidad de la composición, tales como, por ejemplo, agentes tensioactivos, emulsificantes, dispersantes y/o polímeros.

En otra realización, los huéspedes recombinantes que expresan uno o más polipéptidos de la invención se aplican sobre o cerca de una planta susceptible de ser atacada por un insecto plaga. Los huéspedes recombinantes incluyen, sin limitaciones, huéspedes microbianos y virus que afectan insectos, que han sido transformados y que expresan una o más moléculas de ácidos nucleicos (y, por consiguiente, polipéptidos) de la invención. En algunas realizaciones, el huésped recombinante secreta el polipéptido de la invención en el ambiente circundante, con el fin de entrar en contacto con el insecto plaga. En otras realizaciones, los huéspedes recombinantes colonizan uno o más tejidos vegetales susceptibles de ser infestados por insectos.

5.6 Expresión recombinante

Las moléculas de ácidos nucleicos y los polipéptidos de la invención pueden expresarse en forma recombinante usando procedimientos de ADN recombinante y clonación molecular convencionales bien conocidos en la técnica (por ejemplo, Sambrook, Fritsch y Maniatis, *Molecular Cloning: A Laboratory Manual*; Cold Spring Harbor Laboratory Press: Cold Spring Harbor, 1989). Adicionalmente, pueden usarse

procedimientos de ADN recombinante para crear construcciones de ácidos nucleicos apropiadas para usar en la preparación de plantas transgénicas (véase la sección 5.7).

Por consiguiente, un aspecto de la invención se relaciona con vectores, preferiblemente vectores de expresión, que comprenden una molécula de ácido nucleico de la invención, o una variante de ésta. Como se lo usa en la presente documentación, el término "vector" hace referencia a un polinucleótido capaz de transportar otro ácido nucleico al que haya sido unido. Un tipo de vector es un "plásmido", que designa un rizo de ADN circular de cadena doble en el que pueden introducirse segmentos de ADN adicionales. Otro tipo de vector es un vector viral, donde pueden introducirse segmentos de ADN adicionales en el genoma viral.

Determinados vectores son capaces de replicarse en forma autónoma en la célula huésped donde se introducen (por ejemplo, los vectores bacterianos que contienen un origen de replicación en bacterias y los vectores episomales). Otros vectores (por ejemplo, los vectores no episomales) se integran en el genoma de una célula huésped al introducirlos en la célula huésped, y por consiguiente, se replican junto con el genoma del huésped. En general, los vectores de expresión útiles en los procedimientos de ADN recombinante comúnmente toman la forma de plásmidos (vectores). Sin embargo, la invención incluye otras formas de vectores de expresión, tales como vectores virales (por ejemplo, retrovirus con replicación defectuosa).

Los vectores de expresión recombinante de la invención comprenden una molécula de ácido nucleico de la invención en una forma apropiada para expresar la molécula de ácido nucleico en una célula huésped. Esto significa que los vectores de expresión recombinante incluyen una o más secuencias reguladoras apropiadas, seleccionadas teniendo en cuenta las células huésped usadas para la expresión, que están asociadas operativamente con el polinucleótido que se desea expresar. Dentro de un vector de expresión recombinante, el término "asociada operativamente" denota que la secuencia de nucleótidos de interés está unida a las secuencias reguladoras de un modo que permite expresar la secuencia de nucleótidos (por ejemplo, en un sistema de transcripción/traducción *in vitro* o en una célula huésped cuando se introduce el vector en

la célula huésped). El término "secuencia reguladora" incluye promotores, potenciadores y otros elementos de control de la expresión (por ejemplo, señales de poliadenilación). Estas secuencias reguladoras se describen en la técnica (por ejemplo, Goeddel, Gene Expression Technology: Methods in Enzymology, 1990, Academic Press, San Diego, CA). Las secuencias reguladoras incluyen aquellas que dirigen la expresión constitutiva de una secuencia de nucleótidos en muchos tipos de células huésped, y aquellas que dirigen la expresión de la secuencia de nucleótidos solamente en determinadas células huésped (por ejemplo, secuencias reguladoras con especificidad tisular). Aquellos entrenados en la técnica apreciarán que el diseño del vector de expresión puede depender de factores tales como la selección de la célula huésped que se desea transformar, el nivel de expresión deseado para la proteína, el área del organismo en el que se desea la expresión, etcétera. Los vectores de expresión de la invención pueden introducirse en células huésped para producir proteínas o péptidos, incluyendo proteínas o péptidos de fusión, codificados por las moléculas de ácidos nucleicos descriptas en la presente documentación.

En algunas realizaciones, pueden introducirse ácidos nucleicos aislados, que sirven como elementos promotores o potenciadores, en la posición apropiada (generalmente río arriba) de una forma no heteróloga de un polinucleótido de la presente invención, con el fin de regular positiva o negativamente la expresión de un polinucleótido de la presente invención. Por ejemplo, pueden alterarse promotores endógenos *in vivo* a través de mutación, deleción y/o sustitución (véanse la Patente de los EEUU Nº 5565350; la Solicitud Internacional de Patente Nº PCT/US93/03868), o pueden introducirse promotores aislados en una célula vegetal, en la orientación apropiada y a una distancia de un gen conocido de un polinucleótido de la presente invención, con el objeto de controlar la expresión del gen. Puede modularse la expresión genética bajo condiciones apropiadas para el crecimiento de las plantas, de modo de alterar la concentración total y/o alterar la composición de los polipéptidos de la presente invención en la célula vegetal. Por consiguiente, la presente invención provee composiciones y métodos para preparar

promotores y/o potenciadores heterólogos unidos operativamente a una forma nativa, endógena (es decir, no heteróloga) de un polinucleótido de la presente invención.

Si se desea expresar un polipéptido, es generalmente deseable incluir una región de poliadenilación en el extremo 3' de una región codificante de un polinucleótido. La región de poliadenilación puede derivar del gen natural, de una variedad de otros genes vegetales o de ADN-T. La secuencia terminal 3' a agregar puede derivar, por ejemplo, de genes de nopalina sintetasa u octopina sintetasa, o como alternativa, de otros genes vegetales, o menos preferiblemente de otro gen eucariota.

Los vectores de expresión recombinantes de la invención pueden diseñarse para expresar un polipéptido de la invención en células procariotas (por ejemplo, *Enterobacteriaceae*, tales como *Escherichia*; *Bacillaceae*; *Rhizoboceae*, tales como *Rhizobium* y *Rhizobacter*; *Spirillaceae*, tales como photobacterium; *Zymomonas*; *Serratia*; *Aeromonas*; *Vibrio*; *Desulfovibrio*; *Spirillum*; *Lactobacillaceae*; *Pseudomonadaceae*, tales como *Pseudomonas* y *Acetobacter*; *Azotobacteraceae*; y *Nitrobacteraceae*) o eucariotas (por ejemplo, células de insectos, usando vectores de expresión en baculovirus, células de levaduras, células vegetales o células de mamíferos) (véase Goeddel, *supra.* para hallar una descripción sobre células huésped apropiadas). Como alternativa, puede transcribirse y traducirse el vector de expresión recombinante *in vitro*, por ejemplo, secuencias reguladoras promotoras T7 y T7 polimerasa.

La expresión de proteínas en procariotas comúnmente se efectúa en *E. coli*, con vectores que comprenden promotores constitutivos o inducibles que dirigen la expresión de proteínas de fusión o proteínas que no son de fusión. Los vectores de fusión agregan una cantidad de aminoácidos a una proteína codificada, comúnmente en el extremo amino de la proteína recombinante. Estos vectores de fusión típicamente sirven para al menos tres propósitos: 1) incrementar la expresión de la proteína recombinante; 2) incrementar la solubilidad de la proteína recombinante; y/o 3) contribuir en la purificación de la proteína recombinante al actuar como ligandos en purificaciones de afinidad. Comúnmente, en los vectores de expresión de fusión, se introduce un sitio de corte proteolítico en la unión entre la porción de fusión y la proteína recombinante, de modo de

permitir la separación de la proteína recombinante de la porción de fusión después de purificar la proteína de fusión. Estas enzimas, y sus secuencias de reconocimiento conocidas, incluyen el Factor Xa, la trombina y la enteroquinasa. Los vectores de expresión de fusión típicos incluyen pGEX (Pharmacia Biotech Inc; Smith y Johnson, 1988, Gene 67:31-40), pMAL (New England Biolabs, Beverly, MA) y pRIT5 (Pharmacia, Piscataway, NJ), que fusionan glutatión S-transferasa (GST), proteína de unión a maltosa E o proteína A, respectivamente, a la proteína recombinante deseada.

En otra realización, el vector de expresión es un vector de expresión en levadura. Los ejemplos de vectores para expresar en la levadura *S. cerevisiae* incluyen pYepSec1 (Baldari et al., 1987, EMBO J. 6:229-234), pMFa (Kurjan y Herskowitz, 1982, Cell 30:933-943), pJRY88 (Schultz et al., 1987, Gene 54:113-123), pYES2 (Invitrogen Corp., San Diego, CA) y pPicZ (Invitrogen Corp., San Diego, CA).

Como alternativa, el vector de expresión es un vector de expresión en baculovirus. Los vectores para baculovirus disponibles para expresar las proteínas en células de insectos cultivadas (por ejemplo, células Sf 9) incluyen la serie pAc (Smith et al., 1983, Mol. Cell Biol. 3:2156-2165) y la serie pVL (Lucklow y Summers, 1989, Virology 170:31-39).

En aún otra realización, se expresa un ácido nucleico de la invención en células vegetales usando un vector de expresión en plantas, incluyendo, sin limitaciones, el virus en mosaico del tabaco y los vectores de expresión con virus de papa.

En la técnica se conocen otros sistemas de expresión apropiados para células procariotas y eucariotas (véanse, por ejemplo, los capítulos 16 y 17 de Sambrook et al. 1990, Molecular Cloning, A Laboratory Manual, 2ª edición, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY).

Puede usarse una cantidad de promotores en la práctica de la invención. Los promotores pueden seleccionarse sobre la base del resultado deseado. Los ácidos nucleicos pueden combinarse con promotores constitutivos, específicos para tejidos, inducibles u otros, con el fin de obtener expresión en el organismo huésped.

Un "promotor con especificidad tisular" puede dirigir la expresión de los ácidos nucleicos de la presente invención en un tejido, un órgano o un tipo celular específico. Los promotores con especificidad tisular pueden ser inducibles. De forma similar, los promotores con especificidad tisular pueden promover la transcripción dentro de un marco de tiempo o una etapa de desarrollo determinada en dicho tejido. Otros promotores con especificidad tisular pueden ser activos durante el ciclo vital de un tejido particular. Aquellos entrenados en la técnica reconocerán que un promotor con especificidad tisular puede dirigir la expresión de secuencias unidas operativamente en tejidos distintos del tejido blanco. Por consiguiente, como se lo usa en la presente documentación, un promotor con especificidad tisular es uno que dirige la expresión preferiblemente en el tejido o el tipo celular deseado, pero también puede conducir a un cierto grado de expresión en otros tejidos. Puede usarse una cantidad de promotores con especificidad tisular en la presente invención. Con el promotor apropiado, puede realizarse el direccionamiento hacia cualquier órgano, tal como órganos/estructuras vegetativas de los brotes (por ejemplo, hojas, tallos y tubérculos), raíces, flores y órganos/estructuras florales (por ejemplo, brácteas, sépalos, pétalos, estámenes, carpelos, anteras y óvulos), semillas (incluyendo embriones, endosperma y recubrimiento de las semillas) y frutos. Por ejemplo, los promotores que dirigen la expresión de ácidos nucleicos en hojas, raíces o flores son útiles para mejorar la resistencia a las plagas que infectan estos órganos. Para expresar un polinucleótido de la presente invención en los órganos vegetativos aéreos de una planta, pueden usarse promotores específicos para órganos fotosintéticos, tales como el promotor *RBCS* (Khoudi et al., Gene 197:343, 1997). Puede lograrse la expresión específica en raíz de los polinucleótidos de la presente invención bajo el control de un promotor específico para raíz, tal como, por ejemplo, el promotor del gen *ANR1* (Zhang y Forde, Science, 279:407, 1998). Otros ejemplos de promotores incluyen el promotor del gen de glutamina sintetasa de soja específico para raíz (Hirel et al., 1992, Plant Molecular Biology 20:207-218) y el elemento de control específico para raíz del gen GRP 1.8 del poroto francés (Keller et al., 1991, The Plant Cell 3:1051-1061).

Un "promotor constitutivo" se define como un promotor que dirige la expresión de un gen en todos los tejidos, y que es activo bajo casi cualquier condición ambiental y estado del desarrollo o la diferenciación celular. Los ejemplos de promotores constitutivos incluyen la región de inicio de la transcripción del virus en mosaico de la coliflor (CaMV) 35S, el promotor 1' o 2' derivado del ADN-T de *Agrobacterium tumefaciens*, y otras regiones de inicio de la transcripción de varios genes vegetales conocidos por aquellos entrenados en la técnica. Estos genes incluyen, por ejemplo, *ACT11* de *Arabidopsis* (Huang et al. 1996, Plant Mol. Biol. 33:125-139), *Cat3* de *Arabidopsis* (Nº de acceso GenBank U43147, Zhong et al., 1996, Mol. Gen. Genet. 251:196-203), el gen que codifica la proteína transportadora estearoil-acil desaturasa de *Brassica napus* (Nº de acceso Genbank X74782, Solocombe et al. 1994, Plant Physiol. 104:1167-1176), GPc1 de maíz (Nº de acceso Genbank X15596, Martinez et al., 1989, J. Mol. Biol 208:551-565), y Gpc2 de maíz (Nº de acceso Genbank U45855, Manjunath et al., 1997, Plant Mol. Biol. 33:97-112). Puede usarse cualquier promotor constitutivo fuerte, tal como el promotor CaMV 35S, para expresar los polinucleótidos de la presente invención en la planta.

El término "promotor inducible" hace referencia a un promotor que está bajo un control ambiental o de desarrollo preciso. Los ejemplos de condiciones ambientales que pueden desencadenar la transcripción por promotores inducibles incluyen condiciones anaeróbicas, temperatura elevada, la presencia de luz o rocío con sustancias químicas/hormonas.

Los promotores constitutivos apropiados para usar en una célula huésped vegetal incluyen, por ejemplo, el promotor nuclear del promotor Rsyn7 y otros promotores constitutivos relacionados (Publicación Internacional Nº WO 99/43838 y Patente de los EEUU Nº 6072050); el promotor nuclear CaMV 35S (Odell et al., 1985, Nature 313:810-812); el promotor de actina de arroz (McElroy et al., 1990, Pkant Cell 2:163-171); ubiquitina (Christensen et al., 1989, Plant Mol. Biol. 12:619-632 y 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); el promotor ALS (Patente de los EEUU

Nº 5659026) y semejantes (por ejemplo, Patentes de los EEUU Nº 5608149; 5608144; 5604121; 5569597; 5466785; 5399680; 5268463; 5608142 y 6177611).

Otro aspecto de la invención se relaciona con células huésped en las cuales se ha introducido un vector de expresión recombinante de la invención. Los términos "célula huésped" y "célula huésped recombinante" se usan indistintamente en la presente documentación. Puede comprenderse que estos términos no solamente hacen referencia a la célula particular en sí, sino también a la progenie potencial de dicha célula. Como pueden ocurrir algunas modificaciones en las generaciones sucesivas, debido a la mutación o a influencias ambientales, esta progenie, de hecho, puede no ser idéntica a la célula progenitora, pero aún se incluye dentro del alcance del término, tal como se lo usa en la presente documentación.

Por consiguiente, la presente invención provee una célula huésped que contiene un vector de expresión que comprende un ácido nucleico de la invención, o una variante de éste. Una célula huésped puede ser cualquier célula procariota (por ejemplo, *E. coli*, *Bacillus thuringiensis*) o eucariota (por ejemplo, células de insectos, levaduras o células vegetales). La invención también provee un método para expresar un ácido nucleico de la invención para obtener de este modo el polipéptido codificado, que comprende los siguientes pasos: i) cultivar una célula que comprende una molécula de ácido nucleico de la invención bajo condiciones que permiten la producción del polipéptido codificado; y ii) aislar el polipéptido expresado.

Puede introducirse ADN vector en células procariotas o eucariotas mediante procedimientos de transformación o transfección convencionales. Como se los usa en la presente documentación, los términos "transformación" y "transfección" hacen referencia a una variedad de procedimientos reconocidos en la técnica para introducir moléculas de ácidos nucleicos extrañas en una célula huésped, incluyendo co-precipitación con fosfato de calcio o cloruro de calcio, transfección mediada por DEAE-dextrano, lipofección o electroporación. Pueden hallarse métodos apropiados para transformar o transfectar células huésped en la técnica (por ejemplo, Sambrook, et al. *supra*.).

5.7 <u>Producción de plantas transgénicas</u>

Puede usarse cualquier método conocido en la técnica para transformar una planta o una célula vegetal con una molécula de ácido nucleico de la presente invención. Pueden incorporarse moléculas de ácidos nucleicos en ADN vegetal (por ejemplo, ADN genómico o ADN de cloroplasto), o puede mantenérselas sin insertarlas en el ADN de la planta (por ejemplo, mediante el uso de cromosomas artificiales). Los métodos apropiados para introducir moléculas de ácidos nucleicos en células vegetales incluyen microinyección (Crossway et al., 1986, Biotechniques 4:320-334); electroporación (Riggs et al., 1986, *Proc. Natl. Acad. Sci.* 83:5602-5606; D'Halluin et al., 1992, Plant Cell 4:1495-1505); transformación mediada por *Agrobacterium* (Patentes de los EEUU Nº 5563055 y 5981840, Osjoda et al., 1996, Nature Biotechnology 14:745-750; Horsch et al., 1984, Science 233:496-498, Fraley et al., 1983, *Proc. Natl. Acad. Sci.* 80:4803, y Gene Transfer to Plants, Potrykus, editor, Springer-Verlag, Berlín 1995); transferencia directa de genes (Paszkowski et al., 1984, EMBO J. 3:2717-2722); aceleración balística de partículas (Patentes de los EEUU Nº 4945050; 5879918; 5886244; 5932782; Tomes et al., 1995, "Direct DNA Transfer into Intact Plant Cells via Microprojectile Bombardment, en Plant Cell, Tissue, and Organ Culture: Fundamental Methods, editado por Gamborg y Phillips, Springer-Verlag, Berlín; y McCabe et al., 1988, Biotechnology 6:923-926); transformación mediada por virus (Patentes de los EEUU Nº 5889191 5889190 5866785 5589367 y 5316931); transformación de polen (De Wet et al., 1985, en The Experimental Manipulation of Ovule Tissues, editado por Chapman et al., Longman, Nueva York, pp. 197-209); transformación Lec 1 (Solicitud de Patente de los EEUU con Nº serial 09/435054, Publicación Internacional Nº WO 00/28058); transformación mediada por fibrillas (Kaeppler et al., 1990, Plant Cell Reports 9:415-418; Kaeppler et al., 1992, Theor. Appl. Genet. 84:560-566); y tecnología de transformación de cloroplastos (Bogorad, 2000, Trends in Biotechnology 18: 257-263; Rameeh et al., 2004, Methods Mol Biol. 274:301-7; Hou et al., 2003, Transgenic Res. 12:111-4; Kindle et al., 1991, *Proc. Natl. Acad. Sci.* 88:1721-5; Bateman y Purton, 2000, Mol Gen Genet. 263:404-10; Sidorov et al., 1999, Plant J. 19:209-216).

La elección de los protocolos de transformación usados para generar plantas y células vegetales transgénicas puede variar dependiendo del tipo de planta o célula vegetal, es decir, monocotiledónea o dicotiledónea, que se desea transformar. Los ejemplos de protocolos de transformación particularmente apropiados para un tipo de planta particular incluyen aquellos para papa (Tu et al., 1998, Plant Molecular Biology 37:829-838; Chong et al., 2000, Transgenic Research 9:71-78); soja (Christou et al., 1988, Plant Physiol. 87:671-674; McCabe et al., 1988, BioTechnology 6:923-926; Finer y McMullen, 1991, In Vitro Cell Dev. Biol. 27P:175-182; Singh et al., 1998, Theor. Appl. Genet. 96:319-324); maíz (Klein et al., 1988, *Proc. Natl. Acad. Sci.* 85:4305-4309; Klein et al., 1988, Biotechnology 6:559-563; Klein et al., 1988, Plant Physiol. 91:440-444; Fromm et al., 1990, Biotechnology 8:833-839; Tomes et al., 1995, "Direct DNA Transfer into Intact Plant Cells via Microprojectile Bombardment", en Plant Cell, Tissue, and Organ Culture: Fundamental Methods, editado por Gamborg (Springer-Verlag, Berlín)); cereales (Hooykaas-Van Slogteren et al., 1984, Nature 311:763-764; Patente de los EEUU Nº 5736369).

En algunas realizaciones, se usa más de una construcción de transformación para generar las plantas y las células vegetales transgénicas. Pueden incluirse construcciones múltiples en posiciones cis o trans. En realizaciones preferidas, cada construcción tiene un promotor y otras secuencias reguladoras.

Las células vegetales transformadas obtenidas a través de cualquiera de los procedimientos de transformación anteriores pueden cultivarse para regenerar una planta completa que posea el genotipo transformado, y por consiguiente, el fenotipo deseado. Estos procedimientos de regeneración se basan en la manipulación de determinadas fitohormonas en un medio de cultivo de tejido, típicamente se basan en un marcador biocida y/o herbicida que ha sido introducido en combinación con las secuencias de nucleótidos deseadas. La regeneración de plantas a partir de protoplastos cultivados se describe en la técnica (por ejemplo, Evans et al., Protoplasts Isolation and Culture, Handbook of Plant Cell Culture, pp. 124-176, MacMillilan Publishing Company, Nueva York, 1983; y Binding, Regeneration of Plants, Plant Protoplasts, pp. 21-73, CRC Press,

Boca Raton, 1985). También puede efectuarse la regeneración a partir de callos de plantas, explantes, órganos o partes de éstos. Estos procedimientos de regeneración también se describen en la técnica (por ejemplo, Klee et al. 1987, Ann. Rev. of Plant Phys. 38:467-486).

El término "planta" incluye plantas completas, órganos/estructuras de brotes vegetativos (por ejemplo, hojas, tallos y tubérculos), raíces, flores y órganos/estructuras florales (por ejemplo, brácteas, sépalos, pétalos, estámenes, carpelos, anteras y óvulos), semillas (incluyendo embriones, endosperma y recubrimiento de las semillas) y frutos (el ovario maduro), tejido vegetal (por ejemplo, tejido vascular, tejido enterrado y semejantes) y células (por ejemplo, células de guarda, células huevo, tricomas y semejantes), y progenie de éstas. La clase de plantas que puede usarse en los métodos de la presente invención incluye la clase de las plantas superiores e inferiores susceptibles de ser transformadas con los procedimientos descriptos, incluyendo angiospermas (plantas monocotiledóneas y dicotiledóneas), gimnospermas, mohos y algas multicelulares. También se incluyen plantas con una variedad de niveles de ploidía, incluyendo plantas aneuploides, poliploides, diploides, haploides y hemicigotas.

Las moléculas de ácidos nucleicos de la invención pueden usarse para conferir caracteres deseados esencialmente a cualquier planta. Por consiguiente, la invención puede usarse sobre un amplio rango de plantas, incluyendo especies de los géneros *Agrotis, Allium, Ananas, Anacardium, Apium, Arachis, Asparagus, Athamantha, Atropa, Avena, Bambusa, Beta, Brassica, Bromus, Browaalia, Camellia, Cannabis, Carica, Ceratonia. Cicer, Chenopodium, Chicorium, Citrus, Citrullus, Capsicum, Carthamus, Cocos, Coffea, Coix, Cucumis, Cucurbita, Cynodon, Dactylis, Datura, Daucus, Dianthus, Digitalis, Dioscorea, Elaeis, Eliusine, Euphorbia, Festuca, Ficus, Fragaria, Geranium, Glicine, Graminae, Gossyplum, Helianthus, Heterocallis, Hevea, Hibiscus, Hordeum, Hyosclamus, Ipomoea, Lactuca, Lathyrus, Lens, Lilium, Linum, Lolium, Lotus, Lupinus, Lycopersicon, Macadamia, Macrophylla, Malus, Mangifera, Manihot, Majorana, Medicago, Musa, Narcissus, Nemesia, Nicotiana, Onobrychis, Olea, Olyreae, Oryza, Panicum, Panicum, Panieum, Pannisetum, Pennisetum, Petunia, Pelargonium, Persea, Pharoideae,*

Phaseolus, *Phleum*, *Picea*, *Poa*, *Pinus*, *Pistachia*, *Pisum*, *Populus*, *Pseudotsuga*, *Pirus*, *Prunus*, *Pseutotsuga*, *Psidium*, *Quercus*, *Ranunculus*, *Raphanus*, *Ribes*, *Ricinus*, *Rhododendron*, *Rosa*, *Saccharum*, *Salpiglossis*, *Secale*, *Senecio*, *Setaria*, *Sequoia*, *Sinapis*, *Solanum*, *Sorghum*, *Stenotaphrum*, *Theobromus*, *Trigonella*, *Trifolium*, *Trigonella*, *Triticum*, *Tsuga*, *Tulipa*, *Vicia*, *Vitis*, *Vigna* y *Zea*.

En realizaciones específicas, las plantas transgénicas son plantas de maíz, papa, arroz, soja o algodón.

Las plantas transgénicas pueden cultivarse y polinizarse con la misma cepa transformada o con distintas cepas. Pueden cultivarse dos o más generaciones de las plantas para asegurar la expresión de la molécula de ácido nucleico o el polipéptido deseado, y/o el mantenimiento y la herencia estable de la característica fenotípica deseada. Aquellos entrenados en la técnica reconocerán que, después de incorporar en forma estable la molécula de ácido nucleico de la presente invención en las plantas transgénicas y confirmar su operación, puede introducírsela en otras plantas por cruzamiento sexual. Puede usarse cualquiera de una cantidad de procedimientos de cruzamiento convencionales, dependiendo de las especies a cruzar.

5.8 Determinación de la expresión en plantas transgénicas

Puede usarse cualquier método conocido en la técnica para determinar el nivel de expresión de una molécula de ácido nucleico de la invención, o un polipéptido codificado por ésta, en una planta. Por ejemplo, puede determinarse el nivel de expresión de un polipéptido codificado por una molécula de ácido nucleico de la invención en una planta por inmunoensayo, electroforesis cuantitativa en gel, etcétera. Adicionalmente, puede determinarse el nivel de expresión de un polipéptido codificado por una molécula de ácido nucleico de la invención en una planta a través del grado de alteración que presenta el fenotipo de la planta. En una realización específica, la resistencia mejorada a insectos es el fenotipo a analizar.

Como se lo usa en la presente documentación, "resistencia mejorada a insectos" hace referencia a una mayor resistencia de una planta transgénica que expresa un polipéptido de la invención al consumo y/o la infestación por un insecto plaga, en

comparación con una planta que no expresa un polipéptido de la invención. Puede medirse la resistencia mejorada en una cantidad de formas. En una realización, se mide la resistencia mejorada a través del daño reducido en una planta que expresa un polipéptido de la invención, en comparación con una planta que no expresa un polipéptido de la invención, después del mismo período de incubación con insectos. El daño causado por los insectos puede evaluarse en forma visual. Por ejemplo, puede medirse el daño después de la infestación en plantas de algodón buscando directamente señales de alimentación por parte de los insectos en los copos de la planta de algodón. En otra realización, se mide la resistencia mejorada a través de un rendimiento mejorado del cultivo, en una planta que expresa un polipéptido de la invención, en comparación con una planta que no expresa un polipéptido de la invención, después del mismo período de incubación con insectos. En realizaciones particulares, los insectos plaga son de los órdenes Lepidoptera y/o Diptera.

Pueden realizarse las determinaciones usando plantas completas, tejidos de éstas o cultivos de células vegetales.

Los contenidos de todos los artículos publicados, los libros, los manuales de referencia y los resúmenes citados en la presente documentación se incorporan por completo en la presente documentación a modo de referencia, con el fin de describir más completamente el estado de la técnica a la que concierne la invención.

Como pueden efectuarse varios cambios en el tema en cuestión sin apartarse del espíritu y el alcance de la presente invención, se interpreta que todo el tema en cuestión contenido en la descripción anterior y/o definido en las reivindicaciones adjuntas puede interpretarse como descriptivo e ilustrativo de la presente invención. Son posibles modificaciones y variaciones de la presente invención a la luz de las enseñanzas anteriores.

6. EJEMPLOS

6.1 Ejemplo 1: Análisis primario de los insectos

El análisis primario de los insectos permitió identificar cultivos Bt activos de una colección de biodiversidad con actividad contra *Helicoverpa* spp. El análisis se realizó con

muestras de complejos de esporas-cristales a una dosis elevada contra larvas neonatas de *Helicoverpa zea*.

Se prepararon complejos de esporas-cristales en placas de producción con cavidades profundas que contenían 1 ml de medio de esporulación CYS (Yamamoto, 1990, Analytical Chemistry of *Bacillus thuringiensis* 432:46-60). Las placas de producción se incubaron con 10 µl de cultivos de semillas, que habían sido mantenidos congelados a –80°C y se habían incubado a 30°C, a 350 rpm por 3 días, hasta que la mayoría de los cultivos hubieran esporulado y liberado esporas y cristales libres. Se centrifugaron las placas a 4000 rpm por 40 minutos para precipitar las esporas, los cristales y las células no lisadas. Los complejos de esporas-cristales precipitados se suspendieron en 1,2 ml de acetato de potasio 15 mM que contenía 100 µg de lisozima, y se incubó a 30°C, a 250 rpm por 16 horas para asegurar una esporulación y una lisis celular completa. Después de incubar por 16 horas, se recolectaron los complejos de esporas-cristales por centrifugación y se los suspendió en acetato de potasio 15 mM. Este paso con acetato de potasio se repitió una vez. Se preparó la suspensión final de esporas-cristales en 1 ml de acetato de potasio 15 mM, y se la usó para analizar la actividad contra *H. zea*.

El análisis de los insectos se realizó en placas de 96 cavidades poco profundas, cada una de las cuales contenía 150 µl de dieta artificial para insectos. Se colocaron 20 µl de suspensión de esporas-cristales en la dieta para insectos. Se clocaron aproximadamente 5 larvas neonatas en cada cavidad. Se incubaron las placas de ensayos para insectos a 29°C por 3 días. Las respuestas de los insectos ante los cristales Bt incluyeron la inhibición de la alimentación y la mortalidad. Aproximadamente 400 cultivos presentaron una mortalidad sustancial y, por ende, se los identificó como positivos. Cry2Ax estuvo entre los positivos.

6.2 <u>Ejemplo 2: Barajado de ADN para aislar polipéptidos derivados de Cry2Ax</u>

Comenzando con el polipéptido Cry2Ax (SEQ ID N° 2) y el polipéptido Cry2Ab* (Cry2Ab* tiene 2 cambios de aminoácidos respecto de Cry2Ab tipo salvaje; K por R en la posición 36 y M por T en la posición 241 del N° de acceso Genbank M23724), se crearon moldes de ADN sintético para realizar barajado de ADN. Usando una comparación

filogenética de Cry2Ab (Nº de acceso Genbank M23724) y Cry2Ax (SEQ ID Nº 2), se creó una biblioteca donde variaban las 40 posiciones de aminoácidos (véase la sección 5.1) que eran diferentes entre las dos secuencias de polipéptidos. Se crearon bibliotecas de ADN barajado usando barajado dirigido de oligonucleótidos, donde el gen sintético que codificaba Cry2Ax actuó como ADN molde progenitor. Se clonaron las bibliotecas de ADN por PCR en pMAXY3219, reemplazando el gen Cry2Ab*. Se construyeron clones con la toxina de modo tal que se expresaran como una fusión con la proteína de unión a maltosa de *E. coli* (MBP). El análisis primario de los insectos permitió identificar cultivos activos contra *Helicoverpa* spp. El análisis se realizó incorporando una pequeña cantidad de cultivo de *E. coli* que expresaba el polipéptido de fusión MBP::derivado de Cry2Ax a una dosis baja en una dieta artificial, a lo que siguió una infestación con larvas de *H. zea* larvae. El análisis se realizó en placas de 96 cavidades poco profundas, cada una de las cuales contenía 150 µl de dieta artificial para insectos. Se colocaron aproximadamente 0,5 µl de cultivo que expresaba el polipéptido de fusión MBP::derivado de Cry2Ax en la dieta para insectos. Se clocaron aproximadamente 5 larvas neonatas en cada cavidad. Se incubaron las placas de ensayos para insectos a 29°C por 4 días. Las respuestas de los insectos ante las muestras de *E. coli* incluyeron la inhibición de la alimentación y la mortalidad. Aquellas muestras que causaron detención del crecimiento severa o muerte se prepararon para realizar un análisis adicional.

Para el segundo experimento de barajado, se amplificaron los moldes de ADN progenitor de los clones 38 (D_S00503480) (SEQ ID Nº 4) y 44 (D_S00503970) (SEQ ID Nº 8) por PCR en presencia de uracilo, y luego se los fragmentó con uracilo N-glicosilasa. Luego se mezclaron los moldes fragmentados y se los re-ensambló antes de amplificar los moldes recombinantes por PCR. Se creó una biblioteca de estos moldes barajados en pMAXY3219, como se describió previamente. Se indica la secuencia de algunos de los clones aislados del primer y el segundo experimento de barajado en la Tabla 3, donde se detallan los residuos de aminoácidos cambiados.

Con el fin de diversificar adicionalmente uno de los dos aciertos de mayor desempeño en el segundo experimento, se modificó el clon 473R (D_S01037677) (SEQ

ID Nº 18), que contiene los primeros 46 residuos de aminoácidos en la región amino terminal del polipéptido, para que contuviera los residuos hallados en ocho secuencias de polipéptidos Cry2 diferentes (es decir, Cry2Aa, Cry2Ab, Cry2Ac, Cry2Ad, Cry2Ae, Cry2Af, Cry2Ag y Cry2Ax). Además, se reemplazaron dos residuos, I13 y D15, por los residuos conservativos valina y glutamato, respectivamente (véase la Tabla 4). El clon modificado se denominó clon 473N (SEQ ID Nº 8).

6.3 Ejemplo 3: Actividad de los polipéptidos derivados de Cry2Ax

El análisis de las actividades de los clones barajados se realizó en varias etapas. Inicialmente se buscó actividad insecticida elevada en los clones agregando una pequeña cantidad de *E. coli* que expresaban una proteína de fusión clonal a dieta artificial para larvas de *H. zea* de primer estadío. Los clones que provocaron muerte completa o detención completa del crecimiento de las larvas se seleccionaron para continuar los estudios. Aquellos clones que demostraron una actividad insecticida elevada se usaron posteriormente para crear una nueva biblioteca en un vector de expresión de plantas en *Agrobacterium tumefaciens*. Se analizó la biblioteca co-cultivando cada clon en cuatro réplicas con larvas de *N. benthamiana* (usando la infiltración forzada de cada cultivo respectivo), y luego alimentando cada disco correspondiente a larvas de *H. zea* de 3er estadío. Después de un período de incubación de 24 horas, se determinó la actividad de alimentación por observación visual, y se la expresó como una fracción aproximada de área foliar remanente.

Los clones que pasaron esta repetición adicional de los ensayos de expresión en *E. coli*incorporación en la dieta, fueron clonados nuevamente en forma individual en el vector de expresión en plantas pMAXY4384. Se evaluó la eficacia *in planta* como se describió previamente. Se detalla una evaluación final de la actividad *in planta* de los mejores aciertos del ensayo de expresión con múltiples partes en *E. coli* y el abordaje de bibliotecas vegetales en la FIG. 1. A partir de este análisis, varios clones parecieron presentar una mayor actividad insecticida, incluyendo 7K (D_S01000779) (SEQ ID Nº 10), 15K (D_S00999080) (SEQ ID Nº 12), 16K (D_S01000269) (SEQ ID Nº 14), 16R (D_S01037143) (SEQ ID Nº 16) y 473R (D_S01037877) (SEQ ID Nº 18).

6.4 Ejemplo 4: Barajado de ADN para aislar otros polipéptidos derivados de Cry2Ax

Se usaron los clones 44 (D_S00503970) (SEQ ID N° 6), 473R (D_S01037677) (SEQ ID N° 18), que fueron los aciertos de barajado del 1er y el 2° experimento de barajado, como se describe en la sección 6.2, y Cry2Ab*, como moldes para continuar el barajado. Usando estos moldes y barajado dirigido a oligonucleótidos, se crearon polipéptidos derivados con diversidad de aminoácidos respecto de los polipéptidos Cry2 tipo salvaje (es decir, Cry2Ae y Cry2Ag), así como sustituciones de aminoácidos conservativas generadas al azar, y sustituciones al azar dentro de los segmentos de determinadas regiones de rizos estructurales. Se clonaron las bibliotecas de ADN barajadas en pMAXY3219 reemplazando el gen Cry2Ab*. Los clones con toxinas están construidos de modo tal que se expresan como una fusión con la proteína de unión a maltosa de *E. coli* (MBP). Se proporciona un resumen de las secuencias aisladas en Tablas 5-7.

6.5 Ejemplo 5: Actividad de polipéptidos derivados de Cry2Ax adicionales

Con el fin de evaluar la actividad de los polipéptidos derivados barajados contra la plaga de algodón *Helicoverpa zea*, se realizó un análisis de alto desempeño usando dietas artificiales que contenían células completas de *E. coli*, que expresaban una proteína de fusión del clon, como se describió previamente. Los clones con mayor nivel de actividad se analizaron adicionalmente *in planta*, para confirmar que los cambios realizados en cada polipéptido derivado no hubieran presentado un impacto negativo sobre la expresión genética o la acumulación de proteínas en células vegetales. Para iniciar este proceso, se clonó cada polipéptido derivado de Cry2Ax en un vector de expresión en plantas basado en *Agrobacterium tumefaciens*, se los transformó en la cepa huésped de *Agrobacterium* y luego se los dispuso en placas de microtitulación. Luego se analizaron los aciertos co-cultivando cada uno en cuatro réplicas con hojas de *N. benthamiana* (usando infiltración forzada de cada cultivo respectivo), a lo que siguió la alimentación de cada disco correspondiente a larvas de *H. zea* de 3er estadío. Después de un período de incubación de 24 horas, se determinó la actividad de alimentación en cada disco empleando un método de captura y análisis visual como se describió previamente.

Algunos polipéptidos derivados de este proceso mejoraron en comparación con los clones progenitores. Uno de estos clones es D_S01764701 (SEQ ID Nº 134), que presentó una actividad mejorada respecto del clon 44. Los resultados de alimentación de los tres experimentos se presentan en la FIG. 2.

6.6 Ejemplo 6: Plantas transgénicas que expresan el clon 44

Se generaron plantas de tabaco transgénicas que expresaban el clon 44 (D_S00503970) mediante transformación mediada por *Agrobacterium* con selección con glifosato, usando los vectores binarios pMAXY5469 y pMAXY5471. Estos vectores contienen un gen GAT dirigido por dSVBV y una molécula de ácido nucleico del clon 44 dirigida por dMMV (SEQ ID Nº 5). pMAXY5469 difiere de pMAXY5471 porque contiene señales de direccionamiento a plástidos fusionadas a la región codificante del clon 44, lo que permite que esta variante de la toxina se acumule en el compartimiento del plástido. Se generaron aproximadamente 25 transformantes para cada construcción. Se colocaron los discos de hojas que expresaban el clon 44 en un lecho de agar en una bandeja de titulación de 48 cavidades, y luego se los infestó con larvas de *Helicoverpa zea* de 3er estadio y larvas de *Spodoptera exigua* de 4º estadio. Las hojas se incubaron por 24 horas con las larvas, y luego se retiraron las larvas y se observó el área foliar remanente con equipo de captura en video para realizar el cálculo real del área foliar relativa remanente (cantidad de píxeles). Se indican los resultados usando las mejores transformantes para cada vector en la FIG. 3A para *H. zea* y la FIG. 3B para *S. exigua*. Se tomaron 6 discos de hojas de cada planta transgénica para realizar el análisis indicado.

Luego se evaluó la expresión del polipéptido del clon 44 en el plástido (FIG. 4A) o el compartimiento citoplasmático (FIG. 4B) de plantas de tabaco transgénicas por Western blot, usando un anticuerpo policlonal dirigido contra la región N-terminal del polipéptido del clon 44. Los números de los carriles en la FIG. 4 corresponden a los números de las plantas en la FIG. 3.

El anticuerpo policlonal usado en el Western blot se preparó inmunizando pollos con tripsina purificada truncada con el polipéptido del clon 44, y luego purificando

anticuerpos específicos contra Cry2 usando una columna de afinidad preparada con tripsina purificada truncada con el polipéptido del clon 44 como sustrato.

La diferencia más obvia entre los dos tipos de plantas transgénicas es que la inhibición de *S. exigua* es mucho mayor para la toxina acumulada en el plástido (comparando los paneles derecho e izquierdo de la FIG. 3B). Estos datos se correlacionan en general con los datos de expresión (FIG. 4), que muestran que las plantas que contienen el ADN-T derivado de 5469 (FIG. 4A) son capaces de producir mucha más toxina que aquellas de 5471 (FIG. 4B).

Tabla 1: secuencias de Cry2Ax y derivadas de Cry2Ax

Nombre del clon	Tipo	SEQ ID No.
Cry2Ax	ácido nucleico	1
Cry2Ax	polipéptido	2
38 (D_S00503480)	ácido nucleico	3
38 (D_S00503480)	polipéptido	4
44 (D_S00503970)	ácido nucleico	5
44 (D_S00503970)	polipéptido	6
473N	ácido nucleico	7
473N	polipéptido	8
7K (D_S01000779)	ácido nucleico	9
7K (D_S01000779)	polipéptido	10
15K (D_S00999080)	ácido nucleico	11
15K (D_S00999080)	polipéptido	12

Nombre del clon	Tipo	SEQ ID No.
D_S01611723	polipéptido	52
D_S01561293	ácido nucleico	53
D_S01561293	polipéptido	54
D_S01561489	ácido nucleico	55
D_S01561489	polipéptido	56
D_S01561330	ácido nucleico	57
D_S01561330	polipéptido	58
D_S01570511	ácido nucleico	59
D_S01570511	polipéptido	60
D_S01570809	ácido nucleico	61
D_S01570809	polipéptido	62
D_S01570568	ácido nucleico	63

Nombre del clon	Tipo	SEQ ID No.
16K (D_S01000269)	ácido nucleico	13
16K (D_S01000269)	polipéptido	14
16R (D_S01037143)	ácido nucleico	15
16R (D_S01037143)	polipéptido	16
473R (D_S01037677)	ácido nucleico	17
473R (D_S01037677)	polipéptido	18
D_S01466681	ácido nucleico	19
D_S01466681	polipéptido	20
D_S01466770	ácido nucleico	21
D_S01466770	polipéptido	22
D_S01467219	ácido nucleico	23
D_S01467219	polipéptido	24
D_S01466712	ácido nucleico	25

Nombre del clon	Tipo	SEQ ID No.
D_S01570568	polipéptido	64
D_S01572168	ácido nucleico	65
D_S01572168	polipéptido	66
D_S01571315	ácido nucleico	67
D_S01571315	polipéptido	68
D_S01571875	ácido nucleico	69
D_S01571875	polipéptido	70
D_S01572374	ácido nucleico	71
D_S01572374	polipéptido	72
D_S01572905	ácido nucleico	73
D_S01572905	polipéptido	74
D_S01572908	ácido nucleico	75
D_S01572908	polipéptido	76

Nombre del clon	Tipo	SEQ ID No.
D_S01466712	polipéptido	26
D_S01467003	ácido nucleico	27
D_S01467003	polipéptido	28
D_S01460229	ácido nucleico	29
D_S01460229	polipéptido	30
D_S01459398	ácido nucleico	31
D_S01459398	polipéptido	32
D_S01464856	ácido nucleico	33
D_S01464856	polipéptido	34
D_S014657862	ácido nucleico	35
D_S014657862	polipéptido	36
D_S01458733	ácido nucleico	37
D_S01458733	polipéptido	38

Nombre del clon	Tipo	SEQ ID No.
D_S01561856	ácido nucleico	77
D_S01561856	polipéptido	78
D_S01573294	ácido nucleico	79
D_S01573294	polipéptido	80
D_S01571529	ácido nucleico	81
D_S01571529	polipéptido	82
D_S01599948	ácido nucleico	83
D_S01599948	polipéptido	84
D_S01601459	ácido nucleico	85
D_S01601459	polipéptido	86
D_S01602925	ácido nucleico	87
D_S01602925	polipéptido	88
D_S01613034	ácido nucleico	89

Nombre del clon	Tipo	SEQ ID No.
D_S01457892	ácido nucleico	39
D_S01457892	polipéptido	40
D_S01442158	ácido nucleico	41
D_S01442158	polipéptido	42
D_S01443366	ácido nucleico	43
D_S01443366	polipéptido	44
D_S01442132	ácido nucleico	45
D_S01442132	polipéptido	46
D_S01532970	ácido nucleico	47
D_S01532970	polipéptido	48
D_S01532041	ácido nucleico	49
D_S01532041	polipéptido	50
D_S01611723	ácido nucleico	51

Nombre del clon	Tipo	SEQ ID No.
D_S01613034	polipéptido	90
D_S01614407	ácido nucleico	91
D_S01614407	polipéptido	92
D_S01631557	ácido nucleico	93
D_S01631557	polipéptido	94
D_S01633080	ácido nucleico	95
D_S01633080	polipéptido	96
D_S01632237	ácido nucleico	97
D_S01632237	polipéptido	98
D_S01633031	ácido nucleico	99
D_S01633031	polipéptido	100
D_S01632121	ácido nucleico	101
D_S01632121	polipéptido	102

Nombre del clon	Tipo	SEQ ID No.
D_S01764500	ácido nucleico	103
D_S01764500	polipéptido	104
D_S01764502	ácido nucleico	105
D_S01764502	polipéptido	106
D_S01764505	ácido nucleico	107
D_S01764505	polipéptido	108
D_S01764533	ácido nucleico	109
D_S01764533	polipéptido	110
D_S01764543	ácido nucleico	111
D_S01764543	polipéptido	112
D_S01764546	ácido nucleico	113
D_S01764546	polipéptido	114
D_S01764554	ácido nucleico	115
D_S01764554	polipéptido	116
D_S01764568	ácido nucleico	117
D_S01764568	polipéptido	118

Nombre del clon	Tipo	SEQ ID No.
D_S01765112	ácido nucleico	153
D_S01765112	polipéptido	154
D_S01765174	ácido nucleico	155
D_S01765174	polipéptido	156
D_S01765242	ácido nucleico	157
D_S01765242	polipéptido	158
D_S01765308	ácido nucleico	159
D_S01765308	polipéptido	160
D_S01765221	ácido nucleico	161
D_S01765221	polipéptido	162
D_S01765254	ácido nucleico	163
D_S01765254	polipéptido	164
D_S01765231	ácido nucleico	165
D_S01765231	polipéptido	166
D_S01765255	ácido nucleico	167
D_S01765255	polipéptido	168

Nombre del clon	Tipo	SEQ ID No.
D_S01764569	ácido nucleico	119
D_S01764569	polipéptido	120
D_S01764577	ácido nucleico	121
D_S01764577	polipéptido	122
D_S01764642	ácido nucleico	123
D_S01764642	polipéptido	124
D_S01764643	ácido nucleico	125
D_S01764643	polipéptido	126
D_S01764680	ácido nucleico	127
D_S01764680	polipéptido	128
D_S01764685	ácido nucleico	129
D_S01764685	polipéptido	130
D_S01764691	ácido nucleico	131
D_S01764691	polipéptido	132
D_S01764701	ácido nucleico	133
D_S01764701	polipéptido	134
D_S01764706	ácido	135

Nombre del clon	Tipo	SEQ ID No.
D_S01765377	ácido nucleico	169
D_S01765377	polipéptido	170
D_S01765430	ácido nucleico	171
D_S01765430	polipéptido	172
D_S01765446	ácido nucleico	173
D_S01765446	polipéptido	174
D_S01765496	ácido nucleico	175
D_S01765496	polipéptido	176
D_S01764642	ácido nucleico	177
D_S01764642	polipéptido	178
D_S01766041	ácido nucleico	179
D_S01766041	polipéptido	180
D_S01764706	ácido nucleico	181
D_S01764706	polipéptido	182
D_S01766073	ácido nucleico	183
D_S01766073	polipéptido	184
D_S01764643	ácido	185

Nombre del clon	Tipo	SEQ ID No.
	nucleico	
D_S01764708	polipéptido	136
D_S01764723	ácido nucleico	137
D_S01764723	polipéptido	138
D_S02847715	ácido nucleico	139
D_S02847715	polipéptido	140
D_S01765051	ácido nucleico	141
D_S01765051	polipéptido	142
D_S01765068	ácido nucleico	143
D_S01765068	polipéptido	144
D_S01765100	ácido nucleico	145
D_S01765100	polipéptido	146
D_S01765063	ácido nucleico	147
D_S01765063	polipéptido	148
D_S01765119	ácido nucleico	149
D_S01765119	polipéptido	150
D_S01765104	ácido nucleico	151

Nombre del clon	Tipo	SEQ ID No.
	nucleico	
D_S01764643	polipéptido	186
D_S01763985	ácido nucleico	187
D_S01763985	polipéptido	188
D_S01764668	ácido nucleico	189
D_S01764668	polipéptido	190
D_S01764196	ácido nucleico	191
D_S01764196	polipéptido	192
D_S01764728	ácido nucleico	193
D_S01764728	polipéptido	194
D_S01764787	ácido nucleico	195
D_S01764787	polipéptido	196
D_S01764758	ácido nucleico	197
D_S01764758	polipéptido	198
D_S01764768	ácido nucleico	199
D_S01764768	polipéptido	200
D_S01764860	ácido nucleico	201

Nombre del clon	Tipo	SEQ ID No.
D_S01765104	Polipéptido	152

Nombre del clon	Tipo	SEQ ID No.
D_S01764860	Polipéptido	202

Nombre del Clon	Tipo	SEQ ID NO
D_S01765018	ácido nucleico	203
D_S01765018	polipéptido	204
D_S01764947	ácido nucleico	205
D_S01764947	polipéptido	206
D_S01764934	ácido nucleico	207
D_S01764934	polipéptido	208
D_S01764968	ácido nucleico	209
D_S01764968	polipéptido	210
D_S01765008	ácido nucleico	211
D_S01765008	polipéptido	212
D_S01764953	ácido nucleico	213
D_S01764953	polipéptido	214
D_S01764977	ácido	215

Nombre del Clon	Tipo	SEQ ID NO
D_S01766026	ácido nucleico	233
D_S01766026	polipéptido	234
D_S02838294	ácido nucleico	235
D_S02838294	polipéptido	236
D_S02838310	ácido nucleico	237
D_S02838310	polipéptido	238
D_S02838327	ácido nucleico	239
D_S02838327	polipéptido	240
D_S02838328	ácido nucleico	241
D_S02838328	polipéptido	242
D_S02838330	ácido nucleico	243
D_S02838330	polipéptido	244
D_S02838454	ácido	245

Nombre del Clon	Tipo	SEQ ID NO
	nucleico	
D_S01764977	polipéptido	216
D_S01765509	ácido nucleico	217
D_S01765509	polipéptido	218
D_S01765668	ácido nucleico	219
D_S01765668	polipéptido	220
D_S01765621	ácido nucleico	221
D_S01765621	polipéptido	222
D_S01765693	ácido nucleico	223
D_S01765693	polipéptido	224
D_S01765687	ácido nucleico	225
D_S01765687	polipéptido	226
D_S01765765	ácido nucleico	227
D_S01765765	polipéptido	228
D_S01765932	ácido nucleico	229
D_S01765932	polipéptido	230
D_S01766010	ácido nucleico	231

Nombre del Clon	Tipo	SEQ ID NO
	nucleico	
D_S02838454	polipéptido	246
D_S02838470	ácido nucleico	247
D_S02838470	polipéptido	248
D_S02838478	ácido nucleico	249
D_S02838478	polipéptido	250
D_S02838434	ácido nucleico	251
D_S02838434	polipéptido	252
D_S02838549	ácido nucleico	253
D_S02838549	polipéptido	254
D_S02838632	ácido nucleico	255
D_S02838632	polipéptido	256
D_S02838640	ácido nucleico	257
D_S02838640	polipéptido	258
D_S02838648	ácido nucleico	259
D_S02838648	polipéptido	260
Cry2Ab	polipéptido	261

Nombre del Clon	Tipo	SEQ ID NO
D_S01786010	polipéptido	232

Nombre del Clon	Tipo	SEQ ID NO

Tabla 2: Tabla de codones

Aminoácidos			Codón					
Alanina	Ala	A	GCA	GCC	GCG	GCU		
Cisteina	Cys	C	UGC	UGU				
Ácido aspártico	Asp	D	GAC	GAU				
Ácido glutámico	Glu	E	GAA	GAG				
Fenilalanina	Phe	F	UUC	UUU				
Glicina	Gly	G	GGA	GGC	GGG	GGU		
Histidina	His	H	CAC	CAU				
Isoleucina	Ile	I	AUA	AUC	AUU			
Lisina	Lys	K	AAA	AAG				
Leucina	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU
Metionina	Met	M	AUG					
Asparragina	Asn	N	AAC	AAU				
Prolina	Pro	P	CCA	CCC	CCG	CCU		
Glutamina	Gln	Q	CAA	CAG				
Arginina	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU
Serina	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU
Treonina	Thr	T	ACA	ACC	ACG	ACU		
Valina	Val	V	GUA	GUC	GUG	GUU		
Triptofano	Trp	W	UGG					

Tirosina	Tyr	Y	UAC	UAU

Tabla 3: Secuencia de los clones de interés aislados del barajado de ADN

	Progenitores		1er Experimento		2do Experimento				
Posición de aminoácido	2Ab	2Ax	38	44	7K	15K	16K	16R	473R
3	N	H	H	H	H	H	H	H	H
4	S	N	N	N	N	N	N	N	N
20	A	V	A	A	A	A	A	A	A

	Progenitores		1er Experimento		2do Experimento				
Posición de aminoácido	2Ab	2Ax	38	44	7K	15K	16K	16R	473R
355	S	-	S	S	S	S	S	S	S
356	P	V	P	P	P	P	P	P	P
358	N	N	T	N	T	T	T	N	N

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35	V	I	V	V	V	V	V	V	V
37	K	E	E	E	E	E	E	E	E
40	T	M	M	M	M	M	M	M	M
42	W	W	W	W	W	W	R	W	W
45	N	D	D	D	D	D	D	D	D
51	L	V	V	V	V	L	L	V	V
80	N	N	S	N	S	S	S	S	S
163	P	T	T	P	P	P	P	P	P
210	R	Q	R	Q	R	R	Q	R	R
211	D	N	N	N	N	N	N	N	N

Secuencia de Aminoacidos

362	N	S	S	S	S	S	S	S	S
386	E	G	G	G	G	G	G	G	G
388	V	I	V	V	V	V	V	V	V
389	A	N	A	N	A	N	N	A	N
447	E	Q	Q	Q	Q	Q	Q	Q	Q
452	A	E	E	A	E	A	A	A	E
461	A	L	A	L	A	L	L	A	A
477	H	Y	Y	Y	Y	Y	Y	Y	Y
484	S	T	T	S	T	S	T	T	T
490	N	E	E	E	E	E	E	E	E

Secuencia de Aminoacidos

212	Y	H	H	H	H	H	H	H	H		529	N	S	S	S	S	S	S	S	S	
214	K	R	R	R	R	R	R	R	R		570	T	S	S	T	T	S	S	S	T	
230	S	T	S	T	S	S	S	S	T		600	S	D	D	S	S	S	S	S	D	
233	K	R	R	R	R	R	R	R	R		602	S	T	S	S	S	S	S	S	S	
242	M	M	M	M	V	M	M	M	M		603	D	N	N	D	D	D	D	D	N	
318	S	T	S	S	S	S	S	S	S		619	D	E	E	D	D	E	E	D	D	
319	N	Q	Q	Q	Q	Q	Q	Q	Q		625	L	F	F	F	F	F	F	F	F	
330	S	T	T	T	T	T	T	T	T		630	I	L	L	L	L	L	L	L	L	
347	I	V	V	V	V	V	V	V	V		631	S	P	S	P	P	S	S	P	P	

Tabla 4: Comparación de secuencia de polipéptidos Cry2 tipo salvaje con el clon 473N

	PROGENITORES									Clon Modificado	Secuencia de Aminoacidos
Posición de aminoácido	Cry2 Aa	Cry2 Ab	Cry2 Ac	Cry2 Ad	Cry2 Ae	Cry2 Af	Cry2 Ag	Cry2 Ax	473 R	473N	
8	S	S	N	S	N	S	S	S	S	N	
9	S	G	G	G	G	G	E	G	G	E	
11	S	T	N	N	T	T	T	T	T	N	
13	S	I	T	I	I	I	K	I	I	V	
15	S	D	H	D	D	D	G	D	D	E	
17	S	Y	H	Y	Y	Y	Y	Y	Y	H	
21	S	A	A	V	A	A	A	A	A	V	
22	S	H	H	H	H	H	H	H	H	R	
28	S	Q	E	Q	E	Q	E	Q	Q	E	
36	S	Q	E	D	R	Q	Q	Q	Q	E	
37	S	K	K	N	K	E	K	E	E	K	

40	S	T	K	M	M	M	M	M	M	T	
44	S	K	R	K	R	K	R	K	K	R	
45	S	N	T	D	T	D	T	D	D	N	
46	S	N	D	N	D	N	D	N	N	D	

Tabla 5: Secuencia de clones de interés aislados por barajado de ADN usando Cry2Ab* como gen progenitor

Muestra	**1**	**3**	**4**	**7**	**9**	**10**	**11**	**12**	**13**	**14**	**20**	**25**	**26**	**27**	**28**	**29**	**31**	**34**	**36**	**37**	**42**	**46**	**48**	**49**	**51**	**54**	**56**	**64**
Cry2Ab*	M	N	S	N	G	R	T	T	I	C	A	F	S	F	Q	H	S	T	Q	R	W	N	S	L	L	I	G	K
Cry2Ab sec. salvaje																				K								
D_S02838648				D													P			R	R							
D_S02838640																				R								
D_S02838632																			R	R	·			P				
D_S02838470																				R								
D_S02838434																				R								
D_S02838328																				R								

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D_S02838327																		R							
D_S02838310																		R							
D_S01766073																		R							
D_S01766026																		R		D					
D_S01765621																		R							
D_S01765509																		R							
D_S01765496														R				R							
D_s01765255														R				R							
D_S01765119																		R							
D_S01765112								T	R									R				V	V		
D_S01765104					H													R							
D_S01765063																		R							

D_S01765008																		R							
D_S01764977																		R							
D_S01764947												L						R							
D_S01764787																		R							
D_S01764723												L						R							
D_S01764701																		R							
D_S01764691																		R							
D_S01764680											S						S	R							
D_S01764668																		R							
D_S01764642																		R							

Tabla 5: (cont.)

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Muestra	1	3	4	7	9	10	11	12	13	14	20	25	26	27	28	29	31	34	36	37	42	46	48	49	51	54	56	64
D_S01764568																				R								
D_S01764554																				R								
D_S01764548																				R								
D_S01764543																				R								E
D_S01764533																				R								
D_S01764505		H	N								V									R								
D_S01764502								A												R								
D_S01764500																				R								
D_S01764196					S															R								
D_S01763985																				R								
D_S01632237																				R								

D_S01632121							A												R							
D_S01631557																			R							
D_S01614407																			R							
D_S01613034																			R						R	
D_S01602925																			R							
D_S01601459																			R							
D_S01599948																			R							
D_S01532970															R				R							
D_S0153204		H	N										S						R							
D_S01487003																			R							
D_S01486770																			R							
D_S01486712																			R							

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D_S01466681		H																								
D_S014657862	I																	R								
D_S01457892																		R								
D_S01443366																		R								
D_S01442158																		R			L					
D_S01442132																		R								
D_S-1764685																		R								
BY2_Cry2Ab																		R								

Tabla 5: (cont.)

Muestra	70	76	79	80	89	93	96	97	100	101	107	111	118	119	122	123	124	125	126	130	135	137	139
Cry2Ab*	V	S	R	N	N	D	R	E	K	F	N	L	L	T	Q	A	N	V	E	R	F	N	N

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Cry2Ab sec. salvaje																						
D_S02838648				S						L				E								
D_S02838640				S										E								P
D_S02838632																						P
D_S02838470									Q													
D_S02838434				S																	L	
D_S02838328																						
D_S02838327				S					E													
D_S02838310																						
D_S01766073																						
D_S01766026			W						E													

D_S01765621				G							D											
D_S01765509																						
D_S01765496	I																					
D_s01765255																			Q			
D_S01765119									Q													
D_S01765112					D																	
D_S01765104							H					W										
D_S01765083									Q		D											
D_S01765008			W	G																		
D_S01764977			W						Q													
D_S01764947			K	S					Q													
D_S01764787			W																		Y	

D_S01764723			W	G									M									
D_S01764701									Q			D										
D_S01764691																						
D_S01764680																						
D_S01764668			W	G											R							
D_S01764642		L							Q													
D_S01764568																	G	I				

Tabla 5: (cont.)

Muestra	70	76	79	80	89	93	96	97	100	101	107	111	118	119	122	123	124	125	126	130	135	137	139
D_S01764554				S					R														
D_S01764546									Q														

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D_S01764543				S																		
D_S01764533			W																			T
D_S01764505															S							
D_S01764502			W	G					Q					R								
D_S01764500				G																		T
D_S01764196				S		G																
D_S01763985																						
D_S01632237				S																		
D_S01632121				S																		
D_S01631557				S		V													H			
D_S01614407								G	R													
D_S01613034																						

D_S01602925				S																		
D_S01601459				S										E								
D_S01599948				S				G														
D_S01532970																						
D_S0153204																			G			
D_S01467003																						
D_S01466770																						
D_S01466712																						
D_S01466681																						
D_S014657862											S			R						H		
D_S01457892																						
D_S01443366																						

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D_S01442158																						
D_S01442132																						
D_S-1764685																						
BY2_Cry2Ab				S									E									

Tabla 5: (cont.)

Muestra	140	141	142	144	153	154	160	162	164	166	167	168	169	172	178	184	187	191	192	193	197	201
Cry2Ab*	R	N	A	P	T	M	N	L	Q	Q	M	Q	G	L	F	L	S	D	V	I	D	I
Cry2Ab sec. salvaje																						
D_S02838648																					G	
D_S02838640		D	I																			

D_S02838832	L	S	I										Q								
D_S02838470			T																		
D_S02838434															L						
D_S02838328																M					
D_S02838327	L	D	T																		
D_S02838310																					
D_S01766073																					
D_S01766026	Q															M					
D_S01765621																			V		V
D_S01765509										R	V								V		
D_S01765496																					
D_s01765255											V					M			V		

D_S01765119				L																
D_S01765112					A															
D_S01765104								S							M		E			
D_S01765063																				
D_S01765008							S				V				M				V	
D_S01764977																				
D_S01764947																				
D_S01764787											V									
D_S01764723	Q					L				R	V								V	
D_S01764701																				
D_S01764691																				
D_S01764680										R					M				V	

D_S01764668																M					
D_S01764642											V					M				V	
D_S01764568																					

Tabla 5: (cont.)

Muestra	140	141	142	144	153	154	160	162	164	166	167	168	169	172	178	184	187	191	192	193	197	201
D_S01764554																			A			
D_S01764546																						
D_S01764543																						
D_S01764533																				V		
D_S01764505																						
D_S01764502	Q																G			V		

D_S01764500	Q										V										
D_S01764196												R		S							
D_S01763985																					
D_S01632237												R	Q								
D_S01632121																					
D_S01631557																					
D_S01614407																					
D_S01613034																					
D_S01602925																					
D_S01601459																					
D_S01599948																					
D_S01532970																					

D_S0153204																						
D_S01467003																						
D_S01466770																						
D_S01466712			T																			
D_S01466681																						
D_S014657862									M													
D_S01457892																						
D_S01443366																						
D_S01442158																						
D_S01442132																						
D_S-1764685																						
BY2_Cry2Ab																						

Tabla 5: (cont.)

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Muestra	205	210	211	212	214	215	216	218	219	221	226	229	230	233	234	237	238	240	241	242	244	273
Cry2Ab*	T	R	D	Y	K	N	Y	R	D	S	N	Q	S	K	G	T	R	H	D	T	E	G
Cry2Ab sec. salvaje																				M		
D_S02838648																				T		
D_S02838640													T							T		
D_S02838632																				T		
D_S02838470																				T		
D_S02838434					R															T		
D_S02838328																				T		
D_S02838327																				T		

D_S02838310		Q											T						T		
D_S01766073																					
D_S01766026																			T		
D_S01765621								T											T		
D_S01765509																			T		
D_S01765496																			T		
D_s01765255																			T		
D_S01765119																			T		
D_S01765112		Q	N	H	R								T	R							
D_S01765104																			T		
D_S01765063																		G	T		
D_S01765008																			T		

D_S01764977																			T	K	
D_S01764947																			T		
D_S01764787															A				T		
D_S01764723																			T		S
D_S01764701																		G	T		
D_S01764691																			T		
D_S01764680																	R		T		
D_S01764668									E										T		
D_S01764642									E										T		
D_S01764568																			T		

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Tabla 5: (cont.)

Muestra	205	210	211	212	214	215	216	218	219	221	226	229	230	233	234	237	238	240	241	242	244	273
D_S01764554		Q									S									T		
D_S01764546	A																			T		
D_S01764543													T							T		
D_S01764533																				T		
D_S01764505																				T		
D_S01764502	A																		G	T		
D_S01764500															A					T		
D_S01764196		Q			R												G			T		
D_S01763985							H						T							T		

D_S01632237			N										T							T		
D_S01632121		Q											T							T		
D_S01631557												R								T		
D_S01614407													T							T		
D_S01613034			N		R								T							T		
D_S01602925					R								T							T		
D_S01601459		Q	N										T							T		
D_S01599948													T							T		
D_S01532970				F																		
D_S0153204		Q	N	H	R								T	R						T		
D_S01467003																				T		
D_S01466770																				T		

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D_S01466712																			T		
D_S01466681																			T		
D_S014657862						E													T		
D_S01457892																			T		
D_S01443366																			T		
D_S01442158																			T		
D_S01442132																			T		
D_S-1764685										W											
BY2_Cry2Ab			N		R								T						T		

Tabla 5: (cont.)

Muestra	278	279	283	284	285	286	288	291	298	302	305	307	310	311	317	319	321	323	325	330	331	344

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Cry2Ab*	A	S	P	Q	Q	T	S	S	Y	Q	S	Y	N	G	L	N	F	N	V	S	T	S
Cry2Ab sec. salvaje																						
D_S02838648																						
D_S02838640								G														
D_S02838632																						
D_S02838470									H													
D_S02838434																						
D_S02838328																			G			
D_S02838327																						
D_S02838310																						
D_S01766073						A																

D_S01766026																					
D_S01765621																		G			
D_S01765509																		G			
D_S01765496							L														
D_s01765255																		G			
D_S01765119																					
D_S01765112															Q	L					
D_S01765104																		G			
D_S01765063																		G			
D_S01765008																		G			
D_S01764977																					
D_S01764947																					

D_S01764787																		G			
D_S01764723														S							
D_S01764701																		G			
D_S01764691																					
D_S01764680											H							G			
D_S01764668																		G			P
D_S01764642													S								
D_S01764568																					

Tabla 5: (cont.)

Muestra	278	279	283	284	285	286	288	291	298	302	305	307	310	311	317	319	321	323	325	330	331	344
D_S01764554																					A	

D_S01764548																					
D_S01764543		C																			
D_S01764533																		G			
D_S01764505											Q							G			
D_S01764502													S								
D_S01764500	T					A															
D_S01764198																					
D_S01763985			V	T	N																
D_S01632237													S								
D_S01632121													H								
D_S01631557																					
D_S01614407																	S				

164

D_S01613034			V	T	N																
D_S01602925																					
D_S01601459						R													N		
D_S01599948																					
D_S01532970																			T		
D_S0153204																Q			T		
D_S01467003																					
D_S01466770																					
D_S01466712		R																			
D_S01466681																					
D_S014657882													D								
D_S01457892																					

D_S01443366																					
D_S01442158																					
D_S01442132																					
D_S-1764685					R					R											
BY2_Cry2Ab																					

Tabla 5: (cont.)

Muestra	347	358	362	367	383	386	389	391	399	401	403	405	407	408	413	420	435	436	444	445	447	448
Cry2Ab*	I	N	N	L	S	E	A	V	F	T	L	L	S	G	R	P	R	N	H	Y	E	I
Cry2Ab sec. salvaje																						

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D_S02838648																					
D_S02838640																					
D_S02838632																					
D_S02838470																					
D_S02838434																					
D_S02838328																					
D_S02838327																					
D_S02838310																					
D_S01766073				T																	
D_S01766026																					
D_S01765621																					
D_S01765509																					

D_S01765496																					
D_s01765255	V																				
D_S01765119																					
D_S01765112						G	N														
D_S01765104										S	I	I		R							
D_S01765063																					
D_S01765008										S	I	I	C								
D_S01764977																					
D_S01764947																					
D_S01764787																					
D_S01764723																	K				
D_S01764701																					

D_S01764691																				
D_S01764680																				
D_S01764668										S	I	I								
D_S01764642																				
D_S01764568																				

Tabla 5: (cont.)

Muestra	347	358	362	367	383	386	389	391	399	401	403	405	407	408	413	420	435	436	444	445	447	448
D_S01764554																						
D_S01764546																						T
D_S01764543																						

D_S01764533																					
D_S01764505																		Y	F		
D_S01764502																					
D_S01764500																					
D_S01764196																					
D_S01763985																					
D_S01632237																					
D_S01632121																					
D_S01631557																					
D_S01614407																					
D_S01613034																					
D_S01602925																					

D_S01601459																					
D_S01599948														K							
D_S01532970	V		S					L												Q	
D_S0153204						G	N														
D_S01467003															S		D				
D_S01466770																	D				
D_S01466712																					
D_S01466681																					
D_S014657862									L												
D_S01457892																					
D_S01443366																					
D_S01442158																					

D_S01442132																					
D_S-1764685		S		T	R																
BY2_Cry2Ab																					

Tabla 5: (cont.)

Muestra	459	461	476	490	491	492	497	498	500	508	513	517	529	530	537	538	543	545	553	560	566
Cry2Ab*	G	A	H	N	D	Y	I	S	I	Q	I	F	N	N	L	R	S	N	I	V	V
Cry2Ab sec. salvaje																					
D_S02838648																K					
D_S02838640											V										

D_S02838632																				
D_S02838470																				
D_S02838434																				
D_S02838328																				
D_S02838327																				
D_S02838310								G												
D_S01766073																				
D_S01766026																				
D_S01765621									V											
D_S01765509																				
D_S01765496																				
D_s01765255																				

D_S01765119																				
D_S01765112		L	Y	E									S							
D_S01765104					G					-										
D_S01765063																				
D_S01765008																G				
D_S01764977																	P			
D_S01764947																				
D_S01764787																			A	
D_S01764723																				
D_S01764701																				
D_S01764691																				
D_S01764680																				

D_S01764668																			
D_S01764642															W				
D_S01764568																			

Tabla 5: (cont.)

Muestra	459	461	476	490	491	492	497	498	500	508	513	517	529	530	537	538	543	546	553	560	566
D_S01764554																					
D_S01764548																					
D_S01764543	S																				
D_S01764533																					
D_S01764505																					

D_S01764502																				
D_S01764500																		T		
D_S01764196																				A
D_S01763985																				
D_S01632237																				
D_S01632121																				
D_S01631557																				
D_S01614407										R										
D_S01613034																				
D_S01602925																				
D_S01601459																				
D_S01599948																	D			

D_S01532970		L		E																
D_S0153204																P	D		A	
D_S01467003															F			L		
D_S01466770												L	T		F			L		
D_S01466712													T					L		
D_S01466681																				
D_S014657862																				
D_S01457892					G										F					
D_S01443366							M						T					L		
D_S01442158													A		F					
D_S01442132													T							
D_S-1764685						H								Y						

BY2_Cry2Ab																				

Tabla 5: (cont.)

Muestra	567	568	569	582	583	591	592	593	595	598	600	603	612	619	623	624	625	630	631	633
Cry2Ab*	Y	T	A	N	D	I	N	I	N	A	S	D	L	D	I	M	L	I	S	L
Cry2Ab sec. salvaje																				
D_S02838648																				
D_S02838640																				
D_S02838632																				
D_S02838470																				I

D_S02838434																			
D_S02838328	H												F						I
D_S02838327																			
D_S02838310		A																	
D_S01766073																			
D_S01766026							D						F						
D_S01765621																			I
D_S01765509		A											F						I
D_S01765498								M											I
D_s01765255								M											I
D_S01765119																			
D_S01765112																			

D_S01765104								M											
D_S01765063													F		T				
D_S01765008								M					F						I
D_S01764977								M					F						I
D_S01764947								M		V									I
D_S01764787								M					F						
D_S01764723																			
D_S01764701													F		T				
D_S01764691																			
D_S01764680								M											I
D_S01764668								M											
D_S01764642							K	M					F						I

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D_S01764568						V		M								V				I

Tabla 5: (cont.)

Muestra	567	568	569	582	583	591	592	593	595	598	600	603	612	619	623	624	625	630	631	633
D_S01764554																				
D_S01764546								M												
D_S01764543																				
D_S01764533																				I
D_S01764505																				
D_S01764502																				
D_S01764500										.			F							I

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D_S01764196																			
D_S01763985																			
D_S01632237																			
D_S01632121																			
D_S01631557																			
D_S01614407																			
D_S01613034																			
D_S01602925																			
D_S01601459																			
D_S01599948											.		S						
D_S01532970																	F	L	P	
D_S0153204				Y													F			

D_S01467003											G								
D_S01466770												N							I
D_S01466712									T				F						
D_S01466681														E					
D_S014657862										T									
D_S01457892																			I
D_S01443366			V					M					F					G	
D_S01442158																			
D_S01442132			V					M					F						I
D_S-1764885					N														
BY2_Cry2Ab																			

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Tabla 6: Tabla 6: Secuencia de los clones de interés aislados por barajado de ADN, usando el clon 44 como progenitor

MUESTRA	64	143	149	189	192	216	217	225	228	290	345	358	383	418	527	553	600	603	616	619	631
D_S00503970 (CLON PROGENITOR 44)	K	V	S	I	V	Y	T	I	Y	T	G	N	S	Y	E	I	S	D	T	D	P
D_S01765068																	D	N		E	S
D_S01573294						H					S										S
D_S01572908					A																

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D_S01572905			P				A													
D_S01561856		L							H									A		
D_S01561489		A						F					G							
D_S01561330										R				H						
D_S01765221	R											D			G					
D_S01561293	R			V												M				

Tabla 7: Secuencia de clones de interés aislados por barajado de AND usando el clon 473R como progenitor

Muestra	4	12	17	29	31	32	34	38	51	93	96	108	124	137	139	140	141	142	143	144	147	153	167
D_S01037677 (clon progenitor 473)	N	T	Y	H	S	L	T	E	V	D	R	T	N	N	N	R	N	A	V	P	I	T	M
D_S01765231																							
D_S01764643						P																	
D_S01572374																							
D_S01571875																							

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D_S01766010														H	P	T	I	S	H			
D_S01572168					P									T	Q	T		T	R			L
D_S01765242										G												L
D_S01764953			H	R				G					S								V		L
D_S01764728									I			A										M	L
D_S01764758																							L
D_S01571529	S						A																V
D_S01571315											C												V
D_S01570809														D									
D_S01570568																							
D_S01570511		A																					

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Tabla 7 (cont.)

Muestra	168	169	170	177	189	195	223	226	250	266	296	306	315	323	324	350	355	356	357	358	362	372	3
D_S01037677 (clon progenitor 473)	Q	G	Y	L	I	N	Y	N	F	Q	F	N	A	N	I	G	S	P	F	N	S	T	V
D_S01765231														S									
D_S01764643																							
D_S01572374								S								S							
D_S01571875						S																	
D_S01766010				V			H		S			S											I
D_S01572168	H		R																				

D_S01765242	N	N	R																			
D_S01764953	R		H																			
D_S01764728	R	D	P												V							
D_S01764758	G	E									S		V				R	T	A	G	N	S
D_S01571529	E	R										D								D		
D_S01571315	G		F																			
D_S01570809																						
D_S01570568					V					R												
D_S01570511																						

Tabla 7 (cont.)

Muestra	384	390	425	434	446	447	451	455	474	479	492	504	505	527	553	555	565	570	599	611	616	623
D_S01037677 (clon progenitor 473)	D	T	R	V	N	Q	I	S	N	H	Y	Q	V	E	I	N	R	T	S	T	T	I
D_S01765231										R												
D_S01764643														G								
D_S01572374																						
D_S01571875			Q								H								R			
D_S01766010								P				R						A				
D_S01572168		A																				

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D_S01765242	G																				
D_S01764953													A								
D_S01764728									D										A		V
D_S01764758				A																I	
D_S01571529												R				Q					
D_S01571315							T														
D_S01570809					S																
D_S01570568						H									V						
D_S01570511																S					

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LISTADO DE SECUENCIAS

<110> PIONEER HI-BRED INTERNATIONAL, INC.

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<151> 2004-02-25

<160> 261

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<211> 1899

<212> ADN

<213> Bacillus thuringiensis

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cctaatattg ttggtttacc tggtactact acaactcacg cattgcttgc tgcaagggtc 1020

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<213> Bacillus thuringiensis

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20 25 30

Thr Ile Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser Leu
35 40 45

Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys Lys
50 55 60

Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn Leu
65 70 75 80

Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg Glu
85 90 95

Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala Arg
100 105 110

Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe Asn
115 120 125

Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro Leu

130 135 140

Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn Arg
145 150 155 160

Leu Thr Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro Leu
165 170 175

Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val Ile
180 185 190

Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr Tyr
195 200 205

Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys Ile
210 215 220

Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His Asp
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Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr Val
245 250 255

Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser Gly
260 265 270

Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser Phe
275 280 285

Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn Ser
290 295 300

Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Thr Gln Thr Phe
305 310 315 320

Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu Leu
325 330 335

Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile Gly
340 345 350

Ala Val Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro Pro Leu
355 360 365

Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp Arg Gly
370 375 380

Gly Ile Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu Thr Thr
385 390 395 400

Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser Asn Tyr
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Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val Val
420 425 430

Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile Arg Asn
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Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr Met Val
450 455 460

Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu Asn Gly
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Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr Ile Ser
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Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe Ile Ser

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Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln Ser Asn

515 520 525

Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr Asn Leu

530 535 540

Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val Thr Ile

545 550 555 560

Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr Asn Asn

565 570 575

Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn Ile Gly

580 585 590

Asn Val Val Ala Ser Asp Asn Thr Asn Val Pro Leu Asp Ile Asn Val

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Pro Thr Asn Leu Pro Pro Leu Tyr

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Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
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Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
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Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
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Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala

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Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe

115 120 125

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Arg Leu Thr Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro

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Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

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Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

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Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
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Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
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Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
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Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
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Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
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Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
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Gly Ala Ser Pro Phe Thr Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
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Arg Gly Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
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Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
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Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
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Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
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Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu

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Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
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Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
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Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met

610 615 620

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625 630

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cgtcctctgc actacaatca gatcaggaac attgcgtcac cttcaggtac acctggtgga 1380

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cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagc 1800

aacagcgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgttcgttcc gacaaaccta ccaccattgt at 1902

<210> 6

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 6

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn

65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr

625 630

<210> 7

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 7

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gagtggaaga gaaacgacca ttcgctatat gttgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggagc 240

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ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccttgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccac aattccagat ccaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcga aaccatctga ggaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcgagcgac 1800

aacagcaacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

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<210> 8

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 8

Met Gly His Asn Val Leu Asn Asn Glu Arg Asn Thr Val Cys Glu Ala
1 5 10 15

His Asn Val Ala Val Arg Asp Pro Phe Ser Phe Glu His Lys Ser Leu
20 25 30

Asn Thr Val Glu Lys Glu Trp Thr Glu Trp Lys Arg Asn Asp His Ser

35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys

50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser

65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg

85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala

100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe

115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Leu Pro

130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn

145 150 155 160

Arg Leu Pro Gln Phe Gln Ile Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 9

<211> 1902

<212> ADN

<213> Bacillus thuringiensis

<400> 9

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gagtggaaga aggacaatca ttcgctatat gttgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggagc 240

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

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atatcggcag ctacactacg tacttatcga aaccatctga ggaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtca gccttcagag gcctgaatac aaggctccac 720

gatgtgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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aacagcgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgttcgttcc gacaaaccta ccaccattgt at 1902

<210> 10

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 10

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Val Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Thr Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Gly Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 11

<211> 1902

<212> ADN

<213> Bacillus thuringiensis

<400> 11

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tcaaactact gtatcaacac ctatcagtcc gcattccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagc 1800

aacagcgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgaattg 1860

atgaacatca tgttcgttcc gacaaaccta tcaccattgt at 1902

<210> 12

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 12

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Arg Gly Leu Asn Thr Arg Leu His

225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn

290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr

305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu

325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Thr Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Leu Ser Pro Leu Tyr

625 630

<210> 13

<211> 1902

<212> ADN

<213> Bacillus thuringiensis

<400> 13

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gagcggaaga aggacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggagc 240

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ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcag aatcacctgc gcaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

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gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagc 1800

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atgaacatca tgttcgttcc gacaaaccta tcaccattgt at 1902

<210> 14

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 14

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Arg Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr

305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Thr Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Ser Pro Leu Tyr
625 630

<210> 15

<211> 1902

<212> ADN

<213> Bacillus thuringiensis

<400> 15

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gagtggaaga aggacaatca ttcgctatat gttgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggagc 240

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ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcga aaccatctga ggaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtca gccttcagag gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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accatcaacg gtcgagtgta cacagcttca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagc 1800

aacagcgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgttcgttcc gacaaaccta ccaccattgt at 1902

<210> 16

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 16

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu

20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630 .

<210> 17

<211> 1902

<212> ADN

<213> Bacillus thuringiensis

<400> 17

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcga aaccatctga ggaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcgagcgac 1800

aacagcaacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgtttgttcc gacaaaccta ccaccattgt at 1902

<210> 18

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 18

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn

290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr

305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu

325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 19

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 19

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

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gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

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<210> 20

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 20

Met Gly His Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Lys Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His

225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn

290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr

305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu

325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 21

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 21

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ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgctcaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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ggaaactctt acaacctata cttgcgtgtc tccagccttg gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccaccaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

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<210> 22

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 22

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu

20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser

35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys

50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asp Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Leu Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Thr Asn Thr Thr Ala Arg Tyr Thr Phe Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Leu Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asn Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr

625 630

<210> 23

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 23

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaata tgcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

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tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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aacagtgacg tacctctgga cattaacgtt acgttcaact caggcacaca gttcgatttg 1860

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<210> 24

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 24

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn

200

145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro

165 170 175

Leu Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His

225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val His Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr

625 630

<210> 25

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 25

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<210> 26

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 26

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe

115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Thr Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Arg Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Thr Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Leu Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Thr Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 27

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 27

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240

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ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttctca 1260

gactacttca tccgaaacat ctctggagta cctctagtcg ttagggatga agaccttcgt 1320

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cacgccactc aggtgaacaa ccagactcga acattcatca gtgagaagtt tggaaaccaa 1560

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ggaaactctt acaacctata cttgcgtgtc tccagccttg gcaattcaac tatcagggtt 1680

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gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcggt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 28

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 28

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg

85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Ser Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asp Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu

465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Phe Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Leu Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Gly Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 29

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 29

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240

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ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctgcactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatgg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 30

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 30

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys

50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Ala Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Thr
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Met Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 31
<211> 1902
<212> ADN
<213> Bacillus thuringiensis

<400> 31

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaacac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcag aatcacctgc gcaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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ggaacgatga tccacttggc tccagaggac tacaccggat ttacaatcag tcctatccac 1500

gccactcagg tgaacaacca gactcgaacg ttcatcagtg agaagtttgg aaaccaaggc 1560

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aacgacaatg gtgctcgctt cagcgacatc aacatcggaa acgtagtcgc aagcgacaac 1800

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aacatcatgt tcgttccgac aaacctgccg ccattgtatt ag 1902

<210> 32

<211> 633

<212> PRT

<213> Bacillus thuringiensis

<400> 32

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Val Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu

20 25 30

Asp Thr Ile Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser

35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys

50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn

65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg

85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala

100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe

115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro

130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Thr Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Thr Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Val Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro Pro
355 360 365

Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp Arg
370 375 380

Gly Gly Ile Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu Thr

385 390 395 400

Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser Asn

405 410 415

Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val

420 425 430

Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile Arg

435 440 445

Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr Met

450 455 460

Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu Asn

465 470 475 480

Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr Ile

485 490 495

Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe Ile

500 505 510

Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln Ser
515 520 525

Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr Asn
530 535 540

Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val Thr
545 550 555 560

Ile Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr Asn
565 570 575

Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn Ile
580 585 590

Gly Asn Val Val Ala Ser Asp Asn Thr Asn Val Pro Leu Asp Ile Asn
595 600 605

Val Thr Leu Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met Phe
610 615 620

Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 33

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 33

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

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tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

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gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

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atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 34

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 34

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
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Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 35

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 35

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

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<210> 36

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 36

Ile Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Ser Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Arg Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn His Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Met Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Glu Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asp Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu

245

325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Leu Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Thr Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 37

<211> 1902

<212> ADN

<213> Bacillus thuringiensis

<400> 37

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cggttaacac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

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gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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aacatcatgt tcgttccgac aaacctgccg ccattgtatt ag 1902

<210> 38

<211> 633

<212> PRT

<213> Bacillus thuringiensis

<400> 38

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Val Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Ile Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Thr Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn

290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Thr Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Val Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro Pro
355 360 365

Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp Arg
370 375 380

Gly Gly Ile Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu Thr
385 390 395 400

Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser Asn
405 410 415

Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val
420 425 430

Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile Arg
435 440 445

Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr Met
450 455 460

Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu Asn
485 470 475 480

Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr Ile
485 490 495

Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe Ile
500 505 510

Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln Ser
515 520 525

Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr Asn
530 535 540

Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val Thr
545 550 555 560

Ile Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr Asn
565 570 575

Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn Ile
580 585 590

Gly Asn Val Val Ala Ser Asp Asn Thr Asn Val Pro Leu Asp Ile Asn
595 600 605

Val Thr Leu Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met Phe
610 615 620

Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 39

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 39

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gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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<210> 40

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 40

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn

290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr

305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu

325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Gly Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Phe Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr

625 630

<210> 41

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 41

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gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagag ggaatggact 120

gagtggaaga agaacaatca tttgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgctttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

agtggacctc agcaaaccca atcgttcacg agtcaagact ggccattcct gtatagcttg 900

ttccaggtca actccaacta cgtgctgaac ggcttctcag gtgctcgatt gtccaacact 960

ttcccaaaca tcgttggact tccaggaagc actacgactc atgccttgct ggctgcacga 1020

gtcaactact ctggtggaat ctcaagtggc gatattggag cttcaccatt caaccagaac 1080

ttcaactgca gcacattcct gcctcctttg cttacgccat tcgttagatc ctggctcgac 1140

agtggaagtg atcgagaagg agtcgctact gtgaccaact ggcagacaga gagtttcgag 1200

acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

gactacttca tccgaaacat ctctggagta cctctagtcg ttaggaacga agaccttcgt 1320

cgtcctctgc actacaatga gatcaggaac attgcctcac cttcgggtac acctggtgga 1380

gcacgagcat acatggtctc agttcacaac cgtaagaaca acatccatgc agttcatgag 1440

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca acggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 42

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 42

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Leu
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His

225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ala Asn Thr Thr Ala Arg Tyr Thr Phe Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 43

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 43

atgggaaact ctgtccttaa ttccggtcgt accacaatat gtgatgcata caacgtggca 60

gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagag ggaatggact 120

gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

agtggacctc agcaaaccca atcgttcacg agtcaagact ggccattcct gtatagcttg 900

ttccaggtca actccaacta cgtgctgaac ggcttctcag gtgctcgatt gtccaacact 960

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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

gactacttca tccgaaacat ctctggagta cctctagtcg ttaggaacga agaccttcgt 1320

cgtcctctgc actacaatga gatcaggaac attgcctcac cttcaggtac acctggtgga 1380

gcacgagcat acatggtctc agttcacaac cgtaagaaca acatccatgc agttcatgag 1440

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ggaaactctt acaacctata cttgcgtgtc tccagccttg gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagtgaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatgg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttcaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt ggcccattgt attag 1905

<210> 44

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 44

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Met Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Thr Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Leu Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Val Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Met Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Gly Pro Leu Tyr

625 630

<210> 45

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 45

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gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagag ggaatggact 120

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

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accatcaacg gtcgagtgta cacagtgaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatgg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttcaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccaatct attag 1905

<210> 46

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 46

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro

280

165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His

225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Thr Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Val Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Met Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr

625 630

<210> 47

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 47

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gctcacgacc ctttctcatt ccagcgcaaa tcactagaca ctgttcagag ggaatggact 120
gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180
ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240
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atgaacatca tgttcgttcc gacaaaccta ccaccattgt attag 1905

<210> 48

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 48

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln Arg Lys Ser Leu
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Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro

130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn

145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro

165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Arg Asp Phe Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His

225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Leu Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr

625 630

<210> 49

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 49

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

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tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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<210> 50

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 50

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Ser Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala

100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Gly Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu

465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Pro Tyr

530 535 540

Asp Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Ala

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Tyr Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 51

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 51

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gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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<210> 52

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 52

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn

65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 53

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 53

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<210> 54

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 54

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser

35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Arg

50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn

65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg

85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala

100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe

115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro

130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn

145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Val Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Met Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 55

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 55

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gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagga ggagtggatg 120

gagtggaaga aggacaatca ttcgctatat gttgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgcgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccgc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcag aatcacctgc gcaactacac gcgtgactac 660

tcaaactact gtttcaacac ctatcagacc gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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gtcaactact ctggtggagt ttcaagtggc gatattggag cttcgccgtt caaccagaac 1080

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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

gactacttca tccgaaacat ctctggagta cctctagtcg ttaggaacga agaccttcgt 1320

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aacggatcca tgatccactt ggctccagag gactacaccg gatttacaat cagtcctatc 1500

cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacattg gaaacgtagt cgcaagcagc 1800

aacagcgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgttcgttcc gacaaaccta ccaccattgt attag 1905

<210> 56

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 56

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Ala Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Phe Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Gly Asp

370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 57
<211> 1905
<212> ADN
<213> Bacillus thuringiensis

<400> 57
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gagtggaaga aggacaatca ttcgctatat gttgacccga tcgttggaac cgtggcttca 180
ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240
ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300
ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360
ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420
aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480
cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540
gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600
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tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

ggcgattctc tgaggtttga gcagagtaat accacggcaa ggtacactct caggggtaat 1620

ggaaactcct acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtggt cgcaagcagc 1800

aacagcgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgttcgttcc aacaaaccta ccaccattgt attag 1905

<210> 58

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 58

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Arg Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile

325

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn His Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr

625 630

<210> 59

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 59

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcga aaccatctga ggaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

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accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcgagcgac 1800

aacagcaacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgtttgttcc gacaaaccta ccaccattgt attag 1905

<210> 60

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 60

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Ala Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr

305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Ser Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 61

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 61

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<211> 634

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<213> Bacillus thuringiensis

<400> 62

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

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Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asp Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn

290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr

305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu

325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Ser Gln Ile
435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 63

<211> 1902

<212> ADN

<213> Bacillus thuringiensis

<400> 63

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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
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Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Val Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Arg Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn

290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr

305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu

325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn His Ile
435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Val Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile
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Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

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Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

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<211> 1902
<212> ADN
<213> Bacillus thuringiensis

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<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 66

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Pro Leu
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Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Thr Gln Thr Ala Thr Arg
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Leu His Gly Arg Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Ala Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

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Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr

625 630

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<213> Bacillus thuringiensis

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<210> 68

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 68

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Cys
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Val Gly Gly Phe Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val

360

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His

225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn

290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Thr Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr

625 630

<210> 69

<211> 1902

<212> ADN

<213> Bacillus thuringiensis

<400> 69

atgggacaca acgtccttaa ttccggtcgt accacaatat gtgatgcata caacgtggcc 60

gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagga ggagtggatg 120

gagtggaaga aggacaatca ttcgctatat gttgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggagc 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taagtgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcga aaccatctga ggaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

agtggacctc agcaaaccca atcgttcacg agtcaagact ggccattcct gtatagcttg 900

ttccaggtca actccaacta cgtgctgaac ggcttctcag gtgctcgatt gtcccagact 960

ttcccaaaca tcgttggact tccaggaaca actacgactc atgccttgct ggctgcacga 1020

gtcaactact ctggtggagt ttcaagtggc gatattggag cttcgccgtt caaccagaac 1080

ttcagttgca gcacattcct gcctccttig cttacgccat tcgttagatc ctggctcgac 1140

agtggaagtg atcgaggggg agttaatact gtgaccaact ggcagacaga gagtttcgag 1200

acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

gactacttca tccaaaacat ctctggagta cctctagtcg ttaggaacga agaccttcgt 1320

cgtcctctgc actacaatca gatcaggaac attgagtcac cttcaggtac acctggtgga 1380

gcacgagcat acatggtctc agttcacaac cgtaagaaca acatctacgc agttcatgag 1440

aacggaacga tgatccactt ggctccagag gaccacaccg gatttacaat cagtcctatc 1500

cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

ggcgattctc tgaggtttga gcagagtaat accacggcaa ggtacactct caggggtaat 1620

ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcgagggac 1800

aacagcaacg tacctctgga cattaacgtt acgttgaact cgggcacaca gttcgatttg 1860

atgaacatca tgtttgttcc gacaaaccta ccaccattgt at 1902

<210> 70

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 70

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn

145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Ser Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Gln Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp His Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Arg Asp Asn Ser Asn Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 71

<211> 1902

<212> ADN

<213> Bacillus thuringiensis

<400> 71

atgggacaca acgtccttaa ttccggtcgt accacaatat gtgatgcata caacgtggcc 60

gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagga ggagtggatg 120

gagtggaaga aggacaatca ttcgctatat gttgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggagc 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgaga gaccgagaag 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgactggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcga aaccatctga ggaactacac gcgtgactac 660

tcaaactact gtatcagcac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgctttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

agtggacctc agcaaaccca atcgttcacg agtcaagact ggccattcct gtatagcttg 900

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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcgagcgac 1800

aacagcaacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgtttgttcc gacaaaccta ccaccattgt at 1902

<210> 72

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 72

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe

115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Ser Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Ser Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 73

<211> 1902

<212> ADN

<213> Bacillus thuringiensis

<400> 73

atgggacaca acgtccttaa ttccggtcgt accacaatat gtgatgcata caacgtggcc 60
gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagga ggagtggatg 120
gagtggaaga aggacaatca ttcgctatat gttgacccga tcgttggaac cgtggcttca 180
ttcttgctca aaaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240
ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300
ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggc 360
ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420
aacgccgtgc ctttgtctat tacgccgtcc gtcaacacga tgcagcagct attcttgaac 480
cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540
gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcag aatcacctgc gcaactacgc gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcgggtg ctaacctata cgcaagtgga 840

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagc 1800

aacagcgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgttcgttcc gacaaaccta ccaccattgt at 1902

<210> 74

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 74

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg

85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Pro Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn His Leu Arg Asn Tyr Ala Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu

465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 75
<211> 1902
<212> ADN
<213> Bacillus thuringiensis

<400> 75
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ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgccatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcag aatcacctgc gcaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

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cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

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gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagc 1800

aacagcgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgttcgttcc gacaaaccta ccaccattgt at 1902

<210> 76

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 76

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys

50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Ala
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu

465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 77
<211> 1902
<212> ADN
<213> Bacillus thuringiensis

<400> 77

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cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

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gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagc 1800

aacagcgacg tacctctgga cattaacgtt acgttgaact caggcgcaca gttcgatttg 1860

atgaacatca tgttcgttcc gacgaaccta ccaccattgt at 1902

<210> 78

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 78

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu

20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Leu Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr His Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Ala Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr

625 630

<210> 79

<211> 1902

<212> ADN

<213> Bacillus thuringiensis

<400> 79

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tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

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aacagcgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgttcgttcc gacaaaccta tcaccattgt at 1902

<210> 80

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 80

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn His Leu Arg Asn His Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Ser Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Ser Pro Leu Tyr
625 630

<210> 81
<211> 1902
<212> ADN
<213> Bacillus thuringiensis

<400> 81
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atatcggcag ctacactacg tacttatcga aaccatctga ggaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcaagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcgagcgac 1800

aacagcaacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgtttgttcc gacaaaccta ccaccattgt at 1902

<210> 82

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 82

Met Gly His Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Ala Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Val Glu Arg Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asp Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu

325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asp Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile

435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Arg Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Gln Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr

625 630

<210> 83

<211> 1902

<212> ADN

<213> Bacillus thuringiensis

<400> 83

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggtcc 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtgg gaccgagaag 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gactacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagaca gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac gtacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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acaacactcg gtctacgatc aggagcattc acagcaaaag gaaacagcaa ctacttccca 1260

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cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

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ggaaactctt acgacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgttgt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgtcgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt at 1902

<210> 84

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 84

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Gly Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn

290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Lys Gly Asn Ser
405 410 415

420

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asp Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Ser Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 85

<211> 1902

<212> ADN

<213> Bacillus thuringiensis

<400> 85

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggtcc 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attggaaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcag aactacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagaca gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcgggtg ctaacctata cgcaagtgga 840

agtggaccac aacagagaca atcgttcacg agtcaagact ggccattcct gtatagcttg 900

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gtcaactact ctggtggaat ctcaagtggc gatattggag cttcaccatt caaccagaac 1080

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accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt at 1902

<210> 86

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 86

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Glu Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Arg Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn

290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr

305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Asn Thr Thr Thr His Ala Leu

325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 87

<211> 1902

<212> ADN

<213> Bacillus thuringiensis

<400> 87

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aacgccgtgc cttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gactacctga ggaactacac gcgtgactac 660

tcaaactact gtatcaacac ctaccagaca gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ccaacctata cgcaagtgga 840

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accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt at 1902

<210> 88

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 88

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Lys Gly Leu Asn Thr Arg Leu His

225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 89

<211> 1902

<212> ADN

<213> Bacillus thuringiensis

<400> 89

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gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg aactacctga ggaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagaca gccttcaaag gcctgaatac aaggctccac 720

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<210> 90

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 90

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
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Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Arg Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Arg Asn Tyr Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Val Thr Asn Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 91

<211> 1902

<212> ADN

<213> Bacillus thuringiensis

<400> 91

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag tttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

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tcaaactact gtatcaacac ctatcagaca gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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<210> 92

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 92

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Gly Thr Glu Arg Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro

165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Lys Gly Leu Asn Thr Arg Leu His

225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Ser Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Arg Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 93

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 93

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aacgccgtgc ccttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

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atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcggtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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<210> 94

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 94

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Val Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn His Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro

130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Arg Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 95

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

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atatcggcag ctacactacg tacttatagg aactacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagaca gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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cgtcctctgc actacaatga gatcaggaac attgcctcac cttcaggtac acctggtgga 1380

gcacgagcat acatggtctc agttcacaac cgtaagaaca acatccatgc agttcatgag 1440

aacggatcaa tgatccactt ggctccaaac gactacaccg gatttacaat cagtcctatc 1500

cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

ggcgattctc tgaggtttga gcagaacaat accacggcaa ggtacactct caggggtaat 1620

ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 96

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 96

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala

100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe

115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Val Val Pro

130 135 140

Leu Ser Ile Met Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn

145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro

165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Arg Asn Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu

485 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 97

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 97

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga tcctctcgga actaaggtcc 240

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ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggctacctc aattccagat gagacaatac caactcttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg aactacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagaca gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

agtggacctc agcaaaccca atcgttcacg agtcaagact ggccattcct gtatagcttg 900

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ttcaactgca gcacattcct gcctccttig cttacgccat tcgttagatc ctggctcgac 1140

agtggaagtg atcgagaagg agtcgctact gtgaccaact ggcagacaga gagtttcgag 1200

acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

gactacttca tccgaaacat ctctggagta cctctagtcg ttaggaacga agaccttcgt 1320

cgtcctctgc actacaatga gatcaggaac attgcctcac cttcaggtac acctggtgga 1380

gcacgagcat acatggtctc agttcacaac cgtaagaaca acatccatgc agttcatgag 1440

aacggatcaa tgatccactt ggctccaaac gactacaccg gatttacaat cagtcctatc 1500

cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

ggcgattctc tgaggtttga gcagaacaat accacggcaa ggtacactct caggggtaat 1620

ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 98

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 98

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser

65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg

85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala

100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe

115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro

130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn

145 150 155 160

Arg Leu Pro Gln Phe Gln Met Arg Gln Tyr Gln Leu Leu Leu Leu Pro

165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Ser Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 99

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 99

atgggaaact ctgtccttaa ttccggtcgt accacaatat gtgatgcata caacgtggca 60

aacggatcaa tgatccactt ggctccaaac gactacaccg gatttacaat cagtcctatc 1500

cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

ggcgattctc tgaggtttga gcagaacaat accacggcaa ggtacactct caggggtaat 1620

ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 100

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 100

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser

35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys

50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn

65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg

85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala

100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe

115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Val Val Pro

130 135 140

Leu Ser Ile Met Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn

145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 101

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 101

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ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cgattacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcag gactacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagaca gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

agtggacctc agcaaaccca atcgttcacg agtcaagact ggccattcct gtatagcttg 900

ttccaggtca actccaacta cgtgctgcac ggcttctcag gtgctcgatt gtccaacact 960

ttcccaaaca tcgttggact tccaggaagc actacgactc atgccttgct ggctgcacga 1020

gtcaactact ctggtggaat ctcaagtggc gatattggag cttcaccatt caaccagaac 1080

ttcaactgca gcacattcct gcctccttg cttacgccat tcgttagatc ctggctcgac 1140

agtggaagtg atcgagaagg agtcgctact gtgaccaact ggcagacaga gagtttcgag 1200

acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

gactacttca tccgaaacat ctctggagta cctctagtcg ttaggaacga agaccttcgt 1320

cgtcctctgc actacaatga gatcaggaac attgcctcac cttcaggtac acctggtgga 1380

gcacgagcat acatggtctc agttcacaac cgtaagaaca acatccatgc agttcatgag 1440

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 102

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 102

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Ala Thr Ile Cys Asp Ala

1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu His Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

485

370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu

465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 103

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 103

atgggaaact ctgtccttaa ttccggtcgt accacaatat gtgatgcata caacgtggca 60

gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagag ggaatggact 120

gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggggt 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatagg caagttgaca acttcctaaa tcccactcaa 420

aacgcagtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccaagt gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtgggac 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag ccctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cacaagtgga 840

agtggacctc agcaagccca atcgttcacg agtcaagact ggccattcct gtatagcttg 900

ttccaggtca actccaacta cgtgctgaac ggcttctcag gtgctcgatt gtccaacact 960

ttcccaaaca tcgttggact tccaggaagc actacgactc atgccttgct ggctgcacga 1020

gtcaactact ctggtggaat ctcaagtggc gatattggag cttcaccatt caaccagaac 1080

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accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttcaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccaatct attag 1905

<210> 104

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 104

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Gly
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Thr Gln Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Val Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Ala Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Thr Ser Gly Ser Gly Pro Gln Gln Ala Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Thr Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr
625 630

<210> 105

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 105

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actatggggt 240

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ctacgggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcaa 420

aacgcagtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacttggg cttcatcagg gatgtcgtcc taaatgcaga cgagtggggc 600

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tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aagactccac 720

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cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

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accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 106

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 106

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Ala Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Trp Gly
85 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Arg Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Gln Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Gly Phe Ile Arg Asp Val
180 185 190

Val Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Ala Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Gly Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Ser Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr

305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

500

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu

465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 107

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 107

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

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gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

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gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 108

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 108

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Val Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ser Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Gln Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu Tyr Phe Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 109

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 109

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

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atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccaatct attag 1905

<210> 110

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 110

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Trp Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Thr Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Val Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr
625 630

<210> 111
<211> 1905
<212> ADN
<213> Bacillus thuringiensis

<400> 111
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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180
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atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagaca gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcatgtgga 840

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accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctagtacc gacaaacatt agcccattgt attag 1905

<210> 112

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 112

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Glu
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

520

210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Cys Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Ser Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagag ggaatggact 120

gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

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aacgtcgtgc ctttgtctat tatgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg aactacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagaca gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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gcacgagcat acatggtctc agttcacaac cgtaagaaca acatccatgc agttcatgag 1440

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 113

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 113

atgggaaact ccgtccttaa ttccggtcgt accacaatat gtgatgcata caacgtggca 60

gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagag ggaatggact 120

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ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagcaa 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctgcactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgctttta agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

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aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 114

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 114

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Ala Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Thr
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

530

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Met Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 115

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 115

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgccatcc taaatgcaga cgagtggggc 600

atatcggcag ccacactacg tacttatcag gactacctga agaactacac gcgtgactac 660

tcaaactact gtatcagcac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcgggtg ctaacctata cgcaagtgga 840

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accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 116

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 116

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu

20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Arg Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn

145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro

185 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Ala

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Gln Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Ser Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His

225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Ala Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 117

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 117

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gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagag ggaatggact 120

gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgtcggaac cgtggcttca 180

ttcttgctca agaaggtcgg ttctctcgtc ggtaagagga ttctctcgga actaaggaac 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcag gtatcgagga gttcaatcga caagttgaca acttcctaaa tcccaatcgt 420

aacgcagtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

agtggacctc agcaaaccca atcgttcacg agtcaagact ggccattcct gtatagcttg 900

ttccaggtca actccaacta cgtgctgaac ggcttctcag gtgctcgatt gtccaacact 960

ttcccaaaca tcgttggact tccaggaagc actacgactc atgccttgct ggctgcacga 1020

gtcaactact ctggtggaat ctcaagtggc gatattggag cttcaccatt caaccagaac 1080

ttcaactgca gcacattcct gcctcctttg cttacgccat tcgttagatc ctggctcgac 1140

agtggaagtg atcgagaagg agtcgctact gtgaccaact ggcagacaga gagtttcgag 1200

acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

gactacttca tccgaaacat ctctggagta cctctagtcg ttaggaacga agaccttcgt 1320

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gcacgagcat acatggtctc agttcacaac cgtaagaaca acatccatgc agttcatgag 1440

aacggatcaa tgatccactt ggctccaaac gactacaccg gatttacaat cagtcccatc 1500

cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac gtcaacatgg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatcg tgctggtacc gacaaacatt agcccaatct attag 1905

<210> 118

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 118

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Gly Ile Glu Glu Phe

115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Val Asn

580 585 590

Met Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Val
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr
625 630

<210> 119

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 119

atgggaaact ctgtccttaa ttccggtcgt accacaatat gtgatgcata caacgtggca 60

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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agtggaagtg atcgagaagg agtcgctact gtgaccaact ggcagacaga gagtttcgag 1200

acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

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cgtcctctgc actacaatga gatcaggaac attgcctcac cttcaggtac acctggtgga 1380

gcacgagcat acatggtctc agttcacaac cgtaagaaca acatccatgc agttcatgag 1440

aacggatcaa tgatccactt ggctccaaac gactacaccg gatttacaat cagtcctatc 1500

cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 120

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 120

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg

85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 121
<211> 1905
<212> ADN
<213> Bacillus thuringiensis

<400> 121
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gagtggaaga aggacaatca ttcgctatat gttgacccga tcgttggaac cgtggcttca 180
ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

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ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcag aatcacctgc gcaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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gtcaactact ctggtggagt ttcaagtggc gatattggag cttcgccgtt caaccagaac 1080

ttcagttgca gcacattcct gcctccttg cttacgccat tcgttagatc ctggctcgac 1140

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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagc 1800

aacagcgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgttcgttcc gacaaaccta ccaccattgt attag 1905

<210> 122

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 122

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys

50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu

465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 123
<211> 1905
<212> ADN
<213> Bacillus thuringiensis

<400> 123

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gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagag ggaatggact 120

gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

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ctacaggcaa atgtcgagga gttcaataga caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccaagt gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaata tgcacctgag cttcatcagg gatgtcgtcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gagggaatac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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gtaaacgaca atggtgctcg tttcagcgac atcaaaatgg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttcaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc aacaaacatt agcccaatct attag 1905

<210> 124

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 124

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu

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Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser

35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys

50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Leu Glu Leu Arg Asn

65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg

85 90 95

Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala

100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe

115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro

130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Val Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val
180 185 190

Val Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Glu Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Ser Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

643
642

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Trp Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Lys

580 585 590

Met Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr

625 630

<210> 125

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 125

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cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

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tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

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gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcgagcgac 1800

aacagcaacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgtttgttcc gacaaaccta ccaccattgt attag 1905

<210> 126

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 126

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Pro
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Gly Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 127

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 127

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ttcttgctca agaaggtcgg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240

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aacgcagtgc cttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

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gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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<210> 128

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 128

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Ser Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Ser Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Arg Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val
180 185 190

Val Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu Arg
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn His Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu

325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Met Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr
625 630

<210> 129

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 129

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atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 130

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 130

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Trp Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Arg Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Arg Val Asn

290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Ser Gln Asn Phe Asn Cys Ser Thr Phe Thr Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Arg Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp His Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Tyr Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asn Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 131
<211> 1905
<212> ADN

<213> Bacillus thuringiensis

<400> 131

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

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ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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ttcccaaaca tcgttggact tccaggaagc actacgactc atgccttgct ggctgcacga 1020

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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

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gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 132

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 132

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn

290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr

305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu

325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 133

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 133

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgtcggaac cgtggcttca 180

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ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagcaa 300

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ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc tgaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

ggtacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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agtggaagtg atcgagaagg agtcgctact gtgaccaact ggcagacaga gagtttcgag 1200

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gcacgagcat acatggtctc agttcacaac cgtaagaaca acatccatgc agttcatgag 1440

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttcaact caggcacaca gttcgatttg 1860

atgaacacca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 134

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 134

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asp Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His

600

225 230 235 240

Gly Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Thr Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 135

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 135

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

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<210> 136

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 136

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

610

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 137

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 137

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actatggggc 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga aatgacaggt 360

5 ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcaa 420

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cggttacctc aattcagagt gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

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15 ttcccaaaca tcgttggact tccaggaagc actacgactc atgccttgct ggctgcacga 1020

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aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

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<210> 138

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 138

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Leu Phe Gln His Lys Ser Leu
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Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Trp Gly
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Met Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Gln Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Leu Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Arg Val Gln Gly Tyr Gln Leu Leu Leu Leu Pro

165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Val Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Ser Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Ser Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Lys Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 139

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 139

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcatt ggtaagagga ttctctcgga actaaggaac 240

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agggccgtgc acttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gcggctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcagg cgagtggggc 600

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gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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gtaaacgaca atggtgctcg cctcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

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atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 140

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 140

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

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Tyr Asp Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Glu Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Pro Arg Arg Ala Val His

130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn

145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro

165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val

180 185 190

Ile Leu Asn Ala Gly Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Gln Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Lys Gly Leu Asn Thr Arg Leu His

225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Met Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Leu Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 141

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 141

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gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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atgaacatca tgtttgttcc gacaaaccta ccaccattgt attag 1905

<210> 142

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 142

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala

100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe

115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro

130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn

145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro

165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu

465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr

625 630

<210> 143

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 143

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcag aatcacctgc gcaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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aacagcaacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgaattg 1860

atgaacatca tgttcgttcc gacaaaccta tcaccattgt attag 1905

<210> 144

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 144

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn

65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Ser Pro Leu Tyr
625 630

<210> 145

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 145

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gagtggaaga aggacaatca ttcgctatat gttgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggagc 240

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ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcga aaccatctga ggaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

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cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

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accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcgagcgac 1800

aacagcaacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgtttgttcc gacaaaccta ccaccattgt attag 1905

<210> 146

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 146

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser

35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys

50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser

65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg

85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala

100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe

115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro

130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn

145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 147

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 147

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgtcggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaat 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagcaa 300

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ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc tgaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

ggtacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgctttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttcaact caggcacaca gttcgatttg 1860

atgaacacca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 148

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 148

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asp Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

650

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Gly Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Thr Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 149

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 149

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

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aacgccgtgc ttttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 150

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 150

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Leu
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 151

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 151

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gctgctaata tgcacctgag cttcatcagg gaagtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

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aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

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<210> 152

<211> 633

<212> PRT

<213> Bacillus thuringiensis

<400> 152

Met Gly Asn Ser Val Leu Asn Ser Gly His Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
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Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu His
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Trp Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Ser Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Glu Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr

305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Ser Thr Ile Gly Ile Arg Ser Arg Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu

465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Gly Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Thr Arg Thr Phe Ile

500 505 510

Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln Asn

515 520 525

Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr Asn

530 535 540

Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val Thr

545 550 555 560

Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr Asn
565 570 575

Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn Met
580 585 590

Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile Asn
595 600 605

Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met Leu
610 615 620

Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 153

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 153

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gagtggaaga agaacaatca ttcgctatat gttgacccgg tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacgcga tgcagcagct attcttgaac 480

cggttaccac aattccagat gcaaggctac cagttgttgt tactcccgtt attcgcccaa 540

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gtaaacgaca acggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

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<210> 154

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 154

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Thr Arg Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Val Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asp Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Ala Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Leu Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 155

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 155

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<210> 156

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 156

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

680

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn

290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr

305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu

325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr

625 630

<210> 157

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 157

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aacgccgtgc ccttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagct gaataatcgt caattgttgt tactcccgtt attcgcccaa 540

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tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

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<210> 158

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 158

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Gly Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Leu Asn Asn Arg Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Gly
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

690

580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr

625 630

<210> 159

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 159

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240

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ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ttttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

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cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

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accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 160

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 160

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu

20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser

35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys

50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Leu
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His

225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn

290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 161

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 161

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gagtggaaga aggacaatca ttcgctatat gttgacccga tcgttggaac cgtggcttca 180

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ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcag aatcacctgc gcaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgttggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

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gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagc 1800

aacagcgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgttcgttcc gacaaaccta ccaccgttgt attag 1905

<210> 162

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 162

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu

20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Arg
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn

145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro

165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His

225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asp Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Gly Gln

515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr

625 630

<210> 163

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 163

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

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tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 164

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 164

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe

115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 165

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 165

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gagtggaaga aggacaatca ttcgctatat gttgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggagc 240

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcga aaccatctga ggaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

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<210> 166

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 166

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
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Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg

85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Ser Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val Arg Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 167
<211> 1905
<212> ADN
<213> Bacillus thuringiensis

<400> 167
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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccaagt gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

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aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccaatct attag 1905

<210> 168

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 168

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Arg His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys

50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Gln Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Val Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val
180 185 190

Val Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu

465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Met Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr
625 630

<210> 169

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 169

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<210> 170

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 170

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Pro

20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser

35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys

50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser

65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg

85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala

100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe

115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro

130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile

435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu

465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Gly Gln

515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr

625 630

<210> 171

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 171

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tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

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accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagc 1800

aacagcgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgttcgttcc gacaaaccta ccaccattgt attag 1905

<210> 172

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 172

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 173

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 173

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gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagga ggagtggatg 120

gagtggaaga aggacaatca ttcgctatat gttgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggagc 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcga aaccatctga ggaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

agtggacctc agcaaaccca atcgttcacg agtcaagact ggccattcct gtatagcttg 900

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ttcccaaaca tcgttggact tccaggaaca actacgactc atgccttgct ggctgcacga 1020

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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

gactacttca tccgaaacat ctctggagta cctctagtcg ttaggaacga agaccttcgt 1320

cgtcctctgc actacaatca gatcaggaac attgagtcac cttcaggtac acctggtgga 1380

gcacgagcat acatggtctc agttcacaac cgtaagaaca acatctacgc agttcatgag 1440

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cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

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gggaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcgagcgac 1800

aacagcaacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgtttgttcc gacaaaccta ccaccattgt attag 1905

<210> 174

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 174

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu

325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile

435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 175

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 175

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

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ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatcga caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatgg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccaatct attag 1905

<210> 176

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 176

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Arg His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Leu
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn

290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Met Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr
625 630

<210> 177

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 177

atgggaaact ctgtccttaa ttccggtcgt accacaatat gtgatgcata caacgtggca 60

gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagag ggaatggact 120

gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctcttgga actaaggaac 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagcaa 300

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ctacaggcaa atgtcgagga gttcaatagc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccaagt gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaata tgcacctgag cttcatcagg gatgtcgtcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gagggaatac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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ggcgattctc tgaggtttga gcagaacaat accacggcaa ggtacactct ctggggtaat 1620

ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgacggt 1740

gtaaacgaca atggtgctcg tttcagcgac atcaaaatgg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttcaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc aacaaacatt agcccaatct attag 1905

<210> 178

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 178

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Leu Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Val Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val
180 185 190

Val Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Glu Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn

290 295 300

Ser Asn Tyr Val Leu Asn Ser Phe Ser Gly Ala Arg Leu Ser Asn Thr

305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu

325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Trp Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Lys

580 585 590

Met Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr

625 630

<210> 179

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 179

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaagagt 240

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccaaat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gagggactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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ttcccaaaca tcgttggact tccaggaagc actacgactc atgccttgct ggctgcacga 1020

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acaacactcg gtctacggtc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

gactacttca tccgaaacat ctctggagta cctctagtcg ttaggaacga agaccttcgt 1320

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatgg gaaacgtagt cgtaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

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<210> 180

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 180

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Leu Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Lys Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His

225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Met Gly Asn Val Val Val Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr

625 630

<210> 181

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 181

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 182

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 182

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 183

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 183

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 184

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 184

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro

165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His

225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Ala Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Thr Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 185

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 185

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcga aaccatctga ggaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcgagcgac 1800

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<210> 186

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 186

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Pro
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro

130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Gly Gln

515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr

625 630

<210> 187

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 187

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cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

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gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 188

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 188

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala

100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn His Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Val Thr Asn Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu

465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 189

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 189

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cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaata tgcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

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tcaaactact gtatcaacac ctaccagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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<210> 190

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 190

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu

20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser

35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys

50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Trp Gly

65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Arg Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Glu Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Pro Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Ser Thr Ile Gly Ile Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Met Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 191

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 191

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<210> 192

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 192

Met Gly Asn Ser Val Leu Asn Ser Ser Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser

35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Gly Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Arg Gly Tyr Gln Ser Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asp Tyr Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Gly Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Ala Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 193

<211> 1906

<212> ADN

<213> Bacillus thuringiensis

<400> 193

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gagtggaaga aggacaatca ttcgctatat attgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggagc 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

ttcctgaacc agcgactgaa cgcggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc cttgtctat tacgtcgtcc gtcaacatga tgcagcagct attcttgaac 480

cggttacctc aattccagct acgtgatccc caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcga aaccatctga ggaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gccgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcgagcgac 1800

aacagcaacg tacctctgga cattaacgtt gcgttgaact caggcacaca gttcgatttg 1860

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<210> 194

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 194

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Ile Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Ala Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Met Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Leu Arg Asp Pro Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Val Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asp Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile
595 600 605

Asn Val Ala Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Val Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr

625 630

<210> 195

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 195

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actatggaat 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

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ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctata tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccaagt gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc tgaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatgc aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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gtaaacgaca atggtgctcg cttcagcgac atcaacatgg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttcaact caggcacaca gttcgatttg 1860

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<210> 196

<211> 834

<212> PRT

<213> Bacillus thuringiensis

<400> 196

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Trp Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Tyr Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Val Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Ala Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Ala
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Met Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 197

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 197

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagtt aggtgaatat caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcga aaccatctga ggaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcgagcgac 1800

aacagcaacg tacctctgga cattaacgtt acgttgaact caggcataca gttcgatttg 1860

atgaacatca tgtttgttcc gacaaaccta ccaccattgt attag 1905

<210> 198

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 198

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Leu Gly Glu Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Ser Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Val Arg Leu Ser Gln Thr

305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu

325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile

340 345 350

Gly Ala Arg Thr Ala Gly Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Ser Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Ala Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Ile Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr

625 630

<210> 199

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 199

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcag aatcacctgc gcaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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agtggaagtg atcgaggggg agttaatact gtgaccaact ggcagacaga gagtttcgag 1200

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagc 1800

aacagcgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

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<210> 200

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 200

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 201

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 201

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

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ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 202

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 202

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

850

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 203

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 203

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcga aaccatctga ggaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcgagcgac 1800

aacagcaacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgtttgttcc gacaaaccta ccaccattgt attag 1905

<210> 204

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 204

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr

625 630

<210> 205

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 205

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccaaat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gagggactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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gtaaacgaca atggtgctcg cttcagcgac atcaacatgg gaaacgtagt cgtaagcagt 1800

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atgaacatca tgctggtacc gacaaacatt agcccaatct attag 1905

<210> 206

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 206

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Leu Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Lys Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Met Gly Asn Val Val Val Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr

625 630

<210> 207

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 207

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ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actatggaat 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctata tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccaagt gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc tgaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatgc aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

gactacttca tccgaaacat ctctggagta cccctagtcg ttaggaacga agaccttcgt 1320

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cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggct 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatgg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttcaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 208

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 208

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu

20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Trp Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Tyr Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn

145 150 155 160

Arg Leu Pro Gln Phe Gln Val Gln Gly Tyr Gln Leu Leu Leu Leu Pro

165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Ala Arg Leu His

225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Ala
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Met Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 209

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 209

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gagtggaaga aggacaatca ttcgctatat gttgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcag aatcacctgc gcaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

agtggacctc agcaaaccca atcgttcacg agtcaagact ggccattcct gtatagcttg 900

ttccaggtca actccaacta cgtgctgaac ggcttctcag gtgctcgatt gtcccagact 960

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ttcagttgca gcacattcct gcctcctttg cttacgccat tcgttagatc ctggctcgac 1140

agtggaagtg atcgaggggg agttaatact gtgaccaact ggcagacaga gagtttcgag 1200

acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

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cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

ggcgattctc tgaggtttga gcagagtaat accacggcaa ggtacactct caggggtaat 1620

ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagc 1800

aacagcgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgttcgttcc gacaaaccta ccaccattgt attag 1905

<210> 210

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 210

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe

115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr

625 630

<210> 211

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 211

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

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aacgcagtgc ctttgtctat tacgtcgtcc gttaacacga tgcagcagct attcttgagc 480

cggttacctc aattccaagt gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaata tgcacctgag cttcatcagg gatgtcgtcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatgg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttcaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccaatct attag 1905

<210> 212

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 212

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Trp Gly
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg

85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Ser
145 150 155 160

Arg Leu Pro Gln Phe Gln Val Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val
180 185 190

Val Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Ser Thr Ile Gly Ile Arg Cys Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Gly Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Met Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr

625 630

<210> 213

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 213

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gagtggaaga aggacaatca ttcgctatat gttgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggagc 240

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ctacaggcaa gtgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctgt tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagtt gcgtggacac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcga aaccatctga ggaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

agtggacctc agcaaaccca atcgttcacg agtcaagact ggccattcct gtatagcttg 900

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ttcccaaaca tcgttggact tccaggaaca actacgactc atgccttgct ggctgcacga 1020

gtcaactact ctggtggagt ttcaagtggc gatattggag cttcgccgtt caaccagaac 1080

ttcagttgca gcacattcct gcctccttg cttacgccat tcgttagatc ctggctcgac 1140

agtggaagtg atcgaggggg agttaatact gtgaccaact ggcagacaga gagtttcgag 1200

acaacactcg gtctacgatc aggagcattc acagcgagag gaaacagcaa ctacttccca 1260

gactacttca tccgaaacat ctctggagta cctctagtcg ttaggaacga agaccttcgt 1320

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gcacgagcat acatggtctc agttcacaac cgtaagaaca acatctacgc agttcatgag 1440

aacggaacga tgatccactt ggctccagag gactacaccg gatttacaat cagtcctatc 1500

cacgccactc aggcgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

ggcgattctc tgaggtttga gcagagtaat accacggcaa ggtacactct caggggtaat 1620

ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gccgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcgagcgac 1800

aacagcaacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgtttgttcc gacaaaccta ccaccattgt attag 1905

<210> 214

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 214

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

His Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln Arg Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Gly Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys

50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Ser Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Val Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Leu Arg Gly His Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile

435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu

465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Ala Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 215
<211> 1905
<212> ADN
<213> Bacillus thuringiensis

<400> 215

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttactca agaaggtcgg ttctctcgtc ggtaagagga ttctctcgga actatggaat 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagcaa 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gagggactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttga agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

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accatcaacg gtcgggtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatgg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttcaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccaatct attag 1905

<210> 216

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 216

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu

20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser

35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys

50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Trp Asn

65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg

85 90 95

Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala

100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe

115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro

130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Lys Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu

465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Pro Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Met Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr

625 630

<210> 217

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 217

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattcagagt gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcgtcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttcaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccaatct attag 1905

<210> 218

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 218

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Arg Val Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Val Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu

465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Ala Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr
625 630

<210> 219

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 219

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gagtggaaga aggacaatca ttcgctatat gttgacccga tcgttggaac cgtggcttca 180
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aacgccgtgc ccttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480
cggttacctc aattccagct gaataatcgt caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcga aaccatctga ggaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720

gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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gcacgagcat acatggtctc agttcacaac cgtaagaaca acatctacgc agttcatgag 1440

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gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcgagcgac 1800

aacagcaacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgtttgttcc gacaaaccta ccaccattgt attag 1905

<210> 220

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 220

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Gly Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Leu Asn Asn Arg Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu

325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Gly

370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile

435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr

625 630

<210> 221

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 221

atgggaaact ctgtccttaa ttccggtcgt accacaatat gtgatgcata caacgtggca 60

gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagag ggaatggact 120

gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggggt 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

ttcctgaacc agcgactgga cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccaaat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcgtcc taaatgcaga cgagtggggc 600

gtatcggcag ctacactacg tacttatagg gattacctga agaactacac gacggactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

agtggacctc agcaaaccca atcgttcacg agtcaagact ggccattcct gtatagcttg 900

ttccaggtca actccaacta cgtgctgaac ggcttctcag gtgctcgatt gtccaacact 960

ttcccaaaca tcggtggact tccaggaagc actacgactc atgccttgct ggctgcacga 1020

gtcaactact ctggtggaat ctcaagtggc gatattgggg cttcaccatt caaccagaac 1080

ttcaactgca gcacattcct gcctccttg cttacgccat tcgttagatc ctggctcgac 1140

agtggaagtg atcgagaagg agtcgctact gtgaccaact ggcagacaga gagtttcgag 1200

acaacactcg gtctacggtc cggagcattc acagcaagag gaaacagcaa ctacttccca 1260

gactacttca tccgaaacat ctctggagta cctctagtcg ttaggaacga agaccttcgt 1320

cggcctctgc actacaatga gatcaggaac attgcctcac cttcaggtac acctggtgga 1380

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cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac catcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccaatct attag 1905

<210> 222

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 222

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Gly
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asp Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Val Leu Asn Ala Asp Glu Trp Gly Val Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Thr Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn

290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Val His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr
625 630

<210> 223

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 223

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gagtggaaga aggacaatca ttcgctatat gttgacccga tcgttggaac cgtggcttca 180
ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggagc 240
ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300
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ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420
aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480
cggttaccac aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540
gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600
atatcggcag ctacactacg tacttatcga aaccatctga ggaactacac gcgtgactac 660
tcaaactact gtatcaacac ctatcagact gccttccgtg gcctgaatac aaggctccac 720
gatatgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780
tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840
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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

gactacttca tccgaaacat ctctggagta cctctagtcg ttaggaacga agaccttcgt 1320

cgtcctctgc actacaatca gatcaggaac attgagtcac cttcaggtac acctggtgga 1380

gcacgagcat acatggtctc agttcacaac cgtaagaaca acatctacgc agttcgtgag 1440

aacggaacga tgatccactt ggctccagag gactacaccg gatttacaat cagtcctatc 1500

cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

ggcgattctc tgaggtttga gcagagtaat accacggcaa ggtacactct caggggtaat 1620

ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcgagcgac 1800

aacagcaacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgacttg 1860

atgaacatca tgtttgttcc gacaaaccta ccaccattgt attag 1905

<210> 224

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 224

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn

290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr

305 310 315 320

Phe Pro Ser Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu

325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val Arg Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr

625 630

<210> 225

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 225

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gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagag ggaatggact 120

gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgctttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 226

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 226

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His

225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 227

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 227

atgggaaact ctgtccttaa ttccggtcgt accacaatat gtgatgcata caacgtggca 60

gctcacgacc cttcctcatt ccagcacaaa tcactagact ctgttcagag ggaatggact 120

gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtcgg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

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aacgcagtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

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atgaacatca tgctggtacc gacaaacatt agcccaatct attag 1905

<210> 228

<211> 834

<212> PRT

<213> Bacillus thuringiensis

<400> 228

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Ser Ser Phe Gln His Lys Ser Leu
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Asp Ser Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Arg Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val
180 185 190

Val Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu Arg
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn His Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Met Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr

625 630

<210> 229

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 229

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

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<210> 230

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 230

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Trp Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Tyr Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Val Gln Gly Tyr Gln Leu Leu Leu Leu Pro

165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Ala Arg Leu His

225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Ala
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Met Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 231

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 231

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<210> 232

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 232

Met Gly His Asn Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser
35 40 45

Leu Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro His Pro Thr Ile Ser His

130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Val Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn His Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Ser Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Ser Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Gln Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Arg Leu Asp Ser Gly Ser Asp
370 375 380

Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile
435 440 445

Arg Asn Ile Glu Ser Pro Pro Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475 480

Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Arg Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Ala Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Asp Asn Ser Asn Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Phe Val Pro Thr Asn Leu Pro Pro Leu Tyr
625 630

<210> 233
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<212> ADN
<213> Bacillus thuringiensis

<400> 233
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<210> 234

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<212> PRT

<213> Bacillus thuringiensis

<400> 234

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asp His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Trp Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Glu Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala

100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe

115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Gln Asn Ala Val Pro

130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn

145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro

165 170 175

Leu Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu

485 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asp

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 235

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 235

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actatggaat 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctata tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccaagt gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc tgaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatgc aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

agtggacctc agcaaaccca atcgttcacg agtcaagact ggccattcct gtatagcttg 900

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agtggaagtg atcgagaagg agtcgctact gtgaccaact ggcagacaga gagtttcgag 1200

acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

gactacttca tccgaaacat ctctggagta cccctagtcg ttaggaacga agaccttcgt 1320

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cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggct 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatgg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttcaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 236

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 236

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Trp Asn

65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Tyr Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Val Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Ala Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Ala
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Met Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 237

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 237

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gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagag ggaatggact 120

gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcag gactacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagaca gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

agtggacctc agcaaaccca atcgttcacg agtcaagact ggccattcct gtatagcttg 900

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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

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cgtcctctgc actacaatga gatcaggaac attgcctcac cttcaggtac acctggtgga 1380

gcacgagcat acatggtctc agttcacaac cgtaagaaca acatccatgc agttcatgag 1440

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cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

ggcgattctc tgaggtttga gcagaacaat accacggcaa ggtacactct caggggtaat 1620

ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cgcagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 238

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 238

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu

20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser

35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

1085
1054

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu

465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Gly Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Ala Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 239

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 239

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gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagag ggaatggact 120

gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

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gacaccgtgc ccttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caactgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

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accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 240

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 240

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala

1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Glu Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Leu Asp Thr Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu

465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 241

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 241

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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

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cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

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atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

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gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttcaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccaatct attag 1905

<210> 242

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 242

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
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Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

1069
1069

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val His Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

1072
1091

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr
625 630

<210> 243
<211> 1905
<212> ADN
<213> Bacillus thuringiensis

<400> 243
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gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180
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ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctata tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccaagt gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc tgaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

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atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 244

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 244

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Trp Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Tyr Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Val Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Ala Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr

1000

305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Ala
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Met Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 245

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 245

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gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

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atgaacatca tgctggtacc gacaaacatt agcccaatct attag 1905

<210> 246

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 246

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Gly
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asp Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Val Leu Asn Ala Asp Glu Trp Gly Val Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Thr Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Val His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr
625 630

<210> 247

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 247

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atatcggcag ctacactacg tacttatagg gattacctga agaactacac gagggactac 660

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<210> 248

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 248

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Thr Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser

275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu His Ser Leu Phe Gln Val Asn

290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr

305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu

325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Ile Tyr
625 630

<210> 249
<211> 1905
<212> ADN
<213> Bacillus thuringiensis

<400> 249
atgggaaact ctgtccttaa ttccggtcgt accacaatat gtgatgcata caacgtggca 60
gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagag ggaatggact 120
gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180
ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240
ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300
ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360
ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccaatcgt 420
aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480
cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540
gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600
atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

agtggacctc agcaaaccca atcgttcacg agtcaagact ggccattcct gtatagcttg 900

ttccaggtca actccaacta cgtgctgaac ggcttctcag gtgctcgatt gtccaacact 960

ttcccaaaca tcgttggact tccaggaagc actacgactc atgccttgct ggctgcacga 1020

gtcaactact ctggtggaat ctcaagtggc gatattggag cttcaccatt caaccagaac 1080

ttcaactgca gcacattcct gcctcctttg cttacgccat tcgttagatc ctggctcgac 1140

agtggaagtg atcgagaagg agtcgctact gtgaccaact ggcagacaga gagtttcgag 1200

acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

gactacttca tccgaaacat ctctggagta cctctagtcg ttaggaacga agaccttcgt 1320

cgtcctctgc actacaatga gatcaggaac attgcctcac cttcaggtac acctggtgga 1380

gcacgagcat acatggtctc agttcacaac cgtaagaaca acatccatgc agttcatgag 1440

aacggatcaa tgatccactt ggctccaaac gactacaccg gatttacaat cagtcctatc 1500

cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

ggcgattctc tgaggtttga gcagaacaat accacggcaa ggtacactct caggggtaat 1620

ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 250

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 250

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile

340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro

355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp

370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu

385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser

405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 251

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 251

atgggaaact ctgtccttaa ttccggtcgt accacaatat gtgatgcata caacgtggca 60

gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagag ggaatggact 120

gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggtcc 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caggttgaca acctcctaaa tcccaatcgt 420

aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt actcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gactacctga ggaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

agtggacccc agcaaaccca atcgttcacg agtcaagact ggccatttcct gtatagcttg 900

ttccaggtca actccaacta cgtgctgaac ggcttctcag gtgctcgatt gtccaacact 960

ttcccaaaca tcgttggact tccaggaagc actacgactc atgccttgct ggctgcacga 1020

gtcaactact ctggtggaat ctcaagtggc gatattggag cttcaccatt caaccagaac 1080

ttcaactgca gcacattcct gcctccttg cttacgccat tcgttagatc ctggctcgac 1140

agtggaagtg atcgagaagg agtcgctact gtgaccaact ggcagacaga gagtttcgag 1200

acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

gactacttca tccgaaacat ctctggagta cctctagtcg ttaggaacga agaccttcgt 1320

cgtcctctgc actacaatga gatcaggaac attgcctcac cttcaggtac acctggtgga 1380

gcacgagcat acatggtctc agttcacaac cgtaagaaca acatccatgc agttcatgag 1440

aacggatcaa tgatccactt ggctccaaac gactacaccg gatttacaat cagtcctatc 1500

cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

ggcgattctc tgaggtttga gcagaacaat accacggcaa ggtacactct caggggtaat 1620

ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 252

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 252

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Leu Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Leu Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 253

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 253

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gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagag ggaatggact 120

gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatcag gactacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagaca gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

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ggcgattctc tgaggtttga gcagaacaat accacggcaa ggtacactct caggggtaat 1620

ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cgcagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 254

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 254

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Ala Thr Ile Cys Asp Ala

1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu

20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn

145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro

165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val

180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr

195 200 205

Tyr Gln Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys

210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Lys Gly Leu Asn Thr Arg Leu His

225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr

245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser

260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr
485 490 495

Ile Gly Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Ala Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 255

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 255

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gagtggaaga agaacaatca ttcgccatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggaac 240

ttgatcttcc cctccggtag cacaaatctc atgcaggata tactccgtga gaccgagaag 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attgacaggc 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tcccccttg 420

agcattgtgc ccttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacctc aattccagat gcaacaatac caactcttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctaccagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc actgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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ttcccaaaca tcgttggact tccaggaagc actacgactc atgccttgct ggctgcacga 1020

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ttcaactgca gcacattcct gcctcctttg cttacgccat tcgttagatc ctggctcgac 1140

agtggaagtg atcgagaagg agtcgctact gtgaccaact ggcagacaga gagtttcgag 1200

acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

gactacttca tccgaaacat ctctggagta cctctagtcg ttaggaacga agaccttcgt 1320

cgtcctctgc actacaatga gatcaggaac attgcctcac cttcaggtac acctggtgga 1380

gcacgagcat acatggtctc agttcacaac cgtaagaaca acatccatgc agttcatgag 1440

aacggatcaa tgatccactt ggctccaaac gactacaccg gatttacaat cagtcctatc 1500

cacgccactc aggtgaacaa ccagactcga acgttcatca gtgagaagtt tggaaaccaa 1560

ggcgattctc tgaggtttga gcagaacaat accacggcaa ggtacactct caggggtaat 1620

ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 256

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 256

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Arg Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Pro Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe

115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Pro Leu Ser Ile Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gln Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr
450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu
465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 257

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 257

atgggaaact ctgtccttaa ttccggtcgt accacaatat gtgatgcata caacgtggca 60

gctcacgacc ctttctcatt ccagcacaaa tcactagaca ctgttcagag ggaatggact 120

gagtggaaga agaacaatca ttcgctatat ctcgacccga tcgttggaac cgtggcttca 180

ttcttgctca agaaggtggg ttctctcgtt ggtaagagga ttctctcgga actaaggtcc 240

ttgatcttcc cctccggtag cacaaatctc atgcaggaca tactccgtga gaccgagaag 300

ttcctgaacc agcgactgaa cacggacacc ttggcacgag ttaatgctga attggaaggt 360

ctacaggcaa atgtcgagga gttcaatcgc caagttgaca acttcctaaa tccccctaga 420

gacattgtgc ccttgtctat tacgtcgtcc gtcaacacga tgcaacagct attcttgaac 480

cggttacctc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcaga cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagaca gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ccaacctata cgcaagcgga 840

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acaacactcg gtctacgatc aggagcattc acagcaagag gaaacagcaa ctacttccca 1260

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gcacgagcat acatggtctc agttcacaac cgtaagaaca acatccatgc agttcatgag 1440

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cacgccactc aggtgaacaa ccagactcga acgttcgtca gtgagaagtt tggaaaccaa 1560

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accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 258

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 258

Met Gly Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Trp Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg

85 90 95

Glu Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Glu Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Pro Arg Asp Ile Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Gly Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu
420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu

465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Val Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val

545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr

565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn

580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile

595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met

610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr

625 630

<210> 259

<211> 1905

<212> ADN

<213> Bacillus thuringiensis

<400> 259

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gctcacgacc ctttctcatt ccagcacaaa ccactagaca ctgttcagag ggaatggact 120

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aacgccgtgc ctttgtctat tacgtcgtcc gtcaacacga tgcagcagct attcttgaac 480

cggttacccc aattccagat gcaaggctac caattgttgt tactcccgtt attcgcccaa 540

gctgctaatc ttcacctgag cttcatcagg gatgtcatcc taaatgcagg cgagtggggc 600

atatcggcag ctacactacg tacttatagg gattacctga agaactacac gcgtgactac 660

tcaaactact gtatcaacac ctatcagtcc gccttcaaag gcctgaatac aaggctccac 720

gatacgttgg agtttcggac atacatgttc ctgaacgtgt tcgagtatgt ctccatctgg 780

tcgcttttca agtaccagtc attgctggtc tcgtcaggtg ctaacctata cgcaagtgga 840

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ggaaactctt acaacctata cttgcgtgtc tccagcatag gcaattcaac tatcagggtt 1680

accatcaacg gtcgagtgta cacagctaca aacgtcaata ccaccactaa caacgatggt 1740

gtaaacgaca atggtgctcg cttcagcgac atcaacatcg gaaacgtagt cgcaagcagt 1800

aacagtgacg tacctctgga cattaacgtt acgttgaact caggcacaca gttcgatttg 1860

atgaacatca tgctggtacc gacaaacatt agcccattgt attag 1905

<210> 260

<211> 634

<212> PRT

<213> Bacillus thuringiensis

<400> 260

Met Gly Asn Ser Val Leu Asp Ser Gly Arg Thr Thr Ile Cys Asp Ala
1 5 10 15

Tyr Asn Val Ala Ala His Asp Pro Phe Ser Phe Gln His Lys Pro Leu
20 25 30

Asp Thr Val Gln Arg Glu Trp Thr Glu Arg Lys Lys Asn Asn His Ser
35 40 45

Leu Tyr Leu Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys

50 55 60

Lys Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Ser
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Lys Leu Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Glu Gly Leu Gln Ala Asn Val Glu Glu Phe
115 120 125

Asn Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val
180 185 190

Ile Leu Asn Ala Gly Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Arg Asp Tyr Leu Lys Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Ser Ala Phe Lys Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Thr Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Ser Asn Thr
305 310 315 320

Phe Pro Asn Ile Val Gly Leu Pro Gly Ser Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Ile Ser Ser Gly Asp Ile
340 345 350

Gly Ala Ser Pro Phe Asn Gln Asn Phe Asn Cys Ser Thr Phe Leu Pro
355 360 365

Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp
370 375 380

Arg Glu Gly Val Ala Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu
385 390 395 400

Thr Thr Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser
405 410 415

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu

420 425 430

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile

435 440 445

Arg Asn Ile Ala Ser Pro Ser Gly Thr Pro Gly Gly Ala Arg Ala Tyr

450 455 460

Met Val Ser Val His Asn Arg Lys Asn Asn Ile His Ala Val His Glu

465 470 475 480

Asn Gly Ser Met Ile His Leu Ala Pro Asn Asp Tyr Thr Gly Phe Thr

485 490 495

Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe

500 505 510

Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln

515 520 525

Asn Asn Thr Thr Ala Arg Tyr Thr Leu Lys Gly Asn Gly Asn Ser Tyr

530 535 540

Asn Leu Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val
545 550 555 560

Thr Ile Asn Gly Arg Val Tyr Thr Ala Thr Asn Val Asn Thr Thr Thr
565 570 575

Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn
580 585 590

Ile Gly Asn Val Val Ala Ser Ser Asn Ser Asp Val Pro Leu Asp Ile
595 600 605

Asn Val Thr Leu Asn Ser Gly Thr Gln Phe Asp Leu Met Asn Ile Met
610 615 620

Leu Val Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

<210> 261
<211> 632
<212> PRT
<213> Bacillus thuringiensis

<400> 261

Met Asn Asn Val Leu Asn Asn Gly Arg Thr Thr Ile Cys Asp Ala Tyr
1 5 10 15

Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser Leu Asp
20 25 30

Thr Ile Arg Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His Ser Leu
35 40 45

Tyr Val Ala Pro Ile Val Gly Thr Val Ser Ser Phe Leu Leu Lys Lys
50 55 60

Val Gly Ser Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Trp Gly Leu
65 70 75 80

Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg Glu
85 90 95

Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala Arg
100 105 110

Val Asn Ala Glu Leu Glu Gly Leu Gln Ala Asn Ile Arg Glu Phe Asn
115 120 125

Gln Gln Val Asp Asn Phe Leu Asn Pro Thr Gln Asn Pro Val Pro Leu
130 135 140

Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn Arg
145 150 155 160

Leu Pro Gln Phe Arg Val Gln Gly Tyr Gln Leu Leu Leu Leu Pro Leu
165 170 175

Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val Val
180 185 190

Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr Tyr
195 200 205

Gln Asn Tyr Leu Lys Asn Tyr Thr Thr Glu Tyr Ser Asn Tyr Cys Ile
210 215 220

Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His Asp
225 230 235 240

Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr Val
245 250 255

Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser Gly
260 265 270

Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser Phe
275 280 285

Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn Ser
290 295 300

Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Thr Gln Thr Phe
305 310 315 320

Pro Asn Ile Gly Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu Leu
325 330 335

Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile Gly
340 345 350

Ala Val Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro Pro Leu

355 360 365

Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp Arg Gly

370 375 380

Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu Ser Thr

385 390 395 400

Leu Gly Leu Arg Cys Gly Ala Phe Thr Ala Arg Gly Asn Ser Asn Tyr

405 410 415

Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val Val

420 425 430

Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile Arg Asn

435 440 445

Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr Met Val

450 455 460

Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu Asn Gly

465 470 475 480

Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr Ile Ser
485 490 495

Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe Ile Ser
500 505 510

Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln Ser Asn
515 520 525

Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr Asn Leu
530 535 540

Tyr Leu Arg Val Ser Ser Leu Gly Asn Ser Thr Ile Arg Val Thr Ile
545 550 555 560

Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr Asn Asn
565 570 575

Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Leu Asp Ile Asn Met Gly
580 585 590

Asn Val Val Ala Ser Asp Asn Thr Asn Val Pro Leu Asp Ile Asn Val
595 600 605

Thr Phe Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met Phe Val
610 615 620

Pro Thr Asn Leu Pro Pro Ile Tyr
625 630

REIVINDICACIONES:

1. Una molécula de ácido nucleico aislada que comprende cualquiera de SEQ ID Nº 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, o un complemento de ésta.

2. Una molécula de ácido nucleico aislada seleccionada del grupo que consiste en:

a) una molécula de ácido nucleico que comprende una secuencia de nucleótidos que es al menos 95% idéntica a la secuencia de nucleótidos de cualquiera de SEQ ID Nº 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, o un complemento de ésta;

b) una molécula de ácido nucleico que codifica un polipéptido que comprende la secuencia de aminoácidos de cualquiera de SEQ ID Nº 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260;

c) una molécula de ácido nucleico que hibridiza con una sonda de ácido nucleico que consiste en la secuencia de nucleótidos de cualquiera de SEQ ID Nº 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, o un complemento de ésta, después de al menos un lavado en SSC 0,2X a 55ºC por 20 minutos; y

d) un fragmento que comprende al menos 600 nucleótidos consecutivos de cualquiera de SEQ ID Nº 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119,

121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259.

3. La molécula de ácido nucleico aislada de la reivindicación 2, donde la molécula de ácido nucleico codifica un polipéptido que comprende al menos un aminoácido seleccionado del grupo que consiste en H_2, S_7, Q_{27}, Q_{35}, E_{36}, K_{43}, D_{44}, N_{45}, D_{51}, A_{58}, V_{69}, R_{78}, N_{79}, K_{99}, T_{118}, V_{124}, E_{125}, R_{129}, N_{138}, R_{139}, A_{141}, T_{162}, Q_{185}, M_{186}, L_{183}, I_{192}, H_{211}, R_{213}, R_{217}, D_{218}, V_{324}, I_{366}, T_{399}, S_{405}, Q_{446}, I_{551}, S_{587}, I_{591}, L_{610} y L_{631}.

4. La molécula de ácido nucleico aislada de la reivindicación 1 ó 2, donde la molécula de ácido nucleico codifica un polipéptido con actividad insecticida.

5. La molécula de ácido nucleico aislada de la reivindicación 4, donde los dípteros o los lepidópteros son susceptibles a la actividad insecticida del polipéptido.

6. Un vector que comprende una molécula de ácido nucleico de la reivindicación 1 ó 2.

7. El vector de la reivindicación 6, que es un vector de expresión.

8. Una célula huésped que comprende el vector de la reivindicación 6 ó 7.

9. La célula huésped de la reivindicación 8, donde la célula se selecciona del grupo que consiste en una célula vegetal, una célula bacteriana, una célula fúngica.

10. Un polipéptido aislado que comprende cualquiera de SEQ ID Nº 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100,

102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260.

11. Un polipéptido aislado seleccionado del grupo que consiste en:

a) un polipéptido que es al menos 95% idéntico a la secuencia de aminoácidos de cualquiera de SEQ ID Nº 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260;

b) un polipéptido que está codificado por una molécula de ácido nucleico que comprende una secuencia de nucleótidos que es al menos 95% idéntico a cualquiera de SEQ ID Nº 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227,

229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, o un complemento de éstas;

c) un polipéptido que está codificado por una molécula de ácido nucleico que hibridiza con una sonda de ácido nucleico que consiste en la secuencia de nucleótidos de cualquiera de SEQ ID Nº 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, o un complemento de ésta, después de al menos un lavado en SSC 0,2X a 55ºC por 20 minutos;

d) un fragmento que comprende al menos 200 aminoácidos consecutivos de cualquiera de SEQ ID Nº 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260.

12. El polipéptido aislado de la reivindicación 11, donde el polipéptido comprende al menos un aminoácido seleccionado del grupo que consiste en H_2, S_7, Q_{27}, Q_{36}, E_{36}, K_{43}, D_{44}, N_{46}, D_{61}, A_{68}, V_{89}, R_{76}, N_{79}, K_{99}, T_{118}, V_{124}, E_{125}, R_{129}, N_{138}, R_{139}, A_{141}, T_{162}, Q_{165}, M_{166}, L_{183}, I_{192}, H_{211}, R_{213}, R_{217}, D_{218}, V_{324}, I_{366}, T_{366}, S_{405}, Q_{445}, I_{551}, S_{587}, I_{591}, L_{610} y L_{631}.

13. El polipéptido aislado de la reivindicación 10 u 11, donde el polipéptido tiene actividad insecticida.

14. El polipéptido aislado de la reivindicación 13, donde los dípteros o los lepidópteros son susceptibles a la actividad insecticida del polipéptido.

15. Una planta transgénica que comprende un transgen que expresa

(a) un polipéptido de cualquiera de SEQ ID Nº 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260; o

(b) una molécula de ácido nucleico de cualquiera de SEQ ID Nº 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203,

205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259.

16. La planta transgénica de la reivindicación 15, donde la planta se selecciona del grupo que consiste en maíz, soja, papa y algodón.

17. La planta transgénica de la reivindicación 15, donde la planta transgénica presenta mayor resistencia a un insecto plaga en comparación con una planta que no es transgénica.

18. La planta transgénica de la reivindicación 17, donde el insecto plaga es un díptero o un lepidóptero.

19. Una planta transgénica que comprende un transgen que expresa

(a) un polipéptido de la reivindicación 11, o

(b) una molécula de ácido nucleico de la reivindicación 2.

20. La planta transgénica de la reivindicación 19, donde la planta se selecciona del grupo que consiste en maíz, soja, papa y algodón.

21. La planta transgénica de la reivindicación 19, donde la planta transgénica presenta mayor resistencia a un insecto plaga en comparación con una planta que no es transgénica.

22. La planta transgénica de la reivindicación 21, donde el insecto plaga es un díptero o un lepidóptero.

23. Una composición que comprende uno o más polipéptidos de SEQ ID Nº 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98,

100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260 y un agente, donde el agente se selecciona del grupo que consiste en coadyuvantes dispersantes-adhesivos, agentes estabilizadores, aditivos insecticidas, diluyentes, agentes tensioactivos, emulsificantes y dispersantes.

24. La composición de la reivindicación 23, donde la composición comprende además células.

25. La composición de la reivindicación 24, donde las células están completas o lisadas.

26. La composición de la reivindicación 25, donde las células están en suspensión o precipitadas.

27. La composición de la reivindicación 23, donde la composición comprende además un complejo de esporas-cristales de *Bacillus thuringiensis*.

28. La composición de la reivindicación 23, donde el polipéptido está purificado.

NUEVOS POLIPÉPTIDOS CRISTALINOS Y POLINUCLEÓTIDOS DE BACILLUS THURINGIENSIS Y COMPOSICIONES CON LOS MISMOS

RESUMEN

Polipéptidos insecticidas relacionados con polipéptidos Cry 2 de *Bacillus*. También se proveen los ácidos nucleicos que codifican los polipéptidos de la invención. Se proveen métodos para usar los polipéptidos y ácidos nucleicos de la invención para mejorar la resistencia de plantas a la predación por insectos.

#53
1152

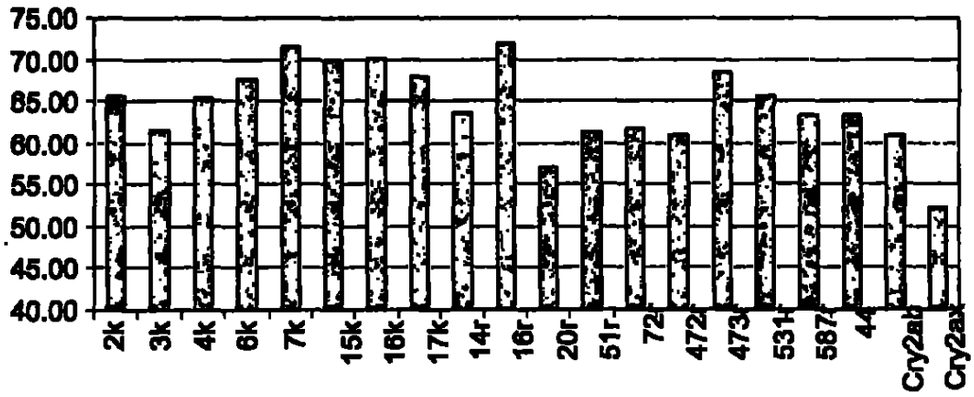

75.00
70.00
65.00
60.00
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45.00
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2k
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15k
16k
17k
14r
16r
20r
51r
72
472
473
531
587
44
Cry2ab
Cry2ax

FIG. 1

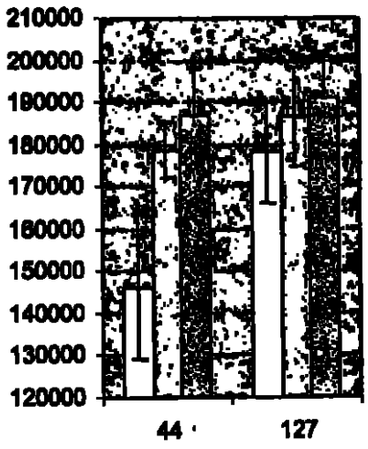

210000
200000
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127

FIG. 2

#55
1154

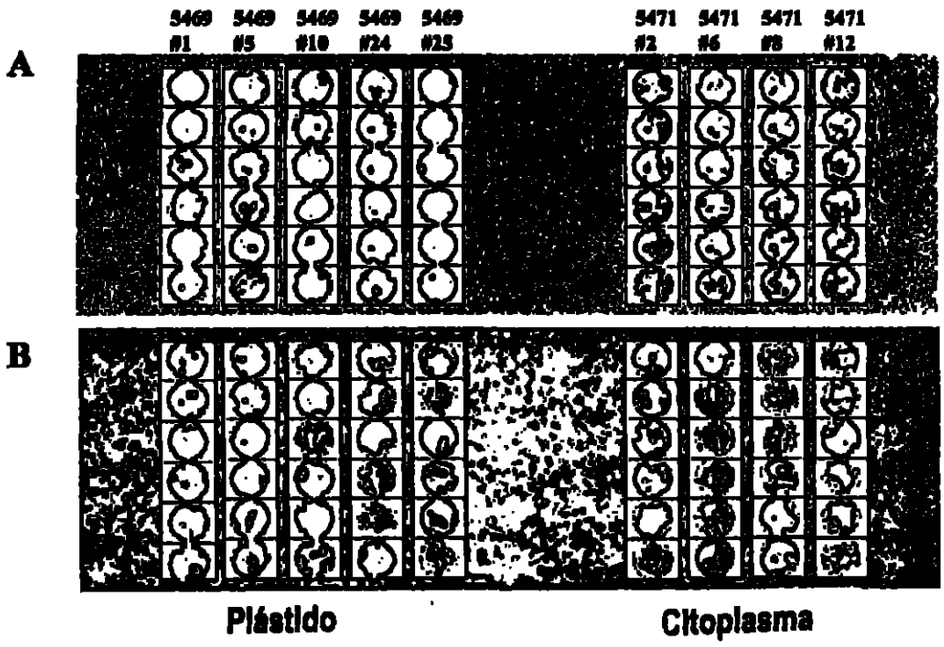

5469 #1
5469 #5
5469 #10
5469 #24
5469 #25
5471 #2
5471 #6
5471 #8
5471 #12
A
B
Plástido
Citoplasma

FIG. 3

456
155

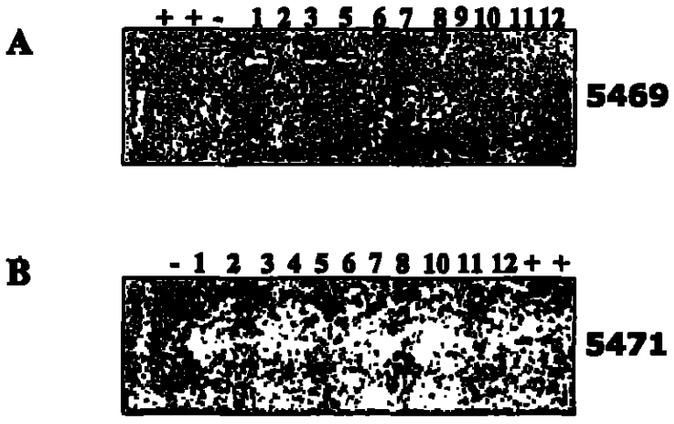


FIG. 4

1157

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO
Rad: 08-064256- -00000-0000
Fec: 2008-08-25 15:08:40 Dep: 2020 NUECREACIONE
Tra: 11 PATENTEYM
Eve: 378 FASENACIONALI
Act 411 PRESENTACION Folios: 1158

1156

Industria y Comercio
SUPERINTENDENCIA

REQUISITOS MINIMOS PARA ADMISION A TRAMITE
PCT

PATENTE DE INVENCION [✓] MODELO DE UTILIDAD [ ]

- ◇ Indicación de que se solicita la concesión de una patente [✓]
- ◇ Datos de identificación del solicitante o de la persona que presenta la solicitud [✓]
- ◇ Descripción de la invención [✓]
- ◇ Dibujos de ser estos pertinentes [ ]
- ◇ Comprobante de pago de las tasas establecidas [✓]

COMPLETA [✓] INCOMPLETA [ ]

DISEÑO INDUSTRIAL [ ]

- ◇ Indicación de que se solicita el registro de Diseño Industrial [ ]
- ◇ Datos de identificación del solicitante o de la persona que presenta la solicitud [ ]
- ◇ Representación gráfica y fotográfica del Diseño Industrial o muestra del material que incorpora el diseño [ ]
- ◇ Comprobante de pago de las tasas establecidas [ ]

COMPLETA [ ] INCOMPLETA [ ]

ESQUEMA DE TRAZADO [ ]

- ◇ Indicación de que se solicita el registro de un Esquema de Trazado [ ]
- ◇ Datos de identificación del solicitante o de la persona que presenta la solicitud [ ]
- ◇ Representación gráfica del esquema trazado [ ]
- ◇ Comprobante de pago de las tasas establecidas [ ]

COMPLETA [ ] INCOMPLETA [ ]

Firma Responsable

Fecha_____

Carrera 13 No. 27-00 Piso 5, 7 y 10
Conmutador: 3 82 08 40
Fax: 350 52 20
E-mail: info@sic.gov.co
www.sic.gov.co
Bogotá, D.C., Colombia

1157 - 1158

PETITORIO

Industria y Comercio
SUPERINTENDENCIA

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO
Rad: 06-084256- -00000-0000
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Tra: 11 PATENTEIYII
Eve: 378 FASENACIONALI
Act 411 PRESENTACION Folios: 1158

FORMULARIO UNICO DE SOLICITUD DE PATENTE
PCT
ENTRADA EN FASE NACIONAL

25/09/06

(1) SOLICITUD DE:

[X] Patente de Invención. [ ] Patente de Modelo de Utilidad.

[X] Capítulo I [ ] Capítulo II

(2) SOLICITANTE (71)

Nombre: PIONEEER HI-BRED INTERNATIONAL, INC.
Dirección: 7100 NW 62nd Avenue, P.O.BOX 1014, Johnston, IA 50131-1014, ESTADOS UNIDOS DE AMERICA
Nacionalidad o Domicilio: Johnston, IA, ESTADOS UNIDOS DE AMERICA
Lugar de Constitución:
Teléfono: Fax
E-mail:

IDENTIFICACIÓN
C.C. [ ] NIT [ ]
C.E. [ ] Otro [ ] Cual:
Número:

(3) REPRESENTANTE O APODERADO (74)

Nombre: MARGARITA CASTELLANOS A.
Dirección: CALLE 94A No. 7A-09
Teléfono: 610 7420 Fax: 610 0706
E-mail: info@castellanosyco.com

IDENTIFICACIÓN
C.C. [X] NIT [ ]
C.E. [ ] Otro Cual [ ]
Número 38779.664 TPA 70.819

(4) INVENTOR (ES) (72)

Nombre: ERICKA BERMUDEZ, ROBIN EMIG, KEVIN MCBRIDE, TAKASHI YAMAMOTO
Dirección: 734 Clubhouse Drive, Aptos, CA 95003, ESTADOS UNIDOS DE AMERICA; 1405 Marshall St. #715, Redwood City, CA 94063, ESTADOS UNIDOS DE AMERICA; 1306 Madina Circle, Davis, CA 95616, ESTADOS UNIDOS DE AMERICA; 3780 Tivoli Garden Terrace, Fremont, CA 94538, ESTADOS UNIDOS DE AMERICA.
Nacionalidad o Domicilio ESTADOUNIDENSES

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Solicitud Internacional No. PCT/US2006/006239 Fecha 23/02/2006
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(6) Título (54) NUEVOS POLIPEPTIDOS CRISTALINOS Y POLINUCLEOTIDOS DE BACILLUS THURINGIENSIS Y COMPOSICIONES CON LOS MISMOS

(7) Clasificación Internacional (51) C12N 15/32 1003 K 14/325 ; C12P 21/02 A01H 5/00

(8) Prioridad SI [X] NO [ ]

(33) País de Origen	(32) Fecha	(31) Número de Solicitud
US	25/02/2004	60/547,884

(9) Comprobante de pago No. 09- **Fecha** Agosto 25 de 2006

Instrucciones para el diligenciamiento del presente formulario, ver reverso de esta página.

REIVINDICACIONES:

1. Una molécula de ácido nucleico aislada que comprende cualquiera de SEQ ID Nº 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, o un complemento de ésta.

2. Una molécula de ácido nucleico aislada seleccionada del grupo que consiste en:

a) una molécula de ácido nucleico que comprende una secuencia de nucleótidos que es al menos 95% idéntica a la secuencia de nucleótidos de cualquiera de SEQ ID Nº 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, o un complemento de ésta;

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REPUBLICA DE COLOMBIA
SUPERINTENDENCIA DE INDUSTRIA Y COMERCI

Bogotá,
2020

Doctor(a)
CASTELLANOS ABONDANO MARGARITA

REFERENCIA	Radicación No.	06 84256
	Solicitud internacional	PCT/US2005/006238
	Fecha inicio fase nacional	25/09/2006
	Trámite	11
	Evento	378
	Actuación	430
	Oficio No.	00013560

Como resultado del examen de forma, realizado con fundamento en el artículo 38 de la Decisión 486 de la Comisión de la Commidad Andina, artículo 27 del Tratado de Cooperación en Materia de Patentes (PCT), regla 51 bis del Reglamento y Circular Única de la Superintendencia de Industria y Comercio, se le commica que:

1. La solicitud no contiene la copia del documento en que consta la cesión del derecho a la patente del inventor al solicitante o a su causante. (Art. 26-k) Decisión 486.

2. La solicitud no contiene el poder debidamente otorgado, con el lleno de los requisitos exigidos por los artículos 63 y subsiguientes del Código de Procedimiento Civil. Adicionalmente, deberá presentar el documento que acredita la existencia y representación legal de la sociedad solicitante, cuando ésta fuere persona jurídica.

En cumplimiento de lo dispuesto por el artículo 39 de la Decisión 486, se le requiere para que dentro del término de dos meses siguientes a la fecha de notificación del presente oficio, complete los requisitos anteriormente enunciados. En caso de no dar cumplimiento al presente requerimiento, la solicitud se considerará abandonada y perderá su prelación.

Notifíquese el presente oficio conforme a lo dispuesto en el numeral 5.2, literal e), del capítulo quinto del título primero de la Circular Unica No.10 de 2001.

ALIX CARMENZA CESPEDES DE VERGEL
Jefe de la división de Nuevas Creaciones

El anterior requerimiento fue notificado por fijación en lista de fecha 24 NOV. 2006
aalvarado