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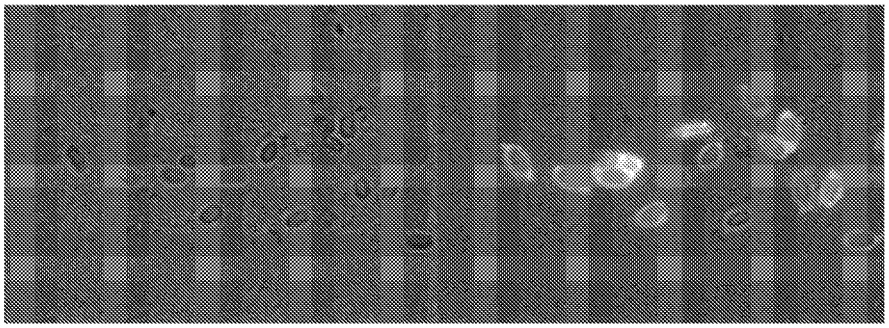
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(54) Title: ENDOSPORE DISPLAY PLATFORMS, PRODUCTS AND METHODS

FIG. 7A



(57) Abstract: Signal sequences useful for targeting proteins and peptides to the surface of endospores produced by *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* family members and methods of using the same are provided. The display of heterologous molecules, such as peptides, polypeptides and other recombinant constructs, on the exosporium of *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* family members, using particular N-terminal targeting sequences and derivatives of the same, and likewise are provided.

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*[Continued on next page]*

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# ENDOSPORE DISPLAY PLATFORMS, PRODUCTS AND METHODS

## CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Patent Application Nos. 62/768,077, 62/768,063, and 62/767,997, which were filed on November 15, 2018, the entire contents of each of which is incorporated herein by reference in its entirety.

## REFERENCE TO SEQUENCE LISTING SUBMITTED ELECTRONICALLY

[0002] The official copy of the sequence listing is submitted electronically via EFS-Web as an ASCII-formatted sequence listing with a file named "BCS189008WO_ST25.txt" created on November 13, 2019, and having a size of 169 kilobytes, and is filed concurrently with the specification. The sequence listing contained in this ASCII-formatted document is part of the specification and is herein incorporated by reference in its entirety.

## TECHNICAL FIELD

**[0003]** The disclosure provides products useful for various applications, such as delivering heterologous molecules of interest to plants. In particular, the disclosure describes endospore display methods and associated targeting sequences. For example, the disclosure provides N-terminal signal sequences useful for various applications, such as targeting heterologous proteins, peptides, and other recombinant constructs to the exosporium of *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus*, as well as endospores and methods of using the same. Such N-terminal signal sequences may be used as targeting signals for fusion proteins expressed in *Brevibacillus, Lysinibacillus*, or *Viridibacillus* species as disclosed herein, resulting in endospores with a molecule of interest localized on the exosporium surface. These endospores may be administered to a host, such as a plant host. The resulting platform is amenable to high through-put screening of proteins of interest for beneficial traits, such as agricultural traits (resistance to herbicides, promotion of plant growth and/or health, protection from insects, protection from fungal, bacterial or viral phytopathogens, etc.) The disclosure provides other related products and methods.

## BACKGROUND OF THE DISCLOSURE

**[0004]** Modern agricultural techniques rely heavily on compositions that promote or enhance plant health and growth in order to improve the yield and quality of crops. Such compositions generally include organic or inorganic fertilizers, nutrients and other chemical compounds that promote proper plant growth and development. However, it is well established

that long-term or overuse of many of these compositions may result in negative side effects, such as soil acidification or destabilization of the nutrient balance in the soil. Moreover, overuse may result in the enrichment of harmful end-products in crops grown for human consumption.

**[0005]** Modern farms also typically rely on the use of a wide variety of chemicals (e.g., insecticides, herbicides, bactericides, nematicides, and fungicides) to control pests and ensure a high yield of commercially-grown crops. Many of these chemical compounds exhibit broad activity and may be potentially harmful to humans and animals in high concentrations. In addition, some chemical compounds exhibit off-target effects. Moreover, at least some of these synthetic compounds are non-biodegradable. In recent years, there has been increasing pressure from consumers for agricultural products that have been raised and harvested with reduced or no exposure to synthetic insecticides or fungicides. A further problem arising with the use of synthetic insecticides or fungicides is that the repeated and/or exclusive use often leads to selection of resistant pests. Normally, resistant pests are also cross-resistant against other active ingredients having the same mode of action. As a result, pest control compositions and compounds are difficult and expensive to develop (e.g., due to safety concerns and the rapid development of resistance).

**[0006]** Genetic engineering methods have also been used to promote plant growth and/or health without reliance on synthetic chemicals. For example, crops can be modified to introduce or modify genes related to plant growth and/or health, and/or to introduce genes that encode natural or synthetic pest control agents. Transgenes may be introduced into a target plant using a viral vector. In recent years, there has been some success reported using bacteria for delivery of recombinant proteins to plants. However, to date, such success is largely limited to members of the *Bacillaceae* family and more specifically, *Bacillus subtilis*, which is the most well-characterized, Gram-positive bacteria and the primary bacterial model for sporulation research. The focus on *B. subtilis* as a delivery and expression platform is further due to the fact that the *B. subtilis* genome and biological pathways related to protein synthesis and secretion are well understood. However, due to the high degree of genetic diversity among bacteria, research findings based on *B. subtilis* studies are often not directly translatable to members inside and outside the *Bacillaceae* family. For example, *B. subtilis* endospores lack the exosporium layer that *B. cereus* family members produce.

**[0007]** Accordingly, while certain methods of delivering heterologous genetic materials are known, there is a need in the art for developing new delivery and expression platforms for such genetic materials.

## BRIEF SUMMARY OF EMBODIMENTS OF THE DISCLOSURE

**[0008]** The disclosure describes methods, compositions and genetic constructs that address the needs identified above by, for example, providing, among other things, a new platform for delivering recombinant enzymes and other molecules of interest (e.g., peptide, protein) to an environment (e.g., plant, field) using spore-forming members of the *Brevibacillus, Lysinibacillus,* or *Viridibacillus* genera.

**[0009]** In one aspect, the disclosure provides recombinant exosporium-producing *Brevibacillus, Lysinibacillus,* or *Viridibacillus* cells that express a fusion protein comprising: (i) at least one heterologous protein or peptide that confers or modifies a plant trait or attribute (e.g., an enzyme involved in the production or activation of a plant growth stimulating compound, an enzyme that degrades or modifies a bacterial, fungal, or plant nutrient source; or an enzyme, protein, or peptide that protects a plant from a pathogen or a pest); and (ii) an N-terminal targeting sequence that localizes the fusion protein to the exosporium of the respective *Brevibacillus, Lysinibacillus,* or *Viridibacillus* cells. This general composition may further include additional components (e.g., that promote plant growth and/or health). Moreover, particular embodiments of the methods disclosed herein provide for an efficient high-throughput screening of heterologous proteins and peptide that confer or otherwise modify plant traits or attributes. When reference is made in this disclosure to N-terminal signal peptides (or targeting sequences), or fusion proteins comprising the same, it is understood that suitable sequences for any such constructs must be selected based on the bacterial genus of the cell or endospore that will express the construct, and that intergeneric use is not envisioned by this disclosure. In other words, N-terminal targeting sequences compatible with *Brevibacillus* are shown in Table 1 and FIGs. 1-3, N-terminal targeting sequences compatible with *Lysinibacillus* are shown in Table 2 and FIGs. 4-5, and N-terminal targeting sequences compatible with *Viridibacillus* are shown in Table 3 and FIG. 6. Variants and fragments of these sequences that retain N-terminal targeting functionality in each of these respective bacterial genera are also disclosed herein.

**[0010]** In another aspect, the disclosure provides a nucleic acid molecule encoding a fusion protein, comprising (a) a first polynucleotide sequence encoding an N-terminal signal peptide, operably linked to (b) a second polynucleotide sequence encoding a polypeptide heterologous to the N-terminal signal peptide, wherein the first polynucleotide sequence comprises: (i) a polynucleotide sequence having at least 60%, 70%, or 80% sequence identity with any of the polynucleotide sequences disclosed in Tables 1 (for *Brevibacillus*), 2 (for *Lysinibacillus*), or 3 (for *Viridibacillus*); or (ii) a polynucleotide sequence comprising a fragment of at least 60 consecutive nucleotides of any of the polynucleotide sequences disclosed in Tables 1 (for *Brevibacillus*), 2 (for *Lysinibacillus*), or 3 (for *Viridibacillus*); and wherein the N-terminal

signal peptide is capable of targeting the fusion protein to an exosporium of a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore.

**[0011]** In selected aspects, the polypeptide heterologous to the N-terminal signal peptide comprises: (a) at least one of a plant growth or immune stimulating protein; (b) an enzyme; (c) a protein; (d) a polypeptide heterologous to *Brevibacillus, Lysinibacillus, or Viridibacillus*; or (e) a therapeutic protein. In selected aspects, the nucleic acid molecule further comprises a third polynucleotide sequence, encoding: (a) a polypeptide comprising one or more protease cleavage sites, wherein the polypeptide is positioned between the N-terminal signal peptide and the polypeptide heterologous to the N-terminal signal peptide; (b) a polypeptide comprising a selectable marker; (c) a polypeptide comprising a visualization marker; (d) a polypeptide comprising a protein recognition/purification domain; or (e) a polypeptide comprising a flexible linker element, which connects the N-terminal signal peptide and the polypeptide heterologous to the N-terminal signal peptide.

**[0012]** In selected aspects, the *Brevibacillus* endospore is an endospore formed by a *Brevibacillus* species, comprising: *B. agri, B. aydinogluensis, B. borstelensis, B. brevis, B. centrosporus, B. choshinensis, B. fluminis, B. formosus, B. fulvus, B. ginsengisoli, B. invocatus, B. laterosporus, B. levickii, B. limnophilus, B. massiliensis, B. nitrificans, B. panacihumi, B. parabrevis, B. reuszeri,* or *B. thermoruber.*

**[0013]** In select aspects, the *Lysinibacillus* endospore is an endospore formed by a *Lysinibacillus* species, comprising: *Lysinibacillus sphaericus, Lysinibacillus boronitolerans, Lysinibacillus fusiformis, Lysinibacillus acetophenoni, Lysinibacillus alkaliphilus, Lysinibacillus chungkukjangi, Lysinibacillus composti, Lysinibacillus contaminans, Lysinibacillus cresolivorans, Lysinibacillus macroides, Lysinibacillus manganicus, Lysinibacillus mangiferihumi, Lysinibacillus massiliensis, Lysinibacillus meyeri, Lysinibacillus odysseyi, Lysinibacillus pakistanensis, Lysinibacillus parviboronicapiens, Lysinibacillus sinduriensis, Lysinibacillus tabacifolii, Lysinibacillus varians, Lysinibacillus xylanilyticus,* or *Lysinibacillus halotolerans.*

**[0014]** In select aspects, the *Viridibacillus* endospore is an endospore formed by a *Viridibacillus* species, comprising: *Viridibacillus arvi, Viridibacillus arenosi*, or *Viridibacillus neidei.*

**[0015]** In selected aspects, the nucleic acid molecule is operatively linked to a promoter element that is heterologous to at least one of the second polynucleotide sequence and *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus.*

**[0016]** In selected aspects, the polypeptide heterologous to the N-terminal signal peptide comprises: (a) at least one of a plant growth or immune stimulating protein; (b) an enzyme; (c) a polypeptide heterologous to *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus;* (d) a therapeutic

protein (e.g., an antibiotic or anti-inflammatory protein); or (e) a protein that provides an agriculturally-significant property, included, but not limited to: insecticidal activity, fungicidal activity, plant growth, health or immune-stimulating activity, and/or improved environmental resistance. Other agriculturally-significant properties include improved crop characteristics including: emergence, crop yields, protein content, oil content, starch content, more developed root system, improved root growth, improved root size maintenance, improved root effectiveness, improved stress tolerance (e.g., against drought, heat, salt, UV, water, cold), reduced ethylene (reduced production and/or inhibition of reception), tillering increase, increase in plant height, bigger leaf blade, less dead basal leaves, stronger tillers, greener leaf color, pigment content, photosynthetic activity, less input needed (such as fertilizers or water), less seeds needed, more productive tillers, earlier flowering, early grain maturity, less plant verse (lodging), increased shoot growth, enhanced plant vigor, increased plant stand and early and better germination.

**[0017]** In selected aspects, the fusion protein further comprises: (a) a polypeptide containing one or more protease cleavage sites, positioned between the N-terminal signal peptide and the polypeptide heterologous to the N-terminal signal peptide; (b) a polypeptide comprising a selectable marker (e.g., a protein that confers resistance to an antibiotic); (c) a polypeptide comprising a visualization element (e.g., a fluorescent tag such as GFP); (d) a polypeptide comprising at least one protein recognition/purification domain (e.g., a HIS-tag); or (e) a polypeptide comprising a flexible linker element, connecting the signal peptide and the polypeptide heterologous to the N-terminal signal peptide.

**[0018]** In an alternative aspect, the disclosure provides a recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cell comprising a bacterial chromosome comprising a nucleic acid molecule of any one of the aspects disclosed herein.

**[0019]** In an alternative aspect, the disclosure provides a vector comprising a nucleic acid molecule of any one of the aspects disclosed herein, wherein the vector comprises a plasmid, an artificial chromosome, or a viral vector.

**[0020]** In selected aspects, the vector further comprising at least one of the following: (a) an origin of replication that provides stable maintenance in a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cell; (b) an origin of replication that provides selectively non-stable maintenance in the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cell; (c) a temperature-sensitive origin of replication that provides selectively non-stable maintenance in the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cell; (d) a polynucleotide encoding a selection marker, operably linked to an expression control sequence; or (e) a polynucleotide encoding a plant growth stimulating protein, operably linked to an expression control sequence;

**[0021]** In alternative aspects, the disclosure provides a recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cell transformed with a vector comprising the nucleic acid molecule of any one of the aspects disclosed herein.

**[0022]** In selected aspects, the *Brevibacillus* cell is a *Brevibacillus* species, comprising: *B. agri, B. aydinogluensis, B. borstelensis, B. brevis, B. centrosporus, B. choshinensis, B. fluminis, B. formosus, B. fulvus, B. ginsengisoli, B. invocatus, B. laterosporus, B. levickii, B. limnophilus, B. massiliensis, B. nitrificans, B. panacihumi, B. parabrevis, B. reuszeri,* or *B. thermoruber.*

**[0023]** In selected aspects, the *Lysinibacillus* cell is a *Lysinibacillus* species, comprising: *Lysinibacillus sphaericus, Lysinibacillus boronitolerans*, *Lysinibacillus fusiformis*, *Lysinibacillus acetophenoni*, *Lysinibacillus alkaliphilus*, *Lysinibacillus chungkukjangi*, *Lysinibacillus composti*, *Lysinibacillus contaminans*, *Lysinibacillus cresolivorans*, *Lysinibacillus macroides*, *Lysinibacillus manganicus*, *Lysinibacillus mangiferihumi*, *Lysinibacillus massiliensis*, *Lysinibacillus meyeri*, *Lysinibacillus odysseyi*, *Lysinibacillus pakistanensis*, *Lysinibacillus parviboronicapiens*, *Lysinibacillus sinduriensis*, *Lysinibacillus tabacifolii*, *Lysinibacillus varians*, *Lysinibacillus xylanilyticus,* or *Lysinibacillus halotolerans.*

**[0024]** In selected aspects, the *Viridibacillus* cell is a *Viridibacillus* species, comprising: *Viridibacillus arvi, Viridibacillus arenosi,* or *Viridibacillus neidei.*

**[0025]** In alternative aspects, the disclosure provides a composition comprising: a) one or more recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells that express the fusion protein of any one of the aspects disclosed herein, wherein the polypeptide heterologous to the N-terminal signal peptide comprises a plant growth or immune stimulating protein; and b) at least one biological control agent; optionally, in a synergistically effective amount.

**[0026]** In alternative aspects, the disclosure provides a seed treated with at least one of the nucleic acids, fusion proteins, bacterial cells or compositions of any one of the aspects disclosed herein.

**[0027]** In alternative aspects, the disclosure provides a method of treating a plant, a seed, a plant part, or the soil surrounding the plant to enhance plant growth and/or promote plant health comprising the step of simultaneously or sequentially applying: a) recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores that express the fusion protein of any of the aspects disclosed herein, wherein the polypeptide heterologous to the N-terminal signal peptide comprises a plant growth or immune stimulating protein; and b) at least one biological control agent; optionally, in a synergistically effective amount.

**[0028]** In alternative aspects, the disclosure provides a method of screening a host plant treated with a recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore, comprising

the following steps: a) applying a composition comprising a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore modified to express a fusion protein according to any of the aspects disclosed herein, to a seed, a seedling, or a vegetative plant capable of being permanently or transiently colonized by a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus*, to produce a treated seed, seedling, or vegetative plant; b) screening the treated seed, seedling, or vegetative plant by detecting and optionally measuring a trait, component, or attribute of the treated seed, seedling, or vegetative plant.

**[0029]** In selected aspects, the screening step comprises one or more of the following: (a) at least one *in vitro* assay comprising detecting and optionally quantifying the presence, level, change in level, activity, or localization of one or more compounds contained in an extract prepared from a cell or tissue sample obtained from the treated seed, seedling, or vegetative plant; and/or (b) at least one *in vivo* assay comprising detecting and optionally quantifying a trait, component, or attribute of the treated seed, seedling, or vegetative plant.

**[0030]** In alternative aspects, the disclosure provides a method of screening heterologous proteins or peptides expressed in a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cell for agriculturally-significant properties, comprising: (a) modifying a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cell to express a fusion protein according to the aspects disclosed herein to produce a recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cell; and (b) screening the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cell by detecting and optionally quantifying a level or activity of a compound produced by the recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cell.

**[0031]** In alternative aspects, the disclosure provides a method of treating a plant, a plant seed, a human, or an animal, comprising: administering to the plant, plant seed, human, or animal a composition comprising an exosporium isolated from an endospore produced by a recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cell; wherein the recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cell expresses the fusion protein of any one of the aspects disclosed herein. In selected aspects, the animal may include animals raised as livestock, such as cattle.

**[0032]** In selected aspects, the composition has been heat-inactivated or sterilized such that no viable *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells remain.

**[0033]** In alternative aspects, the disclosure provides a composition comprising an isolated and/or purified fusion protein according to any one of the aspects disclosed herein.

**[0034]** In alternative aspects, the disclosure provides a composition comprising an isolated and/or purified exosporium produced by a recombinant *Brevibacillus*, *Lysinibacillus*, or

*Viridibacillus* endospore, which has been modified to express a fusion protein according to any of the aspects disclosed herein.

**[0035]** In alternative aspects, the disclosure provides a composition comprising an exosporium produced by a recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore, which has been modified to express a fusion protein according to any of the aspects disclosed herein.

**[0036]** In selected aspects, the exosporium produced by a recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore comprises: (a) a basal layer of an exosporium; (b) a hair-like layer of an exosporium; (c) a mixture of both (a) and( b); (d) a fraction or extract of a crude exosporium obtained from a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore; and/or (e) a fraction or extract of a crude exosporium obtained from a *Brevibacillus, Lysinibacillus*, or *Viridibacillus* endospore that is enriched in an amount or concentration of the fusion protein compared to a same amount of the crude exosporium.

**[0037]** In alternative aspects, the disclosure provides a method of delivering a protein of interest to a plant, seed or field, comprising: applying a composition comprising an exosporium obtained from a recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore to a plant, seed, or field; wherein the recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore has been modified to express a fusion protein according to any of the aspects disclosed herein.

**[0038]** In selected aspects, the composition is applied to a field: (a) pre- or post-planting; (b) pre- or post-emergence; (c) as a powder, suspension or solution; or (d) wherein the composition further comprises one or more additional compounds that stimulate plant growth.

## BRIEF DESCRIPTION OF THE DRAWINGS

**[0039]** **FIG. 1** shows a first sequence alignment of the amino acid sequences of the N-terminal portion of various *Brevibacillus* proteins that possess variants of an N-terminal signal peptide according to an exemplary aspect of the disclosure. A consensus sequence is shown below the alignment.

**[0040]** **FIG. 2** shows a second sequence alignment of the amino acid sequences of the N-terminal portion of various *Brevibacillus* proteins that possess variants of an N-terminal signal peptide according to an exemplary aspect of the disclosure. A consensus sequence is shown below the alignment.

**[0041]** **FIG. 3** shows a third sequence alignment of the amino acid sequences of the N-terminal portion of various *Brevibacillus* proteins that possess variants of an N-terminal signal peptide according to an exemplary aspect of the disclosure. A consensus sequence is shown below the alignment.

**[0042]** **FIG. 4** shows a sequence alignment of the amino acid sequences of the N-terminal portion of various *Lysinibacillus* proteins that possess variants of an N-terminal signal peptide according to an exemplary aspect of the disclosure. A consensus sequence (SEQ ID NO: 41) is shown below the alignment.

**[0043]** **FIG. 5** shows a sequence alignment of the amino acid sequences of the N-terminal portion of various *Lysinibacillus* proteins that possess variants of an N-terminal signal peptide according to another exemplary aspect of the disclosure. A consensus sequence is shown below the alignment.

**[0044]** **FIG. 6** shows a sequence alignment of the amino acid sequences of the N-terminal portion of various proteins identified in *Viridibacillus* sp. strains (e.g., SEQ ID NOs: 181, 185, 189, 193, 197, 201, 205, 209, 213, and 217) that possess variants of an N-terminal signal peptide according to an exemplary aspect of the disclosure. A consensus sequence (i.e., SEQ ID NO: 179) is shown below the alignment. Several groups of *Viridibacillus* sp. strains expressed proteins having an identical N-terminal signal peptide.

**[0045]** **FIG. 7A** shows a brightfield (left) and epifluorescent (right) micrographs (1000x magnification) of a *Brevibacillus* sp. NRRL B-67865 endospore expressing an exemplary N-terminal targeting sequence according to the disclosure, specifically a tdTomato fusion protein construct which is localized to the endospore surface as illustrated by this figure. The fluorescence produced by tdTomato in the right panel corresponds with the image of the spores observed with brightfield microscopy in the left panel indicating correct localization of the tdTomato to the endospore surface.

**[0046]** **FIG. 7B** shows a flow cytometry histogram of *Brevibacillus* sp. NRRL B-67865 endospores expressing the same exemplary N-terminal targeting sequence used to transform the endospores shown in FIG. 7A. Wild-type *Brevibacillus* sp. NRRL B-67865 endospores with no observable tdTomato fluorescence are shown for comparison (dotted line trace, open area). 50,000 events are recorded for each population shown on the figure.

**[0047]** **FIG. 8A** shows a brightfield (left) and epifluorescent (right) micrographs (1000x magnification) of a *Lysinibacillus* sp. NRRL B-67864 endospore expressing an exemplary N-terminal targeting sequence according to the disclosure, specifically a tdTomato fusion protein construct which is localized to the endospore surface as illustrated by this figure. The fluorescence produced by tdTomato in the right panel corresponds with the image of the spores observed with brightfield microscopy in the left panel indicating correct localization of the tdTomato to the endospore surface.

**[0048]** **FIG. 8B** shows a flow cytometry histogram of *Lysinibacillus* sp. NRRL B-67864 endospores expressing the same exemplary N-terminal targeting sequence used to transform

the endospores shown in FIG. 8A. Wild-type *Lysinibacillus* sp. NRRL B-67864 endospores with no observable tdTomato fluorescence are shown for comparison (dotted line trace, open area). 50,000 events are recorded for each population shown on the figure.

**[0049]** **FIG. 9A** shows brightfield (left) and epifluorescent (right) micrographs (1000x magnification) of a *Viridibacillus* sp. NRRL B-67869 endospore expressing an exemplary N-terminal targeting sequence according to the disclosure, specifically a tdTomato fusion protein construct which is localized to the endospore surface as illustrated by this figure. The fluorescence produced by tdTomato in the right panel corresponds with the image of the spores observed with brightfield microscopy in the left panel indicating correct localization of the tdTomato to the endospore surface.

**[0050]** **FIG. 9B** shows a flow cytometry histogram of *Viridibacillus* sp. NRRL B-67869 endospores expressing the same exemplary N-terminal targeting sequence used to transform the endospores shown in FIG. 9A. Wild-type *Viridibacillus* sp. NRRL B-67869 endospores with no observable tdTomato fluorescence are shown for comparison (dotted line trace, open area). 50,000 events are recorded for each population shown on the figure.

## DETAILED DESCRIPTION

**[0051]** The disclosure provides genetic constructs capable of targeting a fusion protein to a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* exosporium, as well as compositions and methods that use these constructs to deliver heterologous molecules of interest (e.g., peptides, proteins) to various environments, such as plants. For example, following treatment with the recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores, treated plants may be screened to detect changes attributable to the heterologous protein delivered via the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores. Such changes may include alterations in the host plant's growth rate or yield; enhanced plant health (e.g., resistance to environmental stress, disease or pests); and the display of enhanced, modified or otherwise new attributes, compared to host plants grown under the same conditions absent treatment with the recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores. The use of a targeting sequence that efficiently targets the heterologous protein to the exosporium also provides a platform for high-throughput screening for useful heterologous proteins that, for example, are capable of enhancing, modifying, and/or conferring new plant traits or attributes.

**[0052]** *Brevibacillus*, *Lysinibacillus*, and *Viridibacillus* bacteria produce endospores that contain an exosporium layer. This structure is absent in *B. subtilis*, which produces endospores that terminate in an outer spore coat. The canonical spore formation process (elucidated based on studies using *B. subtilis*) involves asymmetric cell division of a vegetative cell to form a mother

cell and a forespore, which develop as two distinct compartments separated by an intervening septum. Eventually, the peptidoglycan in the septum is degraded and the forespore is engulfed by the mother cell, forming a cell within a cell. Intercellular communication between the mother cell and forespore coordinates cell-specific gene expression in each cell, resulting in the production of endospore-specific compounds, formation of a cortex layer around the forespore and deposition of the coat.

**[0053]** In some *Bacillus* species, e.g., *B. subtilis*, *B. licheniformis*, and *B. pumilus*, this coat will go on to become the outermost layer of the endospore. In many species of the *B. cereus* group, the forespore is further enclosed by a loose-fitting and balloon-like exosporium composed of a paracrystalline basal layer surrounded by a hair-like nap layer. In these species, the exosporium is separated from the coat by an interstitial connecting region known as the interspace. In either case, after the formation of a terminal coat layer or exosporium, the forespore undergoes a final dehydration and maturation into a complete endospore. The mother cell is subsequently degraded via programmed cell death, resulting in a release of the endospore into the environment. The endospore will then typically remain in a dormant state until more favorable conditions or particular stimuli trigger germination and a return to the vegetative state.

**[0054]** As the outermost surface between the spore and the environment, the coat layer (or exosporium, in exosporium-forming species) serves many critical functions. In particular, this layer acts as a semipermeable barrier to environmental insults and mediates interactions with the soil, and thus plays an important role in maintaining the viability of the spore and in the sensing of conditions that trigger germination of the endospore. The coat layer is also a target of clinical research as it contains cell surface molecules in pathogenic strains of bacteria that contribute to host immune cell recognition. Methods of displaying heterologous proteins on the spore coat of *B. subtilis* have been developed using fusion protein constructs containing a *B. subtilis* spore coat protein such as CotC fused to a protein of interest. However, *B. subtilis* lacks an exosporium and thus studies using this species fail to provide guidance as to how fusion proteins may be targeted to the exosporium produced by other bacterial genera, such as *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus*.

**[0055]** In contrast, the disclosure provides N-terminal constructs and fusion proteins comprising the same that are capable of targeting fusion protein constructs to the exosporium of *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells. The N-terminal signal sequence used to target the fusion protein to the exosporium may comprise a polypeptide having a sequence represented by any of the sequences disclosed herein, provided that such sequence is compatible with the selected bacterial genus (i.e., a sequence shown in Table 1 or FIGs. 1-3 for *Brevibacillus*, Table 2 or FIGs. 4-5 for *Lysinibacillus*, Table 3 or FIG. 6 for *Viridibacillus*, or a fragment or variant of any

of these sequences which retains exosporium-targeting functionality in the corresponding bacterial genus). In select embodiments, this N-terminal signal sequence may comprise a fragment or variant of any of the sequences disclosed herein, sufficient to retain exosporium-targeting functionality in the same bacterial genus. These and other embodiments are described herein.

**[0056]** Throughout the disclosure, the term "comprise" or any derivative thereof (e.g., comprising, comprises) may be replaced with "consist essentially of", "consist of", or the applicable corresponding derivative thereof.

**[0057]** As used herein, "*Brevibacillus*" refers to endospore-producing bacteria classified in the *Brevibacillus* genus. This term encompasses, without limitation, various *Brevibacillus* family members including *B. agri, B. aydinogluensis, B. borstelensis, B. brevis, B. centrosporus, B. choshinensis, B. fluminis, B. formosus, B. fulvus, B. ginsengisoli, B. invocatus, B. laterosporus, B. levickii, B. limnophilus, B. massiliensis, B. nitrificans, B. panacihumi, B. parabrevis, B. reuszeri,* or *B. thermoruber.*

**[0058]** As used herein, "*Lysinibacillus*" refers to endospore-producing bacteria classified in the *Lysinibacillus* genus. This term encompasses, without limitation, various *Lysinibacillus* family members including *Lysinibacillus sphaericus, Lysinibacillus boronitolerans, Lysinibacillus fusiformis, Lysinibacillus acetophenoni, Lysinibacillus alkaliphilus, Lysinibacillus chungkukjangi, Lysinibacillus composti, Lysinibacillus contaminans, Lysinibacillus cresolivorans, Lysinibacillus macroides, Lysinibacillus manganicus, Lysinibacillus mangiferihumi, Lysinibacillus massiliensis, Lysinibacillus meyeri, Lysinibacillus odysseyi, Lysinibacillus pakistanensis, Lysinibacillus parviboronicapiens, Lysinibacillus sinduriensis, Lysinibacillus tabacifolii, Lysinibacillus varians, Lysinibacillus xylanilyticus* and *Lysinibacillus halotolerans.*

**[0059]** As used herein, "*Viridibacillus*" refers to endospore-producing bacteria classified in the *Viridibacillus* genus. This term encompasses, without limitation, various *Viridibacillus* family members including *Viridibacillus arvi, Viridibacillus arenosi,* and *Viridibacillus neidei.*

**[0060]** In certain aspects, the *Brevibacillus* member used to express the fusion protein is *Brevibacillus brevis* (formerly classified as *Bacillus brevis*), the *Lysinibacillus* member used to express the fusion protein is *Lysinibacillus sphaericus* (formerly classified as *Bacillus sphaericus*), and the *Viridibacillus* member used to express the fusion protein is *Viridibacillus arvi* (formerly classified as *Bacillus arvi*). Each of these bacterial species is a Gram-positive, aerobic, and spore-forming bacterium commonly isolated from soils.

**[0061]** Characterization of a bacterium as a *Bacillus brevis*, *Bacillus sphaericus*, or *Bacillus arvi* was previously based solely on simple morphological features and a limited number of biochemical tests. However, recent genomics studies have revealed that several members of the

*Bacillus* genus are quite distinct at the DNA level, resulting in reevaluation of the taxonomic position of multiple species, including the species now identified as *B. brevis*, *L. sphaericus* and *V. arvi*. Strikingly, both 16S rRNA and whole genome analysis of this genus reveals that it is a member of the *Planococcaceae* family rather than the *Bacillaceae* family, as it was originally classified. Previous studies have indicated that *Brevibacillus*, *Lysinibacillus*, and *Viridibacillus* spores possess an exosporium layer. However, unlike the exosporium in the *B. cereus* group, comparatively little is known about the composition and structure of the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* exosporium. Given the general lack of knowledge about the basic composition or structure of the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* exosporium, little is known about the process by which proteins are targeted to the exosporium of members of these genera during formation of this layer.

**[0062]** In certain aspects, the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* member used to express the fusion protein is a bacterium that possesses a 16S rRNA gene that shares at least 97, 98 or 99 percent identity with a 16S rRNA gene of *B. brevis, L. sphaericus*, *V. arvi*, or any of the other exemplary *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* family members disclosed herein. Alternatively, the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* member used to express the fusion protein is a bacterium that possesses a DNA-DNA hybridization value of at least 70 percent to that of *B. brevis*, *L. sphaericus*, *V. arvi*, or any of the other exemplary *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* family members disclosed herein. In another instance, the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* member used to express the fusion protein is a bacterium that possesses an average nucleotide identity of 95, 96, 97, 98, or 99 percent to that of *B. brevis*, *L. sphaericus*, *V. arvi*, or any of the other exemplary *Brevibacillus* family members disclosed herein.

**[0063]** The term "N-terminal signal sequence" generally refers to a polypeptide sequence located at or proximal to the amino terminus of a polypeptide, which directs localization of the polypeptide to a subcellular compartment, or for secretion. It is recognized and understood that this term may be used interchangeably with the terms "N-terminal targeting sequence," "targeting sequence," "signal sequence," and "signal peptide," depending on context. The N-terminal signal sequence may be retained as part of the polypeptide sequence of a mature protein or alternatively cleaved during or after the localization process. This term may be used to specifically refer to a polypeptide sequence located at or proximal to the amino terminus of a polypeptide, which directs localization of the polypeptide to the exosporium of a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore. In this context, the only required functionality of the N-terminal signal sequence is the capability to target the polypeptide of which it is a part to the exosporium of a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore. N-terminal targeting

sequences compatible with *Brevibacillus* are shown in Table 1 and FIGs. 1-3, N-terminal targeting sequences compatible with *Lysinibacillus* are shown in Table 2 and FIGs. 4-5, and N-terminal targeting sequences compatible with *Viridibacillus* are shown in Table 3 and FIG. 6. As noted above, intergeneric use of N-terminal targeting sequences is not envisioned by this disclosure.

**[0064]** A "plant" or "host plant," includes any plant that possesses a rhizosphere or phyllosphere which *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* can colonize, as well as plants that can serve as a transient hosts for *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* bacteria. Colonization is not a requirement for the methods described herein and compositions to function, though it may be preferred in certain aspects of the disclosure.

**[0065]** As used herein, "biological control" is defined as control of a pathogen and/or insect and/or an acarid and/or a nematode by the use of a second organism or a biological molecule. Known mechanisms of biological control include bacteria that control root rot by out-competing fungi for space or nutrients on the surface of the root. Bacterial toxins, such as antibiotics, have been used to control pathogens. The toxin can be isolated and applied directly to the plant or the bacterial species may be administered so it produces the toxin *in situ*. Other means of exerting biological control include the application of certain fungi producing ingredients active against a target phytopathogen, insect, mite or nematode, or attacking the target pest/pathogen. "Biological control" may also encompass microorganisms having a beneficial effect on plant health, growth, vigor, stress response or yield. Application routes include spray application, soil application and seed treatment.

**[0066]** "Hybridization" refers to a reaction in which one or more polynucleotides react to form a complex that is stabilized via hydrogen bonding between the bases of the nucleotide residues. The hydrogen bonding may occur by Watson-Crick base pairing, Hoogstein binding, or in any other sequence-specific manner. The complex may comprise two strands forming a duplex structure, three or more strands forming a multi-stranded complex, a single self-hybridizing strand, or any combination of these. Hybridization reactions can be performed under conditions of different "stringency". In general, a low stringency hybridization reaction is carried out at about 40°C in 10x SSC or a solution of equivalent ionic strength/temperature. A moderate stringency hybridization is typically performed at about 50°C in 6x SSC, and a high stringency hybridization reaction is generally performed at about 60°C in 1x SSC.

**[0067]** As used herein, the term "sequence identity" refers to the degree to which two polynucleotide or amino acid sequences are identical (i.e., on a nucleotide-by-nucleotide or residue-by-residue basis, respectively) over the window of comparison. The percentage of sequence identity is calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of positions at which the identical nucleic acid base (e.g., A,

T, C, G for a polynucleotide sequence) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison (i.e., the window size), and multiplying the result by 100 to yield the percentage of sequence identity. An equivalent calculation can be performed by comparing two aligned amino acid sequences.

**[0068]** With respect to the comparison of amino acid sequences, in addition to the measurement of sequence identity, a comparison may also take into account whether residue changes constitute "conservative" substitutions. Conservative amino acid substitutions refer to the interchangeability of residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, and asparagine-glutamine.

## N-terminal Targeting Sequences

**[0069]** The disclosure provides N-terminal targeting sequences from *Brevibacillus*, *Lysinibacillus*, and *Viridibacillus* bacteria. Under stressful environmental conditions, *Brevibacillus*, *Lysinibacillus*, and *Viridibacillus* family bacteria undergo sporulation and form endospores that can stay dormant for extended periods of time. The outermost layer of *Brevibacillus*, *Lysinibacillus*, and *Viridibacillus* endospores is known as the exosporium and comprises a basal layer, and in some strains, external appendages/filaments/structures comprised of collagen-like protein.

**[0070]** Previously reported studies on the exosporium of bacteria from other genera have determined that the exosporium is predominantly formed by a collagen-like glycoprotein, e.g., BclA, in *B. anthracis* endospores. The basal layer is currently thought to be comprised of a number of different proteins. BclA, the major constituent of the *B. anthracis* surface nap, has been shown to be attached to the exosporium with its amino-terminus (N-terminus) positioned at the basal layer and its carboxy-terminus (C-terminus) extending outward from the spore. It was previously discovered that certain sequences from the N-terminal regions of BclA and BclB could be used to target a peptide or protein to the exosporium of a *B. cereus* family member endospore. *See* U.S. Patent Publication Nos. 2010/0233124 and 2011/0281316, and Thompson, et al.,

"Targeting of the BclA and BclB Proteins to the *Bacillus anthracis* Spore Surface," *Molecular Microbiology*, 70(2):421-34 (2008), the entirety of each of which is hereby incorporated by reference.

**[0071]** Despite the growing body of literature available regarding *B. cereus* exosporium targeting sequences, there are no reported studies identifying homologous N-terminal targeting sequences in *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus*. A bioinformatics analysis of the known exosporium-targeted collagen-like repeat proteins BclA, BclB or BetA fails to reveal any homologous N-terminal targeting sequences in *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus*, suggesting that the exosporium targeting sequences of these proteins is highly specific to the *B. cereus* family. Given the limited characterization of proteins that form and localize to the exosporium of *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus*, one cannot easily deduce the N-terminal signal sequences necessary to target proteins to the exosporium of *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* generally or in particular species within these genera (e.g., *B. brevis*, *L. sphaericus*, or *V. arvi*).

**[0072]** Despite this lack of guidance in the available literature, the inventors have identified N-terminal targeting sequences capable of directing endogenous and fusion proteins to the exosporium of *Brevibacillus*, *Lysinibacillus*, and *Viridibacillus* cells.

**[0073]** For ease of reference, the SEQ ID NOs. for the nucleotide and polypeptide sequences referred to herein are listed in Table 1 below.

**Table 1:** Exemplary *Brevibacillus* N-Terminal Targeting Sequences

| Sequence Identifier | Sequence |
|---|---|
| SEQ ID NO: 1 | MPFSNKIVNGDFETGTLIPWSSXNVAITNLQSHTGFFSALLFGNTANSLLFQAVPVTPGDSFEFFLSIAKLGNLVS PQVNIALLYLDVAATPVGIGLNXTIPVGHLPDNTANIWTTIYETTSVVPATATQALLIIHKIPSLSTADIVVDDIV LLQTSG |
| SEQ ID NO: 2 | MVRTLSKIEDSTYTTLAPINPIMEVVIYLPFSNKVVNGDFETGTLFPWSFTNVSITNLQSHTGFFSALLFGDTANS LLFQAIPVTPGDSFELFLSIAKLGNLVSPQVNIALXYLDVATIPVGIGLNLTIPVGHLPDNTANIWTTIYETTSVVP ATATQALLIINKIPALSTADIVVDDIGILQTSG |
| SEQ ID NO: 3 | MLPLIFPPQGCPAIFPGPTLDPPDPPDPP |
| SEQ ID NO: 4 | MMILTIKIFRKERAKINDKRANAFNKKILPLIFPPQGCPAIFPGPTLDPPDPPDPP |
| SEQ ID NO: 5 | MKELHDIKRIWDEVANTDLEEFTRKNPIYMKSSNGISSSSSTFCWTFIR |
| SEQ ID NO: 6 | MKELHDIKRIWDEVANTDLEEFTRKNPIYMKSSNGISSSSSTFCWTFIRGKT |
| SEQ ID NO: 7 | MVLALSKIGESTYNASVPINLIMEVVIYLPFSNIVENGNFESGTLFPWSFTNAAITDLQSHSGFFSALLFGGTANS LLFQTVPVTPGDSFELFLSIAKSGNLISPQVNIVLIYLDAANIPVGIGLNLTIPVGHLPDNTANIWTTIYETTAVVP ATAIEALLIISKVPAL-STADVILDDIELLQTSG |
| SEQ ID NO: 8 | MKAVIYLPFGNKIVNGNFETGSLVPWNFSNVTINNLQSHTGSFSALFFGNTTNSVLYQTVPVTSGEIFEFFLSIG KIGNLPSPQVNIALIYLNAASTPENIGINIILPVGKLPNNLNNNWSTIYEISSVVPAAATQAMVIIHKIPAPSTADIV VDDIVLVQTGA |
| SEQ ID NO: 9 | MPFGNKIVNGNFETGSLIPWSSSNVAISNLQSHTGSYSALLFGNAANSFLFQAVPVTVGDSFEFFLSIAKIGNLPS PQVDIALIYLNAASTPISNGMSIILPTGHLPDNLNNNWSTIYEISSVVPAMATHAMVIIHKIPSPSTSDIVVDDIVL VQTGA |
| SEQ ID NO: 10 | NKVVNGDFETGTLFPWSFTNVSITNLQSHTGFFSALFFGDTANSLLFQAIPVTPGDSFELFLSIAKLGNLVSPQV NIALLYLDVATIPVGIGLNLTIPVGHLPDNTANIWTTIYETTSVVPATATQALLIINKISALSTADIVVDDIGILQTS G |
| SEQ ID NO: 11 | MFQAVPVTVGDSFEFFLSIAKIGNLPSPEVNIALIYLNVASTPISIGMSIILPIGHLPDNLNNNWSTIYEISSVVPAT ATHAMVIIHKIPSP-STSDIVVDDIVLVQTGA |
| SEQ ID NO: 12 | MKAVIYLPLGNKIVNGNFETGSLVPWNFSNVAIYNLQSHTGSFSALFFGNTTNSVLYQTVPVTSGEIFEFFLSIG KIGNLPSPQVNIALIYLNAASTPENIGINIILPVGKLPNNLNNNWSTIYEISSVVPAAATQAMVIIHKIPAPSTADIV VDDIVLVQTGA |

| Sequence Identifier | Sequence |
|---|---|
| SEQ ID NO: 13 | MPFSNKIVNGDFETGTLIPWSFVNVAITNLQSHTGFFSAQLFGTTANSLLFQAVPVTPGDSFEFFLSIAKLGNLLS PQVNIALLYLDVAATPVGIGLNITIPIGHLPDNAANIWTTIYETTTVVPATATQALLIINKIPTLTTADIVVDDIAL LQVSG |
| SEQ ID NO: 14 | MFLSIAKSGNVISPQVNIVLIYLDVANIPVGIGLNLTIPVGHLPDNTANIWTTIYETTSVVPATAIEALLIINKVPA LSTADVILDDIGLLQTSG |
| SEQ ID NO: 15 | LLPWSFTNAAITDLQSHSGFFSALLFGGTANSLLFQTVPVTPGDSFELFLSIAKSGNLISPQVNIVLIYLDAANIPV GIGLNLTIPVGHLPDNTANIWTTIYETTAVVPATAIEALLIISKVPALSTADVILDDIELLQTSG |
| SEQ ID NO: 16 | MPFSNKIVNGDFETGTLIPWSFTNVAITNLQSHSGFFSARLFGTTVNSLLFQSVPVTPGDSFEFFLSIAKLGTLLSP QVNIALLYLDVTATPVGIGLNITIPIGHLPDNTANIWTTIYETTTVVPATATQALLIINKIPTLTTADIVVDDIELLQ VSG |
| SEQ ID NO: 17 | MSFINKIVNGDFETGTLIPWSFVNVAINPLQSHTGFFSARLFGNTANSLLFQAVPVTPGDSFEFFLSIAKIGNLTSP QVNIVLFYLDALANPISLGLNITIPSGHLPDNVDNNWTTIYETTSAVPATATQALLIINKIPALFTTADIVVDDIAL LQTGAGV |
| SEQ ID NO: 18 | MPFGNKIVNGNFETGSLIPWSSSNVVISNLQSHTGSYSALLFGNEANSLMFQAVPVTVGDSFEFFLSIAKIGNLP SPQVNIALIYLNVASTPISIGMSIILPIGHLPDNLNNNWSTIYEISSVVPATATHAMVIIHKIPSPSTSDIVVDDIVLV QTGA |
| SEQ ID NO: 19 | MPVKNRAVNGDFETGSLVPWNSINVTISNQQSHSGTFSALLFGTSANSLLFQTVPVITGDSFEFFLSIAKIGNLPS PQVNIAVIYVNATSTPLSIGMSVILPVNHLPNNLNNNWLTIYNTTSVVPVTATQAIIIIHKIPAPSTADIVVDDIALI QTGG |
| SEQ ID NO: 20 | MPFSNKIVNGNFETGALIPWSSINVAITNLQSHTGFFSARLFGNTTNSLLFQAVPVTPGDSFEFLLSIAKLGNLVS PQVNIALLYLDVTATPVGIGLNFTIPVGHLPDNTANIWTTIYETTSVVPATATQALLIINKIAALSTADIVVDDIGI LQTSG |
| SEQ ID NO: 21 | MPFSNKIVNGNFETGALIPWSSINVAITNLQSHTGFFSARLFGNTTNSLLFQAVPVTPGDSFEFLLSIAKLGNLVS PQVNIALLYLDVTATPVGIGLNFTIPVGHLPDNTANIWTTIYETTSVVPATAIQALLIIEKVAALTTADVVVDDIQ LLQTSG |
| SEQ ID NO: 22 | MFQAVPVTVGDSFEFFLSIAKIGNLPSPEVNIALIYLNVASTPISIGMSIILPIGHLPDNLNNNWSTIYEISSVVPAT ATHAMVIIHKIPSPSTSDIVVDDIVLVQTGA |
| SEQ ID NO: 23 | MPFGNKIVNGNFETGSLIPWSSSNVVISNLQSHTGSYSALLFGNAANSLMFQAVPVTVGDSFEFFLSIAKIGNLP SPQVNIALIYLNVASTPISIGMSIILPIGHLPDNLNNNWSTIYEISSVVPATATHAMVIIHKIPSPSTSDIVVDDIVLV QTGA |

| Sequence Identifier | Sequence |
|---|---|
| SEQ ID NO: 24 | MPFSNKIVNGNFETGALIPWSSINVAITNLQSHTGFFSARLFGNTTNSLLFQAVPVTLGDSFEFLLSIAKLGNLVS PQVNIALLYLDVTATPVGIGLNFTIPVGHLPDNTANIWTTIYETTSVVPATAIQALLIIEKVAALTTADVVVDDIQ LLQTSG |
| SEQ ID NO: 25 | MVRTLSKIEDSTYTTLAPINPIMEVVIYLPFSNKVVNGDFETGTLFPWSFTNVSITNLQSHTGFFSALLFGDTANS LLFQAIPVTPGDSFELFLSIAKLGNLVSPQVNIALLYLDVATIPVGIGLNLTIPVGHLPDNTANIWTTIYETTSVVP ATATQALLIINKISALSTADIVVDDIGILQTSG |
| SEQ ID NO: 26 | MPFGNKIVNGNFETGSLIPWSSSNVAISNLQSHTGSYSALLFGNAANSFLFQAVPVTVGDSFEFFLSIAKIGNLPS PQVDIALIYLNAASTPISIGMSIILPTGHLPDNLNNNWSTIYEISSVVPAMATHAMVIIHKIPSPSTSDIVVDDIVLV QTGA |
| SEQ ID NO: 27 | MVRTLSKIEDSTYTTLAPINPIMEVVIYLPFSNKVVNGDFETGTLFPWSFTNVSITNLQSHTGFFSAILFGDTANS LLFQAIPVTPGDSFELFLSIAKLGNLVSPQVNIALLYLDVATIPVGIGLNLTIPVGHLPDNTANIWTTIYETTSVVP ANATQALLIINKISALSTADIVVDDIGILQTSG |
| SEQ ID NO: 28 | GDFETGTLFPWSFTNVSITNLQSHTGFFSAILFGDTANSLLFQAIPVTPGDSFELFLSIAKLGNLVSPQVNIALLYL DVATIPVGIGLNLTIPVGHLPDNTANIWTTIYETTSVVPANATQALLIINKISALSTADIVVDDIGILQTSG |
| SEQ ID NO: 29 | MPFGNKIVNGNFETGSLIPWSSSNVAISNLQSHTGSYSALLFGNTANSLMFQAVPVTVGDSFEFFLSIAKIGNLP SAQVNIALIYLNVASTPISIGMSIILPIGHLPDNLNNNWSTIYEISSVVPAMATHAMVIIHKIPSPSTSDIVVDDIVL VQTGA |
| SEQ ID NO: 30 | MPFSNKIVNGDFETGTLIPWSSINVAITNLQSHTGFFSARLFGNTANSLLFQAVPVTPGDSFEFLLSIAKLGNLVS PQVNIALLYLDVTATPVGIGLNLTIPVGHLPDNTADIWTTIYETTSVVPATAIQALLIIEKVPGLTTADVVVDDIE LLQTSG |
| SEQ ID NO: 31 | MPFGNKIVNGNFETGSLIPWSSSNVAISNLQSHTGSYSALLFGNTANSLMFQAVPVTVGDSFEFFLSIAKIGNLP SAQVNIALIYLNVASTPISIGMSIILPIGHLPDNLNNNWSTIYEISSVVPAMATHAMVIIHKIPSPSTSDIVVDDIVF VQTGA |
| SEQ ID NO: 32 | VYLNVVATPIGIGMSTILPIDHLPDNTNKNWTTIYETTSVVPATAIRALVIIHKIPSPSTADIVVDDIVLLQTGL |
| SEQ ID NO: 33 | MPFSNKIVNGDFETGTLIPWSSINVAITNLQSHTGFFSARLFGNIANSLLFQAVPVTPGDSFEFLLSIAKLGNLVSP QVNIALLYLDVTATPVGIGLNLTIPVGHLPDNTANIWTTIYETTSVVPATAIQALLIIEKVASLTTADVVVDDIEL LQTSG |
| SEQ ID NO: 34 | MPFGNKIVNGNFETGSLIPWSSSNVVISNLQSHTGSYSALLFGNAANSLMFQAVPVTVGDSFEFFLSIAKIGNLP SPQVNIALIYLNVASTPISIGMSIILPIDHLPDNLNNNWSTIYEISSVVPATATHAMVIIHKIPSPSTSDIVVDDIVLV QTGA |

| Sequence Identifier | Sequence |
|---|---|
| SEQ ID NO: 35 | MPFSNKIVNGDFETGTLIPWSSINVAITNLQSHTGFFSARLFGNIANSLLFQAVPVTPGDSFEFLLSIAKLGNLVSP QVNIALLYLDVTATPVGIGLNFTIPVGHLPDNTANIWTTIYETTSVVPATAIQALLIIEKVASLTTADVVVDDIEL LQTSG |
| SEQ ID NO: 36 | FELFLSIAKLGNLVSPQVNIALLYLDVATIPVGIGLNLTIPVGHLPDNTANIWTTIYETTSVVPATATQALLIINKI AALSTADIVVDDIGILQTSE |
| SEQ ID NO: 37 | MPFGNKIVNGNFETGSLIPWSSSNVVISNLQSHTGSYSALLFGNATNSLMFQAVPVTVGDSFEFFLSIAKIGNLP SPQVNIALIYLNVASTPISIGMSIILPIGHLPDNLNNNWSTIYEISSVVPATATHAMVIIHKIPSPSTSDIVVDDIVLV QTGA |
| SEQ ID NO: 38 | MPFSNKIVNGDFETGTLIPWSSINVAITNLQSHTGFFSARLFGNIANSLLFQAVPVTPGDSFEFLLSIAKLGNLVSP QVNIALLYLDVTATPVGIGLNFTIPVGHLPDNTANIWTTIYETTSVVPATATQALLIINKIAALSTADIVVDDIGIL QTSE |

**Table 2:** Exemplary *Lysinibacillus* N-Terminal Targeting Sequences

| Sequence Identifier | Sequence |
|---|---|
| SEQ ID NO: 39 | ATGCGCTTTAGCTATAGCCGCAACTTTGATAACTTTAAATGCGATAGCAAATGCAACTATCCGATGAAAT ATAAATGCAACGAATTTGGCTGCAACGGCTATCCGTATGATCTGAGCGGCATTCAGGATCCGATT |
| SEQ ID NO: 40 | ATGCATTTTGGCAACTTTAACCTGGATCGCGTGTGCAGCAAATGCAACAGCTTTCCGTGCTGCTGCAAAAC CGGCCCGATTCCGAGCTGCCCGATTTGGCCGGTGAAACCGACC |
| SEQ ID NO: 41 | MRFSYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYDLSGIQDPI |
| SEQ ID NO: 42 | MHFGNFNLDRVCSKCNSFPCCCKTGPIPSCPIWPVKPT |
| SEQ ID NO: 43 | MRFSYNRNFDNFKCDAKCNYPMKYKCNEFGCNGYPYVYGIEDPI |
| SEQ ID NO: 44 | MRFSYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYDFSGIQDPI |
| SEQ ID NO: 45 | MRFSYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYDFSGIQDPM |
| SEQ ID NO: 46 | MRFSYSRNFDYFKCDSKCNYPMKYKCYEFGCNGYPYDFSGIQDPI |
| SEQ ID NO: 47 | MRFSYSRNSDNFKCDSKCNYPMKYKCNEFGCNGYPYDFSGIQDPI |
| SEQ ID NO: 48 | MRFSYSRNFDNFKCDSKSNYPMKYKCNEFGCNGYPYDFSGIQDPI |
| SEQ ID NO: 49 | MRFSYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYDFLGIQDPI |
| SEQ ID NO: 50 | MRFSYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYDLLGIQDPI |

| Sequence Identifier | Sequence |
|---|---|
| SEQ ID NO: 51 | MRFSYSRNFDNFKCDSKCNYPLKFKCNEFGCNGYPYDFSGIQDPI |
| SEQ ID NO: 52 | MRFSYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYNLSGIQDPI |
| SEQ ID NO: 53 | MRFSYSRNFDNFKCDSKCNYPKKYKCNEFGCNGYPYDLSGIQDPI |
| SEQ ID NO: 54 | MRFSYSRNFDNFKCDSKCNYPLKYKCNEFGCNGYPYDLSGIQDPI |
| SEQ ID NO: 55 | MRLSYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYDFSGIQDPI |
| SEQ ID NO: 56 | LRFSYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYDLSGIQDPI |
| SEQ ID NO: 57 | MRFRYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYDFSGIQDPI |
| SEQ ID NO: 58 | MRVSYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYDFSGIQDPI |
| SEQ ID NO: 59 | MRFSYSRYFDNFKCDSKCNYPMKYKCNEFGCNGYPYDFSGIQDPI |
| SEQ ID NO: 60 | MRISYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYDFSGIQDPM |
| SEQ ID NO: 61 | MRFSYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYDLSGIQEPM |
| SEQ ID NO: 62 | MRFSYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYDLSGIQDLI |
| SEQ ID NO: 63 | MRFSYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYDLSGIQVPI |
| SEQ ID NO: 64 | MRFSYSRNFDNFKCDSKFNYPMKYKCNEFGCNGYPYDLSGIQDPI |
| SEQ ID NO: 65 | MRFSYSRNFDYFKCDSKCNYPMKYKCNEFGCNGYPYDLSGIQDPI |
| SEQ ID NO: 66 | MRFSYSRNFDNFKCDSKCNYPMKNKCNEFGCNGYPYDLSGIQDPI |
| SEQ ID NO: 67 | MRFSYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYDLSAIQDPI |
| SEQ ID NO: 68 | MRFSYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYDLSGFQDPI |
| SEQ ID NO: 69 | MRFSYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYDLSGFQDPT |
| SEQ ID NO: 70 | MRFSYSRNFDNYKCDSKCNYPMKYKCNEFGCNGYPYDLSGIQDPI |
| SEQ ID NO: 71 | MRFSYCRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYDLSGIQDPI |
| SEQ ID NO: 72 | MRFSYSRNLDNFKCDSKCNYPMKYKCNEFGCNGYPYDLSGIQDLI |
| SEQ ID NO: 73 | MRFSYSRNFDNFKCDSKCNYPMKYKCNEFGCIGYPYNLSGIQDPI |
| SEQ ID NO: 74 | MRFSYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYAYNLSGIQDPI |
| SEQ ID NO: 75 | MRFSYSRNLDNFKCDSKCNYPMKYKCNEFGCNGYPYNLSGIQDPI |
| SEQ ID NO: 76 | LRFSYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYNLSGIQDPI |
| SEQ ID NO: 77 | MRFSYIRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYNLSGIQDPI |
| SEQ ID NO: 78 | MRVSDSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYDFSGIQDPI |
| SEQ ID NO: 79 | MRFSYSRNFDNFKCYSKCNYPMKYKCNEFGCNGYPYDLSGFQDPI |
| SEQ ID NO: 80 | MRFSYSRNFDNFKCDSKCNYPMKYKCNEFWCNGYPYDLSGFQDPI |

| Sequence Identifier | Sequence |
|---|---|
| SEQ ID NO: 81 | MRFSNSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPYDLSGFQDPI |
| SEQ ID NO: 82 | MRFSYSRNLDNFKCDSKCNYPMKYKCNEFGCNGYPYDLSGFQDPI |
| SEQ ID NO: 83 | FSYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYAYNLSGIQDPI |
| SEQ ID NO: 84 | MRFSYSRNFDNFKCDSKCNYPMKYKCNEYGCNGYAYNLSGIQDPI |
| SEQ ID NO: 85 | MRLSYSRNLDNFKCDSKCNYPMKYKCNEFGCNGYPYNLSGIQDPI |
| SEQ ID NO: 86 | MRFSYSRNFDNFKCDSKCNYPMKYKCNEFGCNGYPFDFSGFQDPI |
| SEQ ID NO: 87 | MRFSYSRNFDNFKSDTKCNYPMKYKCNEFGCNGYPYDLSGIQDPI |
| SEQ ID NO: 88 | MRFSYNRNFDNFKCDAKCNYPMKYKCNEFGCNGYPYVYGIQDPI |
| SEQ ID NO: 89 | MRFSFNRNFDNFKCDAKCNYPMKYKCNEFGCNGYPYVYGIEDPI |
| SEQ ID NO: 90 | MRFSYNRNFDNFKCDAKCNYPMKYKCNEFGCNGYPYVYGIEDQI |
| SEQ ID NO: 91 | MRFSYIRNFDNFKCDAKCNYPLKYKCNEFGCNGYPYVYGIQEPI |
| SEQ ID NO: 92 | MRFSYNLNFDNFKCDAKCNYPLKYKCNEFGCNGYPYVYGIQEPI |
| SEQ ID NO: 93 | MRFCYYRNFDNFKCDANCYYPMKYKCNEFGCNGYPYVYGIEDPI |
| SEQ ID NO: 94 | MRFSYSRNFDNFKCDSKCNYHMKYKCNEFGCNGYPYVLSDIQDPI |
| SEQ ID NO: 95 | YSRNFDKIKCDSKCNYHMKYKCNEFGCNGYPYDFSGIQDPI |
| SEQ ID NO: 96 | MRFNYNRNNDNFKCDAKCNYPMKFKCNEFGCNGYPYGAYEIQDPV |
| SEQ ID NO: 97 | MRFNYNRNNDNFKCDTKCNYPMKFKCNEFGCNGYPYGAYEIQDPV |
| SEQ ID NO: 98 | MHFGKFKERVCSKCNTFPCCCSPCPPQSCPIWPVKPT |
| SEQ ID NO: 99 | MHFGKFKERVCSKCNTFPCCCSPYPPQSCPIWPVKPT |
| SEQ ID NO: 100 | MHFGNFIDRVCSKCHSFPCCCKTGPIPSCPIWPVKPT |
| SEQ ID NO: 101 | MHFGNFIDRVCSKCHSFPCYCKTGPIPSCPIWPVKPT |
| SEQ ID NO: 102 | MHFGNFIDRVCSKCHSFPCCCKTGPIPSCPIWPVNPT |
| SEQ ID NO: 103 | MHFGNFIDRVCSKCHSFPCCCKAGPIPSCPIWPVKPT |
| SEQ ID NO: 104 | MHFGNFIDRVCSKCHSFPCCCKTGPIPNCPIWPVKPT |
| SEQ ID NO: 105 | MHYGNFIDRVCSKCHSFPCCCKTGPIPSCPIWPVKPT |
| SEQ ID NO: 106 | MHFGNFIVRVCSKCHSFPCCCKTGPIQSCPIWPVKPT |
| SEQ ID NO: 107 | MHFGIIIDRVCSKCHSFPCCCKTGPIPSCPIWPVKPT |
| SEQ ID NO: 108 | MHFGKFIDRVCTKCHSYPCCCKTGPIPSCPIWPVKPT |
| SEQ ID NO: 109 | MHFGKFLDRVCNKCHSFPCCCKTGPIPGCPIWPVKPT |
| SEQ ID NO: 110 | MHFGKFLDRVCSKCHSFPCCCKTGPIPGCPIWPVKPT |

| Sequence Identifier | Sequence |
|---|---|
| SEQ ID NO: 111 | MHFGKFLDRVCSKCNSFPCCCKTGPSPSCPIWPVKPT |
| SEQ ID NO: 112 | MNFGKFLDRVCSKCNSFPCCCKTGPSPSCPIWPVKPT |
| SEQ ID NO: 113 | MLFGKFLDRVCSKCNSFPCCCKTGPSPSCPIWPVKPT |
| SEQ ID NO: 114 | MHFGKFLDRVCSKCNSFPCCCKTGPSPSCPNWPVKPT |
| SEQ ID NO: 115 | MHFGNYLKRVCSKCNSFPCCCRTGPIPSCPVWPVKPT |
| SEQ ID NO: 116 | MHFGNYLKRVCSKCNYFPCCCRTGPIPSCPVWPVKPT |
| SEQ ID NO: 117 | MHFGNYLKRVCSKCNSFPCCCRPGPIPSCPVWPVKPT |
| SEQ ID NO: 118 | MHFGNYLKQVCSKCNSFPCCCRTGPIPSCPVWPVKPT |
| SEQ ID NO: 119 | MHFGNYLKRVCSKCNSFPCCCRTGPIQSCPVWPVKPT |
| SEQ ID NO: 120 | MHFGNYLKQVCNKCNSFPCCCRTGPIPSCPVWPVKPT |
| SEQ ID NO: 121 | MHFGNYLKQVCSKCNSFPCCCRNGPIPSCPVWPVKPT |
| SEQ ID NO: 122 | MHFGNYLKQVCSKCNSFPCCCRTGPIPSCPIWPVKPT |
| SEQ ID NO: 123 | LHFGNYLKQVCSKCNSFPCCCRTGPIPSCPIWPVKPT |
| SEQ ID NO: 124 | MLFGNYLKQVCSKCNSFPCCCRTGPIPSCPIWPVKPT |
| SEQ ID NO: 125 | MHFGNYLKQVSSKCNSFPCCCRNGPIPSCPVWPVKPT |
| SEQ ID NO: 126 | MHFGRFNERVCSKCNTFPCCCNPCAAQSCPIWPVKPT |
| SEQ ID NO: 127 | MHFGRFKERVCSKCNTFPCCCNPCAAQSCPIWPVKPT |
| SEQ ID NO: 128 | MHFGRFNERVCSKCNSFPCCCNPCAAQSCPIWPVKPT |
| SEQ ID NO: 129 | MHFGKFNERVCSKCNTFPCCCNPCAAQSCPIWPVKPS |
| SEQ ID NO: 130 | MHFGRFNERVCSKCNTFPCCCCAAQSCPIWPVKPT |
| SEQ ID NO: 131 | MHFGKFKDSVCSKCNTFPCCCNPCAAQSCPIWPVKPT |
| SEQ ID NO: 132 | MHFGRFNERVCSKCNTFPCCCCAAQSCPIWPVKP |
| SEQ ID NO: 133 | MHFGKFKERVCSKCNSFPCCCSPCPPQSCPIWPVKPT |
| SEQ ID NO: 134 | MHFGKFKDRVCSKCNTFPCCCSPCPPQSCPIWPVKPT |
| SEQ ID NO: 135 | MHFGRFNERVCSKCNTFPCCCSPCDVQSCPIWPVKPT |
| SEQ ID NO: 136 | MQFGRFNERVCSKCTTFPCCCSPCDVQSCPIWPVKPT |
| SEQ ID NO: 137 | MHFGKFNDRICSKCNTFPCCCNPCAPSCPVWPVKP |
| SEQ ID NO: 138 | MHFGNFIDRVCSKCNTFPCCCRGGPVPGCPIWPVKPT |
| SEQ ID NO: 139 | MHFGNFIDRVCSKCKTFPCCCRGGPVPGCPIWPVKPT |
| SEQ ID NO: 140 | MHFGNFIDRVCSKCNTFPCCCRGGPVPGCPIWPVKPP |

| Sequence Identifier | Sequence |
|---|---|
| SEQ ID NO: 141 | MHFGNFIDRVCSKCNTFPCCCRGGPVPGCHIWPVKPT |
| SEQ ID NO: 142 | MHFGNFIDRVCSKCKTFPCCCRGGPVPCCPIWPVKPT |
| SEQ ID NO: 143 | MHFGNFIDRVCSKCKTIPCCCRGGPVPGCPIWPVKPT |
| SEQ ID NO: 144 | MHFGNFIDRVCSKCNTFPCCCKGGPVPGCHIWPVKPT |
| SEQ ID NO: 145 | MHFGNFIDRVCSKCKTFPCCCGSGPVPGCPIWPVKPT |
| SEQ ID NO: 146 | MHFGNFIDRVCSKCKTSPCCCGSGPVPGCPIWPVKPT |
| SEQ ID NO: 147 | MHFGNFIDRVCTKCKIFPRCCRGGPVPGCPIWPVKPT |
| SEQ ID NO: 148 | MHFGKFTDRVCSKCNTFPCCCNTCPAPNCPIWPVKP |
| SEQ ID NO: 149 | MNFGNFNNRICSKCNTFPCCCIPCAPSCPVWPVKPG |
| SEQ ID NO: 150 | MYFGNFLDRICSKCNTFPCCCLSGPILRSPIWPVRPT |
| SEQ ID NO: 151 | MHFGNFLDRVCNKCNTFPCCCLSGPIHRSPIWPVPPAKATR |
| SEQ ID NO: 152 | MQFGKYNDRICRKCNTFPCCCNPSAPSCPGWPVKP |
| SEQ ID NO: 153 | MKFQDFNINKICNNCHSYPCCCHNGPVQRCPVWPVKPT |
| SEQ ID NO: 154 | MKFQDFNINKICNNCHSYPCCCHNGPVHRCPVWPVKPT |
| SEQ ID NO: 155 | MKFQDFNINKICNNCNSYPCCCHNGPVQRCPVWPVKPT |
| SEQ ID NO: 156 | MKFQDFNINKICNNCHSYPCCCHNGPVLRCPVWPVKPT |
| SEQ ID NO: 157 | MKFLDFNINKICNNCHSYPCCCHNGPVHRCPVWPVKPT |
| SEQ ID NO: 158 | MKFQDFNINKICNNCHSYPCCCHKGPVHRCPVWPVKPT |
| SEQ ID NO: 159 | MKFQDFNINKICNICHSYPFCCHNGPVQRCPVWPVKPT |
| SEQ ID NO: 160 | MKFQDFNINMICNNCHSYPCCCHNGPVHRCPVWPVKP |
| SEQ ID NO: 161 | MKFHDFNLNNICGKCLSHPCCCNNGPAQRCPIWPVKPT |
| SEQ ID NO: 162 | MKFHDFNLNNICGKCLSHPCCCNNVPAQRCPIWPVKPT |
| SEQ ID NO: 163 | MKFHDFNLNNICGKCLSHPCCCNNGPVQRCPIWPVKPT |
| SEQ ID NO: 164 | MDFANFKNRICSRCNSFPCNCKRNFPQNCPIWPVKPT |
| SEQ ID NO: 165 | MDFANFKNRICSRCNSFPCNCKRNSPQNCPIWPVKPT |
| SEQ ID NO: 166 | MDFANFKNRICSRCNTFPCNCKRNFPQNCPIWPVKPT |
| SEQ ID NO: 167 | MDFANFKNRICSRCNSFPCNCKGNFPQNCPIWPVKPT |
| SEQ ID NO: 168 | MDFAYFKNRICSRCNSFPCNCKRNFPQNCPIWPVKPT |
| SEQ ID NO: 169 | MDFANFKNRICSRCNSFPCNCIRNIPQNCPIWPVKPT |
| SEQ ID NO: 170 | MDLANFKNRICSRCNSFPCNCKRNFPQNCPIWPVKPT |

| Sequence Identifier | Sequence |
|---|---|
| SEQ ID NO: 171 | MDFANFKNRICSRCNSFPCNCKSNYPQNCSIWPVKPT |
| SEQ ID NO: 172 | MNFEDYFLNNVCSKCKTFPCACIRIPEHHCCIWPVKPT |
| SEQ ID NO: 173 | MNFEDYFLNNVCSKCKTFPCACIRIPGHHCSIWPVKPT |
| SEQ ID NO: 174 | MNFEDYFLNNVHVLCKTFPCACIRIPEHHCCIWPVKPT |
| SEQ ID NO: 175 | MNFEDYFLNNVCSKCRTFPCGCRRIPEHHSCVWPVKPT |
| SEQ ID NO: 176 | MNFEDYFLKNVCSKCRTFPCGCTRIPEQHCCVWPVKPT |
| SEQ ID NO: 177 | MNFHDFILNNICKRCNSYPCRCINRPEQNCSIWPVKPT |

**Table 3:** Exemplary *Viridibacillus* N-Terminal Targeting Sequences

| Sequence Identifier | Sequence |
|---|---|
| SEQ ID NO: 178 | ATGGATTCAAATAAAACGAGGTGTGCTGTTTGTAATAAATATCAATGTTCTTGTAACTCCAAAAAAAGAAGTCCTAA AACAGTTATTAGAGATTTAGATTATATAGATCCATGTGAACCTCTTTATATAATAGATCATTGTCATAATAGA |
| SEQ ID NO: 179 | MDSNKTRCXVCNKYQCSCNHKKRSPKTVIRDLDYIDPCEPLYIIDHCHNR |
| SEQ ID NO: 180 | ATGGACTCAAATAAAACGAGGTGTCCTATTTGTAATAATTATCAATGTTCTTGTAACGCTAAAAAAAGAAGGCCTAC AAGATGTATTAGATATTTAGATTATATAGATCAATGTGAACAATGTGAACCTATTTCTATAATAGATCATTGTCATA ATAGA |
| SEQ ID NO: 181 | MDSNKTRCPICNNYQCSCNAKKRRPTRCIRYLDYIDQCEQCEPISIIDHCHNR |
| SEQ ID NO: 182 | ATGGACTCAAATAAAACGAGGTGTCCTATTTGTAATAATTATCAATGTTCTTGTAACGCTAAAAAAAGAAGGCCTAC AAGATGTATTAGATATTTAGATTATATAGATCAATGTGAACAATGTGAACCTATTTCTATAATAGATCATTGTCATA ATAGAGGTAAAACAGGACCGACCGGAGCAACTGGTGCAACCGGACCAACTGGAGCAACTGGAGCAACAGGACCAA CAGGACCAACTGGAGCAACAGGACCTACAGGAGCAACAGGACCAACAGGTGCAACTGGGGCGACAGGAATCACCG GGCCGACTGGAGCAACGGGAGCAACA |
| SEQ ID NO: 183 | MDSNKTRCPICNNYQCSCNAKKRRPTRCIRYLDYIDQCEQCEPISIIDHCHNRGKTGPTGATGATGPTGATGATGPTGPTG ATGPTGATGPTGATGATGITGPTGATGAT |
| SEQ ID NO: 184 | ATGGAATCAAATAAAACGAGGTGTATTGTTTGTAATAAATATCAATGTTCTTGTAACTCCAAAAAAAGAAGTCCTAA AACAGTTATTAGAGATTTAGATTATATAGATCCATGTGAACCTCTTTATATAATAGATCATTGTCATAATAGA |
| SEQ ID NO: 185 | MESNKTRCIVCNKYQCSCNSKKRSPKTVIRDLDYIDPCEPLYIIDHCHNR |
| SEQ ID NO: 186 | ATGGAATCAAATAAAACGAGGTGTATTGTTTGTAATAAATATCAATGTTCTTGTAACTCCAAAAAAAGAAGTCCTAA AACAGTTATTAGAGATTTAGATTATATAGATCCATGTGAACCTCTTTATATAATAGATCATTGTCATAATAGAGGTA AAACAGGACCAACAGGACCAACGGGACCAACCGGAGTGACTGGAGCAACCGGACCAACAGGAGAAACAGGACCA ACGGGAGCAACCGGAGCAACTGGAGCAACAGGAGCAACAGGTCCAATGGGAGTAACTGGCTCGACCGGAGCAACT GGTGTAACGGGAGCAACAGGAGCAACAGGGTCAACCGGAGCAACAGGTGAAACCGGAGCGACTGGTGAAACCGG A |
| SEQ ID NO: 187 | MESNKTRCIVCNKYQCSCNSKKRSPKTVIRDLDYIDPCEPLYIIDHCHNRGKTGPTGPTGPTGVTGATGPTGETGPTGATG ATGATGATGPMGVTGSTGATGVTGATGATGSTGATGETGATGETG |
| SEQ ID NO: 188 | ATGTATTCAAATAAAAAGAGGTGTGCTGTTTGTAATAAATATCAATGTTCTTGTAACTCCAAAAAAAGAAGTCCTAA AACAGTTATTAGAGATTTAGATTATATAGATCCATGTGAACCTCTTTATATAATAGATCATTGTCATAATAGA |
| SEQ ID NO: 189 | MYSNKKRCAVCNKYQCSCNSKKRSPKTVIRDLDYIDPCEPLYIIDHCHNR |
| SEQ ID NO: 190 | ATGTATTCAAATAAAAAGAGGTGTGCTGTTTGTAATAAATATCAATGTTCTTGTAACTCCAAAAAAAGAAGTCCTAA AACAGTTATTAGAGATTTAGATTATATAGATCCATGTGAACCTCTTTATATAATAGATCATTGTCATAATAGAGGTA AAACAGGACCAACAGGAGCAACAGGTCATACAGGAACAACCGGAACAACAGGAGAGACTGGACCAACAGGAGCA ACAGGAGCAACAGGAATAACGGGAGCAACGGGAGAAACAGGAGCAACAGGACCAACGGGAACAACTGGTGTAAC |

| Sequence Identifier | Sequence |
|---|---|
| | CGGAGAAACCGGAGCAACAGGTCCAACTGGAGAAACTGGTGAAACAGGACCAACGGGAGCAACTGGGAACCGGA<br>GCAACAGGAGAAACAGGAACAACTGGAGCAACAGGAAAAACGGGAACAACAGGAGAAACAGGAGAAACAGGAG<br>CAACAGGAGAAACAGGAAAAACAGG |
| SEQ ID NO: 191 | MYSNKKRCAVCNKYQCSCNSKKRSPKTVIRDLDYIDPCEPLYIIDHCHNRGKTGPTGATGHTGTTGTTGETGPTGATGAT<br>GITGATGETGATGPTGTTGVTGETGATGPTGETGETGPTGATGNRSNRRNRNNWSNRKNGNNRRNRRNRSNRRNRKNR |
| SEQ ID NO: 192 | ATGTATTCAAATAAAAAGAGGTGTGCTGTTTGTAATAAATATCAATGTTCTTGTAACTCCAAAAAAAGAAGTCCTAA<br>AACAGTTATTAGAGATTTAGATTATATAGATCCATGTGAACCTCTTTATATAATAGATCATTGTCATAATAGA |
| SEQ ID NO: 193 | MYSNKKRCAVCNKYQCSCNSKKRSPKTVIRDLDYIDPCEPLYIIDHCHNR |
| SEQ ID NO: 194 | ATGTATTCAAATAAAAAGAGGTGTGCTGTTTGTAATAAATATCAATGTTCTTGTAACTCCAAAAAAAGAAGTCCTAA<br>AACAGTTATTAGAGATTTAGATTATATAGATCCATGTGAACCTCTTTATATAATAGATCATTGTCATAATAGAGGTA<br>AAACAGGACCAACAGGAGCAACAGGTCCTACAGGATCAACGGGACCAACAGGAGTGACTGGACCAACAGGAGCAA<br>CAGGAACAACAGGATCAACAGGAACAACAGGAGCAACAGGAGCAACAGGAGAAACAGGAGCAACAGGACCAACA<br>GGACCAACAGGAGAAACAGGAACAACA |
| SEQ ID NO: 195 | MYSNKKRCAVCNKYQCSCNSKKRSPKTVIRDLDYIDPCEPLYIIDHCHNRGKTGPTGATGPTGSTGPTGVTGPTGATGTT<br>GSTGTTGATGATGETGATGPTGPTGETGTT |
| SEQ ID NO: 196 | ATGGATTCAAATAAAAAGAGGTGTGCTGTTTGTAATAAATATCAATGTTCTTGTAACTCCAAAAAAAGAAGTCCTAA<br>AACAGTTATTAGAGATTTAGATTATATAGATCCATGTGAACCGCTTTATATAATAGATCATTGTCATAATAGA |
| SEQ ID NO: 197 | MDSNKKRCAVCNKYQCSCNSKKRSPKTVIRDLDYIDPCEPLYIIDHCHNR |
| SEQ ID NO: 198 | ATGGATTCAAATAAAAAGAGGTGTGCTGTTTGTAATAAATATCAATGTTCTTGTAACTCCAAAAAAAGAAGTCCTAA<br>AACAGTTATTAGAGATTTAGATTATATAGATCCATGTGAACCGCTTTATATAATAGATCATTGTCATAATAGAGGTA<br>AAACAGGACCAACAGGAGCAACAGGTCCTACAGGATCAATGGGACCAACCGGAGTGACTGGATCAACAGGAGCAA<br>CCGGACCAACAGGGTCAACCGGAGTAACTGGGGAAACAGGATCAACCGGGACAACGGGACCAAGCGGATCAACTG<br>GACCAACTGGTGCAACAGGGTCAACCGGAGAAACCGGAGCAACAGGGTCAACCGGAGCAACTGGAGAAACAGGTC<br>CAACAGGACCAACGGGAACAACTGGTGTAACCGGAGAAACCGGAGCAACAGGTCCAACTGGAGCAACTGGAGCAA<br>CTGGTGAAACAGGTTCAACAGGACCAACGGGAGCAACTGGAGAAACTGGTGAAACAGGTTCAACAGGACCAACGG<br>GAGCAACGGGATCGACTGGAGCAACGGGACCAACGGGAGCAACGGGATCCACTGGAGCAACGGGATCGACTGGAG<br>CAACGGGATCGACTGGAGCAACAGGACCAACAGGAGCAACAGGGTCAACCGGAGAAACAGGACCAACTGGTGAA<br>ACAGGTTCAACGGGAGCAACTGGGTCGACCGGAGCAACAGGTGAAACAGGACCAACGGGAACAACTGGAGTAACC<br>GGAGAAACCGGAGCAACAGGTCCAACAGGAGCAACTGGAGCAACTGGAGAAACTGGTGAAACAGGTTCAACAGGA<br>CCAACGGGAGCAACTGGAGAAACTGGTGAAACAGGTTCAACAGGACCAACGGGAGCAACGGGATCGACTGGAGCA<br>ACGGGACCAACTGGAGCAACGGGATCGACTGGAGCAACGGGATCGACTGGAGCAACGGGATCGACTGGAGCAACA<br>GGACCAACAGGAGCAACAGGGTCAACCGGAGAAACAGGACCAACTGGTGAAACAGGTTCAACGGGAGCAACTGGG<br>TCGACCGGAGCAACAGGTGAAACAGGACCAACGGGAGCAACTGGGTCGACCGGAGCAACTGGTGAAACAGGTGCA<br>ACAGGACCAACAGGACCAACGGGAACAACTGGTGTAACCGGAGCAACAGGTCCAACTGGAGCAACTGGAGAAACA |

| Sequence Identifier | Sequence |
|---|---|
| | GGACCAACGGGAGCGACTGGAGAAGCAGGACCAACAGGGTCAACCGGAGCGACTGGACCAACCGGGGCAACGGG<br>AATCACGGGAGCAACAGGACCAACAGGATCAACTGGTGCAACAGGGTCAACCGGAGAAACTGGATCAACTGGAGA<br>AACCGGACCAACAGGAGCAACTGGTGTAACCGGAGCAACAGGTCCAACTGGAGAAACAGGTTCAACAGGACCAAT<br>GGGAGCAACCGGAGAAACTGGTTCGACCGGATCAACTGGTGTAACGGGAGCAACAGGAGCAACGGGAGAAACCGG<br>AGCAACAGGATCAACGGGAGCAACTGGCACGACCGGAGCAACAGGAGAAACAGGACCAACAGGACCAACTGGGT<br>CCACCGGAGCAACAGGAGAAACAGGTCCAACAGGACCAACGGGAGCAACTGGAGTAACCGGAGCAACAGGAGCA<br>ACGGGAGCAACTGGAGAAACAGGTTCAACAGGACCAATGGGAGCAACCGGAGAAACTGGTTCGACCGGATCAACT<br>GGTGTAACGGGAGCAACAGGAGCGACTGGAGTAACAGGAGCAACTGGTGAAACAGGATCAACGGGAGCAACTGGG<br>TCGACCGGAGCAACAGGTGAAACCGGACCAACAGGTCCAACAGGTCCAACAGGACCAACGGGAACAACTGGTGTA<br>ACCGGAGTAACTGGAGAAACCGGACCAACAGGAGCGACTGGTGAAACAGGTTCAACAGGACCAACGGGAACAACT<br>GGTGTAACCGGAGAAACCGGAGCAACAGGACCAACTGGTGCAACAGGGTCAACCGGAGAAACCGGAGCAACTGGA<br>GAAACAGGTCGAACAGGACCAACGGGAACAACTGGTGTAACCGGAGAAACCGGAGCAACTGGAGAAACAGGACC<br>AACAGGAGCAACGGGATCGACTGGAGCAACAGGACCAACGGGAGCAACTGGGGCGACCGGAGCAACAGGTGAAA<br>CAGGACCAACGGGAGCGACTGGAGAAACAGGAGCAACGGGAGCAACTGGGTCAACCGGAGCAACAGGTCCAACA<br>GGACCAACGGGAACAACTGGAGTAACCGGAGCAACAGGTCCAACTGGAGCAACTGGAGAAACAGGACCAACGGG<br>AGCAACTGGAGAAGCAGGACCAACAGGGTCAACCGGATCGACTGGACCAACCGGGGCAACGGGAATCACGGGAGC<br>AACAGGACCAACAGGAGCAACTGGTGCAACAGGGTCAACCGGAGAAACTGGATCAACTGGAGAAACCGGACCAAC<br>AGGATCAACTGGT |
| SEQ ID NO: 199 | MDSNKKRCAVCNKYQCSCNSKKRSPKTVIRDLDYIDPCEPLYIIDHCHNRGKTGPTGATGPTGSMGPTGVTGSTGATGPT<br>GSTGVTGETGSTGTTGPSGSTGPTGATGSTGETGATGSTGATGETGPTGPTGTTGVTGETGATGPTGATGATGETGSTGP<br>TGATGETGETGSTGPTGATGSTGATGPTGATGSTGATGSTGATGSTGATGPTGATGSTGETGPTGETGSTGATGSTGATG<br>ETGPTGTTGVTGETGATGPTGATGATGETGETGSTGPTGATGETGETGSTGPTGATGSTGATGPTGATGSTGATGSTGAT<br>GSTGATGPTGATGSTGETGPTGETGSTGATGSTGATGETGPTGATGSTGATGETGATGPTGPTGTTGVTGATGPTGATGE<br>TGPTGATGEAGPTGSTGATGPTGATGITGATGPTGSTGATGSTGETGSTGETGPTGATGVTGATGPTGETGSTGPMGATG<br>ETGSTGSTGVTGATGATGETGATGSTGATGTTGATGETGPTGPTGSTGATGETGPTGPTGATGVTGATGATGATGETGS<br>TGPMGATGETGSTGSTGVTGATGATGVTGATGETGSTGATGSTGATGETGPTGPTGPTGPTGTTGVTGVTGETGPTGAT<br>GETGSTGPTGTTGVTGETGATGPTGATGSTGETGATGETGRTGPTGTTGVTGETGATGETGPTGATGSTGATGPTGATG<br>ATGATGETGPTGATGETGATGATGSTGATGPTGPTGTTGVTGATGPTGATGETGPTGATGEAGPTGSTGSTGPTGATGIT<br>GATGPTGATGATGSTGETGSTGETGPTGSTG |
| SEQ ID NO: 200 | ATGGATTCAAATAAAACGAGGTGTGCTGTTTGTAATAAATATCAATGTTCTTGTAACTCCAAAAAAAGAAGTCCTAA<br>AACAGTTATTAGAGATTTAGATTATATAGATCCATGTGAACCTCTTTATATAATAAATCATTGTCATAATAGA |
| SEQ ID NO: 201 | MDSNKTRCAVCNKYQCSCNSKKRSPKTVIRDLDYIDPCEPLYIINHCHNR |
| SEQ ID NO: 202 | ATGGATTCAAATAAAACGAGGTGTGCTGTTTGTAATAAATATCAATGTTCTTGTAACTCCAAAAAAAGAAGTCCTAA<br>AACAGTTATTAGAGATTTAGATTATATAGATCCATGTGAACCTCTTTATATAATAAATCATTGTCATAATAGAGGTA |

| Sequence Identifier | Sequence |
|---|---|
| | AAACTGGACCAACTGGACCAACCGGATCGACCGGACCAACAGGACCAACTGGTGAAACCGGACCAACTGGAGCAA CAGGACCAACAGGAGCTACTGGAGCAACTGGAGCAACTGGTGCAACTGGAGCAACGGGATCAACTGGAGCAACAG GATCAACTGGGGCAGCCGGAGTAACTGGTGAAACAGGACTAACAGGGTCAACCGGAGCGACAGGA |
| SEQ ID NO: 203 | MDSNKTRCAVCNKYQCSCNSKKRSPKTVIRDLDYIDPCEPLYIINHCHNRGKTGPTGPTGSTGPTGPTGETGPTGATGPTG ATGATGATGATGATGSTGATGSTGAAGVTGETGLTGSTGATG |
| SEQ ID NO: 204 | ATGGATTCAAATAAAACGAGGTGTGCTGTTTGTAATAAATATCAATGTTCTTGTAATACCAAAAAAAGAAGTCCTAA AACAGTTATTAGAGATTTAGATTATATAGATCCATGTGAACCTCTTTATATAATAGATCATTGTCATAATAGA |
| SEQ ID NO: 205 | MDSNKTRCAVCNKYQCSCNTKKRSPKTVIRDLDYIDPCEPLYIIDHCHNR |
| SEQ ID NO: 206 | ATGGATTCAAATAAAACGAGGTGTGCTGTTTGTAATAAATATCAATGTTCTTGTAATACCAAAAAAAGAAGTCCTAA AACAGTTATTAGAGATTTAGATTATATAGATCCATGTGAACCTCTTTATATAATAGATCATTGTCATAATAGAGGTA AAACAGGACCAACAGGACCAACAGGAGCAACTGGACCAACCGGACCAACTGGAGCAACAGGGGCAACCGGAGCA ACAGGTCCAACAGGATCAACTGGCGCAACAGGAGCAACTGGACAAACGGGAGCAACTGGAGCAACGGGACCAACA GGAGCAACAGGAGCAACTGGAGAAACAGGAGCAACAGGAGCAACAGGAGCAACAGGAGCAACAGGACCAACGGG AGCAACTGGAGAAACAGGAGCA |
| SEQ ID NO: 207 | MDSNKTRCAVCNKYQCSCNTKKRSPKTVIRDLDYIDPCEPLYIIDHCHNRGKTGPTGPTGATGPTGPTGATGATGATGPT GSTGATGATGQTGATGATGPTGATGATGETGATGATGATGATGPTGATGETGA |
| SEQ ID NO: 208 | ATGGATTCAAATAAAACGAGGTGTGCTGTTTGTAATAAATATCAATGTTCTTGTAACTCCAAAAAAAGAAGTCCTAA AACAGTTATTAGAGATTTAGATTATATAGATCCATGTGAACCTCTTTATATAATAGATCATTGTCATAATAGA |
| SEQ ID NO: 209 | MDSNKTRCAVCNKYQCSCNSKKRSPKTVIRDLDYIDPCEPLYIIDHCHNR |
| SEQ ID NO: 210 | ATGGATTCAAATAAAACGAGGTGTGCTGTTTGTAATAAATATCAATGTTCTTGTAACTCCAAAAAAAGAAGTCCTAA AACAGTTATTAGAGATTTAGATTATATAGATCCATGTGAACCTCTTTATATAATAGATCATTGTCATAATAGAGGTA AAACAGGACCAACAGGAGCAACAGGTCCAACGGGACCAACCGGAGCAACGGGATCAACTGGTCCAACAGGATCAA CTGGAGCAACTGGAGCAACAGGGTCAACCGGAGCGACTGGAGAAACAGGACCAACTGGGGTAACGGGAATCACGG GACCGACTGGTGTAACTGGAGCAACAGGGTTCACAGGACTGACTGGAGCAACTGGAGCGACAGGAAATACAGGTC CAACAGGACCAACCGGAGCA |
| SEQ ID NO: 211 | MDSNKTRCAVCNKYQCSCNSKKRSPKTVIRDLDYIDPCEPLYIIDHCHNRGKTGPTGATGPTGPTGATGSTGPTGSTGAT GATGSTGATGETGPTGVTGITGPTGVTGATGFTGLTGATGATGNTGPTGPTGA |
| SEQ ID NO: 212 | ATGGATTCAAATAAAACGAGGTGTACTGTTTGTAATAAATATCAATGTTCATGTAACCACAAAAAAAGAAGTCCTA AAACAGTTATTAGAGATTTAGATTATATAGATCCATGTGAACCGCTTTATATAATAGATCATTGTCATAATAGA |
| SEQ ID NO: 213 | MDSNKTRCTVCNKYQCSCNHKKRSPKTVIRDLDYIDPCEPLYIIDHCHNR |
| SEQ ID NO: 214 | ATGGATTCAAATAAAACGAGGTGTACTGTTTGTAATAAATATCAATGTTCATGTAACCACAAAAAAAGAAGTCCTA AAACAGTTATTAGAGATTTAGATTATATAGATCCATGTGAACCGCTTTATATAATAGATCATTGTCATAATAGAGGT AAAACAGGTCCAACGGGGCCAACCGGAGCAACTGGAGCAACAGGTGCAACGGGATCAACTGGGCCGACAGGAGTA ACTGGTGCAAACTCATATACAAAACAAACACTGCCAACGACGTCAACAGAGAAGAAA |

| Sequence Identifier | Sequence |
|---|---|
| SEQ ID NO: 215 | MDSNKTRCTVCNKYQCSCNHKKRSPKTVIRDLDYIDPCEPLYIIDHCHNRGKTGPTGPTGATGATGATGSTGPTGVTGAN<br>SYTKQTLPTTSTEKK |
| SEQ ID NO: 216 | ATGGATTCAAATAAAACGAGGTGTACTGTTTGTAATAAATATCAATGTTCATGTAACCCCAAAAAAAGAAGTCCTA<br>AAACAGTTATTAGAGATTTAGATTATATAAATCCATGTGAACCGCTTTATATAATAGATCATTGTCATAATAGA |
| SEQ ID NO: 217 | MDSNKTRCTVCNKYQCSCNPKKRSPKTVIRDLDYINPCEPLYIIDHCHNR |
| SEQ ID NO: 218 | ATGGATTCAAATAAAACGAGGTGTACTGTTTGTAATAAATATCAATGTTCATGTAACCCCAAAAAAAGAAGTCCTA<br>AAACAGTTATTAGAGATTTAGATTATATAAATCCATGTGAACCGCTTTATATAATAGATCATTGTCATAATAGAGGT<br>AAAACAGGTCCAACGGGGCCAACCGGAGCAACCGGAGCAACGGGGCCAACCGGACCAACTGGAGCAACAGGGCC<br>AACCGGAGCGACTGGAGCAACCGGACCAACGGGATCAACAGGTCCTACAGGATCAACCGGAGCAACAGGACCGAC<br>TGGGGCTACAGGAGTAACTGGAGCAACGGGAGCAACTGGAGCAACGGGAGTAACTGGGGCAACAGGACCAACGGG<br>ACCAACAGGGTTAACCGGAGCGACTGGAGCAACAGGAACGACTGGGGCTACAGGAGCAACTGGGGCAACGGGAGT<br>AACTGGAGCAACAGGACCGACTGGGGCAACGGGAGTAACTGGAGCAACGGGAGTAACTGGGGCAACAGGACCAAC<br>TGGAGCAACAGGATCGACTGGAGAAACTGGAACAACAGGAGTAACTGGAGCAACGGGAGTAACTGGAGCAACAGG<br>TCCAACCGGGTCAATCGGATCAACGGGAGCAACTGGGGCAACCGGACCAACTGGAGCAACCGGGGCAACAGGAGC<br>AACCGGACCAACGGGAGAAACCGGACCAACCGGACCAACAGGCCCAACGGGAATCACCGGGCCAACCGGAGCAAC<br>TGGTTCAGGAGGCGTAATCCCATTTGCATCAGGAGGCACAGTAACAATAAATTCACTATTAACTGGGGTACCTAATA<br>CCGGAGGTATTATTGCATTTGGCAATAGTACTACTAGTGTAGGGATTGGTAATGCTACAGTAAATCTTCAAAATATT<br>AATAATGAAGCGTTTGTCGTTCCACATGCTGGAGCAATTACAAATGTTGCTGCATTCTTTAATATTACAGTTGCTCTT<br>AATATAGCTGTTTTAGGTACAGCTACTATTACGGCACAAGTATGGAAATCACAAAATGCATCATCTAACGTATTTGC<br>ACCTTTAGCATCGACTCTTATAAGCTTTACACCATTAGCTGGTGCCATAGCTGCATTTACTACATTAAATGGTGCTCT<br>TGCAAATTTAAATGAACCAGTAAATGTTGGAGATCGTTTAATTATGGTATTCTCTGTGGCTACTACAGGGTTAAGTG<br>TAATAACTGCTATTACAGGTACAGCAAGTGCGGGTATTACAATTAGTTGA |
| SEQ ID NO: 219 | MDSNKTRCTVCNKYQCSCNPKKRSPKTVIRDLDYINPCEPLYIIDHCHNRGKTGPTGPTGATGATGPTGPTGATGPTGAT<br>GATGPTGSTGPTGSTGATGPTGATGVTGATGATGATGVTGATGPTGPTGLTGATGATGTTGATGATGATGVTGATGPT<br>GATGVTGATGVTGATGPTGATGSTGETGTTGVTGATGVTGATGPTGSIGSTGATGATGPTGATGATGATGPTGETGPTG<br>PTGPTGITGPTGATGSGGVIPFASGGTVTINSLLTGVPNTGGIIAFGNSTTSVGIGNATVNLQNINNEAFVVPHAGAITNVA<br>AFFNITVALNIAVLGTATITAQVWKSQNASSNVFAPLASTLISFTPLAGAIAAFTTLNGALANLNEPVNVGDRLIMVFSVA<br>TTGLSVITAITGTASAGITIS |

**[0074]** N-terminal targeting sequences compatible with *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* are shown in Table 1, 2, and 3, respectively. In addition to these sequences, the N-terminal targeting sequence may alternatively comprise a variant sharing at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to any of the sequences disclosed herein, so long as the sequence retains the capability to target the fusion protein to the exosporium of a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore. In some embodiments, a fragment of at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 contiguous amino acids selected from any of the sequences disclosed in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*) may be used. This contiguous segment may include the N-terminal end or the C-terminal end of any of the sequences disclosed herein (e.g., an N-terminal targeting sequence may comprise the last 25 contiguous amino acids of any sequence disclosed herein). In some aspects, the only required functionality is that the sequence maintains the capability to target a fusion protein to the exosporium of a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore.

**[0075]** The N-terminal signal sequence used to target the fusion protein to the exosporium may comprise a polypeptide having a sequence as disclosed in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*). Alternatively, in select embodiments this N-terminal signal sequence may comprise a variant or fragment thereof that targets the fusion protein to the exosporium of a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore and a molecule of interest (e.g., peptide or polypeptide) sequence heterologous to the N-terminal signal sequence. In select embodiments, the N-terminal signal sequence comprises an amino acid sequence having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity with the amino acid sequence of any of the sequences disclosed in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*). In select embodiments, the N-terminal signal sequence comprises a contiguous sequence of at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 amino acids that is identical to a contiguous sequence of the same number amino acids disclosed in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*).

**[0076]** As discussed herein, fusion protein constructs according to several aspects of the disclosure comprise an N-terminal signal sequence or a variant or fragment thereof that targets the fusion protein to the exosporium of a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore and a polypeptide sequence that is heterologous to the N-terminal signal sequence. However, in further aspects, any of the disclosed sequences, as well as the sequential variants and fragments thereof according to any of the disclosed aspects, may be used for other purposes. The disclosure's focus on aspects wherein these sequences function as N-terminal exosporium targeting sequences is not to be construed as a disclaimer of other functionalities.

**[0077]** In some embodiments, the N-terminal signal sequence comprises a polypeptide with an amino acid sequence represented by any of the sequences disclosed in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*). In alternative embodiments, the N-terminal signal sequence comprises a fragment of any of the sequences disclosed in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*), e.g., a polypeptide with an amino acid sequence comprising at least one contiguous subsequence found in any of the sequences disclosed on these tables or figures. In alternative embodiments, the N-terminal signal sequence comprises a variant of any of Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*), e.g., a polypeptide with an amino acid sequence that shares a minimum or exact degree of percentage identity with a sequence disclosed in these tables or figures. In select embodiments, the N-terminal signal sequence may qualify as both a fragment and as a variant, as defined above (e.g., an N-terminal signal sequence comprising a contiguous subsequence of a sequence disclosed herein, as well as a divergent sequence that falls within a disclosed sequence identity range).

**[0078]** In select embodiments, the N-terminal signal sequence comprises an amino acid sequence having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity with an amino acid sequence disclosed in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*).

**[0079]** In select embodiments, the N-terminal signal sequence comprises a contiguous sequence of at least 10, 20 or 25 amino acids that is identical to a contiguous sequence of at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 amino acids of an amino acid sequence disclosed in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*).

**[0080]** In some embodiments, the N-terminal signal sequence comprises a polypeptide with an amino acid sequence encoded by any of the nucleotide sequences disclosed in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*). In alternative embodiments, the N-terminal signal sequence comprises a fragment of a polypeptide with an amino acid sequence encoded by any of the nucleotide sequences disclosed in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*), e.g., a polypeptide with an amino acid sequence comprising at least one contiguous subsequence found in a polypeptide with an amino acid sequence encoded by a nucleotide sequence disclosed in these tables or figures. In alternative embodiments, the N-terminal signal sequence comprises a variant of a polypeptide with an amino acid sequence encoded by a nucleotide sequence any of the nucleotide sequences disclosed in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*), e.g., a polypeptide with an amino acid sequence that shares a minimum or exact degree of percentage identity with a polypeptide with an amino acid sequence encoded by a nucleotide sequence disclosed in these tables or figures. In select embodiments, the N-terminal signal sequence may qualify as both a fragment and as a variant, as defined above, e.g., an N-terminal signal sequence comprising a contiguous subsequence found in a polypeptide with an amino acid sequence disclosed in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*), followed by a divergent sequence that falls within a minimum sequence identity range as described herein.

**[0081]** In select embodiments, the N-terminal signal sequence comprises a nucleotide sequence having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity with any of the nucleotide sequences disclosed herein, e.g., any nucleotide sequences disclosed in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*).

**[0082]** In select embodiments, the N-terminal signal sequence comprises a nucleotide sequence that hybridizes to a nucleic acid probe complementary to a polynucleotide encoding any of the polypeptide sequences disclosed in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*), or a fragment thereof, under moderate or high stringency.

**[0083]** In select embodiments, the N-terminal signal sequence comprises a contiguous sequence of at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 nucleotides that is

identical to a contiguous sequence of the same number of nucleotides in any of the nucleotide sequences disclosed in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*).

**[0084]** With respect to any of the alternative N-terminal targeting sequences contemplated by this disclosure, such as the aforementioned embodiments, the minimum required functionality of such sequences in selected aspects is the capability to target a fusion protein to the exosporium of a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore.

## Fusion Proteins

**[0085]** The disclosure provides fusion proteins comprising an N-terminal targeting sequence linked, directly or indirectly, to at least one molecule of interest (e.g., polypeptide sequence of a protein or peptide of interest, such as at least one plant growth stimulating protein or peptide). In selected embodiments, the indirect linkage may be an intervening spacer, linker or a regulatory sequence. The protein or peptide may comprise, but is not limited to, a peptide hormone, a non-hormone peptide, an enzyme involved in the production or activation of a plant growth stimulating compound or an enzyme that degrades or modifies a bacterial, fungal, or plant nutrient source. In general, any protein of interest capable of expression in a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore and heterologous to the selected N-terminal targeting sequence may be used. The targeting sequence can be any of the targeting sequences described above.

**[0086]** In some embodiments, the fusion proteins can comprise a targeting sequence and at least one protein or peptide that protects a plant from a pathogen. The targeting sequence can be any of the targeting sequences described above.

**[0087]** The fusion protein can be made using standard cloning and molecular biology methods known in the art. For example, a gene encoding a protein or peptide (e.g., a gene encoding a plant growth stimulating protein or peptide) can be amplified by polymerase chain reaction (PCR) and ligated to DNA coding for any of the above-described targeting sequences to form a DNA molecule that encodes the fusion protein. The DNA molecule encoding the fusion protein can be cloned into any suitable vector, for example a plasmid vector. The vector suitably comprises a multiple cloning site into which the DNA molecule encoding the fusion protein can be easily inserted. The vector also suitably contains a selectable marker, such as an antibiotic resistance gene, such that bacteria transformed, transfected, or mated with the vector can be readily identified and isolated. Where the vector is a plasmid, the plasmid suitably also comprises an origin of replication. The DNA encoding the fusion protein is suitably under the control of a sporulation promoter that will cause expression of the fusion protein on the exosporium of a

*Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore (*e.g.*, a native promoter from a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* family member). Alternatively, DNA coding for the fusion protein, e.g., a sequence comprising any of the polynucleotide sequences disclosed in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*) can be integrated into the chromosomal DNA of a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cell.

**[0088]** The fusion protein can also comprise additional polypeptide sequences that are not part of the targeting sequence, or the linked protein of interest (e.g., the plant growth stimulating protein or peptide, the protein or peptide that protects a plant from a pathogen, the protein or peptide that enhances stress resistance in a plant, or the plant binding protein or peptide). For example, the fusion protein can include tags or markers to facilitate purification (e.g., a polyhistidine tag) or visualization (e.g., a fluorescent protein such as GFP or YFP) of the fusion protein itself or of the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells' spores expressing the fusion protein.

**[0089]** Expression of fusion proteins on the exosporium using the targeting sequences described herein is enhanced due to a lack of secondary structure in the amino-termini of these sequences, which allows for native folding of the fused proteins and retention of activity. Proper folding can be further enhanced by the inclusion of a short amino acid linker between the targeting sequence and the fusion partner protein.

**[0090]** Thus, any of the fusion proteins described herein can comprise an amino acid linker between the targeting sequence and the linked protein of interest (e.g., the plant growth stimulating protein or peptide, the protein or peptide that protects a plant from a pathogen, the protein or peptide that enhances stress resistance in a plant, or the plant binding protein or peptide).

**[0091]** The linker can comprise a polyalanine linker or a polyglycine linker. A linker comprising a mixture of both alanine and glycine residues can also be used. For example, where the targeting sequence comprises SEQ ID NO: 4, a fusion protein can have one of the following structures:

No linker: SEQ ID NO: 4—Fusion Partner Protein

Alanine Linker: SEQ ID NO: 4—$A_n$-Fusion Partner Protein

Glycine Linker: SEQ ID NO: 4—$G_n$-Fusion Partner Protein

Mixed Alanine and Glycine Linker: SEQ ID NO: 4—$(A/G)_n$-Fusion Partner Protein

where $A_n$, $G_n$, and $(A/G)_n$ are any number of alanines, any number of glycines, or any number of a mixture of alanines and glycines, respectively.

**[0092]** For example, *n* can be any integer between 1 to 25, such as an integer between 6 to 10. Where the linker comprises a mixture of alanine and glycine residues, any combination

of glycine and alanine residues can be used. The N-terminal targeting sequence represented by SEQ ID NO: 4 (for *Brevibacillus*) may be used, e.g., as shown above. However, any of the other N-terminal targeting sequences disclosed herein (including truncated and variant forms) may be substituted in place of SEQ ID NO: 4 in the exemplary configurations above, e.g., any of the sequences disclosed in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*). In the structures shown above, "Fusion Partner Protein" represents the linked protein of interest (e.g., a plant growth stimulating protein or peptide, the protein or peptide that protects a plant from a pathogen, the protein or peptide that enhances stress resistance in a plant, or the plant binding protein or peptide).

**[0093]** Alternatively, or in addition, the linker can comprise a protease recognition site. Inclusion of a protease recognition site allows for targeted removal, upon exposure to a protease that recognizes the protease recognition site, of the protein of interest (e.g., a plant growth stimulating protein or peptide, the protein or peptide that protects a plant from a pathogen, the protein or peptide that enhances stress resistance in a plant, or the plant binding protein or peptide).

**[0094]** In certain aspects, the fusion protein comprises an enzyme involved in the production or activation of a plant growth stimulating compound, such as an acetoin reductase, an indole-3-acetamide hydrolase, a tryptophan monooxygenase, an acetolactate synthetase, an α-acetolactate decarboxylase, a pyruvate decarboxylase, a diacetyl reductase, a butanediol dehydrogenase, an aminotransferase, a tryptophan decarboxylase, an amine oxidase, an indole-3-pyruvate decarboxylase, an indole-3-acetaldehyde dehydrogenase, a tryptophan side chain oxidase, a nitrile hydrolase, a nitrilase, a peptidase, a protease, an adenosine phosphate isopentenyltransferase, a phosphatase, an adenosine kinase, an adenine phosphoribosyltransferase, CYP735A, a 5'-ribonucleotide phosphohydrolase, an adenosine nucleosidase, a zeatin cis-trans isomerase, a zeatin O-glucosyltransferase, a β-glucosidase, a cis-hydroxylase, a CK cis-hydroxylase, a CK N-glucosyltransferase, a 2,5-ribonucleotide phosphohydrolase, an adenosine nucleosidase, a purine nucleoside phosphorylase, a zeatin reductase, a hydroxylamine reductase, a 2-oxoglutarate dioxygenase, a gibberellic 2B/3B hydrolase, a gibberellin 3-oxidase, a gibberellin 20-oxidase, a chitosanase, a chitinase, a β-1,3-glucanase, a β-1,4-glucanase, a β-1,6-glucanase, an aminocyclopropane-1-carboxylic acid deaminase, an enzyme involved in producing a nod factor, or any combination of the above.

**[0095]** In other aspects, the fusion protein comprises an enzyme that degrades or modifies a bacterial, fungal, or plant nutrient source, such as a cellulase, a lipase, a lignin oxidase, a protease, a glycoside hydrolase, a phosphatase, a nitrogenase, a nuclease, an amidase, a nitrate reductase, a nitrite reductase, an amylase, an ammonia oxidase, a ligninase, a glucosidase, a

phospholipase, a phytase, a pectinase, a glucanase, a sulfatase, a urease, a xylanase, a siderophore, or any combination of the above.

**[0096]** In some embodiments, the fusion protein is expressed under the control of a sporulation promoter native to the targeting sequence, exosporium protein, or exosporium protein fragment of the fusion protein. The fusion protein may be expressed under the control of a high-expression sporulation promoter. In certain aspects, the high-expression sporulation promoter comprises a sigma-K sporulation-specific polymerase promoter sequence. In selected aspects, the fusion protein may be expressed under the control of a promoter that is native to the targeting sequence of the fusion protein. In some cases, the promoter that is native to the targeting sequence will be a high-expression sporulation promoter. In other cases, the promoter that is native to the targeting sequence will not be a high-expression sporulation promoter. In the latter cases, it may be advantageous to replace the native promoter with a high-expression sporulation promoter. Expression of the fusion protein under the control of a high-expression sporulation promoter provides for increased expression of the fusion protein on the exosporium of the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore. The high-expression sporulation promoter can comprise one or more sigma-K sporulation-specific promoter sequences.

**[0097]** As described above, the fusion proteins may comprise a targeting sequence and at least one heterologous protein that may comprise a growth stimulating protein or peptide. The plant growth stimulating protein or peptide can comprise, among other things, a peptide hormone, a non-hormone peptide, an enzyme involved in the production or activation of a plant growth-stimulating compound, or an enzyme that degrades or modifies a bacterial, fungal, or plant nutrient source. The plant growth stimulating protein or peptide can comprise an enzyme involved in the production or activation of a plant growth-stimulating compound. The enzyme involved in the production or activation of a plant growth stimulating compound can be any enzyme that catalyzes any step in a biological synthesis pathway for a compound that stimulates plant growth or alters plant structure, or any enzyme that catalyzes the conversion of an inactive or less active derivative of a compound that stimulates plant growth or alters plant structure into an active or more active form of the compound. Alternatively, the plant growth-stimulating compound can comprise a plant growth hormone, e.g., a cytokinin or a cytokinin derivative, ethylene, an auxin or an auxin derivative, a gibberellic acid or a gibberellic acid derivative, abscisic acid or an abscisic acid derivative, or a jasmonic acid or a jasmonic acid derivative.

**[0098]** Where the enzyme comprises a protease or peptidase, the protease or peptidase can be a protease or peptidase that cleaves proteins, peptides, proproteins, or preproproteins to create a bioactive peptide. The bioactive peptide can be any peptide that exerts a biological activity. The protease or peptidase that cleaves proteins, peptides, proproteins, or preproproteins

to create a bioactive peptide can comprise subtilisin, an acid protease, an alkaline protease, a proteinase, an endopeptidase, an exopeptidase, thermolysin, papain, pepsin, trypsin, pronase, a carboxylase, a serine protease, a glutamic protease, an aspartate protease, a cysteine protease, a threonine protease, or a metalloprotease.

**[0099]** The plant growth stimulating protein can also comprise an enzyme that degrades or modifies a bacterial, fungal, or plant nutrient source. Such enzymes include cellulases, lipases, lignin oxidases, proteases, glycoside hydrolases, phosphatases, nitrogenases, nucleases, amidases, nitrate reductases, nitrite reductases, amylases, ammonia oxidases, ligninases, glucosidases, phospholipases, phytases, pectinases, glucanases, sulfatases, ureases, xylanases, and siderophores. When introduced into a plant growth medium or applied to a plant, seed, or an area surrounding a plant or a plant seed, fusion proteins comprising enzymes that degrade or modify a bacterial, fungal, or plant nutrient source can aid in the processing of nutrients in the vicinity of the plant and result in enhanced uptake of nutrients by the plant or by beneficial bacteria or fungi in the vicinity of the plant. The fusion proteins can comprise a targeting sequence and at least one protein or peptide that protects a plant from a pathogen. The protein or peptide can comprise a protein or peptide that stimulates a plant immune response. For example, the protein or peptide that stimulates a plant immune response can comprise a plant immune system enhancer protein or peptide. The plant immune system enhancer protein or peptide can be any protein or peptide that has a beneficial effect on the immune system of a plant. Alternatively, the protein or peptide that protects a plant from a pathogen can be a protein or peptide that has antibacterial activity, antifungal activity, or both antibacterial and antifungal activity. The protein or peptide that protects a plant from a pathogen can also be a protein or peptide that has insecticidal activity, helminthicidal activity, suppresses insect or worm predation, or a combination thereof. The protein that protects a plant from a pathogen can comprise an enzyme. Suitable enzymes include proteases and lactonases. The proteases and lactonases can be specific for a bacterial signaling molecule (e.g., a bacterial lactone homoserine signaling molecule). The enzyme can also be an enzyme that is specific for a cellular component of a bacterium or fungus.

**[0100]** The fusion proteins can comprise a targeting sequence and at least one protein or peptide that enhances stress resistance in a plant. For example, the protein or peptide that enhances stress resistance in a plant comprises an enzyme that degrades a stress-related compound. Stress-related compounds include, but are not limited to, aminocyclopropane-1-carboxylic acid (ACC), reactive oxygen species, nitric oxide, oxylipins, and phenolics. Specific reactive oxygen species include hydroxyl, hydrogen peroxide, oxygen, and superoxide. The enzyme that degrades a stress-related compound can comprise a superoxide dismutase, an oxidase,

a catalase, an aminocyclopropane-1-carboxylic acid deaminase, a peroxidase, an antioxidant enzyme, or an antioxidant peptide.

**[0101]** The protein or peptide that enhances stress resistance in a plant can also comprise a protein or peptide that protects a plant from an environmental stress. The environmental stress can comprise, for example, drought, flood, heat, freezing, salt, heavy metals, low pH, high pH, or a combination thereof. For instance, the protein or peptide that protects a plant from an environmental stress can comprise an ice nucleation protein, a prolinase, a phenylalanine ammonia lyase, an isochorismate synthase, an isochorismate pyruvate lyase, or a choline dehydrogenase.

**[0102]** The fusion proteins can comprise a targeting sequence and at least plant binding protein or peptide. The plant binding protein or peptide can be any protein or peptide that is capable of specifically or non-specifically binding to any part of a plant (e.g., a plant root or an aerial portion of a plant such as a leaf, stem, flower, or fruit) or to plant matter. Thus, for example, the plant binding protein or peptide can be a root binding protein or peptide, or a leaf binding protein or peptide.

## Recombinant *Brevibacillus*, *Lysinibacillus*, and *Viridibacillus* Endospores and Cells Expressing Fusion Proteins

**[0103]** The fusion proteins described herein can be expressed by recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells (e.g., *B. brevis*, *L. sphaericus* or *V. arvi* cells). The fusion protein can be any of the fusion proteins discussed above, provided that it is compatible with the selected bacterial genus used for expression, i.e., the fusion protein must include an N-terminal signal peptide shown in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*), or a fragment or variant of any one of these sequences, which retains exosporium-targeting functionality in the corresponding bacterial genus. The recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells can co-express two or more of any of the fusion proteins discussed above. For example, the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells can co-express at least one fusion protein that comprises a plant binding protein or peptide, together with at least one fusion protein comprising a plant growth stimulating protein or peptide, at least one fusion protein comprising a protein or peptide that protects a plant from a pathogen, or at least one protein or peptide that enhances stress resistance in a plant.

**[0104]** The recombinant exosporium-producing *Brevibacillus* cells may comprise *Brevibacillus* cells, such as *B. agri, B. aydinogluensis, B. borstelensis, B. brevis, B. centrosporus,*

*B. choshinensis, B. fluminis, B. formosus, B. fulvus, B. ginsengisoli, B. invocatus, B. laterosporus, B. levickii, B. limnophilus, B. massiliensis, B. nitrificans, B. panacihumi, B. parabrevis, B. reuszeri,* or *B. thermoruber* cells.

**[0105]** The recombinant exosporium-producing *Lysinibacillus* cells may comprise *Lysinibacillus* cells, such as *Lysinibacillus sphaericus, Lysinibacillus boronitolerans, Lysinibacillus fusiformis, Lysinibacillus acetophenoni, Lysinibacillus alkaliphilus, Lysinibacillus chungkukjangi, Lysinibacillus composti, Lysinibacillus contaminans, Lysinibacillus cresolivorans, Lysinibacillus macroides, Lysinibacillus manganicus, Lysinibacillus mangiferihumi, Lysinibacillus massiliensis, Lysinibacillus meyeri, Lysinibacillus odysseyi, Lysinibacillus pakistanensis, Lysinibacillus parviboronicapiens, Lysinibacillus sinduriensis, Lysinibacillus tabacifolii, Lysinibacillus varians, Lysinibacillus xylanilyticus,* or *Lysinibacillus halotolerans* cells.

**[0106]** The recombinant exosporium-producing *Viridibacillus* cells may comprise *Viridibacillus* cells, such as *Viridibacillus arvi, Viridibacillus arenosi*, or *Viridibacillus neidei* cells.

**[0107]** To generate recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells expressing a fusion protein, any *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* bacterium may be transformed using standard methods known in the art (*e.g.,* by electroporation, or by conjugation with a cell that has been transformed with a vector encoding the fusion protein). The bacteria can then be screened to identify transformants by any method known in the art. For example, where the vector includes an antibiotic resistance gene, the bacteria can be screened for antibiotic resistance. Alternatively, DNA encoding the fusion protein can be integrated into the chromosomal DNA of a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cell. The recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells can then exposed to conditions that will induce sporulation. Suitable conditions for inducing sporulation are known in the art. For example, the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells can be plated onto agar plates, and incubated at a temperature of about 30°C for several days (e.g., 3 days), or alternatively cultured in Schaeffer Sporulation Medium.

**[0108]** Inactivated strains, non-toxic strains, or genetically manipulated strains of any of the species disclosed herein can also suitably be used. For example, a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* that lacks the Bin toxins can be used. Alternatively or in addition, once the recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* species' spores expressing the fusion protein have been generated, they can be inactivated to prevent further germination once in use. Any method for inactivating bacterial spores that is known in the art can be used.

Suitable methods include, without limitation, heat treatment, gamma irradiation, x-ray irradiation, UV-A irradiation, UV-B irradiation, chemical treatment (e.g., treatment with gluteraldehyde, formaldehyde, hydrogen peroxide, acetic acid, bleach, or any combination thereof), or a combination thereof. Alternatively, spores derived from nontoxigenic strains, or genetically or physically inactivated strains, can be used.

**[0109]** Fusion protein constructs according to the present disclosure comprise an N-terminal signal sequence or a variant or fragment thereof that targets the fusion protein to the exosporium of a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore and a polypeptide sequence that is heterologous to the N-terminal signal sequence. In select embodiments, the N-terminal signal sequence and the polypeptide sequence that is heterologous to the N-terminal signal sequence are directly linked. In other aspects, an intervening linker or spacer sequence may be present. In further aspects, a cleavage sequence or other regulatory sequence may be positioned between the two regions. The polypeptide sequence that is heterologous to the N-terminal signal sequence may comprise one or more functional proteins. In aspects where multiple functional proteins are contained in the polypeptide sequence that is heterologous to the N-terminal signal sequence, at least one spacer, cleavage sequence or other regulatory element may be located between the two or more functional proteins.

**[0110]** The polypeptide sequence that is heterologous to the N-terminal signal sequence may be, for example: (a) a plant growth stimulating protein or peptide; (b) a protein or peptide that protects a plant from a pathogen; (c) a protein or peptide that enhances stress resistance of a plant; (d) a plant binding protein or peptide; (e) a plant immune system enhancer protein or peptide; or (f) a protein or peptide that enhances nutrient uptake. When expressed in *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus*, these fusion proteins are targeted to the exosporium layer of the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore and are physically oriented such that the protein or peptide is displayed on the outside of the spore.

**[0111]** These *Brevibacillus*, *Lysinibacillus*, and *Viridibacillus* exosporium display systems can be used to deliver peptides, enzymes, and other proteins to plants (e.g., to plant foliage, fruits, flowers, stems, or roots) or to a plant growth medium such as soil. Peptides, enzymes, and proteins delivered to the soil or another plant growth medium in this manner persist and exhibit activity in the soil for extended periods of time. Introduction of recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells expressing the fusion proteins described herein into soil or the rhizosphere of a plant may lead to a beneficial enhancement of plant growth in many different soil conditions. The use of a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* exosporium display system to create these enzymes allows them to continue to exert their beneficial effects on the plant and the rhizosphere over the first months

of a plants life, and in some aspects over longer period of time up to and including the life of the plant.

**Isolated and/or Purified Exosporia and Compositions Comprising the Same**

**[0112]** The disclosure provides isolated and/or purified exosporia obtained from recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores that have been modified to express fusion protein constructs as described herein, and compositions comprising the same. In selected aspects, these compositions comprise either the basal layer or the hair-like nap layer of a recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* exosporium. In others, the composition comprises both layers of a recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* exosporium. In selected aspects, the composition may comprise a specific fraction or extract of a recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* exosporium (e.g., an extract comprising exosporium components soluble in a particular solvent).

**[0113]** In other select aspects, the exosporium compositions may further comprise additional components (e.g., any of the plant growth-promoting compounds, pesticides, or other active agents disclosed herein). In additional aspects, the exosporium compositions may be treated to kill or render nonviable vegetative *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells and/or endospores in the composition. In select aspects, the exosporium composition contains no detectable amounts of *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells and/or endospores. In select aspects, the exosporium composition is processed to remove or reduce the level of bacterial toxins and/or immunogenic components in order to produce an exosporium composition that is less toxic or immunogenic, or otherwise more well-tolerated by a plant or animal that may be treated with or exposed to the exosporium composition.

**[0114]** In selected aspects, the exosporium composition comprises substantially intact exosporia collected from recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores (e.g., using sonication). Alternatively, the composition may contain processed exosporia (e.g., ground up, suspended in a fluid, etc.) In alternative aspects, the exosporium composition may be dissolved in a solvent. In each case, the composition may be processed so that a particular subcomponent or compound is enriched. For example, exosporium compositions may be processed to enrich the concentration or amount of the recombinant fusion protein present in the enriched composition compared to the amount or composition in the crude exosporium collected from the recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores.

**[0115]** In select aspects, the exosporium composition comprises an isolated and/or purified *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* exosporium containing a fusion protein according to any aspects described herein. For example, the fusion protein comprises any of the

N-terminal targeting sequences disclosed herein, e.g., any of the sequences disclosed in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*).

**[0116]** The fusion proteins and/or exosporium compositions disclosed herein may be used to deliver a protein of interest to a plant. In select aspects, the fusion proteins or exosporium compositions according to any aspect described herein may be applied directly to a plant (e.g., as a powder, suspension or solution, to a seed, or to a field). In select aspects, the fusion protein or exosporium composition is applied to a field prior to or after seeding, or alternatively prior to or after sprouting (e.g., pre- or post-planting, or pre- or post-emergence).

**[0117]** In alternative aspects, the fusion proteins and/or exosporium compositions disclosed herein may be delivered to a plant, seed, and/or field indirectly by applying recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells to the plant, seed, or field. In these aspects, the fusion protein and/or exosporium composition may be expressed or generated by the recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells (e.g., in the field), resulting in delivery of the fusion protein to the plant, seed, or field.

## Recombinant Exosporium-Producing *Brevibacillus*, *Lysinibacillus*, and *Viridibacillus* Cells Having Plant-Growth Promoting Effects and/or Other Beneficial Attributes

**[0118]** Some *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* bacteria are known to have inherent beneficial attributes. For example, some strains have plant-growth promoting effects. Any of the fusion proteins described herein can be expressed in such strains.

**[0119]** For example, the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells may comprise a plant-growth promoting strain of *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus*. The plant-growth promoting strain of bacteria can comprise a strain of bacteria that produces an insecticidal toxin (*e.g.*, a Bin toxin), produces a fungicidal compound (e.g., a β-1,3-glucanase, a chitosinase, a lyticase, or a combination thereof), produces a nematocidal compound (e.g., a Cry toxin), produces a bacteriocidal compound, is resistant to one or more antibiotics, comprises one or more freely replicating plasmids, binds to plant roots, colonizes plant roots, forms biofilms, solubilizes nutrients, secretes organic acids, or any combination thereof.

## Biological Control Agents

**[0120]** Compositions provided by the disclosure may further include biological control agents. Biological control agents can include, in particular, bacteria, fungi or yeasts, protozoa, viruses, entomopathogenic nematodes, inoculants and botanicals and/or mutants of them having

all identifying characteristics of the respective strain, and/or at least one metabolite produced by the respective strain that exhibits activity against insects, mites, nematodes and/or phytopathogens. The disclosure provides combinations of the above-described recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores with the particular biological control agents described herein and/or to mutants of specific strains of microorganisms described herein, where the mutants have all the identifying characteristics of the respective strain, and/or at least one metabolite produced by the respective strain that exhibits activity against insects, mites, nematodes and/or phytopathogens or promotes plant growth and/or enhances plant health. According to the disclosure, the biological control agents described herein may be employed or used in any physiologic state such as active or dormant.

**Selected Compositions According to the Present Disclosure**

**[0121]** In selected aspects, the disclosure provides compositions comprising (a) a recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cell that expresses a fusion protein comprising: a targeting sequence that localizes the fusion protein, which comprises a heterologous protein of interest, to the exosporium of a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* family member; and (b) at least one further and different particular biological control agent disclosed herein and/or a mutant of a specific strain of a microorganism disclosed herein having all identifying characteristics of the respective strain, and/or at least one metabolite produced by the respective strain that exhibits activity against insects, mites, nematodes and/or phytopathogens in a synergistically effective amount. In alternative aspects, the composition comprises at least one additional fungicide and/or at least one insecticide, with the proviso that the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells, the insecticide and the fungicide are not identical. In another aspect, composition is used for reducing overall damage of plants and plant parts, as well as, losses in harvested fruits or vegetables caused by insects, mites, nematodes and/or phytopathogens. In another aspect, the composition increases the overall plant health.

**[0122]** The term "plant health" generally comprises various sorts of improvements of plants that are not connected to the control of pests. For example, advantageous properties that may be mentioned are improved crop characteristics including: emergence, crop yields, protein content, oil content, starch content, more developed root system, improved root growth, improved root size maintenance, improved root effectiveness, improved stress tolerance (e.g., against drought, heat, salt, UV, water, cold), reduced ethylene (reduced production and/or inhibition of reception), tillering increase, increase in plant height, bigger leaf blade, less dead basal leaves, stronger tillers, greener leaf color, pigment content, photosynthetic activity, less input needed

(such as fertilizers or water), less seeds needed, more productive tillers, earlier flowering, early grain maturity, less plant verse (lodging), increased shoot growth, enhanced plant vigor, increased plant stand and early and better germination.

**[0123]** Compositions provided by the disclosure may be screened to identify potential benefits to plant growth, health, or other positive attributes by comparing plants which are grown under the same environmental conditions, whereby a part of said plants is treated with a composition according to the present disclosure and another part of said plants is not treated with a composition according to the present disclosure. Instead, said other part is not treated at all or is treated with a suitable control (i.e., an application without a composition according to the disclosure such as an application without all active ingredients), an application without the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells as described herein, or an application without a further particular biological control agent disclosed herein.

**[0124]** The composition according to the present disclosure may be applied in any desired manner, such as in the form of a seed coating, soil drench, and/or directly in-furrow and/or as a foliar spray and applied either pre-emergence, post-emergence or both. In other words, the composition can be applied to the seed, the plant or to harvested fruits and vegetables or to the soil wherein the plant is growing or wherein it is desired to grow (plant's locus of growth).

**[0125]** Reducing the overall damage of plants and plant parts often results in healthier plants and/or in an increase in plant vigor and yield. Preferably, the composition according to the present disclosure is used for treating conventional or transgenic plants or seed thereof.

## Methods of Using Recombinant *Brevibacillus*, *Lysinibacillus*, and *Viridibacillus* Constructs and Compositions

**[0126]** The present disclosure also relates to methods for stimulating plant growth using any of the compositions described above comprising recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells that express a fusion protein and at least one of the further particular biological control agents described herein. The method for stimulating plant growth comprises applying to a plant, a seed, a plant part, to the locus surrounding the plant or in which the plant will be planted (e.g., soil or other growth medium) a composition comprising recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells that express a fusion protein comprising: (i) a heterologous protein (e.g., at least one plant growth stimulating protein); and (ii) a targeting sequence; and at least one further particular biological control agent disclosed herein and/or a mutant of a specific strain of a microorganism disclosed herein having all identifying characteristics of the respective strain, and/or at least one metabolite

produced by the respective strain that exhibits activity against insects, mites, nematodes and/or phytopathogens in a synergistically effective amount.

**[0127]** In another aspect of the present disclosure a method for reducing overall damage of plants and plant parts as well as losses in harvested fruits or vegetables caused by insects, mites, nematodes and/or phytopathogens is provided comprising the step of simultaneously or sequentially applying the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells and at least one further particular biological control agent described herein in a synergistically effective amount.

**[0128]** In one embodiment of the present method the composition further comprises at least one fungicide. In one aspect, the at least one fungicide is a synthetic fungicide. In another embodiment, the composition comprises at least one insecticide in addition to the fungicide or in place of the fungicide, provided that the insecticide, the fungicide, the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells and the particular biological control agent disclosed herein are not identical.

**[0129]** The method of the present disclosure includes the following application methods, namely both of the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells and the at least one further particular biological control agent disclosed herein may be formulated into a single, stable composition with an agriculturally acceptable shelf life (so called "solo-formulation"), or being combined before or at the time of use (so called "combined-formulations").

**[0130]** If not mentioned otherwise, the expression "combination" stands for the various combinations of the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells and at least one further particular biological control agent disclosed herein, and optionally at least one fungicide and/or at least one insecticide, in a solo-formulation, in a single "ready-mix" form, in a combined spray mixture composed from solo-formulations, such as a "tank-mix", and especially in a combined use of the single active ingredients when applied in a sequential manner, i.e., one after the other within a reasonably short period, such as a few hours or days, e.g., 2 hours to 7 days. The order of applying the composition according to the present disclosure is not essential for working the present disclosure. Accordingly, the term "combination" also encompasses the presence of the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells and the at least one further particular biological control agent disclosed herein, and optionally at least one fungicide and/or insecticide on or in a plant to be treated or its surrounding, habitat or storage space, e.g., after simultaneously or consecutively applying the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells and the at least one further particular biological control agent disclosed

herein, and optionally at least one fungicide and/or at least one insecticide to a plant or its surrounding, habitat or storage space.

**[0131]** If the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells and the at least one further particular biological control agent described herein, and optionally at least one fungicide and/or at least one insecticide are employed or used in a sequential manner, it is preferred to treat the plants or plant parts (which includes seeds and plants emerging from the seed), harvested fruits and vegetables according to the following method: firstly applying at least one fungicide and/or at least one insecticide on the plant or plant parts, and secondly applying the further particular biological control agent described herein and the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells to the same plant or plant parts. By this application manner the amount of residues of insecticides/fungicides on the plant upon harvesting is as low as possible. The time periods between the first and the second application within a (crop) growing cycle may vary and depend on the effect to be achieved. For example, the first application is done to prevent an infestation of the plant or plant parts with insects, mites, nematodes and/or phytopathogens (this is particularly the case when treating seeds) or to combat the infestation with insects, mites, nematodes and/or phytopathogens (this is particularly the case when treating plants and plant parts) and the second application is done to prevent or control the infestation with insects, mites, nematodes and/or phytopathogens and/or to promote plant growth. Control in this context means that the composition comprising the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells and the particular biological control agent disclosed herein are not able to fully exterminate the pests or phytopathogenic fungi but are able to keep the infestation on an acceptable level.

**[0132]** The present disclosure also provides methods of enhancing the killing, inhibiting, preventative and/or repelling activity of the compositions of the present disclosure by multiple applications. In some other embodiments, the compositions of the present disclosure are applied to a plant and/or plant part for two times, during any desired development stages or under any predetermined pest pressure, at an interval of about 1 hour, about 5 hours, about 10 hours, about 24 hours, about two days, about 3 days, about 4 days, about 5 days, about 1 week, about 10 days, about two weeks, about three weeks, about 1 month or more. Still in some embodiments, the compositions of the present disclosure are applied to a plant and/or plant part for more than two times, for example, 3 times, 4 times, 5 times, 6 times, 7 times, 8 times, 9 times, 10 times, or more, during any desired development stages or under any predetermined pest pressure, at an interval of about 1 hour, about 5 hours, about 10 hours, about 24 hours, about two days, about 3 days, about 4 days, about 5 days, about 1 week, about 10 days, about two weeks, about three

weeks, about 1 month or more. The intervals between each application can vary if it is desired. One skilled in the art will be able to determine the application times and length of interval depending on plant species, plant pest species, and other factors.

**[0133]** By following the before mentioned steps, a very low level of residues of the at least one fungicide and/or at least one insecticide on the treated plant, plant parts, and the harvested fruits and vegetables can be achieved.

**[0134]** If not mentioned otherwise the treatment of plants or plant parts (which includes seeds and plants emerging from the seed), harvested fruits and vegetables with the composition according to the disclosure is carried out directly or by action on their surroundings, habitat or storage space using customary treatment methods, for example dipping, spraying, atomizing, irrigating, evaporating, dusting, fogging, broadcasting, foaming, painting, spreading-on, watering (drenching), drip irrigating. It is furthermore possible to apply the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells, the at least one further particular biological control agent described herein, and optionally the at least one fungicide and/or the at least one insecticide as solo-formulation or combined-formulations by the ultra-low volume method, or to inject the composition according to the present disclosure as a composition or as sole-formulations into the soil (in-furrow).

**[0135]** The term "plant to be treated" encompasses every part of a plant including its root system and the material – e.g., soil or nutrition medium – which is in a radius of at least 10 cm, 20 cm, 30 cm around the caulis or bole of a plant to be treated or which is at least 10 cm, 20 cm, 30 cm around the root system of said plant to be treated, respectively.

**[0136]** The amount of the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells, which is used or employed in combination with at least one further particular biological control agent described herein, optionally in the presence of at least one fungicide and/or the at least one insecticide, depends on the final formulation as well as size or type of the plant, plant parts, seeds, harvested fruits and vegetables to be treated. Usually, the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells to be employed or used according to the disclosure is present in about 1% to about 80% (w/w), preferably in about 1% to about 60% (w/w), more preferably about 10% to about 50% (w/w) of its solo-formulation or combined-formulation with the at least one further particular biological control agent described herein, and optionally the fungicide and/or the at least one insecticide.

**[0137]** Also the amount of the at least one further particular biological control agent disclosed herein which is used or employed in combination with the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells, optionally in the presence of at least one fungicide and/or the at least one insecticide, depends on the final formulation as well as

size or type of the plant, plant parts, seeds, harvested fruit or vegetable to be treated. Usually, the further particular biological control agent described herein to be employed or used according to the disclosure is present in about 0.1% to about 80% (w/w), preferably 1% to about 60% (w/w), more preferably about 10% to about 50% (w/w) of its solo-formulation or combined-formulation with the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells, and optionally the at least one fungicide and/or the at least one insecticide.

**[0138]** Application of the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells may be effected as a foliar spray, as a soil treatment, and/or as a seed treatment/dressing. When used as a foliar treatment, in one embodiment, about 1/16 to about 5 gallons of whole broth are applied per acre. When used as a soil treatment, in one embodiment, about 1 to about 5 gallons of whole broth are applied per acre. When used for seed treatment about 1/32 to about 1/4 gallons of whole broth are applied per acre. For seed treatment, the end-use formulation contains at least $1 \times 10^4$, at least $1 \times 10^5$, at least $1 \times 10^6$, $1 \times 10^7$, at least $1 \times 10^8$, at least $1 \times 10^9$, at least $1 \times 10^{10}$ colony forming units per gram.

**[0139]** The ratio can be calculated based on the amount of the at least one further particular biological control agent disclosed herein, at the time point of applying said component of a combination according to the disclosure to a plant or plant part and the amount of the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells shortly prior (e.g., 48 h, 24 h, 12 h, 6 h, 2 h, 1 h) or at the time point of applying said component of a combination according to the disclosure to a plant or plant part.

**[0140]** The application of the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells and the at least one further particular biological control agent disclosed herein to a plant or a plant part can take place simultaneously or at different times as long as both components are present on or in the plant after the application(s). In cases where the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells and further particular biological control agent disclosed herein are applied at different times and the further particular biological control agent disclosed herein is applied prior to the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells, the skilled person can determine the concentration of further particular biological control agent disclosed herein on/in a plant by chemical analysis known in the art, at the time point or shortly before the time point of applying the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells. Similarly, when the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells are applied to a plant first, the concentration of the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells can be determined using tests

which are also known in the art, at the time point or shortly before the time point of applying the further particular biological control agent disclosed herein.

**[0141]** In another aspect of the present disclosure a seed treated with the composition as described above is provided. The control of insects, mites, nematodes and/or phytopathogens by treating the seed of plants has been known for a long time and is a subject of continual improvements. Nevertheless, the treatment of seed entails a series of problems which cannot always be solved in a satisfactory manner. Thus, it is desirable to develop methods for protecting the seed and the germinating plant that remove the need for, or at least significantly reduce, the additional delivery of crop protection compositions in the course of storage, after sowing or after the emergence of the plants. It is desirable, furthermore, to optimize the amount of active ingredient employed in such a way as to provide the best-possible protection to the seed and the germinating plant from attack by insects, mites, nematodes and/or phytopathogens, but without causing damage to the plant itself by the active ingredient employed. In particular, methods for treating seed ought also to take into consideration the intrinsic insecticidal and/or nematicidal properties of pest-resistant or pest-tolerant transgenic plants, in order to achieve optimum protection of the seed and of the germinating plant with a minimal use of crop protection compositions.

**[0142]** The present disclosure therefore also relates in particular to a method for protecting seed and germinating plants from attack by pests, by treating the seed with the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells as defined above and at least one further biological control agent selected from particular microorganisms disclosed herein and/or a mutant of a specific strain of microorganism disclosed herein having all identifying characteristics of the respective strain, and/or at least one metabolite produced by the respective strain that exhibits activity against insects, mites, nematodes and/or phytopathogens and optionally at least one fungicide and/or optionally at least one insecticide of the disclosure. The method of the disclosure for protecting seed and germinating plants from attack by pests encompasses a method in which the seed is treated simultaneously in one operation with the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells and the at least one further particular biological control agent described herein, and optionally the at least one fungicide and/or the at least one insecticide. It also encompasses a method in which the seed is treated at different times with the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells and the at least one further particular biological control agent disclosed herein, and optionally the at least one fungicide and/or the at least one insecticide.

**[0143]** The disclosure further provides methods of treating seeds for the purpose of protecting the seed and the resultant plant against insects, mites, nematodes and/or

phytopathogens. The disclosure also relates to seed which at the same time has been treated with a the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells and at least one further particular biological control agent described herein, and optionally at least one fungicide and/or the at least one insecticide. The disclosure further relates to seed which has been treated at different times with the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells and the at least one further particular biological control agent disclosed herein and optionally the at least one fungicide and/or the at least one insecticide. In the case of seed which has been treated at different times with the recombinant exosporium-producing *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells and the at least one further particular biological control agent disclosed herein, and optionally the at least one fungicide and/or the at least one insecticide, the individual active ingredients in the composition of the disclosure may be present in different layers on the seed.

**[0144]** Furthermore, the disclosure relates to seed which, following treatment with the composition of the disclosure, is subjected to a film-coating process in order to prevent dust abrasion of the seed.

**[0145]** One of the advantages of the present disclosure is that, owing to the particular systemic properties of the compositions of the disclosure, the treatment of the seed with these compositions provides protection from insects, mites, nematodes and/or phytopathogens not only to the seed itself but also to the plants originating from the seed, after they have emerged. In this way, it may not be necessary to treat the crop directly at the time of sowing or shortly thereafter. A further advantage is to be seen in the fact that, through the treatment of the seed with composition of the disclosure, germination and emergence of the treated seed may be promoted.

**[0146]** The compositions of the disclosure are suitable for protecting seed of any variety of plant which is used in agriculture, in greenhouses, in forestry or in horticulture. More particularly, the seed in question is that of cereals (e.g., wheat, barley, rye, oats and millet), maize, cotton, soybeans, rice, potatoes, sunflower, coffee, tobacco, canola, oilseed rape, beets (e.g., sugar beet and fodder beet), peanuts, vegetables (e.g., tomato, cucumber, bean, brassicas, onions and lettuce), fruit plants, lawns and ornamentals. Particularly important is the treatment of the seed of cereals (such as wheat, barley, rye and oats) maize, soybeans, cotton, canola, oilseed rape and rice.

**[0147]** For the purposes of the present disclosure, the composition of the disclosure is applied alone or in a suitable formulation to the seed. The seed is preferably treated in a condition in which its stability is such that no damage occurs in the course of the treatment. Generally speaking, the seed may be treated at any point in time between harvesting and sowing. Typically, seed is used which has been separated from the plant and has had cobs, hulls, stems, husks, hair or pulp removed. Thus, for example, seed may be used that has been harvested, cleaned and dried

to a moisture content of less than 15% by weight. Alternatively, seed can also be used that after drying has been treated with water, for example, and then dried again.

**[0148]** When treating seed it is necessary, generally speaking, to ensure that the amount of the composition of the disclosure, and/or of other additives, that is applied to the seed is selected such that the germination of the seed is not adversely affected, and/or that the plant which emerges from the seed is not damaged. This is the case in particular with active ingredients which may exhibit phytotoxic effects at certain application rates.

**[0149]** The compositions of the disclosure can be applied directly, in other words without comprising further components and without having been diluted. As a general rule, it is preferable to apply the compositions in the form of a suitable formulation to the seed. Suitable formulations and methods for seed treatment are known to the skilled person and are described in, for example, the following documents: U.S. Patent Nos. 4,272,417 A; 4,245,432 A; 4,808,430 A; 5,876,739 A; U.S. Patent Publication No. 2003/0176428 A1; WO 2002/080675 A1; WO 2002/028186 A2, the contents of each of which being incorporated herein by reference.

**[0150]** The combinations which can be used in accordance with the disclosure may be converted into the customary seed-dressing formulations, such as solutions, emulsions, suspensions, powders, foams, slurries or other coating compositions for seed, and also ULV formulations. These formulations are prepared in a known manner, by mixing composition with customary adjuvants, such as, for example, customary extenders and also solvents or diluents, colorants, wetters, dispersants, emulsifiers, antifoams, preservatives, secondary thickeners, stickers, gibberellins, and also water. Colorants which may be present in the seed-dressing formulations which can be used in accordance with the invention include all colorants which are customary for such purposes. In this context it is possible to use not only pigments, which are of low solubility in water, but also water-soluble dyes. Examples include the colorants known under designations Rhodamin B, C.I. Pigment Red 112, and C.I. Solvent Red 1.

**[0151]** Depending on the plant species or plant cultivars, their location and growth conditions (soils, climate, vegetation period, diet), using or employing the composition according to the present disclosure the treatment according to the disclosure may also result in super-additive ("synergistic") effects. Thus, for example, by using or employing inventive composition in the treatment according to the disclosure, reduced application rates and/or a widening of the activity spectrum and/or an increase in the activity better plant growth, increased tolerance to high or low temperatures, increased tolerance to drought or to water or soil salt content, increased flowering performance, easier harvesting, accelerated maturation, higher harvest yields, bigger fruits, larger plant height, greener leaf color, earlier flowering, higher quality and/or a higher nutritional value of the harvested products, higher sugar concentration within the fruits, better storage stability

and/or processability of the harvested products are possible, which exceed the effects which were actually to be expected.

**[0152]** At certain application rates of the inventive composition in the treatment according to the disclosure may also have a strengthening effect in plants. The defense system of the plant against attack by unwanted phytopathogenic fungi and/or microorganisms and/or viruses is mobilized. Plant-strengthening (resistance-inducing) substances are to be understood as meaning, in the present context, those substances or combinations of substances which are capable of stimulating the defense system of plants in such a way that, when subsequently inoculated with unwanted phytopathogenic fungi and/or microorganisms and/or viruses, the treated plants display a substantial degree of resistance to these phytopathogenic fungi and/or microorganisms and/or viruses. Thus, by using or employing composition according to the present disclosure in the treatment according to the disclosure, plants can be protected against attack by the abovementioned pathogens within a certain period of time after the treatment. The period of time within which protection is effected generally extends from 1 to 10 days, preferably 1 to 7 days, after the treatment of the plants with the active compounds.

**[0153]** Any of the compositions disclosed herein may include one or more agrochemicals. Similarly, the methods of applying compositions according to the disclosure may further comprise introducing at least one agrochemical into the plant growth medium or applying at least one agrochemical to plants or seeds.

**[0154]** The agrochemical can comprise a fertilizer (e.g., a liquid fertilizer), a micronutrient fertilizer material (e.g., boric acid, a borate, a boron frit, copper sulfate, a copper frit, a copper chelate, a sodium tetraborate decahydrate, an iron sulfate, an iron oxide, iron ammonium sulfate, an iron frit, an iron chelate, a manganese sulfate, a manganese oxide, a manganese chelate, a manganese chloride, a manganese frit, a sodium molybdate, molybdic acid, a zinc sulfate, a zinc oxide, a zinc carbonate, a zinc frit, zinc phosphate, a zinc chelate, or a combination thereof), an insecticide (e.g., an organophosphate, a carbamate, a pyrethroid, an acaricide, an alkyl phthalate, boric acid, a borate, a fluoride, sulfur, a haloaromatic substituted urea, a hydrocarbon ester, a biologically-based insecticide, or a combination thereof), an herbicide (e.g., a chlorophenoxy compound, a nitrophenolic compound, a nitrocresolic compound, a dipyridyl compound, an acetamide, an aliphatic acid, an anilide, a benzamide, a benzoic acid, a benzoic acid derivative, anisic acid, an anisic acid derivative, a benzonitrile, benzothiadiazinone dioxide, a thiocarbamate, a carbamate, a carbanilate, chloropyridinyl, a cyclohexenone derivative, a dinitroaminobenzene derivative, a fluorodinitrotoluidine compound, isoxazolidinone, nicotinic acid, isopropylamine, an isopropylamine derivatives, oxadiazolinone, a phosphate, a phthalate, a picolinic acid compound, a triazine, a triazole, a uracil, a urea derivative, endothall, sodium

chlorate, or a combination thereof), a fungicide (e.g., a substituted benzene, a thiocarbamate, an ethylene bis dithiocarbamate, a thiophthalidamide, a copper compound, an organomercury compound, an organotin compound, a cadmium compound, anilazine, benomyl, cyclohexamide, dodine, etridiazole, iprodione, metlaxyl, thiamimefon, triforine, or a combination thereof), a molluscicide, an algicide, a plant growth amendment, a bacterial inoculant (e.g., a bacterial inoculant of the genus *Rhizobium*, a bacterial inoculant of the genus *Bradyrhizobium*, a bacterial inoculant of the genus *Mesorhizobium*, a bacterial inoculant of the genus *Azorhizobium*, a bacterial inoculant of the genus *Allorhizobium*, a bacterial inoculant of the genus *Sinorhizobium*, a bacterial inoculant of the genus *Kluyvera*, a bacterial inoculant of the genus *Azotobacter*, a bacterial inoculant of the genus *Pseudomonas*, a bacterial inoculant of the genus *Azospirillium*, a bacterial inoculant of the genus *Bacillus*, a bacterial inoculant of the genus *Streptomyces*, a bacterial inoculant of the genus *Paenibacillus*, a bacterial inoculant of the genus *Paracoccus*, a bacterial inoculant of the genus *Enterobacter*, a bacterial inoculant of the genus *Alcaligenes*, a bacterial inoculant of the genus *Mycobacterium*, a bacterial inoculant of the genus *Trichoderma*, a bacterial inoculant of the genus *Gliocladium*, a bacterial inoculant of the genus *Glomus*, a bacterial inoculant of the genus *Klebsiella*, or a combination thereof), a fungal inoculant (e.g., a fungal inoculant of the family *Glomeraceae*, a fungal inoculant of the family *Claroidoglomeraceae*, a fungal inoculant of the family *Gigasporaceae*, a fungal inoculant of the family *Acaulosporaceae*, a fungal inoculant of the family *Sacculosporaceae*, a fungal inoculant of the family *Entrophosporaceae*, a fungal inoculant of the family *Pacidsporaceae*, a fungal inoculant of the family *Diversisporaceae*, a fungal inoculant of the family *Paraglomeraceae*, a fungal inoculant of the family *Archaeosporaceae*, a fungal inoculant of the family *Geosiphonaceae*, a fungal inoculant of the family *Ambisporaceae*, a fungal inoculant of the family *Scutellosporaceae*, a fungal inoculant of the family *Dentiscultataceae*, a fungal inoculant of the family *Racocetraceae*, a fungal inoculant of the phylum *Basidiomycota*, a fungal inoculant of the phylum *Ascomycota*, a fungal inoculant of the phylum *Zygomycota*, or a combination thereof), or a combination thereof.

**[0155]** The fertilizer can comprise ammonium sulfate, ammonium nitrate, ammonium sulfate nitrate, ammonium chloride, ammonium bisulfate, ammonium polysulfide, ammonium thiosulfate, aqueous ammonia, anhydrous ammonia, ammonium polyphosphate, aluminum sulfate, calcium nitrate, calcium ammonium nitrate, calcium sulfate, calcined magnesite, calcitic limestone, calcium oxide, calcium nitrate, dolomitic limestone, hydrated lime, calcium carbonate, diammonium phosphate, monoammonium phosphate, magnesium nitrate, magnesium sulfate, potassium nitrate, potassium chloride, potassium magnesium sulfate, potassium sulfate, sodium nitrates, magnesian limestone, magnesia, urea, urea-formaldehydes, urea ammonium nitrate, sulfur-coated urea, polymer-coated urea, isobutylidene diurea, $K_2SO_4$-$(MgSO_4)_2$, kainite,

sylvinite, kieserite, Epsom salts, elemental sulfur, marl, ground oyster shells, fish meal, oil cakes, fish manure, blood meal, rock phosphate, super phosphates, slag, bone meal, wood ash, manure, bat guano, peat moss, compost, green sand, cottonseed meal, feather meal, crab meal, fish emulsion, humic acid, or a combination thereof. The agrochemical can comprise any fungicide, bacterial inoculant, or herbicide, as described herein. The spore-forming bacterium, alone or in combination with the insecticide, can further comprise an effective amount of at least one fungicide.

**[0156]** In general, a "fungicide" is a substance to increase mortality or inhibit the growth rate of fungi. The term "fungus" or "fungi" includes a wide variety of nucleated spore-bearing organisms that are devoid of chlorophyll. Examples of fungi include yeasts, molds, mildews, rusts, and mushrooms. Typical fungicidal ingredients also include captan, fludioxonil, iprodione, tebuconazole, thiabendazole, azoxystrobin, prochloraz, and oxadixyl. Select compositions, plant seeds, or inoculums according to the disclosure may comprise any natural or synthetic fungicide, such as: aldimorph, ampropylfos, ampropylfos potassium, andoprim, anilazine, azaconazole, azoxystrobin, benalaxyl, benodanil, benomyl, benzamacril, benzamacryl-isobutyl, bialaphos, binapacryl, biphenyl, bitertanol, blasticidin-S, boscalid, bromuconazole, bupirimate, buthiobate, calcium polysulphide, capsimycin, captafol, captan, carbendazim, carvon, quinomethionate, chlobenthiazone, chlorfenazole, chloroneb, chloropicrin, chlorothalonil, chlozolinate, clozylacon, cufraneb, cymoxanil, cyproconazole, cyprodinil, cyprofuram, debacarb, dichlorophen, diclobutrazole, diclofluanid, diclomezine, dicloran, diethofencarb, dimethirimol, dimethomorph, dimoxystrobin, diniconazole, diniconazole-M, dinocap, diphenylamine, dipyrithione, ditalimfos, dithianon, dodemorph, dodine, drazoxolon, edifenphos, epoxiconazole, etaconazole, ethirimol, etridiazole, famoxadon, fenapanil, fenarimol, fenbuconazole, fenfuram, fenitropan, fenpiclonil, fenpropidin, fenpropimorph, fentin acetate, fentin hydroxide, ferbam, ferimzone, fluazinam, flumetover, fluopyram, fluoromide, fluquinconazole, flurprimidol, flusilazole, flusulfamide, flutolanil, flutriafol, folpet, fosetyl-aluminium, fosetyl-sodium, fthalide, fuberidazole, furalaxyl, furametpyr, furcarbonil, furconazole, furconazole-cis, furmecyclox, guazatine, hexachlorobenzene, hexaconazole, hymexazole, imazalil,imibenconazole, iminoctadine, iminoctadine albesilate, iminoctadine triacetate, iodocarb, iprobenfos (IBP), iprodione, irumamycin, isoprothiolane, isovaledione, kasugamycin, kresoxim-methyl, copper preparations, such as: copper hydroxide, copper naphthenate, copper oxychloride, copper sulphate, copper oxide, oxine-copper and Bordeaux mixture, mancopper, mancozeb, maneb, meferimzone, mepanipyrim, mepronil, metalaxyl, metconazole, methasulfocarb, methfuroxam, metiram, metomeclam, metsulfovax, mildiomycin, myclobutanil, myclozolin, nickel dimethyldithiocarbamate, nitrothal-isopropyl, nuarimol, ofurace, oxadixyl, oxamocarb, oxolinic

acid, oxycarboxim, oxyfenthiin, paclobutrazole, pefurazoate, penconazole, pencycuron, phosdiphen, pimaricin, piperalin, polyoxin, polyoxorim, probenazole, prochloraz, procymidone, propamocarb, propanosine-sodium, propiconazole, propineb, prothiocinazole, pyrazophos, pyrifenox, pyrimethanil, pyroquilon, pyroxyfur, quinconazole, quintozene (PCNB), sulphur and sulphur preparations, tebuconazole, tecloftalam, tecnazene, tetcyclasis, tetraconazole, thiabendazole, thicyofen, thifluzamide, thiophanate-methyl, tioxymid, tolclofos-methyl, tolylfluanid, triadimefon, triadimenol, triazbutil, triazoxide, trichlamide, tricyclazole, tridemorph, trifloxystrobin, triflumizole, triforine, uniconazole, validamycin A, vinclozolin, viniconazole, zarilamide, zineb, ziramor, or a combination thereof. The fungicide can also comprise a substituted benzene, a thiocarbamate, an ethylene bis dithiocarbamate, a thiophthalidamide, a copper compound, an organomercury compound, an organotin compound, a cadmium compound, anilazine, benomyl, cyclohexamide, dodine, etridiazole, iprodione, metlaxyl, thiamimefon, triforine, or a combination thereof. One of ordinary skill in the art will readily appreciate that other known synthetic or naturally-occurring fungicides used for agricultural purposes may also be selected for inclusion in a composition, plant seed or inoculum according to the disclosure.

**[0157]** If a composition, plant seed, or inoculum comprises a fungicide, the fungicide can be a foliar fungicide. Foliar fungicides include copper, mancozeb, penthiopyrad, triazoles, cyproconazole, metconazole, propiconazole, prothioconazole, tebuconazole, azoxystrobin, pyraclastobin, fluoxastrobin, picoxystrobin, trifloxystrobin, sulfur, boscalid, thiophanate methyl, chlorothanonil, penthiopyrad, difenconazole, flutriafol, cyprodinil, fluzinam, iprodione, penflufen, cyazofamid, flutolanil, cymoxanil, dimethomorph, pyrimethanil, zoxamide, mandipropamid, metrinam, propamocarb, fenamidone, tetraconazole, chloronab, hymexazol, tolclofos, and fenbuconazole. One of ordinary skill in the art will readily appreciate that other known synthetic or naturally-occurring foliar fungicides used for agricultural purposes may also be selected for inclusion in a composition, plant seed or inoculum according to the disclosure.

**[0158]** Compositions, seeds, and inoculants according to the disclosure comprising an insecticide, possess the ability to increase mortality or inhibit growth rate of insects. As used herein, the term "insects" includes all organisms in the class "Insecta". The term "pre-adult" insects refers to any form of an organism prior to the adult stage, including, for example, eggs, larvae, and nymphs. As used herein, the terms "insecticide" and "insecticidal" also encompass "nematicide" and "nematicidal" and "acaricide" and "acaricidal." "Nematicides" and "nematicidal" refers to the ability of a substance to increase mortality or inhibit the growth rate of nematodes. In general, the term "nematode" comprises eggs, larvae, juvenile and mature forms of said organism. "Acaricide" and "acaricidal" refers to the ability of a substance to increase mortality or inhibit growth rate of ectoparasites belonging to the class Arachnida, sub-class Acari.

**[0159]** According to one aspect of the present disclosure, the at least one insecticide comprises: (1) Acetylcholinesterase (AChE) inhibitors, such as, for example, carbamates, for example alanycarb, bendiocarb, benfuracarb, butocarboxim, butoxycarboxim, carbofuran, carbosulfan, ethiofencarb, furathiocarb, isoprocarb, metolcarb, oxamyl, pirimicarb, propoxur, thiofanox, triazamate, trimethacarb, XMC and xylylcarb; or organophosphates, for example acephate, azamethiphos, azinphos-ethyl, azinphos-methyl, cadusafos, chlorethoxyfos, chlorfenvinphos, chlormephos, chlorpyrifos-methyl, coumaphos, cyanophos, demeton-S-methyl, diazinon, dichlorvos/DDVP, dicrotophos, dimethoate, dimethylvinphos, disulfoton, EPN, ethion, famphur, fenitrothion, fosthiazate, heptenophos, imicyafos, isofenphos, isopropyl O-(methoxyaminothiophosphoryl) salicylate, isoxathion, malathion, mecarbam, methidathion, mevinphos, monocrotophos, naled, omethoate, parathion-methyl, phenthoate, phorate, phosmet, phosphamidon, phoxim, pirimiphos -methyl, profenofos, propetamphos, prothiofos, pyraclofos, pyridaphenthion, quinalphos, sulfotep, tebupirimfos, temephos, terbufos, tetrachlorvinphos, thiometon, and triclorfon. (2) GABA-gated chloride channel antagonists, such as, for example, cyclodiene-organochlorines, for example chlordane and/or phenylpyrazoles. (3) Sodium channel modulators/voltage-gated sodium channel blockers such as, for example, pyrethroids, e.g., acrinathrin, allethrin, d-cis-trans allethrin, d-trans allethrin, bifenthrin, bioallethrin, bioallethrin s-cyclopentenyl isomer, bioresmethrin, cycloprothrin, cyhalothrin, lambda-cyhalothrin, gamma-cyhalothrin, empenthrin [(EZ)-(IR)-isomer], esfenvalerate, etofenprox, fenpropathrin, fenvalerate, flucythrinate, flumethrin, tau-fluvalinate, halfenprox, imiprothrin, kadethrin, permethrin, phenothrin [(lR)-trans-isomer], prallethrin, pyrethrins (pyrethrum), resmethrin, tefluthrin, tetramethrin, tetramethrin [(1R)-isomer)], and transfluthrin or DDT or methoxychlor. (4) Nicotinergic acetylcholine receptor (nAChR) agonists, such as, for example, neonicotinoids, e.g., dinotefuran, nitenpyram, and thiamethoxam or nicotine or sulfoxaflor. (5) Allosteric activators of the nicotinergic acetylcholine receptor (nAChR) such as, for example, spinosyns, e.g., spinetoram and spinosad. (6) Chloride channel activators, such as, for example, avermectins/milbemycins, for example abamectin, emamectin benzoate, lepimectin and milbemectin. (7) Juvenile hormone imitators such as, for example, juvenile hormone analogues, e.g., hydroprene, kinoprene and methoprene or fenoxycarb or pyriproxyfen. (8) Active compounds with unknown or nonspecific mechanisms of action such as, for example, alkyl halides, e.g., methyl bromide and other alkyl halides; or chloropicrine or sulphuryl fluoride or borax or tartar emetic. (9) Selective antifeedants, for example pymetrozine or flonicamid. (10) Mite growth inhibitors, for example clofentezine, hexythiazox and diflovidazin or etoxazole. (11) Microbial disrupters of the insect gut membrane, for example *Bacillus thuringiensis* subspecies *israelensis*, *Lysinibacillus sphaericus*, *Bacillus thuringiensis* subspecies *aizawai*, *Bacillus*

*thuringiensis* subspecies *kurstaki*, *Bacillus thuringiensis* subspecies *tenebrionis*, and Bt plant proteins: CrylAb, CrylAc, CrylFa, Cry2Ab, mCry3A, Cry3Ab, Cry3Bb, Cry34/35Abl. (12) Oxidative phosphorylation inhibitors, ATP disrupters such as, for example, diafenthiuron or organotin compounds, for example azocyclotin, cyhexatin and fenbutatin oxide or propargite or tetradifon. (13) Oxidative phosphorylation decouplers acting by interrupting the H proton gradient such as, for example, chlorfenapyr, DNOC and sulfluramid. (14) Nicotinergic acetylcholine receptor antagonists such as, for example, bensultap, cartap hydrochloride, thiocylam, and thiosultap-sodium. (15) Chitin biosynthesis inhibitors, type 0, such as, for example, bistrifluron, chlorfluazuron, diflubenzuron, flucycloxuron, flufenoxuron, hexaflumuron, lufenuron, novaluron, noviflumuron, and teflubenzuron. (16) Chitin biosynthesis inhibitors, type 1, for example buprofezin. (17) Moulting inhibitors (in particular for Diptera, i.e., dipterans) such as, for example, cyromazine. (18) Ecdysone receptor agonists such as, for example, chromafenozide, halofenozide, methoxyfenozide and tebufenozide. (19) Octopaminergic agonists. (20) Complex-Ill electron transport inhibitors such as, for example, hydramethylnone or acequinocyl or fluacrypyrim. (21) Complex-I electron transport inhibitors, for example from the group of the METI acaricides, e.g., fenazaquin, fenpyroximate, pyrimidifen, pyridaben, tebufenpyrad and tolfenpyrad or rotenone (Derris). (22) Voltage-gated sodium channel blockers, for example indoxacarb or metaflumizone. (23) Inhibitors of acetyl-CoA carboxylase. (24) Complex-IV electron transport inhibitors such as, for example, phosphines, e.g., aluminium phosphide, calcium phosphide, phosphine and zinc phosphide or cyanide. (25) Complex II electron transport inhibitors, such as, for example, cyenopyrafen and cyflumetofen. (26) Ryanodine receptor effectors, such as, for example, diamides, e.g., chlorantraniliprole, which is also known by the trade name RYNAXYPYR™, and cyantraniliprole, or any combination of one or more of the compounds or classes of compounds identified above.

**[0160]** One of ordinary skill in the art will readily appreciate that other known synthetic or naturally-occurring insecticides used for agricultural purposes may also be selected for inclusion in a composition, plant seed or inoculum according to the disclosure.

## Screening Methods

**[0161]** The fusion protein constructs and recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells disclosed herein may be used as a platform for high-throughput screening of heterologous proteins that generate new and/or modified plant attributes, as discussed throughout the disclosure. Such attributes may include commercially significant improvements in plant yields and other plant characteristics, such as: altered plant protein or oil content/composition, altered plant carbohydrate content/composition; altered seed carbohydrate content/composition, altered

seed oil or protein composition; increased tolerance to environmental or chemical stresses (e.g., resistance to cold or heat, drought, insecticides or herbicides); delayed senescence or disease resistance; growth improvement, health enhancement; herbivore resistance; improved nitrogen fixation or nitrogen utilization; improved root architecture or length; improved water use efficiency; increased biomass; increased seed weight; increased shoot length; increased yield; modified kernel mass or moisture content; metal tolerance; pathogen or pest resistance; photosynthetic capability improvement; salinity tolerance; vigor improvement; increased dry and/or fresh weight of mature seeds, increased number of mature seeds per plant; increased chlorophyll content; a detectable modulation in the level of a metabolite or in the metabolome relative to a reference plant/seed; a detectable modulation in the level of a transcript or in the transcriptome relative to a reference plant/seed; a detectable modulation in the level of a protein or in the proteome relative to a reference plant; and combinations of any of the traits or attributes above. Moreover, the preceding list is intended as a non-limiting set of examples. One of ordinary skill will appreciate that the high-throughput delivery platform disclosed herein is suitable for screening for various other plant traits and attributes discussed elsewhere in the disclosure or otherwise known in the art.

**[0162]** Endospores produced by recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells modified to express a fusion protein according to the disclosure may be applied to plant cells grown *in vitro*, a host plant seed, seedling, or to a vegetative or otherwise mature plant. The heterologous protein may in turn modify or confer a trait or attribute to the plant cells grown *in vitro*, host plant seed, seedling or mature plant. In select embodiments, the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores may be used to inoculate a seed and the resulting new or modified trait or attribute may be immediately apparent, whereas on other embodiments it may not become apparent until a later stage of development of the host plant.

**[0163]** In some embodiments, the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* bacterium used to deliver the fusion protein is exogenous to the host plant species. In others, the selected *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* bacterium is an endogenous endophyte known to colonize the host plant species. The host plant may be any suitable plant disclosed here (a monocot, dicot, conifer, etc.)

**[0164]** The recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* bacterium used to deliver the fusion protein may be used to inoculate a host plant seed, seedling, vegetative or otherwise mature plant specimen by way of a coating or spray, or any other method of applying endospores to a host plant known in the art. When applied as a liquid, for example, as a solution or suspension, the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores may be mixed or suspended in aqueous solutions. Suitable liquid diluents or carriers include aqueous solutions,

petroleum distillates, or other liquid carriers. Solid compositions can be prepared by dispersing the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores in and on an appropriately divided solid carrier, such as peat, wheat, bran, vermiculite, clay, talc, bentonite, diatomaceous earth, fuller's earth, pasteurized soil, and the like. When such formulations comprise wettable powders, dispersing agents such as non-ionic, anionic, amphoteric, or cationic dispersing and emulsifying agents can be used.

**[0165]** *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores may be applied directly to the surface of host plant seeds or to the leaves and stem of a vegetative plant directly, or as part of a composition comprising additional components. The additional components may include one or more compounds that enhance the rate of colonization, compounds that enhance plant growth or health, pesticides or herbicides, or any other compounds disclosed herein as suitable for promoting cultivation and growth of plants. Moreover, the composition may include additional *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores that have been modified to express fusion proteins comprising different amino acid sequences. For example, a composition may comprise a first *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore that expresses a fusion protein comprising a plant growth promoting factor as well as a second *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore that expresses a fusion protein that comprises a protein that enhances pesticide-resistance.

**[0166]** In select embodiments, the recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore which is coated onto the seed of a host plant is capable, upon germination of the seed into a vegetative state, of localizing to a different tissue of the plant. For example, the recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells can be capable of localizing to any one of the tissues in the plant, including: the root, adventitious root, seminal root, root hair, shoot, leaf, flower, bud, tassel, meristem, pollen, pistil, ovaries, stamen, fruit, stolon, rhizome, nodule, tuber, trichome, guard cells, hydathode, petal, sepal, glume, rachis, vascular cambium, phloem, and xylem. In other embodiments, the recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells may be capable of localizing to the root and/or the root hair of the plant. In alternative embodiments, the recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells may be capable of localizing to the photosynthetic tissues, for example, leaves and shoots of the plant; or to the vascular tissues of the plant, for example, in the xylem and phloem.

**[0167]** In other embodiments, the recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells are capable of localizing to the reproductive tissues (flower, pollen, pistil, ovaries, stamen, fruit) of the plant. In still another embodiment, the recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells colonize a fruit or seed tissue of the plant. In still another embodiment, the recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells are able to

colonize the plant such that it is present on the surface of the plant (e.g., the plant exterior or the phyllosphere of the plant). In still other embodiments, the recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells are capable of localizing to substantially all, or all, tissues of the plant.

**[0168]** Compositions comprising the recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores designed for application to a host plant may comprise a seed coating composition, a root treatment, or a foliar application composition. The seed coating composition, or the root treatment, or the foliar application composition may comprise a fungicide, an antibacterial agent, an herbicide, a nematicide, an insecticide, a plant growth regulator, a nutrient, or combinations thereof. The seed coating composition, or the root treatment, or the foliar application composition can further comprise an agriculturally acceptable carrier, a tackifier, a microbial stabilizer, or a combination thereof. In select embodiments, the seed coating composition, or the root treatment, or the foliar application composition can contain a second bacteria, including but not limited to a rhizobial bacterial preparation. The compositions may also contain a surfactant. In one embodiment, the surfactant is present at a concentration of between 0.01% v/v to 10% v/v. In another embodiment, the surfactant is present at a concentration of between 0.1% v/v to 1% v/v. In some embodiments, the composition may include a microbial stabilizer (e.g., a stabilizer).

**[0169]** Upon inoculation, a treated host plant (e.g., a treated seed, seedling, vegetative or otherwise mature plant) may be screened for the existence of new or modified attributes or traits. Screening can occur at any time point following treatment. In select embodiments, a seed may be treated and screening may not occur until the seed has sprouted or reached a more advanced stage of development. In other embodiments, a seed, seedling or vegetative plant may be treated and screening may not occur until the treated plant has produced a harvested end product which may comprise the sample to be screened for a new or modified trait or attribute.

**[0170]** During screening, various tests may be performed both *in vitro* and *in vivo* to determine what benefits, if any, are conferred upon the treated host plant. *In vivo* screening assays include tests that measure phenotypic traits or attributes of a plant or seed (e.g., assays measuring plant growth rate or height; crop yield; resistance to an environmental stress such as heat, cold, or salinity; resistance to biological pathogens or insect pests; resistance to chemical treatments such as insecticides or herbicides). *In vitro* screening assays include, but are not limited to, tests that measure the composition or properties of plant extracts, tissue samples, cell samples, and the like. In some embodiments, *in vitro* screening may comprise purifying and measuring the amount or activity of a given protein, enzyme, gene transcript, metabolite or other compound found in the cells or tissue of the treated host plant. In other embodiments, screening may comprise visual

inspection of the structure of cells or tissue of the treated host plant, whether by the naked eye or via microscopy.

**[0171]** In alternative embodiments, screening may comprise assays of recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores or vegetative cells modified to express a fusion protein according to the present disclosure, as opposed to assays directed to treated host plants. In these embodiments, the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* family member cells or endospores may be subject to *in vitro* assays of one or more activities, such as but not limited to the ability to liberate complexed phosphates or complexed iron (e.g., through secretion of siderophores); production of phytohormones; production of antibacterial, antifungal, or insecticidal, or nematicidal compounds; production and/or secretion of ACC deaminase, acetoin, pectinase, cellulase, or RNase. Screening methods directed to the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* family member cells or endospores, rather than vegetative plants, are particularly advantageous in that such methods may allow detection of useful heterologous proteins sooner than methods directed to treated host plants.

## DEPOSIT INFORMATION

**[0172]** Samples of the *Brevibacillus, Lysinibacillus, and Viridibacillus* strains of the invention have been deposited with the Agricultural Research Service Culture Collection located at the National Center for Agricultural Utilization Research, Agricultural Research Service, U.S. Department of Agriculture (NRRL), 1815 North University Street, Peoria, IL 61604, U.S.A., under the Budapest Treaty. *The Brevibacillus* and *Lysinibacillus* strains NRRL B-67865, and NRRL B-67864, respectively, both were deposited on October 10, 2019. The *Viridibacillus* strain NRRL B-67869 was deposited on October 17, 2019.

**[0173]** The *Brevibacillus, Lysinibacillus, and Viridibacillus* strains have been deposited under conditions that assure that access to the culture will be available during the pendency of this patent application to one determined by the Commissioner of Patents and Trademarks to be entitled thereto under 37 C.F.R. § 1.14 and 35 U.S.C. §122. However, it should be understood that the availability of a deposit does not constitute a license to practice the subject invention in derogation of patent rights granted by governmental action.

**[0174]** The following non-limiting examples are provided to further illustrate the present disclosure.

## EXAMPLES

### Example 1: General Protocol For Preparing Recombinant *Brevibacillus, Lysinibacillus, or Viridibacillus* Endospores.

**[0175]** To create a fusion construct, a polynucleotide encoding one or more heterologous proteins may be fused to a polynucleotide encoding the amino acids of any N-terminal targeting sequence disclosed herein, e.g., a polynucleotide encoding any of the amino acid sequences disclosed in Table 1 or FIGs. 1-3 (for *Brevibacillus*), Table 2 or FIGs. 4-5 (for *Lysinibacillus*), or Table 3 or FIG. 6 (for *Viridibacillus*), or a fragment or variant thereof that retains exosporium-targeting functionality when expressed in the respective bacterial genus. The fusion construct may be under the control of the native promoter of the disclosed N-terminal targeting sequence. Such constructs may be generated using the splicing by overlapping extension (SOE) technique or Gibson assembly resulting in a linear amplicon. At this stage, the protocol may also be modified to fuse the N-terminal targeting sequence to an in-frame coding sequence for a tag (e.g., GFP) or to insert a linker or protease recognition sequence between the N-terminal targeting sequence and the heterologous protein. Regardless of whether the optional tag, linker, and/or protease recognition sequence is included, correct amplicons may then be selected and cloned into a suitable shuttle vector (e.g., pHP13 for *E. coli/Brevibacillus*), and correct vector constructs screened by DNA sequencing. This vector construct may be electroporated into untransformed *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells. Correct transformants may then be grown in a suitable sporulation medium (e.g., Schaeffer's Sporulation Medium broth overnight at 30°C) until sporulation has occurred (typically 2 – 3 days). Spores expressing the fusion construct may be harvested and then be subjected to one or more *in vitro* screening assays, applied directly to a host plant or seed, or applied to a host plant or seed which is then later subjected to one or more *in vitro* or *in vivo* screening assays.

### Example 2: Use of Recombinant *Brevibacillus, Lysinibacillus*, or *Viridibacillus* Endospores for Delivery of a Fusion Protein Involved in the Production of a Plant Growth Promoting Compound to a Seed, Seedling, Plant, or Plant Part.

**[0176]** Enzymes responsible for the production of plant growth promoting compounds can be delivered to plants using the *Brevibacillus*, *Lysinibacillus*, and *Viridibacillus* endospore delivery systems disclosed herein. For example, butanediol dehydrogenase converts acetoin to 2,3-butanediol. 2,3-butanediol is a plant growth promoting compound. *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores expressing this enzyme can be applied as a seed treatment or seed coating or delivered to the area surrounding a seed, seedling, plant, or plant part by drip or spray.

**Example 3: Use of Recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* Endospores for Delivery of More Than One Fusion Protein on a Single *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* Endospore to a Seed, Seedling, Plant, or Plant Part.**

**[0177]** A single recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore can be used to display more than one heterologous fusion protein. This is accomplished by constructing two (or more) separate fusion proteins. The coding sequence for each heterologous protein to be displayed on the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore surface is fused separately to an N-terminal targeting sequence under control of its native promoters. The fusion protein constructs can be cloned either into the same plasmid vector or different plasmid vectors and introduced into *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* cells by electroporation. The resulting *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores will then express a mixture of both heterologous proteins on the spore surface. This is particularly useful for stacking multiple proteinaceous invertebrate toxins to mitigate pest resistance.

**Example 4: Use of More Than One Recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* Endospores in Combination, Each Displaying One or More Different Fusion Proteins to a Seed, Seedling, Plant, or Plant Part.**

**[0178]** In certain cases, delivery of more than one *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore in combination each expressing one or more different heterologous proteins (as described above) are provided. For example, the delivery of nitrogen fixation enzymes to the area surrounding the roots of a plant reduces the need for chemical nitrogen fertilizers. Nitrogen fixation in bacteria may require, at minimum, eight or nine different enzymes and potentially upwards of twenty different enzymes depending on the species. Here, delivery of a combination of *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores each expressing different enzyme components of the nitrogen fixation pathway may useful. For example, *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores heterologously displaying NifH, NifD, and NifK may be combined in a mixture with *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores heterologously displaying NifE, NifN, and NifD and delivered to the area surrounding the roots.

**Example 5: Use of Recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* Endospores for Delivery of an Invertebrate Toxin That Kills Invertebrate Plant Pests to the Area Surrounding a Seed, Seedling, Plant, or Plant Part or as a Seed Treatment.**

**[0179]** Proteinaceous toxins antagonistic towards invertebrates including but not limited to insects or nematodes can be delivered using the *Brevibacillus*, *Lysinibacillus*, or

*Viridibacillus* endospore systems disclosed herein. For example, Cry toxins including but not limited to Cry5B and Cry21A which are both insecticidal and nematicidal may be fused to the N-terminal targeting sequence for expression in *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores. *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores expressing Cry toxins or other proteinaceous invertebrate toxins can be applied as a seed treatment or seed coating or delivered to the area surrounding a seed, seedling, plant, or plant part by drip or spray for protection against invertebrate plant pathogens.

**Example 6: Use of *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* Endospores for Delivery of a Peptide, Protein, or Enzyme That is Antagonistic Towards Bacterial Plant Pests to the Area Surrounding a Seed, Seedling, Plant, or Plant Part or as a Seed Treatment.**

**[0180]** Bacteriocins are small peptides produced by bacteria with antagonistic activity towards other bacteria. Due to the fact that bacteriocins are ribosomally synthesized as opposed to other antimicrobial molecules (e.g., bacitracin), which are synthesized by large non-ribosomal peptide synthetases, bacteriocins are especially well suited for delivery using the *Brevibacillus* endospore system. The coding sequence for one or more bacteriocins may be fused to the N-terminal targeting sequence for expression in *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores. *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores expressing bacteriocins can be applied as a seed treatment or seed coating or delivered to the area surrounding a seed, seedling, plant, or plant part by drip or spray for protection against bacterial plant pathogens.

**Example 7: Use of *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* Endospores for Delivery of a Peptide, Protein, or Enzyme That is Antagonistic Towards Fungal Plant Pests to the Area Surrounding a Seed, Seedling, Plant, or Plant Part or as a Seed Treatment.**

**[0181]** The primary cell wall component of fungi is chitin. Chitinase is an enzyme that degrades chitin and can be expressed on the surface of *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores to protect against fungal plant pathogens by destroying their cell walls. *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores expressing chitinase can be applied as a seed treatment or seed coating or delivered to the area surrounding a seed, seedling, plant, or plant part by drip or spray.

**Example 8: Use of *Brevibacillus, Lysinibacillus*, or *Viridibacillus* Endospores for Delivery of an Enzyme That Degrades or Modifies a Bacterial, Fungal, or Plant Nutrient Source to the Area Surrounding a Seed, Seedling, Plant, or Plant Part or as a Seed Treatment.**

**[0182]** Enzymes responsible for the degradation or modification of a bacterial, fungal, or plant nutrient source can be delivered to plants using recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores. For example, a glycoside hydrolase which breaks down complex polysaccharides can be used to make available simple sugars for beneficial rhizobacteria by treating a plant or seed with recombinant *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores expressing this (or another) enzyme of interest.

**Example 9: Use of *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* Endospores for Assessing Responses to Plant Growth Promoting Biocontrol Agents by Screening of Genomic DNA Libraries Derived from Plant Growth Promoting Biocontrol Agents.**

**[0183]** Many of the biocontrol strains used today are recalcitrant to exogenous DNA uptake rendering researchers unable to generate targeted genetic modifications of said strains. Due to this challenge, elucidating the mechanism of action of the plant growth promoting effects of these biocontrol strains is incredibly difficult. *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores present a novel approach for identifying specific genes responsible for the underlying plant growth promoting effects of biocontrol strains. First, the N-terminal targeting sequence and native promoter are cloned into a suitable shuttle vector (e.g., pHP13 for *Brevibacillus*), resulting in a vector suitable for heterologous protein expression on *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores. All cloning steps and plasmid propagation are performed in *E. coli*. Next, total gDNA is extracted from a target plant growth promoting biocontrol strain. The gDNA is sheared into fragments (enzymatically or sonically) and ligated into the above described vector for expression of heterologous proteins on *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores to generate a gDNA library comprised of all the genetic material originating from the biocontrol strain of interest. The resulting vector library is introduced into a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* member by electroporation and the bacteria are plated onto agar plates containing an appropriate antibiotic selection agent to select for successful transformants. Individual transformants, each expressing a different fragment of the target biocontrol strain's gDNA, are assessed for plant growth promoting effects. These effects can include but are not limited to enhanced greening, improved germination, increased plant vigor, increased root length, increased root mass, increased plant height, increased leaf area, or resistance to pests. The vector in *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore transformants found to modulate the

above mentioned plant health parameters can be sequenced to identify the genetic determinants originating from the biocontrol strain responsible for the observed plant growth promoting effects.

**Example 10: Use of *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores for Identifying Novel or Uncharacterized Toxins Antagonistic Against Plant Invertebrate, Bacterial, and Fungal Plant Pathogens.**

**[0184]** Many of the biocontrol strains in use today are recalcitrant to exogenous DNA uptake rendering researchers unable to generate targeted genetic modifications of said strains. Due to this challenge, elucidating the mechanism of action by which biocontrol strains are toxic towards invertebrate, bacterial, and fungal plant pathogens is incredibly difficult. *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores present a novel approach for identifying specific genes responsible for the underlying plant protective effects of biocontrol strains. First, the N-terminal targeting sequence and native promoter are cloned into a suitable shuttle vector (e.g., pHP13 for *Brevibacillus*) resulting in a vector suitable for heterologous protein expression on *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores. All cloning steps and plasmid propagation are performed in *E. coli*. Next, total gDNA is extracted from a target plant growth promoting biocontrol strain. The gDNA is sheared into fragments (enzymatically or sonically) and ligated into the above described vector for expression of heterologous proteins on *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores to generate a gDNA library comprised of all the genetic material originating from the biocontrol strain of interest. The resulting vector library is introduced into a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* member by electroporation and the bacteria are plated onto agar plates containing an appropriate antibiotic selection agent to select for successful transformants. Individual transformants, each expressing a different fragment of the target biocontrol strain's gDNA, are assessed for antagonist activity towards invertebrate, bacterial, and fungal plant pathogens. The vector in *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* transformants that are found to be antagonistic towards the above plant pathogens can be sequenced to identify the genetic determinants originating from the biocontrol strain responsible for the observed plant protective effects.

**Example 11: Use of Purified Exosporiums from *Brevibacillus, Lysinibacillus*, or *Viridibacillus* Endospores as a Treatment to a Seed, Seedling, Plant, or Plant Part to Improve Plant Health.**

**[0185]** There may be a need to deliver plant health promoting proteins/enzymes using the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore systems disclosed herein without viable *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores. To that end, the exosporium

from a *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore (e.g., produced by a cell modified to product a heterologous protein using the N-terminal targeting sequences disclosed herein) can be stripped away from the *Brevibacillus* endospore via sufficient agitation through sonication. The stripped exosporiums are then further purified through filtration. The resulting purified exosporiums can be applied as a seed treatment or seed coating or delivered to the area surrounding a seed, seedling, plant, or plant part by drip or spray.

**Example 12: Use of Non-viable *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* Endospores as a Treatment to a Seed, Seedling, Plant, or Plant Part for the Purposes of Protecting Plants from Pathogens or Improving Plant Health.**

**[0186]** There may be a need to deliver plant health promoting proteins/enzymes or plant protection proteins/enzymes using the *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospore delivery systems disclosed herein, with non-viable (dead) *Brevibacillus* endospores. *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores can be inactivated and rendered non-viable via sufficient heat treatment, UV light, gamma irradiation, or high-pressure processing. The resulting non-viable *Brevibacillus*, *Lysinibacillus*, or *Viridibacillus* endospores can be applied as a seed treatment or seed coating or delivered to the area surrounding a seed, seedling, plant, or plant part by drip or spray.

**Example 13: A General Protocol for Preparing Recombinant *Brevibacillus* Endospores Displaying tandem-dimer Tomato (tdTomato).**

**[0187]** The complete genome of *Brevibacillus* sp. NRRL B-67865 was searched for ORFs containing collagen-like GXX repeats by bioinformatics analysis. Sequences from ORFs containing collagen-like repeats were compiled and trimmed to yield only N-terminal amino acids upstream from collagen-like repeats. This general protocol was used to identify endogenous *Brevibacillus* sp. NRRL B-67865 proteins having the N-terminal targeting sequences disclosed in Table 1 and FIGs. 1-3. For example, this approach was used to identify the N-terminal targeting sequence represented by SEQ ID NO: 3, which was found to be directly upstream of a CLR repeat domain (SEQ ID NO: 220) and under the control of a native promoter encoded by SEQ ID NO: 221.

**Table 4:** CLR and Promoter Sequences Associated With an Exemplary *Brevibacillus* Exosporium-Targeted Protein

| Sequence Identifier | SEQUENCE |
|---|---|
| SEQ ID NO: 220 | GVTGATGATGPTGATGATGATGPTGVTGATGAAGGDTGATGATGQTGE TGVAGATGATGQTGETGVAGATGATGQTGETGVAGATGATGQTGETGV AGATGATGQTGETGVAGATGATGQTGETGVAGATGATGQTGETGVAGA TGATGQTGETGVAGATGATGQTGETGVAGATGATGQTGETGKAGATGA TGQTGETGVTGATGATGQTGETGEAGATGAAGQTGETGVTGATGATGQ TGETGVAGATGATGQTGETGVAGATGATGATGQTGETGVVGATGATGQ TGETGVVGATGATGQTGETGVAGATGATGATGQTGETGVAGATGATGQ TGETGVAGATGATGQTGETGVAGATGATGQTGETGVAGATGATGQTGE AGVAGVTGATG |
| SEQ ID NO: 221 | TGAAAAGATGGGGAATTCTCCATCTTTTTTCTTTTGTCTGGAGTGGTGA GATATACGACATACAACGAATGAGCATAACATGAATAGTTTATAAAAT CGCAAAAAATTTTTCGGAAGGAGAGAGCGAAAATTAACAATAAGCGG GCTAACGCATTCAATAAGAAG |

**[0188]** To create fusion constructs, the gene coding for tdTomato was fused to a DNA segment encoding the amino acids of the disclosed N-terminal targeting sequence (SEQ ID NO: 3) of *Brevibacillus* sp. NRRL B-67865 under control of the native promoter of the disclosed N-terminal targeting sequences by gene synthesis and cloned into an *E. coli/Brevibacillus* shuttle vector, pAP13. The resulting vector construct was introduced into *Brevibacillus* sp. NRRL B-67865 by electroporation similar to that described by Huang *et al.* (2010), "Production of an In Vitro-Derived Deletion Mutation of *Brevibacillus laterosporus* by Constructing a Homology-Driven Integration Vector," Current Microbiology, 61:401–406, doi:10.1007/s00284-010-9627-0. Correct transformants were then grown in a glucose-based broth medium at 30°C until sporulation. *Brevibacillus* sp. NRRL B-67865 spores expressing the fusion construct were then examined by epifluorescent microscopy. TdTomato is visible on spores expressing the fusion construct (**FIG. 7A**). *Brevibacillus* sp. NRRL B-67865 spores were also examined by flow cytometry. Spores expressing the fusion construct are significantly more fluorescent than wild-type spores (**FIG. 7B**).

**Example 14: A General Protocol for Preparing Recombinant *Lysinibacillus* Endospores Displaying tandem-dimer Tomato (tdTomato).**

**[0189]** The complete genome of *Lysinibacillus* sp. NRRL B-67864 was searched for ORFs containing collagen-like GXX repeats by bioinformatics analysis. Sequences from ORFs containing collagen-like repeats were compiled and trimmed to yield only N-terminal amino acids upstream from collagen-like repeats. This general protocol was used to identify endogenous *Lysinibacillus* sp. NRRL B-67864 proteins having the N-terminal targeting sequences disclosed

in Table 2 and FIGs. 4-5. For example, this approach was used to identify the N-terminal targeting sequence represented by SEQ ID NO: 43, which was found to be directly upstream of a CLR repeat domain (SEQ ID NO: 222 and under the control of a native promoter encoded by SEQ ID NO: 223.

**Table 5:** CLR and Promoter Sequences Associated With an Exemplary *Lysinibacillus* Exosporium-Targeted Protein

| **Sequence Identifier** | **SEQUENCE** |
|---|---|
| SEQ ID NO: 222 | GVTGATGATGATGAQGPPGAPGPQGVAGAMGPRGEIGPQGVAGA TGATGPQGEMGLQGVAGVTGASGPQGEIGPQGVAGVTGAPGPQG EIGPQGVAGATGVPGPQGEIGPQGVAGETGATGPQGEMGLQGVAG VTGATGPQGEMGPQGVAGVTGATGPQGEIGPQGVAGVTGAPGPQ GEIGPQGVAGVTGAPGPQGEMGLQGVAGVTGATGPQGIIGATGLR GLAGITGATGERGLAGITGATGVQGVAGSTGATGSQGITGATGVQ GVTGSTGATGSQGITGATGVQGVTGSTGATGSQGITGATGVQGVT GSTGATGSQGITGATGVQGVAGSTGATGSQGITGATGVQGVTGST GATGARGTTGVTGTTGPSGSGLMEVFLSTDQSVGNNDFLGTGNSS ASFVRSSIVIPENATIRSLTLNIRDHALSAGQTASAQIFVSTNCGFTSV ATGIIATVTGPNSSTTPNCCAKVIANYPVSSCTLLSVQVSTTGGAFS NGVSATVLFNTV |
| SEQ ID NO: 223 | TGTTGAAACATATTATTGAGCATTGGGTTTTATATGACCTAATGT TCTTTTTATTTTAAGATACATATTTAAATCATTCTAATATTCTAG GTGCATTAATTATCTCAATAAGTAGACTTTTGAATATGATAAAA AGGGACAGGAGGTGAAGTCGCA |

**[0190]** To create fusion constructs, the gene coding for tdTomato was fused to a DNA segment encoding the amino acids of the disclosed N-terminal targeting sequence (SEQ ID NO: 43) of *Lysinibacillus* sp. NRRL B-67864 under control of the native promoter of the disclosed N-terminal targeting sequences by gene synthesis and cloned into an *E. coli/Lysinibacillus* shuttle vector, pAP13. The resulting vector construct was introduced into *Lysinibacillus* sp. NRRL B-67864 by electroporation similar to that described by Taylor and Burke (1990), "Transformation of an entomopathic strain of *Bacillus sphaericus* by high voltage electroporation," *FEMS Microbiology Letters*, 66:125-128, doi.org/10.1111/j.1574-6968.1990.tb03983.x. Correct transformants were then grown in a glucose-based broth medium at 30°C until sporulation. *Lysinibacillus* sp. NRRL B-67864 spores expressing the fusion construct were then examined by epifluorescent microscopy. TdTomato is visible on spores expressing the fusion construct (**FIG. 8A**). *Lysinibacillus* sp. NRRL B-67864 spores were also examined by flow cytometry. Spores expressing the fusion construct are significantly more fluorescent than wild-type spores (**FIG. 8B**).

**Example 15: A General Protocol for Preparing Recombinant *Viridibacillus* Endospores Displaying tandem-dimer Tomato (tdTomato).**

**[0191]** The approach described in Examples 13 and 14 was used to identify N-terminal targeting sequences in *Viridibacillus*. This approach led to the identification of the N-terminal targeting sequence represented by SEQ ID NO: 197, which was found to be directly upstream of a CLR repeat domain (SEQ ID NO: 224 and under the control of a native promoter encoded by SEQ ID NO: 225).

**Table 6:** CLR and Promoter Sequences Associated With an Exemplary *Viridibacillus* Exosporium-Targeted Protein

| **Sequence Identifier** | **SEQUENCE** |
|---|---|
| SEQ ID NO: 224 | GKTGPTGATGPTGSMGPTGVTGSTGATGPTGSTGVTGETGSTGTTG<br>PSGSTGPTGATGSTGETGATGSTGATGETGPTGPTGTTGVTGETGA<br>TGPTGATGATGETGSTGPTGATGETGETGSTGPTGATGSTGATGPT<br>GATGSTGATGSTGATGSTGATGPTGATGSTGETGPTGETGSTGATG<br>STGATGETGPTGTTGVTGETGATGPTGATGATGETGETGSTGPTGA<br>TGETGETGSTGPTGATGSTGATGPTGATGSTGATGSTGATGSTGAT<br>GPTGATGSTGETGPTGETGSTGATGSTGATGETGPTGATGSTGATG<br>ETGATGPTGPTGTTGVTGATGPTGATGETGPTGATGEAGPTGSTGA<br>TGPTGATGITGATGPTGSTGATGSTGETGSTGETGPTGATGVTGAT<br>GPTGETGSTGPMGATGETGSTGSTGVTGATGATGETGATGSTGAT<br>GTTGATGETGPTGPTGSTGATGETGPTGPTGATGVTGATGATGAT<br>GETGSTGPMGATGETGSTGSTGVTGATGATGVTGATGETGSTGAT<br>GSTGATGETGPTGPTGPTGPTGTTGVTGVTGETGPTGATGETGSTG<br>PTGTTGVTGETGATGPTGATGSTGETGATGETGRTGPTGTTGVTGE<br>TGATGETGPTGATGSTGATGPTGATGATGATGETGPTGATGETGA<br>TGATGSTGATGPTGPTGTTGVTGATGPTGATGETGPTGATGEAGPT<br>GSTGSTGPTGATGITGATGPTGATGATGSTGETGSTGETGPTGSTG |
| SEQ ID NO: 225 | ATATTTTAGAAAGTGAAAAATACAGATAAAAGCCTTTGCTGATT<br>CATTTTTCTGGATTTATTTAAAAGAACGATTGGAGAGTATTCTTC<br>AGCCGTATCTTTTTTTTGTTGCTAAAAATATTAATAATTTTACTT<br>GAGGATTTTAATAGATTAAGAAATTTTTAATTCTGATACCTATAT<br>TGTATTACAGGAATATTTTAGAAATAAGCATATCCCATTTTCATT<br>TTACAGTTTAATAGCATGCTAGAGAAATACATAATTATCAGACT<br>ACCATGAATGAGATGATTATCCGATTTTTTTCTGTCACATTACAA<br>TTGTCCAATATCAATCTATTTCACGAGAATAGTATGTATATGATG<br>GGAGGTGATAATA |

**[0192]** To create fusion constructs, the gene coding for tdTomato was fused to a DNA segment encoding the amino acids of the disclosed N-terminal targeting sequence (SEQ ID NO: 197) of *Viridibacillus* sp. NRRL B-67869 under control of the native promoter of the disclosed N-terminal targeting sequences by gene synthesis and cloned into an *E. coli/Viridibacillus* shuttle

vector, pAP13. The resulting vector construct was introduced into *Viridibacillus* sp. NRRL B-67869 by electroporation using LBSP media, ampicillin treatment, and washing with TSMMKK buffer similar to that described by Zhang *et al.* (2015), "Development of an Efficient Electroporation Method for Iturin A-Producing *Bacillus subtilis* ZK," International Journal of Molecular Sciences, 16:7334-7351, doi:10.3390/ijms16047334. Correct transformants were then grown in a glucose-based broth medium at 30°C until sporulation. *Viridibacillus* sp. NRRL B-67869 spores expressing the fusion construct were then examined by epifluorescent microscopy. TdTomato is visible on spores expressing the fusion construct (**FIG. 9A**). *Viridibacillus* sp. NRRL B-67869 spores were also examined by flow cytometry. Spores expressing the fusion construct are significantly more fluorescent than wild-type spores (**FIG. 9B**).

# CLAIMS

**We claim:**

1. A nucleic acid molecule encoding a fusion protein, comprising (a) a first polynucleotide sequence encoding an N-terminal signal peptide, operably linked to (b) a second polynucleotide sequence encoding a polypeptide heterologous to the N-terminal signal peptide, wherein the first polynucleotide sequence comprises:

(i) a polynucleotide sequence having at least 60%, 70%, 80% or 90% sequence identity with a polynucleotide sequence encoding an amino acid sequence represented by any one of SEQ ID NOs: 1-38, or shown in **Table 1** or **FIGs. 1-3**; or

(ii) a polynucleotide sequence comprising a fragment of at least 15, 30, 45, 60, 75, 90, 105, 120 or 150, 210, 270, 330, 390 or 450 consecutive nucleotides of a polynucleotide sequence encoding an amino acid sequence shown in **Table 1** or **FIGs. 1-3**; and

wherein the N-terminal signal peptide is capable of targeting the fusion protein to an exosporium of a *Brevibacillus* endospore.

2. The nucleic acid molecule of claim 1, wherein the fragment includes:

(a) the first nucleotide of a polynucleotide sequence encoding any amino acid sequence shown in **Table 1** or **FIGs. 1-3**; or

(b) the last nucleotide of a polynucleotide sequence encoding any amino acid sequence shown in **Table 1** or **FIGs. 1-3**.

3. The nucleic acid molecule of claim 1 or 2, wherein the first polynucleotide sequence comprises a polynucleotide sequence having at least 60%, 70%, 80% or 90% sequence identity with a polynucleotide sequence encoding any amino acid sequence shown in **Table 1** or **FIGs. 1-3**.

4. The nucleic acid molecule of any one of claims 1-3, wherein the fragment encodes amino acids 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 1-35, 1-40 or 1-45, 1-50, 1-75, 1-100, 1-125 or 1-150 of any one the amino acid sequences shown in **Table 1** or **FIGs. 1-3**.

5. The nucleic acid molecule of any one of claims 1-4, wherein the polypeptide heterologous to the N-terminal signal peptide comprises:

(a) a plant growth-stimulating protein;

(b) an enzyme;

(c) a protein;

(d) a polypeptide heterologous to *Brevibacillus;*

(e) a therapeutic protein; or

(f) a plant immune-stimulating protein.

6. The nucleic acid molecule of any one of claims 1-5, further comprising a third polynucleotide sequence, encoding:

(a) a polypeptide comprising one or more protease cleavage sites, wherein the polypeptide is positioned between the N-terminal signal peptide and the polypeptide heterologous to the N-terminal signal peptide;

(b) a polypeptide comprising a selectable marker;

(c) a polypeptide comprising a visualization marker;

(d) a polypeptide comprising a protein recognition/purification domain; or

(e) a polypeptide comprising a flexible linker element, which connects the N-terminal signal peptide and the polypeptide heterologous to the N-terminal signal peptide.

7. The nucleic acid molecule of any one of claims 1-6, the *Brevibacillus* endospore is an endospore formed by a *Brevibacillus* species, comprising: *B. agri, B. aydinogluensis, B. borstelensis, B. brevis, B. centrosporus, B. choshinensis, B. fluminis, B. formosus, B. fulvus, B. ginsengisoli, B. invocatus, B. laterosporus, B. levickii, B. limnophilus, B. massiliensis, B. nitrificans, B. panacihumi, B. parabrevis, B. reuszeri,* or *B. thermorube*; or an endospore formed by a bacterium that possesses a 16S rRNA gene that shares at least 97%, 98% or 99% identity with a 16S rRNA gene of a *Brevibacillus* species.

8. The nucleic acid molecule of any one of claims 1-7, operatively linked to a promoter element that is heterologous to at least one of the second polynucleotide sequences and *Brevibacillus*.

9. The nucleic acid molecule of any one of claims 1-8, wherein the first polynucleotide sequence comprises:

a codon-optimized polynucleotide sequence having at least 60%, 70%, 80% or 90% sequence identity with a polynucleotide sequence encoding an amino acid sequence shown in **Table 1** or **FIGs. 1-3**, which is expressed at a higher rate or level in the *Brevibacillus* endospore

compared to the polynucleotide sequence encoding an amino acid sequence shown in **Table 1** or **FIGs. 1-3**, under identical conditions.

10. A fusion protein comprising an N-terminal signal peptide operably linked to a polypeptide heterologous to the N-terminal signal peptide, wherein the N-terminal signal peptide comprises:

(a) a polypeptide comprising an amino acid sequence having at least 60%, 70%, 80% or 90% sequence identity with any one of SEQ ID NOs: 1-6 or an amino acid sequence shown in **Table 1** or **FIGs. 1-3**; or

(b) a polypeptide comprising a fragment of at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 125 or 150 consecutive amino acids from the amino acid sequence of any one of SEQ ID NOs: 1-38 or an amino acid sequence shown in **Table 1** or **FIGs. 1-3**;

wherein the N-terminal signal peptide is capable of targeting the fusion protein to an exosporium of a *Brevibacillus* endospore.

11. The fusion protein of claim 10, wherein the fragment includes:

(a) the first amino acid of any one of SEQ ID NOs: 1-38 or an amino acid sequence shown in **Table 1** or **FIGs. 1-3**; or

(b) the last amino acid of any one of SEQ ID NOs: 1-38 or an amino acid sequence shown in **Table 1** or **FIGs. 1-3**.

12. The fusion protein of claim 10 or 11, wherein the polypeptide sequence comprises a sequence having at least 60%, 70%, 80% or 90% sequence identity with the amino acid sequence of any one of SEQ ID NOs: 1-38 or an amino acid sequence shown in **Table 1** or **FIGs. 1-3**.

13. The fusion protein of any one of claims 10 to 12, wherein the fragment comprises amino acids 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 1-35, 1-40, 1-45, 1-50, 1-75, 1-100, 1-125 or 1-150 of any one of SEQ ID NO: 1-38 or of an amino acid sequence shown in **Table 1** or **FIGs. 1-3**.

14. The fusion protein of any one of claims 10 to 13, wherein the polypeptide heterologous to the N-terminal signal peptide comprises:

(a) a plant growth-stimulating protein;

(b) an enzyme;

(c) a protein;

(d) a polypeptide heterologous to *Brevibacillus;*

(e) a therapeutic protein; or

(f) a plant immune-stimulating protein.

15. The fusion protein of any one of claims 10 to 14, wherein the fusion protein further comprises:

(a) a polypeptide containing one or more protease cleavage sites, positioned between the N-terminal signal peptide and the polypeptide heterologous to the N-terminal signal peptide;

(b) a polypeptide comprising a selectable marker;

(c) a polypeptide comprising a visualization marker;

(d) a polypeptide comprising at least one protein recognition/purification domain; or

(e) a polypeptide comprising a flexible linker element, connecting the signal peptide and the polypeptide heterologous to the N-terminal signal peptide.

16. The fusion protein of any one of claims 10 to 15, wherein the *Brevibacillus* endospore is an endospore formed by a *Brevibacillus* species, comprising: *B. agri, B. aydinogluensis, B. borstelensis, B. brevis, B. centrosporus, B. choshinensis, B. fluminis, B. formosus, B. fulvus, B. ginsengisoli, B. invocatus, B. laterosporus, B. levickii, B. limnophilus, B. massiliensis, B. nitrificans, B. panacihumi, B. parabrevis, B. reuszeri, or B. thermorube*; or an endospore formed by a bacterium that possesses a 16S rRNA gene that shares at least 97%, 98% or 99% identity with a 16S rRNA gene of a *Brevibacillus* species.

17. A recombinant *Brevibacillus* cell comprising a bacterial chromosome comprising the nucleic acid molecule of any one of claims 1-9.

18. A vector comprising the nucleic acid molecule of any one of claims 1-9, wherein the vector comprises a plasmid, an artificial chromosome, or a viral vector.

19. The vector of claim 18, further comprising at least one of the following:

(a) an origin of replication that provides stable maintenance in a *Brevibacillus* cell;

(b) an origin of replication that provides selectively non-stable maintenance in a *Brevibacillus* cell;

(c) a temperature-sensitive origin of replication that provides selectively non-stable maintenance in a *Brevibacillus* cell;

(d) a polynucleotide encoding a selection marker, operably linked to an expression control sequence; or

(e) a polynucleotide encoding a plant growth stimulating protein, operably linked to an expression control sequence.

20. A recombinant *Brevibacillus* cell transformed with a vector comprising the nucleic acid molecule of any one of claims 1-9.

21. The recombinant *Brevibacillus* cell of claim 20, wherein the *Brevibacillus* cell is a *Brevibacillus* species, comprising: *B. agri, B. aydinogluensis, B. borstelensis, B. brevis, B. centrosporus, B. choshinensis, B. fluminis, B. formosus, B. fulvus, B. ginsengisoli, B. invocatus, B. laterosporus, B. levickii, B. limnophilus, B. massiliensis, B. nitrificans, B. panacihumi, B. parabrevis, B. reuszeri,* or *B. thermoruber*; or a bacterium that possesses a 16S rRNA gene that shares at least 97%, 98% or 99% identity with a 16S rRNA gene of a *Brevibacillus* species.

22. A method of displaying a heterologous fusion protein on an exosporium of a *Brevibacillus* endospore, the method comprising:

(a) transforming a *Brevibacillus* cell capable of sporulation with a recombinant vector comprising the nucleic acid molecule of any one of claims 1-9; and

(b) expressing the fusion protein encoded by the nucleic acid molecule of any one of claims 1-9 under sporulation conditions such that the fusion protein is targeted to the exosporium of the *Brevibacillus* endospore resulting from the sporulation,

wherein the N-terminal signal peptide comprises: (i) a polypeptide comprising an amino acid sequence having at least 60%, 70%, or 80% sequence identity with the amino acid sequence of any one of SEQ ID NOs: 1-38 or an amino acid sequence shown in **Table 1** or **FIGs. 1-3**; or (ii) a fragment of at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 125 or 150 consecutive amino acids of the amino acid sequence of any one of SEQ ID NOs: 1-38 or an amino acid sequence shown in **Table 1** or **FIGs. 1-3**.

23. A composition comprising:

(a) one or more recombinant exosporium-producing *Brevibacillus* cells that express the fusion protein of any one of claims 10-16, wherein the polypeptide heterologous to the N-terminal signal peptide comprises a plant growth or immune stimulating protein; and

(b) at least one biological control agent; optionally,

in a synergistically effective amount.

24. A seed treated with the nucleic acid of any one of claims 1-9, the fusion protein of any one of claims 10-16, the recombinant bacterial cell of claim 20 or 21, or the composition of claim 23.

25. A method of treating a plant, a seed, a plant part, or the soil surrounding the plant to enhance plant growth and/or promote plant health comprising the step of simultaneously or sequentially applying:

(a) recombinant exosporium-producing *Brevibacillus* endospores that express the fusion protein of any one of claims 10-16, wherein the polypeptide heterologous to the N-terminal signal peptide comprises a plant growth or immune stimulating protein; and

(b) at least one biological control agent; optionally,

in a synergistically effective amount.

26. A method of screening a host plant treated with a recombinant *Brevibacillus* endospore, comprising the following steps:

(a) applying a composition comprising a *Brevibacillus* endospore modified to express a fusion protein according to any one of claims 10-16, to a seed, a seedling, or a vegetative plant capable of being permanently or transiently colonized by a *Brevibacillus*, to produce a treated seed, seedling, or vegetative plant; and

(b) screening the treated seed, seedling, or vegetative plant by detecting and optionally measuring a trait, component, or attribute of the treated seed, seedling, or vegetative plant.

27. The method of claim 26, wherein the screening step comprises one or more of the following:

(a) at least one *in vitro* assay comprising detecting and optionally quantifying the presence, level, change in level, activity, or localization of one or more compounds contained in an extract prepared from a cell or tissue sample obtained from the treated seed, seedling, or vegetative plant; and/or

(b) at least one *in vivo* assay comprising detecting and optionally quantifying a trait, component, or attribute of the treated seed, seedling, or vegetative plant.

28. A method of screening heterologous proteins or peptides expressed in a *Brevibacillus* cell for agriculturally-significant properties, comprising:

(a) modifying a *Brevibacillus* cell to express a fusion protein according to any one of claims 10-16 to produce a recombinant *Brevibacillus* cell; and

(b) screening the *Brevibacillus* cell by detecting and optionally quantifying a level or activity of a compound produced by the recombinant *Brevibacillus* cell.

29. A method of treating a plant, a seed, a human, or an animal, comprising:

administering to the plant, seed, human, or animal a composition comprising an exosporium isolated from an endospore produced by a recombinant *Brevibacillus* cell;

wherein the recombinant *Brevibacillus* cell expresses the fusion protein of any one of claims 10-16.

30. The method of claim 29, wherein the composition has been heat-inactivated or sterilized such that no viable *Brevibacillus* cells remain.

31. A composition comprising an isolated and/or purified fusion protein according to any one of claims 10-16.

32. A composition comprising an isolated and/or purified exosporium produced by a recombinant *Brevibacillus* endospore, which has been modified to express a fusion protein according to any one of claims 10-16.

33. A composition comprising an exosporium produced by a recombinant *Brevibacillus* endospore, which has been modified to express a fusion protein according to any one of claims 10-16.

34. The composition of claim 33, wherein the exosporium produced by a recombinant *Brevibacillus* endospore comprises:

(a) a basal layer of an exosporium;

(b) a hair-like layer of an exosporium;

(c) a mixture of both a) and b);

(d) a fraction or extract of a crude exosporium obtained from a *Brevibacillus* endospore; and/or

(e) a fraction or extract of a crude exosporium obtained from a *Brevibacillus* endospore that is enriched in an amount or concentration of the fusion protein compared to a same amount of the crude exosporium.

35. A method of delivering a protein of interest to a plant, seed or field, comprising:

applying a composition comprising an exosporium obtained from a recombinant *Brevibacillus* endospore to a plant, seed, or field;

wherein the recombinant *Brevibacillus* endospore has been modified to express a fusion protein according to any one of claims 10-16.

36. The method of claim 35, wherein the composition is applied to a field:

(a) pre- or post-planting;

(b) pre- or post-emergence;

(c) as a powder, suspension or solution; and/or

(d) wherein the composition further comprises one or more additional compounds that stimulate plant growth or protect plants from pests.

37. A nucleic acid molecule encoding a fusion protein, comprising (a) a first polynucleotide sequence encoding an N-terminal signal peptide, operably linked to (b) a second polynucleotide sequence encoding a polypeptide heterologous to the N-terminal signal peptide, wherein the first polynucleotide sequence comprises:

(i) a polynucleotide sequence having at least 60%, 70%, 80% or 90% sequence identity with any one of SEQ ID NOs: 39 or 40, or with a polynucleotide sequence encoding an amino acid sequence represented by any one of SEQ ID NOs. 41-177 or shown in **Table 2** or **FIGs. 4-5**; or

(ii) a polynucleotide sequence comprising a fragment of at least 15, 30, 45, 60, 75, 90, 105, 120 or 135 consecutive nucleotides from SEQ ID NOs: 39 or 40, or from a polynucleotide sequence encoding an amino acid sequence represented by any one of SEQ ID NOs. 41-177 or shown in **Table 2** or **FIGs. 4-5**; and

wherein the N-terminal signal peptide is capable of targeting the fusion protein to an exosporium of a *Lysinibacillus* endospore.

38. The nucleic acid molecule of claim 37, wherein the fragment includes:

(a) the first nucleotide of a polynucleotide sequence encoding an amino acid sequence shown in **Table 2** or **FIGs. 4-5**; or

(b) the last nucleotide of a polynucleotide sequence encoding an amino acid sequence shown in **Table 2** or **FIGs. 4-5**.

39. The nucleic acid molecule of claim 37 or 38, wherein the first polynucleotide sequence comprises a polynucleotide sequence having at least 60%, 70%, 80% or 90% sequence

identity with SEQ ID NOs: 39 or 40, or a polynucleotide sequence encoding an amino acid sequence shown in **Table 2** or **FIGs. 4-5**.

40. The nucleic acid molecule of any one of claims 37-39, wherein the fragment encodes amino acids 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 1-35, 1-40 or 1-45 of SEQ ID NO: 7 or 8 or any one of the amino acid sequences shown in **Table 2** or **FIGs. 4-5**.

41. The nucleic acid molecule of any one of claims 37-40, wherein the polypeptide heterologous to the N-terminal signal peptide comprises:

(a) a plant growth-stimulating protein;

(b) an enzyme;

(c) a protein;

(d) a polypeptide heterologous to *Lysinibacillus;*

(e) a therapeutic protein; or

(f) a plant immune-stimulating protein.

42. The nucleic acid molecule of any one of claims 37-41, further comprising a third polynucleotide sequence, encoding:

(a) a polypeptide comprising one or more protease cleavage sites, wherein the polypeptide is positioned between the N-terminal signal peptide and the polypeptide heterologous to the N-terminal signal peptide;

(b) a polypeptide comprising a selectable marker;

(c) a polypeptide comprising a visualization marker;

(d) a polypeptide comprising a protein recognition/purification domain; or

(e) a polypeptide comprising a flexible linker element, which connects the N-terminal signal peptide and the polypeptide heterologous to the N-terminal signal peptide.

43. The nucleic acid molecule of any one of claims 37-42, the *Lysinibacillus* endospore is an endospore formed by a *Lysinibacillus* species, comprising: *Lysinibacillus sphaericus, Lysinibacillus boronitolerans*, *Lysinibacillus fusiformis*, *Lysinibacillus acetophenoni*, *Lysinibacillus alkaliphilus*, *Lysinibacillus chungkukjangi*, *Lysinibacillus composti*, *Lysinibacillus contaminans*, *Lysinibacillus cresolivorans*, *Lysinibacillus macroides*, *Lysinibacillus manganicus*, *Lysinibacillus mangiferihumi*, *Lysinibacillus massiliensis*, *Lysinibacillus meyeri*, *Lysinibacillus odysseyi*, *Lysinibacillus pakistanensis*, *Lysinibacillus parviboronicapiens*, *Lysinibacillus*

*sinduriensis*, *Lysinibacillus tabacifolii*, *Lysinibacillus varians*, *Lysinibacillus xylanilyticus.* or *Lysinibacillus halotolerans*; or

an endospore formed by a bacterium that possesses a 16S rRNA gene that shares at least 97, 98 or 99% identity with a 16S rRNA gene of a *Lysinibacillus* species.

44. The nucleic acid molecule of any one of claims 37-43, operatively linked to a promoter element that is heterologous to at least one of the second polynucleotide sequences and *Lysinibacillus*.

45. The nucleic acid molecule of any one of claims 37-44, wherein the first polynucleotide sequence comprises:

a codon-optimized polynucleotide sequence having at least 60%, 70%, 80% or 90% sequence identity with a polynucleotide sequence encoding an amino acid sequence shown in **Table 2** or **FIGs. 4-5**, which is expressed at a higher rate or level in the *Lysinibacillus* endospore compared to the polynucleotide sequence encoding an amino acid sequence shown in **Table 2** or **FIGs. 4-5**, under identical conditions.

46. A fusion protein comprising an N-terminal signal peptide operably linked to a polypeptide heterologous to the N-terminal signal peptide, wherein the N-terminal signal peptide comprises:

(a) a polypeptide comprising an amino acid sequence having at least 60%, 70%, 80% or 90% sequence identity with the amino acid sequence of any one of SEQ ID NOs: 41-177 or an amino acid sequence shown in **Table 2** or **FIGs. 4-5**; or

(b) a polypeptide comprising a fragment of at least 5, 10, 15, 20, 25, 30, 35, 40 or 45 consecutive amino acids of any one of SEQ ID NOs: 41-177 or an amino acid sequence shown in **Table 2** or **FIGs. 4-5**;

wherein the N-terminal signal peptide is capable of targeting the fusion protein to an exosporium of a *Lysinibacillus* endospore.

47. The fusion protein of claim 46, wherein the fragment includes:

(a) the first amino acid of any one of SEQ ID NOs: 41-177 or an amino acid sequence shown in **Table 2** or **FIGs. 4-5**; or

(b) the last amino acid of any one of SEQ ID NOs: 41-177 or an amino acid sequence shown in **Table 2** or **FIGs. 4-5**.

48. The fusion protein of claim 46 or 47, wherein the polypeptide sequence comprises a an amino acid sequence having at least 60%, 70%, 80% or 90% sequence identity with any one of SEQ ID NOs: 41-177 or an amino acid sequence shown in **Table 2** or **FIGs. 4-5**.

49. The fusion protein of any one of claims 46 to 48, wherein the fragment comprises amino acids 1-5, 1-10, 1-15, 1-20, 1-25, 1-30, 1-35, 1-40 or 1-45 of any one of SEQ ID NOs: 41-177 or an amino acid sequence shown in **Table 2** or **FIGs. 4-5**.

50. The fusion protein of any one of claims 46 to 49, wherein the polypeptide heterologous to the N-terminal signal peptide comprises:

(a) a plant growth-stimulating protein;

(b) an enzyme;

(c) a protein;

(d) a polypeptide heterologous to *Lysinibacillus;*

(e) a therapeutic protein; or

(f) a plant immune-stimulating protein.

51. The fusion protein of any one of claims 46 to 50, wherein the fusion protein further comprises:

(a) a polypeptide containing one or more protease cleavage sites, positioned between the N-terminal signal peptide and the polypeptide heterologous to the N-terminal signal peptide;

(b) a polypeptide comprising a selectable marker;

(c) a polypeptide comprising a visualization marker;

(d) a polypeptide comprising at least one protein recognition/purification domain; or

(e) a polypeptide comprising a flexible linker element, connecting the signal peptide and the polypeptide heterologous to the N-terminal signal peptide.

52. The fusion protein of any one of claims 46 to 51, wherein the *Lysinibacillus* endospore is an endospore formed by a *Lysinibacillus* species, comprising: *Lysinibacillus sphaericus, Lysinibacillus boronitolerans*, *Lysinibacillus fusiformis*, *Lysinibacillus acetophenoni*, *Lysinibacillus alkaliphilus*, *Lysinibacillus chungkukjangi*, *Lysinibacillus composti*, *Lysinibacillus contaminans*, *Lysinibacillus cresolivorans*, *Lysinibacillus macroides*, *Lysinibacillus manganicus*, *Lysinibacillus mangiferihumi*, *Lysinibacillus massiliensis*, *Lysinibacillus meyeri*, *Lysinibacillus odysseyi*, *Lysinibacillus pakistanensis*, *Lysinibacillus parviboronicapiens*, *Lysinibacillus*

*sinduriensis*, *Lysinibacillus tabacifolii*, *Lysinibacillus varians*, *Lysinibacillus xylanilyticus,* or *Lysinibacillus halotolerans*; or

an endospore formed by a bacterium that possesses a 16S rRNA gene that shares at least 97, 98 or 99% identity with a 16S rRNA gene of a *Lysinibacillus* species.

53. A recombinant *Lysinibacillus* cell comprising a bacterial chromosome comprising the nucleic acid molecule of any one of claims 37-45.

54. A vector comprising the nucleic acid molecule of any one of claims 37-45, wherein the vector comprises a plasmid, an artificial chromosome, or a viral vector.

55. The vector of claim 54, further comprising at least one of the following:

(a) an origin of replication that provides stable maintenance in a *Lysinibacillus* cell;

(b) an origin of replication that provides selectively non-stable maintenance in a *Lysinibacillus* cell;

(c) a temperature-sensitive origin of replication that provides selectively non-stable maintenance in a *Lysinibacillus* cell;

(d) a polynucleotide encoding a selection marker, operably linked to an expression control sequence; or

(e) a polynucleotide encoding a plant growth stimulating protein, operably linked to an expression control sequence.

56. A recombinant *Lysinibacillus* cell transformed with a vector comprising the nucleic acid molecule of any one of claims 37-45.

57. The recombinant *Lysinibacillus* cell of claim 56, wherein the *Lysinibacillus* cell is a *Lysinibacillus* species, comprising: *Lysinibacillus sphaericus, Lysinibacillus boronitolerans*, *Lysinibacillus fusiformis*, *Lysinibacillus acetophenoni*, *Lysinibacillus alkaliphilus*, *Lysinibacillus chungkukjangi*, *Lysinibacillus composti*, *Lysinibacillus contaminans*, *Lysinibacillus cresolivorans*, *Lysinibacillus macroides*, *Lysinibacillus manganicus*, *Lysinibacillus mangiferihumi*, *Lysinibacillus massiliensis*, *Lysinibacillus meyeri*, *Lysinibacillus odysseyi*, *Lysinibacillus pakistanensis*, *Lysinibacillus parviboronicapiens*, *Lysinibacillus sinduriensis*, *Lysinibacillus tabacifolii*, *Lysinibacillus varians*, *Lysinibacillus xylanilyticus,* or *Lysinibacillus halotolerans*; or a bacterium that possesses a 16S rRNA gene that shares at least 97%, 98% or 99% identity with a 16S rRNA gene of a *Lysinibacillus* species.

58. A method of displaying a heterologous fusion protein on an exosporium of a *Lysinibacillus* endospore, the method comprising:

(a) transforming a *Lysinibacillus* cell capable of sporulation with a recombinant vector comprising the nucleic acid molecule of any one of claims 37-45; and

(b) expressing the fusion protein encoded by the nucleic acid molecule of any one of claims 37-45 under sporulation conditions such that the fusion protein is targeted to the exosporium of the *Lysinibacillus* endospore resulting from the sporulation,

wherein the N-terminal signal peptide comprises: (i) a polypeptide comprising an amino acid sequence having at least 60%, 70%, or 80% sequence identity with the amino acid sequence of any one of SEQ ID NOs: 41-177 or an amino acid sequence shown in **Table 2** or **FIGs. 4-5**; or (ii) a fragment of at least 5, 10, 15, 20, 25, 30, 35, 40 or 45 consecutive amino acids of any one of SEQ ID NOs: 41-177 or an amino acid sequence shown in **Table 2** or **FIGs. 4-5**.

59. A composition comprising:

(a) one or more recombinant exosporium-producing *Lysinibacillus* cells that express the fusion protein of any one of claims 46-52, wherein the polypeptide heterologous to the N-terminal signal peptide comprises a plant growth or immune stimulating protein; and

(b) at least one biological control agent; optionally,

in a synergistically effective amount.

60. A seed treated with the nucleic acid of any one of claims 37-45, the fusion protein of any one of claims 46-52, the recombinant bacterial cell of claims 56 or 57, or the composition of claim 59.

61. A method of treating a plant, a seed, a plant part, or the soil surrounding the plant to enhance plant growth and/or promote plant health comprising the step of simultaneously or sequentially applying:

(a) recombinant exosporium-producing *Lysinibacillus* endospores that express the fusion protein of any one of claims 46-52, wherein the polypeptide heterologous to the N-terminal signal peptide comprises a plant growth or immune stimulating protein; and

(b) at least one biological control agent; optionally,

in a synergistically effective amount.

62. A method of screening a host plant treated with a recombinant *Lysinibacillus* endospore, comprising the following steps:

(a) applying a composition comprising a *Lysinibacillus* endospore modified to express a fusion protein according to any one of claims 46-52, to a seed, a seedling, or a vegetative plant capable of being permanently or transiently colonized by a *Lysinibacillus*, to produce a treated seed, seedling, or vegetative plant; and

(b) screening the treated seed, seedling, or vegetative plant by detecting and optionally measuring a trait, component, or attribute of the treated seed, seedling, or vegetative plant.

63. The method of claim 62, wherein the screening step comprises one or more of the following:

(a) at least one *in vitro* assay comprising detecting and optionally quantifying the presence, level, change in level, activity, or localization of one or more compounds contained in an extract prepared from a cell or tissue sample obtained from the treated seed, seedling, or vegetative plant; and/or

(b) at least one *in vivo* assay comprising detecting and optionally quantifying a trait, component, or attribute of the treated seed, seedling, or vegetative plant.

64. A method of screening heterologous proteins or peptides expressed in a *Lysinibacillus* cell for agriculturally-significant properties, comprising:

(a) modifying a *Lysinibacillus* cell to express a fusion protein according to any one of claims 46-52 to produce a recombinant *Lysinibacillus* cell; and

(b) screening the *Lysinibacillus* cell by detecting and optionally quantifying a level or activity of a compound produced by the recombinant *Lysinibacillus* cell.

65. A method of treating a plant, a seed, a human, or an animal, comprising:

administering to the plant, seed, human, or animal a composition comprising an exosporium isolated from an endospore produced by a recombinant *Lysinibacillus* cell;

wherein the recombinant *Lysinibacillus* cell expresses the fusion protein of any one of claims 46-52.

66. The method of claim 65, wherein the composition has been heat-inactivated or sterilized such that no viable *Lysinibacillus* cells remain.

67. A composition comprising an isolated and/or purified fusion protein according to any one of claims 46-52.

68. A composition comprising an isolated and/or purified exosporium produced by a recombinant *Lysinibacillus* endospore, which has been modified to express a fusion protein according to any one of claims 46-52.

69. A composition comprising an exosporium produced by a recombinant *Lysinibacillus* endospore, which has been modified to express a fusion protein according to any one of claims 46-52.

70. The composition of claim 69, wherein the exosporium produced by a recombinant *Lysinibacillus* endospore comprises:

(a) a basal layer of an exosporium;

(b) a hair-like layer of an exosporium;

(c) a mixture of both a) and b);

(d) a fraction or extract of a crude exosporium obtained from a *Lysinibacillus* endospore; and/or

(e) a fraction or extract of a crude exosporium obtained from a *Lysinibacillus* endospore that is enriched in an amount or concentration of the fusion protein compared to a same amount of the crude exosporium.

71. A method of delivering a protein of interest to a plant, seed or field, comprising:

applying a composition comprising an exosporium obtained from a recombinant *Lysinibacillus* endospore to a plant, seed, or field;

wherein the recombinant *Lysinibacillus* endospore has been modified to express a fusion protein according to any one of claims 46-52.

72. The method of claim 71, wherein the composition is applied to a field:

(a) pre- or post-planting;

(b) pre- or post-emergence;

(c) as a powder, suspension or solution; and/or

(d) wherein the composition further comprises one or more additional compounds that stimulate plant growth or protect plants from pests.

73. A nucleic acid molecule encoding a fusion protein, comprising (a) a first polynucleotide sequence encoding an N-terminal signal peptide, operably linked to (b) a second

polynucleotide sequence encoding a polypeptide heterologous to the N-terminal signal peptide, wherein the first polynucleotide sequence comprises:

(i) a polynucleotide sequence having at least 60%, 70%, 80% or 90% sequence identity with any one of the polynucleotide sequences shown in **Table 3** or **FIG. 6**; or

(ii) a polynucleotide sequence comprising a fragment of at least 30, 60, 90, 120 or 150 consecutive nucleotides of any one of the polynucleotide sequences shown in **Table 3** or **FIG. 6**; and

wherein the N-terminal signal peptide is capable of targeting the fusion protein to an exosporium of a *Viridibacillus* endospore.

74. The nucleic acid molecule of claim 73, wherein the fragment includes:

(a) the first nucleotide of any one of the polynucleotide sequences shown in **Table 3** or **FIG. 6**; or

(b) the last nucleotide of any one of the polynucleotide sequences shown in **Table 3** or **FIG. 6**.

75. The nucleic acid molecule of claim 73 or 74, wherein the first polynucleotide sequence comprises a polynucleotide sequence having at least 60%, 70%, 80% or 90% sequence identity with any one of SEQ ID NOs: 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, or 218.

76. The nucleic acid molecule of any one of claims 73-75, wherein the fragment encodes amino acids 1-10, 1-20, 1-30, 1-40 or 1-50 of any one of SEQ ID NOs: 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, or 219.

77. The nucleic acid molecule of any one of claims 73-76, wherein the polypeptide heterologous to the N-terminal signal peptide comprises:

(a) a plant growth-stimulating protein;

(b) an enzyme;

(c) a protein;

(d) a polypeptide heterologous to *Viridibacillus;*

(e) a therapeutic protein; or

(f) a plant immune-stimulating protein.

78. The nucleic acid molecule of any one of claims 73-77, further comprising a third polynucleotide sequence, encoding:

(a) a polypeptide comprising one or more protease cleavage sites, wherein the polypeptide is positioned between the N-terminal signal peptide and the polypeptide heterologous to the N-terminal signal peptide;

(b) a polypeptide comprising a selectable marker;

(c) a polypeptide comprising a visualization marker;

(d) a polypeptide comprising a protein recognition/purification domain; or

(e) a polypeptide comprising a flexible linker element, which connects the N-terminal signal peptide and the polypeptide heterologous to the N-terminal signal peptide.

79. The nucleic acid molecule of any one of claims 73-78, wherein the *Viridibacillus* endospore is an endospore formed by a *Viridibacillus* species, comprising: *Viridibacillus arvi, Viridibacillus arenosi*, or *Viridibacillus neidei*; or

an endospore formed by a bacterium that possesses a 16S rRNA gene that shares at least 97, 98 or 99% identity with a 16S rRNA gene of a *Viridibacillus* species.

80. The nucleic acid molecule of any one of claims 73-79, operatively linked to a promoter element that is heterologous to at least one of the second polynucleotide sequences and *Viridibacillus*.

81. The nucleic acid molecule of any one of claims 73-80, wherein the first polynucleotide sequence comprises:

a codon-optimized polynucleotide sequence having at least 60%, 70%, 80% or 90% sequence identity with any one of the polynucleotide sequences shown in **Table 3** or **FIG. 6**, which is expressed at a higher rate or level in the *Viridibacillus* endospore compared to the polynucleotide sequence shown in **Table 3** or **FIG. 6**, under identical conditions.

82. A fusion protein comprising an N-terminal signal peptide operably linked to a polypeptide heterologous to the N-terminal signal peptide, wherein the N-terminal signal peptide comprises:

(a) a polypeptide comprising an amino acid sequence having at least 60%, 70%, 80% or 90% sequence identity with any one of the amino acid sequences shown in **Table 3** or **FIG. 6**; or

(b) a polypeptide comprising a fragment of at least 10, 20, 30, 40 or 50 consecutive amino acids of any one of the amino acid sequences shown in **Table 3** or **FIG. 6**;

wherein the N-terminal signal peptide is capable of targeting the fusion protein to an exosporium of a *Viridibacillus* endospore.

83. The fusion protein of claim 82, wherein the fragment includes:

(a) the first amino acid of any one of the sequences shown in **Table 3** or **FIG. 6**; or

(b) the last amino acid of any one of the sequences shown in **Table 3** or **FIG. 6**.

84. The fusion protein of claim 82 or 83, wherein the polypeptide sequence comprises a sequence having at least 60%, 70%, 80% or 90% sequence identity with any one of the sequences shown in **Table 3** or **FIG. 6**.

85. The fusion protein of any one of claims 82 to 84, wherein the fragment comprises amino acids 1-10, 1-20, 1-30, 1-40 or 1-50 of any one of the amino acid sequences shown in **Table 3** or **FIG. 6**.

86. The fusion protein of any one of claims 82 to 85, wherein the polypeptide heterologous to the N-terminal signal peptide comprises:

(a) a plant growth-stimulating protein;

(b) an enzyme;

(c) a protein;

(d) a polypeptide heterologous to *Viridibacillus;*

(e) a therapeutic protein; or

(f) a plant immune-stimulating protein.

87. The fusion protein of any one of claims 82 to 86, wherein the fusion protein further comprises:

(a) a polypeptide containing one or more protease cleavage sites, positioned between the N-terminal signal peptide and the polypeptide heterologous to the N-terminal signal peptide;

(b) a polypeptide comprising a selectable marker;

(c) a polypeptide comprising a visualization marker;

(d) a polypeptide comprising at least one protein recognition/purification domain; or

(e) a polypeptide comprising a flexible linker element, connecting the signal peptide and the polypeptide heterologous to the N-terminal signal peptide.

88. The fusion protein of any one of claims 82 to 87, wherein the *Viridibacillus* endospore is an endospore formed by a *Viridibacillus* species, comprising: *Viridibacillus arvi, Viridibacillus arenosi*, or *Viridibacillus neidei*; or an endospore formed by a bacterium that possesses a 16S rRNA gene that shares at least 97, 98 or 99% identity with a 16S rRNA gene of a *Viridibacillus* species.

89. A recombinant *Viridibacillus* cell comprising a bacterial chromosome comprising the nucleic acid molecule of any one of claims 73-81.

90. A vector comprising the nucleic acid molecule of any one of claims 73-81, wherein the vector comprises a plasmid, an artificial chromosome, or a viral vector.

91. The vector of claim 90, further comprising at least one of the following:

(a) an origin of replication that provides stable maintenance in a *Viridibacillus* cell;

(b) an origin of replication that provides selectively non-stable maintenance in a *Viridibacillus* cell;

(c) a temperature-sensitive origin of replication that provides selectively non-stable maintenance in a *Viridibacillus* cell;

(d) a polynucleotide encoding a selection marker, operably linked to an expression control sequence; or

(e) a polynucleotide encoding a plant growth stimulating protein, operably linked to an expression control sequence.

92. A recombinant *Viridibacillus* cell transformed with a vector comprising the nucleic acid molecule of any one of claims 73-81.

93. The recombinant *Viridibacillus* cell of claim 92, wherein the *Viridibacillus* cell is a *Viridibacillus* species, comprising: *Viridibacillus arvi, Viridibacillus arenosi*, or *Viridibacillus neidei*; or a bacterium that possesses a 16S rRNA gene that shares at least 97, 98 or 99% identity with a 16S rRNA gene of a *Viridibacillus* species.

94. A method of displaying a heterologous fusion protein on an exosporium of a *Viridibacillus* endospore, the method comprising:

(a) transforming a *Viridibacillus* cell capable of sporulation with a recombinant vector comprising the nucleic acid molecule of any one of claims 73-81; and

(b) expressing the fusion protein encoded by the nucleic acid molecule of any one of claims 73-81 under sporulation conditions such that the fusion protein is targeted to the exosporium of the *Viridibacillus* endospore resulting from the sporulation,

wherein the N-terminal signal peptide comprises: (i) a polypeptide comprising an amino acid sequence having at least 60%, 70%, or 80% sequence identity with any one of the amino acid sequences shown in **Table 3** or **FIG. 6**; or (ii) a fragment of at least 10, 20, 30, 40 or 50 consecutive amino acids of any one of the amino acid sequences shown in **Table 3** or **FIG. 6**.

95. A composition comprising:

(a) one or more recombinant exosporium-producing *Viridibacillus* cells that express the fusion protein of any one of claims 82-88, wherein the polypeptide heterologous to the N-terminal signal peptide comprises a plant growth or immune stimulating protein; and

(b) at least one biological control agent; optionally,

in a synergistically effective amount.

96. A seed treated with the nucleic acid of any one of claims 73-81, the fusion protein of any one of claims 82-88, the recombinant bacterial cell of claim 92 or 93, or the composition of claim 95.

97. A method of treating a plant, a seed, a plant part, or the soil surrounding the plant to enhance plant growth and/or promote plant health comprising the step of simultaneously or sequentially applying:

(a) recombinant exosporium-producing *Viridibacillus* endospores that express the fusion protein of any one of claims 82-88, wherein the polypeptide heterologous to the N-terminal signal peptide comprises a plant growth or immune stimulating protein; and

(b) at least one biological control agent; optionally,

in a synergistically effective amount.

98. A method of screening a host plant treated with a recombinant *Viridibacillus* endospore, comprising the following steps:

(a) applying a composition comprising a *Viridibacillus* endospore modified to express a fusion protein according to any one of claims 82-88, to a seed, a seedling, or a vegetative plant capable of being permanently or transiently colonized by a *Viridibacillus*, to produce a treated seed, seedling, or vegetative plant; and

(b) screening the treated seed, seedling, or vegetative plant by detecting and optionally measuring a trait, component, or attribute of the treated seed, seedling, or vegetative plant.

99. The method of claim 98, wherein the screening step comprises one or more of the following:

(a) at least one *in vitro* assay comprising detecting and optionally quantifying the presence, level, change in level, activity, or localization of one or more compounds contained in an extract prepared from a cell or tissue sample obtained from the treated seed, seedling, or vegetative plant; and/or

(b) at least one *in vivo* assay comprising detecting and optionally quantifying a trait, component, or attribute of the treated seed, seedling, or vegetative plant.

100. A method of screening heterologous proteins or peptides expressed in a *Viridibacillus* cell for agriculturally-significant properties, comprising:

(a) modifying a *Viridibacillus* cell to express a fusion protein according to any one of claims 10-16 to produce a recombinant *Viridibacillus* cell; and

(b) screening the *Viridibacillus* cell by detecting and optionally quantifying a level or activity of a compound produced by the recombinant *Viridibacillus* cell.

101. A method of treating a plant, a seed, a human, or an animal, comprising:

administering to the plant, seed, human, or animal a composition comprising an exosporium isolated from an endospore produced by a recombinant *Viridibacillus* cell;

wherein the recombinant *Viridibacillus* cell expresses the fusion protein of any one of claims 82-88.

102. The method of claim 101, wherein the composition has been heat-inactivated or sterilized such that no viable *Viridibacillus* cells remain.

103. A composition comprising an isolated and/or purified fusion protein according to any one of claims 82-88.

104. A composition comprising an isolated and/or purified exosporium produced by a recombinant *Viridibacillus* endospore, which has been modified to express a fusion protein according to any one of claims 82-88.

105. A composition comprising an exosporium produced by a recombinant *Viridibacillus* endospore, which has been modified to express a fusion protein according to any one of claims 82-88.

106. The composition of claim 105, wherein the exosporium produced by a recombinant *Viridibacillus* endospore comprises:

(a) a basal layer of an exosporium;

(b) a hair-like layer of an exosporium;

(c) a mixture of both a) and b);

(d) a fraction or extract of a crude exosporium obtained from a *Viridibacillus* endospore; and/or

(e) a fraction or extract of a crude exosporium obtained from a *Viridibacillus* endospore that is enriched in an amount or concentration of the fusion protein compared to a same amount of the crude exosporium.

107. A method of delivering a protein of interest to a plant, seed or field, comprising:

applying a composition comprising an exosporium obtained from a recombinant *Viridibacillus* endospore to a plant, seed, or field;

wherein the recombinant *Viridibacillus* endospore has been modified to express a fusion protein according to any one of claims 82-88.

108. The method of claim 107, wherein the composition is applied to a field:

(a) pre- or post-planting;

(b) pre- or post-emergence;

(c) as a powder, suspension or solution; and/or

(d) wherein the composition further comprises one or more additional compounds that stimulate plant growth or protect plants from pests.

FIG. 1

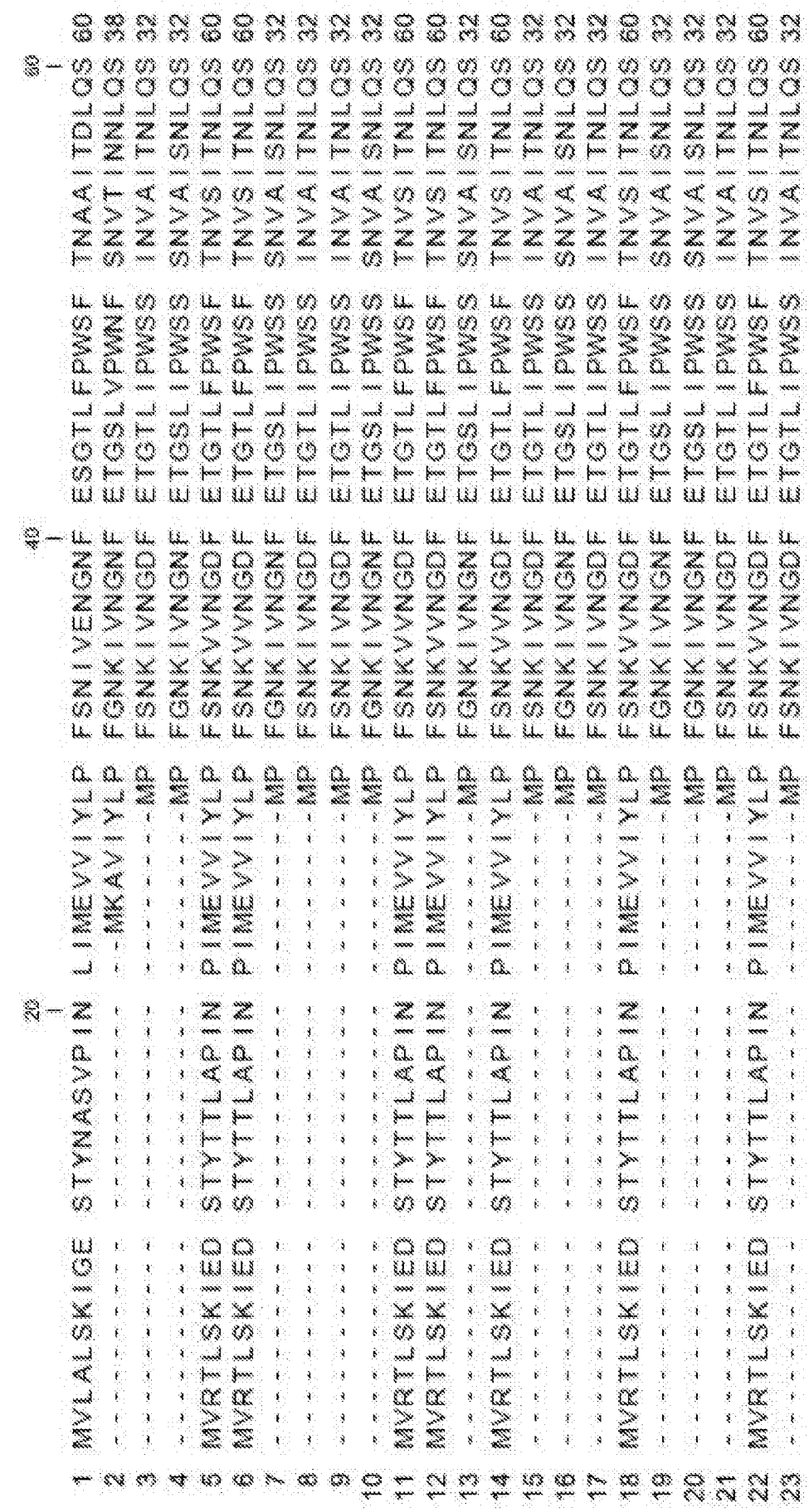

1 MVLALSKIGE STYNASVPIN LIMEVVIYLP FSNIVENGNF ESGTLFPWSF TNAAITDLQS 60
2 ---------- ---------- --MKAVIYLP FGNKIVNGNF ETGSLVPWNF SNVTINNLQS 38
3 ---------- ---------- ---------- FSNKIVNGDF ETGTLIPWSS INVAITNLQS 32
4 ---------- ---------- ---------- FGNKIVNGNF ETGSLIPWSS SNVAISNLQS 32
5 MVRTLSKIED STYTTLAPIN PIMEVVIYLP FSNKVVNGDF ETGTLFPWSF TNVSITNLQS 60
6 MVRTLSKIED STYTTLAPIN PIMEVVIYLP FSNKVVNGDF ETGTLFPWSF TNVSITNLQS 60
7 ---------- ---------- ---------- FGNKIVNGNF ETGSLIPWSS SNVAISNLQS 32
8 ---------- ---------- ---------- FSNKIVNGDF ETGTLIPWSS INVAITNLQS 32
9 ---------- ---------- ---------- FSNKIVNGDF ETGTLIPWSS INVAITNLQS 32
10 ---------- ---------- ---------- FGNKIVNGNF ETGSLIPWSS SNVAISNLQS 32
11 MVRTLSKIED STYTTLAPIN PIMEVVIYLP FSNKVVNGDF ETGTLFPWSF TNVSITNLQS 60
12 MVRTLSKIED STYTTLAPIN PIMEVVIYLP FSNKVVNGDF ETGTLFPWSF TNVSITNLQS 60
13 ---------- ---------- ---------- FGNKIVNGNF ETGSLIPWSS SNVAISNLQS 32
14 MVRTLSKIED STYTTLAPIN PIMEVVIYLP FSNKVVNGDF ETGTLFPWSF TNVSITNLQS 60
15 ---------- ---------- ---------- FSNKIVNGDF ETGTLIPWSS INVAITNLQS 32
16 ---------- ---------- ---------- FGNKIVNGNF ETGSLIPWSS SNVAISNLQS 32
17 ---------- ---------- ---------- FSNKIVNGDF ETGTLIPWSS INVAITNLQS 32
18 MVRTLSKIED STYTTLAPIN PIMEVVIYLP FSNKVVNGDF ETGTLFPWSF TNVSITNLQS 60
19 ---------- ---------- ---------- FGNKIVNGNF ETGSLIPWSS SNVAISNLQS 32
20 ---------- ---------- ---------- FGNKIVNGNF ETGSLIPWSS SNVAISNLQS 32
21 ---------- ---------- ---------- FSNKIVNGDF ETGTLIPWSS INVAITNLQS 32
22 MVRTLSKIED STYTTLAPIN PIMEVVIYLP FSNKVVNGDF ETGTLFPWSF TNVSITNLQS 60
23 ---------- ---------- ---------- FSNKIVNGDF ETGTLIPWSS INVAITNLQS 32

FIG. 1 (continued)

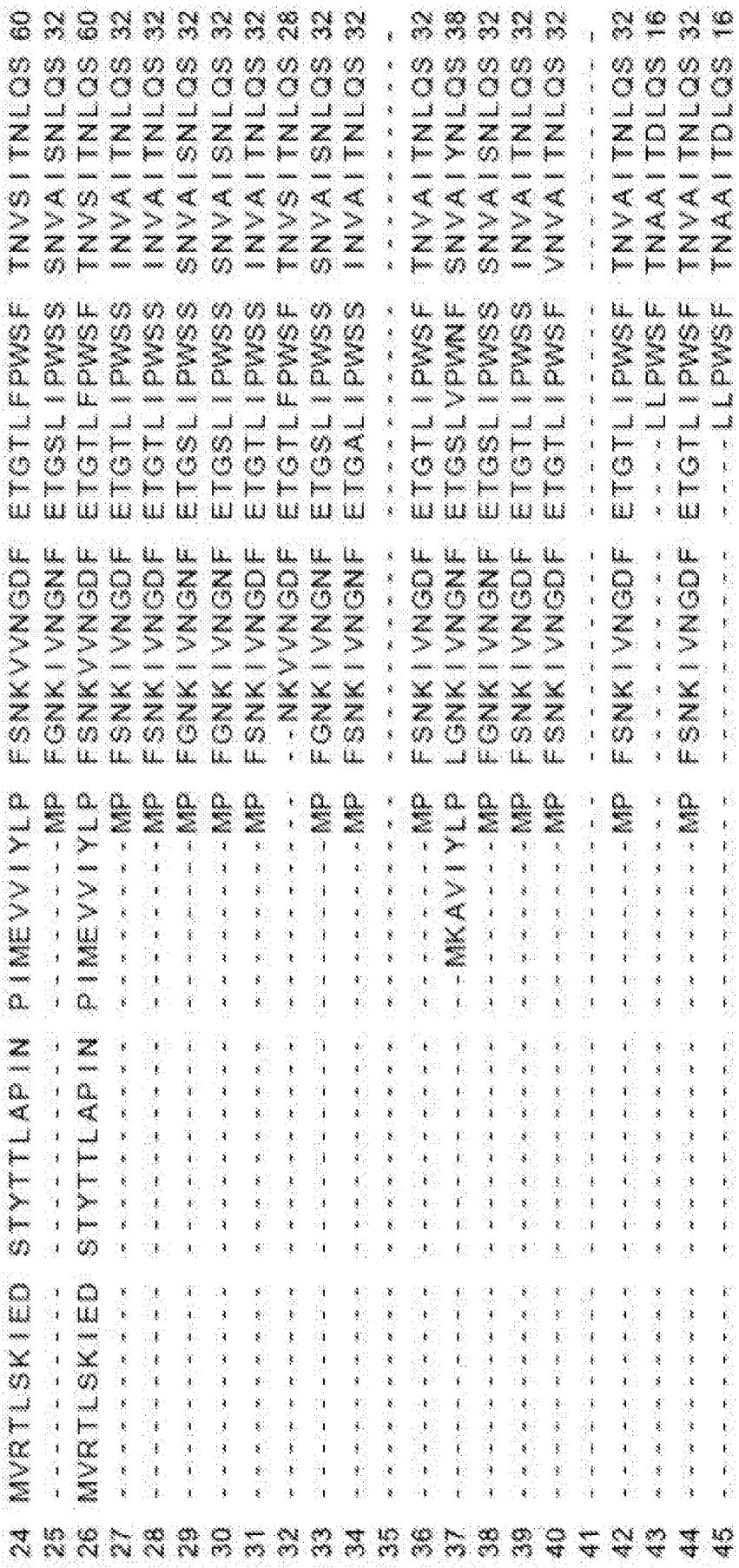


FIG. 1 (continued)

```
46 ------------------------------MP FSNKIVNGDF ETGTLIPWSF TNVAITNLQS 32
47 ------------------------------MS FINKIVNGDF ETGTLIPWSF VNVAITNLQS 32
48 ------------------------------MS FINKIVNGDF ETGTLIPWSF VNVAINPLQS 32
49 ------------------------------MS FINKIVNGDF ETGTLIPWSF VNVAINPLQS 32
50 ------------------------------MP FSNKIVNGDF ETGTLIPWSS INVAITNLQS 32
51 ------------------------------MP FGNKIVNGNF ETGSLIPWSS SNVVISNLQS 32
52 ------------------------------MP VKNRAVNGDF ETGSLVPWNS INVTISNQQS 32
53 ------------------------------ ---------- ---------- ---------- -
54 ------------------------------MP FSNKIVNGNF ETGALIPWSS INVAITNLQS 32
55 ------------------------------MP FSNKIVNGNF ETGALIPWSS INVAITNLQS 32
56 ------------------------------ ---------- ---------- ---------- -
57 ------------------------------MP FGNKIVNGNF ETGSLIPWSS SNVVISNLQS 32
58 ------------------------------MP FSNKIVNGNF ETGALIPWSS INVAITNLQS 32
59 ------------------------------MP FSNKIVNGNF ETGALIPWSS INVAITNLQS 32
60 ------------------------------MP FGNKIVNGNF ETGSLIPWSS SNVVISNLQS 32
61 ------------------------------MP FSNKIVNGNF ETGALIPWSS INVAITNLQS 32
62 MVRTLSKIED STYTTLAPIN PIMEVVIYLP FSNKVVNGDF ETGTLFPWSF TNVSITNLQS 60
63 ------------------------------MP FSNKIVNGDF ETGTLIPWSS INVAITNLQS 32
64 ------------------------------MP FGNKIVNGNF ETGSLIPWSS SNVAISNLQS 32
65 ------------------------------MP FSNKIVNGDF ETGTLIPWSS INVAITNLQS 32
66 MVRTLSKIED STYTTLAPIN PIMEVVIYLP FSNKVVNGDF ETGTLFPWSF TNVSITNLQS 60
67 ------------------------------MP FGNKIVNGNF ETGSLIPWSS SNVAISNLQS 32
68 ------------------------------MP FSNKIVNGDF ETGTLIPWSS INVAITNLQS 32
69 MVRTLSKIED STYTTLAPIN PIMEVVIYLP FSNKVVNGDF ETGTLFPWSF TNVSITNLQS 60
70 ------------------------------MP FGNKIVNGNF ETGSLIPWSS SNVAISNLQS 32
```

FIG. 1 (continued)

```
71  ----------  ----------  ---MP  FSNKIVNGDF  ETGTLIPWSS  INVAITNLQS  32
72  MVRTLSKIED  STYTTLAPIN  PIMEVVIYLP  FSNKVVNGDF  ETGTLFPWSF  TNVSITNLQS  60
73  ----------  ----------  ---MP  FGNKIVNGNF  ETGSLIPWSS  SNVAISNLQS  32
74  ----------  ----------  ---MP  FSNKIVNGDF  ETGTLIPWSS  INVAITNLQS  32
75  ----------  ----------  ------  ----GDF  ETGTLFPWSF  TNVSITNLQS  23
76  ----------  ----------  ---MP  FGNKIVNGNF  ETGSLIPWSS  SNVAISNLQS  32
77  ----------  ----------  ---MP  FSNKIVNGDF  ETGTLIPWSS  INVAITNLQS  32
78  ----------  ----------  ---MP  FGNKIVNGNF  ETGSLIPWSS  SNVAISNLQS  32
79  ----------  ----------  ------  ----------  ----------  ----------  -
80  ----------  ----------  ---MP  FSNKIVNGDF  ETGTLIPWSS  INVAITNLQS  32
81  ----------  ----------  ---MP  FSNKIVNGDF  ETGTLIPWSS  INVAITNLQS  32
82  ----------  ----------  ---MP  FGNKIVNGNF  ETGSLIPWSS  SNVVISNLQS  32
83  ----------  ----------  ---MP  FGNKIVNGNF  ETGSLIPWSS  SNVVISNLQS  32
84  ----------  ----------  ---MP  FGNKIVNGNF  ETGSLIPWSS  SNVVISNLQS  32
85  ----------  ----------  ---MP  FGNKIVNGNF  ETGSLIPWSS  SNVVISNLQS  32

86  ----------  ----------  ---MP  FSNKIVNGDF  ETGTLIPWSS  INVAITNLQS  32
87  ----------  ----------  ------  ----------  ----------  ----------  -
88  ----------  ----------  ---MP  FGNKIVNGNF  ETGSLIPWSS  SNVVISNLQS  32
89  ----------  ----------  ---MP  FGNKIVNGNF  ETGSLIPWSS  SNVVISNLQS  32
90  ----------  ----------  ---MP  FSNKIVNGDF  ETGTLIPWSS  INVAITNLQS  32

Consensus  ----------  ----------  ---MP  FSNKIVNGDF  ETGTLIPWSS  XNVAITNLQS
```

**FIG. 1 (continued)**

```
                                80                            100                           120
                                 |                              |                             |
 1 HSGFFSALLF GGTANSLLFQ TVPVTPGDSF ELFLSIAKSG NLISPQVNIV LIYLDAANIP 120
 2 HTGSFSALFF GNTTNSVLYQ TVPVTSGEIF EFFLSIGKIG NLPSPQVNIA LIYLNAASTP 98
 3 HTGFFSARLF GNTANSLLFQ AVPVTPGDSF EFLLSIAKLG NLVSPQVNIA LLYLDVTATP 92
 4 HTGSYSALLF GNAANSFLFQ AVPVTVGDSF EFFLSIAKIG NLPSPQVDIA LIYLNAASTP 92
 5 HTGFFSALLF GDTANSLLFQ AIPVTPGDSF ELFLSIAKLG NLVSPQVNIA LLYLDVATIP 120
 6 HTGFFSALLF GDTANSLLFQ AIPVTPGDSF ELFLSIAKLG NLVSPQVNIA LLYLDVATIP 120
 7 HTGSYSALLF GNAANSFLFQ AVPVTVGDSF EFFLSIAKIG NLPSPQVDIA LIYLNAASTP 92
 8 HTGFFSARLF GNTANSLLFQ AVPVTPGDSF EFLLSIAKLG NLVSPQVNIA LLYLDVTATP 92
 9 HTGFFSARLF GNTANSLLFQ AVPVTPGDSF EFLLSIAKLG NLVSPQVNIA LLYLDVTATP 92
10 HTGSYSALLF GNAANSFLFQ AVPVTVGDSF EFFLSIAKIG NLPSPQVDIA LIYLNAASTP 92
11 HTGFFSALLF GDTANSLLFQ AIPVTPGDSF ELFLSIAKLG NLVSPQVNIA LLYLDVATIP 120
12 HTGFFSALLF GDTANSLLFQ AIPVTPGDSF ELFLSIAKLG NLVSPQVNIA LLYLDVATIP 120
13 HTGSYSALLF GNAANSFLFQ AVPVTVGDSF EFFLSIAKIG NLPSPQVDIA LIYLNAASTP 92
14 HTGFFSALLF GDTANSLLFQ AIPVTPGDSF ELFLSIAKLG NLVSPQVNIA LLYLDVATIP 120
15 HTGFFSARLF GNTANSLLFQ AVPVTPGDSF EFLLSIAKLG NLVSPQVNIA LLYLDVTATP 92
16 HTGSYSALLF GNAANSFLFQ AVPVTVGDSF EFFLSIAKIG NLPSPQVDIA LIYLNAASTP 92
17 HTGFFSARLF GNTANSLLFQ AVPVTPGDSF EFLLSIAKLG NLVSPQVNIA LLYLDVTATP 92
18 HTGFFSALLF GDTANSLLFQ AIPVTPGDSF ELFLSIAKLG NLVSPQVNIA LLYLDVATIP 120
19 HTGSYSALLF GNAANSFLFQ AVPVTVGDSF EFFLSIAKIG NLPSPQVDIA LIYLNAASTP 92
20 HTGSYSALLF GNAANSFLFQ AVPVTVGDSF EFFLSIAKIG NLPSPQVDIA LIYLNAASTP 92
21 HTGFFSARLF GNTANSLLFQ AVPVTPGDSF EFLLSIAKLG NLVSPQVNIA LLYLDVTATP 92
22 HTGFFSALLF GDTANSLLFQ AIPVTPGDSF ELFLSIAKLG NLVSPQVNIA LLYLDVATIP 120
23 HTGFFSARLF GNTANSLLFQ AVPVTPGDSF EFLLSIAKLG NLVSPQVNIA LLYLDVTATP 92
```

FIG. 1 (continued)

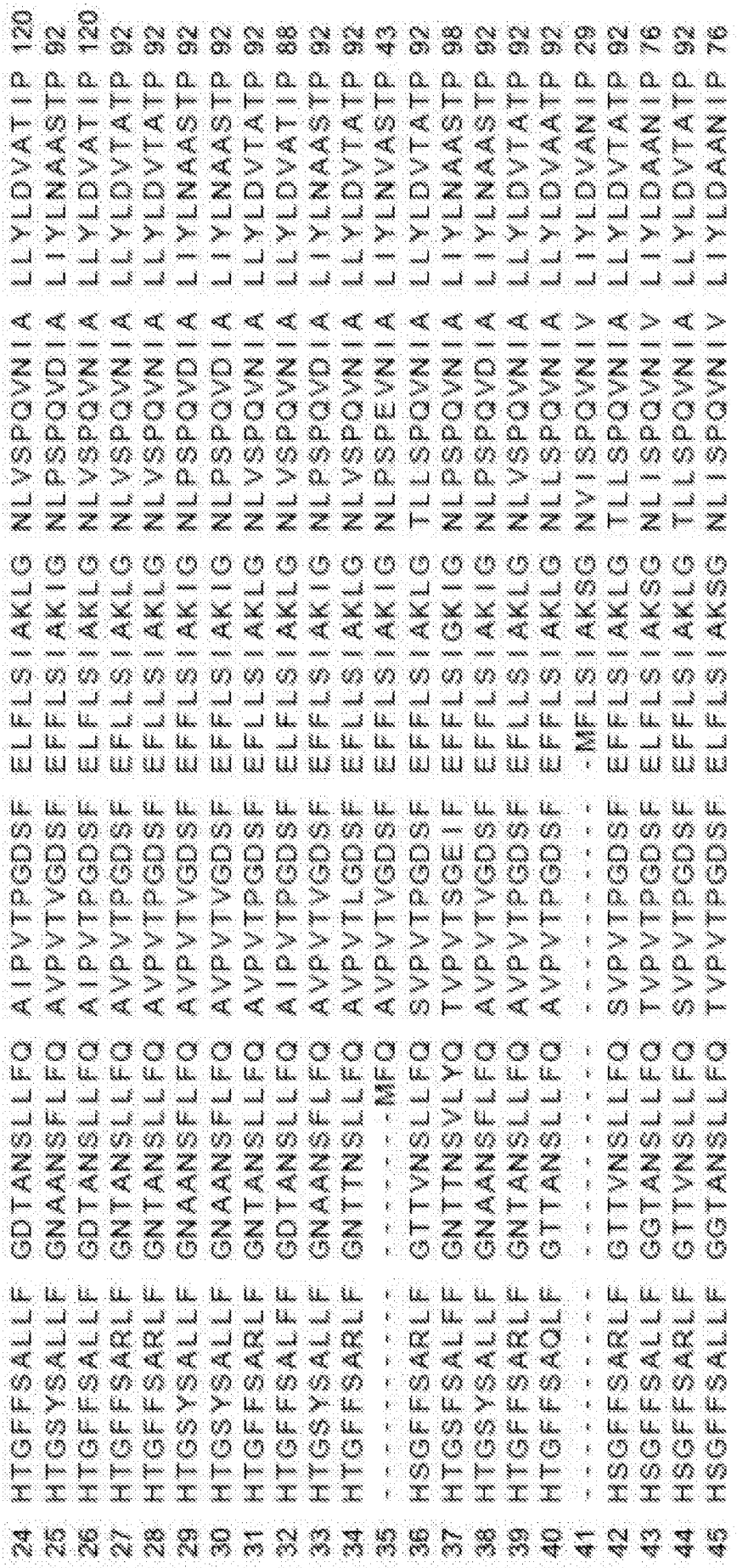


FIG. 1 (continued)



FIG. 1 (continued)

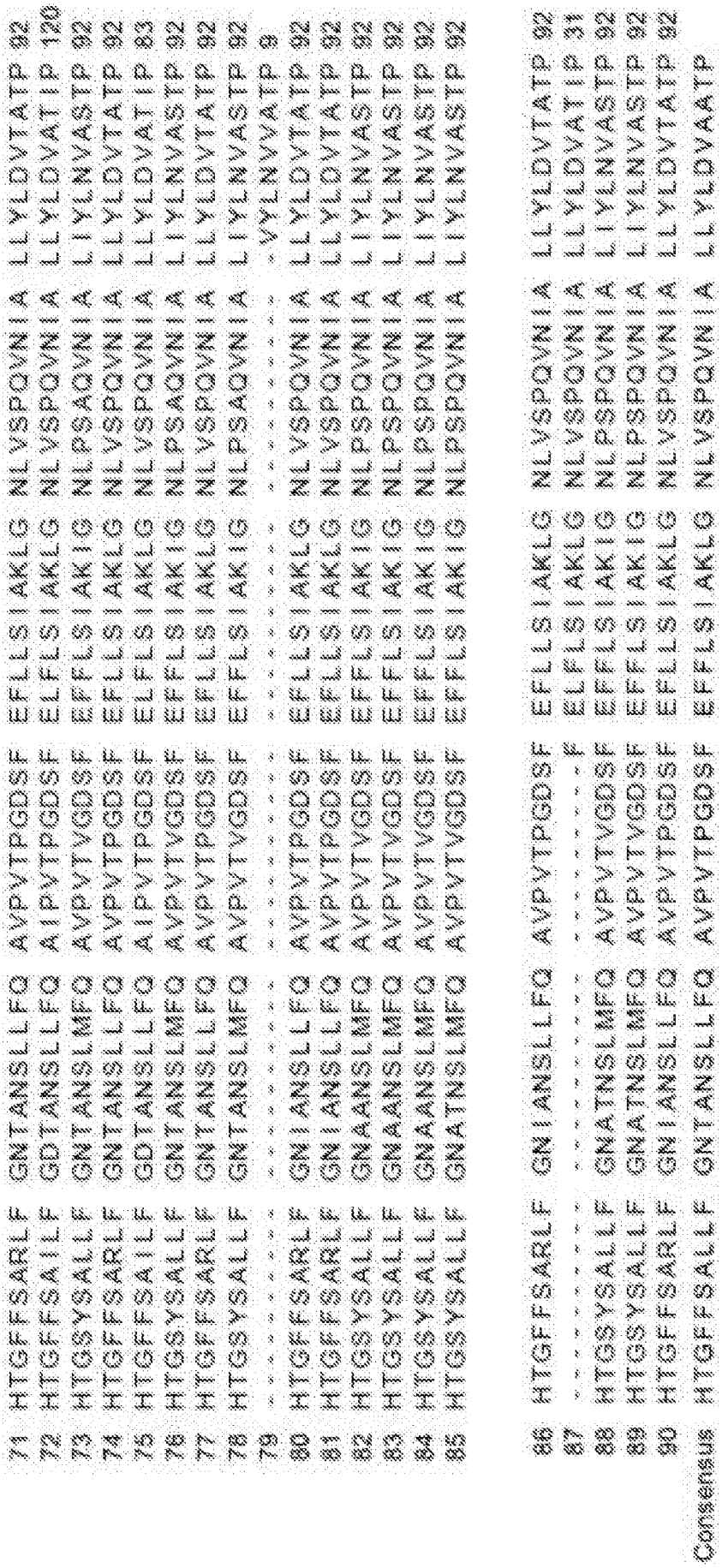


FIG. 1 (continued)

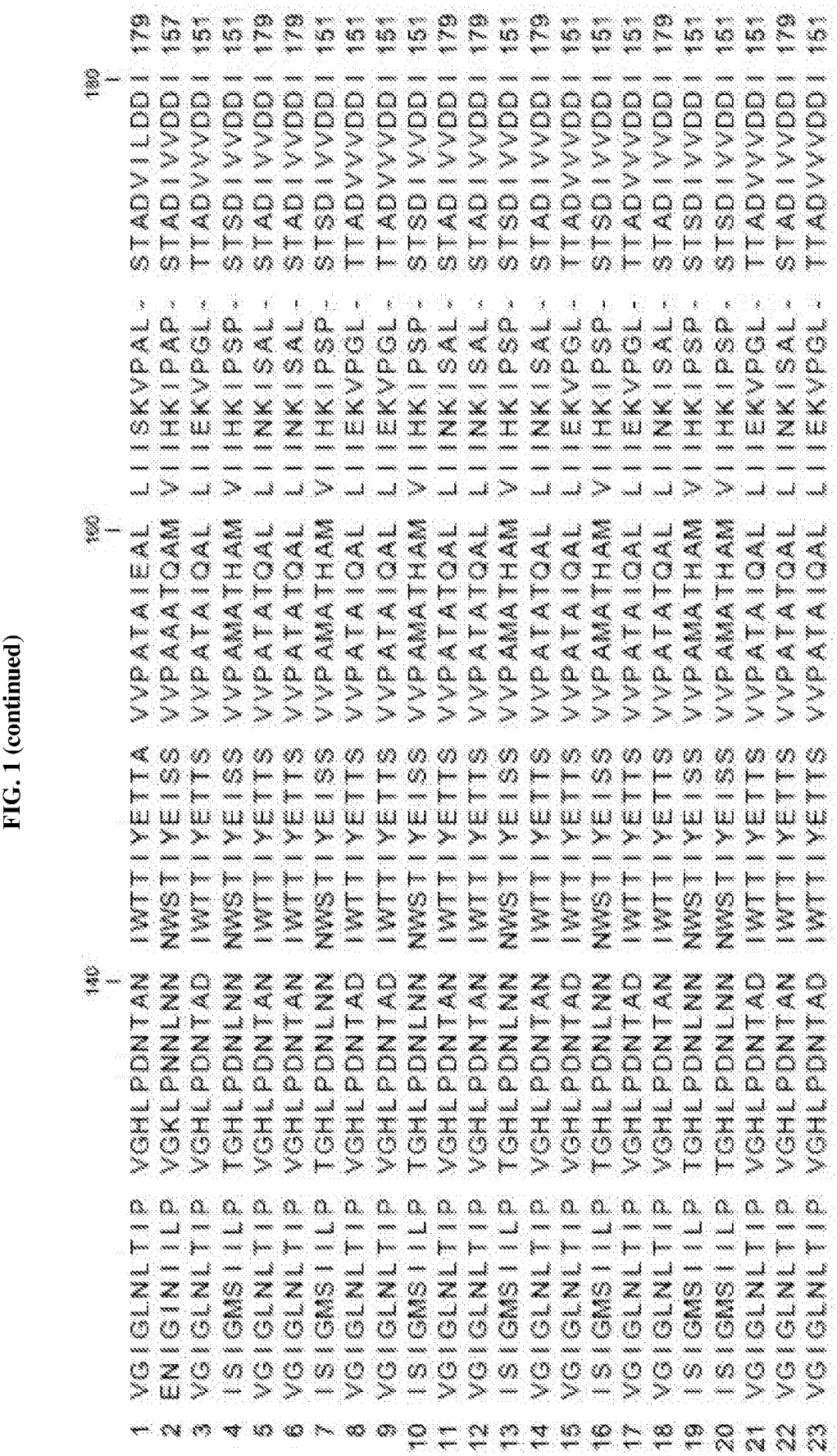


FIG. 1 (continued)

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 24 | VGIGLNLTIP | VGHLPDNTAN | IWTTIYETTS | VVPATATQAL | LIINKISAL- | STADIVVDDI | 179 |
| 25 | ISIGMSILLP | TGHLPDNLNN | NMSTIYEISS | VVPAMATHAM | VIIHKIPSP- | STSDIVVDDI | 151 |
| 26 | VGIGLNLTIP | VGHLPDNTAN | IWTTIYETTS | VVPATATQAL | LIINKISAL- | STADIVVDDI | 179 |
| 27 | VGIGLNLTIP | VGHLPDNTAD | IWTTIYETTS | VVPATAIQAL | LIIEKVPGL- | TTADVVVDDI | 151 |
| 28 | VGIGLNLTIP | VGHLPDNTAD | IWTTIYETTS | VVPATAIQAL | LIIEKVPGL- | TTADVVVDDI | 151 |
| 29 | ISIGMSILLP | TGHLPDNLNN | NMSTIYEISS | VVPAMATHAM | VIIHKIPSP- | STSDIVVDDI | 151 |
| 30 | ISNGMSILLP | TGHLPDNLNN | NMSTIYEISS | VVPAMATHAM | VIIHKIPSP- | STSDIVVDDI | 151 |
| 31 | VGIGLNLTIP | VGHLPDNTAD | IWTTIYETTS | VVPATAIQAL | LIIEKVPGL- | TTADVVVDDI | 151 |
| 32 | VGIGLNLTIP | VGHLPDNTAN | IWTTIYETTS | VVPATATQAL | LIINKISAL- | STADIVVDDI | 147 |
| 33 | ISIGMSILLP | TGHLPDNLNN | NMSTIYEISS | VVPAMATHAM | VIIHKIPSP- | STSDIVVDDI | 151 |
| 34 | VGIGLNFTIP | VGHLPDNTAN | IWTTIYETTS | VVPATAIQAL | LIIEKVAAL- | TTADVVVDDI | 151 |
| 35 | ISIGMSILLP | IGHLPDNLNN | NMSTIYEISS | VVPATATHAM | VIIHKIPSP- | STSDIVVDDI | 102 |
| 36 | VGIGLNITIP | IGHLPDNTAN | IWTTIYETTT | VVPATATQAL | LIINKIPTL- | TTADIVVDDI | 151 |
| 37 | ENIGINILLP | VGKLPNNLNN | NMSTIYEISS | VVPAAATQAM | VIIHKIPAP- | STADIVVDDI | 157 |
| 38 | ISIGMSILLP | TGHLPDNLNN | NMSTIYEISS | VVPAMATHAM | VIIHKIPSP- | STSDIVVDDI | 151 |
| 39 | VGIGLNLTIP | VGHLPDNTAD | IWTTIYETTS | VVPATAIQAL | LIIEKVPGL- | TTADVVVDDI | 151 |
| 40 | VGIGLNITIP | IGHLPDNAAN | IWTTIYETTT | VVPATATQAL | LIINKIPTL- | TTADIVVDDI | 151 |
| 41 | VGIGLNLTIP | VGHLPDNTAN | IWTTIYETTS | VVPATAIEAL | LIINKVPAL- | STADVILDDI | 88 |
| 42 | VGIGLNITIP | IGHLPDNTAN | IWTTIYETTT | VVPATATQAL | LIINKIPTL- | TTADIVVDDI | 151 |
| 43 | VGIGLNLTIP | VGHLPDNTAN | IWTTIYETTA | VVPATAIEAL | LIISKVPAL- | STADVILDDI | 135 |
| 44 | VGIGLNITIP | IGHLPDNTAN | IWTTIYETTT | VVPATATQAL | LIINKIPTL- | TTADIVVDDI | 151 |
| 45 | VGIGLNLTIP | VGHLPDNTAN | IWTTIYETTA | VVPATAIEAL | LIISKVPAL- | STADVILDDI | 135 |

FIG. 1 (continued)

```
46 VGIGLNITIP IGHLPDNTAN IWTTIYETTT VVPATATQAL LIINKIPTL- TTADIVVDDI 151
47 ISLGLNITIP SGHLPDNVDN NWTTIYETTS AVPATATQAL LIINKIPALF TTADIVVDDI 152
48 ISLGLNITIP SGHLPDNVDN NWTTIYETTS AVPATATQAL LIINKIPALF TTADIVVDDI 152
49 ISLGLNITIP SGHLPDNVDN NWTTIYETTS AVPATATQAL LIINKIPALF TTADIVVDDI 152
50 VGIGLNLTIP VGHLPDNTAN IWTTIYETTS VVPATAIQAL LIIEKVASL- TTADVVVDDI 151
51 ISIGMSIILP IGHLPDNLNN NWSTIYEISS VVPATATHAM VIIHKIPSP- STSDIVVDDI 151
52 LSIGMSVILP VNHLPNNLNN NWLTIYNTTS VVPVTATQAI IIIHKIPAP- STADIVVDDI 151
53 ISIGMSIILP IGHLPDNLNN NWSTIYEISS VVPATATHAM VIIHKIPSP- STSDIVVDDI 102
54 VGIGLNFTIP VGHLPDNTAN IWTTIYETTS VVPATATQAL LIINKIAAL- STADIVVDDI 151
55 VGIGLNFTIP VGHLPDNTAN IWTTIYETTS VVPATAIQAL LIIEKVAAL- TTADVVVDDI 151
56 ISIGMSIILP IGHLPDNLNN NWSTIYEISS VVPATATHAM VIIHKIPSP- STSDIVVDDI 102
57 ISIGMSIILP IDHLPDNLNN NWSTIYEISS VVPATATHAM VIIHKIPSP- STSDIVVDDI 151
58 VGIGLNFTIP VGHLPDNTAN IWTTIYETTS VVPATAIQAL LIIEKVAAL- TTADVVVDDI 151
59 VGIGLNFTIP VGHLPDNTAN IWTTIYETTS VVPATAIQAL LIIEKVAAL- TTADVVVDDI 151
60 ISIGMSIILP IGHLPDNLNN NWSTIYEISS VVPATATHAM VIIHKIPSP- STSDIVVDDI 151
61 VGIGLNFTIP VGHLPDNTAN IWTTIYETTS VVPATAIQAL LIIEKVAAL- TTADVVVDDI 151
62 VGIGLNLTIP VGHLPDNTAN IWTTIYETTS VVPATATQAL LIINKISAL- STADIVVDDI 179
63 VGIGLNLTIP VGHLPDNTAD IWTTIYETTS VVPATAIQAL LIIEKVPGL- TTADVVVDDI 151
64 ISIGMSIILP TGHLPDNLNN NWSTIYEISS VVPAMATHAM VIIHKIPSP- STSDIVVDDI 151
65 VGIGLNLTIP VGHLPDNTAD IWTTIYETTS VVPATAIQAL LIIEKVPGL- TTADVVVDDI 151
66 VGIGLNLTIP VGHLPDNTAN IWTTIYETTS VVPANATQAL LIINKISAL- STADIVVDDI 179
67 ISIGMSIILP IGHLPDNLNN NWSTIYEISS VVPAMATHAM VIIHKIPSP- STSDIVVDDI 151
68 VGIGLNLTIP VGHLPDNTAD IWTTIYETTS VVPATAIQAL LIIEKVPGL- TTADVVVDDI 151
69 VGIGLNLTIP VGHLPDNTAN IWTTIYETTS VVPANATQAL LIINKISAL- STADIVVDDI 179
70 ISIGMSIILP IGHLPDNLNN NWSTIYEISS VVPAMATHAM VIIHKIPSP- STSDIVVDDI 151
```

FIG. 1 (continued)

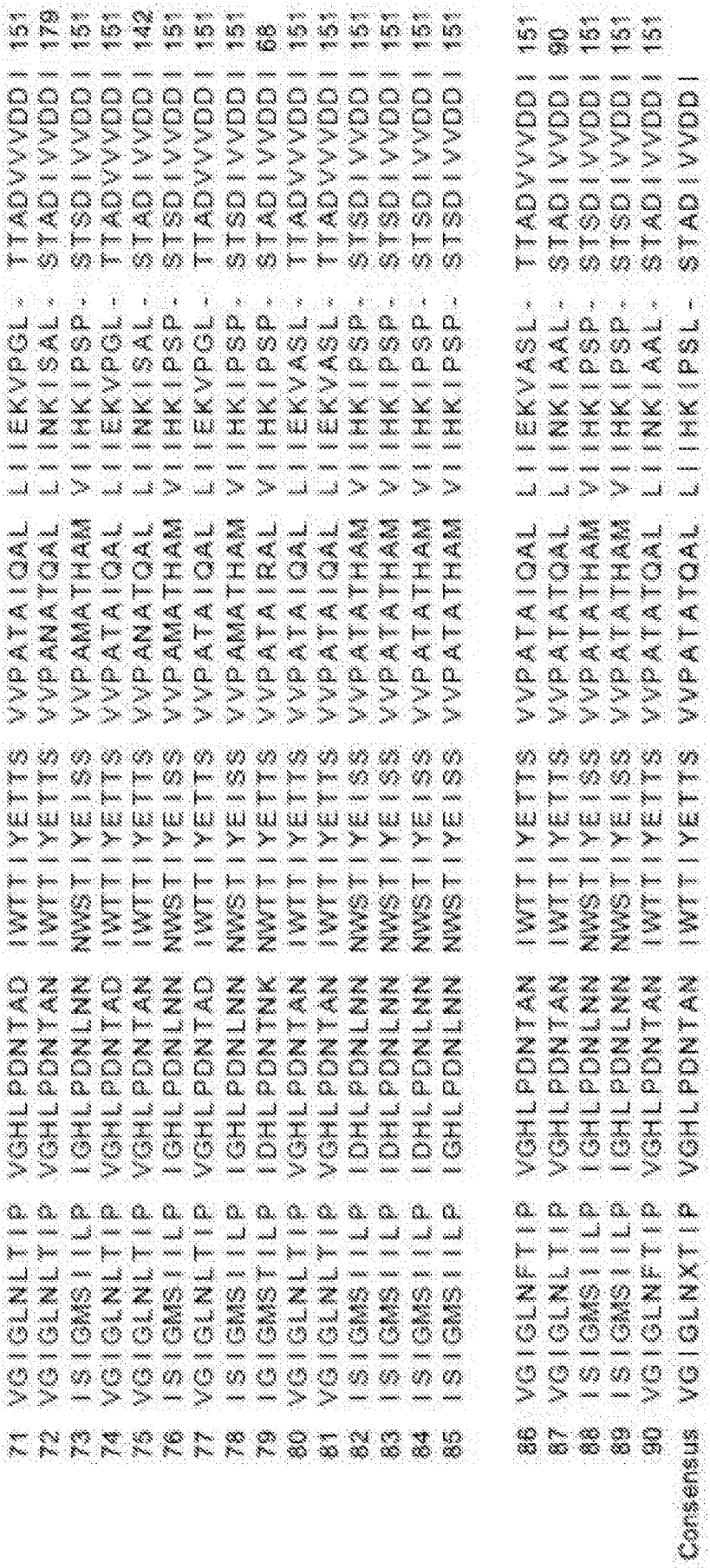


**FIG. 1 (continued)**

| | | |
|---|---|---|
| 1 | ELLQTSG- - | 186 |
| 2 | VLVQTGA- - | 164 |
| 3 | ELLQTSG- - | 158 |
| 4 | VLVQTGA- - | 158 |
| 5 | GILQTSG- - | 186 |
| 6 | GILQTSG- - | 186 |
| 7 | VLVQTGA- - | 158 |
| 8 | ELLQTSG- - | 158 |
| 9 | ELLQTSG- - | 158 |
| 10 | VLVQTGA- - | 158 |
| 11 | GILQTSG- - | 186 |
| 12 | GILQTSG- - | 186 |
| 13 | VLVQTGA- - | 158 |
| 14 | GILQTSG- - | 186 |
| 15 | ELLQTSG- - | 158 |
| 16 | VLVQTGA- - | 158 |
| 17 | ELLQTSG- - | 158 |
| 18 | GILQTSG- - | 186 |
| 19 | VLVQTGA- - | 158 |
| 20 | VLVQTGA- - | 158 |
| 21 | ELLQTSG- - | 158 |
| 22 | GILQTSG- - | 186 |
| 23 | ELLQTSG- - | 158 |
| 24 | GILQTSG- - | 186 |
| 25 | VLVQTGA- - | 158 |
| 26 | GILQTSG- - | 186 |
| 27 | ELLQTSG- - | 158 |
| 28 | ELLQTSG- - | 158 |
| 29 | VLVQTGA- - | 158 |
| 30 | VLVQTGA- - | 158 |
| 31 | ELLQTSG- - | 158 |
| 32 | GILQTSG- - | 154 |
| 33 | VLVQTGA- - | 158 |
| 34 | QLLQTSG- - | 158 |
| 35 | VLVQTGA- - | 109 |
| 36 | ELLQVSG- - | 158 |
| 37 | VLVQTGA- - | 164 |
| 38 | VLVQTGA- - | 158 |
| 39 | ELLQTSG- - | 158 |
| 40 | ALLQVSG- - | 158 |
| 41 | GLLQTSG- - | 95 |
| 42 | ELLQVSG- - | 158 |
| 43 | ELLQTSG- - | 142 |
| 44 | ELLQVSG- - | 158 |
| 45 | ELLQTSG- - | 142 |

**FIG. 1 (continued)**

```
46 ELLQVSG-- 158
47 ALLQTGAGV 161
48 ALLQTGAGV 161
49 ALLQTGAGV 161
50 ELLQTSG-- 158
51 VLVQTGA-- 158
52 ALIQTGG-- 158
53 VLVQTGA-- 109
54 GILQTSG-- 158
55 QLLQTSG-- 158
56 VLVQTGA-- 109
57 VLVQTGA-- 158
58 QLLQTSG-- 158
59 QLLQTSG-- 158
60 VLVQTGA-- 158
61 QLLQTSG-- 158
62 GILQTSG-- 186
63 ELLQTSG-- 158
64 VLVQTGA-- 158
65 ELLQTSG-- 158
66 GILQTSG-- 186
67 VLVQTGA-- 158
68 ELLQTSG-- 158
69 GILQTSG-- 186
70 VLVQTGA-- 158
71 ELLQTSG-- 158
72 GILQTSG-- 186
73 VLVQTGA-- 158
74 ELLQTSG-- 158
75 GILQTSG-- 149
76 VLVQTGA-- 158
77 ELLQTSG-- 158
78 VFVQTGA-- 158
79 VLLQTGL-- 75
80 ELLQTSG-- 158
81 ELLQTSG-- 158
82 VLVQTGA-- 158
83 VLVQTGA-- 158
84 VLVQTGA-- 158
85 VLVQTGA-- 158
86 ELLQTSG-- 158
87 GILQTSE-- 97
88 VLVQTGA-- 158
89 VLVQTGA-- 158
90 GILQTSE-- 158
Consensus VLLQTSG--
```

FIG. 2

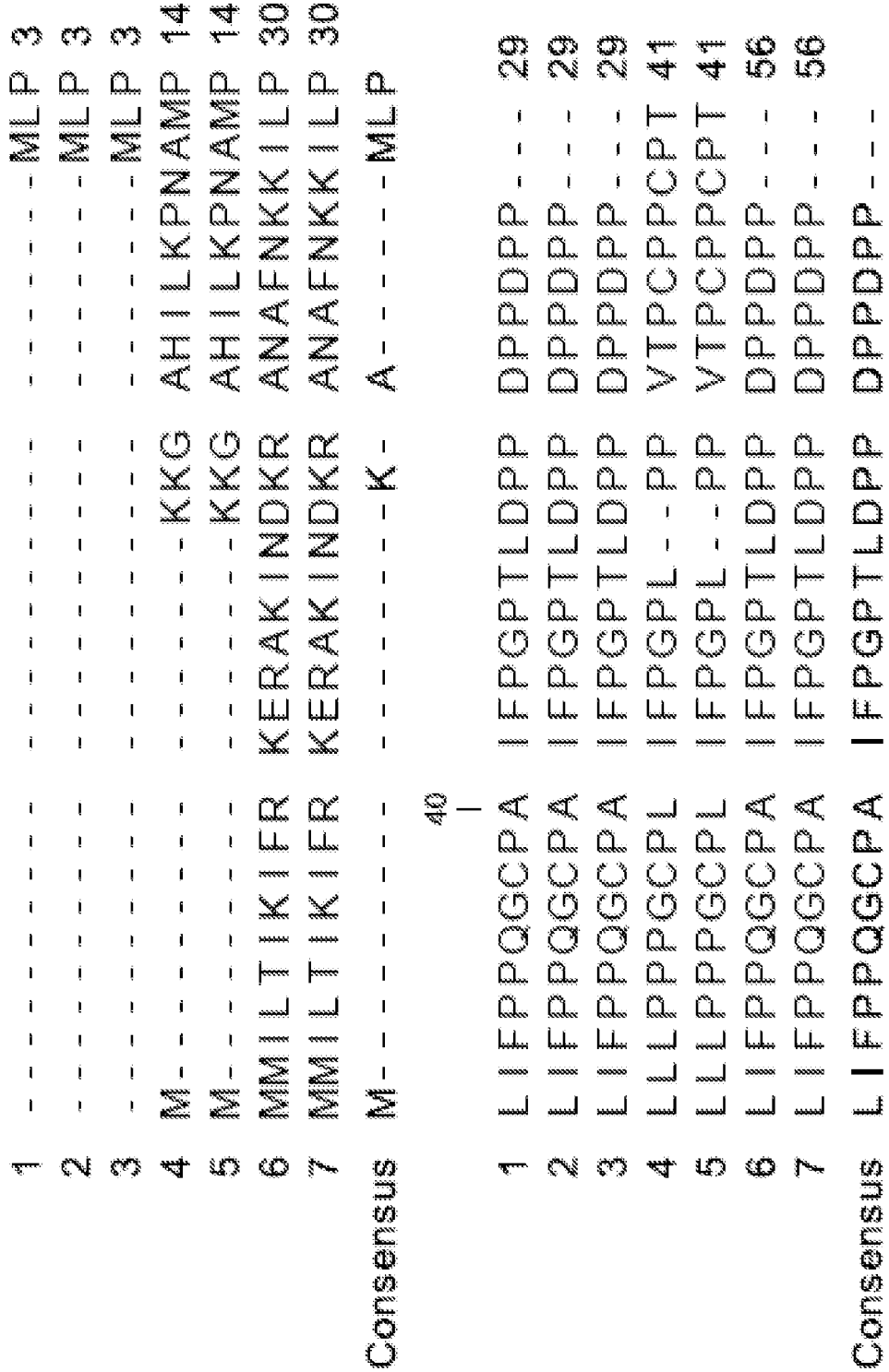

20
40
1 ----------MLP 3
2 ----------MLP 3
3 ----------MLP 3
4 M----------KKGAHILKPNAMP 14
5 M----------KKGAHILKPNAMP 14
6 MMILTIKIFRKERAKINDKRANAFNKKILP 30
7 MMILTIKIFRKERAKINDKRANAFNKKILP 30
Consensus M----------K-A----------MLP
1 LIFPPQGCPALIFPGPTLDPPDPPDPP---29
2 LIFPPQGCPALIFPGPTLDPPDPPDPP---29
3 LIFPPQGCPALIFPGPTLDPPDPPDPP---29
4 LLLPPPGCPLIFPGPL--PPVTPPCPPCPT 41
5 LLLPPPGCPLIFPGPL--PPVTPPCPPCPT 41
6 LIFPPQGCPALIFPGPTLDPPDPPDPP---56
7 LIFPPQGCPALIFPGPTLDPPDPPDPP---56
Consensus LIFPPQGCPALIFPGPTLDPPDPPDPP---

FIG. 3

```
                                    20
                                    |
 1  ---MKELNDI  KRIWDEIKHT  DLDEFTKKNP 27
 2  ---MKELHDI  KRIWDEVANT  DLEEFTRKNP 27
 3  -----ELHDI  RRIWDEIKHT  DLDEFAKKNP 25
 4  ---MKELHDI  KRIWDEVVNT  DLEEFTRKNP 27
 5  ---MKELNEI  KRIWDEIKHT  DLDEFTKKNP 27
 6  ---MKELHDI  KRIWDEVVNT  DLEEFTRKNP 27
 7  ---MKELHDI  KRIWDEVVNT  DLEEFTRKNP 27
 8  ---MKELHDI  KRIWDEVVNT  DLEEFTRKNP 27
 9  ---MKELHDI  KRIWDEIKHT  DLDEFAKKNP 27
10  ----------  ----------  ----------- -
11  ---MKELHDI  KRIWDEVANT  DLEEFTRKNP 27
12  ---MKELHDI  KRIWDEVANT  DLEEFTRKNP 27
13  ---MKELHDI  KRIWDEVANT  DLEEFTRKNP 27
14  ----------  ----------  ----------- -
15  ---MKELHDI  KRIWDEVANT  DLEEFTRKNP 27
16  ---MKELHDI  KRIWDEVANT  DLEEFTRKNP 27
17  ----------  ----DEIKHT  DLDEFTKKNP 16
18  MWIVKELNDI  KRIWDEVANT  DLEEFTRKNP 30
Consensus  ---MKELHDI  KRIWDEVANT  DLEEFTRKNP

                        40
                        |
 1  MLMKRSCYIS  SSSSTFCCTF  IR 49
 2  IYMKSSNSIS  SSSSTFCWTF  IR 49
 3  IHIKRSCHLS  STSSTFCCTF  IR 47
 4  IYMKSPYGMS  SSSSTFCWTF  IR 49
 5  MHMKRSCNIP  SSSSTFCCTF  IR 49
 6  IYMKSPYGMS  SSSSTFCWTF  IR 49
 7  IYMKSPYGMS  SSSSTFCWTF  IR 49
 8  IYMKSPYGMS  SSSSTFCWTF  IR 49
 9  IHIKRSCHLS  STSSTFCCTF  IR 49
10  --MKRSCYIS  SSSSTFCCTF  IR 20
11  IYMKSSNGIS  SSSFTFCWTF  IR 49
12  IYMKSSNSIS  SSSSTFCWTF  IR 49
13  IYMKSSNSIS  SSSSTFCWTF  IR 49
14  --TTCANGFS  CSSVSICCTF  IC 20
15  IYMKSSNGIS  SSSFTFCWTF  IR 49
16  IYMKSSNSIS  SSSSTFCWTF  IR 49
17  MLMKRSCYIS  SSSSTFCCTF  IR 38
18  IYMKSSNGIS  SSSFTFCWTF  IR 52
Consensus  IYMKSSNGIS  SSSSTFCWTF  IR
```

FIG. 4

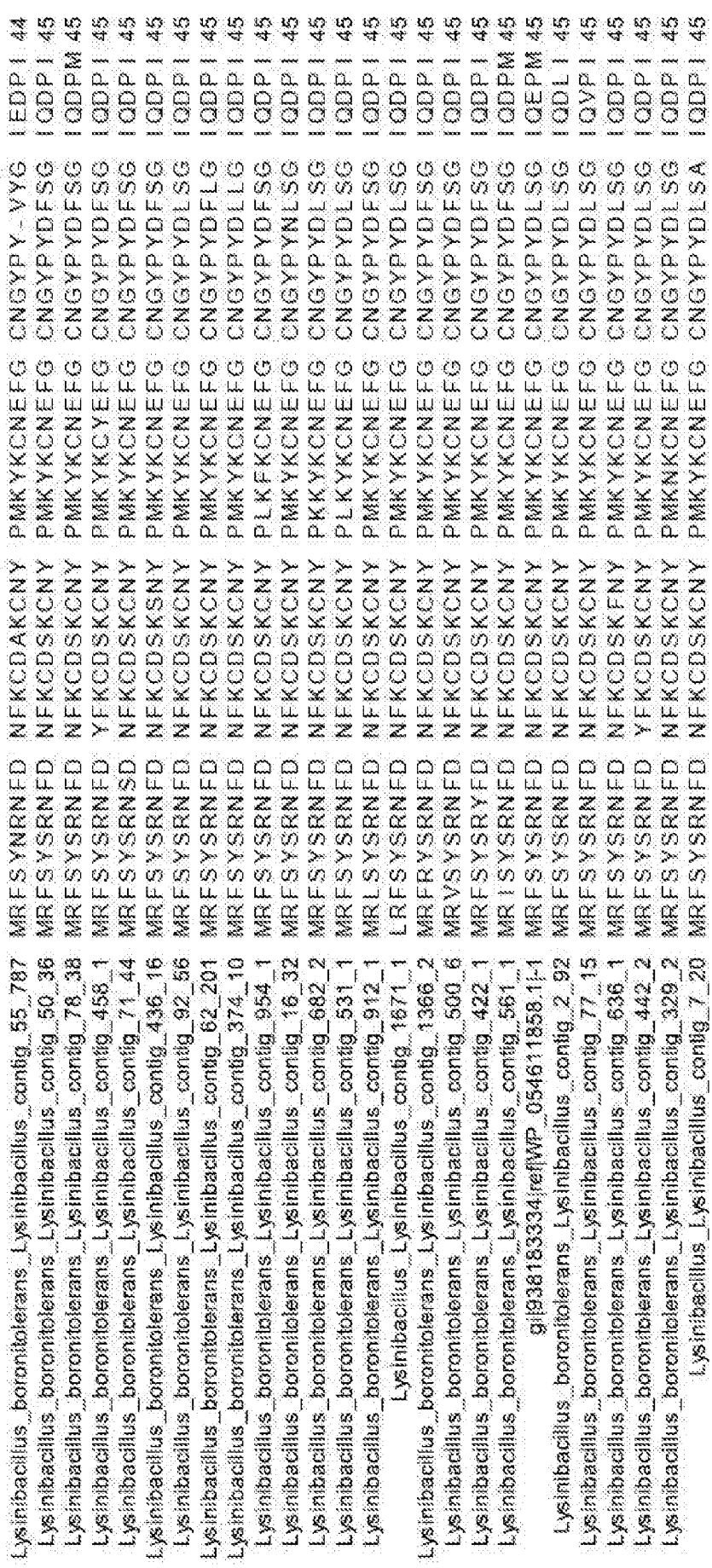

20
40
Lysinibacillus_boronitolerans_Lysinibacillus_contig_55_787 MRFSYNRNFD NFKCDAKCNY PMKYKCNEFG CNGYPY-VYG IEDPI 44
Lysinibacillus_boronitolerans_Lysinibacillus_contig_50_36 MRFSYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYDFSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_78_38 MRFSYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYDFSG IQDPM 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_458_1 MRFSYSRNFD YFKCDSKCNY PMKYKCYEFG CNGYPYDFSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_71_44 MRFSYSRNSD NFKCDSKCNY PMKYKCNEFG CNGYPYDFSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_436_16 MRFSYSRNFD NFKCDSKSNY PMKYKCNEFG CNGYPYDFSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_92_56 MRFSYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYDLSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_62_201 MRFSYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYDFLG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_374_10 MRFSYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYDLLG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_954_1 MRFSYSRNFD NFKCDSKCNY PLKFKCNEFG CNGYPYDFSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_16_32 MRFSYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYNLSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_682_2 MRFSYSRNFD NFKCDSKCNY PKKYKCNEFG CNGYPYDLSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_531_1 MRFSYSRNFD NFKCDSKCNY PLKYKCNEFG CNGYPYDLSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_912_1 MRLSYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYDFSG IQDPI 45
Lysinibacillus_Lysinibacillus_contig_1671_1 LRFSYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYDLSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_1366_2 MRFRYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYDFSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_500_6 MRVSYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYDFSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_422_1 MRFSYSRYFD NFKCDSKCNY PMKYKCNEFG CNGYPYDFSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_561_1 MRISYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYDFSG IQDPM 45
gi|938183334|ref|WP_054611858.1|-1 MRFSYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYDLSG IQEPM 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_2_92 MRFSYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYDLSG IQDLI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_77_15 MRFSYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYDLSG IQVPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_636_1 MRFSYSRNFD NFKCDSKFNY PMKYKCNEFG CNGYPYDLSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_442_2 MRFSYSRNFD YFKCDSKCNY PMKYKCNEFG CNGYPYDLSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_329_2 MRFSYSRNFD NFKCDSKCNY PMKNKCNEFG CNGYPYDLSG IQDPI 45
Lysinibacillus_Lysinibacillus_contig_7_20 MRFSYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYDLSA IQDPI 45

FIG. 4 (continued)

```
Lysinibacillus_boronitolerans_Lysinibacillus_contig_256_2   MRFSYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYDLSG FQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_913_1   MRFSYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYDLSG FQDPT 45
          Lysinibacillus_Lysinibacillus_contig_30_11        MRFSYSRNFD NYKCDSKCNY PMKYKCNEFG CNGYPYDLSG IQDPI 45
          Lysinibacillus_Lysinibacillus_contig_1268_1       MRFSYCRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYDLSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_478_3   MRFSYSRNLD NFKCDSKCNY PMKYKCNEFG CNGYPYDLSG IQDLI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_453_2   MRFSYSRNFD NFKCDSKCNY PMKYKCNEFG CIGYPYNLSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_439_2   MRFSYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYAYNLSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_978_1   MRFSYSRNLD NFKCDSKCNY PMKYKCNEFG CNGYPYNLSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_1644_1  LRFSYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYNLSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_377_1   MRFSYIRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYNLSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_530_2   MRVSDSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYDFSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_192_4   MRFSYSRNFD NFKCYSKCNY PMKYKCNEFG CNGYPYDLSG FQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_384_4   MRFSYSRNFD NFKCDSKCNY PMKYKCNEFW CNGYPYDLSG FQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_624_4   MRFSNSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPYDLSG FQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_1359_1  MRFSYSRNLD NFKCDSKCNY PMKYKCNEFG CNGYPYDLSG FQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_946_2   - - FSYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYAYNLSG IQDPI 43
Lysinibacillus_boronitolerans_Lysinibacillus_contig_775_1   MRFSYSRNFD NFKCDSKCNY PMKYKCNEYG CNGYAYNLSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_130_8   MRLSYSRNLD NFKCDSKCNY PMKYKCNEFG CNGYPYNLSG IQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_302_3   MRFSYSRNFD NFKCDSKCNY PMKYKCNEFG CNGYPFDFSG FQDPI 45
Lysinibacillus_boronitolerans_Lysinibacillus_contig_633_1   MRFSYSRNFD NFKSDTKCNY PMKYKCNEFG CNGYPYDLSG IQDPI 45
```

FIG. 5


20
1
40
1
Lysinibacillus_boronitolerans_Lysinibacillus_contig_83_1 MHFGKF-KER VCSKCNTFPC CCSPCPPQSC PIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_1374_1 MHFGKF-KER VCSKCNTFPC CCSPYPPQSC PIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_330_1 MHFGNF-IDR VCSKCHSFPC CCKTGPIPSC PIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_368_1 MHFGNF-IDR VCSKCHSFPC YCKTGPIPSC PIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_1438_2 MHFGNF-IDR VCSKCHSFPC CCKTGPIPSC PIWPVNPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_876_1 MHFGNF-IDR VCSKCHSFPC CCKAGPIPSC PIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_1177_1 MHFGNF-IDR VCSKCHSFPC CCKTGPIPNC PIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_247_6 MHYGNF-IDR VCSKCHSFPC CCKTGPIPSC PIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_1131_2 MHFGNF-IVR VCSKCHSFPC CCKTGPIQSC PIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_2225_1 MHFGII-IDR VCSKCHSFPC CCKTGPIPSC PIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_19_10 MHFGKF-IDR VCTKCHSYPC CCKTGPIPSC PIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_2372_1 MHFGKF-LDR VCNKCHSFPC CCKTGPIPGC PIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_6_1 MHFGKF-LDR VCSKCHSFPC CCKTGPIPGC PIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_968_1 MHFGKF-LDR VCSKCNSFPC CCKTGPSPSC PIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_850_1 MNFGKF-LDR VCSKCNSFPC CCKTGPSPSC PIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_215_9 MLFGKF-LDR VCSKCNSFPC CCKTGPSPSC PIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_37_16 MHFGKF-LDR VCSKCNSFPC CCKTGPSPSC PMWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_23_30 MHFGNY-LKR VCSKCNSFPC CCRTGPIPSC PVWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_1735_2 MHFGNY-LKR VCSKCNYFPC CCRTGPIPSC PVWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_90_14 MHFGNY-LKR VCSKCNSFPC CCRPGPIPSC PVWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_115_1 MHFGNY-LKQ VCSKCNSFPC CCRTGPIPSC PVWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_1000_2 MHFGNY-LKR VCSKCNSFPC CCRTGPIQSC PVWPVKPT-- -- 37
gi|738204586|ref|WP_036160504.1| MHFGNY-LKQ VCNKCNSFPC CCRTGPIPSC PVWPVKPT-- -- 37

FIG. 5 (continued)

```
Lysinibacillus_boronitolerans_Lysinibacillus_contig_168_4   MHFGNY-LKQ  VCNKCNSFPC  CCRTGPIPSC  PVWPVKPT--  --  37
  Lysinibacillus_boronitolerans_Lysinibacillus_contig_4_31  MHFGNY-LKQ  VCSKCNSFPC  CCRNGPIPSC  PVWPVKPT--  --  37
      Lysinibacillus_Lysinibacillus_contig_393_1            MHFGNY-LKQ  VCSKCNSFPC  CCRTGPIPSC  PIWPVKPT--  --  37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_446_1   LHFGNY-LKQ  VCSKCNSFPC  CCRTGPIPSC  PIWPVKPT--  --  37
      Lysinibacillus_Lysinibacillus_contig_252_4            MLFGNY-LKQ  VCSKCNSFPC  CCRTGPIPSC  PIWPVKPT--  --  37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_646_2   MHFGNY-LKQ  VSSKCNSFPC  CCRNGPIPSC  PVWPVKPT--  --  37
  Lysinibacillus_boronitolerans_Lysinibacillus_contig_7_37  MHFGRF-NER  VCSKCNTFPC  CCNPCAAQSC  PIWPVKPT--  --  37
    Lysinibacillus_boronitolerans_Lysinibacillus_contig_3_1 MHFGRF-KER  VCSKCNTFPC  CCNPCAAQSC  PIWPVKPT--  --  37
      Lysinibacillus_Lysinibacillus_contig_1352_2           MHFGRF-NER  VCSKCNSFPC  CCNPCAAQSC  PIWPVKPT--  --  37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_363_1   MHFGKF-NER  VCSKCNTFPC  CCNPCAAQSC  PIWPVKPS--  --  37
  Lysinibacillus_Lysinibacillus_contig_483_1                MHFGRF-NER  VCSKCNTFPC  CC--CAAQSC  PIWPVKPT--  --  35
      Lysinibacillus_Lysinibacillus_contig_68_6             MHFGKF-KDS  VCSKCNTFPC  CCNPCAAQSC  PIWPVKPT--  --  37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_30_62   MHFGRF-NER  VCSKCNTFPC  CC--CAAQSC  PIWPVKP---  --  34
Lysinibacillus_boronitolerans_Lysinibacillus_contig_25_15   MHFGKF-KER  VCSKCNSFPC  CCSPCPPQSC  PIWPVKPT--  --  37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_23_65   MHFGKF-KDR  VCSKCNTFPC  CCSPCPPQSC  PIWPVKPT--  --  37
      Lysinibacillus_Lysinibacillus_contig_1419_1           MHFGRF-NER  VCSKCNTFPC  CCSPCDVQSC  PIWPVKPT--  --  37
          Lysinibacillus_contig_2646_1                      MQFGRF-NER  VCSKCTTFPC  CCSPCDVQSC  PIWPVKPT--  --  37
```

FIG. 5 (continued)

```
Lysinibacillus_boronitolerans_Lysinibacillus_contig_256_5      MHFGKF-NDR ICSKCNTFPC CCNPC-APSC PVWPVKP--- -- 35
                Lysinibacillus_Lysinibacillus_contig_43_5      MHFGNF-IDR VCSKCNTFPC CCRGGPVPGC PIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_13_15      MHFGNF-IDR VCSKCKTFPC CCRGGPVPGC PIWPVKPT-- -- 37
          Lysinibacillus_Lysinibacillus_contig_172_1           MHFGNF-IDR VCSKCNTFPC CCRGGPVPGC PIWPVKPP-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_133_74     MHFGNF-IDR VCSKCNTFPC CCRGGPVPGC HIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_47_11      MHFGNF-IDR VCSKCKTFPC CCRGGPVPCC PIWPVKPT-- -- 37
          Lysinibacillus_Lysinibacillus_contig_1087_2          MHFGNF-IDR VCSKCKTIPC CCRGGPVPGC PIWPVKPT-- -- 37
                Lysinibacillus_Lysinibacillus_contig_251_1     MHFGNF-IDR VCSKCNTFPC CCKGGPVPGC HIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_208_5      MHFGNF-IDR VCSKCKTFPC CCGSGPVPGC PIWPVKPT-- -- 37
          Lysinibacillus_Lysinibacillus_contig_130_6           MHFGNF-IDR VCSKCKTSPC CCGSGPVPGC PIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_362_67     MHFGNF-IDR VCTKCKIFPR CCRGGPVPGC PIWPVKPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_87_15      MHFGKF-TDR VCSKCNTFPC CCNTCPAPNC PIWPVKP--- -- 36
  Lysinibacillus_boronitolerans_Lysinibacillus_contig_90_8     MNFGNF-NNR ICSKCNTFPC CCIPC-APSC PVWPVKPG-- -- 36
Lysinibacillus_boronitolerans_Lysinibacillus_contig_63_78      MYFGNF-LDR ICSKCNTFPC CCLSGPILRS PIWPVRPT-- -- 37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_21_79      MHFGNF-LDR VCNKCNTFPC CCLSGPIHRS PIWPVPPAKA TR 41
Lysinibacillus_boronitolerans_Lysinibacillus_contig_420_1      MQFGKY-NDR ICRKCNTFPC CCNPS-APSC PGWPVKP--- -- 35
          Lysinibacillus_Lysinibacillus_contig_47_10           MKFQDFNINK ICNNCHSYPC CCHNGPVQRC PVWPVKPT-- -- 38
                Lysinibacillus_Lysinibacillus_contig_45_6      MKFQDFNINK ICNNCHSYPC CCHNGPVHRC PVWPVKPT-- -- 38
          Lysinibacillus_Lysinibacillus_contig_69_1            MKFQDFNINK ICNNCNSYPC CCHNGPVQRC PVWPVKPT-- -- 38
          Lysinibacillus_Lysinibacillus_contig_26_16           MKFQDFNINK ICNNCHSYPC CCHNGPVLRC PVWPVKPT-- -- 38
Lysinibacillus_boronitolerans_Lysinibacillus_contig_21_1       MKFLDFNINK ICNNCHSYPC CCHNGPVHRC PVWPVKPT-- -- 38
```

FIG. 5 (continued)

```
Lysinibacillus_boronitolerans_Lysinibacillus_contig_47_11  MHFGNF-IDR  VCSKCKTFPC  CCRGGPVPCC  PIWPVKPT--  --  37
          Lysinibacillus_Lysinibacillus_contig_1087_2      MHFGNF-IDR  VCSKCKTIPC  CCRGGPVPGC  PIWPVKPT--  --  37
               Lysinibacillus_Lysinibacillus_contig_251_1  MHFGNF-IDR  VCSKCNTFPC  CCKGGPVPGC  HIWPVKPT--  --  37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_208_5  MHFGNF-IDR  VCSKCKTFPC  CCGSGPVPGC  PIWPVKPT--  --  37
          Lysinibacillus_Lysinibacillus_contig_130_8       MHFGNF-IDR  VCSKCKTSPC  CCGSGPVPGC  PIWPVKPT--  --  37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_362_67 MHFGNF-IDR  VCTKCKIFPR  CCRGGPVPGC  PIWPVKPT--  --  37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_87_15  MHFGKF-TDR  VCSKCNTFPC  CCNTCPAPNC  PIWPVKP---  --  36
     Lysinibacillus_boronitolerans_Lysinibacillus_contig_60_8  MNFGNF-MNR  ICSKCNTFPC  CCIPC-APSC  PVWPVKPG--  --  36
Lysinibacillus_boronitolerans_Lysinibacillus_contig_63_78  MYFGNF-LDR  ICSKCNTFPC  CCLSGPILRS  PIWPVRPT--  --  37
Lysinibacillus_boronitolerans_Lysinibacillus_contig_21_79  MHFGNF-LDR  VCNKCNTFPC  CCLSGPIHRS  PIWPVPPAKA  TR  41
Lysinibacillus_boronitolerans_Lysinibacillus_contig_420_1  MQFGKY-NDR  ICRKCNTFPC  CCNPS-APSC  PGWPVKP---  --  35
          Lysinibacillus_Lysinibacillus_contig_47_10       MKFQDFNINK  ICNNCHSYPC  CCHNGPVQRC  PVWPVKPT--  --  38
               Lysinibacillus_Lysinibacillus_contig_45_6   MKFQDFNINK  ICNNCHSYPC  CCHNGPVHRC  PVWPVKPT--  --  38
               Lysinibacillus_Lysinibacillus_contig_69_1   MKFQDFNINK  ICNNCNSYPC  CCHNGPVQRC  PVWPVKPT--  --  38
          Lysinibacillus_Lysinibacillus_contig_28_16       MKFQDFNINK  ICNNCHSYPC  CCHNGPVLRC  PVWPVKPT--  --  38
Lysinibacillus_boronitolerans_Lysinibacillus_contig_21_1   MKFLDFNINK  ICNNCHSYPC  CCHNGPVHRC  PVWPVKPT--  --  38
```

**FIG. 6**

```
                                               20                           40
                                               |                            |
Viridibacillus_arenosi  MDSNKTRCPI CNNYQCSCNA KKRRPTRCIR YLDYIDQCEQ CEPISIIDHC HNR 53
Viridibacillus_arenosi  MDSNKTRCPI CNNYQCSCNA KKRRPTRCIR YLDYIDQCEQ CEPISIIDHC HNR 53
    Viridibacillus_arvi MDSNKTRCTV CNKYQCSCNH KKRSPKTVIR DLDYIDPCE- --PLYIIDHC HNR 50
  Viridibacillus_arvi-1 MDSNKTRCTV CNKYQCSCNH KKRSPKTVIR DLDYIDPCE- --PLYIIDHC HNR 50
    Viridibacillus_arvi MDSNKTRCTV CNKYQCSCNH KKRSPKTVIR DLDYIDPCE- --PLYIIDHC HNR 50
    Viridibacillus_arvi MDSNKTRCTV CNKYQCSCNH KKRSPKTVIR DLDYIDPCE- --PLYIIDHC HNR 50
    Viridibacillus_arvi MDSNKTRCTV CNKYQCSCNH KKRSPKTVIR DLDYIDPCE- --PLYIIDHC HNR 50
    Viridibacillus_arvi MDSNKTRCTV CNKYQCSCNH KKRSPKTVIR DLDYIDPCE- --PLYIIDHC HNR 50
    Viridibacillus_arvi MDSNKTRCTV CNKYQCSCNH KKRSPKTVIR DLDYIDPCE- --PLYIIDHC HNR 50
    Viridibacillus_arvi MDSNKTRCTV CNKYQCSCNH KKRSPKTVIR DLDYIDPCE- --PLYIIDHC HNR 50
    Viridibacillus_arvi MDSNKTRCAV CNKYQCSCNT KKRSPKTVIR DLDYIDPCE- --PLYIIDHC HNR 50
    Viridibacillus_arvi MDSNKTRCAV CNKYQCSCNT KKRSPKTVIR DLDYIDPCE- --PLYIIDHC HNR 50
    Viridibacillus_arvi MDSNKTRCAV CNKYQCSCNT KKRSPKTVIR DLDYIDPCE- --PLYIIDHC HNR 50
    Viridibacillus_arvi MDSNKTRCAV CNKYQCSCNT KKRSPKTVIR DLDYIDPCE- --PLYIIDHC HNR 50
    Viridibacillus_arvi MDSNKTRCAV CNKYQCSCNS KKRSPKTVIR DLDYIDPCE- --PLYIIDHC HNR 50
    Viridibacillus_arvi MDSNKTRCAV CNKYQCSCNS KKRSPKTVIR DLDYIDPCE- --PLYIIDHC HNR 50
    Viridibacillus_arvi MESNKTRCIV CNKYQCSCNS KKRSPKTVIR DLDYIDPCE- --PLYIIDHC HNR 50
    Viridibacillus_arvi MYSNKKRCAV CNKYQCSCNS KKRSPKTVIR DLDYIDPCE- --PLYIIDHC HNR 50
    Viridibacillus_arvi MYSNKKRCAV CNKYQCSCNS KKRSPKTVIR DLDYIDPCE- --PLYIIDHC HNR 50
    Viridibacillus_arvi MDSNKKRCAV CNKYQCSCNS KKRSPKTVIR DLDYIDPCE- --PLYIIDHC HNR 50
    Viridibacillus_arvi MDSNKTRCAV CNKYQCSCNS KKRSPKTVIR DLDYIDPCE- --PLYIINHC HNR 50
    Viridibacillus_arvi MDSNKTRCTV CNKYQCSCNP KKRSPKTVIR DLDYINPCE- --PLYIIDHC HNR 50
    Viridibacillus_arvi MDSNKTRCTV CNKYQCSCNP KKRSPKTVIR DLDYINPCE- --PLYIIDHC HNR 50
              Consensus MDSNKTRCXV CNKYQCSCNH KKRSPKTVIR DLDYIDPCE- --PLYIIDHC HNR
```

FIG. 7A

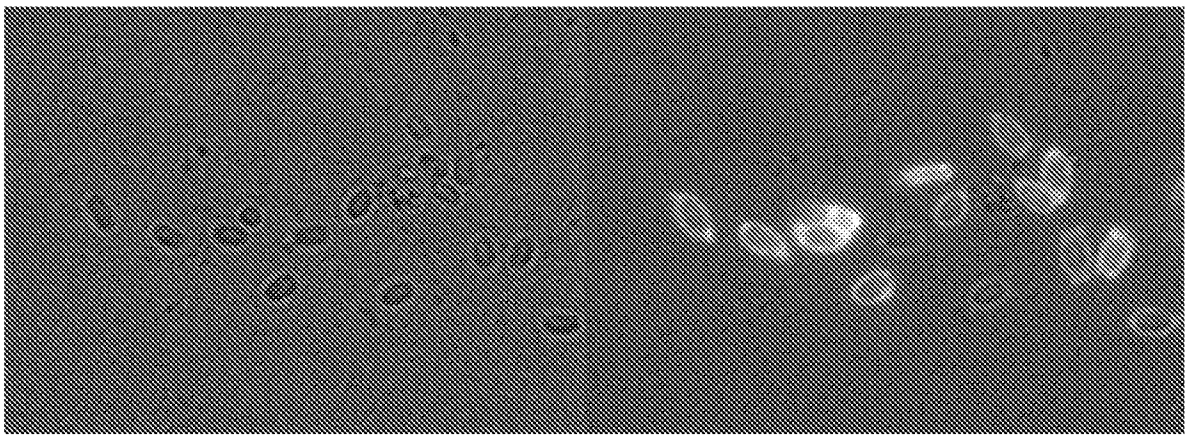


FIG. 7B

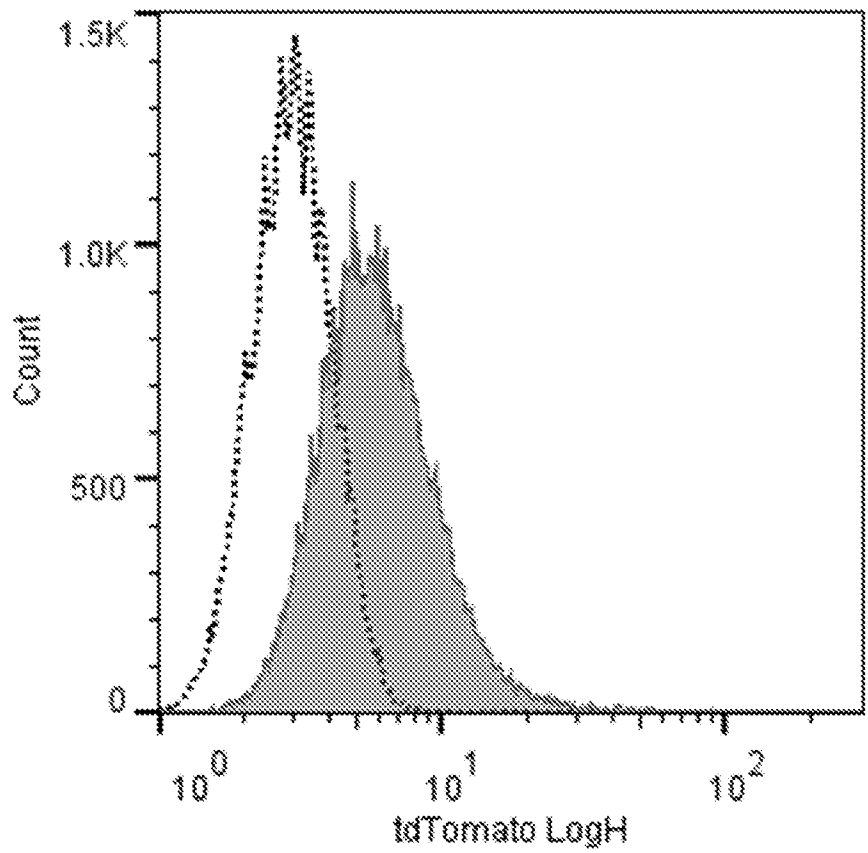


FIG. 8A

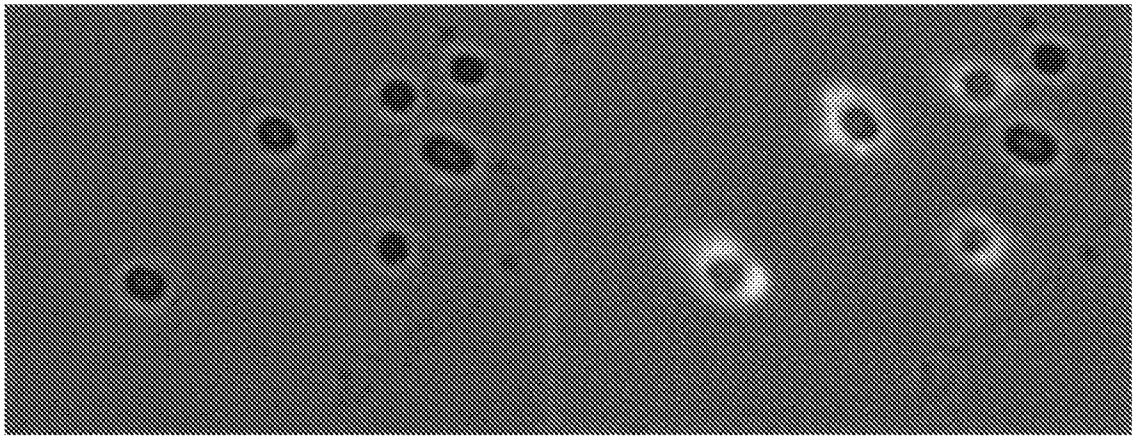


FIG. 8B

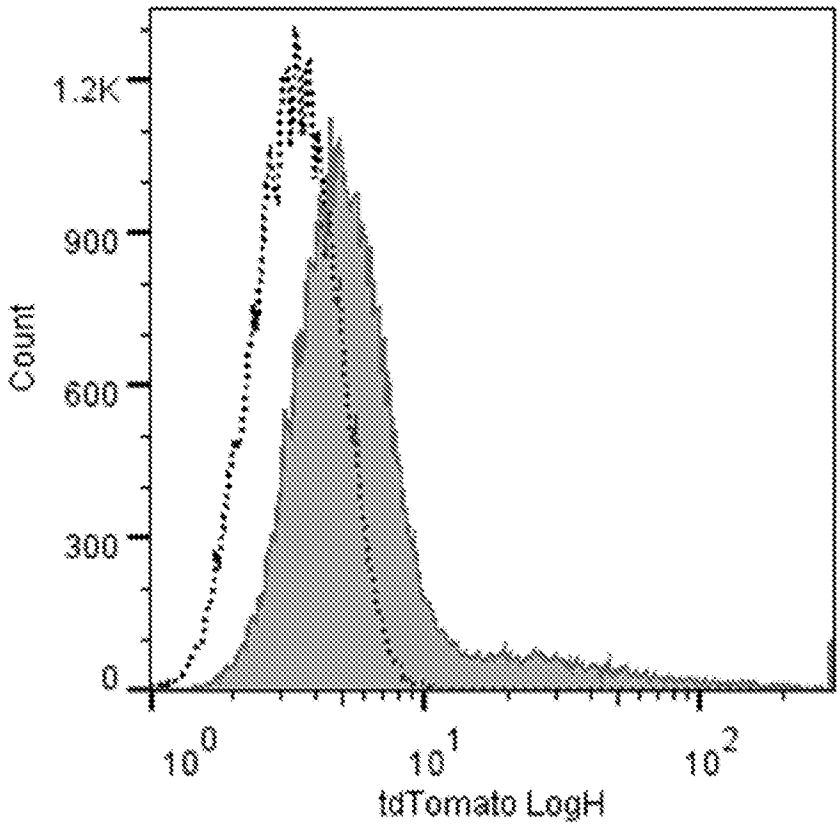


FIG. 9A

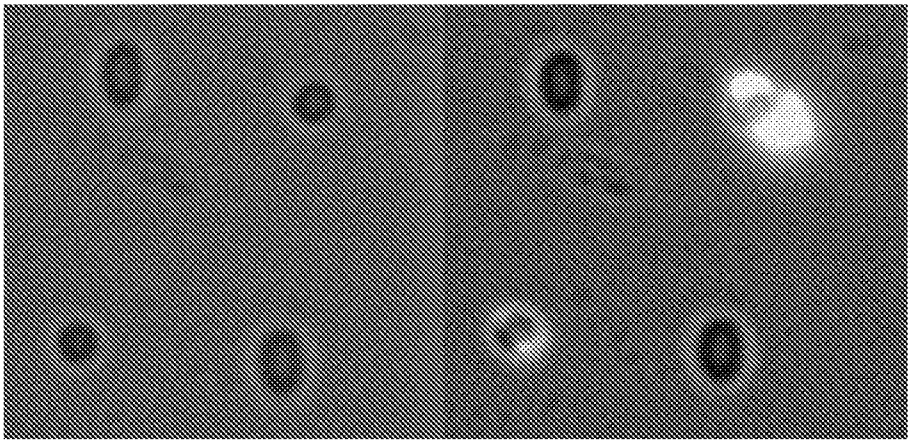
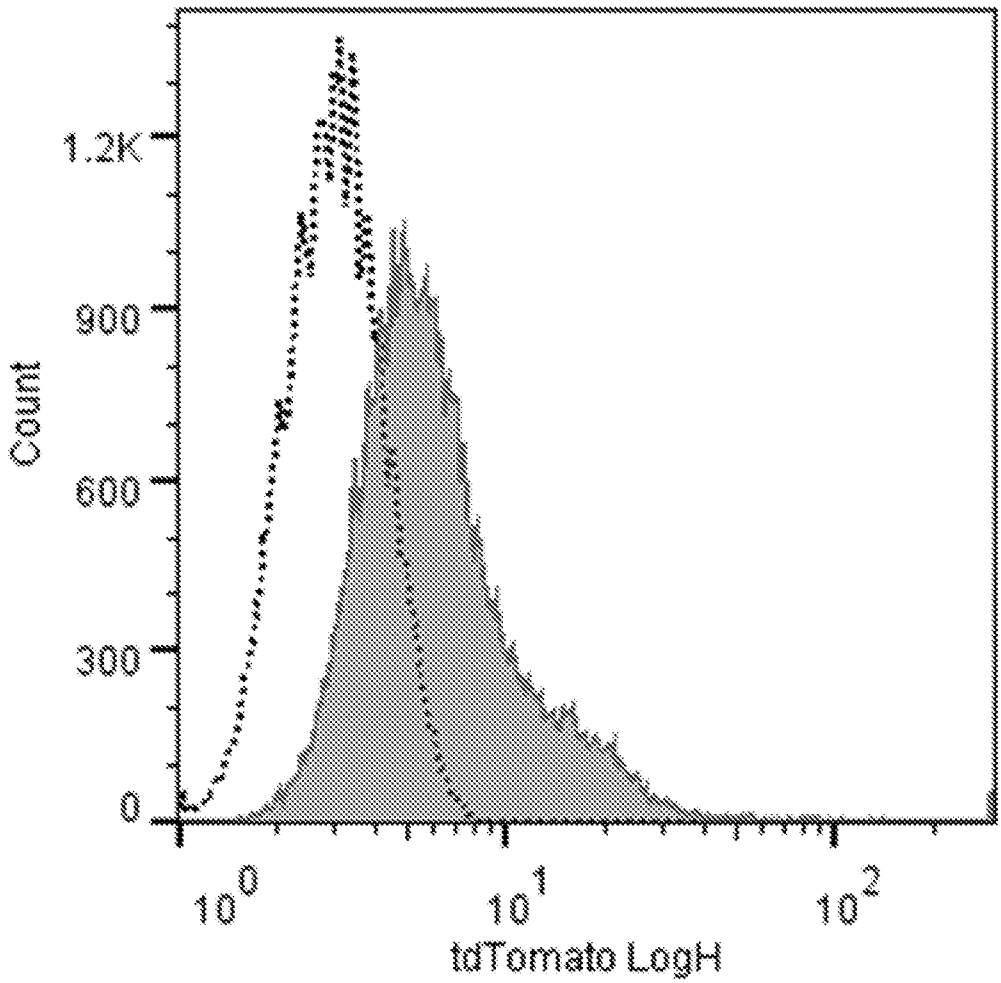


FIG. 9B



SEQUENCE LISTING

<110> Bayer CropScience LP

<120> ENDOSPORE DISPLAY PLATFORMS, PRODUCTS AND METHODS

<130> BCS189008 WO

<150> 62/768,077
<151> 2018-11-15

<150> 62/768,063
<151> 2018-11-15

<150> 62/767,997
<151> 2018-11-15

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<220>
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<222> (99)..(99)
<223> Xaa can be any naturally occurring amino acid

<400> 1

Met Pro Phe Ser Asn Lys Ile Val Asn Gly Asp Phe Glu Thr Gly Thr
1 5 10 15

Leu Ile Pro Trp Ser Ser Xaa Asn Val Ala Ile Thr Asn Leu Gln Ser
20 25 30

His Thr Gly Phe Phe Ser Ala Leu Leu Phe Gly Asn Thr Ala Asn Ser
35 40 45

```
Leu Leu Phe Gln Ala Val Pro Val Thr Pro Gly Asp Ser Phe Glu Phe
    50                  55                  60

Phe Leu Ser Ile Ala Lys Leu Gly Asn Leu Val Ser Pro Gln Val Asn
65                  70                  75                  80

Ile Ala Leu Leu Tyr Leu Asp Val Ala Ala Thr Pro Val Gly Ile Gly
                85                  90                  95

Leu Asn Xaa Thr Ile Pro Val Gly His Leu Pro Asp Asn Thr Ala Asn
            100                 105                 110

Ile Trp Thr Thr Ile Tyr Glu Thr Thr Ser Val Val Pro Ala Thr Ala
        115                 120                 125

Thr Gln Ala Leu Leu Ile Ile His Lys Ile Pro Ser Leu Ser Thr Ala
    130                 135                 140

Asp Ile Val Val Asp Asp Ile Val Leu Leu Gln Thr Ser Gly
145                 150                 155
```

<210>  2
<211>  186
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<220>
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<220>
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<222>  (112)..(112)
<223>  Xaa can be any naturally occurring amino acid

<400>  2

```
Met Val Arg Thr Leu Ser Lys Ile Glu Asp Ser Thr Tyr Thr Thr Leu
1               5                   10                  15

Ala Pro Ile Asn Pro Ile Met Glu Val Val Ile Tyr Leu Pro Phe Ser
            20                  25                  30

Asn Lys Val Val Asn Gly Asp Phe Glu Thr Gly Thr Leu Phe Pro Trp
        35                  40                  45
```

```
Ser Phe Thr Asn Val Ser Ile Thr Asn Leu Gln Ser His Thr Gly Phe
    50                  55                  60

Phe Ser Ala Leu Leu Phe Gly Asp Thr Ala Asn Ser Leu Leu Phe Gln
65                  70                  75                  80

Ala Ile Pro Val Thr Pro Gly Asp Ser Phe Glu Leu Phe Leu Ser Ile
                85                  90                  95

Ala Lys Leu Gly Asn Leu Val Ser Pro Gln Val Asn Ile Ala Leu Xaa
            100                 105                 110

Tyr Leu Asp Val Ala Thr Ile Pro Val Gly Ile Gly Leu Asn Leu Thr
        115                 120                 125

Ile Pro Val Gly His Leu Pro Asp Asn Thr Ala Asn Ile Trp Thr Thr
    130                 135                 140

Ile Tyr Glu Thr Thr Ser Val Val Pro Ala Thr Ala Thr Gln Ala Leu
145                 150                 155                 160

Leu Ile Ile Asn Lys Ile Pro Ala Leu Ser Thr Ala Asp Ile Val Val
                165                 170                 175

Asp Asp Ile Gly Ile Leu Gln Thr Ser Gly
            180                 185


<210>  3
<211>  29
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  3

Met Leu Pro Leu Ile Phe Pro Pro Gln Gly Cys Pro Ala Ile Phe Pro
1               5                   10                  15

Gly Pro Thr Leu Asp Pro Pro Asp Pro Pro Asp Pro Pro
            20                  25
```

<210> 4
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 4

Met Met Ile Leu Thr Ile Lys Ile Phe Arg Lys Glu Arg Ala Lys Ile
1 5 10 15

Asn Asp Lys Arg Ala Asn Ala Phe Asn Lys Lys Ile Leu Pro Leu Ile
20 25 30

Phe Pro Pro Gln Gly Cys Pro Ala Ile Phe Pro Gly Pro Thr Leu Asp
35 40 45

Pro Pro Asp Pro Pro Asp Pro Pro
50 55

<210> 5
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 5

Met Lys Glu Leu His Asp Ile Lys Arg Ile Trp Asp Glu Val Ala Asn
1 5 10 15

Thr Asp Leu Glu Glu Phe Thr Arg Lys Asn Pro Ile Tyr Met Lys Ser
20 25 30

Ser Asn Gly Ile Ser Ser Ser Ser Ser Thr Phe Cys Trp Thr Phe Ile
35 40 45

Arg

<210> 6
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 6

Met Lys Glu Leu His Asp Ile Lys Arg Ile Trp Asp Glu Val Ala Asn
1 5 10 15

Thr Asp Leu Glu Glu Phe Thr Arg Lys Asn Pro Ile Tyr Met Lys Ser
20 25 30

Ser Asn Gly Ile Ser Ser Ser Ser Ser Thr Phe Cys Trp Thr Phe Ile
35 40 45

Arg Gly Lys Thr
50

<210> 7
<211> 187
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<220>
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<222> (170)..(170)
<223> Xaa can be any naturally occurring amino acid

<400> 7

Met Val Leu Ala Leu Ser Lys Ile Gly Glu Ser Thr Tyr Asn Ala Ser
1 5 10 15

Val Pro Ile Asn Leu Ile Met Glu Val Val Ile Tyr Leu Pro Phe Ser
20 25 30

Asn Ile Val Glu Asn Gly Asn Phe Glu Ser Gly Thr Leu Phe Pro Trp
35 40 45

```
Ser Phe Thr Asn Ala Ala Ile Thr Asp Leu Gln Ser His Ser Gly Phe
    50                  55                  60

Phe Ser Ala Leu Leu Phe Gly Gly Thr Ala Asn Ser Leu Leu Phe Gln
65                  70                  75                  80

Thr Val Pro Val Thr Pro Gly Asp Ser Phe Glu Leu Phe Leu Ser Ile
                85                  90                  95

Ala Lys Ser Gly Asn Leu Ile Ser Pro Gln Val Asn Ile Val Leu Ile
            100                 105                 110

Tyr Leu Asp Ala Ala Asn Ile Pro Val Gly Ile Gly Leu Asn Leu Thr
        115                 120                 125

Ile Pro Val Gly His Leu Pro Asp Asn Thr Ala Asn Ile Trp Thr Thr
    130                 135                 140

Ile Tyr Glu Thr Thr Ala Val Val Pro Ala Thr Ala Ile Glu Ala Leu
145                 150                 155                 160

Leu Ile Ile Ser Lys Val Pro Ala Leu Xaa Ser Thr Ala Asp Val Ile
                165                 170                 175

Leu Asp Asp Ile Glu Leu Leu Gln Thr Ser Gly
            180                 185
```

<210>  8
<211>  164
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  8

```
Met Lys Ala Val Ile Tyr Leu Pro Phe Gly Asn Lys Ile Val Asn Gly
1               5                   10                  15

Asn Phe Glu Thr Gly Ser Leu Val Pro Trp Asn Phe Ser Asn Val Thr
            20                  25                  30
```

```
Ile Asn Asn Leu Gln Ser His Thr Gly Ser Phe Ser Ala Leu Phe Phe
        35                  40                  45

Gly Asn Thr Thr Asn Ser Val Leu Tyr Gln Thr Val Pro Val Thr Ser
    50                  55                  60

Gly Glu Ile Phe Glu Phe Phe Leu Ser Ile Gly Lys Ile Gly Asn Leu
65                  70                  75                  80

Pro Ser Pro Gln Val Asn Ile Ala Leu Ile Tyr Leu Asn Ala Ala Ser
                85                  90                  95

Thr Pro Glu Asn Ile Gly Ile Asn Ile Ile Leu Pro Val Gly Lys Leu
            100                 105                 110

Pro Asn Asn Leu Asn Asn Asn Trp Ser Thr Ile Tyr Glu Ile Ser Ser
        115                 120                 125

Val Val Pro Ala Ala Ala Thr Gln Ala Met Val Ile Ile His Lys Ile
    130                 135                 140

Pro Ala Pro Ser Thr Ala Asp Ile Val Val Asp Asp Ile Val Leu Val
145                 150                 155                 160

Gln Thr Gly Ala
```

<210> 9
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 9

```
Met Pro Phe Gly Asn Lys Ile Val Asn Gly Asn Phe Glu Thr Gly Ser
1               5                   10                  15

Leu Ile Pro Trp Ser Ser Ser Asn Val Ala Ile Ser Asn Leu Gln Ser
            20                  25                  30
```

```
His Thr Gly Ser Tyr Ser Ala Leu Leu Phe Gly Asn Ala Ala Asn Ser
        35                  40                  45


Phe Leu Phe Gln Ala Val Pro Val Thr Val Gly Asp Ser Phe Glu Phe
    50                  55                  60


Phe Leu Ser Ile Ala Lys Ile Gly Asn Leu Pro Ser Pro Gln Val Asp
65                  70                  75                  80


Ile Ala Leu Ile Tyr Leu Asn Ala Ala Ser Thr Pro Ile Ser Asn Gly
                85                  90                  95


Met Ser Ile Ile Leu Pro Thr Gly His Leu Pro Asp Asn Leu Asn Asn
            100                 105                 110


Asn Trp Ser Thr Ile Tyr Glu Ile Ser Ser Val Val Pro Ala Met Ala
        115                 120                 125


Thr His Ala Met Val Ile Ile His Lys Ile Pro Ser Pro Ser Thr Ser
    130                 135                 140


Asp Ile Val Val Asp Asp Ile Val Leu Val Gln Thr Gly Ala
145                 150                 155


<210>  10
<211>  154
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  10

Asn Lys Val Val Asn Gly Asp Phe Glu Thr Gly Thr Leu Phe Pro Trp
1               5                   10                  15


Ser Phe Thr Asn Val Ser Ile Thr Asn Leu Gln Ser His Thr Gly Phe
            20                  25                  30


Phe Ser Ala Leu Phe Phe Gly Asp Thr Ala Asn Ser Leu Leu Phe Gln
        35                  40                  45
```

```
Ala Ile Pro Val Thr Pro Gly Asp Ser Phe Glu Leu Phe Leu Ser Ile
    50                  55                  60


Ala Lys Leu Gly Asn Leu Val Ser Pro Gln Val Asn Ile Ala Leu Leu
65                  70                  75                  80


Tyr Leu Asp Val Ala Thr Ile Pro Val Gly Ile Gly Leu Asn Leu Thr
                85                  90                  95


Ile Pro Val Gly His Leu Pro Asp Asn Thr Ala Asn Ile Trp Thr Thr
            100                 105                 110


Ile Tyr Glu Thr Thr Ser Val Val Pro Ala Thr Ala Thr Gln Ala Leu
        115                 120                 125


Leu Ile Ile Asn Lys Ile Ser Ala Leu Ser Thr Ala Asp Ile Val Val
    130                 135                 140


Asp Asp Ile Gly Ile Leu Gln Thr Ser Gly
145                 150


<210>  11
<211>  110
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence


<220>
<221>  misc_feature
<222>  (93)..(93)
<223>  Xaa can be any naturally occurring amino acid

<400>  11

Met Phe Gln Ala Val Pro Val Thr Val Gly Asp Ser Phe Glu Phe Phe
1               5                   10                  15


Leu Ser Ile Ala Lys Ile Gly Asn Leu Pro Ser Pro Glu Val Asn Ile
            20                  25                  30


Ala Leu Ile Tyr Leu Asn Val Ala Ser Thr Pro Ile Ser Ile Gly Met
        35                  40                  45
```

Ser Ile Ile Leu Pro Ile Gly His Leu Pro Asp Asn Leu Asn Asn Asn
    50                  55                  60

Trp Ser Thr Ile Tyr Glu Ile Ser Ser Val Val Pro Ala Thr Ala Thr
65                  70                  75                  80

His Ala Met Val Ile Ile His Lys Ile Pro Ser Pro Xaa Ser Thr Ser
                85                  90                  95

Asp Ile Val Val Asp Asp Ile Val Leu Val Gln Thr Gly Ala
            100                 105                 110

<210>  12
<211>  164
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  12

Met Lys Ala Val Ile Tyr Leu Pro Leu Gly Asn Lys Ile Val Asn Gly
1               5                   10                  15

Asn Phe Glu Thr Gly Ser Leu Val Pro Trp Asn Phe Ser Asn Val Ala
            20                  25                  30

Ile Tyr Asn Leu Gln Ser His Thr Gly Ser Phe Ser Ala Leu Phe Phe
        35                  40                  45

Gly Asn Thr Thr Asn Ser Val Leu Tyr Gln Thr Val Pro Val Thr Ser
    50                  55                  60

Gly Glu Ile Phe Glu Phe Phe Leu Ser Ile Gly Lys Ile Gly Asn Leu
65                  70                  75                  80

Pro Ser Pro Gln Val Asn Ile Ala Leu Ile Tyr Leu Asn Ala Ala Ser
                85                  90                  95

Thr Pro Glu Asn Ile Gly Ile Asn Ile Ile Leu Pro Val Gly Lys Leu
            100                 105                 110

```
Pro Asn Asn Leu Asn Asn Asn Trp Ser Thr Ile Tyr Glu Ile Ser Ser
        115                 120                 125


Val Val Pro Ala Ala Ala Thr Gln Ala Met Val Ile Ile His Lys Ile
    130                 135                 140


Pro Ala Pro Ser Thr Ala Asp Ile Val Val Asp Asp Ile Val Leu Val
145                 150                 155                 160


Gln Thr Gly Ala
```

<210> 13
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 13

```
Met Pro Phe Ser Asn Lys Ile Val Asn Gly Asp Phe Glu Thr Gly Thr
1               5                   10                  15


Leu Ile Pro Trp Ser Phe Val Asn Val Ala Ile Thr Asn Leu Gln Ser
            20                  25                  30


His Thr Gly Phe Phe Ser Ala Gln Leu Phe Gly Thr Thr Ala Asn Ser
        35                  40                  45


Leu Leu Phe Gln Ala Val Pro Val Thr Pro Gly Asp Ser Phe Glu Phe
    50                  55                  60


Phe Leu Ser Ile Ala Lys Leu Gly Asn Leu Leu Ser Pro Gln Val Asn
65                  70                  75                  80


Ile Ala Leu Leu Tyr Leu Asp Val Ala Ala Thr Pro Val Gly Ile Gly
                85                  90                  95


Leu Asn Ile Thr Ile Pro Ile Gly His Leu Pro Asp Asn Ala Ala Asn
            100                 105                 110
```

```
Ile Trp Thr Thr Ile Tyr Glu Thr Thr Thr Val Val Pro Ala Thr Ala
        115                 120                 125


Thr Gln Ala Leu Leu Ile Ile Asn Lys Ile Pro Thr Leu Thr Thr Ala
    130                 135                 140


Asp Ile Val Val Asp Asp Ile Ala Leu Leu Gln Val Ser Gly
145                 150                 155


<210>  14
<211>  95
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  14

Met Phe Leu Ser Ile Ala Lys Ser Gly Asn Val Ile Ser Pro Gln Val
1               5                   10                  15


Asn Ile Val Leu Ile Tyr Leu Asp Val Ala Asn Ile Pro Val Gly Ile
            20                  25                  30


Gly Leu Asn Leu Thr Ile Pro Val Gly His Leu Pro Asp Asn Thr Ala
        35                  40                  45


Asn Ile Trp Thr Thr Ile Tyr Glu Thr Thr Ser Val Val Pro Ala Thr
    50                  55                  60


Ala Ile Glu Ala Leu Leu Ile Ile Asn Lys Val Pro Ala Leu Ser Thr
65                  70                  75                  80


Ala Asp Val Ile Leu Asp Asp Ile Gly Leu Leu Gln Thr Ser Gly
                85                  90                  95


<210>  15
<211>  142
<212>  PRT
<213>  Artificial Sequence

<220>
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<223>  N-terminal Signal Sequence

<400>  15

```
Leu Leu Pro Trp Ser Phe Thr Asn Ala Ala Ile Thr Asp Leu Gln Ser
1               5                   10                  15


His Ser Gly Phe Phe Ser Ala Leu Leu Phe Gly Gly Thr Ala Asn Ser
            20                  25                  30


Leu Leu Phe Gln Thr Val Pro Val Thr Pro Gly Asp Ser Phe Glu Leu
        35                  40                  45


Phe Leu Ser Ile Ala Lys Ser Gly Asn Leu Ile Ser Pro Gln Val Asn
    50                  55                  60


Ile Val Leu Ile Tyr Leu Asp Ala Ala Asn Ile Pro Val Gly Ile Gly
65                  70                  75                  80


Leu Asn Leu Thr Ile Pro Val Gly His Leu Pro Asp Asn Thr Ala Asn
                85                  90                  95


Ile Trp Thr Thr Ile Tyr Glu Thr Thr Ala Val Val Pro Ala Thr Ala
            100                 105                 110


Ile Glu Ala Leu Leu Ile Ile Ser Lys Val Pro Ala Leu Ser Thr Ala
        115                 120                 125


Asp Val Ile Leu Asp Asp Ile Glu Leu Leu Gln Thr Ser Gly
    130                 135                 140
```

<210>  16
<211>  158
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  16

```
Met Pro Phe Ser Asn Lys Ile Val Asn Gly Asp Phe Glu Thr Gly Thr
1               5                   10                  15
```

```
Leu Ile Pro Trp Ser Phe Thr Asn Val Ala Ile Thr Asn Leu Gln Ser
            20                  25                  30


His Ser Gly Phe Phe Ser Ala Arg Leu Phe Gly Thr Thr Val Asn Ser
        35                  40                  45


Leu Leu Phe Gln Ser Val Pro Val Thr Pro Gly Asp Ser Phe Glu Phe
    50                  55                  60


Phe Leu Ser Ile Ala Lys Leu Gly Thr Leu Leu Ser Pro Gln Val Asn
65                  70                  75                  80


Ile Ala Leu Leu Tyr Leu Asp Val Thr Ala Thr Pro Val Gly Ile Gly
                85                  90                  95


Leu Asn Ile Thr Ile Pro Ile Gly His Leu Pro Asp Asn Thr Ala Asn
            100                 105                 110


Ile Trp Thr Thr Ile Tyr Glu Thr Thr Thr Val Val Pro Ala Thr Ala
        115                 120                 125


Thr Gln Ala Leu Leu Ile Ile Asn Lys Ile Pro Thr Leu Thr Thr Ala
    130                 135                 140


Asp Ile Val Val Asp Asp Ile Glu Leu Leu Gln Val Ser Gly
145                 150                 155


<210>  17
<211>  161
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  17

Met Ser Phe Ile Asn Lys Ile Val Asn Gly Asp Phe Glu Thr Gly Thr
1               5                   10                  15


Leu Ile Pro Trp Ser Phe Val Asn Val Ala Ile Asn Pro Leu Gln Ser
            20                  25                  30
```

```
His Thr Gly Phe Phe Ser Ala Arg Leu Phe Gly Asn Thr Ala Asn Ser
        35                  40                  45

Leu Leu Phe Gln Ala Val Pro Val Thr Pro Gly Asp Ser Phe Glu Phe
    50                  55                  60

Phe Leu Ser Ile Ala Lys Ile Gly Asn Leu Thr Ser Pro Gln Val Asn
65                  70                  75                  80

Ile Val Leu Phe Tyr Leu Asp Ala Leu Ala Asn Pro Ile Ser Leu Gly
                85                  90                  95

Leu Asn Ile Thr Ile Pro Ser Gly His Leu Pro Asp Asn Val Asp Asn
            100                 105                 110

Asn Trp Thr Thr Ile Tyr Glu Thr Thr Ser Ala Val Pro Ala Thr Ala
        115                 120                 125

Thr Gln Ala Leu Leu Ile Ile Asn Lys Ile Pro Ala Leu Phe Thr Thr
    130                 135                 140

Ala Asp Ile Val Val Asp Asp Ile Ala Leu Leu Gln Thr Gly Ala Gly
145                 150                 155                 160

Val
```

<210> 18
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 18

```
Met Pro Phe Gly Asn Lys Ile Val Asn Gly Asn Phe Glu Thr Gly Ser
1               5                   10                  15

Leu Ile Pro Trp Ser Ser Ser Asn Val Val Ile Ser Asn Leu Gln Ser
            20                  25                  30
```

```
His Thr Gly Ser Tyr Ser Ala Leu Leu Phe Gly Asn Glu Ala Asn Ser
        35                  40                  45


Leu Met Phe Gln Ala Val Pro Val Thr Val Gly Asp Ser Phe Glu Phe
    50                  55                  60


Phe Leu Ser Ile Ala Lys Ile Gly Asn Leu Pro Ser Pro Gln Val Asn
65                  70                  75                  80


Ile Ala Leu Ile Tyr Leu Asn Val Ala Ser Thr Pro Ile Ser Ile Gly
                85                  90                  95


Met Ser Ile Ile Leu Pro Ile Gly His Leu Pro Asp Asn Leu Asn Asn
            100                 105                 110


Asn Trp Ser Thr Ile Tyr Glu Ile Ser Ser Val Val Pro Ala Thr Ala
        115                 120                 125


Thr His Ala Met Val Ile Ile His Lys Ile Pro Ser Pro Ser Thr Ser
    130                 135                 140


Asp Ile Val Val Asp Asp Ile Val Leu Val Gln Thr Gly Ala
145                 150                 155


<210>  19
<211>  158
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  19

Met Pro Val Lys Asn Arg Ala Val Asn Gly Asp Phe Glu Thr Gly Ser
1               5                   10                  15


Leu Val Pro Trp Asn Ser Ile Asn Val Thr Ile Ser Asn Gln Gln Ser
            20                  25                  30


His Ser Gly Thr Phe Ser Ala Leu Leu Phe Gly Thr Ser Ala Asn Ser
        35                  40                  45
```

```
Leu Leu Phe Gln Thr Val Pro Val Ile Thr Gly Asp Ser Phe Glu Phe
    50                  55                  60

Phe Leu Ser Ile Ala Lys Ile Gly Asn Leu Pro Ser Pro Gln Val Asn
65                  70                  75                  80

Ile Ala Val Ile Tyr Val Asn Ala Thr Ser Thr Pro Leu Ser Ile Gly
                85                  90                  95

Met Ser Val Ile Leu Pro Val Asn His Leu Pro Asn Asn Leu Asn Asn
            100                 105                 110

Asn Trp Leu Thr Ile Tyr Asn Thr Thr Ser Val Val Pro Val Thr Ala
        115                 120                 125

Thr Gln Ala Ile Ile Ile Ile His Lys Ile Pro Ala Pro Ser Thr Ala
    130                 135                 140

Asp Ile Val Val Asp Asp Ile Ala Leu Ile Gln Thr Gly Gly
145                 150                 155
```

<210> 20
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 20

```
Met Pro Phe Ser Asn Lys Ile Val Asn Gly Asn Phe Glu Thr Gly Ala
1               5                   10                  15

Leu Ile Pro Trp Ser Ser Ile Asn Val Ala Ile Thr Asn Leu Gln Ser
            20                  25                  30

His Thr Gly Phe Phe Ser Ala Arg Leu Phe Gly Asn Thr Thr Asn Ser
        35                  40                  45

Leu Leu Phe Gln Ala Val Pro Val Thr Pro Gly Asp Ser Phe Glu Phe
    50                  55                  60
```

```
Leu Leu Ser Ile Ala Lys Leu Gly Asn Leu Val Ser Pro Gln Val Asn
65                  70                  75                  80


Ile Ala Leu Leu Tyr Leu Asp Val Thr Ala Thr Pro Val Gly Ile Gly
                85                  90                  95


Leu Asn Phe Thr Ile Pro Val Gly His Leu Pro Asp Asn Thr Ala Asn
            100                 105                 110


Ile Trp Thr Thr Ile Tyr Glu Thr Thr Ser Val Val Pro Ala Thr Ala
        115                 120                 125


Thr Gln Ala Leu Leu Ile Ile Asn Lys Ile Ala Ala Leu Ser Thr Ala
    130                 135                 140


Asp Ile Val Val Asp Asp Ile Gly Ile Leu Gln Thr Ser Gly
145                 150                 155


<210>  21
<211>  158
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  21

Met Pro Phe Ser Asn Lys Ile Val Asn Gly Asn Phe Glu Thr Gly Ala
1               5                   10                  15


Leu Ile Pro Trp Ser Ser Ile Asn Val Ala Ile Thr Asn Leu Gln Ser
            20                  25                  30


His Thr Gly Phe Phe Ser Ala Arg Leu Phe Gly Asn Thr Thr Asn Ser
        35                  40                  45


Leu Leu Phe Gln Ala Val Pro Val Thr Pro Gly Asp Ser Phe Glu Phe
    50                  55                  60


Leu Leu Ser Ile Ala Lys Leu Gly Asn Leu Val Ser Pro Gln Val Asn
65                  70                  75                  80
```

```
Ile Ala Leu Leu Tyr Leu Asp Val Thr Ala Thr Pro Val Gly Ile Gly
                85                  90                  95


Leu Asn Phe Thr Ile Pro Val Gly His Leu Pro Asp Asn Thr Ala Asn
            100                 105                 110


Ile Trp Thr Thr Ile Tyr Glu Thr Thr Ser Val Val Pro Ala Thr Ala
        115                 120                 125


Ile Gln Ala Leu Leu Ile Ile Glu Lys Val Ala Ala Leu Thr Thr Ala
    130                 135                 140


Asp Val Val Val Asp Asp Ile Gln Leu Leu Gln Thr Ser Gly
145                 150                 155


<210>  22
<211>  109
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  22

Met Phe Gln Ala Val Pro Val Thr Val Gly Asp Ser Phe Glu Phe Phe
1               5                   10                  15


Leu Ser Ile Ala Lys Ile Gly Asn Leu Pro Ser Pro Glu Val Asn Ile
            20                  25                  30


Ala Leu Ile Tyr Leu Asn Val Ala Ser Thr Pro Ile Ser Ile Gly Met
        35                  40                  45


Ser Ile Ile Leu Pro Ile Gly His Leu Pro Asp Asn Leu Asn Asn Asn
    50                  55                  60


Trp Ser Thr Ile Tyr Glu Ile Ser Ser Val Val Pro Ala Thr Ala Thr
65                  70                  75                  80


His Ala Met Val Ile Ile His Lys Ile Pro Ser Pro Ser Thr Ser Asp
                85                  90                  95
```

Ile Val Val Asp Asp Ile Val Leu Val Gln Thr Gly Ala
100 105

<210> 23
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 23

Met Pro Phe Gly Asn Lys Ile Val Asn Gly Asn Phe Glu Thr Gly Ser
1 5 10 15

Leu Ile Pro Trp Ser Ser Ser Asn Val Val Ile Ser Asn Leu Gln Ser
20 25 30

His Thr Gly Ser Tyr Ser Ala Leu Leu Phe Gly Asn Ala Ala Asn Ser
35 40 45

Leu Met Phe Gln Ala Val Pro Val Thr Val Gly Asp Ser Phe Glu Phe
50 55 60

Phe Leu Ser Ile Ala Lys Ile Gly Asn Leu Pro Ser Pro Gln Val Asn
65 70 75 80

Ile Ala Leu Ile Tyr Leu Asn Val Ala Ser Thr Pro Ile Ser Ile Gly
85 90 95

Met Ser Ile Ile Leu Pro Ile Gly His Leu Pro Asp Asn Leu Asn Asn
100 105 110

Asn Trp Ser Thr Ile Tyr Glu Ile Ser Ser Val Val Pro Ala Thr Ala
115 120 125

Thr His Ala Met Val Ile Ile His Lys Ile Pro Ser Pro Ser Thr Ser
130 135 140

Asp Ile Val Val Asp Asp Ile Val Leu Val Gln Thr Gly Ala
145 150 155

<210> 24
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 24

Met Pro Phe Ser Asn Lys Ile Val Asn Gly Asn Phe Glu Thr Gly Ala
1 5 10 15

Leu Ile Pro Trp Ser Ser Ile Asn Val Ala Ile Thr Asn Leu Gln Ser
20 25 30

His Thr Gly Phe Phe Ser Ala Arg Leu Phe Gly Asn Thr Thr Asn Ser
35 40 45

Leu Leu Phe Gln Ala Val Pro Val Thr Leu Gly Asp Ser Phe Glu Phe
50 55 60

Leu Leu Ser Ile Ala Lys Leu Gly Asn Leu Val Ser Pro Gln Val Asn
65 70 75 80

Ile Ala Leu Leu Tyr Leu Asp Val Thr Ala Thr Pro Val Gly Ile Gly
85 90 95

Leu Asn Phe Thr Ile Pro Val Gly His Leu Pro Asp Asn Thr Ala Asn
100 105 110

Ile Trp Thr Thr Ile Tyr Glu Thr Thr Ser Val Val Pro Ala Thr Ala
115 120 125

Ile Gln Ala Leu Leu Ile Ile Glu Lys Val Ala Ala Leu Thr Thr Ala
130 135 140

Asp Val Val Val Asp Asp Ile Gln Leu Leu Gln Thr Ser Gly
145 150 155

<210> 25
<211> 186
<212> PRT
<213> Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  25

```
Met Val Arg Thr Leu Ser Lys Ile Glu Asp Ser Thr Tyr Thr Thr Leu
1               5                  10                  15


Ala Pro Ile Asn Pro Ile Met Glu Val Val Ile Tyr Leu Pro Phe Ser
            20                  25                  30


Asn Lys Val Val Asn Gly Asp Phe Glu Thr Gly Thr Leu Phe Pro Trp
        35                  40                  45


Ser Phe Thr Asn Val Ser Ile Thr Asn Leu Gln Ser His Thr Gly Phe
    50                  55                  60


Phe Ser Ala Leu Leu Phe Gly Asp Thr Ala Asn Ser Leu Leu Phe Gln
65                  70                  75                  80


Ala Ile Pro Val Thr Pro Gly Asp Ser Phe Glu Leu Phe Leu Ser Ile
                85                  90                  95


Ala Lys Leu Gly Asn Leu Val Ser Pro Gln Val Asn Ile Ala Leu Leu
            100                 105                 110


Tyr Leu Asp Val Ala Thr Ile Pro Val Gly Ile Gly Leu Asn Leu Thr
        115                 120                 125


Ile Pro Val Gly His Leu Pro Asp Asn Thr Ala Asn Ile Trp Thr Thr
    130                 135                 140


Ile Tyr Glu Thr Thr Ser Val Val Pro Ala Thr Ala Thr Gln Ala Leu
145                 150                 155                 160


Leu Ile Ile Asn Lys Ile Ser Ala Leu Ser Thr Ala Asp Ile Val Val
                165                 170                 175


Asp Asp Ile Gly Ile Leu Gln Thr Ser Gly
            180                 185
```

<210> 26
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 26

Met Pro Phe Gly Asn Lys Ile Val Asn Gly Asn Phe Glu Thr Gly Ser
1 5 10 15

Leu Ile Pro Trp Ser Ser Ser Asn Val Ala Ile Ser Asn Leu Gln Ser
20 25 30

His Thr Gly Ser Tyr Ser Ala Leu Leu Phe Gly Asn Ala Ala Asn Ser
35 40 45

Phe Leu Phe Gln Ala Val Pro Val Thr Val Gly Asp Ser Phe Glu Phe
50 55 60

Phe Leu Ser Ile Ala Lys Ile Gly Asn Leu Pro Ser Pro Gln Val Asp
65 70 75 80

Ile Ala Leu Ile Tyr Leu Asn Ala Ala Ser Thr Pro Ile Ser Ile Gly
85 90 95

Met Ser Ile Ile Leu Pro Thr Gly His Leu Pro Asp Asn Leu Asn Asn
100 105 110

Asn Trp Ser Thr Ile Tyr Glu Ile Ser Ser Val Val Pro Ala Met Ala
115 120 125

Thr His Ala Met Val Ile Ile His Lys Ile Pro Ser Pro Ser Thr Ser
130 135 140

Asp Ile Val Val Asp Asp Ile Val Leu Val Gln Thr Gly Ala
145 150 155

<210> 27
<211> 186
<212> PRT
<213> Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  27

```
Met Val Arg Thr Leu Ser Lys Ile Glu Asp Ser Thr Tyr Thr Thr Leu
1               5                  10                  15


Ala Pro Ile Asn Pro Ile Met Glu Val Val Ile Tyr Leu Pro Phe Ser
            20                  25                  30


Asn Lys Val Val Asn Gly Asp Phe Glu Thr Gly Thr Leu Phe Pro Trp
        35                  40                  45


Ser Phe Thr Asn Val Ser Ile Thr Asn Leu Gln Ser His Thr Gly Phe
    50                  55                  60


Phe Ser Ala Ile Leu Phe Gly Asp Thr Ala Asn Ser Leu Leu Phe Gln
65                  70                  75                  80


Ala Ile Pro Val Thr Pro Gly Asp Ser Phe Glu Leu Phe Leu Ser Ile
                85                  90                  95


Ala Lys Leu Gly Asn Leu Val Ser Pro Gln Val Asn Ile Ala Leu Leu
            100                 105                 110


Tyr Leu Asp Val Ala Thr Ile Pro Val Gly Ile Gly Leu Asn Leu Thr
        115                 120                 125


Ile Pro Val Gly His Leu Pro Asp Asn Thr Ala Asn Ile Trp Thr Thr
    130                 135                 140


Ile Tyr Glu Thr Thr Ser Val Val Pro Ala Asn Ala Thr Gln Ala Leu
145                 150                 155                 160


Leu Ile Ile Asn Lys Ile Ser Ala Leu Ser Thr Ala Asp Ile Val Val
                165                 170                 175


Asp Asp Ile Gly Ile Leu Gln Thr Ser Gly
            180                 185
```

<210> 28
<211> 149
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 28

Gly Asp Phe Glu Thr Gly Thr Leu Phe Pro Trp Ser Phe Thr Asn Val
1 5 10 15

Ser Ile Thr Asn Leu Gln Ser His Thr Gly Phe Phe Ser Ala Ile Leu
20 25 30

Phe Gly Asp Thr Ala Asn Ser Leu Leu Phe Gln Ala Ile Pro Val Thr
35 40 45

Pro Gly Asp Ser Phe Glu Leu Phe Leu Ser Ile Ala Lys Leu Gly Asn
50 55 60

Leu Val Ser Pro Gln Val Asn Ile Ala Leu Leu Tyr Leu Asp Val Ala
65 70 75 80

Thr Ile Pro Val Gly Ile Gly Leu Asn Leu Thr Ile Pro Val Gly His
85 90 95

Leu Pro Asp Asn Thr Ala Asn Ile Trp Thr Thr Ile Tyr Glu Thr Thr
100 105 110

Ser Val Val Pro Ala Asn Ala Thr Gln Ala Leu Leu Ile Ile Asn Lys
115 120 125

Ile Ser Ala Leu Ser Thr Ala Asp Ile Val Val Asp Asp Ile Gly Ile
130 135 140

Leu Gln Thr Ser Gly
145

<210> 29
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  29

Met Pro Phe Gly Asn Lys Ile Val Asn Gly Asn Phe Glu Thr Gly Ser
1               5                  10                  15

Leu Ile Pro Trp Ser Ser Ser Asn Val Ala Ile Ser Asn Leu Gln Ser
            20                  25                  30

His Thr Gly Ser Tyr Ser Ala Leu Leu Phe Gly Asn Thr Ala Asn Ser
        35                  40                  45

Leu Met Phe Gln Ala Val Pro Val Thr Val Gly Asp Ser Phe Glu Phe
    50                  55                  60

Phe Leu Ser Ile Ala Lys Ile Gly Asn Leu Pro Ser Ala Gln Val Asn
65                  70                  75                  80

Ile Ala Leu Ile Tyr Leu Asn Val Ala Ser Thr Pro Ile Ser Ile Gly
                85                  90                  95

Met Ser Ile Ile Leu Pro Ile Gly His Leu Pro Asp Asn Leu Asn Asn
            100                 105                 110

Asn Trp Ser Thr Ile Tyr Glu Ile Ser Ser Val Val Pro Ala Met Ala
        115                 120                 125

Thr His Ala Met Val Ile Ile His Lys Ile Pro Ser Pro Ser Thr Ser
    130                 135                 140

Asp Ile Val Val Asp Asp Ile Val Leu Val Gln Thr Gly Ala
145                 150                 155

<210>  30
<211>  158
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400> 30

Met Pro Phe Ser Asn Lys Ile Val Asn Gly Asp Phe Glu Thr Gly Thr
1 5 10 15

Leu Ile Pro Trp Ser Ser Ile Asn Val Ala Ile Thr Asn Leu Gln Ser
20 25 30

His Thr Gly Phe Phe Ser Ala Arg Leu Phe Gly Asn Thr Ala Asn Ser
35 40 45

Leu Leu Phe Gln Ala Val Pro Val Thr Pro Gly Asp Ser Phe Glu Phe
50 55 60

Leu Leu Ser Ile Ala Lys Leu Gly Asn Leu Val Ser Pro Gln Val Asn
65 70 75 80

Ile Ala Leu Leu Tyr Leu Asp Val Thr Ala Thr Pro Val Gly Ile Gly
85 90 95

Leu Asn Leu Thr Ile Pro Val Gly His Leu Pro Asp Asn Thr Ala Asp
100 105 110

Ile Trp Thr Thr Ile Tyr Glu Thr Thr Ser Val Val Pro Ala Thr Ala
115 120 125

Ile Gln Ala Leu Leu Ile Ile Glu Lys Val Pro Gly Leu Thr Thr Ala
130 135 140

Asp Val Val Val Asp Asp Ile Glu Leu Leu Gln Thr Ser Gly
145 150 155

<210> 31
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 31

Met Pro Phe Gly Asn Lys Ile Val Asn Gly Asn Phe Glu Thr Gly Ser
1 5 10 15

```
Leu Ile Pro Trp Ser Ser Ser Asn Val Ala Ile Ser Asn Leu Gln Ser
            20                  25                  30

His Thr Gly Ser Tyr Ser Ala Leu Leu Phe Gly Asn Thr Ala Asn Ser
        35                  40                  45

Leu Met Phe Gln Ala Val Pro Val Thr Val Gly Asp Ser Phe Glu Phe
    50                  55                  60

Phe Leu Ser Ile Ala Lys Ile Gly Asn Leu Pro Ser Ala Gln Val Asn
65                  70                  75                  80

Ile Ala Leu Ile Tyr Leu Asn Val Ala Ser Thr Pro Ile Ser Ile Gly
                85                  90                  95

Met Ser Ile Ile Leu Pro Ile Gly His Leu Pro Asp Asn Leu Asn Asn
            100                 105                 110

Asn Trp Ser Thr Ile Tyr Glu Ile Ser Ser Val Val Pro Ala Met Ala
        115                 120                 125

Thr His Ala Met Val Ile Ile His Lys Ile Pro Ser Pro Ser Thr Ser
    130                 135                 140

Asp Ile Val Val Asp Asp Ile Val Phe Val Gln Thr Gly Ala
145                 150                 155
```

<210>  32
<211>  75
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  32

```
Val Tyr Leu Asn Val Val Ala Thr Pro Ile Gly Ile Gly Met Ser Thr
1               5                   10                  15

Ile Leu Pro Ile Asp His Leu Pro Asp Asn Thr Asn Lys Asn Trp Thr
            20                  25                  30
```

```
Thr Ile Tyr Glu Thr Thr Ser Val Val Pro Ala Thr Ala Ile Arg Ala
        35                  40                  45


Leu Val Ile Ile His Lys Ile Pro Ser Pro Ser Thr Ala Asp Ile Val
    50                  55                  60


Val Asp Asp Ile Val Leu Leu Gln Thr Gly Leu
65                  70                  75


<210>  33
<211>  158
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  33

Met Pro Phe Ser Asn Lys Ile Val Asn Gly Asp Phe Glu Thr Gly Thr
1               5                   10                  15


Leu Ile Pro Trp Ser Ser Ile Asn Val Ala Ile Thr Asn Leu Gln Ser
            20                  25                  30


His Thr Gly Phe Phe Ser Ala Arg Leu Phe Gly Asn Ile Ala Asn Ser
        35                  40                  45


Leu Leu Phe Gln Ala Val Pro Val Thr Pro Gly Asp Ser Phe Glu Phe
    50                  55                  60


Leu Leu Ser Ile Ala Lys Leu Gly Asn Leu Val Ser Pro Gln Val Asn
65                  70                  75                  80


Ile Ala Leu Leu Tyr Leu Asp Val Thr Ala Thr Pro Val Gly Ile Gly
                85                  90                  95


Leu Asn Leu Thr Ile Pro Val Gly His Leu Pro Asp Asn Thr Ala Asn
            100                 105                 110


Ile Trp Thr Thr Ile Tyr Glu Thr Thr Ser Val Val Pro Ala Thr Ala
        115                 120                 125
```

Ile Gln Ala Leu Leu Ile Ile Glu Lys Val Ala Ser Leu Thr Thr Ala
130 135 140

Asp Val Val Val Asp Asp Ile Glu Leu Leu Gln Thr Ser Gly
145 150 155

<210> 34
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 34

Met Pro Phe Gly Asn Lys Ile Val Asn Gly Asn Phe Glu Thr Gly Ser
1 5 10 15

Leu Ile Pro Trp Ser Ser Ser Asn Val Val Ile Ser Asn Leu Gln Ser
20 25 30

His Thr Gly Ser Tyr Ser Ala Leu Leu Phe Gly Asn Ala Ala Asn Ser
35 40 45

Leu Met Phe Gln Ala Val Pro Val Thr Val Gly Asp Ser Phe Glu Phe
50 55 60

Phe Leu Ser Ile Ala Lys Ile Gly Asn Leu Pro Ser Pro Gln Val Asn
65 70 75 80

Ile Ala Leu Ile Tyr Leu Asn Val Ala Ser Thr Pro Ile Ser Ile Gly
85 90 95

Met Ser Ile Ile Leu Pro Ile Asp His Leu Pro Asp Asn Leu Asn Asn
100 105 110

Asn Trp Ser Thr Ile Tyr Glu Ile Ser Ser Val Val Pro Ala Thr Ala
115 120 125

Thr His Ala Met Val Ile Ile His Lys Ile Pro Ser Pro Ser Thr Ser
130 135 140

Asp Ile Val Val Asp Asp Ile Val Leu Val Gln Thr Gly Ala
145 150 155

<210> 35
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 35

Met Pro Phe Ser Asn Lys Ile Val Asn Gly Asp Phe Glu Thr Gly Thr
1 5 10 15

Leu Ile Pro Trp Ser Ser Ile Asn Val Ala Ile Thr Asn Leu Gln Ser
20 25 30

His Thr Gly Phe Phe Ser Ala Arg Leu Phe Gly Asn Ile Ala Asn Ser
35 40 45

Leu Leu Phe Gln Ala Val Pro Val Thr Pro Gly Asp Ser Phe Glu Phe
50 55 60

Leu Leu Ser Ile Ala Lys Leu Gly Asn Leu Val Ser Pro Gln Val Asn
65 70 75 80

Ile Ala Leu Leu Tyr Leu Asp Val Thr Ala Thr Pro Val Gly Ile Gly
85 90 95

Leu Asn Phe Thr Ile Pro Val Gly His Leu Pro Asp Asn Thr Ala Asn
100 105 110

Ile Trp Thr Thr Ile Tyr Glu Thr Thr Ser Val Val Pro Ala Thr Ala
115 120 125

Ile Gln Ala Leu Leu Ile Ile Glu Lys Val Ala Ser Leu Thr Thr Ala
130 135 140

Asp Val Val Val Asp Asp Ile Glu Leu Leu Gln Thr Ser Gly
145 150 155

<210> 36
<211> 97
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 36

Phe Glu Leu Phe Leu Ser Ile Ala Lys Leu Gly Asn Leu Val Ser Pro
1 5 10 15

Gln Val Asn Ile Ala Leu Leu Tyr Leu Asp Val Ala Thr Ile Pro Val
20 25 30

Gly Ile Gly Leu Asn Leu Thr Ile Pro Val Gly His Leu Pro Asp Asn
35 40 45

Thr Ala Asn Ile Trp Thr Thr Ile Tyr Glu Thr Thr Ser Val Val Pro
50 55 60

Ala Thr Ala Thr Gln Ala Leu Leu Ile Ile Asn Lys Ile Ala Ala Leu
65 70 75 80

Ser Thr Ala Asp Ile Val Val Asp Asp Ile Gly Ile Leu Gln Thr Ser
85 90 95

Glu

<210> 37
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 37

Met Pro Phe Gly Asn Lys Ile Val Asn Gly Asn Phe Glu Thr Gly Ser
1 5 10 15

```
Leu Ile Pro Trp Ser Ser Ser Asn Val Val Ile Ser Asn Leu Gln Ser
            20                  25                  30

His Thr Gly Ser Tyr Ser Ala Leu Leu Phe Gly Asn Ala Thr Asn Ser
        35                  40                  45

Leu Met Phe Gln Ala Val Pro Val Thr Val Gly Asp Ser Phe Glu Phe
    50                  55                  60

Phe Leu Ser Ile Ala Lys Ile Gly Asn Leu Pro Ser Pro Gln Val Asn
65                  70                  75                  80

Ile Ala Leu Ile Tyr Leu Asn Val Ala Ser Thr Pro Ile Ser Ile Gly
                85                  90                  95

Met Ser Ile Ile Leu Pro Ile Gly His Leu Pro Asp Asn Leu Asn Asn
            100                 105                 110

Asn Trp Ser Thr Ile Tyr Glu Ile Ser Ser Val Val Pro Ala Thr Ala
        115                 120                 125

Thr His Ala Met Val Ile Ile His Lys Ile Pro Ser Pro Ser Thr Ser
    130                 135                 140

Asp Ile Val Val Asp Asp Ile Val Leu Val Gln Thr Gly Ala
145                 150                 155
```

<210> 38
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 38

```
Met Pro Phe Ser Asn Lys Ile Val Asn Gly Asp Phe Glu Thr Gly Thr
1               5                   10                  15

Leu Ile Pro Trp Ser Ser Ile Asn Val Ala Ile Thr Asn Leu Gln Ser
            20                  25                  30
```

His Thr Gly Phe Phe Ser Ala Arg Leu Phe Gly Asn Ile Ala Asn Ser
35 40 45

Leu Leu Phe Gln Ala Val Pro Val Thr Pro Gly Asp Ser Phe Glu Phe
50 55 60

Leu Leu Ser Ile Ala Lys Leu Gly Asn Leu Val Ser Pro Gln Val Asn
65 70 75 80

Ile Ala Leu Leu Tyr Leu Asp Val Thr Ala Thr Pro Val Gly Ile Gly
85 90 95

Leu Asn Phe Thr Ile Pro Val Gly His Leu Pro Asp Asn Thr Ala Asn
100 105 110

Ile Trp Thr Thr Ile Tyr Glu Thr Thr Ser Val Val Pro Ala Thr Ala
115 120 125

Thr Gln Ala Leu Leu Ile Ile Asn Lys Ile Ala Ala Leu Ser Thr Ala
130 135 140

Asp Ile Val Val Asp Asp Ile Gly Ile Leu Gln Thr Ser Glu
145 150 155

<210> 39
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 39
atgcgcttta gctatagccg caactttgat aactttaaat gcgatagcaa atgcaactat 60

ccgatgaaat ataaatgcaa cgaatttggc tgcaacggct atccgtatga tctgagcggc 120

attcaggatc cgatt 135

<210> 40
<211> 114
<212> DNA
<213> Artificial Sequence

<220>

<223>  N-terminal Signal Sequence

<400>  40
atgcattttg gcaactttaa cctggatcgc gtgtgcagca aatgcaacag ctttccgtgc  60

tgctgcaaaa ccggcccgat tccgagctgc ccgatttggc cggtgaaacc gacc  114


<210>  41
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  41

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1  5  10  15


Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20  25  30


Gly Tyr Pro Tyr Asp Leu Ser Gly Ile Gln Asp Pro Ile
        35  40  45


<210>  42
<211>  38
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  42

Met His Phe Gly Asn Phe Asn Leu Asp Arg Val Cys Ser Lys Cys Asn
1  5  10  15


Ser Phe Pro Cys Cys Cys Lys Thr Gly Pro Ile Pro Ser Cys Pro Ile
            20  25  30


Trp Pro Val Lys Pro Thr
        35


<210>  43
<211>  44

<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  43

Met Arg Phe Ser Tyr Asn Arg Asn Phe Asp Asn Phe Lys Cys Asp Ala
1               5                   10                  15


Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30


Gly Tyr Pro Tyr Val Tyr Gly Ile Glu Asp Pro Ile
        35                  40


<210>  44
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  44

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15


Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30


Gly Tyr Pro Tyr Asp Phe Ser Gly Ile Gln Asp Pro Ile
        35                  40                  45


<210>  45
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  45

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30

Gly Tyr Pro Tyr Asp Phe Ser Gly Ile Gln Asp Pro Met
        35                  40                  45

<210>  46
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  46

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Tyr Phe Lys Cys Asp Ser
1               5                   10                  15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Tyr Glu Phe Gly Cys Asn
            20                  25                  30

Gly Tyr Pro Tyr Asp Phe Ser Gly Ile Gln Asp Pro Ile
        35                  40                  45

<210>  47
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  47

Met Arg Phe Ser Tyr Ser Arg Asn Ser Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30

Gly Tyr Pro Tyr Asp Phe Ser Gly Ile Gln Asp Pro Ile
        35                  40                  45

<210> 48
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 48

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1 5 10 15

Lys Ser Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
20 25 30

Gly Tyr Pro Tyr Asp Phe Ser Gly Ile Gln Asp Pro Ile
35 40 45

<210> 49
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 49

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1 5 10 15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
20 25 30

Gly Tyr Pro Tyr Asp Phe Leu Gly Ile Gln Asp Pro Ile
35 40 45

<210> 50
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 50

```
Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15


Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30


Gly Tyr Pro Tyr Asp Leu Leu Gly Ile Gln Asp Pro Ile
        35                  40                  45
```

<210>  51
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  51

```
Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15


Lys Cys Asn Tyr Pro Leu Lys Phe Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30


Gly Tyr Pro Tyr Asp Phe Ser Gly Ile Gln Asp Pro Ile
        35                  40                  45
```

<210>  52
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  52

```
Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15


Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30


Gly Tyr Pro Tyr Asn Leu Ser Gly Ile Gln Asp Pro Ile
        35                  40                  45
```

<210> 53
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 53

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1 5 10 15

Lys Cys Asn Tyr Pro Lys Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
20 25 30

Gly Tyr Pro Tyr Asp Leu Ser Gly Ile Gln Asp Pro Ile
35 40 45

<210> 54
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 54

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1 5 10 15

Lys Cys Asn Tyr Pro Leu Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
20 25 30

Gly Tyr Pro Tyr Asp Leu Ser Gly Ile Gln Asp Pro Ile
35 40 45

<210> 55
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 55

Met Arg Leu Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1 5 10 15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
20 25 30

Gly Tyr Pro Tyr Asp Phe Ser Gly Ile Gln Asp Pro Ile
35 40 45

<210> 56
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 56

Leu Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1 5 10 15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
20 25 30

Gly Tyr Pro Tyr Asp Leu Ser Gly Ile Gln Asp Pro Ile
35 40 45

<210> 57
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 57

Met Arg Phe Arg Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1 5 10 15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
20 25 30

Gly Tyr Pro Tyr Asp Phe Ser Gly Ile Gln Asp Pro Ile
35 40 45

<210> 58
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 58

Met Arg Val Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1 5 10 15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
20 25 30

Gly Tyr Pro Tyr Asp Phe Ser Gly Ile Gln Asp Pro Ile
35 40 45

<210> 59
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 59

Met Arg Phe Ser Tyr Ser Arg Tyr Phe Asp Asn Phe Lys Cys Asp Ser
1 5 10 15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
20 25 30

Gly Tyr Pro Tyr Asp Phe Ser Gly Ile Gln Asp Pro Ile
35 40 45

<210> 60
<211> 45
<212> PRT
<213> Artificial Sequence

<220>

<223>  N-terminal Signal Sequence

<400>  60

Met Arg Ile Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15


Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30


Gly Tyr Pro Tyr Asp Phe Ser Gly Ile Gln Asp Pro Met
        35                  40                  45


<210>  61
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  61

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15


Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30


Gly Tyr Pro Tyr Asp Leu Ser Gly Ile Gln Glu Pro Met
        35                  40                  45


<210>  62
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  62

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15


Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30

Gly Tyr Pro Tyr Asp Leu Ser Gly Ile Gln Asp Leu Ile
35 40 45

<210> 63
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 63

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1 5 10 15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
20 25 30

Gly Tyr Pro Tyr Asp Leu Ser Gly Ile Gln Val Pro Ile
35 40 45

<210> 64
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 64

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1 5 10 15

Lys Phe Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
20 25 30

Gly Tyr Pro Tyr Asp Leu Ser Gly Ile Gln Asp Pro Ile
35 40 45

<210> 65
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  65

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Tyr Phe Lys Cys Asp Ser
1               5                   10                  15


Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30


Gly Tyr Pro Tyr Asp Leu Ser Gly Ile Gln Asp Pro Ile
        35                  40                  45


<210>  66
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  66

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15


Lys Cys Asn Tyr Pro Met Lys Asn Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30


Gly Tyr Pro Tyr Asp Leu Ser Gly Ile Gln Asp Pro Ile
        35                  40                  45


<210>  67
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  67

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30

Gly Tyr Pro Tyr Asp Leu Ser Ala Ile Gln Asp Pro Ile
        35                  40                  45

<210>  68
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  68

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30

Gly Tyr Pro Tyr Asp Leu Ser Gly Phe Gln Asp Pro Ile
        35                  40                  45

<210>  69
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  69

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30

Gly Tyr Pro Tyr Asp Leu Ser Gly Phe Gln Asp Pro Thr
        35                  40                  45

<210>  70
<211>  45

<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  70

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Tyr Lys Cys Asp Ser
1               5                   10                  15


Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30


Gly Tyr Pro Tyr Asp Leu Ser Gly Ile Gln Asp Pro Ile
        35                  40                  45


<210>  71
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  71

Met Arg Phe Ser Tyr Cys Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15


Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30


Gly Tyr Pro Tyr Asp Leu Ser Gly Ile Gln Asp Pro Ile
        35                  40                  45


<210>  72
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  72

Met Arg Phe Ser Tyr Ser Arg Asn Leu Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30

Gly Tyr Pro Tyr Asp Leu Ser Gly Ile Gln Asp Leu Ile
        35                  40                  45

<210>  73
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  73

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Ile
            20                  25                  30

Gly Tyr Pro Tyr Asn Leu Ser Gly Ile Gln Asp Pro Ile
        35                  40                  45

<210>  74
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  74

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30

Gly Tyr Ala Tyr Asn Leu Ser Gly Ile Gln Asp Pro Ile
        35                  40                  45

<210> 75
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 75

Met Arg Phe Ser Tyr Ser Arg Asn Leu Asp Asn Phe Lys Cys Asp Ser
1 5 10 15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
20 25 30

Gly Tyr Pro Tyr Asn Leu Ser Gly Ile Gln Asp Pro Ile
35 40 45

<210> 76
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 76

Leu Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1 5 10 15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
20 25 30

Gly Tyr Pro Tyr Asn Leu Ser Gly Ile Gln Asp Pro Ile
35 40 45

<210> 77
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 77

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Met Arg Phe Ser Tyr Ile Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15


Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30


Gly Tyr Pro Tyr Asn Leu Ser Gly Ile Gln Asp Pro Ile
        35                  40                  45


<210>  78
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  78

Met Arg Val Ser Asp Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15


Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30


Gly Tyr Pro Tyr Asp Phe Ser Gly Ile Gln Asp Pro Ile
        35                  40                  45


<210>  79
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  79

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Tyr Ser
1               5                   10                  15


Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30


Gly Tyr Pro Tyr Asp Leu Ser Gly Phe Gln Asp Pro Ile
        35                  40                  45
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<210> 80
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 80

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1 5 10 15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Trp Cys Asn
20 25 30

Gly Tyr Pro Tyr Asp Leu Ser Gly Phe Gln Asp Pro Ile
35 40 45

<210> 81
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 81

Met Arg Phe Ser Asn Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1 5 10 15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
20 25 30

Gly Tyr Pro Tyr Asp Leu Ser Gly Phe Gln Asp Pro Ile
35 40 45

<210> 82
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 82

Met Arg Phe Ser Tyr Ser Arg Asn Leu Asp Asn Phe Lys Cys Asp Ser
1 5 10 15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
20 25 30

Gly Tyr Pro Tyr Asp Leu Ser Gly Phe Gln Asp Pro Ile
35 40 45

<210> 83
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 83

Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser Lys Cys
1 5 10 15

Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn Gly Tyr
20 25 30

Ala Tyr Asn Leu Ser Gly Ile Gln Asp Pro Ile
35 40

<210> 84
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 84

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1 5 10 15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Tyr Gly Cys Asn
20 25 30

Gly Tyr Ala Tyr Asn Leu Ser Gly Ile Gln Asp Pro Ile
35 40 45

<210> 85
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 85

Met Arg Leu Ser Tyr Ser Arg Asn Leu Asp Asn Phe Lys Cys Asp Ser
1 5 10 15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
20 25 30

Gly Tyr Pro Tyr Asn Leu Ser Gly Ile Gln Asp Pro Ile
35 40 45

<210> 86
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 86

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1 5 10 15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
20 25 30

Gly Tyr Pro Phe Asp Phe Ser Gly Phe Gln Asp Pro Ile
35 40 45

<210> 87
<211> 45
<212> PRT
<213> Artificial Sequence

<220>

<223>  N-terminal Signal Sequence

<400>  87

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Ser Asp Thr
1               5                   10                  15


Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30


Gly Tyr Pro Tyr Asp Leu Ser Gly Ile Gln Asp Pro Ile
        35                  40                  45


<210>  88
<211>  44
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  88

Met Arg Phe Ser Tyr Asn Arg Asn Phe Asp Asn Phe Lys Cys Asp Ala
1               5                   10                  15


Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30


Gly Tyr Pro Tyr Val Tyr Gly Ile Gln Asp Pro Ile
        35                  40


<210>  89
<211>  44
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  89

Met Arg Phe Ser Phe Asn Arg Asn Phe Asp Asn Phe Lys Cys Asp Ala
1               5                   10                  15


Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30

Gly Tyr Pro Tyr Val Tyr Gly Ile Glu Asp Pro Ile
35 40

<210> 90
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 90

Met Arg Phe Ser Tyr Asn Arg Asn Phe Asp Asn Phe Lys Cys Asp Ala
1 5 10 15

Lys Cys Asn Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
20 25 30

Gly Tyr Pro Tyr Val Tyr Gly Ile Glu Asp Gln Ile
35 40

<210> 91
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 91

Met Arg Phe Ser Tyr Ile Arg Asn Phe Asp Asn Phe Lys Cys Asp Ala
1 5 10 15

Lys Cys Asn Tyr Pro Leu Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
20 25 30

Gly Tyr Pro Tyr Val Tyr Gly Ile Gln Glu Pro Ile
35 40

<210> 92
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  92

Met Arg Phe Ser Tyr Asn Leu Asn Phe Asp Asn Phe Lys Cys Asp Ala
1               5                   10                  15


Lys Cys Asn Tyr Pro Leu Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30


Gly Tyr Pro Tyr Val Tyr Gly Ile Gln Glu Pro Ile
        35                  40


<210>  93
<211>  44
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  93

Met Arg Phe Cys Tyr Tyr Arg Asn Phe Asp Asn Phe Lys Cys Asp Ala
1               5                   10                  15


Asn Cys Tyr Tyr Pro Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30


Gly Tyr Pro Tyr Val Tyr Gly Ile Glu Asp Pro Ile
        35                  40


<210>  94
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  94

Met Arg Phe Ser Tyr Ser Arg Asn Phe Asp Asn Phe Lys Cys Asp Ser
1               5                   10                  15

Lys Cys Asn Tyr His Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30

Gly Tyr Pro Tyr Val Leu Ser Asp Ile Gln Asp Pro Ile
        35                  40                  45

<210>  95
<211>  41
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  95

Tyr Ser Arg Asn Phe Asp Lys Ile Lys Cys Asp Ser Lys Cys Asn Tyr
1               5                   10                  15

His Met Lys Tyr Lys Cys Asn Glu Phe Gly Cys Asn Gly Tyr Pro Tyr
            20                  25                  30

Asp Phe Ser Gly Ile Gln Asp Pro Ile
        35                  40

<210>  96
<211>  45
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  96

Met Arg Phe Asn Tyr Asn Arg Asn Asn Asp Asn Phe Lys Cys Asp Ala
1               5                   10                  15

Lys Cys Asn Tyr Pro Met Lys Phe Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30

Gly Tyr Pro Tyr Gly Ala Tyr Glu Ile Gln Asp Pro Val
        35                  40                  45

<210>  97
<211>  45

<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  97

Met Arg Phe Asn Tyr Asn Arg Asn Asn Asp Asn Phe Lys Cys Asp Thr
1               5                   10                  15


Lys Cys Asn Tyr Pro Met Lys Phe Lys Cys Asn Glu Phe Gly Cys Asn
            20                  25                  30


Gly Tyr Pro Tyr Gly Ala Tyr Glu Ile Gln Asp Pro Val
        35                  40                  45


<210>  98
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  98

Met His Phe Gly Lys Phe Lys Glu Arg Val Cys Ser Lys Cys Asn Thr
1               5                   10                  15


Phe Pro Cys Cys Cys Ser Pro Cys Pro Pro Gln Ser Cys Pro Ile Trp
            20                  25                  30


Pro Val Lys Pro Thr
        35


<210>  99
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  99

Met His Phe Gly Lys Phe Lys Glu Arg Val Cys Ser Lys Cys Asn Thr
1               5                   10                  15

Phe Pro Cys Cys Cys Ser Pro Tyr Pro Pro Gln Ser Cys Pro Ile Trp
            20                  25                  30

Pro Val Lys Pro Thr
        35

<210>  100
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  100

Met His Phe Gly Asn Phe Ile Asp Arg Val Cys Ser Lys Cys His Ser
1               5                   10                  15

Phe Pro Cys Cys Cys Lys Thr Gly Pro Ile Pro Ser Cys Pro Ile Trp
            20                  25                  30

Pro Val Lys Pro Thr
        35

<210>  101
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  101

Met His Phe Gly Asn Phe Ile Asp Arg Val Cys Ser Lys Cys His Ser
1               5                   10                  15

Phe Pro Cys Tyr Cys Lys Thr Gly Pro Ile Pro Ser Cys Pro Ile Trp
            20                  25                  30

Pro Val Lys Pro Thr
        35

<210> 102
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 102

Met His Phe Gly Asn Phe Ile Asp Arg Val Cys Ser Lys Cys His Ser
1 5 10 15

Phe Pro Cys Cys Cys Lys Thr Gly Pro Ile Pro Ser Cys Pro Ile Trp
20 25 30

Pro Val Asn Pro Thr
35

<210> 103
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 103

Met His Phe Gly Asn Phe Ile Asp Arg Val Cys Ser Lys Cys His Ser
1 5 10 15

Phe Pro Cys Cys Cys Lys Ala Gly Pro Ile Pro Ser Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 104
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 104

Met His Phe Gly Asn Phe Ile Asp Arg Val Cys Ser Lys Cys His Ser
1               5                   10                  15

Phe Pro Cys Cys Cys Lys Thr Gly Pro Ile Pro Asn Cys Pro Ile Trp
            20                  25                  30

Pro Val Lys Pro Thr
        35

<210>  105
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  105

Met His Tyr Gly Asn Phe Ile Asp Arg Val Cys Ser Lys Cys His Ser
1               5                   10                  15

Phe Pro Cys Cys Cys Lys Thr Gly Pro Ile Pro Ser Cys Pro Ile Trp
            20                  25                  30

Pro Val Lys Pro Thr
        35

<210>  106
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  106

Met His Phe Gly Asn Phe Ile Val Arg Val Cys Ser Lys Cys His Ser
1               5                   10                  15

Phe Pro Cys Cys Cys Lys Thr Gly Pro Ile Gln Ser Cys Pro Ile Trp
            20                  25                  30

Pro Val Lys Pro Thr
        35

<210>  107
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  107

Met His Phe Gly Ile Ile Ile Asp Arg Val Cys Ser Lys Cys His Ser
1               5                   10                  15


Phe Pro Cys Cys Cys Lys Thr Gly Pro Ile Pro Ser Cys Pro Ile Trp
            20                  25                  30


Pro Val Lys Pro Thr
        35


<210>  108
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  108

Met His Phe Gly Lys Phe Ile Asp Arg Val Cys Thr Lys Cys His Ser
1               5                   10                  15


Tyr Pro Cys Cys Cys Lys Thr Gly Pro Ile Pro Ser Cys Pro Ile Trp
            20                  25                  30


Pro Val Lys Pro Thr
        35


<210>  109
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400> 109

Met His Phe Gly Lys Phe Leu Asp Arg Val Cys Asn Lys Cys His Ser
1 5 10 15

Phe Pro Cys Cys Cys Lys Thr Gly Pro Ile Pro Gly Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 110
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 110

Met His Phe Gly Lys Phe Leu Asp Arg Val Cys Ser Lys Cys His Ser
1 5 10 15

Phe Pro Cys Cys Cys Lys Thr Gly Pro Ile Pro Gly Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 111
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 111

Met His Phe Gly Lys Phe Leu Asp Arg Val Cys Ser Lys Cys Asn Ser
1 5 10 15

Phe Pro Cys Cys Cys Lys Thr Gly Pro Ser Pro Ser Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 112
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 112

Met Asn Phe Gly Lys Phe Leu Asp Arg Val Cys Ser Lys Cys Asn Ser
1 5 10 15

Phe Pro Cys Cys Cys Lys Thr Gly Pro Ser Pro Ser Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 113
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 113

Met Leu Phe Gly Lys Phe Leu Asp Arg Val Cys Ser Lys Cys Asn Ser
1 5 10 15

Phe Pro Cys Cys Cys Lys Thr Gly Pro Ser Pro Ser Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 114
<211> 37
<212> PRT
<213> Artificial Sequence

<220>

<223>  N-terminal Signal Sequence

<400>  114

Met His Phe Gly Lys Phe Leu Asp Arg Val Cys Ser Lys Cys Asn Ser
1               5                   10                  15


Phe Pro Cys Cys Cys Lys Thr Gly Pro Ser Pro Ser Cys Pro Asn Trp
            20                  25                  30


Pro Val Lys Pro Thr
        35


<210>  115
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  115

Met His Phe Gly Asn Tyr Leu Lys Arg Val Cys Ser Lys Cys Asn Ser
1               5                   10                  15


Phe Pro Cys Cys Cys Arg Thr Gly Pro Ile Pro Ser Cys Pro Val Trp
            20                  25                  30


Pro Val Lys Pro Thr
        35


<210>  116
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  116

Met His Phe Gly Asn Tyr Leu Lys Arg Val Cys Ser Lys Cys Asn Tyr
1               5                   10                  15


Phe Pro Cys Cys Cys Arg Thr Gly Pro Ile Pro Ser Cys Pro Val Trp
            20                  25                  30

Pro Val Lys Pro Thr
35

<210> 117
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 117

Met His Phe Gly Asn Tyr Leu Lys Arg Val Cys Ser Lys Cys Asn Ser
1 5 10 15

Phe Pro Cys Cys Cys Arg Pro Gly Pro Ile Pro Ser Cys Pro Val Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 118
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 118

Met His Phe Gly Asn Tyr Leu Lys Gln Val Cys Ser Lys Cys Asn Ser
1 5 10 15

Phe Pro Cys Cys Cys Arg Thr Gly Pro Ile Pro Ser Cys Pro Val Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 119
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  119

Met His Phe Gly Asn Tyr Leu Lys Arg Val Cys Ser Lys Cys Asn Ser
1               5                   10                  15


Phe Pro Cys Cys Cys Arg Thr Gly Pro Ile Gln Ser Cys Pro Val Trp
            20                  25                  30


Pro Val Lys Pro Thr
        35


<210>  120
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  120

Met His Phe Gly Asn Tyr Leu Lys Gln Val Cys Asn Lys Cys Asn Ser
1               5                   10                  15


Phe Pro Cys Cys Cys Arg Thr Gly Pro Ile Pro Ser Cys Pro Val Trp
            20                  25                  30


Pro Val Lys Pro Thr
        35


<210>  121
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  121

Met His Phe Gly Asn Tyr Leu Lys Gln Val Cys Ser Lys Cys Asn Ser
1               5                   10                  15

Phe Pro Cys Cys Cys Arg Asn Gly Pro Ile Pro Ser Cys Pro Val Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 122
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 122

Met His Phe Gly Asn Tyr Leu Lys Gln Val Cys Ser Lys Cys Asn Ser
1 5 10 15

Phe Pro Cys Cys Cys Arg Thr Gly Pro Ile Pro Ser Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 123
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 123

Leu His Phe Gly Asn Tyr Leu Lys Gln Val Cys Ser Lys Cys Asn Ser
1 5 10 15

Phe Pro Cys Cys Cys Arg Thr Gly Pro Ile Pro Ser Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 124
<211> 37

<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  124

Met Leu Phe Gly Asn Tyr Leu Lys Gln Val Cys Ser Lys Cys Asn Ser
1               5                   10                  15


Phe Pro Cys Cys Cys Arg Thr Gly Pro Ile Pro Ser Cys Pro Ile Trp
            20                  25                  30


Pro Val Lys Pro Thr
        35


<210>  125
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  125

Met His Phe Gly Asn Tyr Leu Lys Gln Val Ser Ser Lys Cys Asn Ser
1               5                   10                  15


Phe Pro Cys Cys Cys Arg Asn Gly Pro Ile Pro Ser Cys Pro Val Trp
            20                  25                  30


Pro Val Lys Pro Thr
        35


<210>  126
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  126

Met His Phe Gly Arg Phe Asn Glu Arg Val Cys Ser Lys Cys Asn Thr
1               5                   10                  15

Phe Pro Cys Cys Cys Asn Pro Cys Ala Ala Gln Ser Cys Pro Ile Trp
            20                  25                  30

Pro Val Lys Pro Thr
        35

<210>  127
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  127

Met His Phe Gly Arg Phe Lys Glu Arg Val Cys Ser Lys Cys Asn Thr
1               5                   10                  15

Phe Pro Cys Cys Cys Asn Pro Cys Ala Ala Gln Ser Cys Pro Ile Trp
            20                  25                  30

Pro Val Lys Pro Thr
        35

<210>  128
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  128

Met His Phe Gly Arg Phe Asn Glu Arg Val Cys Ser Lys Cys Asn Ser
1               5                   10                  15

Phe Pro Cys Cys Cys Asn Pro Cys Ala Ala Gln Ser Cys Pro Ile Trp
            20                  25                  30

Pro Val Lys Pro Thr
        35

<210> 129
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 129

Met His Phe Gly Lys Phe Asn Glu Arg Val Cys Ser Lys Cys Asn Thr
1 5 10 15

Phe Pro Cys Cys Cys Asn Pro Cys Ala Ala Gln Ser Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Ser
35

<210> 130
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 130

Met His Phe Gly Arg Phe Asn Glu Arg Val Cys Ser Lys Cys Asn Thr
1 5 10 15

Phe Pro Cys Cys Cys Cys Ala Ala Gln Ser Cys Pro Ile Trp Pro Val
20 25 30

Lys Pro Thr
35

<210> 131
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 131

Met His Phe Gly Lys Phe Lys Asp Ser Val Cys Ser Lys Cys Asn Thr
1               5                   10                  15

Phe Pro Cys Cys Cys Asn Pro Cys Ala Ala Gln Ser Cys Pro Ile Trp
            20                  25                  30

Pro Val Lys Pro Thr
        35

<210>  132
<211>  34
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  132

Met His Phe Gly Arg Phe Asn Glu Arg Val Cys Ser Lys Cys Asn Thr
1               5                   10                  15

Phe Pro Cys Cys Cys Cys Ala Ala Gln Ser Cys Pro Ile Trp Pro Val
            20                  25                  30

Lys Pro

<210>  133
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  133

Met His Phe Gly Lys Phe Lys Glu Arg Val Cys Ser Lys Cys Asn Ser
1               5                   10                  15

Phe Pro Cys Cys Cys Ser Pro Cys Pro Pro Gln Ser Cys Pro Ile Trp
            20                  25                  30

Pro Val Lys Pro Thr
        35

<210> 134
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 134

Met His Phe Gly Lys Phe Lys Asp Arg Val Cys Ser Lys Cys Asn Thr
1 5 10 15

Phe Pro Cys Cys Cys Ser Pro Cys Pro Pro Gln Ser Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 135
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 135

Met His Phe Gly Arg Phe Asn Glu Arg Val Cys Ser Lys Cys Asn Thr
1 5 10 15

Phe Pro Cys Cys Cys Ser Pro Cys Asp Val Gln Ser Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 136
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 136

Met Gln Phe Gly Arg Phe Asn Glu Arg Val Cys Ser Lys Cys Thr Thr
1 5 10 15

Phe Pro Cys Cys Cys Ser Pro Cys Asp Val Gln Ser Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 137
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 137

Met His Phe Gly Lys Phe Asn Asp Arg Ile Cys Ser Lys Cys Asn Thr
1 5 10 15

Phe Pro Cys Cys Cys Asn Pro Cys Ala Pro Ser Cys Pro Val Trp Pro
20 25 30

Val Lys Pro
35

<210> 138
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 138

Met His Phe Gly Asn Phe Ile Asp Arg Val Cys Ser Lys Cys Asn Thr
1 5 10 15

Phe Pro Cys Cys Cys Arg Gly Gly Pro Val Pro Gly Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 139
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 139

Met His Phe Gly Asn Phe Ile Asp Arg Val Cys Ser Lys Cys Lys Thr
1 5 10 15

Phe Pro Cys Cys Cys Arg Gly Gly Pro Val Pro Gly Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 140
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 140

Met His Phe Gly Asn Phe Ile Asp Arg Val Cys Ser Lys Cys Asn Thr
1 5 10 15

Phe Pro Cys Cys Cys Arg Gly Gly Pro Val Pro Gly Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Pro
35

<210> 141
<211> 37
<212> PRT
<213> Artificial Sequence

<220>

<223>  N-terminal Signal Sequence

<400>  141

```
Met His Phe Gly Asn Phe Ile Asp Arg Val Cys Ser Lys Cys Asn Thr
1               5                   10                  15


Phe Pro Cys Cys Cys Arg Gly Gly Pro Val Pro Gly Cys His Ile Trp
            20                  25                  30


Pro Val Lys Pro Thr
        35
```

<210>  142
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  142

```
Met His Phe Gly Asn Phe Ile Asp Arg Val Cys Ser Lys Cys Lys Thr
1               5                   10                  15


Phe Pro Cys Cys Cys Arg Gly Gly Pro Val Pro Cys Cys Pro Ile Trp
            20                  25                  30


Pro Val Lys Pro Thr
        35
```

<210>  143
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  143

```
Met His Phe Gly Asn Phe Ile Asp Arg Val Cys Ser Lys Cys Lys Thr
1               5                   10                  15


Ile Pro Cys Cys Cys Arg Gly Gly Pro Val Pro Gly Cys Pro Ile Trp
            20                  25                  30
```

Pro Val Lys Pro Thr
35

<210> 144
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 144

Met His Phe Gly Asn Phe Ile Asp Arg Val Cys Ser Lys Cys Asn Thr
1 5 10 15

Phe Pro Cys Cys Cys Lys Gly Gly Pro Val Pro Gly Cys His Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 145
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 145

Met His Phe Gly Asn Phe Ile Asp Arg Val Cys Ser Lys Cys Lys Thr
1 5 10 15

Phe Pro Cys Cys Cys Gly Ser Gly Pro Val Pro Gly Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 146
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  146

Met His Phe Gly Asn Phe Ile Asp Arg Val Cys Ser Lys Cys Lys Thr
1               5                   10                  15


Ser Pro Cys Cys Cys Gly Ser Gly Pro Val Pro Gly Cys Pro Ile Trp
            20                  25                  30


Pro Val Lys Pro Thr
        35


<210>  147
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  147

Met His Phe Gly Asn Phe Ile Asp Arg Val Cys Thr Lys Cys Lys Ile
1               5                   10                  15


Phe Pro Arg Cys Cys Arg Gly Gly Pro Val Pro Gly Cys Pro Ile Trp
            20                  25                  30


Pro Val Lys Pro Thr
        35


<210>  148
<211>  36
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  148

Met His Phe Gly Lys Phe Thr Asp Arg Val Cys Ser Lys Cys Asn Thr
1               5                   10                  15

Phe Pro Cys Cys Cys Asn Thr Cys Pro Ala Pro Asn Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro
35

<210> 149
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 149

Met Asn Phe Gly Asn Phe Asn Asn Arg Ile Cys Ser Lys Cys Asn Thr
1 5 10 15

Phe Pro Cys Cys Cys Ile Pro Cys Ala Pro Ser Cys Pro Val Trp Pro
20 25 30

Val Lys Pro Gly
35

<210> 150
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 150

Met Tyr Phe Gly Asn Phe Leu Asp Arg Ile Cys Ser Lys Cys Asn Thr
1 5 10 15

Phe Pro Cys Cys Cys Leu Ser Gly Pro Ile Leu Arg Ser Pro Ile Trp
20 25 30

Pro Val Arg Pro Thr
35

<210> 151
<211> 41

<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  151

Met His Phe Gly Asn Phe Leu Asp Arg Val Cys Asn Lys Cys Asn Thr
1               5                   10                  15


Phe Pro Cys Cys Cys Leu Ser Gly Pro Ile His Arg Ser Pro Ile Trp
            20                  25                  30


Pro Val Pro Pro Ala Lys Ala Thr Arg
        35                  40


<210>  152
<211>  35
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  152

Met Gln Phe Gly Lys Tyr Asn Asp Arg Ile Cys Arg Lys Cys Asn Thr
1               5                   10                  15


Phe Pro Cys Cys Cys Asn Pro Ser Ala Pro Ser Cys Pro Gly Trp Pro
            20                  25                  30


Val Lys Pro
        35


<210>  153
<211>  38
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  153

Met Lys Phe Gln Asp Phe Asn Ile Asn Lys Ile Cys Asn Asn Cys His
1               5                   10                  15

Ser Tyr Pro Cys Cys Cys His Asn Gly Pro Val Gln Arg Cys Pro Val
            20                  25                  30

Trp Pro Val Lys Pro Thr
        35

<210>  154
<211>  38
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  154

Met Lys Phe Gln Asp Phe Asn Ile Asn Lys Ile Cys Asn Asn Cys His
1               5                   10                  15

Ser Tyr Pro Cys Cys Cys His Asn Gly Pro Val His Arg Cys Pro Val
            20                  25                  30

Trp Pro Val Lys Pro Thr
        35

<210>  155
<211>  38
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  155

Met Lys Phe Gln Asp Phe Asn Ile Asn Lys Ile Cys Asn Asn Cys Asn
1               5                   10                  15

Ser Tyr Pro Cys Cys Cys His Asn Gly Pro Val Gln Arg Cys Pro Val
            20                  25                  30

Trp Pro Val Lys Pro Thr
        35

<210> 156
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 156

Met Lys Phe Gln Asp Phe Asn Ile Asn Lys Ile Cys Asn Asn Cys His
1 5 10 15

Ser Tyr Pro Cys Cys Cys His Asn Gly Pro Val Leu Arg Cys Pro Val
20 25 30

Trp Pro Val Lys Pro Thr
35

<210> 157
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 157

Met Lys Phe Leu Asp Phe Asn Ile Asn Lys Ile Cys Asn Asn Cys His
1 5 10 15

Ser Tyr Pro Cys Cys Cys His Asn Gly Pro Val His Arg Cys Pro Val
20 25 30

Trp Pro Val Lys Pro Thr
35

<210> 158
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 158

Met Lys Phe Gln Asp Phe Asn Ile Asn Lys Ile Cys Asn Asn Cys His
1               5                   10                  15

Ser Tyr Pro Cys Cys Cys His Lys Gly Pro Val His Arg Cys Pro Val
            20                  25                  30

Trp Pro Val Lys Pro Thr
        35

<210>  159
<211>  38
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  159

Met Lys Phe Gln Asp Phe Asn Ile Asn Lys Ile Cys Asn Ile Cys His
1               5                   10                  15

Ser Tyr Pro Phe Cys Cys His Asn Gly Pro Val Gln Arg Cys Pro Val
            20                  25                  30

Trp Pro Val Lys Pro Thr
        35

<210>  160
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  160

Met Lys Phe Gln Asp Phe Asn Ile Asn Met Ile Cys Asn Asn Cys His
1               5                   10                  15

Ser Tyr Pro Cys Cys Cys His Asn Gly Pro Val His Arg Cys Pro Val
            20                  25                  30

Trp Pro Val Lys Pro
        35

<210> 161
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 161

Met Lys Phe His Asp Phe Asn Leu Asn Asn Ile Cys Gly Lys Cys Leu
1 5 10 15

Ser His Pro Cys Cys Cys Asn Asn Gly Pro Ala Gln Arg Cys Pro Ile
20 25 30

Trp Pro Val Lys Pro Thr
35

<210> 162
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 162

Met Lys Phe His Asp Phe Asn Leu Asn Asn Ile Cys Gly Lys Cys Leu
1 5 10 15

Ser His Pro Cys Cys Cys Asn Asn Val Pro Ala Gln Arg Cys Pro Ile
20 25 30

Trp Pro Val Lys Pro Thr
35

<210> 163
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 163

Met Lys Phe His Asp Phe Asn Leu Asn Asn Ile Cys Gly Lys Cys Leu
1 5 10 15

Ser His Pro Cys Cys Cys Asn Asn Gly Pro Val Gln Arg Cys Pro Ile
20 25 30

Trp Pro Val Lys Pro Thr
35

<210> 164
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 164

Met Asp Phe Ala Asn Phe Lys Asn Arg Ile Cys Ser Arg Cys Asn Ser
1 5 10 15

Phe Pro Cys Asn Cys Lys Arg Asn Phe Pro Gln Asn Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 165
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 165

Met Asp Phe Ala Asn Phe Lys Asn Arg Ile Cys Ser Arg Cys Asn Ser
1 5 10 15

Phe Pro Cys Asn Cys Lys Arg Asn Ser Pro Gln Asn Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 166
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 166

Met Asp Phe Ala Asn Phe Lys Asn Arg Ile Cys Ser Arg Cys Asn Thr
1 5 10 15

Phe Pro Cys Asn Cys Lys Arg Asn Phe Pro Gln Asn Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 167
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 167

Met Asp Phe Ala Asn Phe Lys Asn Arg Ile Cys Ser Arg Cys Asn Ser
1 5 10 15

Phe Pro Cys Asn Cys Lys Gly Asn Phe Pro Gln Asn Cys Pro Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 168
<211> 37
<212> PRT
<213> Artificial Sequence

<220>

<223>  N-terminal Signal Sequence

<400>  168

Met Asp Phe Ala Tyr Phe Lys Asn Arg Ile Cys Ser Arg Cys Asn Ser
1               5                   10                  15


Phe Pro Cys Asn Cys Lys Arg Asn Phe Pro Gln Asn Cys Pro Ile Trp
            20                  25                  30


Pro Val Lys Pro Thr
        35


<210>  169
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  169

Met Asp Phe Ala Asn Phe Lys Asn Arg Ile Cys Ser Arg Cys Asn Ser
1               5                   10                  15


Phe Pro Cys Asn Cys Ile Arg Asn Ile Pro Gln Asn Cys Pro Ile Trp
            20                  25                  30


Pro Val Lys Pro Thr
        35


<210>  170
<211>  37
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  170

Met Asp Leu Ala Asn Phe Lys Asn Arg Ile Cys Ser Arg Cys Asn Ser
1               5                   10                  15


Phe Pro Cys Asn Cys Lys Arg Asn Phe Pro Gln Asn Cys Pro Ile Trp
            20                  25                  30

Pro Val Lys Pro Thr
35

<210> 171
<211> 37
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 171

Met Asp Phe Ala Asn Phe Lys Asn Arg Ile Cys Ser Arg Cys Asn Ser
1 5 10 15

Phe Pro Cys Asn Cys Lys Ser Asn Tyr Pro Gln Asn Cys Ser Ile Trp
20 25 30

Pro Val Lys Pro Thr
35

<210> 172
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 172

Met Asn Phe Glu Asp Tyr Phe Leu Asn Asn Val Cys Ser Lys Cys Lys
1 5 10 15

Thr Phe Pro Cys Ala Cys Ile Arg Ile Pro Glu His His Cys Cys Ile
20 25 30

Trp Pro Val Lys Pro Thr
35

<210> 173
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  173

Met Asn Phe Glu Asp Tyr Phe Leu Asn Asn Val Cys Ser Lys Cys Lys
1               5                   10                  15


Thr Phe Pro Cys Ala Cys Ile Arg Ile Pro Gly His His Cys Ser Ile
            20                  25                  30


Trp Pro Val Lys Pro Thr
        35


<210>  174
<211>  38
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  174

Met Asn Phe Glu Asp Tyr Phe Leu Asn Asn Val His Val Leu Cys Lys
1               5                   10                  15


Thr Phe Pro Cys Ala Cys Ile Arg Ile Pro Glu His His Cys Cys Ile
            20                  25                  30


Trp Pro Val Lys Pro Thr
        35


<210>  175
<211>  38
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  175

Met Asn Phe Glu Asp Tyr Phe Leu Asn Asn Val Cys Ser Lys Cys Arg
1               5                   10                  15

Thr Phe Pro Cys Gly Cys Arg Arg Ile Pro Glu His His Ser Cys Val
            20                  25                  30

Trp Pro Val Lys Pro Thr
        35

<210>  176
<211>  38
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  176

Met Asn Phe Glu Asp Tyr Phe Leu Lys Asn Val Cys Ser Lys Cys Arg
1               5                   10                  15

Thr Phe Pro Cys Gly Cys Thr Arg Ile Pro Glu Gln His Cys Cys Val
            20                  25                  30

Trp Pro Val Lys Pro Thr
        35

<210>  177
<211>  38
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  177

Met Asn Phe His Asp Phe Ile Leu Asn Asn Ile Cys Lys Arg Cys Asn
1               5                   10                  15

Ser Tyr Pro Cys Arg Cys Ile Asn Arg Pro Glu Gln Asn Cys Ser Ile
            20                  25                  30

Trp Pro Val Lys Pro Thr
        35

<210>  178
<211>  150

<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 178
atggattcaa ataaaacgag gtgtgctgtt tgtaataaat atcaatgttc ttgtaactcc 60

aaaaaaagaa gtcctaaaac agttattaga gatttagatt atatagatcc atgtgaacct 120

ctttatataa tagatcattg tcataataga 150

<210> 179
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<220>
<221> misc_feature
<222> (9)..(9)
<223> Xaa can be any naturally occurring amino acid

<400> 179

Met Asp Ser Asn Lys Thr Arg Cys Xaa Val Cys Asn Lys Tyr Gln Cys
1 5 10 15

Ser Cys Asn His Lys Lys Arg Ser Pro Lys Thr Val Ile Arg Asp Leu
20 25 30

Asp Tyr Ile Asp Pro Cys Glu Pro Leu Tyr Ile Ile Asp His Cys His
35 40 45

Asn Arg
50

<210> 180
<211> 159
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 180
atggactcaa ataaaacgag gtgtcctatt tgtaataatt atcaatgttc ttgtaacgct 60

aaaaaaagaa ggcctacaag atgtattaga tatttagatt atatagatca atgtgaacaa 120

tgtgaaccta tttctataat agatcattgt cataataga 159

<210> 181
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 181

Met Asp Ser Asn Lys Thr Arg Cys Pro Ile Cys Asn Asn Tyr Gln Cys
1 5 10 15

Ser Cys Asn Ala Lys Lys Arg Arg Pro Thr Arg Cys Ile Arg Tyr Leu
20 25 30

Asp Tyr Ile Asp Gln Cys Glu Gln Cys Glu Pro Ile Ser Ile Ile Asp
35 40 45

His Cys His Asn Arg
50

<210> 182
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 182
atggactcaa ataaaacgag gtgtcctatt tgtaataatt atcaatgttc ttgtaacgct 60

aaaaaaagaa ggcctacaag atgtattaga tatttagatt atatagatca atgtgaacaa 120

tgtgaaccta tttctataat agatcattgt cataatagag gtaaaacagg accgaccgga 180

gcaactggtg caaccggacc aactggagca actggagcaa caggaccaac aggaccaact 240

ggagcaacag gacctacagg agcaacagga ccaacaggtg caactggggc gacaggaatc 300

accgggccga ctggagcaac gggagcaaca 330

<210> 183
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 183

Met Asp Ser Asn Lys Thr Arg Cys Pro Ile Cys Asn Asn Tyr Gln Cys
1 5 10 15

Ser Cys Asn Ala Lys Lys Arg Arg Pro Thr Arg Cys Ile Arg Tyr Leu
20 25 30

Asp Tyr Ile Asp Gln Cys Glu Gln Cys Glu Pro Ile Ser Ile Ile Asp
35 40 45

His Cys His Asn Arg Gly Lys Thr Gly Pro Thr Gly Ala Thr Gly Ala
50 55 60

Thr Gly Pro Thr Gly Ala Thr Gly Ala Thr Gly Pro Thr Gly Pro Thr
65 70 75 80

Gly Ala Thr Gly Pro Thr Gly Ala Thr Gly Pro Thr Gly Ala Thr Gly
85 90 95

Ala Thr Gly Ile Thr Gly Pro Thr Gly Ala Thr Gly Ala Thr
100 105 110

<210> 184
<211> 150
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 184
atggaatcaa ataaaacgag gtgtattgtt tgtaataaat atcaatgttc ttgtaactcc 60

aaaaaaagaa gtcctaaaac agttattaga gatttagatt atatagatcc atgtgaacct 120

ctttatataa tagatcattg tcataataga 150

<210> 185
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 185

Met Glu Ser Asn Lys Thr Arg Cys Ile Val Cys Asn Lys Tyr Gln Cys
1 5 10 15

Ser Cys Asn Ser Lys Lys Arg Ser Pro Lys Thr Val Ile Arg Asp Leu
20 25 30

Asp Tyr Ile Asp Pro Cys Glu Pro Leu Tyr Ile Ile Asp His Cys His
35 40 45

Asn Arg
50

<210> 186
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 186
atggaatcaa ataaaacgag gtgtattgtt tgtaataaat atcaatgttc ttgtaactcc 60

aaaaaaagaa gtcctaaaac agttattaga gatttagatt atatagatcc atgtgaacct 120

ctttatataa tagatcattg tcataataga ggtaaaacag gaccaacagg accaacggga 180

ccaaccggag tgactggagc aaccggacca acaggagaaa caggaccaac gggagcaacc 240

ggagcaactg gagcaacagg agcaacaggt ccaatgggag taactggctc gaccggagca 300

actggtgtaa cgggagcaac aggagcaaca gggtcaaccg gagcaacagg tgaaaccgga 360

gcgactggtg aaaccgga 378

<210> 187
<211> 126

<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  187

Met Glu Ser Asn Lys Thr Arg Cys Ile Val Cys Asn Lys Tyr Gln Cys
1               5                   10                  15


Ser Cys Asn Ser Lys Lys Arg Ser Pro Lys Thr Val Ile Arg Asp Leu
            20                  25                  30


Asp Tyr Ile Asp Pro Cys Glu Pro Leu Tyr Ile Ile Asp His Cys His
        35                  40                  45


Asn Arg Gly Lys Thr Gly Pro Thr Gly Pro Thr Gly Pro Thr Gly Val
    50                  55                  60


Thr Gly Ala Thr Gly Pro Thr Gly Glu Thr Gly Pro Thr Gly Ala Thr
65                  70                  75                  80


Gly Ala Thr Gly Ala Thr Gly Ala Thr Gly Pro Met Gly Val Thr Gly
                85                  90                  95


Ser Thr Gly Ala Thr Gly Val Thr Gly Ala Thr Gly Ala Thr Gly Ser
            100                 105                 110


Thr Gly Ala Thr Gly Glu Thr Gly Ala Thr Gly Glu Thr Gly
        115                 120                 125


<210>  188
<211>  150
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Artificial Sequence

<400>  188
atgtattcaa ataaaaagag gtgtgctgtt tgtaataaat atcaatgttc ttgtaactcc       60

aaaaaaagaa gtcctaaaac agttattaga gatttagatt atatagatcc atgtgaacct      120

ctttatataa tagatcattg tcataataga                                       150

<210> 189
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 189

Met Tyr Ser Asn Lys Lys Arg Cys Ala Val Cys Asn Lys Tyr Gln Cys
1 5 10 15

Ser Cys Asn Ser Lys Lys Arg Ser Pro Lys Thr Val Ile Arg Asp Leu
20 25 30

Asp Tyr Ile Asp Pro Cys Glu Pro Leu Tyr Ile Ile Asp His Cys His
35 40 45

Asn Arg
50

<210> 190
<211> 474
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 190
atgtattcaa ataaaaagag gtgtgctgtt tgtaataaat atcaatgttc ttgtaactcc 60

aaaaaaagaa gtcctaaaac agttattaga gatttagatt atatagatcc atgtgaacct 120

ctttatataa tagatcattg tcataataga ggtaaaacag gaccaacagg agcaacaggt 180

catacaggaa caaccggaac aacaggagag actggaccaa caggagcaac aggagcaaca 240

ggaataacgg gagcaacggg agaaacagga gcaacaggac caacgggaac aactggtgta 300

accggagaaa ccggagcaac aggtccaact ggagaaactg gtgaaacagg accaacggga 360

gcaactggga accggagcaa caggagaaac aggaacaact ggagcaacag gaaaaacggg 420

aacaacagga gaaacaggag aaacaggagc aacaggagaa acaggaaaaa cagg 474

<210> 191
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 191

```
Met Tyr Ser Asn Lys Lys Arg Cys Ala Val Cys Asn Lys Tyr Gln Cys
1               5                  10                  15


Ser Cys Asn Ser Lys Lys Arg Ser Pro Lys Thr Val Ile Arg Asp Leu
            20                  25                  30


Asp Tyr Ile Asp Pro Cys Glu Pro Leu Tyr Ile Ile Asp His Cys His
        35                  40                  45


Asn Arg Gly Lys Thr Gly Pro Thr Gly Ala Thr Gly His Thr Gly Thr
    50                  55                  60


Thr Gly Thr Thr Gly Glu Thr Gly Pro Thr Gly Ala Thr Gly Ala Thr
65                  70                  75                  80


Gly Ile Thr Gly Ala Thr Gly Glu Thr Gly Ala Thr Gly Pro Thr Gly
                85                  90                  95


Thr Thr Gly Val Thr Gly Glu Thr Gly Ala Thr Gly Pro Thr Gly Glu
            100                 105                 110


Thr Gly Glu Thr Gly Pro Thr Gly Ala Thr Gly Asn Arg Ser Asn Arg
        115                 120                 125


Arg Asn Arg Asn Asn Trp Ser Asn Arg Lys Asn Gly Asn Asn Arg Arg
    130                 135                 140


Asn Arg Arg Asn Arg Ser Asn Arg Arg Asn Arg Lys Asn Arg
145                 150                 155
```

<210> 192
<211> 150
<212> DNA
<213> Artificial Sequence

<220>
<223>  Artificial Sequence

<400>  192
atgtattcaa ataaaaagag gtgtgctgtt tgtaataaat atcaatgttc ttgtaactcc  60

aaaaaaagaa gtcctaaaac agttattaga gatttagatt atatagatcc atgtgaacct  120

ctttatataa tagatcattg tcataataga  150


<210>  193
<211>  50
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  193

Met Tyr Ser Asn Lys Lys Arg Cys Ala Val Cys Asn Lys Tyr Gln Cys
1               5                   10                  15


Ser Cys Asn Ser Lys Lys Arg Ser Pro Lys Thr Val Ile Arg Asp Leu
            20                  25                  30


Asp Tyr Ile Asp Pro Cys Glu Pro Leu Tyr Ile Ile Asp His Cys His
        35                  40                  45


Asn Arg
    50


<210>  194
<211>  330
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Artificial Sequence

<400>  194
atgtattcaa ataaaaagag gtgtgctgtt tgtaataaat atcaatgttc ttgtaactcc  60

aaaaaaagaa gtcctaaaac agttattaga gatttagatt atatagatcc atgtgaacct  120

ctttatataa tagatcattg tcataataga ggtaaaacag gaccaacagg agcaacaggt  180

cctacaggat caacgggacc aacaggagtg actggaccaa caggagcaac aggaacaaca  240

ggatcaacag gaacaacagg agcaacagga gcaacaggag aaacaggagc aacaggacca 300

acaggaccaa caggagaaac aggaacaaca 330

<210> 195
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 195

Met Tyr Ser Asn Lys Lys Arg Cys Ala Val Cys Asn Lys Tyr Gln Cys
1 5 10 15

Ser Cys Asn Ser Lys Lys Arg Ser Pro Lys Thr Val Ile Arg Asp Leu
20 25 30

Asp Tyr Ile Asp Pro Cys Glu Pro Leu Tyr Ile Ile Asp His Cys His
35 40 45

Asn Arg Gly Lys Thr Gly Pro Thr Gly Ala Thr Gly Pro Thr Gly Ser
50 55 60

Thr Gly Pro Thr Gly Val Thr Gly Pro Thr Gly Ala Thr Gly Thr Thr
65 70 75 80

Gly Ser Thr Gly Thr Thr Gly Ala Thr Gly Ala Thr Gly Glu Thr Gly
85 90 95

Ala Thr Gly Pro Thr Gly Pro Thr Gly Glu Thr Gly Thr Thr
100 105 110

<210> 196
<211> 150
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 196
atggattcaa ataaaaagag gtgtgctgtt tgtaataaat atcaatgttc ttgtaactcc 60

aaaaaaagaa gtcctaaaac agttattaga gatttagatt atatagatcc atgtgaaccg 120

ctttatataa tagatcattg tcataataga 150

<210> 197
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 197

Met Asp Ser Asn Lys Lys Arg Cys Ala Val Cys Asn Lys Tyr Gln Cys
1 5 10 15

Ser Cys Asn Ser Lys Lys Arg Ser Pro Lys Thr Val Ile Arg Asp Leu
20 25 30

Asp Tyr Ile Asp Pro Cys Glu Pro Leu Tyr Ile Ile Asp His Cys His
35 40 45

Asn Arg
50

<210> 198
<211> 2484
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 198
atggattcaa ataaaaagag gtgtgctgtt tgtaataaat atcaatgttc ttgtaactcc 60

aaaaaaagaa gtcctaaaac agttattaga gatttagatt atatagatcc atgtgaaccg 120

ctttatataa tagatcattg tcataataga ggtaaaacag gaccaacagg agcaacaggt 180

cctacaggat caatgggacc aaccggagtg actggatcaa caggagcaac cggaccaaca 240

gggtcaaccg gagtaactgg ggaaacagga tcaaccggga caacgggacc aagcggatca 300

actggaccaa ctggtgcaac agggtcaacc ggagaaaccg gagcaacagg gtcaaccgga 360

gcaactggag aaacaggtcc aacaggacca acgggaacaa ctggtgtaac cggagaaacc 420

ggagcaacag gtccaactgg agcaactgga gcaactggtg aaacaggttc aacaggacca 480

acgggagcaa ctggagaaac tggtgaaaca ggttcaacag gaccaacggg agcaacggga 540

tcgactggag caacgggacc aacgggagca acgggatcca ctggagcaac gggatcgact 600

ggagcaacgg gatcgactgg agcaacagga ccaacaggag caacagggtc aaccggagaa 660

acaggaccaa ctggtgaaac aggttcaacg ggagcaactg ggtcgaccgg agcaacaggt 720

gaaacaggac caacgggaac aactggagta accggagaaa ccggagcaac aggtccaaca 780

ggagcaactg gagcaactgg agaaactggt gaaacaggtt caacaggacc aacgggagca 840

actggagaaa ctggtgaaac aggttcaaca ggaccaacgg gagcaacggg atcgactgga 900

gcaacgggac caactggagc aacgggatcg actggagcaa cgggatcgac tggagcaacg 960

ggatcgactg gagcaacagg accaacagga gcaacagggt caaccggaga aacaggacca 1020

actggtgaaa caggttcaac gggagcaact gggtcgaccg gagcaacagg tgaaacagga 1080

ccaacgggag caactgggtc gaccggagca actggtgaaa caggtgcaac aggaccaaca 1140

ggaccaacgg gaacaactgg tgtaaccgga gcaacaggtc caactggagc aactggagaa 1200

acaggaccaa cgggagcgac tggagaagca ggaccaacag ggtcaaccgg agcgactgga 1260

ccaaccgggg caacgggaat cacgggagca acaggaccaa caggatcaac tggtgcaaca 1320

gggtcaaccg gagaaactgg atcaactgga gaaaccggac caacaggagc aactggtgta 1380

accggagcaa caggtccaac tggagaaaca ggttcaacag gaccaatggg agcaaccgga 1440

gaaactggtt cgaccggatc aactggtgta acgggagcaa caggagcaac gggagaaacc 1500

ggagcaacag gatcaacggg agcaactggc acgaccggag caacaggaga aacaggacca 1560

acaggaccaa ctgggtccac cggagcaaca ggagaaacag gtccaacagg accaacggga 1620

gcaactggag taaccggagc aacaggagca acgggagcaa ctggagaaac aggttcaaca 1680

ggaccaatgg gagcaaccgg agaaactggt tcgaccggat caactggtgt aacgggagca 1740

acaggagcga ctggagtaac aggagcaact ggtgaaacag gatcaacggg agcaactggg 1800

tcgaccggag caacaggtga aaccggacca acaggtccaa caggtccaac aggaccaacg 1860

ggaacaactg gtgtaaccgg agtaactgga gaaaccggac caacaggagc gactggtgaa 1920

acaggttcaa caggaccaac gggaacaact ggtgtaaccg gagaaaccgg agcaacagga 1980

ccaactggtg caacagggtc aaccggagaa accggagcaa ctggagaaac aggtcgaaca 2040

ggaccaacgg gaacaactgg tgtaaccgga gaaaccggag caactggaga aacaggacca 2100

acaggagcaa cgggatcgac tggagcaaca ggaccaacgg gagcaactgg ggcgaccgga 2160

gcaacaggtg aaacaggacc aacgggagcg actggagaaa caggagcaac gggagcaact 2220

gggtcaaccg gagcaacagg tccaacagga ccaacgggaa caactggagt aaccggagca 2280

acaggtccaa ctggagcaac tggagaaaca ggaccaacgg gagcaactgg agaagcagga 2340

ccaacagggt caaccggatc gactggacca accggggcaa cgggaatcac gggagcaaca 2400

ggaccaacag gagcaactgg tgcaacaggg tcaaccggag aaactggatc aactggagaa 2460

accggaccaa caggatcaac tggt 2484

<210> 199
<211> 828
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 199

Met Asp Ser Asn Lys Lys Arg Cys Ala Val Cys Asn Lys Tyr Gln Cys
1 5 10 15

Ser Cys Asn Ser Lys Lys Arg Ser Pro Lys Thr Val Ile Arg Asp Leu
20 25 30

Asp Tyr Ile Asp Pro Cys Glu Pro Leu Tyr Ile Ile Asp His Cys His
35 40 45

Asn Arg Gly Lys Thr Gly Pro Thr Gly Ala Thr Gly Pro Thr Gly Ser
50 55 60

Met Gly Pro Thr Gly Val Thr Gly Ser Thr Gly Ala Thr Gly Pro Thr
65 70 75 80

Gly Ser Thr Gly Val Thr Gly Glu Thr Gly Ser Thr Gly Thr Thr Gly
85 90 95

Pro Ser Gly Ser Thr Gly Pro Thr Gly Ala Thr Gly Ser Thr Gly Glu
100 105 110

```
Thr Gly Ala Thr Gly Ser Thr Gly Ala Thr Gly Glu Thr Gly Pro Thr
        115                 120                 125

Gly Pro Thr Gly Thr Thr Gly Val Thr Gly Glu Thr Gly Ala Thr Gly
    130                 135                 140

Pro Thr Gly Ala Thr Gly Ala Thr Gly Glu Thr Gly Ser Thr Gly Pro
145                 150                 155                 160

Thr Gly Ala Thr Gly Glu Thr Gly Glu Thr Gly Ser Thr Gly Pro Thr
                165                 170                 175

Gly Ala Thr Gly Ser Thr Gly Ala Thr Gly Pro Thr Gly Ala Thr Gly
            180                 185                 190

Ser Thr Gly Ala Thr Gly Ser Thr Gly Ala Thr Gly Ser Thr Gly Ala
        195                 200                 205

Thr Gly Pro Thr Gly Ala Thr Gly Ser Thr Gly Glu Thr Gly Pro Thr
    210                 215                 220

Gly Glu Thr Gly Ser Thr Gly Ala Thr Gly Ser Thr Gly Ala Thr Gly
225                 230                 235                 240

Glu Thr Gly Pro Thr Gly Thr Thr Gly Val Thr Gly Glu Thr Gly Ala
                245                 250                 255

Thr Gly Pro Thr Gly Ala Thr Gly Ala Thr Gly Glu Thr Gly Glu Thr
            260                 265                 270

Gly Ser Thr Gly Pro Thr Gly Ala Thr Gly Glu Thr Gly Glu Thr Gly
        275                 280                 285

Ser Thr Gly Pro Thr Gly Ala Thr Gly Ser Thr Gly Ala Thr Gly Pro
    290                 295                 300

Thr Gly Ala Thr Gly Ser Thr Gly Ala Thr Gly Ser Thr Gly Ala Thr
305                 310                 315                 320
```

```
Gly Ser Thr Gly Ala Thr Gly Pro Thr Gly Ala Thr Gly Ser Thr Gly
                325                 330                 335

Glu Thr Gly Pro Thr Gly Glu Thr Gly Ser Thr Gly Ala Thr Gly Ser
            340                 345                 350

Thr Gly Ala Thr Gly Glu Thr Gly Pro Thr Gly Ala Thr Gly Ser Thr
        355                 360                 365

Gly Ala Thr Gly Glu Thr Gly Ala Thr Gly Pro Thr Gly Pro Thr Gly
    370                 375                 380

Thr Thr Gly Val Thr Gly Ala Thr Gly Pro Thr Gly Ala Thr Gly Glu
385                 390                 395                 400

Thr Gly Pro Thr Gly Ala Thr Gly Glu Ala Gly Pro Thr Gly Ser Thr
                405                 410                 415

Gly Ala Thr Gly Pro Thr Gly Ala Thr Gly Ile Thr Gly Ala Thr Gly
            420                 425                 430

Pro Thr Gly Ser Thr Gly Ala Thr Gly Ser Thr Gly Glu Thr Gly Ser
        435                 440                 445

Thr Gly Glu Thr Gly Pro Thr Gly Ala Thr Gly Val Thr Gly Ala Thr
    450                 455                 460

Gly Pro Thr Gly Glu Thr Gly Ser Thr Gly Pro Met Gly Ala Thr Gly
465                 470                 475                 480

Glu Thr Gly Ser Thr Gly Ser Thr Gly Val Thr Gly Ala Thr Gly Ala
                485                 490                 495

Thr Gly Glu Thr Gly Ala Thr Gly Ser Thr Gly Ala Thr Gly Thr Thr
            500                 505                 510

Gly Ala Thr Gly Glu Thr Gly Pro Thr Gly Pro Thr Gly Ser Thr Gly
        515                 520                 525

Ala Thr Gly Glu Thr Gly Pro Thr Gly Pro Thr Gly Ala Thr Gly Val
    530                 535                 540
```

```
Thr Gly Ala Thr Gly Ala Thr Gly Ala Thr Gly Glu Thr Gly Ser Thr
545                 550                 555                 560

Gly Pro Met Gly Ala Thr Gly Glu Thr Gly Ser Thr Gly Ser Thr Gly
                565                 570                 575

Val Thr Gly Ala Thr Gly Ala Thr Gly Val Thr Gly Ala Thr Gly Glu
            580                 585                 590

Thr Gly Ser Thr Gly Ala Thr Gly Ser Thr Gly Ala Thr Gly Glu Thr
        595                 600                 605

Gly Pro Thr Gly Pro Thr Gly Pro Thr Gly Pro Thr Gly Thr Thr Gly
    610                 615                 620

Val Thr Gly Val Thr Gly Glu Thr Gly Pro Thr Gly Ala Thr Gly Glu
625                 630                 635                 640

Thr Gly Ser Thr Gly Pro Thr Gly Thr Thr Gly Val Thr Gly Glu Thr
                645                 650                 655

Gly Ala Thr Gly Pro Thr Gly Ala Thr Gly Ser Thr Gly Glu Thr Gly
            660                 665                 670

Ala Thr Gly Glu Thr Gly Arg Thr Gly Pro Thr Gly Thr Thr Gly Val
        675                 680                 685

Thr Gly Glu Thr Gly Ala Thr Gly Glu Thr Gly Pro Thr Gly Ala Thr
    690                 695                 700

Gly Ser Thr Gly Ala Thr Gly Pro Thr Gly Ala Thr Gly Ala Thr Gly
705                 710                 715                 720

Ala Thr Gly Glu Thr Gly Pro Thr Gly Ala Thr Gly Glu Thr Gly Ala
                725                 730                 735

Thr Gly Ala Thr Gly Ser Thr Gly Ala Thr Gly Pro Thr Gly Pro Thr
            740                 745                 750
```

```
Gly Thr Thr Gly Val Thr Gly Ala Thr Gly Pro Thr Gly Ala Thr Gly
        755                 760                 765


Glu Thr Gly Pro Thr Gly Ala Thr Gly Glu Ala Gly Pro Thr Gly Ser
    770                 775                 780


Thr Gly Ser Thr Gly Pro Thr Gly Ala Thr Gly Ile Thr Gly Ala Thr
785                 790                 795                 800


Gly Pro Thr Gly Ala Thr Gly Ala Thr Gly Ser Thr Gly Glu Thr Gly
                805                 810                 815


Ser Thr Gly Glu Thr Gly Pro Thr Gly Ser Thr Gly
            820                 825


<210>  200
<211>  150
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Artificial Sequence

<400>  200
atggattcaa ataaaacgag gtgtgctgtt tgtaataaat atcaatgttc ttgtaactcc       60

aaaaaaagaa gtcctaaaac agttattaga gatttagatt atatagatcc atgtgaacct      120

ctttatataa taaatcattg tcataataga                                       150


<210>  201
<211>  50
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  201

Met Asp Ser Asn Lys Thr Arg Cys Ala Val Cys Asn Lys Tyr Gln Cys
1               5                   10                  15


Ser Cys Asn Ser Lys Lys Arg Ser Pro Lys Thr Val Ile Arg Asp Leu
            20                  25                  30
```

Asp Tyr Ile Asp Pro Cys Glu Pro Leu Tyr Ile Ile Asn His Cys His
        35                  40                  45

Asn Arg
    50

<210>  202
<211>  369
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Artificial Sequence

<400>  202
atggattcaa ataaaacgag gtgtgctgtt tgtaataaat atcaatgttc ttgtaactcc  60

aaaaaaagaa gtcctaaaac agttattaga gatttagatt atatagatcc atgtgaacct  120

ctttatataa taaatcattg tcataataga ggtaaaactg gaccaactgg accaaccgga  180

tcgaccggac caacaggacc aactggtgaa accggaccaa ctggagcaac aggaccaaca  240

ggagctactg gagcaactgg agcaactggt gcaactggag caacgggatc aactggagca  300

acaggatcaa ctggggcagc cggagtaact ggtgaaacag gactaacagg gtcaaccgga  360

gcgacagga  369

<210>  203
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  203

Met Asp Ser Asn Lys Thr Arg Cys Ala Val Cys Asn Lys Tyr Gln Cys
1               5                  10                  15

Ser Cys Asn Ser Lys Lys Arg Ser Pro Lys Thr Val Ile Arg Asp Leu
            20                  25                  30

Asp Tyr Ile Asp Pro Cys Glu Pro Leu Tyr Ile Ile Asn His Cys His
        35                  40                  45

Asn Arg Gly Lys Thr Gly Pro Thr Gly Pro Thr Gly Ser Thr Gly Pro
50 55 60

Thr Gly Pro Thr Gly Glu Thr Gly Pro Thr Gly Ala Thr Gly Pro Thr
65 70 75 80

Gly Ala Thr Gly Ala Thr Gly Ala Thr Gly Ala Thr Gly Ala Thr Gly
85 90 95

Ser Thr Gly Ala Thr Gly Ser Thr Gly Ala Ala Gly Val Thr Gly Glu
100 105 110

Thr Gly Leu Thr Gly Ser Thr Gly Ala Thr Gly
115 120

<210> 204
<211> 150
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 204
atggattcaa ataaaacgag gtgtgctgtt tgtaataaat atcaatgttc ttgtaatacc 60

aaaaaaagaa gtcctaaaac agttattaga gatttagatt atatagatcc atgtgaacct 120

ctttatataa tagatcattg tcataataga 150

<210> 205
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 205

Met Asp Ser Asn Lys Thr Arg Cys Ala Val Cys Asn Lys Tyr Gln Cys
1 5 10 15

Ser Cys Asn Thr Lys Lys Arg Ser Pro Lys Thr Val Ile Arg Asp Leu
20 25 30

Asp Tyr Ile Asp Pro Cys Glu Pro Leu Tyr Ile Ile Asp His Cys His
        35                  40                  45

Asn Arg
    50

<210>  206
<211>  399
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Artificial Sequence

<400>  206
atggattcaa ataaaacgag gtgtgctgtt tgtaataaat atcaatgttc ttgtaatacc  60

aaaaaaagaa gtcctaaaac agttattaga gatttagatt atatagatcc atgtgaacct  120

ctttatataa tagatcattg tcataataga ggtaaaacag gaccaacagg accaacagga  180

gcaactggac caaccggacc aactggagca acaggggcaa ccggagcaac aggtccaaca  240

ggatcaactg gcgcaacagg agcaactgga caaacgggag caactggagc aacgggacca  300

acaggagcaa caggagcaac tggagaaaca ggagcaacag gagcaacagg agcaacagga  360

gcaacaggac caacgggagc aactggagaa acaggagca                          399

<210>  207
<211>  133
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  207

Met Asp Ser Asn Lys Thr Arg Cys Ala Val Cys Asn Lys Tyr Gln Cys
1               5                   10                  15

Ser Cys Asn Thr Lys Lys Arg Ser Pro Lys Thr Val Ile Arg Asp Leu
            20                  25                  30

Asp Tyr Ile Asp Pro Cys Glu Pro Leu Tyr Ile Ile Asp His Cys His
        35                  40                  45

```
Asn Arg Gly Lys Thr Gly Pro Thr Gly Pro Thr Gly Ala Thr Gly Pro
    50                  55                  60

Thr Gly Pro Thr Gly Ala Thr Gly Ala Thr Gly Ala Thr Gly Pro Thr
65                  70                  75                  80

Gly Ser Thr Gly Ala Thr Gly Ala Thr Gly Gln Thr Gly Ala Thr Gly
                85                  90                  95

Ala Thr Gly Pro Thr Gly Ala Thr Gly Ala Thr Gly Glu Thr Gly Ala
            100                 105                 110

Thr Gly Ala Thr Gly Ala Thr Gly Ala Thr Gly Pro Thr Gly Ala Thr
        115                 120                 125

Gly Glu Thr Gly Ala
    130
```

<210>  208
<211>  150
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Artificial Sequence

<400>  208

```
atggattcaa ataaaacgag gtgtgctgtt tgtaataaat atcaatgttc ttgtaactcc       60

aaaaaaagaa gtcctaaaac agttattaga gatttagatt atatagatcc atgtgaacct      120

ctttatataa tagatcattg tcataataga                                       150
```

<210>  209
<211>  50
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  209

```
Met Asp Ser Asn Lys Thr Arg Cys Ala Val Cys Asn Lys Tyr Gln Cys
1               5                   10                  15
```

Ser Cys Asn Ser Lys Lys Arg Ser Pro Lys Thr Val Ile Arg Asp Leu
            20                  25                  30

Asp Tyr Ile Asp Pro Cys Glu Pro Leu Tyr Ile Ile Asp His Cys His
        35                  40                  45

Asn Arg
    50

<210>  210
<211>  399
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Artificial Sequence

<400>  210
atggattcaa ataaaacgag gtgtgctgtt tgtaataaat atcaatgttc ttgtaactcc       60

aaaaaaagaa gtcctaaaac agttattaga gatttagatt atatagatcc atgtgaacct      120

ctttatataa tagatcattg tcataataga ggtaaaacag gaccaacagg agcaacaggt      180

ccaacgggac caaccggagc aacgggatca actggtccaa caggatcaac tggagcaact      240

ggagcaacag ggtcaaccgg agcgactgga gaaacaggac caactggggt aacgggaatc      300

acgggaccga ctggtgtaac tggagcaaca gggttcacag gactgactgg agcaactgga      360

gcgacaggaa atacaggtcc aacaggacca accggagca                              399

<210>  211
<211>  133
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  211

Met Asp Ser Asn Lys Thr Arg Cys Ala Val Cys Asn Lys Tyr Gln Cys
1               5                   10                  15

Ser Cys Asn Ser Lys Lys Arg Ser Pro Lys Thr Val Ile Arg Asp Leu
            20                  25                  30

Asp Tyr Ile Asp Pro Cys Glu Pro Leu Tyr Ile Ile Asp His Cys His
35 40 45

Asn Arg Gly Lys Thr Gly Pro Thr Gly Ala Thr Gly Pro Thr Gly Pro
50 55 60

Thr Gly Ala Thr Gly Ser Thr Gly Pro Thr Gly Ser Thr Gly Ala Thr
65 70 75 80

Gly Ala Thr Gly Ser Thr Gly Ala Thr Gly Glu Thr Gly Pro Thr Gly
85 90 95

Val Thr Gly Ile Thr Gly Pro Thr Gly Val Thr Gly Ala Thr Gly Phe
100 105 110

Thr Gly Leu Thr Gly Ala Thr Gly Ala Thr Gly Asn Thr Gly Pro Thr
115 120 125

Gly Pro Thr Gly Ala
130

<210> 212
<211> 150
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 212
atggattcaa ataaaacgag gtgtactgtt tgtaataaat atcaatgttc atgtaaccac 60

aaaaaaagaa gtcctaaaac agttattaga gatttagatt atatagatcc atgtgaaccg 120

ctttatataa tagatcattg tcataataga 150

<210> 213
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 213

Met Asp Ser Asn Lys Thr Arg Cys Thr Val Cys Asn Lys Tyr Gln Cys
1  5  10  15

Ser Cys Asn His Lys Lys Arg Ser Pro Lys Thr Val Ile Arg Asp Leu
            20  25  30

Asp Tyr Ile Asp Pro Cys Glu Pro Leu Tyr Ile Ile Asp His Cys His
        35  40  45

Asn Arg
    50

<210>  214
<211>  285
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Artificial Sequence

<400>  214
atggattcaa ataaaacgag gtgtactgtt tgtaataaat atcaatgttc atgtaaccac  60

aaaaaaagaa gtcctaaaac agttattaga gatttagatt atatagatcc atgtgaaccg  120

ctttatataa tagatcattg tcataataga ggtaaaacag gtccaacggg gccaaccgga  180

gcaactggag caacaggtgc aacgggatca actgggccga caggagtaac tggtgcaaac  240

tcatatacaa aacaaacact gccaacgacg tcaacagaga agaaa  285

<210>  215
<211>  95
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  215

Met Asp Ser Asn Lys Thr Arg Cys Thr Val Cys Asn Lys Tyr Gln Cys
1  5  10  15

Ser Cys Asn His Lys Lys Arg Ser Pro Lys Thr Val Ile Arg Asp Leu
            20  25  30

```
Asp Tyr Ile Asp Pro Cys Glu Pro Leu Tyr Ile Ile Asp His Cys His
        35                  40                  45


Asn Arg Gly Lys Thr Gly Pro Thr Gly Pro Thr Gly Ala Thr Gly Ala
    50                  55                  60


Thr Gly Ala Thr Gly Ser Thr Gly Pro Thr Gly Val Thr Gly Ala Asn
65                  70                  75                  80


Ser Tyr Thr Lys Gln Thr Leu Pro Thr Thr Ser Thr Glu Lys Lys
                85                  90                  95


<210>  216
<211>  150
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Artificial Sequence

<400>  216
atggattcaa ataaaacgag gtgtactgtt tgtaataaat atcaatgttc atgtaacccc       60

aaaaaaagaa gtcctaaaac agttattaga gatttagatt atataaatcc atgtgaaccg      120

ctttatataa tagatcattg tcataataga                                       150


<210>  217
<211>  50
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  217

Met Asp Ser Asn Lys Thr Arg Cys Thr Val Cys Asn Lys Tyr Gln Cys
1               5                   10                  15


Ser Cys Asn Pro Lys Lys Arg Ser Pro Lys Thr Val Ile Arg Asp Leu
            20                  25                  30


Asp Tyr Ile Asn Pro Cys Glu Pro Leu Tyr Ile Ile Asp His Cys His
        35                  40                  45
```

Asn Arg
50

<210> 218
<211> 1266
<212> DNA
<213> Artificial Sequence

<220>
<223> Artifical Sequence

<400> 218
atggattcaa ataaaacgag gtgtactgtt tgtaataaat atcaatgttc atgtaacccc 60

aaaaaaagaa gtcctaaaac agttattaga gatttagatt atataaatcc atgtgaaccg 120

ctttatataa tagatcattg tcataataga ggtaaaacag gtccaacggg gccaaccgga 180

gcaaccggag caacggggcc aaccggacca actggagcaa cagggccaac cggagcgact 240

ggagcaaccg gaccaacggg atcaacaggt cctacaggat caaccggagc aacaggaccg 300

actggggcta caggagtaac tggagcaacg ggagcaactg gagcaacggg agtaactggg 360

gcaacaggac caacgggacc aacagggtta accggagcga ctggagcaac aggaacgact 420

ggggctacag gagcaactgg ggcaacggga gtaactggag caacaggacc gactggggca 480

acgggagtaa ctggagcaac gggagtaact ggggcaacag gaccaactgg agcaacagga 540

tcgactggag aaactggaac aacaggagta actggagcaa cgggagtaac tggagcaaca 600

ggtccaaccg ggtcaatcgg atcaacggga gcaactgggg caaccggacc aactggagca 660

accggggcaa caggagcaac cggaccaacg ggagaaaccg gaccaaccgg accaacaggc 720

ccaacgggaa tcaccgggcc aaccggagca actggttcag gaggcgtaat cccatttgca 780

tcaggaggca cagtaacaat aaattcacta ttaactgggg tacctaatac cggaggtatt 840

attgcatttg gcaatagtac tactagtgta gggattggta atgctacagt aaatcttcaa 900

aatattaata atgaagcgtt tgtcgttcca catgctggag caattacaaa tgttgctgca 960

ttctttaata ttacagttgc tcttaatata gctgttttag gtacagctac tattacggca 1020

caagtatgga aatcacaaaa tgcatcatct aacgtatttg cacctttagc atcgactctt 1080

ataagcttta caccattagc tggtgccata gctgcattta ctacattaaa tggtgctctt 1140

gcaaatttaa atgaaccagt aaatgttgga gatcgtttaa ttatggtatt ctctgtggct 1200

actacagggt taagtgtaat aactgctatt acaggtacag caagtgcggg tattacaatt 1260

agttga 1266

<210> 219
<211> 421
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal Signal Sequence

<400> 219

Met Asp Ser Asn Lys Thr Arg Cys Thr Val Cys Asn Lys Tyr Gln Cys
1 5 10 15

Ser Cys Asn Pro Lys Lys Arg Ser Pro Lys Thr Val Ile Arg Asp Leu
20 25 30

Asp Tyr Ile Asn Pro Cys Glu Pro Leu Tyr Ile Ile Asp His Cys His
35 40 45

Asn Arg Gly Lys Thr Gly Pro Thr Gly Pro Thr Gly Ala Thr Gly Ala
50 55 60

Thr Gly Pro Thr Gly Pro Thr Gly Ala Thr Gly Pro Thr Gly Ala Thr
65 70 75 80

Gly Ala Thr Gly Pro Thr Gly Ser Thr Gly Pro Thr Gly Ser Thr Gly
85 90 95

Ala Thr Gly Pro Thr Gly Ala Thr Gly Val Thr Gly Ala Thr Gly Ala
100 105 110

Thr Gly Ala Thr Gly Val Thr Gly Ala Thr Gly Pro Thr Gly Pro Thr
115 120 125

Gly Leu Thr Gly Ala Thr Gly Ala Thr Gly Thr Thr Gly Ala Thr Gly
130 135 140

Ala Thr Gly Ala Thr Gly Val Thr Gly Ala Thr Gly Pro Thr Gly Ala
145 150 155 160

```
Thr Gly Val Thr Gly Ala Thr Gly Val Thr Gly Ala Thr Gly Pro Thr
                165                 170                 175

Gly Ala Thr Gly Ser Thr Gly Glu Thr Gly Thr Thr Gly Val Thr Gly
            180                 185                 190

Ala Thr Gly Val Thr Gly Ala Thr Gly Pro Thr Gly Ser Ile Gly Ser
        195                 200                 205

Thr Gly Ala Thr Gly Ala Thr Gly Pro Thr Gly Ala Thr Gly Ala Thr
    210                 215                 220

Gly Ala Thr Gly Pro Thr Gly Glu Thr Gly Pro Thr Gly Pro Thr Gly
225                 230                 235                 240

Pro Thr Gly Ile Thr Gly Pro Thr Gly Ala Thr Gly Ser Gly Gly Val
                245                 250                 255

Ile Pro Phe Ala Ser Gly Gly Thr Val Thr Ile Asn Ser Leu Leu Thr
            260                 265                 270

Gly Val Pro Asn Thr Gly Gly Ile Ile Ala Phe Gly Asn Ser Thr Thr
        275                 280                 285

Ser Val Gly Ile Gly Asn Ala Thr Val Asn Leu Gln Asn Ile Asn Asn
    290                 295                 300

Glu Ala Phe Val Val Pro His Ala Gly Ala Ile Thr Asn Val Ala Ala
305                 310                 315                 320

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

Thr Ile Thr Ala Gln Val Trp Lys Ser Gln Asn Ala Ser Ser Asn Val
            340                 345                 350

Phe Ala Pro Leu Ala Ser Thr Leu Ile Ser Phe Thr Pro Leu Ala Gly
        355                 360                 365

Ala Ile Ala Ala Phe Thr Thr Leu Asn Gly Ala Leu Ala Asn Leu Asn
    370                 375                 380
```

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Glu Pro Val Asn Val Gly Asp Arg Leu Ile Met Val Phe Ser Val Ala
385                 390                 395                 400


Thr Thr Gly Leu Ser Val Ile Thr Ala Ile Thr Gly Thr Ala Ser Ala
                405                 410                 415


Gly Ile Thr Ile Ser
            420


<210>  220
<211>  395
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  220

Gly Val Thr Gly Ala Thr Gly Ala Thr Gly Pro Thr Gly Ala Thr Gly
1               5                   10                  15


Ala Thr Gly Ala Thr Gly Pro Thr Gly Val Thr Gly Ala Thr Gly Ala
            20                  25                  30


Ala Gly Gly Asp Thr Gly Ala Thr Gly Ala Thr Gly Gln Thr Gly Glu
        35                  40                  45


Thr Gly Val Ala Gly Ala Thr Gly Ala Thr Gly Gln Thr Gly Glu Thr
    50                  55                  60


Gly Val Ala Gly Ala Thr Gly Ala Thr Gly Gln Thr Gly Glu Thr Gly
65                  70                  75                  80


Val Ala Gly Ala Thr Gly Ala Thr Gly Gln Thr Gly Glu Thr Gly Val
                85                  90                  95


Ala Gly Ala Thr Gly Ala Thr Gly Gln Thr Gly Glu Thr Gly Val Ala
            100                 105                 110


Gly Ala Thr Gly Ala Thr Gly Gln Thr Gly Glu Thr Gly Val Ala Gly
        115                 120                 125
```

```
Ala Thr Gly Ala Thr Gly Gln Thr Gly Glu Thr Gly Val Ala Gly Ala
    130                 135                 140

Thr Gly Ala Thr Gly Gln Thr Gly Glu Thr Gly Val Ala Gly Ala Thr
145                 150                 155                 160

Gly Ala Thr Gly Gln Thr Gly Glu Thr Gly Val Ala Gly Ala Thr Gly
                165                 170                 175

Ala Thr Gly Gln Thr Gly Glu Thr Gly Lys Ala Gly Ala Thr Gly Ala
            180                 185                 190

Thr Gly Gln Thr Gly Glu Thr Gly Val Thr Gly Ala Thr Gly Ala Thr
        195                 200                 205

Gly Gln Thr Gly Glu Thr Gly Glu Ala Gly Ala Thr Gly Ala Ala Gly
    210                 215                 220

Gln Thr Gly Glu Thr Gly Val Thr Gly Ala Thr Gly Ala Thr Gly Gln
225                 230                 235                 240

Thr Gly Glu Thr Gly Val Ala Gly Ala Thr Gly Ala Thr Gly Gln Thr
                245                 250                 255

Gly Glu Thr Gly Val Ala Gly Ala Thr Gly Ala Thr Gly Ala Thr Gly
            260                 265                 270

Gln Thr Gly Glu Thr Gly Val Val Gly Ala Thr Gly Ala Thr Gly Gln
        275                 280                 285

Thr Gly Glu Thr Gly Val Val Gly Ala Thr Gly Ala Thr Gly Gln Thr
    290                 295                 300

Gly Glu Thr Gly Val Ala Gly Ala Thr Gly Ala Thr Gly Ala Thr Gly
305                 310                 315                 320

Gln Thr Gly Glu Thr Gly Val Ala Gly Ala Thr Gly Ala Thr Gly Gln
                325                 330                 335
```

```
Thr Gly Glu Thr Gly Val Ala Gly Ala Thr Gly Ala Thr Gly Gln Thr
            340                 345                 350


Gly Glu Thr Gly Val Ala Gly Ala Thr Gly Ala Thr Gly Gln Thr Gly
        355                 360                 365


Glu Thr Gly Val Ala Gly Ala Thr Gly Ala Thr Gly Gln Thr Gly Glu
    370                 375                 380


Ala Gly Val Ala Gly Val Thr Gly Ala Thr Gly
385                 390                 395


<210>  221
<211>  165
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Artificial Sequence

<400>  221
tgaaaagatg gggaattctc catcttttt cttttgtctg gagtggtgag atatacgaca       60

tacaacgaat gagcataaca tgaatagttt ataaaatcgc aaaaaatttt tcggaaggag      120

agagcgaaaa ttaacaataa gcgggctaac gcattcaata agaag                      165


<210>  222
<211>  510
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  222

Gly Val Thr Gly Ala Thr Gly Ala Thr Gly Ala Thr Gly Ala Gln Gly
1               5                   10                  15


Pro Pro Gly Ala Pro Gly Pro Gln Gly Val Ala Gly Ala Met Gly Pro
            20                  25                  30


Arg Gly Glu Ile Gly Pro Gln Gly Val Ala Gly Ala Thr Gly Ala Thr
        35                  40                  45
```

```
Gly Pro Gln Gly Glu Met Gly Leu Gln Gly Val Ala Gly Val Thr Gly
    50                  55                  60

Ala Ser Gly Pro Gln Gly Glu Ile Gly Pro Gln Gly Val Ala Gly Val
65                  70                  75                  80

Thr Gly Ala Pro Gly Pro Gln Gly Glu Ile Gly Pro Gln Gly Val Ala
                85                  90                  95

Gly Ala Thr Gly Val Pro Gly Pro Gln Gly Glu Ile Gly Pro Gln Gly
            100                 105                 110

Val Ala Gly Glu Thr Gly Ala Thr Gly Pro Gln Gly Glu Met Gly Leu
        115                 120                 125

Gln Gly Val Ala Gly Val Thr Gly Ala Thr Gly Pro Gln Gly Glu Met
    130                 135                 140

Gly Pro Gln Gly Val Ala Gly Val Thr Gly Ala Thr Gly Pro Gln Gly
145                 150                 155                 160

Glu Ile Gly Pro Gln Gly Val Ala Gly Val Thr Gly Ala Pro Gly Pro
                165                 170                 175

Gln Gly Glu Ile Gly Pro Gln Gly Val Ala Gly Val Thr Gly Ala Pro
            180                 185                 190

Gly Pro Gln Gly Glu Met Gly Leu Gln Gly Val Ala Gly Val Thr Gly
        195                 200                 205

Ala Thr Gly Pro Gln Gly Ile Ile Gly Ala Thr Gly Leu Arg Gly Leu
    210                 215                 220

Ala Gly Ile Thr Gly Ala Thr Gly Glu Arg Gly Leu Ala Gly Ile Thr
225                 230                 235                 240

Gly Ala Thr Gly Val Gln Gly Val Ala Gly Ser Thr Gly Ala Thr Gly
                245                 250                 255

Ser Gln Gly Ile Thr Gly Ala Thr Gly Val Gln Gly Val Thr Gly Ser
            260                 265                 270
```

```
Thr Gly Ala Thr Gly Ser Gln Gly Ile Thr Gly Ala Thr Gly Val Gln
        275                 280                 285

Gly Val Thr Gly Ser Thr Gly Ala Thr Gly Ser Gln Gly Ile Thr Gly
    290                 295                 300

Ala Thr Gly Val Gln Gly Val Thr Gly Ser Thr Gly Ala Thr Gly Ser
305                 310                 315                 320

Gln Gly Ile Thr Gly Ala Thr Gly Val Gln Gly Val Ala Gly Ser Thr
                325                 330                 335

Gly Ala Thr Gly Ser Gln Gly Ile Thr Gly Ala Thr Gly Val Gln Gly
            340                 345                 350

Val Thr Gly Ser Thr Gly Ala Thr Gly Ala Arg Gly Thr Thr Gly Val
        355                 360                 365

Thr Gly Thr Thr Gly Pro Ser Gly Ser Gly Leu Met Glu Val Phe Leu
    370                 375                 380

Ser Thr Asp Gln Ser Val Gly Asn Asn Asp Phe Leu Gly Thr Gly Asn
385                 390                 395                 400

Ser Ser Ala Ser Phe Val Arg Ser Ser Ile Val Ile Pro Glu Asn Ala
                405                 410                 415

Thr Ile Arg Ser Leu Thr Leu Asn Ile Arg Asp His Ala Leu Ser Ala
            420                 425                 430

Gly Gln Thr Ala Ser Ala Gln Ile Phe Val Ser Thr Asn Cys Gly Phe
        435                 440                 445

Thr Ser Val Ala Thr Gly Ile Ile Ala Thr Val Thr Gly Pro Asn Ser
    450                 455                 460

Ser Thr Thr Pro Asn Cys Cys Ala Lys Val Ile Ala Asn Tyr Pro Val
465                 470                 475                 480
```

```
Ser Ser Cys Thr Leu Leu Ser Val Gln Val Ser Thr Thr Gly Gly Ala
                485                 490                 495


Phe Ser Asn Gly Val Ser Ala Thr Val Leu Phe Asn Thr Val
            500                 505                 510


<210>  223
<211>  156
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Artifical Sequence

<400>  223
tgttgaaaca tattattgag cattgggttt tatatgacct aatgttcttt ttattttaag       60

atacatattt aaatcattct aatattctag gtgcattaat tatctcaata agtagacttt      120

tgaatatgat aaaaagggac aggaggtgaa gtcgca                                156


<210>  224
<211>  778
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  N-terminal Signal Sequence

<400>  224

Gly Lys Thr Gly Pro Thr Gly Ala Thr Gly Pro Thr Gly Ser Met Gly
1               5                   10                  15


Pro Thr Gly Val Thr Gly Ser Thr Gly Ala Thr Gly Pro Thr Gly Ser
            20                  25                  30


Thr Gly Val Thr Gly Glu Thr Gly Ser Thr Gly Thr Thr Gly Pro Ser
        35                  40                  45


Gly Ser Thr Gly Pro Thr Gly Ala Thr Gly Ser Thr Gly Glu Thr Gly
    50                  55                  60


Ala Thr Gly Ser Thr Gly Ala Thr Gly Glu Thr Gly Pro Thr Gly Pro
65                  70                  75                  80
```

```
Thr Gly Thr Thr Gly Val Thr Gly Glu Thr Gly Ala Thr Gly Pro Thr
                85                  90                  95

Gly Ala Thr Gly Ala Thr Gly Glu Thr Gly Ser Thr Gly Pro Thr Gly
            100                 105                 110

Ala Thr Gly Glu Thr Gly Glu Thr Gly Ser Thr Gly Pro Thr Gly Ala
        115                 120                 125

Thr Gly Ser Thr Gly Ala Thr Gly Pro Thr Gly Ala Thr Gly Ser Thr
    130                 135                 140

Gly Ala Thr Gly Ser Thr Gly Ala Thr Gly Ser Thr Gly Ala Thr Gly
145                 150                 155                 160

Pro Thr Gly Ala Thr Gly Ser Thr Gly Glu Thr Gly Pro Thr Gly Glu
                165                 170                 175

Thr Gly Ser Thr Gly Ala Thr Gly Ser Thr Gly Ala Thr Gly Glu Thr
            180                 185                 190

Gly Pro Thr Gly Thr Thr Gly Val Thr Gly Glu Thr Gly Ala Thr Gly
        195                 200                 205

Pro Thr Gly Ala Thr Gly Ala Thr Gly Glu Thr Gly Glu Thr Gly Ser
    210                 215                 220

Thr Gly Pro Thr Gly Ala Thr Gly Glu Thr Gly Glu Thr Gly Ser Thr
225                 230                 235                 240

Gly Pro Thr Gly Ala Thr Gly Ser Thr Gly Ala Thr Gly Pro Thr Gly
                245                 250                 255

Ala Thr Gly Ser Thr Gly Ala Thr Gly Ser Thr Gly Ala Thr Gly Ser
            260                 265                 270

Thr Gly Ala Thr Gly Pro Thr Gly Ala Thr Gly Ser Thr Gly Glu Thr
        275                 280                 285

Gly Pro Thr Gly Glu Thr Gly Ser Thr Gly Ala Thr Gly Ser Thr Gly
    290                 295                 300
```

```
Ala Thr Gly Glu Thr Gly Pro Thr Gly Ala Thr Gly Ser Thr Gly Ala
305                 310                 315                 320

Thr Gly Glu Thr Gly Ala Thr Gly Pro Thr Gly Pro Thr Gly Thr Thr
                325                 330                 335

Gly Val Thr Gly Ala Thr Gly Pro Thr Gly Ala Thr Gly Glu Thr Gly
            340                 345                 350

Pro Thr Gly Ala Thr Gly Glu Ala Gly Pro Thr Gly Ser Thr Gly Ala
        355                 360                 365

Thr Gly Pro Thr Gly Ala Thr Gly Ile Thr Gly Ala Thr Gly Pro Thr
    370                 375                 380

Gly Ser Thr Gly Ala Thr Gly Ser Thr Gly Glu Thr Gly Ser Thr Gly
385                 390                 395                 400

Glu Thr Gly Pro Thr Gly Ala Thr Gly Val Thr Gly Ala Thr Gly Pro
                405                 410                 415

Thr Gly Glu Thr Gly Ser Thr Gly Pro Met Gly Ala Thr Gly Glu Thr
            420                 425                 430

Gly Ser Thr Gly Ser Thr Gly Val Thr Gly Ala Thr Gly Ala Thr Gly
        435                 440                 445

Glu Thr Gly Ala Thr Gly Ser Thr Gly Ala Thr Gly Thr Thr Gly Ala
    450                 455                 460

Thr Gly Glu Thr Gly Pro Thr Gly Pro Thr Gly Ser Thr Gly Ala Thr
465                 470                 475                 480

Gly Glu Thr Gly Pro Thr Gly Pro Thr Gly Ala Thr Gly Val Thr Gly
                485                 490                 495

Ala Thr Gly Ala Thr Gly Ala Thr Gly Glu Thr Gly Ser Thr Gly Pro
            500                 505                 510
```

```
Met Gly Ala Thr Gly Glu Thr Gly Ser Thr Gly Ser Thr Gly Val Thr
        515                 520                 525

Gly Ala Thr Gly Ala Thr Gly Val Thr Gly Ala Thr Gly Glu Thr Gly
    530                 535                 540

Ser Thr Gly Ala Thr Gly Ser Thr Gly Ala Thr Gly Glu Thr Gly Pro
545                 550                 555                 560

Thr Gly Pro Thr Gly Pro Thr Gly Pro Thr Gly Thr Thr Gly Val Thr
                565                 570                 575

Gly Val Thr Gly Glu Thr Gly Pro Thr Gly Ala Thr Gly Glu Thr Gly
            580                 585                 590

Ser Thr Gly Pro Thr Gly Thr Thr Gly Val Thr Gly Glu Thr Gly Ala
        595                 600                 605

Thr Gly Pro Thr Gly Ala Thr Gly Ser Thr Gly Glu Thr Gly Ala Thr
    610                 615                 620

Gly Glu Thr Gly Arg Thr Gly Pro Thr Gly Thr Thr Gly Val Thr Gly
625                 630                 635                 640

Glu Thr Gly Ala Thr Gly Glu Thr Gly Pro Thr Gly Ala Thr Gly Ser
                645                 650                 655

Thr Gly Ala Thr Gly Pro Thr Gly Ala Thr Gly Ala Thr Gly Ala Thr
            660                 665                 670

Gly Glu Thr Gly Pro Thr Gly Ala Thr Gly Glu Thr Gly Ala Thr Gly
        675                 680                 685

Ala Thr Gly Ser Thr Gly Ala Thr Gly Pro Thr Gly Pro Thr Gly Thr
    690                 695                 700

Thr Gly Val Thr Gly Ala Thr Gly Pro Thr Gly Ala Thr Gly Glu Thr
705                 710                 715                 720

Gly Pro Thr Gly Ala Thr Gly Glu Ala Gly Pro Thr Gly Ser Thr Gly
                725                 730                 735
```

Ser Thr Gly Pro Thr Gly Ala Thr Gly Ile Thr Gly Ala Thr Gly Pro
740 745 750

Thr Gly Ala Thr Gly Ala Thr Gly Ser Thr Gly Glu Thr Gly Ser Thr
755 760 765

Gly Glu Thr Gly Pro Thr Gly Ser Thr Gly
770 775

<210> 225
<211> 371
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificical Sequence

<400> 225
atattttaga aagtgaaaaa tacagataaa agcctttgct gattcatttt tctggattta 60

tttaaaagaa cgattggaga gtattcttca gccgtatctt ttttttgttg ctaaaaatat 120

taataatttt acttgaggat tttaatagat taagaaattt ttaattctga tacctatatt 180

gtattacagg aatattttag aaataagcat atcccatttt cattttacag tttaatagca 240

tgctagagaa atacataatt atcagactac catgaatgag atgattatcc gatttttttc 300

tgtcacatta caattgtcca atatcaatct atttcacgag aatagtatgt atatgatggg 360

aggtgataat a 371