



US 20250250556A1

(19) **United States**

(12) **Patent Application Publication** (10) **Pub. No.: US 2025/0250556 A1**
Oehlenschlaeger et al. (43) **Pub. Date:** **Aug. 7, 2025**

(54) **POLYPEPTIDES HAVING PEPTIDOGLYCAN DEGRADING ACTIVITY AND POLYNUCLEOTIDES ENCODING SAME**

(71) Applicant: **Novozymes A/S**, Bagsvaerd (DK)

(72) Inventors: **Christian Berg Oehlenschlaeger**, Valby (DK); **Dorotea Raventos Segura**, Runsted (DK); **Jesper Salomon**, Holte (DK); **Fabian Barrientos Garcia**, Birkerod (DK); **Lillian Eva Tang Baltsen**, Bagsvaerd (DK); **Christian Bech Rosen**, Kobenhavn (DK)

(73) Assignee: **Novozymes A/S**, Bagsvaerd (DK)

(21) Appl. No.: **19/095,734**

(22) Filed: **Mar. 31, 2025**

Related U.S. Application Data

(62) Division of application No. 18/586,709, filed on Feb. 26, 2024, now Pat. No. 12,297,470, which is a divi-

sion of application No. 17/298,836, filed on Jun. 1, 2021, now Pat. No. 11,959,111, filed as application No. PCT/EP2019/086399 on Dec. 19, 2019.

(30) **Foreign Application Priority Data**

Dec. 21, 2018 (EP) 18215408.8

Publication Classification

(51) **Int. Cl.**
C12N 9/80 (2006.01)
C11D 3/386 (2006.01)

(52) **U.S. Cl.**
CPC *C12N 9/80* (2013.01); *C11D 3/38636* (2013.01); *C12Y 305/01028* (2013.01)

(57) **ABSTRACT**

The present invention relates to cleaning compositions comprising polypeptides having peptidoglycan degradation activity, as well as use of the cleaning compositions for cleaning of an item such as a textile or a surface.

Specification includes a Sequence Listing.

POLYPEPTIDES HAVING PEPTIDOGLYCAN DEGRADING ACTIVITY AND POLYNUCLEOTIDES ENCODING SAME

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a division of U.S. application Ser. No. 18/586,709 filed Feb. 26, 2024, now pending, which is a division of U.S. application Ser. No. 17/298,836 filed on Jun. 1, 2021, now U.S. Pat. No. 11,959,111, which is a 35 U.S.C. 371 national application of international application no. PCT/EP2019/086399 filed Dec. 19, 2019, which claims priority or the benefit under 35 U.S.C. 119 of EP application no. 18215408.8 filed Dec. 21, 2018. The disclosure of each application is fully incorporated herein by reference.

REFERENCE TO A SEQUENCE LISTING

[0002] This application contains a Sequence Listing in computer readable form, which is incorporated herein by reference. The Sequence Listing was created on Mar. 7, 2025 and is named SQ.xml and is 193,658 bytes in size.

BACKGROUND OF THE INVENTION

Field of the Invention

[0003] The present invention relates to polypeptides having peptidoglycan degrading activity, polynucleotides encoding the polypeptides and catalytic domains belonging to peptidoglycan degrading enzyme families. The invention further relates to compositions comprising such polypeptides, in particular cleaning compositions, use of polypeptides having peptidoglycan degrading activity in cleaning processes and/or for removal or reduction of bacterial-derived peptidoglycan, and methods for removal or reduction of peptidoglycan. The invention further relates to nucleic acid constructs, vectors, and host cells comprising polynucleotides encoding the polypeptides as well as methods of producing and using the polypeptides and catalytic domains.

Description of the Related Art

[0004] Enzymes have been used in detergents for decades. Usually, a cocktail of various enzymes is added to detergent compositions. The enzyme cocktail often comprises various enzymes, wherein each enzyme targets a specific substrate, e.g., amylases are active towards starch stains, proteases on protein stains and so forth. Textiles and surfaces such as laundry and dishes become soiled with many different types of soiling. The soiling may be composed of proteins, grease, starch etc. Complex stains composed of different organic materials such as food stains, sebum, dead cell material, EPS (extracellular polymeric matrix) from, e.g., biofilm are difficult to remove completely with traditional ADW (automatic dishwashing) and laundry detergent compositions. Contributing to the organic matter is peptidoglycan, originating from the bacterial cell wall. Bacteria are present in high numbers in laundry items. When the bacteria lyse, the destroyed cells leave a high amount of cell wall-derived peptidoglycan in the textile or on hard surfaces such as the inner surfaces of a washing machine. This peptidoglycan substrate may be sticky or gluing, which when present on textile attracts soils and may cause redeposition or back-staining of soil, resulting in a greying of the textile. Also,

malodors from, e.g., sweat, cigarette smoke and pollution are particularly difficult to remove from, e.g., textiles. Malodor is a growing problem, particularly in laundry, with the changed habits of lower temperature washing, front loading wash machines that save water but leave behind residual water between loads, thus allowing bacterial biofilms to flourish, line drying clothes to save energy rather than appliance drying, and the increased popularity of synthetic fabrics, such as athletic wear, that appear to retain odors more than natural fabrics. In conventional detergent compositions such as laundry detergents the above problems are often solved by adding perfumes. This solution is not completely effective, however, as it is short term and furthermore only serves to mask malodor rather than dealing with the underlying cause of malodor. There is thus a need in the art for new solutions for overcoming the problems of malodor and redeposition.

SUMMARY OF THE INVENTION

[0005] The invention relates to a cleaning composition comprising a peptidoglycan degradation enzyme, at least one surfactant and at least one additional cleaning component selected from builders and bleach components. The cleaning composition may, e.g., comprise a peptidoglycan degradation enzyme, at least 5 wt % anionic surfactants, and at least one additional cleaning component selected from at least one builder and at least one bleach component.

[0006] The invention further relates to the use of such a composition for cleaning of an item such as a textile or a surface. The invention further relates to a method of cleaning an item, comprising the steps of:

[0007] a) contacting the item with a solution comprising a peptidoglycan degradation enzyme having peptidoglycan lyase activity and preferably N-acetylmuramyl-L-alanine amidase activity; and a cleaning component, wherein the cleaning component is selected from 5 to 60 wt % of at least one surfactant; 5 to 50 wt % of at least one builder; and 1 to 20 wt % of at least one bleach component; and optionally

[0008] b) rinsing the item,
wherein the item is preferably a textile.

Overview of Sequences

SEQ ID NO: 1 DNA encoding full length polypeptide from *Hamadaea tsunoensis*

SEQ ID NO: 2 polypeptide derived from SEQ ID NO: 1

SEQ ID NO: 3 mature polypeptide obtained from *Hamadaea tsunoensis*

SEQ ID NO: 4 DNA encoding full length polypeptide from *Micromonospora maritima*

SEQ ID NO: 5 polypeptide derived from SEQ ID NO: 4

SEQ ID NO: 6 mature polypeptide obtained from *Micromonospora maritima*

SEQ ID NO: 7 DNA encoding full length polypeptide from *Paenibacillus* sp.

SEQ ID NO: 8 polypeptide derived from SEQ ID NO: 7

SEQ ID NO: 9 mature polypeptide obtained from *Paenibacillus* sp.

SEQ ID NO: 10 DNA encoding full length polypeptide from *Nonomuraea* sp.

SEQ ID NO: 11 polypeptide derived from SEQ ID NO: 10

SEQ ID NO: 12 mature polypeptide obtained from *Nonomuraea* sp.

SEQ ID NO: 13 DNA encoding full length polypeptide from *Lysobacter antibioticus*
SEQ ID NO: 14 polypeptide derived from SEQ ID NO: 13
SEQ ID NO: 15 mature polypeptide obtained from *Lysobacter antibioticus*
SEQ ID NO: 16 DNA encoding full length polypeptide from *Micromonospora* sp.
SEQ ID NO: 17 polypeptide derived from SEQ ID NO: 16
SEQ ID NO: 18 mature polypeptide obtained from *Micromonospora* sp.
SEQ ID NO: 19 DNA encoding full length polypeptide from *Nonomuraea coxensis*
SEQ ID NO: 20 polypeptide derived from SEQ ID NO: 19
SEQ ID NO: 21 mature polypeptide obtained from *Nonomuraea coxensis*
SEQ ID NO: 22 DNA encoding full length polypeptide from *Micromonospora fulvopurpurea*
SEQ ID NO: 23 polypeptide derived from SEQ ID NO: 22
SEQ ID NO: 24 mature polypeptide obtained from *Micromonospora fulvopurpurea*
SEQ ID NO: 25 DNA encoding full length polypeptide from *Alicyclobacillus* sp.
SEQ ID NO: 26 polypeptide derived from SEQ ID NO: 25
SEQ ID NO: 27 mature polypeptide obtained from *Alicyclobacillus* sp.
SEQ ID NO: 28 DNA encoding full length polypeptide from *Halomonas* sp.
SEQ ID NO: 29 polypeptide derived from SEQ ID NO: 28
SEQ ID NO: 30 mature polypeptide obtained from *Halomonas* sp.
SEQ ID NO: 31 DNA encoding full length polypeptide from *Pseudomonas peli*
SEQ ID NO: 32 polypeptide derived from SEQ ID NO: 31
SEQ ID NO: 33 mature polypeptide obtained from *Pseudomonas peli*
SEQ ID NO: 34 DNA encoding full length polypeptide from *Halomonas* sp.
SEQ ID NO: 35 polypeptide derived from SEQ ID NO: 34
SEQ ID NO: 36 mature polypeptide obtained from *Halomonas* sp.
SEQ ID NO: 37 DNA encoding full length polypeptide from *Pseudomonas pseudoalcaligenes*
SEQ ID NO: 38 polypeptide derived from SEQ ID NO: 37
SEQ ID NO: 39 mature polypeptide obtained from *Pseudomonas pseudoalcaligenes*
SEQ ID NO: 40 DNA encoding full length polypeptide from *Tumebacillus* sp.
SEQ ID NO: 41 polypeptide derived from SEQ ID NO: 40
SEQ ID NO: 42 mature polypeptide obtained from *Tumebacillus* sp.
SEQ ID NO: 43 DNA encoding full length polypeptide from *Nonomuraea dietziae*
SEQ ID NO: 44 polypeptide derived from SEQ ID NO: 43
SEQ ID NO: 45 mature polypeptide obtained from *Nonomuraea dietziae*
SEQ ID NO: 46 DNA encoding full length polypeptide from *Laceyella sacchari*
SEQ ID NO: 47 polypeptide derived from SEQ ID NO: 46
SEQ ID NO: 48 mature polypeptide obtained from *Laceyella sacchari*
SEQ ID NO: 49 DNA encoding full length polypeptide from *Thermostaphylospora chromogena*
SEQ ID NO: 50 polypeptide derived from SEQ ID NO: 49
SEQ ID NO: 51 mature polypeptide obtained from *Thermostaphylospora chromogena*
SEQ ID NO: 52 DNA encoding full length polypeptide from *Kribbella aluminosa*
SEQ ID NO: 53 polypeptide derived from SEQ ID NO: 52
SEQ ID NO: 54 mature polypeptide obtained from *Kribbella aluminosa*
SEQ ID NO: 55 DNA encoding full length polypeptide from *Streptomyces griseus*
SEQ ID NO: 56 polypeptide derived from SEQ ID NO: 55
SEQ ID NO: 57 mature polypeptide obtained from *Streptomyces griseus*
SEQ ID NO: 58 DNA encoding full length polypeptide from *Micromonospora peucetia*
SEQ ID NO: 59 polypeptide derived from SEQ ID NO: 58
SEQ ID NO: 60 mature polypeptide obtained from *Micromonospora peucetia*
SEQ ID NO: 61 DNA encoding full length polypeptide from *Bacillus* sp.
SEQ ID NO: 62 polypeptide derived from SEQ ID NO: 61
SEQ ID NO: 63 mature polypeptide obtained from *Bacillus* sp.
SEQ ID NO: 64 DNA encoding full length polypeptide from *Bacillus sporothermodurans*
SEQ ID NO: 65 polypeptide derived from SEQ ID NO: 64
SEQ ID NO: 66 mature polypeptide obtained from *Bacillus sporothermodurans*
SEQ ID NO: 67 DNA encoding full length polypeptide from *Paenibacillus pini*
SEQ ID NO: 68 polypeptide derived from SEQ ID NO: 67
SEQ ID NO: 69 mature polypeptide obtained from *Paenibacillus pini*
SEQ ID NO: 70 DNA encoding full length polypeptide from *Bacillus cohnii*
SEQ ID NO: 71 polypeptide derived from SEQ ID NO: 70
SEQ ID NO: 72 mature polypeptide obtained from *Bacillus cohnii*
SEQ ID NO: 73 DNA encoding full length polypeptide from *Kribbella* sp.
SEQ ID NO: 74 polypeptide derived from SEQ ID NO: 73
SEQ ID NO: 75 mature polypeptide obtained from *Kribbella* sp.
SEQ ID NO: 76 DNA encoding full length polypeptide from *Bacillus* sp.
SEQ ID NO: 77 polypeptide derived from SEQ ID NO: 76
SEQ ID NO: 78 mature polypeptide obtained from *Bacillus* sp.
SEQ ID NO: 79 DNA encoding full length polypeptide from *Bacillus* sp.
SEQ ID NO: 80 polypeptide derived from SEQ ID NO: 79
SEQ ID NO: 81 mature polypeptide obtained from *Bacillus* sp.
SEQ ID NO: 82 DNA encoding full length polypeptide from *Bacillus* sp.
SEQ ID NO: 83 polypeptide derived from SEQ ID NO: 82
SEQ ID NO: 84 mature polypeptide obtained from *Bacillus* sp.
SEQ ID NO: 85 DNA encoding full length polypeptide from *Streptomyces* sp.
SEQ ID NO: 86 polypeptide derived from SEQ ID NO: 85
SEQ ID NO: 87 mature polypeptide obtained from *Streptomyces* sp.
SEQ ID NO: 88 DNA encoding full length polypeptide from *Bacillus* sp.

SEQ ID NO: 89 polypeptide derived from SEQ ID NO: 88
 SEQ ID NO: 90 mature polypeptide obtained from *Bacillus* sp.
 SEQ ID NO: 91 DNA encoding full length polypeptide from *Bacillus* sp.
 SEQ ID NO: 92 polypeptide derived from SEQ ID NO: 91
 SEQ ID NO: 93 mature polypeptide obtained from *Bacillus* sp.
 SEQ ID NO: 94 DNA encoding full length polypeptide from *Nonomuraea guangzhouensis*
 SEQ ID NO: 95 polypeptide derived from SEQ ID NO: 94
 SEQ ID NO: 96 mature polypeptide obtained from *Nonomuraea guangzhouensis*
 SEQ ID NO: 97 DNA encoding full length polypeptide from *Nonomuraea guangzhouensis*
 SEQ ID NO: 98 polypeptide derived from SEQ ID NO: 97
 SEQ ID NO: 99 mature polypeptide obtained from *Nonomuraea guangzhouensis*
 SEQ ID NO: 100 DNA encoding full length polypeptide from *Bacillus cohnii*
 SEQ ID NO: 101 polypeptide derived from SEQ ID NO: 100
 SEQ ID NO: 102 mature polypeptide obtained from *Bacillus cohnii*
 SEQ ID NO: 103 DNA encoding full length polypeptide from *Halomonas* sp.
 SEQ ID NO: 104 polypeptide derived from SEQ ID NO: 103
 SEQ ID NO: 105 mature polypeptide obtained from *Halomonas* sp.
 SEQ ID NO: 106 DNA encoding full length polypeptide from *Lysobacter capsici*
 SEQ ID NO: 107 polypeptide derived from SEQ ID NO: 106
 SEQ ID NO: 108 mature polypeptide obtained from *Lysobacter capsica*
 SEQ ID NO: 109 MKKPLGKIVASTALLISVAFSSSIASA (signal peptide)
 SEQ ID NO: 110 HHHHHHPR (His-tag)
 SEQ ID NO: 111 Motif

Definitions

[0009] Peptidoglycan degrading enzymes: The term “peptidoglycan degrading enzyme” means an enzyme having activity towards peptidoglycan. Peptidoglycan (PGN) is a major component of the bacterial cell envelope in both Gram-positive and Gram-negative bacteria (Human et al., 2009, *J. Innate Immun.* 1: 88-97). The peptidoglycan structure of both Gram-positive and Gram-negative bacteria comprises repeating disaccharide backbones of N-acetylglucosamine (NAG) and β -(1-4)-N-acetylmuramic acid (NAM) that are cross-linked by peptide stem chains attached to the NAM residues (Bourhis et al., 2007, *Microbes Infect.* 9(5): 629-636). The peptide and glycopeptide fragments of PGN are commonly referred to as “muropeptides.” PGN hydrolases are defined by their catalytic specificities. Two classes of these enzymes digest the PGN glycan backbone, N-acetylmuramidases which cleave PGN between the NAG-NAM bond upstream of NAM and N-acetylglucosaminidases which cleave the NAM-NAG bond. In contrast, N-acetylmuramyl-L-alanine amidases cleave between NAM and the first alanine of the peptide chain. Thus, catalysis by N-acetylmuramyl-L-alanine amidases separate the PGN sugar backbones from the stem peptide chain (Fournier et al., 2005, *Clin. Microbiol. Rev.* 18(3): 521-540). The

enzymes of the invention comprise an N-acetylmuramyl-L-alanine amidase (EC 3.5.1.28) domain. In the context of the present invention, N-acetylmuramyl-L-alanine amidases may also be termed peptidoglycan amidohydrolases. The enzymes of the invention comprise in addition to the amidase domain also a peptidoglycan lyase domain (GH23-like). The GH 23 family comprises lysozyme type G (EC 3.2.1.17), peptidoglycan lyase (EC 4.2.2.n1, peptidoglycan lytic extransglycosylase, and 4.2.2.n2, peptidoglycan lytic endotransglycosylase) and chitinases (EC 3.2.1.14). The domain comprised by the enzymes of the invention is a peptidoglycan lyase domain (EC 4.2.2.n1 or 4.2.2.n2). Peptidoglycan lyases are also termed lytic transglycosylases. Peptidoglycan lyases of GH23 constitute Family 1 of the organizational scheme of Blackburn and Clarke (Blackburn et al., 2001, *J. Mol. Evol.* 52(1): 78-84). The enzymes of this family cleave the β -1,4-linkage between N-acetylmuramyl and N-acetylglucosaminyl residues in peptidoglycan. However, unlike lysozyme, peptidoglycan lyases are not hydrolases but rather catalyze an intramolecular transglycosylation to the C-6 hydroxyl group of the muramyl residue, leading to the generation of a terminal 1,6-anhydromuramic acid product that is an acetal, and not a hemiacetal (Höltje, 1975, *J. Bacteriol.* 124(3):1067-1076. The enzymes of the invention are thus distinct from lysozymes.

[0010] The enzymes of the invention preferably comprise an N-acetylmuramyl-L-alanine amidase (EC 3.5.1.28) domain as well as a peptidoglycan lyase domain (EC 4.2.2.n1 or 4.2.2.n2). Thus, in the present invention peptidoglycan degrading enzymes are preferably N-acetylmuramyl-L-alanine amidases (EC 3.5.1.28) and peptidoglycan lyases (EC 4.2.2.n1 or 4.2.2.n2) having amidase and lyase activity towards peptidoglycan.

[0011] For purposes of the present invention, peptidoglycan lyase activity and N-acetylmuramyl-L-alanine amidase activity may be determined according to the procedures described below in the example section.

[0012] The term “allelic variant” means any of two or more alternative forms of a gene occupying the same chromosomal locus. Allelic variation arises naturally through mutation, and may result in polymorphism within populations. Gene mutations can be silent (no change in the encoded polypeptide) or may encode polypeptides having altered amino acid sequences. An allelic variant of a polypeptide is a polypeptide encoded by an allelic variant of a gene.

[0013] A biofilm is organic matter produced by any group of microorganisms in which cells stick to each other or stick to a surface, such as a textile, dishware or hard surface or another kind of surface. These adherent cells are frequently embedded within a self-produced matrix of extracellular polymeric substance (EPS). Biofilm EPS is a polymeric conglomeration generally composed of extracellular DNA, proteins, and polysaccharides. Biofilms may form on living or non-living surfaces. The microbial cells growing in a biofilm are physiologically distinct from planktonic cells of the same organism, which, by contrast, are single cells that may float or swim in a liquid medium. Bacteria living in a biofilm usually have significantly different properties from planktonic bacteria of the same species, as the dense and protected environment of the film allows them to cooperate and interact in various ways. One benefit of this environment for the microorganisms is increased resistance to detergents and antibiotics, as the dense extracellular matrix and the

outer layer of cells protect the interior of the community. The biofilm living bacteria do not lose their ability to live as planktonic cells if the biofilm matrix is compromised. On laundry, biofilm- or EPS-producing bacteria can be found among the following species: *Acinetobacter* sp., *Aeromicrobium* sp., *Brevundimonas* sp., *Microbacterium* sp., *Micrococcus luteus*, *Pseudomonas* sp., *Staphylococcus epidermidis*, and *Stenotrophomonas* sp. In one aspect, the biofilm- or EPS-producing strain is *Pseudomonas*, for example *Pseudomonas aeruginosa*, *Pseudomonas alcaliphila* or *Pseudomonas fluorescens*.

[0014] The term "catalytic domain" means the region of an enzyme containing the catalytic machinery of the enzyme.

[0015] The term "cDNA" means a DNA molecule that can be prepared by reverse transcription from a mature, spliced, mRNA molecule obtained from a eukaryotic or prokaryotic cell. cDNA lacks intron sequences that may be present in the corresponding genomic DNA. The initial, primary RNA transcript is a precursor to mRNA that is processed through a series of steps, including splicing, before appearing as mature spliced mRNA.

[0016] The term "clade" means a group of polypeptides clustered together on the basis of homologous features traced to a common ancestor. Polypeptide clades can be visualized as phylogenetic trees and a clade is a group of polypeptides that consists of a common ancestor and all its lineal descendants. Example 6 describes the generation of phylogenetic trees.

[0017] The term "coding sequence" means a polynucleotide which directly specifies the amino acid sequence of a polypeptide. The boundaries of the coding sequence are generally determined by an open reading frame, which begins with a start codon such as ATG, GTG, or TTG and ends with a stop codon such as TAA, TAG, or TGA. The coding sequence may be a genomic DNA, cDNA, synthetic DNA, or a combination thereof.

[0018] The term "control sequences" means nucleic acid sequences necessary for expression of a polynucleotide encoding a mature polypeptide of the present invention. Each control sequence may be native (i.e., from the same gene) or foreign (i.e., from a different gene) to the polynucleotide encoding the polypeptide or native or foreign to each other. Such control sequences include, but are not limited to, a leader, polyadenylation sequence, propeptide sequence, promoter, signal peptide sequence, and transcription terminator. At a minimum, the control sequences include a promoter, and transcriptional and translational stop signals. The control sequences may be provided with linkers for the purpose of introducing specific restriction sites facilitating ligation of the control sequences with the coding region of the polynucleotide encoding a polypeptide.

[0019] The term "cleaning component" means, e.g., a detergent adjunct ingredient that is different from the polypeptides of this invention. The precise nature of these additional cleaning or adjunct components, and levels of incorporation thereof, will depend on the physical form of the composition and the nature of the operation for which it is to be used. Suitable cleaning components include, but are not limited to the components described below, such as surfactants, builders and co-builders, flocculating aid, chelating agents, dye transfer inhibitors, enzymes (other than the enzymes of the invention), enzyme stabilizers, enzyme inhibitors, catalytic materials, bleach activators,

hydrogen peroxide, sources of hydrogen peroxide, pre-formed peracids, polymeric agents, clay soil removal/anti-redeposition agents, brighteners, suds suppressors, dyes, perfumes, structure elasticizing agents, fabric softeners, carriers, hydrotropes, fabric hueing agents, anti-foaming agents, dispersants, processing aids, and/or pigments.

[0020] The term "cleaning composition" includes "detergent composition" and refers to compositions that find use in the removal of undesired compounds from items to be cleaned, such as textiles. The detergent composition may be used to, e.g., clean textiles for both household cleaning and industrial cleaning. The term encompasses any materials/compounds selected for the particular type of cleaning composition desired and the form of the product (e.g., liquid, gel, powder, granulate, paste, or spray compositions) and includes, but is not limited to, detergent compositions such as liquid and/or solid laundry detergents and fine fabric detergents; fabric fresheners; fabric softeners; and textile and laundry pre-spotters/pretreatment. In addition to containing the enzyme of the invention, the detergent formulation may contain one or more additional enzymes (such as proteases, amylases, lipases, cutinases, cellulases, endoglucanases, xyloglucanases, pectinases, pectin lyases, xanthanases, peroxidases, haloperoxidases, catalases, mannanases, nucleases or any mixture thereof), and/or detergent adjunct ingredients such as surfactants, builders, chelators or chelating agents, bleach system or bleach components, polymers, fabric conditioners, foam boosters, suds suppressors, dyes, perfume, tarnish inhibitors, optical brighteners, bactericides, fungicides, soil suspending agents, anti-corrosion agents, enzyme inhibitors or stabilizers, enzyme activators, transferase(s), hydrolytic enzymes, oxidoreductases, bluing agents and fluorescent dyes, antioxidants, and solubilizers.

[0021] The term "expression" includes any step involved in the production of a polypeptide including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification, and secretion.

[0022] The term "expression vector" means a linear or circular DNA molecule that comprises a polynucleotide encoding a polypeptide and is operably linked to control sequences that provide for its expression.

[0023] The term "fragment" means a polypeptide having one or more amino acids absent from the amino and/or carboxyl terminus of a mature polypeptide or domain; wherein the fragment has peptidoglycan degradation activity.

[0024] The term "host cell" means any cell type that is susceptible to transformation, transfection, transduction, or the like with a nucleic acid construct or expression vector comprising a polynucleotide of the present invention. The term "host cell" encompasses any progeny of a parent cell that is not identical to the parent cell due to mutations that occur during replication.

[0025] The term "isolated" means a substance in a form or environment that does not occur in nature. Non-limiting examples of isolated substances include (1) any non-naturally occurring substance, (2) any substance including, but not limited to, any enzyme, variant, nucleic acid, protein, peptide or cofactor, that is at least partially removed from one or more or all of the naturally occurring constituents with which it is associated in nature; (3) any substance modified by the hand of man relative to that substance found in nature; or (4) any substance modified by increasing the amount of the substance relative to other components with

which it is naturally associated (e.g., recombinant production in a host cell; multiple copies of a gene encoding the substance; and use of a stronger promoter than the promoter naturally associated with the gene encoding the substance). An isolated substance may be present in a fermentation broth sample; e.g., a host cell may be genetically modified to express the polypeptide of the invention. The fermentation broth from that host cell will comprise the isolated polypeptide. It will be apparent to persons skilled in the art that the polypeptides disclosed herein are preferably in isolated form.

[0026] The term "laundering" relates to both household laundering and industrial laundering and means the process of treating textiles with a solution containing a cleaning or detergent composition of the present invention. The laundering process can for example be carried out using, e.g., a household or an industrial washing machine or can be carried out by hand.

[0027] The term "malodor" means an odor which is not desired on clean items. The cleaned item should smell fresh and clean without malodors adhered to the item. One example of malodor is compounds with an unpleasant smell, which may be produced by microorganisms. Another example is unpleasant smells which can be sweat or body odor adhered to an item which has been in contact with human or animal. Another example of malodor can be the odor from spices, which sticks to items for example curry or other spices which smell strongly.

[0028] The term "mature polypeptide" means a polypeptide in its mature form following N terminal processing (e.g., removal of signal peptide).

[0029] In one aspect, the mature polypeptide is amino acids 1 to 431 of SEQ ID NO: 2. Amino acids -29 to -1 of SEQ ID NO: 2 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 485 of SEQ ID NO: 5. Amino acids -30 to -1 of SEQ ID NO: 5 are a signal peptide.

[0030] In one aspect, the mature polypeptide is amino acids 1 to 483 of SEQ ID NO: 8. Amino acids -26 to -1 of SEQ ID NO: 8 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 471 of SEQ ID NO: 11. Amino acids -22 to -1 of SEQ ID NO: 11 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 639 of SEQ ID NO: 14. In one aspect, the mature polypeptide is amino acids 1 to 484 of SEQ ID NO: 17. Amino acids -31 to -1 of SEQ ID NO: 17 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 480 of SEQ ID NO: 20. Amino acids -30 to -1 of SEQ ID NO: 20 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 485 of SEQ ID NO: 23. Amino acids -31 to -1 of SEQ ID NO: 23 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 491 of SEQ ID NO: 26. Amino acids -28 to -1 of SEQ ID NO: 26 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 289 of SEQ ID NO: 29. Amino acids -19 to -1 of SEQ ID NO: 29 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 245 of SEQ ID NO: 32. Amino acids -15 to -1 of SEQ ID NO: 32 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 280 of SEQ ID NO: 35. Amino acids -19 to -1 of SEQ ID NO: 35 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 238 of SEQ ID NO: 38. Amino acids -22 to -1 of SEQ ID NO: 38 are a signal peptide. In one aspect, the mature

polypeptide is amino acids 1 to 498 of SEQ ID NO: 41. Amino acids -23 to -1 of SEQ ID NO: 41 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 476 of SEQ ID NO: 44. Amino acids -25 to -1 of SEQ ID NO: 44 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 474 of SEQ ID NO: 47. Amino acids -28 to -1 of SEQ ID NO: 47 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 473 of SEQ ID NO: 50. Amino acids -29 to -1 of SEQ ID NO: 50 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 414 of SEQ ID NO: 53. Amino acids -25 to -1 of SEQ ID NO: 53 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 412 of SEQ ID NO: 56. Amino acids -31 to -1 of SEQ ID NO: 56 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 637 of SEQ ID NO: 59. Amino acids -35 to -1 of SEQ ID NO: 59 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 599 of SEQ ID NO: 62. Amino acids -33 to -1 of SEQ ID NO: 62 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 605 of SEQ ID NO: 65. Amino acids -31 to -1 of SEQ ID NO: 65 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 610 of SEQ ID NO: 68. Amino acids -36 to -1 of SEQ ID NO: 68 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 216 of SEQ ID NO: 71. Amino acids -20 to -1 of SEQ ID NO: 71 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 425 of SEQ ID NO: 74. Amino acids -26 to -1 of SEQ ID NO: 74 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 304 of SEQ ID NO: 77. Amino acids -25 to -1 of SEQ ID NO: 77 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 306 of SEQ ID NO: 80. Amino acids -29 to -1 of SEQ ID NO: 80 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 306 of SEQ ID NO: 83. Amino acids -23 to -1 of SEQ ID NO: 83 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 632 of SEQ ID NO: 86. Amino acids -35 to -1 of SEQ ID NO: 86 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 216 of SEQ ID NO: 89. Amino acids -24 to -1 of SEQ ID NO: 89 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 306 of SEQ ID NO: 92. Amino acids -27 to -1 of SEQ ID NO: 92 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 453 of SEQ ID NO: 95. Amino acids -29 to -1 of SEQ ID NO: 95 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 473 of SEQ ID NO: 98. Amino acids -29 to -1 of SEQ ID NO: 98 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 209 of SEQ ID NO: 101. Amino acids -27 to -1 of SEQ ID NO: 101 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 281 of SEQ ID NO: 104. Amino acids -24 to -1 of SEQ ID NO: 104 are a signal peptide. In one aspect, the mature polypeptide is amino acids 1 to 582 of SEQ ID NO: 107. Amino acids -57 to -1 of SEQ ID NO: 107 are a signal peptide.

[0031] It is known in the art that a host cell may produce a mixture of two or more different mature polypeptides (i.e., with a different C-terminal and/or N-terminal amino acid) expressed by the same polynucleotide. It is also known in the art that different host cells process polypeptides differently, and thus, one host cell expressing a polynucleotide

may produce a different mature polypeptide (e.g., having a different C-terminal and/or N-terminal amino acid) as compared to another host cell expressing the same polynucleotide.

[0032] The term “mature polypeptide coding sequence” means a polynucleotide that encodes a mature polypeptide having peptidoglycan degrading activity.

[0033] In one aspect, the mature polypeptide coding sequence is nucleotides 88 to 1380 of SEQ ID NO: 1 and nucleotides 1 to 87 of SEQ ID NO: 1 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 91 to 1545 of SEQ ID NO: 4 and nucleotides 1 to 90 of SEQ ID NO: 4 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 79 to 1527 of SEQ ID NO: 7 and nucleotides 1 to 78 of SEQ ID NO: 7 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 67 to 1479 of SEQ ID NO: 10 and nucleotides 1 to 66 of SEQ ID NO: 10 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 1 to 1917 of SEQ ID NO: 13. In one aspect, the mature polypeptide coding sequence is nucleotides 94 to 1545 of SEQ ID NO: 16 and nucleotides 1 to 93 of SEQ ID NO: 16 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 91 to 1530 of SEQ ID NO: 19 and nucleotides 1 to 90 of SEQ ID NO: 19 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 94 to 1548 of SEQ ID NO: 22 and nucleotides 1 to 93 of SEQ ID NO: 22 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 85 to 1557 of SEQ ID NO: 25 and nucleotides 1 to 84 of SEQ ID NO: 25 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 58 to 924 of SEQ ID NO: 28 and nucleotides 1 to 57 of SEQ ID NO: 28 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 46 to 780 of SEQ ID NO: 31 and nucleotides 1 to 45 of SEQ ID NO: 31 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 58 to 897 of SEQ ID NO: 34 and nucleotides 1 to 57 of SEQ ID NO: 34 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 67 to 780 of SEQ ID NO: 37 and nucleotides 1 to 66 of SEQ ID NO: 37 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 70 to 1563 of SEQ ID NO: 40 and nucleotides 1 to 69 of SEQ ID NO: 40 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 76 to 1503 of SEQ ID NO: 43 and nucleotides 1 to 75 of SEQ ID NO: 43 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 85 to 1506 of SEQ ID NO: 46 and nucleotides 1 to 84 of SEQ ID NO: 46 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 88 to 1506 of SEQ ID NO: 49 and nucleotides 1 to 87 of SEQ ID NO: 49 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 76 to 1317 of SEQ ID NO: 52 and nucleotides 1 to 75 of SEQ ID NO: 52 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 94 to 1329 of SEQ ID NO: 55 and nucleotides 1 to 93 of SEQ ID NO: 55 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 106 to 2016 of SEQ ID NO: 58 and

nucleotides 1 to 105 of SEQ ID NO: 58 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 100 to 1896 of SEQ ID NO: 61 and nucleotides 1 to 99 of SEQ ID NO: 61 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 94 to 1908 of SEQ ID NO: 64 and nucleotides 1 to 93 of SEQ ID NO: 64 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 109 to 1938 of SEQ ID NO: 67 and nucleotides 1 to 108 of SEQ ID NO: 67 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 61 to 708 of SEQ ID NO: 70 and nucleotides 1 to 60 of SEQ ID NO: 70 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 79 to 1353 of SEQ ID NO: 73 and nucleotides 1 to 78 of SEQ ID NO: 73 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 76 to 987 of SEQ ID NO: 76 and nucleotides 1 to 75 of SEQ ID NO: 76 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 73 to 990 of SEQ ID NO: 79 and nucleotides 1 to 72 of SEQ ID NO: 79 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 70 to 987 of SEQ ID NO: 82 and nucleotides 1 to 69 of SEQ ID NO: 82 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 106 to 2001 of SEQ ID NO: 85 and nucleotides 1 to 105 of SEQ ID NO: 85 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 73 to 720 of SEQ ID NO: 88 and nucleotides 1 to 72 of SEQ ID NO: 88 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 82 to 999 of SEQ ID NO: 91 and nucleotides 1 to 81 of SEQ ID NO: 91 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 88 to 1446 of SEQ ID NO: 94 and nucleotides 1 to 87 of SEQ ID NO: 94 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 88 to 1506 of SEQ ID NO: 97 and nucleotides 1 to 87 of SEQ ID NO: 97 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 82 to 708 of SEQ ID NO: 100 and nucleotides 1 to 81 of SEQ ID NO: 100 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 73 to 915 of SEQ ID NO: 103 and nucleotides 1 to 72 of SEQ ID NO: 103 encode a signal peptide. In one aspect, the mature polypeptide coding sequence is nucleotides 172 to 1917 of SEQ ID NO: 106 and nucleotides 1 to 171 of SEQ ID NO: 106 encode a signal peptide.

[0034] The term “nucleic acid construct” means a nucleic acid molecule, either single- or double-stranded, which is isolated from a naturally occurring gene or is modified to contain segments of nucleic acids in a manner that would not otherwise exist in nature or which is synthetic, which comprises one or more control sequences.

[0035] The term “operably linked” means a configuration in which a control sequence is placed at an appropriate position relative to the coding sequence of a polynucleotide such that the control sequence directs expression of the coding sequence.

[0036] The relatedness between two amino acid sequences or between two nucleotide sequences is described by the parameter “sequence identity”. For purposes of the present

invention, the sequence identity between two amino acid sequences is determined using the Needleman-Wunsch algorithm (Needleman and Wunsch, 1970, *J. Mol. Biol.* 48: 443-453) as implemented in the Needle program of the EMBOSS package (EMBOSS: The European Molecular Biology Open Software Suite, Rice et al., 2000, Trends Genet. 16: 276-277), preferably version 5.0.0 or later. The parameters used are gap open penalty of 10, gap extension penalty of 0.5, and the EBLOSUM62 (EMBOSS version of BLOSUM62) substitution matrix. The output of Needle labeled “longest identity” (obtained using the -nobrief option) is used as the percent identity and is calculated as follows:

(Identical Residues × 100)/

(Length of Alignment–Total Number of Gaps in Alignment)

[0037] For purposes of the present invention, the sequence identity between two deoxyribonucleotide sequences is determined using the Needleman-Wunsch algorithm (Needleman and Wunsch, 1970, *supra*) as implemented in the Needle program of the EMBOSS package (EMBOSS: The European Molecular Biology Open Software Suite, Rice et al., 2000, *supra*), preferably version 5.0.0 or later. The parameters used are gap open penalty of 10, gap extension penalty of 0.5, and the EDNAFULL (EMBOSS version of NCBI NUC4.4) substitution matrix. The output of Needle labeled “longest identity” (obtained using the -nobrief option) is used as the percent identity and is calculated as follows:

(Identical Deoxyribonucleotides × 100)/

(Length of Alignment–Total Number of Gaps in Alignment)

[0038] The term “very low stringency conditions” means for probes of at least 100 nucleotides in length, prehybridization and hybridization at 42° C. in 5×SSPE, 0.3% SDS, 200 micrograms/ml sheared and denatured salmon sperm DNA, and 25% formamide, following standard Southern blotting procedures for 12 to 24 hours. The carrier material is finally washed three times each for 15 minutes using 2×SSC, 0.2% SDS at 45° C.

[0039] The term “low stringency conditions” means for probes of at least 100 nucleotides in length, prehybridization and hybridization at 42° C. in 5×SSPE, 0.3% SDS, 200 micrograms/ml sheared and denatured salmon sperm DNA, and 25% formamide, following standard Southern blotting procedures for 12 to 24 hours. The carrier material is finally washed three times each for 15 minutes using 2×SSC, 0.2% SDS at 50° C.

[0040] The term “medium stringency conditions” means for probes of at least 100 nucleotides in length, prehybridization and hybridization at 42° C. in 5×SSPE, 0.3% SDS, 200 micrograms/ml sheared and denatured salmon sperm DNA, and 35% formamide, following standard Southern blotting procedures for 12 to 24 hours. The carrier material is finally washed three times each for 15 minutes using 2×SSC, 0.2% SDS at 55° C.

[0041] The term “medium-high stringency conditions” means for probes of at least 100 nucleotides in length, prehybridization and hybridization at 42° C. in 5×SSPE, 0.3% SDS, 200 micrograms/ml sheared and denatured salmon sperm DNA, and 35% formamide, following standard Southern blotting procedures for 12 to 24 hours. The carrier material is finally washed three times each for 15 minutes using 2×SSC, 0.2% SDS at 60° C.

[0042] The term “high stringency conditions” means for probes of at least 100 nucleotides in length, prehybridization and hybridization at 42° C. in 5×SSPE, 0.3% SDS, 200 micrograms/ml sheared and denatured salmon sperm DNA, and 50% formamide, following standard Southern blotting procedures for 12 to 24 hours. The carrier material is finally washed three times each for 15 minutes using 2×SSC, 0.2% SDS at 65° C.

[0043] The term “very high stringency conditions” means for probes of at least 100 nucleotides in length, prehybridization and hybridization at 42° C. in 5×SSPE, 0.3% SDS, 200 micrograms/ml sheared and denatured salmon sperm DNA, and 50% formamide, following standard Southern blotting procedures for 12 to 24 hours. The carrier material is finally washed three times each for 15 minutes using 2×SSC, 0.2% SDS at 70° C.

[0044] The term “variant” means a polypeptide having peptidoglycan degrading activity comprising an alteration, i.e., a substitution, insertion, and/or deletion, at one or more positions. A substitution means replacement of the amino acid occupying a position with a different amino acid; a deletion means removal of the amino acid occupying a position; and an insertion means adding an amino acid adjacent to and immediately following the amino acid occupying a position.

[0045] Nomenclature: For purposes of the present invention, the nomenclature [E/Q] or [EQ] means that the amino acid at this position may be a glutamic acid (Glu, E) or a glutamine (Gln, Q). Likewise, the nomenclature [V/G/A/I] or [VGA/I] means that the amino acid at this position may be a valine (Val, V), glycine (Gly, G), alanine (Ala, A) or isoleucine (Ile, I), and so forth for other combinations as described herein. Unless otherwise limited further, the amino acid X is defined such that it may be any of the 20 natural amino acids.

DETAILED DESCRIPTION OF THE INVENTION

[0046] As mentioned in the background section above, textiles and surfaces such as laundry and dishes may become soiled with many different types of soiling. A single complex stain such as a food stain, sebum, dead cells debris, EPS or biofilm related stains is often composed of different organic material such as proteins, polysaccharides, grease etc., which are often difficult to remove completely with traditional detergent compositions. Further, such stains may give rise to disadvantages such as redeposition or malodor. The polypeptides of the invention address this problem, providing good cleaning effects on complex stains such as biofilm and EPS as well as reduced redeposition and malodor from, e.g., textiles and tableware. The polypeptides of the invention are peptidoglycan degrading enzymes having hydrolase activity and preferably N-acetylmuramyl-L-alanine amidase activity. The polypeptides of the invention comprise an amidase domain, preferably an Amidase_2 domain as defined in PFAM (PF01510, Pfam version 31.0; Finn, 2016,

Nucleic Acids Research, Database Issue 44: D279-D285). Also, clusters or clades are described herein, defined by specific motifs shared by the polypeptides of the specific clades. A phylogenetic tree was constructed of polypeptide sequences containing an Amidase_2 domain. The phylogenetic tree was constructed from a multiple alignment of mature polypeptide sequences containing at least one Amidase_2 domain as described in Example 6.

[0047] One embodiment of the invention relates to a peptidoglycan degrading enzyme having hydrolase activity and preferably N-acetylmuramyl-L-alanine amidase activity. One embodiment of the invention relates to a peptidoglycan degrading enzyme having hydrolase activity and preferably N-acetylmuramyl-L-alanine amidase activity, wherein the polypeptide comprises the motif N[IV]X[AG][GAS]A[AY][LV]L (SEQ ID NO: 111), where X can be any naturally occurring amino acid, situated in positions corresponding to positions 85 to 93 in *Micromonospora maritima* (SEQ ID NO: 6).

[0048] The polypeptides containing an Amidase_2 domain can be separated into distinct sub-clusters. The sub-clusters are defined by one or more short sequence motifs, as well as containing an Amidase_2 domain as defined in PFAM (PF01510, Pfam version 31.0). We denote one sub-cluster comprising the motif N[IV]X[AG][GAS]A[AY][LV]L (SEQ ID NO: 111) as the PGL clade. All polypeptide sequences containing an Amidase_2 domain as well as the motif will be denoted as belonging to the PGL clade.

[0049] In an embodiment, the present invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO: 2 of at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have peptidoglycan degrading activity. In one aspect, the polypeptides differ by up to 10 amino acids, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, from the mature polypeptide of SEQ ID NO: 2.

[0050] In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO: 2 of at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least 70% of the peptidoglycan degrading activity of the mature polypeptide of SEQ ID NO: 2.

[0051] In an embodiment, the present invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO: 5 of at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have peptidoglycan degrading activity. In one aspect, the polypeptides differ by up to 10 amino acids, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, from the mature polypeptide of SEQ ID NO: 5.

[0052] In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO: 5 of at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least 70% of the peptidoglycan degrading activity of the mature polypeptide of SEQ ID NO: 5.

[0053] In an embodiment, the present invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO: 8 of at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have peptidoglycan degrading activity. In one aspect, the polypeptides differ by up to 10 amino acids, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, from the mature polypeptide of SEQ ID NO: 8.

[0054] In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO: 8 of at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least 70% of the peptidoglycan degrading activity of the mature polypeptide of SEQ ID NO: 8.

[0055] In an embodiment, the present invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO: 11 of at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have peptidoglycan degrading activity. In one aspect, the polypeptides differ by up to 10 amino acids, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, from the mature polypeptide of SEQ ID NO: 11.

[0056] In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO: 11 of at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least 70% of the peptidoglycan degrading activity of the mature polypeptide of SEQ ID NO: 11.

[0057] In an embodiment, the present invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO: 14 of at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have peptidoglycan degrading activity. In one aspect, the polypeptides differ by up to 10 amino acids, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, from the mature polypeptide of SEQ ID NO: 14.

[0058] In a particular embodiment, the invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO: 14 of at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least 70% of the peptidoglycan degrading activity of the mature polypeptide of SEQ ID NO: 14.

[0059] In an embodiment, the present invention relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO: 17 of at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have peptidoglycan degrading activity. In one aspect, the polypeptides differ by up to 10 amino acids, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, from the mature polypeptide of SEQ ID NO: 17.

ing of: SEQ ID NO: 6, SEQ ID NO: 9, SEQ ID NO: 12, SEQ ID NO: 15, SEQ ID NO: 18, SEQ ID NO: 21, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 42, SEQ ID NO: 45, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 60, SEQ ID NO: 63, SEQ ID NO: 66, SEQ ID NO: 69, SEQ ID NO: 75, SEQ ID NO: 87, SEQ ID NO: 96, SEQ ID NO: 99 and SEQ ID NO: 108 and polypeptides having at least 90% sequence identity thereto, and wherein the polypeptide has peptidoglycan degradation activity.

[0162] One embodiment of the invention relates to a polypeptide wherein the polypeptide comprises the motif N[IV]X[AG][GAS]A[AY][LV]L (SEQ ID NO: 111), wherein the polypeptide is selected from the group consisting of: SEQ ID NO: 6, SEQ ID NO: 9, SEQ ID NO: 12, SEQ ID NO: 15, SEQ ID NO: 18, SEQ ID NO: 21, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 42, SEQ ID NO: 45, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 60, SEQ ID NO: 63, SEQ ID NO: 66, SEQ ID NO: 69, SEQ ID NO: 75, SEQ ID NO: 87, SEQ ID NO: 96, SEQ ID NO: 99 and SEQ ID NO: 108 and polypeptides having at least 95% sequence identity thereto, and wherein the polypeptide has peptidoglycan degradation activity.

[0163] One embodiment of the invention relates to a polypeptide wherein the polypeptide comprises the motif N[IV]X[AG][GAS]A[AY][LV]L (SEQ ID NO: 111), wherein the polypeptide is selected from the group consisting of: SEQ ID NO: 6, SEQ ID NO: 9, SEQ ID NO: 12, SEQ ID NO: 15, SEQ ID NO: 18, SEQ ID NO: 21, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 42, SEQ ID NO: 45, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 60, SEQ ID NO: 63, SEQ ID NO: 66, SEQ ID NO: 69, SEQ ID NO: 75, SEQ ID NO: 87, SEQ ID NO: 96, SEQ ID NO: 99 and SEQ ID NO: 108 and polypeptides having at least 98% sequence identity thereto, and wherein the polypeptide has peptidoglycan degradation activity.

[0164] One embodiment of the invention relates to a polypeptide wherein the polypeptide comprises the motif N[IV]X[AG][GAS]A[AY][LV]L (SEQ ID NO: 111), wherein the polypeptide is selected from the group consisting of: SEQ ID NO: 6, SEQ ID NO: 9, SEQ ID NO: 12, SEQ ID NO: 15, SEQ ID NO: 18, SEQ ID NO: 21, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 42, SEQ ID NO: 45, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 60, SEQ ID NO: 63, SEQ ID NO: 66, SEQ ID NO: 69, SEQ ID NO: 75, SEQ ID NO: 87, SEQ ID NO: 96, SEQ ID NO: 99 and SEQ ID NO: 108 and polypeptides having at least 99% sequence identity thereto, and wherein the polypeptide has peptidoglycan degradation activity.

[0165] In any of the embodiments disclosed herein, the polypeptide has preferably been isolated, i.e., the polypeptide is in an "isolated" form or environment as defined above.

[0166] One polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 2 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 3. In another aspect, the polypeptide comprises or consists of amino acids 1 to 431 of SEQ ID NO: 2.

[0167] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 5 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another

aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 6. In another aspect, the polypeptide comprises or consists of amino acids 1 to 485 of SEQ ID NO: 5.

[0168] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 8 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 9. In another aspect, the polypeptide comprises or consists of amino acids 1 to 483 of SEQ ID NO: 8.

[0169] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 11 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 12. In another aspect, the polypeptide comprises or consists of amino acids 1 to 471 of SEQ ID NO: 11.

[0170] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 14 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 15. In another aspect, the polypeptide comprises or consists of amino acids 1 to 639 of SEQ ID NO: 14.

[0171] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 17 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 18. In another aspect, the polypeptide comprises or consists of amino acids 1 to 484 of SEQ ID NO: 17.

[0172] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 20 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 21. In another aspect, the polypeptide comprises or consists of amino acids 1 to 480 of SEQ ID NO: 20.

[0173] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 23 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 24. In another aspect, the polypeptide comprises or consists of amino acids 1 to 485 of SEQ ID NO: 23.

[0174] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 26 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 27. In another aspect, the polypeptide comprises or consists of amino acids 1 to 491 of SEQ ID NO: 26.

[0175] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 29 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another

aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 78. In another aspect, the polypeptide comprises or consists of amino acids 1 to 304 of SEQ ID NO: 77.

[0192] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 80 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 81. In another aspect, the polypeptide comprises or consists of amino acids 1 to 306 of SEQ ID NO: 80.

[0193] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 83 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 84. In another aspect, the polypeptide comprises or consists of amino acids 1 to 306 of SEQ ID NO: 83.

[0194] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 86 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 87. In another aspect, the polypeptide comprises or consists of amino acids 1 to 632 of SEQ ID NO: 86.

[0195] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 89 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 90. In another aspect, the polypeptide comprises or consists of amino acids 1 to 216 of SEQ ID NO: 89.

[0196] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 92 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 93. In another aspect, the polypeptide comprises or consists of amino acids 1 to 306 of SEQ ID NO: 92.

[0197] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 95 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 96. In another aspect, the polypeptide comprises or consists of amino acids 1 to 453 of SEQ ID NO: 95.

[0198] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 98 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 99. In another aspect, the polypeptide comprises or consists of amino acids 1 to 473 of SEQ ID NO: 98.

[0199] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 101 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another

aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 102. In another aspect, the polypeptide comprises or consists of amino acids 1 to 209 of SEQ ID NO: 101.

[0200] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 104 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 105. In another aspect, the polypeptide comprises or consists of amino acids 1 to 281 of SEQ ID NO: 104.

[0201] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 107 or an allelic variant thereof; or is a fragment thereof having peptidoglycan degradation activity. In another aspect, the polypeptide comprises or consists of the mature polypeptide shown in SEQ ID NO: 108. In another aspect, the polypeptide comprises or consists of amino acids 1 to 582 of SEQ ID NO: 107.

[0202] In another embodiment, the present invention relates to a polypeptide having peptidoglycan degradation activity encoded by a polynucleotide that hybridizes under very low stringency conditions, low stringency conditions, medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with (i) SEQ ID NO: 1, SEQ ID NO: 4, SEQ ID NO: 7, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 19, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 28, SEQ ID NO: 31, SEQ ID NO: 34, SEQ ID NO: 37, SEQ ID NO: 40, SEQ ID NO: 43, SEQ ID NO: 46, SEQ ID NO: 49, SEQ ID NO: 52, SEQ ID NO: 55, SEQ ID NO: 58, SEQ ID NO: 61, SEQ ID NO: 64, SEQ ID NO: 67, SEQ ID NO: 70, SEQ ID NO: 73, SEQ ID NO: 76, SEQ ID NO: 79, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 94, SEQ ID NO: 97, SEQ ID NO: 100, SEQ ID NO: 103 or SEQ ID NO: 106, (ii) the mature polypeptide coding sequence of SEQ ID NO: 1, SEQ ID NO: 4, SEQ ID NO: 7, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 19, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 28, SEQ ID NO: 31, SEQ ID NO: 34, SEQ ID NO: 37, SEQ ID NO: 40, SEQ ID NO: 43, SEQ ID NO: 46, SEQ ID NO: 49, SEQ ID NO: 52, SEQ ID NO: 55, SEQ ID NO: 58, SEQ ID NO: 61, SEQ ID NO: 64, SEQ ID NO: 67, SEQ ID NO: 70, SEQ ID NO: 73, SEQ ID NO: 76, SEQ ID NO: 79, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 94, SEQ ID NO: 97, SEQ ID NO: 100, SEQ ID NO: 103 or SEQ ID NO: 106, or (iii) the full-length complement of (i) or (ii) (Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, 2d edition, Cold Spring Harbor, New York). Such polypeptides have preferably been isolated.

[0203] The polynucleotide of SEQ ID NO: 1, SEQ ID NO: 4, SEQ ID NO: 7, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 19, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 28, SEQ ID NO: 31, SEQ ID NO: 34, SEQ ID NO: 37, SEQ ID NO: 40, SEQ ID NO: 43, SEQ ID NO: 46, SEQ ID NO: 49, SEQ ID NO: 52, SEQ ID NO: 55, SEQ ID NO: 58, SEQ ID NO: 61, SEQ ID NO: 64, SEQ ID NO: 67, SEQ ID NO: 70, SEQ ID NO: 73, SEQ ID NO: 76, SEQ ID NO: 79, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 94, SEQ ID NO: 97, SEQ ID NO: 100, SEQ ID NO: 103, SEQ ID NO: 106 or a subsequence thereof, as well as a fragment thereof may be

used to design nucleic acid probes to identify and clone DNA encoding polypeptides having peptidoglycan degradation activity from strains of different genera or species according to methods well known in the art. In particular, such probes can be used for hybridization with the genomic DNA or cDNA of a cell of interest, following standard Southern blotting procedures, in order to identify and isolate the corresponding gene therein. Such probes can be considerably shorter than the entire sequence, but should be at least 15, e.g., at least 25, at least 35, or at least 70 nucleotides in length. Preferably, the nucleic acid probe is at least 100 nucleotides in length, e.g., at least 200 nucleotides, at least 300 nucleotides, at least 400 nucleotides, at least 500 nucleotides, at least 600 nucleotides, at least 700 nucleotides, at least 800 nucleotides, or at least 900 nucleotides in length. Both DNA and RNA probes can be used. The probes are typically labeled for detecting the corresponding gene (for example, with 32 P, 33 H, 35 S, biotin, or avidin). Such probes are encompassed by the present invention.

[0204] A genomic DNA or cDNA library prepared from such other strains may be screened for DNA that hybridizes with the probes described above and encodes a polypeptide having peptidoglycan degradation activity. Genomic or other DNA from such other strains may be separated by agarose or polyacrylamide gel electrophoresis, or other separation techniques. DNA from the libraries or the separated DNA may be transferred to and immobilized on nitrocellulose or another suitable carrier material. In order to identify a clone or DNA that hybridizes with SEQ ID NO: 1, SEQ ID NO: 4, SEQ ID NO: 7, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 19, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 28, SEQ ID NO: 31, SEQ ID NO: 34, SEQ ID NO: 37, SEQ ID NO: 40, SEQ ID NO: 43, SEQ ID NO: 46, SEQ ID NO: 49, SEQ ID NO: 52, SEQ ID NO: 55, SEQ ID NO: 58, SEQ ID NO: 61, SEQ ID NO: 64, SEQ ID NO: 67, SEQ ID NO: 70, SEQ ID NO: 73, SEQ ID NO: 76, SEQ ID NO: 79, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 94, SEQ ID NO: 97, SEQ ID NO: 100, SEQ ID NO: 103, SEQ ID NO: 106 or a subsequence thereof, the carrier material is used in a Southern blot.

[0205] For purposes of the present invention, hybridization indicates that the polynucleotide hybridizes to a labeled nucleic acid probe corresponding to (i) SEQ ID NO: 1, SEQ ID NO: 4, SEQ ID NO: 7, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 19, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 28, SEQ ID NO: 31, SEQ ID NO: 34, SEQ ID NO: 37, SEQ ID NO: 40, SEQ ID NO: 43, SEQ ID NO: 46, SEQ ID NO: 49, SEQ ID NO: 52, SEQ ID NO: 55, SEQ ID NO: 58, SEQ ID NO: 61, SEQ ID NO: 64, SEQ ID NO: 67, SEQ ID NO: 70, SEQ ID NO: 73, SEQ ID NO: 76, SEQ ID NO: 79, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 94, SEQ ID NO: 97, SEQ ID NO: 100, SEQ ID NO: 103 or SEQ ID NO: 106; (ii) the mature polypeptide coding sequence of SEQ ID NO: 1, SEQ ID NO: 4, SEQ ID NO: 7, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 19, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 28, SEQ ID NO: 31, SEQ ID NO: 34, SEQ ID NO: 37, SEQ ID NO: 40, SEQ ID NO: 43, SEQ ID NO: 46, SEQ ID NO: 49, SEQ ID NO: 52, SEQ ID NO: 55, SEQ ID NO: 58, SEQ ID NO: 61, SEQ ID NO: 64, SEQ ID NO: 67, SEQ ID NO: 70, SEQ ID NO: 73, SEQ ID NO: 76, SEQ ID NO: 79, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 94, SEQ ID

NO: 97, SEQ ID NO: 100, SEQ ID NO: 103 or SEQ ID NO: 106; (iii) the full-length complement thereof; or (iv) a subsequence thereof, under very low to very high stringency conditions. Molecules to which the nucleic acid probe hybridizes under these conditions can be detected using, for example, X-ray film or any other detection means known in the art.

[0206] In another embodiment, the present invention relates to a polypeptide having peptidoglycan degradation activity encoded by a polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 1 of at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%.

[0207] In another embodiment, the present invention relates to a polypeptide having peptidoglycan degradation activity encoded by a polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 4 of at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%.

[0208] In another embodiment, the present invention relates to a polypeptide having peptidoglycan degradation activity encoded by a polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 7 of at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%.

[0209] In another embodiment, the present invention relates to a polypeptide having peptidoglycan degradation activity encoded by a polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 10 of at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%.

[0210] In another embodiment, the present invention relates to a polypeptide having peptidoglycan degradation activity encoded by a polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 13 of at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%.

[0211] In another embodiment, the present invention relates to a polypeptide having peptidoglycan degradation activity encoded by a polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 16 of at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%.

[0212] In another embodiment, the present invention relates to a polypeptide having peptidoglycan degradation activity encoded by a polynucleotide having a sequence

duced into the polypeptide shown SEQ ID NO: 105 is up to 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

[0277] In another embodiment, the present invention relates to variants of the polypeptide shown in SEQ ID NO: 108 comprising a substitution, deletion, and/or insertion at one or more positions. In an embodiment, the number of amino acid substitutions, deletions and/or insertions introduced into the polypeptide shown SEQ ID NO: 108 is up to 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

[0278] The amino acid changes in any of the embodiments above or elsewhere herein may be of a minor nature, that is conservative amino acid substitutions or insertions that do not significantly affect the folding and/or activity of the protein; small deletions, typically of 1-30 amino acids; small amino- or carboxyl-terminal extensions, such as an amino-terminal methionine residue; a small linker peptide of up to 20-25 residues; or a small extension that facilitates purification by changing net charge or another function, such as a poly-histidine tag, an antigenic epitope or a binding domain.

[0279] Examples of conservative substitutions are within the groups of basic amino acids (arginine, lysine and histidine), acidic amino acids (glutamic acid and aspartic acid), polar amino acids (glutamine and asparagine), hydrophobic amino acids (leucine, isoleucine and valine), aromatic amino acids (phenylalanine, tryptophan and tyrosine), and small amino acids (glycine, alanine, serine, threonine and methionine). Amino acid substitutions that do not generally alter specific activity are known in the art and are described, for example, by H. Neurath and R. L. Hill, 1979, In, *The Proteins*, Academic Press, New York. Common substitutions are Ala/Ser, Val/Ile, Asp/Glu, Thr/Ser, Ala/Gly, Ala/Thr, Ser/Asn, Ala/Val, Ser/Gly, Tyr/Phe, Ala/Pro, Lys/Arg, Asp/Asn, Leu/Ile, Leu/Val, Ala/Glu, and Asp/Gly.

[0280] Essential amino acids in a polypeptide can be identified according to procedures known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham and Wells, 1989, *Science* 244: 1081-1085). In the latter technique, single alanine mutations are introduced at every residue in the molecule, and the resultant molecules are tested for peptidoglycan degradation activity to identify amino acid residues that are critical to the activity of the molecule. See also, Hilton et al., 1996, *J. Biol. Chem.* 271: 4699-4708. The active site of the enzyme or other biological interaction can also be determined by physical analysis of structure, as determined by such techniques as nuclear magnetic resonance, crystallography, electron diffraction, or photoaffinity labeling, in conjunction with mutation of putative contact site amino acids. See, for example, de Vos et al., 1992, *Science* 255: 306-312; Smith et al., 1992, *J. Mol. Biol.* 224: 899-904; Wlodaver et al., 1992, *FEBS Lett.* 309: 59-64. The identity of essential amino acids can also be inferred from an alignment with a related polypeptide.

[0281] Single or multiple amino acid substitutions, deletions, and/or insertions can be made and tested using known methods of mutagenesis, recombination, and/or shuffling, followed by a relevant screening procedure, such as those disclosed by Reidhaar-Olson and Sauer, 1988, *Science* 241: 53-57; Bowie and Sauer, 1989, *Proc. Natl. Acad. Sci. USA* 86: 2152-2156; WO 95/17413; or WO 95/22625. Other methods that can be used include error-prone PCR, phage display (e.g., Lowman et al., 1991, *Biochemistry* 30: 10832-10837; U.S. Pat. No. 5,223,409; WO 92/06204), and region-

directed mutagenesis (Derbyshire et al., 1986, *Gene* 46: 145; Ner et al., 1988, *DNA* 7:127).

[0282] Mutagenesis/shuffling methods can be combined with high-throughput, automated screening methods to detect activity of cloned, mutagenized polypeptides expressed by host cells (Ness et al., 1999, *Nature Biotechnology* 17: 893-896). Mutagenized DNA molecules that encode active polypeptides can be recovered from the host cells and rapidly sequenced using standard methods in the art. These methods allow the rapid determination of the importance of individual amino acid residues in a polypeptide.

[0283] The polypeptide may be a hybrid polypeptide in which a region of one polypeptide is fused at the N-terminus or the C-terminus of a region of another polypeptide.

[0284] The polypeptide may be a fusion polypeptide or cleavable fusion polypeptide in which another polypeptide is fused at the N-terminus or the C-terminus of the polypeptide of the present invention. A fusion polypeptide is produced by fusing a polynucleotide encoding another polypeptide to a polynucleotide of the present invention. Techniques for producing fusion polypeptides are known in the art, and include ligating the coding sequences encoding the polypeptides so that they are in frame and that expression of the fusion polypeptide is under control of the same promoter(s) and terminator. Fusion polypeptides may also be constructed using intein technology in which fusion polypeptides are created post-translationally (Cooper et al., 1993, *EMBO J.* 12: 2575-2583; Dawson et al., 1994, *Science* 266: 776-779).

[0285] A fusion polypeptide can further comprise a cleavage site between the two polypeptides. Upon secretion of the fusion protein, the site is cleaved releasing the two polypeptides. Examples of cleavage sites include, but are not limited to, the sites disclosed in Martin et al., 2003, *J. Ind. Microbiol. Biotechnol.* 3: 568-576; Svetina et al., 2000, *J. Biotechnol.* 76: 245-251; Rasmussen-Wilson et al., 1997, *Appl. Environ. Microbiol.* 63: 3488-3493; Ward et al., 1995, *Biotechnology* 13: 498-503; and Contreras et al., 1991, *Biotechnology* 9: 378-381; Eaton et al., 1986, *Biochemistry* 25: 505-512; Collins-Racie et al., 1995, *Biotechnology* 13: 982-987; Carter et al., 1989, *Proteins: Structure, Function, and Genetics* 6: 240-248; and Stevens, 2003, *Drug Discovery World* 4: 35-48.

Sources of Polypeptides Having Peptidoglycan Degradation Activity

[0286] A polypeptide having peptidoglycan degradation activity of the present invention may be obtained from microorganisms of any genus. For purposes of the present invention, the term "obtained from" as used herein in connection with a given source shall mean that the polypeptide encoded by a polynucleotide is produced by the source or by a strain in which the polynucleotide from the source has been inserted. In one aspect, the polypeptide obtained from a given source is secreted extracellularly. In one aspect, the polypeptide is an *Alicyclobacillus* polypeptide. In one aspect, the polypeptide is a *Tumebacillus* polypeptide. In one aspect, the polypeptide is a *Halomonas* polypeptide. In one aspect, the polypeptide is a *Kribbella* polypeptide, e.g., a polypeptide obtained from *Kribbella aluminosa*. In one aspect, the polypeptide is a *Streptomyces* polypeptide, e.g., a polypeptide obtained from *Streptomyces griseus*. In one aspect, the polypeptide is a *Nonomuraea* polypeptide, e.g., a polypeptide obtained from *Nonomuraea*

coxensis, *Nonomuraea dietziae* or *Nonomuraea guangzhouensis*. In one aspect, the polypeptide is a *Micromonospora* polypeptide, e.g., a polypeptide obtained from *Micromonospora peuceia*, *Micromonospora fulvopurpurea* or *Micromonospora maritima*. In one aspect, the polypeptide is a *Laceyella* polypeptide, e.g., a polypeptide obtained from *Laceyella sacchari*. In one aspect, the polypeptide is a *Bacillus* polypeptide, e.g., a polypeptide obtained from *Bacillus sporothermodurans* or *Bacillus cohnii*. In one aspect, the polypeptide is a *Lysobacter* polypeptide, e.g., a polypeptide obtained from *Lysobacter antibioticus* or *Lysobacter capsica*. In one aspect, the polypeptide is a *Hamadaea* polypeptide, e.g., a polypeptide obtained from *Hamadaea tsunoensis*. In one aspect, the polypeptide is a *Paenibacillus* polypeptide, e.g., a polypeptide obtained from *Paenibacillus pini*. In one aspect, the polypeptide is a *Thermostaphylospora* polypeptide, e.g., a polypeptide obtained from *Thermostaphylospora chromogena*. In one aspect, the polypeptide is a *Pseudomonas* polypeptide, e.g., a polypeptide obtained from *Pseudomonas peli* or *Pseudomonas pseudoalcaligenes*.

[0287] It will be understood that for the aforementioned species, the invention encompasses both the perfect and imperfect states, and other taxonomic equivalents, e.g., anamorphs, regardless of the species name by which they are known. Those skilled in the art will readily recognize the identity of appropriate equivalents.

[0288] Strains of these species are readily accessible to the public in a number of culture collections, such as the American Type Culture Collection (ATCC), Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ), Centraalbureau Voor Schimmelcultures (CBS), and Agricultural Research Service Patent Culture Collection, Northern Regional Research Center (NRRL).

[0289] The polypeptide may be identified and obtained from other sources including microorganisms isolated from nature (e.g., soil, composts, water, etc.) or DNA samples obtained directly from natural materials (e.g., soil, composts, water, etc.) using the above-mentioned probes. Techniques for isolating microorganisms and DNA directly from natural habitats are well known in the art. A polynucleotide encoding the polypeptide may then be obtained by similarly screening a genomic DNA or cDNA library of another microorganism or mixed DNA sample. Once a polynucleotide encoding a polypeptide has been detected with the probe(s), the polynucleotide can be isolated or cloned by utilizing techniques that are known to those of ordinary skill in the art (see, e.g., Sambrook et al., 1989, supra).

Nucleic Acid Constructs

[0290] The present invention also relates to nucleic acid constructs comprising a polynucleotide of the present invention operably linked to one or more control sequences that direct the expression of the coding sequence in a suitable host cell under conditions compatible with the control sequences.

[0291] The polynucleotide may be manipulated in a variety of ways to provide for expression of the polypeptide. Manipulation of the polynucleotide prior to its insertion into a vector may be desirable or necessary depending on the expression vector. The techniques for modifying polynucleotides utilizing recombinant DNA methods are well known in the art.

[0292] The control sequence may be a promoter, a polynucleotide that is recognized by a host cell for expression of a polynucleotide encoding a polypeptide of the present invention. The promoter contains transcriptional control sequences that mediate the expression of the polypeptide. The promoter may be any polynucleotide that shows transcriptional activity in the host cell including variant, truncated, and hybrid promoters, and may be obtained from genes encoding extracellular or intracellular polypeptides either homologous or heterologous to the host cell.

[0293] Examples of suitable promoters for directing transcription of the nucleic acid constructs of the present invention in a bacterial host cell are the promoters obtained from the *Bacillus amyloliquefaciens* alpha-amylase gene (amyQ), *Bacillus licheniformis* alpha-amylase gene (amyL), *Bacillus licheniformis* penicillinase gene (penP), *Bacillus stearothermophilus* maltogenic amylase gene (amyM), *Bacillus subtilis* levansucrase gene (sacB), *Bacillus subtilis* xyIA and xyIB genes, *Bacillus thuringiensis* cryIIIa gene (Agaisse and Lereclus, 1994, *Molecular Microbiology* 13: 97-107), *E. Coli* lac operon, *E. Coli* trc promoter (Egon et al., 1988, Gene 69: 301-315), *Streptomyces coelicolor* agarase gene (daga), and prokaryotic beta-lactamase gene (Villa-Kamroff et al., 1978, *Proc. Natl. Acad. Sci. USA* 75: 3727-3731), as well as the tac promoter (DeBoer et al., 1983, *Proc. Natl. Acad. Sci. USA* 80: 21-25). Further promoters are described in "Useful proteins from recombinant bacteria" in Gilbert et al., 1980, *Scientific American* 242: 74-94; and in Sambrook et al., 1989, supra. Examples of tandem promoters are disclosed in WO 99/43835.

[0294] Examples of suitable promoters for directing transcription of the nucleic acid constructs of the present invention in a filamentous fungal host cell are promoters obtained from the genes for *Aspergillus nidulans* acetamidase, *Aspergillus niger* neutral alpha-amylase, *Aspergillus niger* acid stable alpha-amylase, *Aspergillus niger* or *Aspergillus awamori* glucoamylase (g&aA), *Aspergillus oryzae* TAKA amylase, *Aspergillus oryzae* alkaline protease, *Aspergillus oryzae* triose phosphate isomerase, *Fusarium oxysporum* trypsin-like protease (WO 96/00787), *Fusarium venenatum* amyloglucosidase (WO 00/56900), *Fusarium venenatum* Daria (WO 00/56900), *Fusarium venenatum* Quinn (WO 00/56900), *Rhizomucor miehei* lipase, *Rhizomucor miehei* aspartic proteinase, *Trichoderma reesei* beta-glucosidase, *Trichoderma reesei* cellobiohydrolase I, *Trichoderma reesei* cellobiohydrolase II, *Trichoderma reesei* endoglucanase I, *Trichoderma reesei* endoglucanase II, *Trichoderma reesei* endoglucanase III, *Trichoderma reesei* endoglucanase V, *Trichoderma reesei* xylanase I, *Trichoderma reesei* xylanase II, *Trichoderma reesei* xylanase III, *Trichoderma reesei* beta-xylosidase, and *Trichoderma reesei* translation elongation factor, as well as the NA2-tpi promoter (a modified promoter from an *Aspergillus* neutral alpha-amylase gene in which the untranslated leader has been replaced by an untranslated leader from an *Aspergillus* triose phosphate isomerase gene; non-limiting examples include modified promoters from an *Aspergillus niger* neutral alpha-amylase gene in which the untranslated leader has been replaced by an untranslated leader from an *Aspergillus nidulans* or *Aspergillus oryzae* triose phosphate isomerase gene); and variant, truncated, and hybrid promoters thereof. Other promoters are described in U.S. Pat. No. 6,011,147.

[0295] In a yeast host, useful promoters are obtained from the genes for *Saccharomyces cerevisiae* enolase (ENO-1),

Saccharomyces cerevisiae galactokinase (GAL1), *Saccharomyces cerevisiae* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH1, ADH2/GAP), *Saccharomyces cerevisiae* triose phosphate isomerase (TPI), *Saccharomyces cerevisiae* metallothionein (CUP1), and *Saccharomyces cerevisiae* 3-phosphoglycerate kinase. Other useful promoters for yeast host cells are described by Romanos et al., 1992, Yeast 8: 423-488.

[0296] The control sequence may also be a transcription terminator, which is recognized by a host cell to terminate transcription. The terminator is operably linked to the 3'-terminus of the polynucleotide encoding the polypeptide. Any terminator that is functional in the host cell may be used in the present invention.

[0297] Preferred terminators for bacterial host cells are obtained from the genes for *Bacillus clausii* alkaline protease (aprH), *Bacillus licheniformis* alpha-amylase (amyL), and *Escherichia coli* ribosomal RNA (rmB).

[0298] Preferred terminators for filamentous fungal host cells are obtained from the genes for *Aspergillus nidulans* acetamidase, *Aspergillus nidulans* anthranilate synthase, *Aspergillus niger* glucoamylase, *Aspergillus niger* alpha-glucosidase, *Aspergillus oryzae* TAKA amylase, *Fusarium oxysporum* trypsin-like protease, *Trichoderma reesei* beta-glucosidase, *Trichoderma reesei* cellobiohydrolase 1, *Trichoderma reesei* cellobiohydrolase 11, *Trichoderma reesei* endoglucanase I, *Trichoderma reesei* endoglucanase II, *Trichoderma reesei* endoglucanase III, *Trichoderma reesei* endoglucanase V, *Trichoderma reesei* xylanase I, *Trichoderma reesei* xylanase II, *Trichoderma reesei* xylanase III, *Trichoderma reesei* beta-xylanidase, and *Trichoderma reesei* translation elongation factor.

[0299] Preferred terminators for yeast host cells are obtained from the genes for *Saccharomyces cerevisiae* enolase, *Saccharomyces cerevisiae* cytochrome C (CYC1), and *Saccharomyces cerevisiae* glyceraldehyde-3-phosphate dehydrogenase. Other useful terminators for yeast host cells are described by Romanos et al., 1992, supra.

[0300] The control sequence may also be an mRNA stabilizer region downstream of a promoter and upstream of the coding sequence of a gene which increases expression of the gene.

[0301] Examples of suitable mRNA stabilizer regions are obtained from a *Bacillus thuringiensis* cryIIIa gene (WO 94/25612) and a *Bacillus subtilis* SP82 gene (Hue et al., 1995, *Journal of Bacteriology* 177: 3465-3471).

[0302] The control sequence may also be a leader, a nontranslated region of an mRNA that is important for translation by the host cell. The leader is operably linked to the 5'-terminus of the polynucleotide encoding the polypeptide. Any leader that is functional in the host cell may be used.

[0303] Preferred leaders for filamentous fungal host cells are obtained from the genes for *Aspergillus oryzae* TAKA amylase and *Aspergillus nidulans* triose phosphate isomerase.

[0304] Suitable leaders for yeast host cells are obtained from the genes for *Saccharomyces cerevisiae* enolase (ENO-1), *Saccharomyces cerevisiae* 3-phosphoglycerate kinase, *Saccharomyces cerevisiae* alpha-factor, and *Saccharomyces cerevisiae* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH2/GAP).

[0305] The control sequence may also be a polyadenylation sequence, a sequence operably linked to the 3'-terminus of the polynucleotide and, when transcribed, is recognized by the host cell as a signal to add polyadenosine residues to transcribed mRNA. Any polyadenylation sequence that is functional in the host cell may be used.

[0306] Preferred polyadenylation sequences for filamentous fungal host cells are obtained from the genes for *Aspergillus nidulans* anthranilate synthase, *Aspergillus niger* glucoamylase, *Aspergillus niger* alpha-glucosidase *Aspergillus oryzae* TAKA amylase, and *Fusarium oxysporum* trypsin-like protease.

[0307] Useful polyadenylation sequences for yeast host cells are described by Guo and Sherman, 1995, *Mol. Cellular Biol.* 15: 5983-5990.

[0308] The control sequence may also be a signal peptide coding region that encodes a signal peptide linked to the N-terminus of a polypeptide and directs the polypeptide into the cell's secretory pathway. The 5'-end of the coding sequence of the polynucleotide may inherently contain a signal peptide coding sequence naturally linked in translation reading frame with the segment of the coding sequence that encodes the polypeptide. Alternatively, the 5'-end of the coding sequence may contain a signal peptide coding sequence that is foreign to the coding sequence. A foreign signal peptide coding sequence may be required where the coding sequence does not naturally contain a signal peptide coding sequence. Alternatively, a foreign signal peptide coding sequence may simply replace the natural signal peptide coding sequence in order to enhance secretion of the polypeptide. However, any signal peptide coding sequence that directs the expressed polypeptide into the secretory pathway of a host cell may be used.

[0309] Effective signal peptide coding sequences for bacterial host cells are the signal peptide coding sequences obtained from the genes for *Bacillus* NCIB 11837 malto-
genic amylase, *Bacillus licheniformis* subtilisin, *Bacillus licheniformis* beta-lactamase, *Bacillus stearothermophilus* alpha-amylase, *Bacillus stearothermophilus* neutral proteases (nprT, nprS, nprM), and *Bacillus subtilis* prsA. Further signal peptides are described by Simonen and Palva, 1993, *Microbiological Reviews* 57: 109-137.

[0310] Effective signal peptide coding sequences for filamentous fungal host cells are the signal peptide coding sequences obtained from the genes for *Aspergillus niger* neutral amylase, *Aspergillus niger* glucoamylase, *Aspergillus oryzae* TAKA amylase, *Hericium insolens* cellulase, *Humicola insolens* endoglucanase V, *Humicola lanuginosa* lipase, and *Rhizomucor miehei* aspartic proteinase.

[0311] Useful signal peptides for yeast host cells are obtained from the genes for *Saccharomyces cerevisiae* alpha-factor and *Saccharomyces cerevisiae* invertase. Other useful signal peptide coding sequences are described by Romanos et al., 1992, supra.

[0312] The control sequence may also be a propeptide coding sequence that encodes a propeptide positioned at the N-terminus of a polypeptide. The resultant polypeptide is known as a proenzyme or propolypeptide (or a zymogen in some cases). A propolypeptide is generally inactive and can be converted to an active polypeptide by catalytic or autocatalytic cleavage of the propeptide from the propolypeptide. The propeptide coding sequence may be obtained from the genes for *Bacillus subtilis* alkaline protease (aprE), *Bacillus subtilis* neutral protease (npr7), *Myceliophthora*

thermophila laccase (WO 95/33836), *Rhizomucor miehei* aspartic proteinase, and *Saccharomyces cerevisiae* alpha-factor.

[0313] Where both signal peptide and propeptide sequences are present, the propeptide sequence is positioned next to the N-terminus of a polypeptide and the signal peptide sequence is positioned next to the N-terminus of the propeptide sequence.

[0314] It may also be desirable to add regulatory sequences that regulate expression of the polypeptide relative to the growth of the host cell. Examples of regulatory sequences are those that cause expression of the gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Regulatory sequences in prokaryotic systems include the lac, tac, and trp operator systems. In yeast, the ADH2 system or GAL1 system may be used. In filamentous fungi, the *Aspergillus niger* glucoamylase promoter, *Aspergillus oryzae* TAKA alpha-amylase promoter, and *Aspergillus oryzae* glucoamylase promoter, *Trichoderma reesei* cellobiohydrolyase I promoter, and *Trichoderma reesei* cellobiohydrolase II promoter may be used. Other examples of regulatory sequences are those that allow for gene amplification. In eukaryotic systems, these regulatory sequences include the dihydrofolate reductase gene that is amplified in the presence of methotrexate, and the metallothionein genes that are amplified with heavy metals. In these cases, the polynucleotide encoding the polypeptide would be operably linked to the regulatory sequence.

Expression Vectors

[0315] The present invention also relates to recombinant expression vectors comprising a polynucleotide of the present invention, a promoter, and transcriptional and translational stop signals. The various nucleotide and control sequences may be joined together to produce a recombinant expression vector that may include one or more convenient restriction sites to allow for insertion or substitution of the polynucleotide encoding the polypeptide at such sites. Alternatively, the polynucleotide may be expressed by inserting the polynucleotide or a nucleic acid construct comprising the polynucleotide into an appropriate vector for expression. In creating the expression vector, the coding sequence is located in the vector so that the coding sequence is operably linked with the appropriate control sequences for expression.

[0316] The recombinant expression vector may be any vector (e.g., a plasmid or virus) that can be conveniently subjected to recombinant DNA procedures and can bring about expression of the polynucleotide. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. The vector may be a linear or closed circular plasmid.

[0317] The vector may be an autonomously replicating vector, i.e., a vector that exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g., a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome. The vector may contain any means for assuring self-replication. Alternatively, the vector may be one that, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. Furthermore, a single vector or

plasmid or two or more vectors or plasmids that together contain the total DNA to be introduced into the genome of the host cell, or a transposon, may be used.

[0318] The vector preferably contains one or more selectable markers that permit easy selection of transformed, transfected, transduced, or the like cells. A selectable marker is a gene the product of which provides for biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like.

[0319] Examples of bacterial selectable markers are *Bacillus licheniformis* or *Bacillus subtilis* dal genes, or markers that confer antibiotic resistance such as ampicillin, chloramphenicol, kanamycin, neomycin, spectinomycin, or tetracycline resistance. Suitable markers for yeast host cells include, but are not limited to, ADE2, HIS3, LEU2, LYS2, MET3, TRP1, and URA3. Selectable markers for use in a filamentous fungal host cell include, but are not limited to, adeA (phosphoribosylaminoimidazole-succinocarboxamide synthase), adeB (phosphoribosyl-aminoimidazole synthase), amdS (acetamidase), argB (ornithine carbamoyltransferase), bar (phosphinothricin acetyltransferase), hph (hygromycin phosphotransferase), niaD (nitrate reductase), pyrG (orotidine-5'-phosphate decarboxylase), sc (sulfate adenyltransferase), and trpC (anthranilate synthase), as well as equivalents thereof. Preferred for use in an *Aspergillus* cell are *Aspergillus nidulans* or *Aspergillus oryzae* amdS and pyrG genes and a *Streptomyces hygroscopicus* bargene. Preferred for use in a *Trichoderma* cell are adeA, adeB, amdS, hph, and pyrG genes.

[0320] The selectable marker may be a dual selectable marker system as described in WO 2010/039889. In one aspect, the dual selectable marker is an hph-tk dual selectable marker system.

[0321] The vector preferably contains an element(s) that permits integration of the vector into the host cell's genome or autonomous replication of the vector in the cell independent of the genome.

[0322] For integration into the host cell genome, the vector may rely on the polynucleotide's sequence encoding the polypeptide or any other element of the vector for integration into the genome by homologous or non-homologous recombination. Alternatively, the vector may contain additional polynucleotides for directing integration by homologous recombination into the genome of the host cell at a precise location(s) in the chromosome(s). To increase the likelihood of integration at a precise location, the integrational elements should contain a sufficient number of nucleic acids, such as 100 to 10,000 base pairs, 400 to 10,000 base pairs, and 800 to 10,000 base pairs, which have a high degree of sequence identity to the corresponding target sequence to enhance the probability of homologous recombination. The integrational elements may be any sequence that is homologous with the target sequence in the genome of the host cell. Furthermore, the integrational elements may be non-encoding or encoding polynucleotides. On the other hand, the vector may be integrated into the genome of the host cell by non-homologous recombination.

[0323] For autonomous replication, the vector may further comprise an origin of replication enabling the vector to replicate autonomously in the host cell in question. The origin of replication may be any plasmid replicator mediating autonomous replication that functions in a cell. The term

“origin of replication” or “plasmid replicator” means a polynucleotide that enables a plasmid or vector to replicate *in vivo*.

[0324] Examples of bacterial origins of replication are the origins of replication of plasmids pBR322, pUC19, pACYC177, and pACYC184 permitting replication in *E. coli*, and pUB110, pE194, pTA1060, and pAMβ1 permitting replication in *Bacillus*.

[0325] Examples of origins of replication for use in a yeast host cell are the 2 micron origin of replication, ARS1, ARS4, the combination of ARS1 and CEN3, and the combination of ARS4 and CEN6.

[0326] Examples of origins of replication useful in a filamentous fungal cell are AMA1 and ANS1 (Gems et al., 1991, *Gene* 98: 61-67; Cullen et al., 1987, *Nucleic Acids Res.* 15: 9163-9175; WO 00/24883). Isolation of the AMA1 gene and construction of plasmids or vectors comprising the gene can be accomplished according to the methods disclosed in WO 00/24883.

[0327] More than one copy of a polynucleotide of the present invention may be inserted into a host cell to increase production of a polypeptide. An increase in the copy number of the polynucleotide can be obtained by integrating at least one additional copy of the sequence into the host cell genome or by including an amplifiable selectable marker gene with the polynucleotide where cells containing amplified copies of the selectable marker gene, and thereby additional copies of the polynucleotide, can be selected for by cultivating the cells in the presence of the appropriate selectable agent.

[0328] The procedures used to ligate the elements described above to construct the recombinant expression vectors of the present invention are well known to one skilled in the art (see, e.g., Sambrook et al., 1989, *supra*).

Host Cells

[0329] The present invention also relates to recombinant host cells, comprising a polynucleotide of the present invention operably linked to one or more control sequences that direct the production of a polypeptide of the present invention. A construct or vector comprising a polynucleotide is introduced into a host cell so that the construct or vector is maintained as a chromosomal integrant or as a self-replicating extra-chromosomal vector as described earlier. The term “host cell” encompasses any progeny of a parent cell that is not identical to the parent cell due to mutations that occur during replication. The choice of a host cell will to a large extent depend upon the gene encoding the polypeptide and its source.

[0330] The host cell may be any cell useful in the recombinant production of a polypeptide of the present invention, e.g., a prokaryote or a eukaryote.

[0331] The prokaryotic host cell may be any Gram-positive or Gram-negative bacterium. Gram-positive bacteria include, but are not limited to, *Bacillus*, *Clostridium*, *Enterococcus*, *Geobacillus*, *Lactobacillus*, *Lactococcus*, *Oceanobacillus*, *Staphylococcus*, *Streptococcus*, and *Streptomyces*. Gram-negative bacteria include, but are not limited to, *Campylobacter*, *E. coli*, *Flavobacterium*, *Fusobacterium*, *Helicobacter*, *Ilyobacter*, *Neissena*, *Pseudomonas*, *Salmonella*, and *Ureaplasma*.

[0332] The bacterial host cell may be any *Bacillus* cell including, but not limited to, *Bacillus alkalophilus*, *Bacillus altitudinis*, *Bacillus amyloliquefaciens*, *B. amyloliquefa-*

cians subsp. *plantarum*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus dausii*, *Bacillus coagulans*, *Bacillus firmus*, *Bacillus laetus*, *Bacillus lents*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus methylotrophicus*, *Bacillus pumilus*, *Bacillus safensis*, *Bacillus stearothermophilus*, *Bacillus subtilis*, and *Bacillus thuringiensis* cells.

[0333] The bacterial host cell may also be any *Streptococcus* cell including, but not limited to, *Streptococcus equisimilis*, *Streptococcus pyogenes*, *Streptococcus uberis*, and *Streptococcus equi* subsp. *Zooepidemicus* cells.

[0334] The bacterial host cell may also be any *Streptomyces* cell including, but not limited to, *Streptomyces achromogenes*, *Streptomyces avermitilis*, *Streptomyces coelicolor*, *Streptomyces griseus*, and *Streptomyces lividans* cells.

[0335] The introduction of DNA into a *Bacillus* cell may be effected by protoplast transformation (see, e.g., Chang and Cohen, 1979, *Mol. Gen. Genet.* 168: 111-115), competent cell transformation (see, e.g., Young and Spizizen, 1961, *J. Bacteriol.* 81: 823-829, or Dubnau and Davidoff-Abelson, 1971, *J. Mol. Biol.* 56: 209-221), electroporation (see, e.g., Shigekawa and Dower, 1988, *Biotechniques* 6: 742-751), or conjugation (see, e.g., Koehler and Thorne, 1987, *J. Bacteriol.* 169: 5271-5278). The introduction of DNA into an *E. coli* cell may be effected by protoplast transformation (see, e.g., Hanahan, 1983, *J. Mol. Biol.* 166: 557-580) or electroporation (see, e.g., Dower et al., 1988, *Nucleic Acids Res.* 16: 6127-6145). The introduction of DNA into a *Streptomyces* cell may be effected by protoplast transformation, electroporation (see, e.g., Gong et al., 2004, *Folia Microbiol.* (Praha) 49: 399-405), conjugation (see, e.g., Mazodier et al., 1989, *J. Bacteriol.* 171: 3583-3585), or transduction (see, e.g., Burke et al., 2001, *Proc. Natl. Acad. Sci. USA* 98: 6289-6294). The introduction of DNA into a *Pseudomonas* cell may be effected by electroporation (see, e.g., Choi et al., 2006, *J. Microbiol. Methods* 64: 391-397) or conjugation (see, e.g., Pinedo and Smets, 2005, *Appl. Environ. Microbiol.* 71: 51-57). The introduction of DNA into a *Streptococcus* cell may be effected by natural competence (see, e.g., Perry and Kuramitsu, 1981, *Infect. Immun.* 32:1295-1297), protoplast transformation (see, e.g., Catt and Jollick, 1991, *Microbios* 68: 189-207), electroporation (see, e.g., Buckley et al., 1999, *Appl. Environ. Microbiol.* 65: 3800-3804), or conjugation (see, e.g., Clewell, 1981, *Microbiol. Rev.* 45: 409-436). However, any method known in the art for introducing DNA into a host cell can be used.

[0336] The host cell may also be a eukaryote, such as a mammalian, insect, plant, or fungal cell.

[0337] The host cell may be a fungal cell. “Fungi” as used herein includes the phyla Ascomycota, Basidiomycota, Chytridiomycota, and Zygomycota as well as the Oomycota and all mitosporic fungi (as defined by Hawksworth et al., In, *Ainsworth and Bisby's Dictionary of The Fungi*, 8th edition, 1995, CAB International, University Press, Cambridge, UK).

[0338] The fungal host cell may be a yeast cell. “Yeast” as used herein includes ascosporogenous yeast (Endomycetales), basidiosporogenous yeast, and yeast belonging to the Fungi Imperfected (Blastomycetes). Since the classification of yeast may change in the future, for the purposes of this invention, yeast shall be defined as described in Biology and Activities of Yeast (Skinner, Passmore, and Davenport, editors, *Soc. App. Bacteriol. Symposium Series No. 9*, 1980).

[0339] The yeast host cell may be a *Candida*, *Hansenula*, *Kluyveromyces*, *Pichia*, *Saccharomyces*, *Schizosaccharomy-*

ces, or Yarrowia cell, such as a *Kluyveromyces lactis*, *Saccharomyces carlsbergensis*, *Saccharomyces cerevisiae*, *Saccharomyces diastaticus*, *Saccharomyces douglasii*, *Saccharomyces kluyveri*, *Saccharomyces norbensis*, *Saccharomyces oviformis*, or *Yarrowia lipolytica* cell.

[0340] The fungal host cell may be a filamentous fungal cell. "Filamentous fungi" include all filamentous forms of the subdivision Eumycota and Oomycota (as defined by Hawksworth et al., 1995, supra). The filamentous fungi are generally characterized by a mycelial wall composed of chitin, cellulose, glucan, chitosan, mannan, and other complex polysaccharides. Vegetative growth is by hyphal elongation and carbon catabolism is obligately aerobic. In contrast, vegetative growth by yeasts such as *Saccharomyces cerevisiae* is by budding of a unicellular thallus and carbon catabolism may be fermentative.

[0341] The filamentous fungal host cell may be an *Acremonium*, *Aspergillus*, *Aureobasidium*, *Bjerkandera*, *Ceriporiopsis*, *Chrysosporium*, *Coprinus*, *Coriolus*, *Cryptococcus*, *Filibasidium*, *Fusarium*, *Humicola*, *Magnaporthe*, *Mucor*, *Myceliophthora*, *Neocalhimastix*, *Neurospora*, *Paecilomyces*, *Penicillium*, *Phanerochaete*, *Phlebia*, *Piromyces*, *Pleurrotus*, *Schizophyllum*, *Talaromyces*, *Thermoascus*, *Thielavia*, *Tolypocladium*, *Trametes*, or *Trichoderma* cell.

[0342] For example, the filamentous fungal host cell may be an *Aspergillus awamori*, *Aspergillus foetidus*, *Aspergillus fumigatus*, *Aspergillus japonicus*, *Aspergillus nidulans*, *Aspergillus niger*, *Aspergillus oryzae*, *Bjerkandera adusta*, *Ceriporiopsis aneirina*, *Ceriporiopsis caregiea*, *Ceriporiopsis gilvescens*, *Ceriporiopsis pannocinta*, *Ceriporiopsis rivulosa*, *Ceriporiopsis subrufa*, *Ceriporiopsis subvermispora*, *Chrysosporium inops*, *Chrysosporium keratinophilum*, *Chrysosporium lucknowense*, *Chrysosporium merdarium*, *Chrysosporium pannicola*, *Chrysosporium queenslandicum*, *Chrysosporium tropicum*, *Chrysosporium zonatum*, *Coprinus cinereus*, *Coriolus hirsutus*, *Fusarium bactridioides*, *Fusarium cerealis*, *Fusarium crookwellense*, *Fusarium culmorum*, *Fusarium graminearum*, *Fusarium gramininum*, *Fusarium heterosporum*, *Fusarium negundi*, *Fusarium oxysporum*, *Fusarium reticulatum*, *Fusarium roseum*, *Fusarium sambucinum*, *Fusarium sarcochroum*, *Fusarium sporotrichioides*, *Fusarium sulphureum*, *Fusarium torulosum*, *Fusarium trichothecioïdes*, *Fusarium venenatum*, *Humicola insolens*, *Humicola lanuginose*, *Mucor miehei*, *Myceliophthora thermophila*, *Neurospora crassa*, *Penicillium purpurogenum*, *Phanerochaete chrysosporium*, *Phlebia radiata*, *Pleurotus eryngii*, *Thielavia terrestris*, *Trametes villosa*, *Trametes versicolor*, *Trichoderma harzianum*, *Trichoderma koningii*, *Trichoderma longibrachiatum*, *Trichoderma reesei*, or *Trichoderma viride* cell.

[0343] Fungal cells may be transformed by a process involving protoplast formation, transformation of the protoplasts, and regeneration of the cell wall in a manner known per se. Suitable procedures for transformation of *Aspergillus* and *Trichoderma* host cells are described in EP 238023, Yelton et al., 1984, *Proc. Natl. Acad. Sci. USA* 81: 1470-1474, and Christensen et al., 1988, *Bio/Technology* 6:1419-1422. Suitable methods for transforming *Fusarium* species are described by Malardier et al., 1989, *Gene* 78: 147-156, and WO 96/00787. Yeast may be transformed using the procedures described by Becker and Guarente, In Abelson, J. N. and Simon, M. I., editors, *Guide to Yeast Genetics and Molecular Biology, Methods in Enzymology*, Volume 194,

pp 182-187, Academic Press, Inc., New York; Ito et al., 1983, *J. Bacteriol.* 153:163; and Hinnen et al., 1978, *Proc. Natl. Acad. Sci. USA* 75:1920.

Methods of Production

[0344] The present invention also relates to methods of producing a polypeptide of the present invention, comprising (a) cultivating a cell, which in its wild-type form produces the polypeptide, under conditions conducive for production of the polypeptide; and optionally, (b) recovering the polypeptide.

[0345] The present invention also relates to recombinant methods of producing a polypeptide of the present invention, comprising (a) cultivating a recombinant host cell of the present invention capable of expressing the polypeptide under conditions conducive for production of the polypeptide; and optionally, (b) recovering the polypeptide.

[0346] One embodiment of the invention relates to a method of producing a polypeptide, wherein the polypeptide is selected from the group consisting of: SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 9, SEQ ID NO: 12, SEQ ID NO: 15, SEQ ID NO: 18, SEQ ID NO: 21, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 30, SEQ ID NO: 33, SEQ ID NO: 36, SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 45, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 57, SEQ ID NO: 60, SEQ ID NO: 63, SEQ ID NO: 66, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 75, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 84, SEQ ID NO: 87, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO: 96, SEQ ID NO: 99, SEQ ID NO: 102, SEQ ID NO: 105, SEQ ID NO: 108, and polypeptides having at least at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% hereto, comprising (a) cultivating a recombinant host cell of the present invention capable of expressing one of the polypeptides under conditions conducive for production of the polypeptide; and optionally, (b) recovering the polypeptide.

[0347] The host cells are cultivated in a nutrient medium suitable for production of the polypeptide using methods known in the art. For example, the cells may be cultivated by shake flask cultivation, or small-scale or large-scale fermentation (including continuous, batch, fed-batch, or solid-state fermentations) in laboratory or industrial fermentors in a suitable medium and under conditions allowing the polypeptide to be expressed and/or isolated. The cultivation takes place in a suitable nutrient medium comprising carbon and nitrogen sources and inorganic salts, using procedures known in the art. Suitable media are available from commercial suppliers or may be prepared according to published compositions (e.g., in catalogues of the American Type Culture Collection). If the polypeptide is secreted into the nutrient medium, the polypeptide can be recovered directly from the medium. If the polypeptide is not secreted, it can be recovered from cell lysates.

[0348] The polypeptide may be detected using methods known in the art that are specific for the polypeptides. These detection methods include, but are not limited to, use of specific antibodies, formation of an enzyme product, or disappearance of an enzyme substrate. For example, an enzyme assay may be used to determine the activity of the polypeptide.

[0349] The polypeptide may be recovered using methods known in the art. For example, the polypeptide may be recovered from the nutrient medium by conventional procedures including, but not limited to, collection, centrifugation, filtration, extraction, spray-drying, evaporation, or precipitation. In one aspect, a fermentation broth comprising the polypeptide is recovered.

[0350] The polypeptide may be purified by a variety of procedures known in the art including, but not limited to, chromatography (e.g., ion exchange, affinity, hydrophobic, chromatofocusing, and size exclusion), electrophoretic procedures (e.g., preparative isoelectric focusing), differential solubility (e.g., ammonium sulfate precipitation), SDS-PAGE, or extraction (see, e.g., *Protein Purification*, Janson and Ryden, editors, VCH Publishers, New York, 1989) to obtain substantially pure polypeptides.

[0351] In an alternative aspect, the polypeptide is not recovered, but rather a host cell of the present invention expressing the polypeptide is used as a source of the polypeptide. Another option is to use a supernatant in which the polypeptide has been expressed as a source of the polypeptide.

Formulation of Enzyme in Granules

[0352] Non-dusting granulates may be produced, e.g., as disclosed in U.S. Pat. Nos. 4,106,991 and 4,661,452 and may optionally be coated by methods known in the art. Examples of waxy coating materials are poly(ethylene oxide) products (polyethyleneglycol, PEG) with mean molar weights of 1000 to 20000; ethoxylated nonylphenols having from 16 to 50 ethylene oxide units; ethoxylated fatty alcohols in which the alcohol contains from 12 to 20 carbon atoms and in which there are 15 to 80 ethylene oxide units; fatty alcohols; fatty acids; and mono-, di- and triglycerides of fatty acids. Examples of film-forming coating materials suitable for application by fluid bed techniques are given in GB 1483591. Liquid enzyme preparations may, for instance, be stabilized by adding a polyol such as propylene glycol, a sugar or sugar alcohol, lactic acid or boric acid according to established methods. Protected enzymes may be prepared according to the method disclosed in EP 238216.

[0353] The composition(s) of the invention may be formulated as a granule, for example as a co-granule that combines one or more enzymes. Each enzyme will then be present in more granules, securing a more uniform distribution of enzymes in the detergent. This also reduces the physical segregation of different enzymes due to different particle sizes. Methods for producing multi-enzyme co-granulates for the detergent industry are disclosed in the IP.com disclosure IPCOM000200739D.

[0354] Another example of formulation of enzymes by the use of co-granulates is disclosed in WO 2013/188331, which relates to a detergent composition comprising (a) a multi-enzyme co-granule; (b) less than 10 wt % zeolite (anhydrous basis); and (c) less than 10 wt % phosphate salt (anhydrous basis), wherein said enzyme co-granule comprises from 10 to 98 wt % moisture sink component and the composition additionally comprises from 20 to 80 wt % detergent moisture sink component. WO 2013/188331 also relates to a method of treating and/or cleaning a surface, preferably a fabric surface comprising the steps of (i) contacting said surface with the detergent composition in aqueous wash liquor, (ii) rinsing and/or drying the surface.

[0355] A multi-enzyme co-granule may comprise an enzyme of the invention and one or more enzymes selected from the group consisting of proteases, lipases, cellulases, xyloglucanases, perhydrolases, peroxidases, lipoxygenases, laccases, hemicellulases, proteases, cellulases, cellobiose dehydrogenases, xylanases, phospholipases, esterases, cutinases, pectinases, mannanases, pectate lyases, keratinases, reductases, oxidases, phenoloxidases, ligninases, pullulanases, tannases, pentosanases, lichenases, glucanases, arabinosidases, hyaluronidases, chondroitinase, amylases, nucleases, hexosaminidases and mixtures thereof.

[0356] An embodiment of the invention relates to an enzyme granule/particle comprising the enzyme of the invention. The granule is composed of a core, and optionally one or more coatings (outer layers) surrounding the core. Typically, the granule/particle size, measured as equivalent spherical diameter (volume based average particle size), of the granule is 20-2000 μm , particularly 50-1500 μm , 100-1500 μm or 250-1200 μm .

[0357] The core may include additional materials such as fillers, fibre materials (cellulose or synthetic fibers), stabilizing agents, solubilizing agents, suspension agents, viscosity regulating agents, light spheres, plasticizers, salts, lubricants and fragrances.

[0358] The core may include binders, such as synthetic polymer, wax, fat, or carbohydrate.

[0359] The core may comprise a salt of a multivalent cation, a reducing agent, an antioxidant, a peroxide decomposing catalyst and/or an acidic buffer component, typically as a homogenous blend.

[0360] The core may consist of an inert particle with the enzyme absorbed into it, or applied onto the surface, e.g., by fluid bed coating.

[0361] The core may have a diameter of 20-2000 μm , particularly 50-1500 μm , 100-1500 μm or 250-1200 μm .

[0362] The core can be prepared by granulating a blend of the ingredients, e.g., by a method comprising granulation techniques such as crystallization, precipitation, pan-coating, fluid bed coating, fluid bed agglomeration, rotary atomization, extrusion, prilling, spheroidization, size reduction methods, drum granulation, and/or high shear granulation.

[0363] Methods for preparing the core can be found in *Handbook of Powder Technology: Particle size enlargement* by C. E. Capes; Volume 1; 1980; Elsevier.

[0364] The core of the enzyme granule/particle may be surrounded by at least one coating, e.g., to improve the storage stability, to reduce dust formation during handling, or for coloring the granule. The optional coating(s) may include a salt coating, or other suitable coating materials, such as polyethylene glycol (PEG), methyl hydroxy-propyl cellulose (MHPC) and polyvinyl alcohol (PVA). Examples of enzyme granules with multiple coatings are shown in WO 93/07263 and WO 97/23606.

[0365] The coating may be applied in an amount of at least 0.1% by weight of the core, e.g., at least 0.5%, 1% or 5%. The amount may be at most 100%, 70%, 50%, 40% or 30%.

[0366] The coating is preferably at least 0.1 μm thick, particularly at least 0.5 μm , at least 1 μm or at least 5 μm . In a particular embodiment, the thickness of the coating is below 100 μm . In a more particular embodiment the thickness of the coating is below 60 μm . In an even more particular embodiment the total thickness of the coating is below 40 μm .

[0367] The coating should encapsulate the core unit by forming a substantially continuous layer. A substantially continuous layer is to be understood as a coating having few or no holes, so that the core unit it is encapsulating/enclosing has few or none uncoated areas. The layer or coating should be homogeneous in thickness.

[0368] The coating can further contain other materials as known in the art, e.g., fillers, antisticking agents, pigments, dyes, plasticizers and/or binders, such as titanium dioxide, kaolin, calcium carbonate or talc.

[0369] A salt coating may comprise at least 60% by weight w/w of a salt, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or at least 99% by weight w/w.

[0370] The salt may be added from a salt solution where the salt is completely dissolved or from a salt suspension wherein the fine particles is less than 50 µm, such as less than 10 µm or less than 5 µm.

[0371] The salt coating may comprise a single salt or a mixture of two or more salts. The salt may be water soluble, in particular, having a solubility at least 0.1 grams in 100 g of water at 20° C., preferably at least 0.5 g per 100 g water, e.g., at least 1 g per 100 g water, e.g., at least 5 g per 100 g water.

[0372] The salt may be an inorganic salt, e.g., salts of sulfate, sulfite, phosphate, phosphonate, nitrate, chloride or carbonate or salts of simple organic acids (less than 10 carbon atoms, e.g., 6 or less carbon atoms) such as citrate, malonate or acetate. Examples of cations in these salts are alkali or earth alkali metal ions, the ammonium ion or metal ions of the first transition series, such as sodium, potassium, magnesium, calcium, zinc or aluminum. Examples of anions include chloride, bromide, iodide, sulfate, sulfite, bisulfite, thiosulfate, phosphate, monobasic phosphate, dibasic phosphate, hypophosphate, dihydrogen pyrophosphate, tetraborate, borate, carbonate, bicarbonate, metasilicate, citrate, malate, maleate, malonate, succinate, lactate, formate, acetate, butyrate, propionate, benzoate, tartrate, ascorbate or gluconate. In particular alkali- or earth alkali metal salts of sulfate, sulfite, phosphate, phosphonate, nitrate, chloride or carbonate or salts of simple organic acids such as citrate, malonate or acetate may be used.

[0373] The salt in the coating may have a constant humidity at 20° C. above 60%, particularly above 70%, above 80% or above 85%, or it may be another hydrate form of such a salt (e.g., anhydrate). The salt coating may be as described in WO 00/01793 or WO 2006/034710.

[0374] Specific examples of suitable salts are NaCl (CH_{20° C.}=76%), Na₂CO₃ (CH_{20° C.}=92%), NaNO₃ (CH_{20° C.}=73%), Na₂HPO₄ (CH_{20° C.}=95%), Na₃PO₄ (CH_{25° C.}=92%), NH₄Cl (CH_{20° C.}=79.5%), (NH₄)₂HPO₄ (CH_{20° C.}=93.0%), NH₄H₂PO₄ (CH_{20° C.}=93.1%), (NH₄)₂SO₄ (CH_{20° C.}=81.1%), KCl (CH_{20° C.}=85%), K₂HPO₄ (CH_{20° C.}=92%), KH₂PO₄ (CH_{20° C.}=96.5%), KNO₃ (CH_{20° C.}=93.5%), Na₂SO₄ (CH_{20° C.}=93%), K₂SO₄ (CH_{20° C.}=98%), KHSO₄ (CH_{20° C.}=86%), MgSO₄ (CH_{20° C.}=90%), ZnSO₄ (CH_{20° C.}=90%) and sodium citrate (CH_{25° C.}=86%). Other examples include NaH₂PO₄, (NH₄)₂HPO₄, CuSO₄, Mg(NO₃)₂ and magnesium acetate.

[0375] The salt may be in anhydrous form, or it may be a hydrated salt, i.e., a crystalline salt hydrate with bound water(s) of crystallization, such as described in WO 99/32595. Specific examples include anhydrous sodium sulfate (Na₂SO₄), anhydrous magnesium sulfate (MgSO₄),

magnesium sulfate heptahydrate (MgSO₄·7H₂O), zinc sulfate heptahydrate (ZnSO₄·7H₂O), sodium phosphate dibasic heptahydrate (Na₂HPO₄·7H₂O), magnesium nitrate hexahydrate (Mg(No₃)₂(6H₂O)), sodium citrate dihydrate and magnesium acetate tetrahydrate. Preferably the salt is applied as a solution of the salt, e.g., using a fluid bed.

[0376] Thus, in a further aspect, the present invention provides a granule, which comprises:

[0377] (a) a core comprising an enzyme according to the invention,

[0378] (b) optionally a coating consisting of one or more layer(s) surrounding the core; and

[0379] (c) preferably the granule is a co-granulate comprising one or more additional enzyme, preferably selected from proteases, amylases, cellulases.

[0380] In one embodiment, the present invention provides a granule, which comprises:

[0381] (a) a core comprising a polypeptide having peptidoglycan removal activity, wherein the polypeptide comprises the motif N[IV]X[AG][GAS]A[AY][LV]L (SEQ ID NO: 111),

[0382] (b) optionally a coating consisting of one or more layer(s) surrounding the core; and

[0383] (c) preferably the granule is a co-granulate comprising one or more additional enzyme, preferably selected from proteases, amylases, cellulases.

[0384] In one embodiment, the present invention provides a granule, which comprises:

[0385] (a) a core comprising a polypeptide having peptidoglycan removal activity, wherein the polypeptide is selected from the group consisting of: SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 9, SEQ ID NO: 12, SEQ ID NO: 15, SEQ ID NO: 18, SEQ ID NO: 21, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 30, SEQ ID NO: 33, SEQ ID NO: 36, SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 45, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 57, SEQ ID NO: 60, SEQ ID NO: 63, SEQ ID NO: 66, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 75, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 84, SEQ ID NO: 87, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO: 96, SEQ ID NO: 99, SEQ ID NO: 102, SEQ ID NO: 105, SEQ ID NO: 108 and polypeptides having at least at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% hereto,

[0386] (b) optionally a coating consisting of one or more layer(s) surrounding the core; and

[0387] (c) preferably the granule is a co-granulate comprising one or more additional enzyme, preferably selected from proteases, amylases, cellulases.

Fermentation Broth Formulations or Cell Compositions

[0388] The present invention also relates to a fermentation broth formulation or a cell composition comprising a polypeptide of the present invention. The fermentation broth product further comprises additional ingredients used in the fermentation process, such as, for example, cells (including the host cells containing the gene encoding the polypeptide of the present invention which are used to produce the polypeptide of interest), cell debris, biomass, fermentation media and/or fermentation products. In some embodiments,

the composition is a cell-killed whole broth containing organic acid(s), killed cells and/or cell debris, and culture medium.

[0389] The term "fermentation broth" as used herein refers to a preparation produced by cellular fermentation that undergoes no or minimal recovery and/or purification. For example, fermentation broths are produced when microbial cultures are grown to saturation, incubated under carbon-limiting conditions to allow protein synthesis (e.g., expression of enzymes by host cells) and secretion into cell culture medium. The fermentation broth can contain unfractionated or fractionated contents of the fermentation materials derived at the end of the fermentation. Typically, the fermentation broth is unfractionated and comprises the spent culture medium and cell debris present after the microbial cells (e.g., filamentous fungal cells) are removed, e.g., by centrifugation. In some embodiments, the fermentation broth contains spent cell culture medium, extracellular enzymes, and viable and/or nonviable microbial cells.

[0390] In an embodiment, the fermentation broth formulation and cell compositions comprise a first organic acid component comprising at least one 1-5 carbon organic acid and/or a salt thereof and a second organic acid component comprising at least one 6 or more carbon organic acid and/or a salt thereof. In a specific embodiment, the first organic acid component is acetic acid, formic acid, propionic acid, a salt thereof, or a mixture of two or more of the foregoing and the second organic acid component is benzoic acid, cyclohexanecarboxylic acid, 4-methylvaleric acid, phenylacetic acid, a salt thereof, or a mixture of two or more of the foregoing.

[0391] In one aspect, the composition contains at least one organic acid, and optionally further contains killed cells and/or cell debris. In one embodiment, the killed cells and/or cell debris are removed from a cell-killed whole broth to provide a composition that is free of these components.

[0392] The fermentation broth formulations or cell compositions may further comprise a preservative and/or antimicrobial (e.g., bacteriostatic) agent, including, but not limited to, sorbitol, sodium chloride, potassium sorbate, and others known in the art.

[0393] The cell-killed whole broth or composition may contain the unfractionated contents of the fermentation materials derived at the end of the fermentation. Typically, the cell-killed whole broth or composition contains the spent culture medium and cell debris present after the microbial cells (e.g., filamentous fungal cells) are grown to saturation, incubated under carbon-limiting conditions to allow protein synthesis. In some embodiments, the cell-killed whole broth or composition contains the spent cell culture medium, extracellular enzymes, and killed filamentous fungal cells. In some embodiments, the microbial cells present in the cell-killed whole broth or composition can be permeabilized and/or lysed using methods known in the art.

[0394] A whole broth or cell composition as described herein is typically a liquid, but may contain insoluble components, such as killed cells, cell debris, culture media components, and/or insoluble enzyme(s). In some embodiments, insoluble components may be removed to provide a clarified liquid composition.

[0395] The whole broth formulations and cell compositions of the present invention may be produced by a method described in WO 90/15861 or WO 2010/096673.

Compositions

[0396] The present invention also relates to compositions comprising a polypeptide of the present invention. Preferably, the compositions are enriched in such a polypeptide. The term "enriched" indicates that the peptidoglycan degradation activity of the composition has been increased, e.g., with an enrichment factor of at least 1.1.

[0397] The compositions may comprise a polypeptide of the present invention as the major enzymatic component, e.g., a mono-component composition. Alternatively, the compositions may comprise multiple enzymatic activities, such as one or more enzymes selected from the group consisting of hydrolase, isomerase, ligase, lyase, oxidoreductase, or transferase, e.g., an alpha-galactosidase, alpha-glucosidase, aminopeptidase, amylase, beta-galactosidase, beta-glucosidase, beta-xylosidase, carbohydrolase, carboxypeptidase, catalase, cellobiohydrolase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase, deoxyribonuclease, endoglucanase, esterase, glucoamylase, invertase, laccase, lipase,mannosidase, mutanase, oxidase, pectinolytic enzyme, peroxidase, phytase, polyphenoloxidase, proteolytic enzyme, ribonuclease, transglutaminase, or xylanase.

[0398] The invention relates to cleaning compositions, e.g., detergent compositions comprising peptidoglycan degradation enzyme in combination with one or more additional cleaning composition components. The choice of additional components is within the skill of the artisan and includes conventional ingredients, including the exemplary non-limiting components set forth below.

[0399] One aspect of the invention relates to a cleaning composition comprising a polypeptide having peptidoglycan degradation activity, wherein the polypeptide comprises the motif N[IV]X[AG][GAS]A[AY][LV]L (SEQ ID NO: 111), and at least one cleaning component.

[0400] One aspect of the invention relates to a cleaning composition comprising:

[0401] a) a polypeptide having peptidoglycan degradation activity, wherein the polypeptide is selected from the group consisting of:

[0402] i. a polypeptide having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 3,

[0403] ii. a polypeptide having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 6,

[0404] iii. a polypeptide having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 9,

[0405] iv. a polypeptide having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 12,

at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 78,

[0428] xxvii. a polypeptide having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 81,

[0429] xxviii. a polypeptide having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 84,

[0430] xxix. a polypeptide having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 87,

[0431] xxx. a polypeptide having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 90,

[0432] xxxi. a polypeptide having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 93,

[0433] xxxii. a polypeptide having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 96,

[0434] xxxiii. a polypeptide having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 99,

[0435] xxxiv. a polypeptide having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 102,

[0436] xxxv. a polypeptide having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 105, and

[0437] xxxvi. a polypeptide having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 108, and

[0438] b) at least one cleaning component, preferably selected from surfactants, builders, bleach components, polymers, dispersing agents and additional enzymes.

[0439] One embodiment relates to a cleaning composition comprising:

[0440] a) a polypeptide having peptidoglycan removal activity and which comprises the motif N[IV]X[AG] [GAS]A[AY][LV]L (SEQ ID NO: 111), wherein the polypeptide is selected from the group consisting of: SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 9, SEQ ID NO: 12, SEQ ID NO: 15, SEQ ID NO: 18, SEQ ID NO: 21, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 30, SEQ ID NO: 33, SEQ ID NO: 36, SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 45, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 57, SEQ ID NO: 60, SEQ ID NO: 63, SEQ ID NO: 66, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 75, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 84, SEQ ID NO: 87, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO: 96, SEQ ID NO: 99, SEQ ID NO: 102, SEQ ID NO: 105, SEQ ID NO: 108 and polypeptides having at least at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% hereto; and

[0441] b) at least one cleaning component, preferably selected from surfactants, builders, bleach components, polymers, dispersing agents and additional enzymes.

[0442] The peptidoglycan degradation enzyme may be included in the cleaning composition of the present invention at a level of at least 0.0001 to at least 100, at least 0.001 to at least 100, at least 0.01 to at least 100, at least 0.02 to at least 100, at least 0.01 to at least 100, at least 0.1 to at least 100, at least 0.2 to at least 100, at least 0.5 to at least 100 mg/mL, preferably, the concentration of peptidoglycan degradation enzyme in the cleaning composition, e.g., detergent is in the range 0.01 to 100, 0.1 to 50 or 1 to 10 mg/ml. Thus, the detergent composition may comprise at least 0.00008%, preferably at least 0.002%, 0.003%, 0.004%, 0.005%, 0.006%, 0.008%, 0.01%, 0.02%, 0.03%, 0.05%, 0.1%, 0.2%, 0.3%, 0.4%, 0.6%, 0.7%, 0.8%, 0.9% or 1.0% of peptidoglycan degradation enzyme protein.

[0443] The choice of cleaning components may include, for textile care, the consideration of the type of textile to be cleaned, the type and/or degree of soiling, the temperature at which cleaning is to take place, and the formulation of the detergent product. Although components mentioned below are categorized by general header according to a particular functionality, this is not to be construed as a limitation, as a component may comprise additional functionalities as will be appreciated by the skilled artisan.

Surfactants

[0444] The cleaning composition may comprise one or more surfactants, which may be anionic and/or cationic and/or non-ionic and/or semi-polar and/or zwitterionic, or a mixture thereof. In a particular embodiment, the detergent composition includes a mixture of one or more nonionic surfactants and one or more anionic surfactants. The surfactant(s) is typically present at a level of from about 1% to 70% by weight, such as about 1 wt % to about 40 wt %, or about 3 wt % to about 20 wt %, or about 3 wt % to about 10 wt %.

[0445] The surfactant(s) is chosen based on the desired cleaning application, and may include any conventional surfactant(s) known in the art.

[0446] When included therein the detergent will usually contain from about 1% to about 70% by weight of an anionic surfactant, such as from about 5 wt % to about 50 wt %, including from about 5 wt % to about 20 wt %, or from about 15 wt % to about 20 wt %, or from about 20 wt % to about 25 wt % or at least 30 wt %, at least 40 wt % or at least 50 wt % of an anionic surfactant. Non-limiting examples of anionic surfactants include sulfates and sulfonates, in particular, alkylbenzenesulfonates, such as linear alkylbenzenesulfonates (LAS), isomers of LAS, branched alkylbenzenesulfonates (BABS), phenylalkanesulfonates, alpha-olefinsulfonates (AOS), olefin sulfonates, alkene sulfonates, alkane-2,3-diylibis(sulfates), hydroxyalkanesulfonates and disulfonates, alkyl sulfates (AS) such as sodium dodecyl sulfate (SDS), fatty alcohol sulfates (FAS), primary alcohol sulfates (PAS), alcohol ethersulfates (AES or AEOS or FES, also known as alcohol ethoxysulfates or fatty alcohol ether sulfates), secondary alkanesulfonates (SAS), paraffin sulfonates (PS), ester sulfonates, sulfonated fatty acid glycerol esters, alpha-sulfo fatty acid methyl esters (alpha-SFMe or SES) including methyl ester sulfonate (MES), alkyl- or alkenylsuccinic acid, dodeceny/tetradecenyl succinic acid (DTSA), fatty acid derivatives of amino acids, diesters and monoesters of sulfo-succinic acid or salt of fatty acids (soap), and combinations thereof.

[0447] When included therein the detergent will usually contain from about 1% to about 40% by weight of a cationic surfactant, for example from about 0.5% to about 30%, in particular, from about 1% to about 20%, from about 3% to about 10%, such as from about 3% to about 5%, from about 8% to about 12% or from about 10% to about 12%. Non-limiting examples of cationic surfactants include alkyldimethyllethanolamine quat (ADMEAQ), cetyltrimethylammonium bromide (CTAB), dimethyldistearylammnonium chloride (DSDMAC), and alkylbenzyldimethylammnonium, alkyl quaternary ammonium compounds, alkoxylated quaternary ammonium (AQA) compounds, ester quats, and combinations thereof.

[0448] When included therein, the detergent will usually contain from about 0.2% to about 40% by weight of a nonionic surfactant, for example from about 0.5 wt % to about 30 wt %, in particular from about 1 wt % to about 20 wt %, from about 3 wt % to about 10 wt %, such as from about 3% wt to about 5 wt %, from about 8 wt % to about 12 wt %, or from about 10 wt % to about 12 wt %. Non-limiting examples of nonionic surfactants include alcohol ethoxylates (AE or AEO), alcohol propoxylates, propoxylated fatty alcohols (PFA), alkoxylated fatty acid alkyl esters, such as ethoxylated and/or propoxylated fatty acid alkyl esters, alkylphenol ethoxylates (APE), nonylphenol ethoxylates (NPE), alkylpolyglycosides (APG), alkoxylated amines, fatty acid monoethanolamides (FAM), fatty acid diethanolamides (FADA), ethoxylated fatty acid monoethanolamides (EFAM), propoxylated fatty acid monoethanolamides (PFAM), polyhydroxyalkyl fatty acid amides, or N-acyl N-alkyl derivatives of glucosamine (glucamides, GA, or fatty acid glucamides, FAGA), as well as products available under the trade names SPAN and TWEEN, and combinations thereof.

[0449] When included therein the detergent will usually contain from about 0.01% to about 10% by weight of a

semipolar surfactant. Non-limiting examples of semipolar surfactants include amine oxides (AO) such as alkyldimethylamineoxide, N-(coco alkyl)-N,N-dimethylamine oxide and N-(tallow-alkyl)-N,N-bis(2-hydroxyethyl)amine oxide, and combinations thereof.

[0450] When included therein the detergent will usually contain from about 0.01% to about 10% by weight of a zwitterionic surfactant. Non-limiting examples of zwitterionic surfactants include betaines such as alkyldimethylbetaines, sulfobetaines, and combinations thereof.

[0451] Typically, more than one surfactant is present in the cleaning composition, e.g., at least one anionic and at least one non-ionic surfactant. Preferably the amount of all surfactant present (total amount) i.e., the amount of anionic, non-ionic, zwitterionic and cationic surfactant present is preferably from about 1 wt % to 80 wt % by weight, such as about 1 wt % to 70 wt %, such as about 1 wt % to 50 wt % such as about 1 wt % to about 40 wt %, or about 5 wt % to about 40 wt %, or about 10 wt % to about 60 wt %. The ratio between the surfactants present depends on the specific composition but the weight ratios may be when an anionic and non-ionic surfactant is included in the composition a weight ratio of the anionic to nonionic surfactant from; 30:1 to 10:1, 20:1 to 1:10, 25:1 to 1:2, 20:1 to 1:5.

[0452] One embodiment relates to a cleaning composition comprising a peptidoglycan degrading enzyme, preferably having N-acetylmuramyl-L-alanine amidase and peptidoglycan lyase activity and wherein the cleaning component is at least one surfactant, preferably anionic and/or nonionic, preferably wherein the composition comprises from 1 to 70 wt %, preferably from 5 to 40 wt % surfactant, wherein the surfactant preferably is selected from alkylbenzenesulfonates, e.g., LAS, alkyl sulfates (AS) and mixtures thereof, preferably the cleaning composition comprises at least 20 wt % alkylbenzenesulfonate surfactant.

[0453] One embodiment relates to a cleaning composition comprising a peptidoglycan degrading enzyme, preferably having N-acetylmuramyl-L-alanine amidase and peptidoglycan lyase activity, wherein the cleaning composition comprises at least one anionic surfactant and wherein the cleaning composition additionally comprises a nonionic surfactant, and preferably wherein the weight ratio of the anionic to nonionic surfactant is from 25:1 to 1:2 or from 1.5:1 to 1:10.

Builders and Co-Builders

[0454] The cleaning composition may contain about 0-65% by weight, such as about 5% to about 50%, such as about 0.5% to about 20% of a detergent builder or co-builder, or a mixture thereof. In a dish wash detergent, the level of builder is typically 40-65%, particularly 50-65%. The builder and/or co-builder may particularly be a chelating agent that forms water-soluble complexes with Ca and Mg. Any builder and/or co-builder known in the art for use in cleaning detergents may be utilized. Non-limiting examples of builders include zeolites, diphosphates (pyrophosphates), triphosphates such as sodium tripolyphosphate (STP or STPP), carbonates such as sodium carbonate, soluble silicates such as sodium metasilicate, layered silicates (e.g., SKS-6 from Hoechst), ethanolamines such as 2-aminoethan-1-ol (MEA), diethanolamine (DEA, also known as 2,2'-iminodiethan-1-ol), triethanolamine (TEA, also known as 2,2',2"-nitrilotriethan-1-ol), and (carboxymethyl)inulin (CMI), and combinations thereof.

[0455] The detergent composition may also contain 0-50% by weight, such as about 5% to about 30%, of a detergent co-builder. The detergent composition may include a co-builder alone, or in combination with a builder, for example a zeolite builder. Non-limiting examples of co-builders include homopolymers of polyacrylates or copolymers thereof, such as poly(acrylic acid) (PAA) or copoly (acrylic acid/maleic acid) (PAA/PMA). Further non-limiting examples include citrate, chelators such as aminocarboxylates, aminopolycarboxylates and phosphonates, and alkyl- or alkenylsuccinic acid. Additional specific examples include 2,2',2"-nitrilotriacetic acid (NTA), ethylenediaminetetraacetic acid (EDTA), diethylenetriaminepentaacetic acid (DTPA), iminodisuccinic acid (IDS), ethylenediamine-N,N'-disuccinic acid (EDDS), methylglycinediacetic acid (MGDA), glutamic acid-N,N-diacetic acid (GLDA), 1-hydroxyethane-1,1-diphosphonic acid (HEDP), ethylenediaminetetra(methyleneephosphonic acid) (EDTMA), diethylenetriaminepentakis-(methyleneephosphonic acid) (DTMPA or DTPMPA), N-(2-hydroxyethyl)iminodiacetic acid (EDG), aspartic acid-N-monoacetic acid (ASMA), aspartic acid-N,N-diacetic acid (ASDA), aspartic acid-N-monopropionic acid (ASMP), iminodisuccinic acid (IDA), N-(2-sulfomethyl)-aspartic acid (SMAS), N-(2-sulfoethyl)-aspartic acid (SEAS), N-(2-sulfomethyl)-glutamic acid (SMGL), N-(2-sulfoethyl)-glutamic acid (SEGL), N-methyliminoacetic acid (MIDA), α -alanine-N,N-diacetic acid (α -ALDA), serine-N,N-diacetic acid (SEDA), isoserine-N, N-diacetic acid (ISDA), phenylalanine-N,N-diacetic acid (PHDA), anthranilic acid-N,N-diacetic acid (ANDA), sulfanilic acid-N,N-diacetic acid (SLDA), taurine-N,N-diacetic acid (TUDA) and sulfomethyl-N,N-diacetic acid (SMDA), N-(2-hydroxyethyl)ethylenediamine-N,N',N"-triacetic acid (HEDTA), diethanolglycine (DEG), diethylenetriamine penta(methyleneephosphonic acid) (DTPMP), aminotris(methyleneephosphonic acid) (ATMP), and combinations and salts thereof. Further exemplary builders and/or co-builders are described in, e.g., WO 2009/102854, U.S. Pat. No. 5,977,053.

Bleaching Systems

[0456] The cleaning composition may contain 0-30% by weight, such as about 1% to about 20%, such as about 0.01% to about 10% of a bleaching system. Any bleaching system comprising components known in the art for use in cleaning detergents may be utilized. Suitable bleaching system components include sources of hydrogen peroxide; sources of peracids; and bleach catalysts or boosters.

Sources of Hydrogen Peroxide:

[0457] Suitable sources of hydrogen peroxide are inorganic persalts, including alkali metal salts such as sodium percarbonate and sodium perborates (usually mono- or tetrahydrate), and hydrogen peroxide-urea (1/1).

Sources of Peracids:

[0458] Peracids may be (a) incorporated directly as pre-formed peracids or (b) formed in situ in the wash liquor from hydrogen peroxide and a bleach activator (perhydrolysis) or

(c) formed in situ in the wash liquor from hydrogen peroxide and a perhydrolase and a suitable substrate for the latter, e.g., an ester.

[0459] a) Suitable preformed peracids include, but are not limited to, peroxycarboxylic acids such as peroxybenzoic acid and its ring-substituted derivatives, peroxy- α -naphthoic acid, peroxyphthalic acid, peroxylauric acid, peroxystearic acid, ε -phthalimidoperoxycaproic acid [phthalimidoperoxyhexanoic acid (PAP)], and o-carboxybenzamidoperoxycaproic acid; aliphatic and aromatic diperoxydicarboxylic acids such as diperoxydodecanedioic acid, diperoxyazelaic acid, diperoxysebacic acid, diperoxybrassylic acid, 2-decyldiperoxybutanedioic acid, and diperoxyphthalic, -isophthalic and -terephthalic acids; perimidic acids; peroxymonosulfuric acid; peroxydisulfuric acid; peroxyphosphoric acid; peroxysilicic acid; and mixtures of said compounds. It is understood that the peracids mentioned may in some cases be best added as suitable salts, such as alkali metal salts (e.g., Oxone®) or alkaline earth-metal salts.

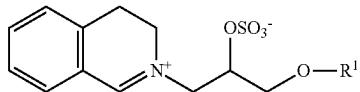
[0460] b) Suitable bleach activators include those belonging to the class of esters, amides, imides, nitriles or anhydrides and, where applicable, salts thereof. Suitable examples are tetraacetyl ethylenediamine (TAED), sodium 4-[3,5,5-trimethylhexanoyl]oxy]benzene-1-sulfonate (ISONOBS), sodium 4-(dodecanoxyloxy)benzene-1-sulfonate (LOBS), sodium 4-(decanoxyloxy)benzene-1-sulfonate, 4-(decanoxyloxy)benzoic acid (DOBA), sodium 4-(nonanoyloxy)benzene-1-sulfonate (NOBS), and/or those disclosed in WO 98/17767. A particular family of bleach activators of interest was disclosed in EP 624154 and particularly preferred in that family is acetyl triethyl citrate (ATC). ATC or a short chain triglyceride like triacetin has the advantage that they are environmentally friendly. Furthermore, acetyl triethyl citrate and triacetin have good hydrolytical stability in the product upon storage and are efficient bleach activators. Finally, ATC is multifunctional, as the citrate released in the perhydrolysis reaction may function as a builder.

Bleach Catalysts and Boosters

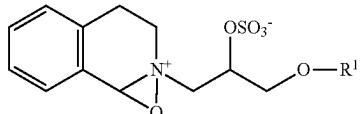
[0461] The bleaching system may also include a bleach catalyst or booster. Some non-limiting examples of bleach catalysts that may be used in the compositions of the present invention include manganese oxalate, manganese acetate, manganese-collagen, cobalt-amine catalysts and manganese triazacyclononane (MnTACN) catalysts; particularly preferred are complexes of manganese with 1,4,7-trimethyl-1,4,7-triazacyclononane (Me3-TACN) or 1,2,4,7-tetramethyl-1,4,7-triazacyclononane (Me4-TACN), in particular Me3-TACN, such as the dinuclear manganese complex [(Me3-TACN)Mn(O)3Mn(Me3-TACN)](PF6)2, and [2,2',2"-nitritolistris(ethane-1,2-diylazanyllylidene- κ N-methanyllylidene)triphenolato- κ 3O]manganese(III). The bleach catalysts may also be other metal compounds; such as iron or cobalt complexes.

[0462] In some embodiments, where a source of a peracid is included, an organic bleach catalyst or bleach booster may be used having one of the following formulae:

[0463] (i)



[0464] (ii)



(iii) and mixtures thereof; wherein each R1 is independently a branched alkyl group containing from 9 to 24 carbons or linear alkyl group containing from 11 to 24 carbons, preferably each R1 is independently a branched alkyl group containing from 9 to 18 carbons or linear alkyl group containing from 11 to 18 carbons, more preferably each R1 is independently selected from the group consisting of 2-propylheptyl, 2-butyloctyl, 2-pentylnonyl, 2-hexyldecyl, dodecyl, tetradecyl, hexadecyl, octadecyl, isononyl, isodecyl, isotridecyl and isopentadecyl.

[0465] Other exemplary bleaching systems are described in, e.g., WO 2007/087258, WO 2007/087244, WO 2007/087259, EP 1867708 (Vitamin K) and WO 2007/087242. Suitable photobleaches may for example be sulfonated zinc or aluminum phthalocyanines.

Metal Care Agents

[0466] Metal care agents may prevent or reduce the tarnishing, corrosion or oxidation of metals, including aluminium, stainless steel and non-ferrous metals, such as silver and copper. Suitable examples include one or more of the following:

[0467] (a) benzatriazoles, including benzotriazole or bis-benzotriazole and substituted derivatives thereof. Benzotriazole derivatives are those compounds in which the available substitution sites on the aromatic ring are partially or completely substituted. Suitable substituents include linear or branch-chain Ci-C20-alkyl groups (e.g., C1-C20- alkyl groups) and hydroxyl, thio, phenyl or halogen such as fluorine, chlorine, bromine and iodine.

[0468] (b) metal salts and complexes chosen from the group consisting of zinc, manganese, titanium, zirconium, hafnium, vanadium, cobalt, gallium and cerium salts and/or complexes, the metals being in one of the oxidation states II, III, IV, V or VI. In one aspect, suitable metal salts and/or metal complexes may be chosen from the group consisting of Mn(II) sulphate, Mn(II) citrate, Mn(II) stearate, Mn(II) acetylacetone, K⁺TiF₆ (e.g., K₂TiF₆), K⁺ZrF₆ (e.g., K₂ZrF₆), CoSO₄, Co(NO₃)₂ and Ce(NO₃)₃, zinc salts, for example zinc sulphate, hydrozincite or zinc acetate;

[0469] (c) silicates, including sodium or potassium silicate, sodium disilicate, sodium metasilicate, crystalline phyllosilicate and mixtures thereof.

[0470] Further suitable organic and inorganic redox-active substances that act as silver/copper corrosion inhibitors are

disclosed in WO 94/26860 and WO 94/26859. Preferably, the composition of the invention comprises from 0.1 to 5% by weight of the composition of a metal care agent, preferably the metal care agent is a zinc salt.

Hydrotropes

[0471] The cleaning composition may contain 0-10% by weight, for example 0-5% by weight, such as about 0.5 to about 5%, or about 3% to about 5%, of a hydrotrope. Any hydrotrope known in the art for use in detergents may be utilized. Non-limiting examples of hydrotropes include sodium benzenesulfonate, sodium p-toluene sulfonate (STS), sodium xylene sulfonate (SXS), sodium cumene sulfonate (SCS), sodium cymene sulfonate, amine oxides, alcohols and polyglycolethers, sodium hydroxynaphthoate, sodium hydroxynaphthalene sulfonate, sodium ethylhexyl sulfate, and combinations thereof.

Polymers

[0472] The cleaning composition may contain 0-10% by weight, such as 0.5-5%, 2-5%, 0.5-2% or 0.2-1% of a polymer. Any polymer known in the art for use in detergents may be utilized. The polymer may function as a co-builder as mentioned above, or may provide antiredeposition, fiber protection, soil release, dye transfer inhibition, grease cleaning and/or anti-foaming properties. Some polymers may have more than one of the above-mentioned properties and/or more than one of the below-mentioned motifs. Exemplary polymers include (carboxymethyl)cellulose (CMC), poly(vinyl alcohol) (PVA), poly(vinylpyrrolidone) (PVP), poly(ethyleneglycol) or poly(ethylene oxide) (PEG), ethoxylated poly(ethyleneimine), carboxymethyl inulin (CMI), and polycarboxylates such as PAA, PAA/PMA, poly-aspartic acid, and lauryl methacrylate/acrylic acid copolymers, hydrophobically modified CMC (HM-CMC) and silicones, copolymers of terephthalic acid and oligomeric glycols, copolymers of poly(ethylene terephthalate) and poly(oxyethylene terephthalate) (PET-POET), PVP, poly(vinylimidazole) (PVI), poly(vinylpyridine-N-oxide) (PVPO or PVPNO) and polyvinylpyrrolidone-vinylimidazole (PVPVI). Suitable examples include PVP-K15, PVP-K30, ChromaBond S-400, ChromaBond S-403E and Chromabond S-100 from Ashland Aqualon, and SokalanM HP 165, SokalanO HP 50 (Dispersing agent), Sokalan® HP 53 (Dispersing agent), SokalanM HP 59 (Dispersing agent), SokalanS HP 56 (dye transfer inhibitor), SokalanO HP 66 K (dye transfer inhibitor) from BASF. Further exemplary polymers include sulfonated polycarboxylates, polyethylene oxide and polypropylene oxide (PEO-PPO) and diquatammonium ethoxy sulfate. Other exemplary polymers are disclosed in, e.g., WO 2006/130575. Salts of the above-mentioned polymers are also contemplated. Particularly preferred polymer is ethoxylated homopolymer SokalanM HP 20 from BASF, which helps to prevent redeposition of soil in the wash liquor.

Fabric Hueing Agents

[0473] The cleaning compositions of the present invention may also include fabric hueing agents such as dyes or pigments, which when formulated in detergent compositions can deposit onto a fabric when said fabric is contacted with a wash liquor comprising said detergent compositions and thus altering the tint of said fabric through absorption/

reflection of visible light. Fluorescent whitening agents emit at least some visible light. In contrast, fabric hueing agents alter the tint of a surface as they absorb at least a portion of the visible light spectrum. Suitable fabric hueing agents include dyes and dye-clay conjugates, and may also include pigments. Suitable dyes include small molecule dyes and polymeric dyes. Suitable small molecule dyes include small molecule dyes selected from the group consisting of dyes falling into the Colour Index (C.I.) classifications of Direct Blue, Direct Red, Direct Violet, Acid Blue, Acid Red, Acid Violet, Basic Blue, Basic Violet and Basic Red, or mixtures thereof, for example as described in WO 2005/003274, WO 2005/003275, WO 2005/003276 and EP1876226 (hereby incorporated by reference). The detergent composition preferably comprises from about 0.00003 wt % to about 0.2 wt %, from about 0.00008 wt % to about 0.05 wt %, or even from about 0.0001 wt % to about 0.04 wt % fabric hueing agent. The composition may comprise from 0.0001 wt % to 0.2 wt % fabric hueing agent, this may be especially preferred when the composition is in the form of a unit dose pouch. Suitable hueing agents are also disclosed in, e.g., WO 2007/087257 and WO 2007/087243.

Dispersants

[0474] The cleaning compositions of the present invention can also contain dispersants. In particular, powdered detergents may comprise dispersants. Suitable water-soluble organic materials include the homo- or co-polymeric acids or their salts, in which the polycarboxylic acid comprises at least two carboxyl radicals separated from each other by not more than two carbon atoms. Suitable dispersants are for example described in Powdered Detergents, Surfactant science series volume 71, Marcel Dekker, Inc.

Dye Transfer Inhibiting Agents

[0475] The cleaning compositions of the present invention may also include one or more dye transfer inhibiting agents. Suitable polymeric dye transfer inhibiting agents include, but are not limited to, polyvinylpyrrolidone polymers, polyamine N-oxide polymers, copolymers of N-vinylpyrrolidone and N-vinylimidazole, polyvinyloxazolidones and polyvinylimidazoles or mixtures thereof. When present in a subject composition, the dye transfer inhibiting agents may be present at levels from about 0.0001% to about 10%, from about 0.01% to about 5% or even from about 0.1% to about 3% by weight of the composition.

Fluorescent Whitening Agent

[0476] The cleaning compositions of the present invention will preferably also contain additional components that may tint articles being cleaned, such as fluorescent whitening agents or optical brighteners. Where present the brightener is preferably at a level of about 0.01% to about 0.5%. Any fluorescent whitening agent suitable for use in a laundry detergent composition may be used in the composition of the present invention. The most commonly used fluorescent whitening agents are those belonging to the classes of diaminostilbene-sulfonic acid derivatives, diarylpyrazoline derivatives and bisphenyl-distyryl derivatives. Examples of the diaminostilbene-sulfonic acid derivative type of fluorescent whitening agents include the sodium salts of: 4,4'-bis-(2-diethanolamino-4-anilino-s-triazin-6-ylamino) stilbene-2,2'-disulfonate, 4,4'-bis-(2,4-dianilino-s-triazin-6-ylamino)

stilbene-2,2'-disulfonate, 4,4'-bis-(2-anilino-4-(N-methyl-N-2-hydroxy-ethylamino)-s-triazin-6-ylamino) stilbene-2,2'-disulfonate, 4,4'-bis-(4-phenyl-1,2,3-triazol-2-yl)stilbene-2,2'-disulfonate and sodium 5-(2H-naphtho[1,2-d][1,2,3]triazol-2-yl)-2-[*(E*)-2-phenylvinyl]-benzenesulfonate.

Preferred fluorescent whitening agents are Tinopal DMS and Tinopal CBS available from Ciba-Geigy AG, Basel, Switzerland. Tinopal DMS is the disodium salt of 4,4'-bis-(2-morpholino-4-anilino-s-triazin-6-ylamino) stilbene-2,2'-disulfonate. Tinopal CBS is the disodium salt of 2,2'-bis-(phenyl-styryl)-disulfonate. Also preferred are fluorescent whitening agents is the commercially available Parawhite KX, supplied by Paramount Minerals and Chemicals, Mumbai, India. Other fluorescers suitable for use in the invention include the 1,3-diaryl pyrazolines and the 7-alkylaminocoumarins. Suitable fluorescent brightener levels include lower levels of from about 0.01, from 0.05, from about 0.1 or even from about 0.2 wt % to upper levels of 0.5 or even 0.75 wt %.

Soil Release Polymers

[0477] The cleaning compositions of the present invention may also include one or more soil release polymers which aid the removal of soils from fabrics such as cotton and polyester based fabrics, in particular the removal of hydrophobic soils from polyester based fabrics. The soil release polymers may for example be nonionic or anionic terephthalate based polymers, polyvinyl caprolactam and related copolymers, vinyl graft copolymers, polyester polyamides see for example Chapter 7 in Powdered Detergents, Surfactant science series volume 71, Marcel Dekker, Inc. Another type of soil release polymers is amphiphilic alkoxyLATED grease cleaning polymers comprising a core structure and a plurality of alkoxylate groups attached to that core structure. The core structure may comprise a polyalkylenimine structure or a polyalkanolamine structure as described in detail in WO 2009/087523 (hereby incorporated by reference). Furthermore, random graft co-polymers are suitable soil release polymers. Suitable graft co-polymers are described in more detail in WO 2007/138054, WO 2006/108856 and WO 2006/113314 (hereby incorporated by reference). Suitable polyethylene glycol polymers include random graft copolymers comprising: (i) hydrophilic backbone comprising polyethylene glycol; and (ii) side chain(s) selected from the group consisting of: C4-C25 alkyl group, polypropylene, polybutylene, vinyl ester of a saturated C1-C6 mono-carboxylic acid, CI-C 6 alkyl ester of acrylic or methacrylic acid, and mixtures thereof. Suitable polyethylene glycol polymers have a polyethylene glycol backbone with random grafted polyvinyl acetate side chains. The average molecular weight of the polyethylene glycol backbone can be in the range of from 2,000 Da to 20,000 Da, or from 4,000 Da to 8,000 Da. The molecular weight ratio of the polyethylene glycol backbone to the polyvinyl acetate side chains can be in the range of from 1:1 to 1:5, or from 1:1.2 to 1-2. The average number of graft sites per ethylene oxide units can be less than 1, or less than 0.8, the average number of graft sites per ethylene oxide units can be in the range of from 0.5 to 0.9, or the average number of graft sites per ethylene oxide units can be in the range of from 0.1 to 0.5, or from 0.2 to 0.4. A suitable polyethylene glycol polymer is Sokalan HP22. Other soil release polymers are substituted polysaccharide structures especially substituted cellulosic structures such as modified cellulose derivatives such as those

described in EP 1867808 or WO 2003/040279 (both are hereby incorporated by reference). Suitable cellulosic polymers include cellulose, cellulose ethers, cellulose esters, cellulose amides and mixtures thereof. Suitable cellulosic polymers include anionically modified cellulose, nonionically modified cellulose, cationically modified cellulose, zwitterionically modified cellulose, and mixtures thereof. Suitable cellulosic polymers include methyl cellulose, carboxy methyl cellulose, ethyl cellulose, hydroxyl ethyl cellulose, hydroxyl propyl methyl cellulose, ester carboxy methyl cellulose, and mixtures thereof.

Anti-Redeposition Agents

[0478] The cleaning compositions of the present invention may also include one or more anti-redeposition agents such as carboxymethylcellulose (CMC), polyvinyl alcohol (PVA), polyvinylpyrrolidone (PVP), polyoxyethylene and/or polyethyleneglycol (PEG), homopolymers of acrylic acid, copolymers of acrylic acid and maleic acid, and ethoxylated polyethyleneimines. The cellulose based polymers described under soil release polymers above may also function as anti-redeposition agents.

Rheology Modifiers

[0479] The cleaning compositions of the present invention may also include one or more rheology modifiers, structurants or thickeners, as distinct from viscosity reducing agents. The rheology modifiers are selected from the group consisting of non-polymeric crystalline, hydroxy-functional materials, polymeric rheology modifiers which impart shear thinning characteristics to the aqueous liquid matrix of a liquid detergent composition. The rheology and viscosity of the detergent can be modified and adjusted by methods known in the art, for example as shown in EP 2169040.

[0480] Other suitable cleaning composition components include, but are not limited to, anti-shrink agents, anti-wrinkling agents, bactericides, binders, carriers, dyes, enzyme stabilizers, fabric softeners, fillers, foam regulators, hydrotropes, perfumes, pigments, sod suppressors, solvents, and structurants for liquid detergents and/or structure elasticizing agents.

Polymers

[0481] The cleaning composition may contain 0-10% by weight, such as 0.5-5%, 2-5%, 0.5-2% or 0.2-1% of a polymer. Any polymer known in the art for use in detergents may be utilized. The polymer may function as a co-builder as mentioned above, or may provide antiredeposition, fiber protection, soil release, dye transfer inhibition, grease cleaning and/or anti-foaming properties. Some polymers may have more than one of the above-mentioned properties and/or more than one of the below-mentioned motifs. Exemplary polymers include (carboxymethyl)cellulose (CMC), poly(vinyl alcohol) (PVA), poly(vinylpyrrolidone) (PVP), poly(ethyleneglycol) or poly(ethylene oxide) (PEG), ethoxylated poly(ethyleneimine), carboxymethyl inulin (CMI), and polycarboxylates such as PAA, PAA/PMA, poly-aspartic acid, and lauryl methacrylate/acrylic acid copolymers, hydrophobically modified CMC (HM-CMC) and silicones, copolymers of terephthalic acid and oligomeric glycols, copolymers of poly(ethylene terephthalate) and poly(oxyethene terephthalate) (PET-POET), PVP, poly(vinylimidazole) (PVI), poly(vinylpyridine-N-oxide)

(PVPO or PVPNO) and polyvinylpyrrolidone-vinylimidazole (PVPVI). Suitable examples include PVP-K15, PVP-K30, ChromaBond S-400, ChromaBond S-403E and Chromabond S-100 from Ashland Aqualon, and Sokalan® HP 165, Sokalan® HP 50 (Dispersing agent), Sokalan® HP 53 (Dispersing agent), Sokalan® HP 59 (Dispersing agent), Sokalan® HP 56 (dye transfer inhibitor), Sokalan® HP 66 K (dye transfer inhibitor) from BASF. Further exemplary polymers include sulfonated polycarboxylates, polyethylene oxide and polypropylene oxide (PEO-PPO) and diquat-mium ethoxy sulfate. Other exemplary polymers are disclosed in, e.g., WO 2006/130575. Salts of the above-mentioned polymers are also contemplated. Particularly preferred polymer is ethoxylated homopolymer Sokalan® HP 20 from BASF, which helps to prevent redeposition of soil in the wash liquor.

Enzymes

[0482] The cleaning composition may comprise one or more additional enzymes such as one or more lipase, cutinase, an amylase, carboxhydrase, cellulase, pectinase, mannanase, arabinase, galactanase, xylanase, oxidase, e.g., a laccase, and/or peroxidase. In general, the properties of the selected enzyme(s) should be compatible with the selected detergent, (i.e., pH-optimum, compatibility with other enzymatic and non-enzymatic ingredients, etc.), and the enzyme(s) should be present in effective amounts.

Mannanases

[0483] Suitable mannanases include those of bacterial or fungal origin. Chemically or genetically modified mutants are included. The mannanase may be an alkaline mannanase of Family 5 or 26. It may be a wild-type from *Bacillus* or *Humicola*, particularly *B. agaradhaerens*, *B. licheniformis*, *B. halodurans*, *B. clausii*, or *H. insolens*. Suitable mannanases are described in WO 1999/064619. A commercially available mannanase is Mannaway (Novozymes A/S).

Cellulases

[0484] Suitable cellulases include complete cellulases or mono-component endoglucanases of bacterial or fungal origin. Chemically or genetically modified mutants are included. The cellulase may for example be a mono-component or a mixture of mono-component endo-1,4-beta-glucanase often just termed endoglucanases. Suitable cellulases include a fungal cellulase from *Humicola insolens* (U.S. Pat. No. 4,435,307) or from *Trichoderma*, e.g., *T. reesei* or *T. viride*. Examples of cellulases are described in EP 495257. Other suitable cellulases are from *Thielavia*, e.g., *Thielavia terrestris* as described in WO 96/29397 or *Fusarium oxysporum* as described in WO 91/17244 or from *Bacillus* as described in, WO 02/099091 and JP 2000210081. Other examples are cellulase variants such as those described in WO 94/07998, EP 531315, U.S. Pat. Nos. 5,457,046, 5,686,593, 5,763,254, WO 95/24471, WO 98/12307 Commercially available cellulases include Car-ezyme®, Celluzyme®, Celluclean®, Cellulast® and Endolase®; Renozyme®; Whitezyme® (Novozymes A/S) Puradax®, Puradax HA, and Puradax EG (available from Genencor).

Proteases

[0485] Suitable proteases may be of any origin, but are preferably of bacterial or fungal origin, optionally in the

form of protein engineered or chemically modified mutants. The protease may be an alkaline protease, such as a serine protease or a metalloprotease. A serine protease may for example be of the S1 family, such as trypsin, or the S8 family such as a subtilisin. A metalloprotease may for example be a thermolysin, e.g., from the M4 family, or another metalloprotease such as those from the M5, M7 or M35 families.

[0486] The term "subtilases" refers to a sub-group of serine proteases according to Siezen et al., 1991, Protein Eng. 4: 719-737 and Siezen et al., 1997, Protein Sci. 6: 501-523. Serine proteases are a subgroup of proteases characterized by having a serine in the active site, which forms a covalent adduct with the substrate. The subtilases may be divided into six subdivisions, the Subtilisin family, the Thermitase family, the Proteinase K family, the Lantibiotic peptidase family, the Kexin family and the Pyrolysin family. [0487] Although proteases suitable for detergent use may be obtained from a variety of organisms, including fungi such as *Aspergillus*, detergent proteases have generally been obtained from bacteria and in particular from *Bacillus*. Examples of *Bacillus* species from which subtilases have been derived include *Bacillus lenthus*, *Bacillus alkalophilus*, *Bacillus subtilis*, *Bacillus amyloliquefaciens*, *Bacillus licheniformis*, *Bacillus pumilus* and *Bacillus gibsonii*. Particular subtilisins include subtilisin lenthus, subtilisin Novo, subtilisin Carlsberg, subtilisin BPN', subtilisin 309, subtilisin 147 and subtilisin 168 and, e.g., protease PD138 (described in WO 93/18140). Other useful proteases are, e.g., those described in WO 01/16285 and WO 02/16547.

[0488] Examples of trypsin-like proteases include the *Fusarium* protease described in WO 94/25583 and WO 2005/040372, and the chymotrypsin proteases derived from *Cellumonas* described in WO 2005/052161 and WO 2005/052146.

[0489] Examples of metalloproteases include the neutral metalloproteases described in WO 2007/044993 such as those derived from *Bacillus amyloliquefaciens*, as well as, e.g., the metalloproteases described in WO 2015/158723 and WO 2016/075078.

[0490] Examples of useful proteases are the protease variants described in WO 89/06279 WO 92/19729, WO 96/34946, WO 98/20115, WO 98/20116, WO 99/11768, WO 01/44452, WO 2003/006602, WO 2004/003186, WO 2004/041979, WO 2007/006305, WO 2011/036263, WO 2014/207227, WO 2016/087617 and WO 2016/174234. Preferred protease variants may, for example, comprise one or more of the mutations selected from the group consisting of: S3T, V4I, S9R, S9E, A15T, S24G, S24R, K27R, N42R, S55P, G59E, G59D, N60D, N60E, V66A, N74D, S85R, A96S, S97G, S97D, S97A, S97SD, S99E, S99D, S99G, S99M, S99N, S99R, S99H, S101A, V102I, V102Y, V102N, S104A, G116V, G116R, H118D, H118N, A120S, S126L, P127Q, S128A, S154D, A156E, G157D, G157P, S158E, Y161A, R164S, Q176E, N179E, S182E, Q185N, A188P, G189E, V193M, N198D, V199I, Q200L, Y203W, S206G, L211Q, L211D, N212D, N212S, M216S, A226V, K229L, Q230H, Q239R, N246K, S253D, N255W, N255D, N255E, L256E, L256D T268A and R269H, wherein position numbers correspond to positions of the *Bacillus lenthus* protease shown in SEQ ID NO: 1 of WO 2016/001449. Protease variants having one or more of these mutations are preferably variants of the *Bacillus lenthus* protease (Savinase®, also known as subtilisin 309) shown in SEQ ID NO: 1 of

WO 2016/001449 or of the *Bacillus amyloliquefaciens* protease (BPN') shown in SEQ ID NO: 2 of WO 2016/001449. Such protease variants preferably have at least 80% sequence identity to SEQ ID NO: 1 or to SEQ ID NO: 2 of WO 2016/001449.

[0491] Another protease of interest is the alkaline protease from *Bacillus lenthus* DSM 5483, as described for example in WO 91/02792, and variants thereof which are described for example in WO 92/21760, WO 95/23221, EP 1921147, EP 1921148 and WO 2016/096711.

[0492] The protease may alternatively be a variant of the TY145 protease having SEQ ID NO: 1 of WO 2004/067737, for example a variant comprising a substitution at one or more positions corresponding to positions 27, 109, 111, 171, 173, 174, 175, 180, 182, 184, 198, 199 and 297 of SEQ ID NO: 1 of WO 2004/067737, wherein said protease variant has a sequence identity of at least 75% but less than 100% to SEQ ID NO: 1 of WO 2004/067737. TY145 variants of interest are described in, e.g., WO 2015/014790, WO 2015/014803, WO 2015/014804, WO 2016/097350, WO 2016/097352, WO 2016/097357 and WO 2016/097354.

[0493] Examples of preferred proteases include:

[0494] (a) variants of SEQ ID NO: 1 of WO 2016/001449 comprising two or more substitutions selected from the group consisting of S9E, N43R, N76D, Q206L, Y209W, S259D and L262E, for example a variant with the substitutions S9E, N43R, N76D, V205I, Q206L, Y209W, S259D, N261W and L262E, or with the substitutions S9E, N43R, N76D, N185E, S188E, Q191N, A194P, Q206L, Y209W, S259D and L262E, wherein position numbers are based on the numbering of SEQ ID NO: 2 of WO 2016/001449;

[0495] (b) a variant of the polypeptide of SEQ ID NO: 1 of WO 2016/001449 with the mutation S99SE, wherein position numbers are based on the numbering of SEQ ID NO: 2 of WO 2016/001449;

[0496] (c) a variant of the polypeptide of SEQ ID NO: 1 of WO 2016/001449 with the mutation S99AD, wherein position numbers are based on the numbering of SEQ ID NO: 2 of WO 2016/001449;

[0497] (d) a variant of the polypeptide of SEQ ID NO: 1 of WO 2016/001449 with the substitutions Y167A+R170S+A194P, wherein position numbers are based on the numbering of SEQ ID NO: 2 of WO 2016/001449;

[0498] (e) a variant of the polypeptide of SEQ ID NO: 1 of WO 2016/001449 with the substitutions S9R+A15T+V68A+N218D+Q245R, wherein position numbers are based on the numbering of SEQ ID NO: 2 of WO 2016/001449;

[0499] (f) a variant of the polypeptide of SEQ ID NO: 1 of WO 2016/001449 with the substitutions S9R+A15T+G61E+V68A+A194P+V205I+Q245R+N261D, wherein position numbers are based on the numbering of SEQ ID NO: 2 of WO 2016/001449;

[0500] (g) a variant of the polypeptide of SEQ ID NO: 1 of WO 2016/001449 with the substitutions S99D+S101R/E+S103A+V104I+G160S; for example a variant of SEQ ID NO: 1 of WO 2016/001449 with the substitutions S3T+V41+S99D+S101EE+S103A+V104I+G160S+V205I, wherein position numbers are based on the numbering of SEQ ID NO: 2 of WO 2016/001449;

[0501] (h) a variant of the polypeptide of SEQ ID NO: 2 of WO 2016/001449 with the substitutions S24G+

S53G+S78N+S101N+G128A/S+Y217Q, wherein position numbers are based on the numbering of SEQ ID NO: 2 of WO 2016/001449;

[0502] (i) the polypeptide disclosed in GENESEQ under accession number BER84782, corresponding to SEQ ID NO: 302 in WO 2017/210295;

[0503] (j) a variant of the polypeptide of SEQ ID NO: 1 of WO 2016/001449 with the substitutions S99D+S101E+S103A+V104I+S156D+G160S+L262E, wherein position numbers are based on the numbering of SEQ ID NO: 2 of WO 2016/001449;

[0504] (k) a variant of the polypeptide of SEQ ID NO: 1 of WO 2016/001449 with the substitutions S9R+A15T+G61E+V68A+N76D+S99G+N218D+Q245R, wherein position numbers are based on the numbering of SEQ ID NO: 2 of WO 2016/001449;

[0505] (l) a variant of the polypeptide of SEQ ID NO: 1 of WO 2016/001449 with the substitutions V68A+S106A, wherein position numbers are based on the numbering of SEQ ID NO: 2 of WO 2016/001449; and

[0506] (m) a variant of the polypeptide of SEQ ID NO: 1 of WO 2004/067737 with the substitutions S27K+N109K+S111E+S171E+S173P+G174K+S175P+F180Y+G182A+L184F+Q198E+N199+T297P, wherein position numbers are based on the numbering of SEQ ID NO: 1 of WO 2004/067737.

[0507] Suitable commercially available protease enzymes include those sold under the trade names Alcalase®, Duralase™, Durazym™, Relase®, Relase® Ultra, Savinase®, Savinase® Ultra, Primase™, Polarzyme®, Kannase®, Liquanase®, Liquanase® Ultra, Ovozyme®, Coronase®, Coronase® Ultra, Blaze®, Blaze Euity® 100T, Blaze Euity® 125T, Blaze Euity® 150T, Blaze Euity® 200T, Neutraser®, Everlase®, Esperase®, Progress® Uno, Progress® In and Progress® Excel (Novozymes A/S), those sold under the tradename Maxatase™, Maxacal™, Maxapem®, Purafect® Ox, Purafect® OxP, Puramax®, FN2™, FN3™, FN4™, Excellase®, Excellenz™ P1000, Excellenz™ P1250, Eraserm, Preferenz® P100, Purafect Prime, Preferenz P110™, Effecten™ P1000™, Purafect®, Effecten™ P1050™, Purafect® Ox, Effecten™ P2000, Purafast™, Properase®, Opticlean™ and Optimase® (Danisco/DuPont), BLAP (sequence shown in FIG. 29 of U.S. Pat. No. 5,352,604) and variants hereof (Henkel AG), and KAP (*Bacillus alkalophilus* subtilisin) from Kao.

Lipases and Cutinases

[0508] Suitable lipases and cutinases include those of bacterial or fungal origin. Chemically modified or protein engineered mutant enzymes are included. Examples include lipase from *Thermomyces*, e.g., from *T. lanuginosus* (previously named *Humicola lanuginosa*) as described in EP 258068 and EP 305216, cutinase from Huricola, e.g., *H. insolens* (WO 96/13580), lipase from strains of *Pseudomonas* (some of these now renamed to *Burkholderia*), e.g., *P. alcaligenes* or *P. pseudoalcaligenes* (EP 218272), *P. cepacia* (EP 331376), *P.* sp. strain SD705 (WO 95/06720 & WO 96/27002), *P. wisconsinensis* (WO 96/12012), GDSL-type *Streptomyces* lipases (WO 2010/065455), cutinase from *Magnaporthe grisea* (WO 2010/107560), cutinase from *Pseudomonas mendocina* (U.S. Pat. No. 5,389,536), lipase from *Thermobifida fusca* (WO 2011/084412), *Geobacillus stearothermophilus* lipase (WO 2011/084417), lipase from

Bacillus subtilis (WO 2011/084599), and lipase from *Streptomyces griseus* (WO 2011/150157) and *S. pristinaespiralis* (WO 2012/137147).

[0509] Other examples are lipase variants such as those described in EP 407225, WO 92/05249, WO 94/01541, WO 94/25578, WO 95/14783, WO 95/30744, WO 95/35381, WO 95/22615, WO 96/00292, WO 97/04079, WO 97/07202, WO 00/34450, WO 00/60063, WO 01/92502, WO 2007/087508 and WO 2009/109500.

[0510] Preferred commercial lipase products include Lipolase™, Lipext™, Upolex™ and Lipoclean™ (Novozymes A/S), Lumafast (originally from Genencor) and Lipomax (originally from Gist-Brocades). Still other examples are lipases sometimes referred to as acyltransferases or perhydrolases, e.g., acyltransferases with homology to *Candida antarctica* lipase A (WO 2010/111143), acyltransferase from *Mycobacterium smegmatis* (WO 2005/056782), perhydrolases from the CE 7 family (WO 2009/067279), and variants of the *M. smegmatis* perhydrolase in particular the S54V variant used in the commercial product Gentle Power Bleach from Huntsman Textile Effects Pte Ltd (WO 2010/100028).

Amylases

[0511] Suitable amylases may be an alpha-amylase or a glucoamylase and may be of bacterial or fungal origin. Chemically modified or protein engineered mutants are included. Amylases include, for example, alpha-amylases obtained from *Bacillus*, e.g., a special strain of *Bacillus licheniformis*, described in more detail in GB 1,296,839.

[0512] Suitable amylases include amylases having SEQ ID NO: 2 in WO 95/10603 or variants having 90% sequence identity to SEQ ID NO: 3 thereof. Preferred variants are described in WO 94/02597, WO 94/18314, WO 97/43424 and SEQ ID NO: 4 of WO 99/19467, such as variants with substitutions in one or more of the following positions: 15, 23, 105, 106, 124, 128, 133, 154, 156, 178, 179, 181, 188, 190, 197, 201, 202, 207, 208, 209, 211, 243, 264, 304, 305, 391, 408, and 444.

[0513] Different suitable amylases include amylases having SEQ ID NO: 6 in WO 02/10355 or variants thereof having 90% sequence identity to SEQ ID NO: 6. Preferred variants of SEQ ID NO: 6 are those having a deletion in positions 181 and 182 and a substitution in position 193.

[0514] Other amylases which are suitable are hybrid alpha-amylase comprising residues 1-33 of the alpha-amylase derived from *B. amyloliquefaciens* shown in SEQ ID NO: 6 of WO 2006/066594 and residues 36-483 of the *B. licheniformis* alpha-amylase shown in SEQ ID NO: 4 of WO 2006/066594 or variants having 90% sequence identity thereof. Preferred variants of this hybrid alpha-amylase are those having a substitution, a deletion or an insertion in one of more of the following positions: G48, T49, G107, H156, A181, N190, M197, 1201, A209 and Q264. Most preferred variants of the hybrid alpha-amylase comprising residues 1-33 of the alpha-amylase derived from *B. amyloliquefaciens* shown in SEQ ID NO: 6 of WO 2006/066594 and residues 36-483 of SEQ ID NO: 4 are those having the substitutions:

[0515] M197T;

[0516] H156Y+A181T+N190F+A209V+Q264S; or

[0517] G48A+T49I+G107A+H156Y+A181T+N190F+I201F+A209V+Q264S.

[0518] Further amylases which are suitable are amylases having SEQ ID NO: 6 in WO 99/19467 or variants thereof having 90% sequence identity to SEQ ID NO: 6. Preferred variants of SEQ ID NO: 6 are those having a substitution, a deletion or an insertion in one or more of the following positions: R181, G182, H183, G184, N195, 1206, E212, E216 and K269. Particularly preferred amylases are those having deletion in positions R181 and G182, or positions H183 and G184.

[0519] Additional amylases which can be used are those having SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 2 or SEQ ID NO: 7 of WO 96/23873 or variants thereof having 90% sequence identity to SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3 or SEQ ID NO: 7. Preferred variants of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3 or SEQ ID NO: 7 are those having a substitution, a deletion or an insertion in one or more of the following positions: 140, 181, 182, 183, 184, 195, 206, 212, 243, 260, 269, 304 and 476, using SEQ ID NO: 2 of WO 96/23873 for numbering. More preferred variants are those having a deletion in two positions selected from 181, 182, 183 and 184, such as 181 and 182, 182 and 183, or positions 183 and 184. Most preferred amylase variants of SEQ ID NO: 1, SEQ ID NO: 2 or SEQ ID NO: 7 are those having a deletion in positions 183 and 184 and a substitution in one or more of positions 140, 195, 206, 243, 260, 304 and 476.

[0520] Other amylases which can be used are amylases having SEQ ID NO: 2 of WO 2008/153815, SEQ ID NO: 10 in WO 01/66712 or variants thereof having 90% sequence identity to SEQ ID NO: 2 of WO 2008/153815 or 90% sequence identity to SEQ ID NO: 10 in WO 01/66712. Preferred variants of SEQ ID NO: 10 in WO 01/66712 are those having a substitution, a deletion or an insertion in one of more of the following positions: 176, 177, 178, 179, 190, 201, 207, 211 and 264.

[0521] Further suitable amylases are amylases having SEQ ID NO: 2 of WO 2009/061380 or variants having 90% sequence identity to SEQ ID NO: 2 thereof. Preferred variants of SEQ ID NO: 2 are those having a truncation of the C-terminus and/or a substitution, a deletion or an insertion in one of more of the following positions: Q87, Q98, S125, N128, T131, T165, K178, R180, S181, T182, G183, M201, F202, N225, S243, N272, N282, Y305, R309, D319, Q320, Q359, K444 and G475. More preferred variants of SEQ ID NO: 2 are those having the substitution in one of more of the following positions: Q87E,R, Q98R, S125A, N128C, T131I, T165I, K178L, T182G, M201L, F202Y, N225E,R, N272E,R, S243Q,A,E,D, Y305R, R309A, Q320R, Q359E, K444E and G475K and/or deletion in position R180 and/or S181 or of T182 and/or G183. Most preferred amylase variants of SEQ ID NO: 2 are those having the substitutions:

[0522] N128C+K178L+T182G+Y305R+G475K;

[0523] N128C+K178L+T182G+F202Y+Y305R+D319T+G475K;

[0524] S125A+N128C+K178L+T182G+Y305R+G475K; or

[0525] S125A+N128C+T131I+T165I+K178L+T182G+Y305R+G475K;

wherein the variants are C-terminally truncated and optionally further comprise a substitution at position 243 and/or a deletion at position 180 and/or position 181.

[0526] Further suitable amylases are amylases having SEQ ID NO: 1 of WO 2013/184577 or variants having 90%

sequence identity to SEQ ID NO: 1 thereof. Preferred variants of SEQ ID NO: 1 are those having a substitution, a deletion or an insertion in one of more of the following positions: K176, R178, G179, T180, G181, E187, N192, M199, 1203, S241, R458, T459, D460, G476 and G477. More preferred variants of SEQ ID NO: 1 are those having the substitution in one of more of the following positions: K176L, E187P, N192FYH, M199L, I203YF, S241QADN, R458N, T459S, D460T, G476K and G477K and/or deletion in position R178 and/or S179 or of T180 and/or G181. Most preferred amylase variants of SEQ ID NO: 1 are those having the substitutions:

[0527] E187P+I203Y+G476K

[0528] E187P+I203Y+R458N+T459S+D460T+G476K

wherein the variants optionally further comprise a substitution at position 241 and/or a deletion at position 178 and/or position 179.

[0529] Further suitable amylases are amylases having SEQ ID NO: 1 of WO 2010/104675 or variants having 90% sequence identity to SEQ ID NO: 1 thereof. Preferred variants of SEQ ID NO: 1 are those having a substitution, a deletion or an insertion in one of more of the following positions: N21, D97, V128 K177, R179, S180, I181, G182, M200, L204, E242, G477 and G478. More preferred variants of SEQ ID NO: 1 are those having the substitution in one of more of the following positions: N21D, D97N, V128I K177L, M200L, L204YF, E242QA, G477K and G478K and/or deletion in position R179 and/or S180 or of I181 and/or G182. Most preferred amylase variants of SEQ ID NO: 1 are those having the substitutions:

[0530] N21D+D97N+V128I,

wherein the variants optionally further comprise a substitution at position 200 and/or a deletion at position 180 and/or position 181.

[0531] Other suitable amylases are the alpha-amylase having SEQ ID NO: 12 in WO 01/66712 or a variant having at least 90% sequence identity to SEQ ID NO: 12. Preferred amylase variants are those having a substitution, a deletion or an insertion in one of more of the following positions of SEQ ID NO: 12 in WO 01/66712: R28, R118, N174; R181, G182, D183, G184, G186, W189, N195, M202, Y298, N299, K302, S303, N306, R310, N314; R320, H324, E345, Y396, R400, W439, R444, N445, K446, Q449, R458, N471, N484. Particular preferred amylases include variants having a deletion of D183 and G184 and having the substitutions R118K, N195F, R320K and R458K, and a variant additionally having substitutions in one or more position selected from the group: M9, G149, G182, G186, M202, T257, Y295, N299, M323, E345 and A339, most preferred a variant that additionally has substitutions in all these positions.

[0532] Other examples are amylase variants such as those described in WO 2011/098531, WO 2013/001078 and WO 2013/001087.

[0533] Commercially available amylases are DuramyTM, TermamylTM, FungamylTM, StainzymeTM, Stainzyme PlusTM, NatalaseTM, Liquozyme X and BANTM (from Novozymes A/S), and RapidaseTM, PurastarTM/EffectenzTM, Powerase, PreferenTM S1000, PreferenTM S100, PreferenTM S110 and PreferenTM S210 (from Genencor International Inc./DuPont).

Peroxidases/Oxidases

[0534] A peroxidase may be an enzyme comprised by the enzyme classification EC 1.11.1.7, as set out by the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (IUBMB), or any fragment derived therefrom, exhibiting peroxidase activity. Suitable peroxidases include those of plant, bacterial or fungal origin. Chemically modified or protein engineered mutants are included. Examples of useful peroxidases include peroxidases from *Coprinopsis*, e.g., from *C. cinerea* (EP 179486), and variants thereof as those described in WO 93/24618, WO 95/10602, and WO 98/15257. A peroxidase may also include a haloperoxidase enzyme, such as chloroperoxidase, bromoperoxidase and compounds exhibiting chloroperoxidase or bromoperoxidase activity. Haloperoxidases are classified according to their specificity for halide ions. Chloroperoxidases (E.C. 1.11.1.10) catalyze formation of hypochlorite from chloride ions. The haloperoxidase may be a chloroperoxidase. Preferably, the haloperoxidase is a vanadium haloperoxidase, i.e., a vanadate-containing haloperoxidase. In a preferred method the vanadate-containing haloperoxidase is combined with a source of chloride ion. Haloperoxidases have been isolated from many different fungi, in particular from the fungus group dematiaceous hyphomycetes, such as *Caldariomyces*, e.g., *C. fumago*, *Altemaria*, *Curvularia*, e.g., *C. verruculosa* and *C. inaequalis*, *Drechslera*, *Ulocladium* and *Botrytis*. *Haloperoxidases have also been isolated from bacteria such as Pseudomonas*, e.g., *P. pyrrocinia* and *Streptomyces*, e.g., *S. aureofaciens*. The haloperoxidase may be derivable from *Curvularia* sp., in particular *Curvularia verruculosa* or *Curvularia inaequalis*, such as *C. inaequalis* CBS 102.42 as described in WO 95/27046; or *C. verruculosa* CBS 147.63 or *C. verruculosa* CBS 444.70 as described in WO 97/04102; or from *Drechslera hartlebii* as described in WO 01/79459, *Dendryphiella salina* as described in WO 01/79458, *Phaeochoconis crotalariae* as described in WO 01/79461, or *Geniculosporium* sp. as described in WO 01/79460.

[0535] Oxidases include any laccase enzyme comprised by the enzyme classification EC 1.10.3.2, or any fragment derived therefrom exhibiting laccase activity, or a compound exhibiting a similar activity, such as a catechol oxidase (EC 1.10.3.1), an o-aminophenol oxidase (EC 1.10.3.4), or a bilirubin oxidase (EC 1.3.3.5). Preferred laccase enzymes are enzymes of microbial origin. The enzymes may be derived from plants, bacteria or fungi (including filamentous fungi and yeasts). Suitable examples from fungi include a laccase derivable from a strain of *Aspergillus*, *Neurospora*, e.g., *N. crassa*, *Podospora*, *Borytis*, *Collybia*, *Fomes*, *Lentinus*, *Pleurotus*, *Trametes*, e.g., *T. villosa* and *T. versicolor*, *Rhizoctonia*, e.g., *R. solani*, *Coprinopsis*, e.g., *C. cinerea*, *C. comatus*, *C. friesii*, and *C. plicatilis*, *Psathyrella*, e.g., *P. condelleana*, *Panaeolus*, e.g., *P. papilionaceus*, *Myceliophthora*, e.g., *M. thermophila* *Schytalidium*, e.g., *S. thermophilum*, *Polyporus*, e.g., *P. pinsitus*, *Phlebia*, e.g., *P. radiata* (WO 92/01046), or *Coriolus*, e.g., *C. hirsutus* (JP 2238885). Suitable examples from bacteria include a laccase derivable from a strain of *Bacillus*. A laccase derived from *Coprinopsis* or *Myceliophthora* is preferred; in particular a laccase derived from *Coprinopsis cinerea*, as disclosed in WO 97/08325; or from *Myceliophthora thermophila*, as disclosed in WO 95/33836.

Microorganisms

[0536] The detergent additive as well as the detergent composition may also comprise one or more microorganisms, such as one or more fungi, yeast, or bacteria. In an embodiment, the one or more microorganisms are dehydrated (for example by lyophilization) bacteria or yeast, such as a strain of *Lactobacillus*. In another embodiment, the microorganisms are one or more microbial spores (as opposed to vegetative cells), such as bacterial spores; or fungal spores, conidia, hypha. Preferably, the one or more spores are *Bacillus* endospores; even more preferably the one or more spores are endospores of *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, or *Bacillus megaterium*. The microorganisms may be included in the detergent composition or additive in the same way as enzymes (see above).

Formulation of Detergent Products

[0537] The cleaning composition of the present invention may be formulated, for example, as a hand or machine laundry detergent composition including a laundry additive composition suitable for pre-treatment of stained fabrics and a rinse added fabric softener composition, or be formulated as a detergent composition for use in general household hard surface cleaning operations, or be formulated for hand or machine dishwashing operations. In a specific aspect, the present invention provides a detergent additive comprising one or more enzymes as described herein. The cleaning composition of the invention may be in any convenient form, e.g., a bar, a homogenous tablet, a tablet having two or more layers, a pouch having one or more compartments, a regular or compact powder, a granule, a paste, a gel, or a regular, compact or concentrated liquid.

[0538] Pouches can be configured as single or multicompartments. It can be of any form, shape and material which is suitable for holding the composition, e.g., without allowing the release of the composition to release of the composition from the pouch prior to water contact. The pouch is made from water soluble film which encloses an inner volume. Said inner volume can be divided into compartments of the pouch. Preferred films are polymeric materials preferably polymers which are formed into a film or sheet. Preferred polymers, copolymers or derivates thereof are selected polyacrylates, and water-soluble acrylate copolymers, methyl cellulose, carboxy methyl cellulose, sodium dextrin, ethyl cellulose, hydroxyethyl cellulose, hydroxypropyl methyl cellulose, malto dextrin, poly methacrylates, most preferably polyvinyl alcohol copolymers and, hydroxypropyl methyl cellulose (HPMC). Preferably the level of polymer in the film for example PVA is at least about 60%. Preferred average molecular weight will typically be about 20,000 to about 150,000. Films can also be of blended compositions comprising hydrolytically degradable and water-soluble polymer blends such as polylactide and polyvinyl alcohol (known under the Trade reference M8630 as sold by MonoSol LLC, Indiana, USA) plus plasticisers like glycerol, ethylene glycerol, propylene glycol, sorbitol and mixtures thereof. The pouches can comprise a solid laundry cleaning composition or part components and/or a liquid cleaning composition or part components separated by the water-soluble film. The compartment for liquid components can be different in composition than compartments containing solids: US 2009/0011970.

[0539] Detergent ingredients can be separated physically from each other by compartments in water dissolvable pouches or in different layers of tablets. Thereby negative storage interaction between components can be avoided. Different dissolution profiles of each of the compartments can also give rise to delayed dissolution of selected components in the wash solution.

[0540] A liquid or gel detergent, which is not unit dosed, may be aqueous, typically containing at least 20% by weight and up to 95% water, such as up to about 70% water, up to about 65% water, up to about 55% water, up to about 45% water, up to about 35% water. Other types of liquids, including without limitation, alkanols, amines, diols, ethers and polyols may be included in an aqueous liquid or gel. An aqueous liquid or gel detergent may contain from 0-30% organic solvent. A liquid or gel detergent may be non-aqueous.

Uses

[0541] The present invention is also directed to methods for using the compositions thereof. Laundry/textile/fabric (Household laundry washing, Industrial laundry washing). Hard surface cleaning (ADW, car wash, Industrial surface).

Use of Cleaning Composition

[0542] The detergent composition of the present invention may be formulated, for example, as a hand or machine laundry detergent composition including a laundry additive composition suitable for pre-treatment of stained fabrics and a rinse added fabric softener composition, or be formulated as a detergent composition for use in general household hard surface cleaning operations, or be formulated for hand or machine dishwashing operations. In a specific aspect, the present invention provides a detergent additive comprising one or more enzymes as described herein.

Methods

[0543] The invention further relates to a method of treating a method of treating a fabric comprising:

[0544] (a) contacting the fabric with an aqueous solution of peptidoglycan degradation enzyme, preferably having N-acetylmuramyl-L-alanine amidase and peptidoglycan lyase activity; and optionally

[0545] (b) rinsing and drying the textile.

[0546] The invention further relates to a method for cleaning or laundering an item comprising the steps of:

[0547] a. exposing an item to a wash liquor comprising at least one peptidoglycan degradation enzyme, preferably having N-acetylmuramyl-L-alanine amidase and/or peptidoglycan lyase activity or a detergent composition comprising such enzyme;

[0548] b. completing at least one wash cycle; and optionally

[0549] c. rinsing the item,
wherein the item is a fabric.

[0550] The invention further relates to a method for cleaning or laundering an item comprising the steps of:

[0551] a. exposing an item to a wash liquor comprising a polypeptide or a detergent composition comprising a polypeptide, preferably wherein the polypeptide has N-acetylmuramyl-L-alanine amidase and/or peptidoglycan lyase activity;

[0552] b. completing at least one wash cycle; and optionally

[0553] c. rinsing the item,
wherein the item is a fabric.

[0554] The invention further relates to a method for cleaning or laundering an item comprising the steps of:

[0555] a. exposing an item to a wash liquor comprising a polypeptide or a detergent composition comprising a polypeptide, preferably wherein the polypeptide has N-acetylmuramyl-L-alanine amidase and/or peptidoglycan lyase activity and wherein the polypeptide comprises the motif N[IV]X[AG][GAS]A[AY][LV]L (SEQ ID NO: 111);

[0556] b. completing at least one wash cycle; and optionally

[0557] c. rinsing the item,
wherein the item is a fabric.

[0558] The invention further relates to a method for cleaning or laundering an item comprising the steps of:

[0559] a. exposing an item to a wash liquor comprising a polypeptide or a detergent composition comprising a polypeptide, preferably wherein the is selected from the group consisting of: SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 9, SEQ ID NO: 12, SEQ ID NO: 15, SEQ ID NO: 18, SEQ ID NO: 21, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 30, SEQ ID NO: 33, SEQ ID NO: 36, SEQ ID NO: 39, SEQ ID NO: 42, SEQ ID NO: 45, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 57, SEQ ID NO: 60, SEQ ID NO: 63, SEQ ID NO: 66, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 75, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 84, SEQ ID NO: 87, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO: 96, SEQ ID NO: 99, SEQ ID NO: 102, SEQ ID NO: 105, SEQ ID NO: 108 and polypeptides having at least at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% hereto;

[0560] b. completing at least one wash cycle; and optionally

[0561] c. rinsing the item,
wherein the item is a fabric.

[0562] The pH of the liquid solution is in the range of 1 to 11, such as in the range 5.5 to 11, such as in the range of 7 to 9, in the range of 7 to 8 or in the range of 7 to 8.5.

[0563] The wash liquor may have a temperature in the range of 5° C. to 95° C., or in the range of 10° C. to 80° C., in the range of 10° C. to 70° C., in the range of 10° C. to 60° C., in the range of 10° C. to 50° C., in the range of 15° C. to 40° C. or in the range of 20° C. to 30° C. In one aspect, the temperature of the wash liquor is 30° C.

[0564] The concentration of the peptidoglycan degradation enzyme in the wash liquor is typically in the range of at least 0.00001 ppm to at least 10 ppm, at least 0.00002 ppm to at least 10 ppm, at least 0.0001 ppm to at least 10 ppm, at least 0.0002 ppm to at least 10 ppm, at least 0.002 ppm to at least 10 ppm, at least 0.01 ppm to at least 10 ppm, at least 0.02 ppm to at least 10 ppm, at least 0.1 ppm to at least 10 ppm, at least 0.2 ppm to at least 10 ppm, at least 0.5 ppm to at least 5 ppm.

[0565] The present invention is further described by the following examples that should not be construed as limiting the scope of the invention.

EXAMPLES

Media and Solutions

[0566] Model detergent A: 12 wt % LAS, 1.1 wt % AEO Biosoft N25-7 (NI), 7 wt % AEOS (SLES), 6 wt % MPG, 3 wt % ethanol, 3 wt % TEA (triethanolamine), 2.75 wt % cocoa soap, 2.75 wt % soya soap, 2 wt % glycerol, 2 wt % sodium hydroxide, 2 wt % sodium citrate, 1 wt % sodium formiate, 0.2 wt % DTMPA, 0.2 wt % PCA.

[0567] Model detergent O: 4 wt % sodium dodecylbenzenesulfonate (LAS), 8 wt % sodium lauryl ether sulfate (SLES/AEOS), 1 wt % soap (soy fatty acid), 4 wt % alcohol ethoxylate (AEO), 0.4 wt % triethanolamine (TEA), 2 wt % sodium citrate, 0.02 wt % calcium chloride dihydrate.

[0568] For Example 4, a wash liquor of model detergent A was prepared by dissolving 3.33 g/l of the detergent in water with a hardness of 150 dH.

[0569] For Example 5, 2.67 g/l model O and 0.44 g/l model A, respectively, were dissolved in tap water.

Assays

Peptidoglycan-Degrading Activity Measurement

[0570] The peptidoglycan-degrading activity was estimated using the Invitrogen™ EnzChek™ Lysozyme Assay Kit (ThermoFisher, E22013) as recommended by the manufacturer. The DQ™ substrate supplied with the kit was dissolved in miliQ-H₂O to yield a 1.0 mg/ml substrate stock solution. This solution was further diluted to 50 µg/ml by mixing 50 µl stock substrate solution with 950 µl 1× Reaction buffer supplied with the kit. Concentrated enzyme solution was diluted to 2 µg/ml in the 1× Reaction buffer. 50 µl of the 50 µg/ml substrate solution was mixed with either 50 µl 1× Reaction buffer or 50 µl 2 µg/ml enzyme solution to yield a final enzyme concentration in the reaction of 1 µg/ml. The sample was incubated at 37° C. and fluorescence development was measured using a POLARstar Omega plate reader spectrophotometer (BMG LABTECH) with an excitation wavelength of 485 nm emission wavelength of 520 nm and a gain of 1500.

[0571] Fluorescence units were plotted against time and the initial slope was estimated. The results are given in the table below. Clear peptidoglycan-degrading enzyme activity is observed for the enzyme.

Enzyme	Initial slope (fluorescence units/min)
No enzyme	-189.64
SEQ ID NO: 6	13228

Example 1: Cloning and Expression of Polypeptides: Strains and DNA

[0572] DNA encoding the genes of SEQ ID NO: 1, SEQ ID NO: 4, SEQ ID NO: 7, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 19, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 28, SEQ ID NO: 31, SEQ ID NO: 34, SEQ ID NO: 37, SEQ ID NO: 40, SEQ ID NO: 43, SEQ ID NO: 46, SEQ ID NO: 49, SEQ ID NO: 52, SEQ ID NO: 55, SEQ ID NO: 58, SEQ ID NO: 61, SEQ ID NO: 64, SEQ ID NO: 67, SEQ ID NO: 70, SEQ ID NO: 73, SEQ ID NO: 76, SEQ ID NO: 79, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID

NO: 88, SEQ ID NO: 91, SEQ ID NO: 94, SEQ ID NO: 97, SEQ ID NO: 100, SEQ ID NO: 103 and SEQ ID NO: 106 was isolated from bacterial strains and environmental bacterial communities isolated from soil samples collected in different countries (see Table 1). Chromosomal DNA from the different strains and bacterial communities was subjected to full genome sequencing using Illumina technology. The genome sequences were analyzed for protein sequences that contained an Amidase_2 domain, as defined in PFAM (PF01510, Pfam version 31.0 Finn (2016). Nucleic Acids Research, Database Issue 44: D279-D285).

TABLE 1

Enzyme Donor	Country of origin
SEQ ID NO: Alicyclobacillus sp.	Denmark
3 Hamadaea tsunoensis	Japan
6 Micromonospora maritima	United States
9 Paenibacillus sp.	United States
12 Nonomuraea sp.	United Kingdom
15 Lysobacter antibioticus	China
18 Micromonospora sp.	United Kingdom
21 Nonomuraea coxensis	Philippines 1990
24 Micromonospora fulvopurpurea	unknown strain isolated 1970
27 Alicyclobacillus sp.	Denmark
30 Halomonas sp.	United States
33 Pseudomonas peli	United States
36 Halomonas sp.	United States
39 Pseudomonas pseudoalcaligenes	United States
42 Tumbacillus sp.	United States
45 Nonomuraea dietiae	United Kingdom
48 Laceyella sacchari	Denmark
51 Thermostaphylospora chromogena	Unknown, date of sampling 22 Aug. 1990
54 Kribbella aluminosa	China
57 Streptomyces griseus	United States
60 Micromonospora peucetia	United Kingdom
63 Bacillus sp.	Japan
66 Bacillus sporothermodurans	Denmark
69 Paenibacillus pini	Sweden
72 Bacillus cohnii	United States
75 Kribbella sp.	United Kingdom
78 Bacillus sp.	United States
81 Bacillus sp.	United States
84 Bacillus sp.	United States
87 Streptomyces sp.	China
90 Bacillus sp.	United States
93 Bacillus sp.	United States
96 Nonomuraea guangzhouensis	United Kingdom
99 Nonomuraea guangzhouensis	United Kingdom
102 Bacillus cohnii	Denmark
105 Halomonas sp.	United States
108 Lysobacter capsica	United States

Example 2: Cloning and Expression of Polypeptides of the Invention

[0573] DNA encoding the mature peptides of peptidoglycan degradation enzyme genes SEQ ID NO: 1, SEQ ID NO: 4, SEQ ID NO: 7, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 19, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 28, SEQ ID NO: 31, SEQ ID NO: 34, SEQ ID NO: 37, SEQ ID NO: 40, SEQ ID NO: 43, SEQ ID NO: 46, SEQ ID NO: 49, SEQ ID NO: 52, SEQ ID NO: 55, SEQ ID NO: 58, SEQ ID NO: 61, SEQ ID NO: 64, SEQ ID NO: 67, SEQ ID NO: 70, SEQ ID NO: 73, SEQ ID NO: 76, SEQ ID NO: 79, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 94, SEQ ID NO: 97, SEQ ID NO: 100, SEQ ID NO: 103 and SEQ ID NO: 106 was

amplified from the genomic DNA of the corresponding bacterial strains by standard PCR techniques using specific primers containing an overhang to cloning vector. The amplified PCR fragments were inserted into a *Bacillus* expression vector as described in WO 2012/025577. Briefly, the DNA encoding the mature peptide of the gene was cloned in frame to a *Bacillus clausii* secretion signal (BcSP; with the following amino acid sequence: MKKPLGKIVAS-TALLISVAFSSSIASA (SEQ ID NO: 109). BcSP replaced the native secretion signal in the gene. Downstream of the BcSP sequence, an affinity tag sequence was introduced to ease the purification process (His-tag; with the following amino acid sequence: HHHHHHPR (SEQ ID NO: 110) The gene that was expressed therefore comprised the BcSP sequence followed by the His-tag sequence followed by the mature wild type gene sequence. The final expression plasmid (BcSP-His-tag-PGLGene) was transformed into a *Bacillus subtilis* expression host. The BcSP-fusion gene was integrated by homologous recombination into the *Bacillus subtilis* host cell genome upon transformation. The gene construct was expressed under the control of a triple promoter system (as described in WO 99/43835). The gene coding for chloramphenicol acetyltransferase was used as marker (as described in (Diderichsen et al., 1993, *Plasmid* 30: 312-315)). Transformants were selected on LB media agar

inoculated per 10 ml TSB glass tube, whirl mixed and incubated over night at 30° C. with 200 rpm shaking. Then the bacteria are transferred to 50 ml Falcon tubes at 3000 rpm 20° C. for 5 min in a Sorvall centrifuge. The supernatant is removed and re-suspended in 10 ml PBS per tube. Cells are washed twice, added to a 50 ml tube and mixed. A solution of the culture is made with an OD600 of 0.5 as measured in a CLARIOstar® reader. 100 mL is prepared and kept under constant stirring throughout the test.

[0576] A detergent solution containing 3.33 g/L model A detergent is prepared by mixing 0.167 g Model A detergent with 50 mL of tap water in a 100 mL BlueCap bottle, stirring for 2-5 min before use. This solution is used for the first and last rows in the setup where no bacteria is added (see below). A detergent solution with bacteria is made by preparing a tap water solution containing *M. luteus* with an OD600 of 0.5 and 0.33 g Model A detergent, stirring for 2-5 min. This is used as a mix for wells of 48-well plates (Thermo Scientific, Nunc A/S, non-treated, PS, sterile, cat.no. 150787). A setup of blanks and enzymes is created so as to randomize the positions for repetitions in the plates to account for the systematic molding variation. An example may look like the following:

	1 No bacteria added	2 bacteria added	3 bacteria added	4 bacteria added	5 bacteria added	6 bacteria added	7 bacteria added	8 No bacteria added
A	Control, no enzyme	Blank, no enzyme	Enz1	Enz3	Enz2	Enz4	Ref	Control, no enzyme
B	Control, no enzyme	Blank, no enzyme	Enz1	Enz3	Enz2	Enz4	Ref	Control, no enzyme
C	Control, no enzyme	Blank, no enzyme	Enz1	Enz3	Enz2	Enz4	Ref	Control, no enzyme
D	Control, no enzyme	Ref	Enz2	Enz4	Enz1	Enz3	Blank, no enzyme	Control, no enzyme
E	Control, no enzyme	Ref	Enz2	Enz4	Enz1	Enz3	Blank, no enzyme	Control, no enzyme
F	Control, no enzyme	Ref	Enz2	Enz4	Enz1	Enz3	Blank, no enzyme	Control, no enzyme

supplemented with 6 microgram of chloramphenicol per ml. One recombinant *Bacillus subtilis* clone containing the PGL expression construct was selected and was cultivated on a rotary shaking table in 500 ml baffled Erlenmeyer flasks each containing 100 ml yeast extract-based media. After 3-5 days' cultivation time at 30° C. to 37° C., the enzyme-containing supernatant was harvested by centrifugation and the enzymes were purified by His-tag purification.

Example 3: His Tag Purification Method

[0574] The His-tagged enzymes were purified by immobilized metal chromatography (IMAC) using Ni²⁺ as the metal ion on 5 mL HisTrap Excel columns (GE Healthcare Life Sciences). The purification took place at pH 7 and the bound protein was eluted with imidazole. The purity of the purified enzymes was checked by SDS-PAGE and the concentration of the enzyme determined by Absorbance 280 nm after a buffer exchange in 50 mM HEPES, 100 mM NaCl pH 7.0.

Example 4: Attachment of *Micrococcus luteus*

[0575] *M. luteus* is taken from -80° C. frozen stock and grown on TSA plates for 3 days. From here one colony is

[0577] Detergent mix+/-bacteria is added to the wells by adding 0.5 mL *M. luteus* test solution to each well. 10 µL enzyme solution with the prepared concentration is added according to the setup. The plate is allowed to incubate at 30° C. for 1.5 h. After incubation, the solution is removed from the plates by turning the plate upside down on paper towel in a zip-lock bag. The plate is turned and punched two times, then rinsed with 0.75 mL 0.9% NaCl solution. Solution is removed from the plates by turning the plate upside down on paper towel in a zip-lock bag. The plate is turned and punched two times, and the rinsing and punching step is repeated. 0.5 mL crystal violet 0.095% is added to each well. It is allowed to incubate 15 min on the table, then the supernatant is removed from the plates by turning the plate upside down on paper towel in a zip-lock bag and punching the plate hard twice to secure best removal, repeating until drops of unbound dye solution are removed, followed by gentle rinsing with 1 mL 0.9% NaCl. The rinse solution is removed and punched as described earlier. The color in the wells is dissolved with 0.5 mL 96% ethanol, giving a quick shake by hand until the liquid is clear. Absorbance 595 is measured in the CLARIOstar® reader and if it is higher than 3 the samples are diluted in new wells.

[0578] The results, measured as follows, are provided in Table 2 below:

$$Y\% \text{ attachment inhibition from } A_{590} = (1 - (A_{590\text{control}}/A_{590\text{enzx}})) * 100\%.$$

$A_{590\text{control}} = A_{590}$ attachment in detergent solution of *M. luteus*;

$A_{590\text{enzx}} = A_{590}$ attachment in detergent + enzyme.

TABLE 2

Inhibition of attachment of <i>M. luteus</i>			
Enzyme	Model A pH 7.0 Y % attachment inhibition	Model A pH 7.8 Y % attachment inhibition	1 × PBS pH 6.0 Y % attachment inhibition
Day 1			
SEQ ID NO: 6 (1 ppm)	46.9	43	30.5
SEQ ID NO: 30 (10 ppm)	—	-3.5	39.9
Day 4			
SEQ ID NO: 6 (1 ppm)	41.8	45.6	22.4
SEQ ID NO: 12 (1 ppm)	40.9	17.5	—
SEQ ID NO: 12 (10 ppm)	40.8	33.9	72.9
Day 14			
SEQ ID NO: 6 (1 ppm)	—	52.4	43.2
SEQ ID NO: 15 (0.01 ppm)	—	23.5	—
SEQ ID NO: 15 (0.1 ppm)	—	51.5	—
SEQ ID NO: 15 (0.5 ppm)	—	60.1	—
SEQ ID NO: 15 (1 ppm)	—	65.2	—
SEQ ID NO: 15 (2 ppm)	—	59.1	—
SEQ ID NO: 15 (5 ppm)	—	62.6	17.5
Day 22			
SEQ ID NO: 6 (1 ppm)	—	50.7	—
SEQ ID NO: 21 (1 ppm)	—	5.4	—
SEQ ID NO: 21 (10 ppm)	—	34.8	—
Day 23			
SEQ ID NO: 6 (1 ppm)	—	57.1	—
SEQ ID NO: 99 (1 ppm)	—	42.7	—
SEQ ID NO: 99 (10 ppm)	—	47.5	—
Day 25			
SEQ ID NO: 6 (1 ppm)	—	73.9	—
SEQ ID NO: 18 (1 ppm)	—	67.1	—
SEQ ID NO: 18 (10 ppm)	—	88.2	—
Day 28			
SEQ ID NO: 6 (1 ppm)	—	32.5	—
SEQ ID NO: 108 (1 ppm)	—	13.3	—
SEQ ID NO: 108 (2.5 ppm)	—	17.1	—
SEQ ID NO: 108 (5 ppm)	—	21.2	—
SEQ ID NO: 108 (10 ppm)	—	24.6	—
Day 29			
SEQ ID NO: 6 (1 ppm)	—	31.8	—
SEQ ID NO: 9 (1 ppm)	—	17.8	—
SEQ ID NO: 9 (10 ppm)	—	52	—
Day 30			
SEQ ID NO: 6 (1 ppm)	—	34.5	—
SEQ ID NO: 27 (1 ppm)	—	1.3	—
SEQ ID NO: 27 (10 ppm)	—	4.2	—
SEQ ID NO: 45 (1 ppm)	—	20.1	—
SEQ ID NO: 45 (10 ppm)	—	27.3	—

TABLE 2-continued

Inhibition of attachment of <i>M. luteus</i>			
Enzyme	Model A pH 7.0 Y % attachment inhibition	Model A pH 7.8 Y % attachment inhibition	1 × PBS pH 6.0 Y % attachment inhibition
Day 31			
SEQ ID NO: 6 (1 ppm)	—	30.7	—
SEQ ID NO: 48 (10 ppm)	—	12	—
SEQ ID NO: 69 (10 ppm)	—	3.2	—
Day 32			
SEQ ID NO: 6 (1 ppm)	—	34.4	—
SEQ ID NO: 87 (1 ppm)	—	4.1	—
SEQ ID NO: 87 (10 ppm)	—	10	—

[0579] The test results have a certain day to day variation, due to, e.g., fluctuations in lab temperature and humidity as well as slight variations in day-to-day cell viability, and the attachment inhibition results should therefore be compared for the same day. Our experience with the assay and the enzymes has shown that the day-to-day fluctuations in attachment and inhibition patterns in general give the same pattern in performance between the enzymes when they are repeated another day. Some enzymes work better at pH 6.0 and 7.0 and others perform optimally at pH 7.8, which has been tested for selected enzymes. SEQ ID NO: 6 is used as a reference enzyme to control the assay and measure the day to day variation.

[0580] Conclusion: In this experiment, SEQ ID NO: 6 shows robust inhibitory effects of *M. luteus* attachment at pH 6, pH 7 and pH 7.8. 10 ppm of SEQ ID NO: 30 shows an inhibitory effect on *M. luteus* on par with the effect of SEQ ID NO: 6 at a concentration of 1 ppm at pH 6, but no performance at pH 7.8. SEQ ID NO: 12 shows good performance at pH 7 compared to the control enzyme SEQ ID NO: 6. The performance of SEQ ID NO: 12 is less prominent at pH 7.8, but there is still a significant effect. SEQ ID NO: 15 can be dosed very low (0.01 ppm) and still give robust anti-attachment benefits at pH 7.8. At 0.5 ppm and 1.0 ppm there is a tendency for the inhibitory effect of SEQ ID NO: 15 to be higher than that of SEQ ID NO: 6 at a pH of 7.8. At pH 6 performance seems to be lower for SEQ ID NO: 15 at 5 ppm compared to SEQ ID NO: 6 at 1 ppm. SEQ ID Nos: 21, 99, 108, 9, 27, 45, 48, 69 and 87 also show inhibitory attachment benefits. SEQ ID NO: 18 gives very high anti-attachment performance on *M. luteus* at pH 7.8 using 1 ppm and it increases using 10 ppm.

Example 5: Preparation of Crude Cell Wall Extracts from *Micrococcus luteus* and OD Drop Activity Assay

Preparation of Cell Wall Extracts

[0581] Cell wall extracts from *Micrococcus luteus* were prepared following the protocol described by Mukamolova et al., 2006, *Molecular Microbiology* 59(1): 84-98. Briefly, *M. luteus* cells grown overnight in 1L LB medium were centrifuged at 10,000 g for 30 minutes, washed with deionized water, resuspended in 200 ml 5% (w/v) SDS and boiled for 20 minutes. Following centrifugation, the pellet was resuspended in 100 ml 4% (w/v) SDS and boiled again for 20 min. The pellet was then thoroughly washed six times

with 100 ml hot (65° C.) water to remove the SDS. Finally, it was washed with 10 ml acetone, air dried overnight, weighed and stored at -20° C.

OD Drop Assay Using Crude Cell Wall Extracts from *M. luteus*

[0582] 0.6 g of *M. luteus* cell wall extracts prepared as described above were resuspended in 15 ml of deionized water (stock solution 40 mg/ml) and passed through a syringe needle to disrupt the large flakes. This stock solution was stored at 4° C.

[0583] A cell wall extract working solution was prepared from the stock solution at 0.75 mg/ml in 50 mM MES (2-(N-morpholino) ethanesulfonic acid) pH 6 buffer and two model detergents, model O and A (2.67 g/L model O and 0.44 g/L model A, respectively, in tap water). These working solutions were prepared fresh each time when running an OD drop assay.

[0584] Next, 150 µL aliquots of the crude cell wall extract working solution were dispensed in the wells of a 96-well microtiter plate (Thermo Scientific, Nunclon Delta Surface, cat #167008) and mixed with 50 µL of a solution containing 80 ppm of a purified enzyme (3, 6, 9, 12, 15, 18, 21, 24, 27, 30, 33, 36, 39, 42, 45, 48, 51, 54, 57, 60, 63, 66, 69, 72, 75, 78, 81, 84, 87, 90, 93, 96, 99, 102, 105 or 108) in 50 mM HEPES 100 mM NaCl pH7 buffer, or the HEPES buffer as a control, and incubated at 30° C. with shaking at 600 rpm in an Eppendorf ThermoMixer C. The absorbance of the samples was measured at 600 nm in a SpectraMax M3 instrument at time=0 and after overnight incubation with the enzyme. Enzymes were tested in duplicate. The average of the OD drop measurements (calculated by the OD obtained after overnight incubation minus OD at time 0) are listed in Table 3 below.

TABLE 3

OD drop values (OD after overnight incubation minus OD time 0)			
SEQ ID NO:	MES + HEPES	Model A	Model O
3	0.27	0.03	0.00
6	0.42	0.13	0.21
9	0.20	0.03	0.00
12	0.35	0.20	0.46
15	0.65	0.79	0.54
18	0.71	0.90	0.82
21	0.10	0.02	0.00
24	0.12	0.00	0.00
27	0.08	0.03	0.00
30	0.15	0.49	0.50
33	0.36	0.15	0.32
36	0.12	0.00	0.00
39	0.36	0.25	0.36
42	0.21	0.02	0.00
45	0.30	0.03	0.00
48	0.10	0.03	0.00
51	0.23	0.00	0.00
54	0.03	0.17	0.23
57	0.23	0.33	0.58
60	0.11	0.23	0.30
63	0.18	0.15	0.30
66	0.47	0.16	0.40
69	0.46	0.16	0.23
72	0.45	0.17	0.29
75	0.53	0.20	0.55
78	0.29	0.19	0.32
81	0.64	0.16	0.27
84	0.60	0.15	0.35
87	0.35	0.17	0.30
90	0.18	0.16	0.23

TABLE 3-continued

OD drop values (OD after overnight incubation minus OD time 0)			
SEQ ID NO:	MES + HEPES	Model A	Model O
93	0.78	0.19	0.10
96	0.36	0.15	0.14
99	0.27	0.72	0.66
102	0.25	0.16	0.21
105	0.10	0.15	0.25
108	0.60	0.03	0.16

[0585] The results in Table 3 show that enzymes giving an OD drop can hydrolyze cell wall extracts present in the solution.

Example 6: Construction of the PGL Domain, Clades and Phylogenetic Trees

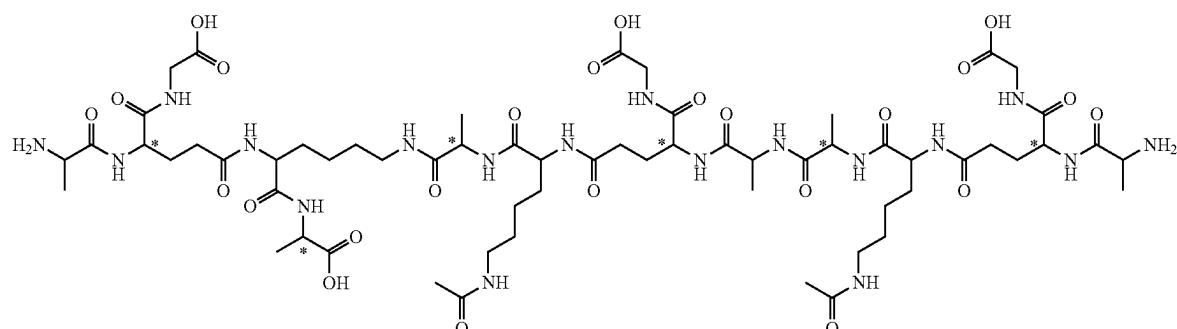
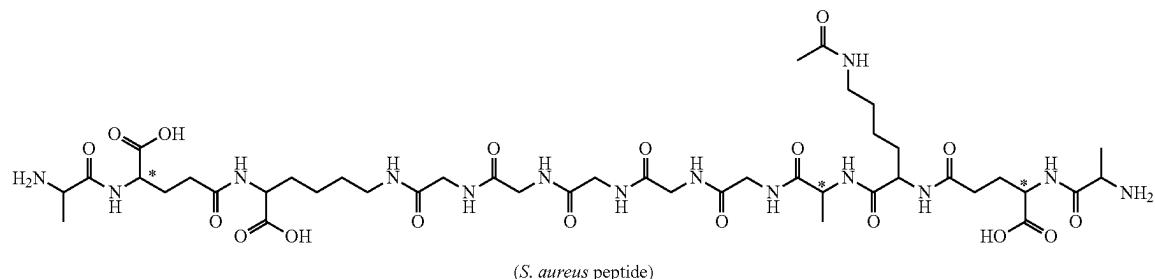
[0586] The polypeptides of the invention have hydrolase activity and comprise the Amidase_2 domain as well as clusters such as clades. A phylogenetic tree was constructed from polypeptide sequences containing an Amidase_2 domain, as defined in PFAM (PF01510, Pfam version 31.0 Finn (2016). Nucleic Acids Research, Database Issue 44: D279-D285). The phylogenetic tree was constructed from a multiple alignment of mature polypeptide sequences containing at least one Amidase_2 domain. The sequences were aligned using the MUSCLE algorithm version 3.8.31 (Edgar, 2004, *Nucleic Acids Research* 32(5): 1792-1797), and a tree was constructed using FastTree version 2.1.8 (Price et al., 2010, *PloS one* 5(3)) and visualized using iTOL (Letunic & Bork, 2007, *Bioinformatics* 23(1): 127-128).

[0587] Analysis of the phylogenetic tree showed that the polypeptides containing an Amidase_2 domain may be separated into distinct sub-clusters. The sub-clusters are defined by one or more short sequence motifs, as well as by containing an Amidase_2 domain as defined in PFAM (PF01510, Pfam version 31.0). We denoted one sub-cluster comprising the motif N[IV]X[AG][GAS]A[AY][LV]L (SEQ ID NO: 111), situated in positions corresponding to positions 324 to 328 in *Micromonospora maritima* (SEQ ID NO: 6), as the PGL clade. All polypeptide sequences containing an Amidase_2 domain as well as the motif will be denoted as belonging to the PGL clade. Polypeptides included in the clade are SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 9, SEQ ID NO: 12, SEQ ID NO: 15, SEQ ID NO: 18, SEQ ID NO: 21, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 42, SEQ ID NO: 45, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 60, SEQ ID NO: 63, SEQ ID NO: 66, SEQ ID NO: 69, SEQ ID NO: 75, SEQ ID NO: 87, SEQ ID NO: 96, SEQ ID NO: 99 and SEQ ID NO: 108.

Example 7: N-Acetylmuramyl-L-Alanine Amidase Assay

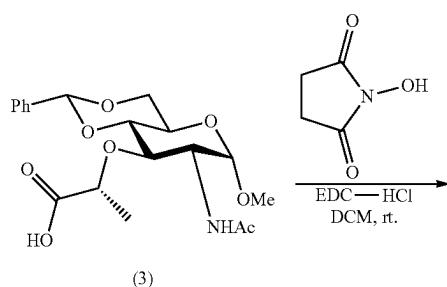
Substrate Synthesis

[0588] The organic syntheses of peptidoglycan fragments (1) and (2) was performed in three steps from commercially available methyl 2-acetamido-4,6-O-benzylidene-2-deoxy- α -D-glucopyranoside and the appropriate peptide sequences. Both peptides used (here named *S. aureus* peptide and *M. luteus* peptide; see below) were synthesized and provided by TAG Copenhagen A/S. In the structural formulas below, an asterisk (*) denotes D-stereochemistry.

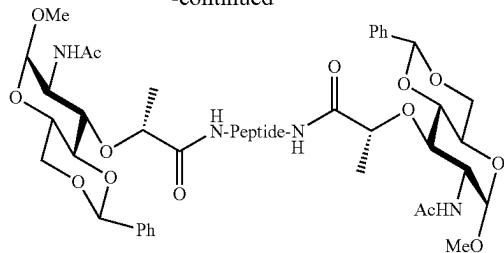


[0589] Synthesis of the peptides modified with muramic acid derivatives was performed, cf. the schematic overview below, by initially coupling methyl 2-acetamido-4,6-O-benzylidene-2-deoxy- α -D-glucopyranoside to (S)-2-chloropropionic acid using the protocol from Hesek et al., *J. Org. Chem.* 2004, 69, 778-784 to result in compound (3). Then the corresponding muramic acid NHS-ester derivative (4) was synthesized by treating 200 mg of (3) with N-(3-Dimethylaminopropyl)-N-ethylcarbodiimide hydrochloride (EDC-HCl, 1.5 eq.) and N-hydroxysuccinimide (1.15 eq.) in anhydrous dichloromethane (DCM, 2 mL) at room temperature (rt) for 4 hours before the solution was diluted with DCM (10 mL), washed with 2.5% NaHSO₄ and brine, dried over anhydrous NaSO₄, filtered and concentrated in vacuo. The desired product (4) was used without further purification in 2.1 eq. to couple to a peptide (20 mg) in anhydrous dimethylformamide (DMF, 300 μ L) at room temperature in the presence of triethylamine (TEA, 3.5 eq.) by overnight reaction. The desired products (*S. aureus* substrate 1, or *M. luteus* substrate 2) were used without further purification for amidase assessment.

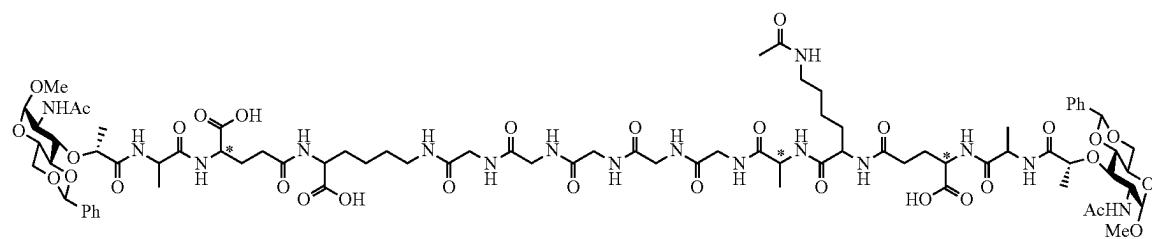
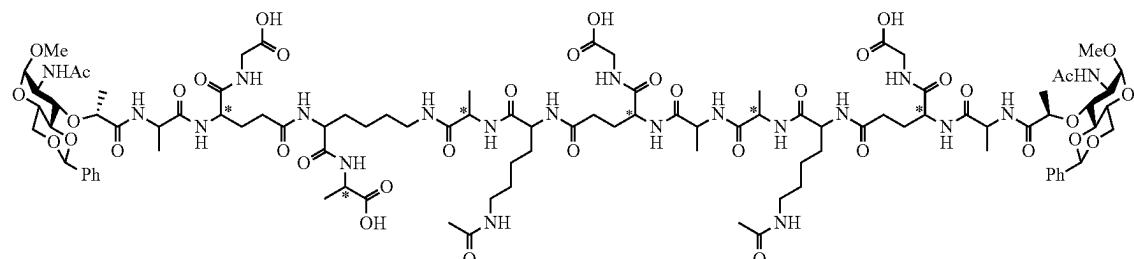
-continued



-continued

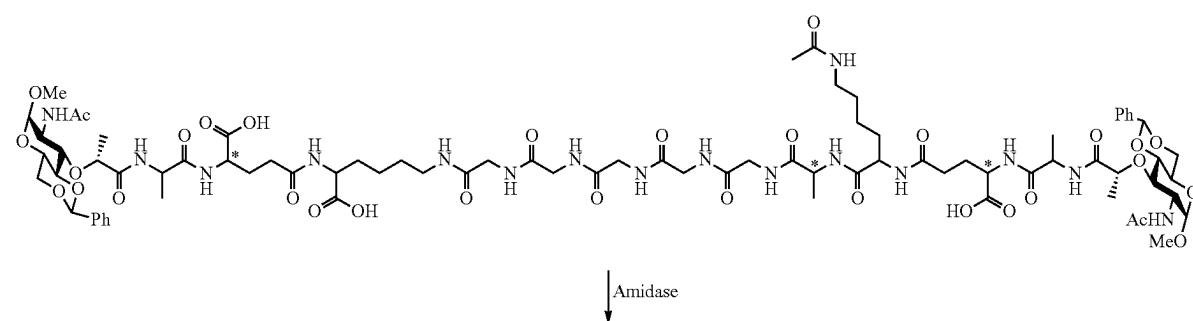


[0590] The result is the following modified peptides, *S. aureus* substrate 1 and *M. luteus* substrate 2:

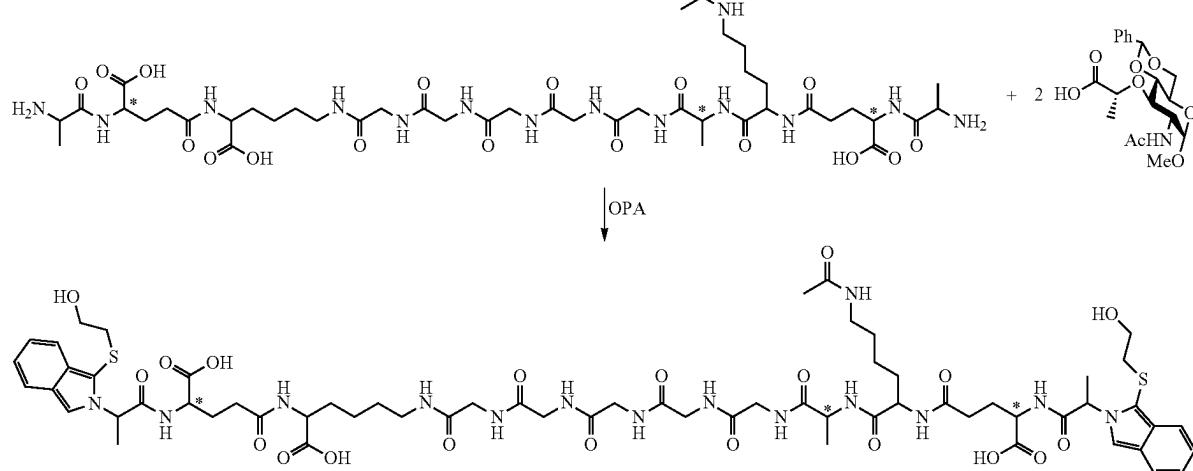
(1; *S. aureus* substrate)(2; *M. luteus* substrate)

Amidase Assay

[0591] The amidases cleave between the peptide and the muramic acid (MurNAc) motifs to liberate one or two new N-termini, as illustrated in the following:



-continued



[0592] When exposed to standard o-phthalaldehyde (OPA) assay conditions, the newly formed peptide amines (N-termini) react to yield a fluorescent readout (excitation=340 nm, emission=455 nm). OPA solution is prepared by dissolving 800 mg o-phthalaldehyde in 10 mL 95% EtOH followed by addition of 1 L 0.5 M borate buffer (pH 9.0) containing 2 mL 2-mercaptoethanol.

[0593] Amidase reactions were performed by incubating and shaking the amidase (20 pg/mL final conc.) with the MurNAc-peptide-MurNAc substrate (substrate 1 or 2, 5 mM final conc.) in 50 mM MES buffer (pH 6.0, 100 mM NaCl) at 37° C. overnight, before the reaction products were analyzed by OPA assay and MALDI-TOF.

[0594] Amidase assessment (OPA assay) was performed by adding 100 µL OPA solution to 10 µL reaction sample. The mixture was transferred to a 96-well plate and monitored in a spectrophotometer (excitation=340 nm, emission=455 nm) after 5 min of incubation. The non-modified *S. aureus* and *M. luteus* peptides (i.e., with amino termini as shown above) were included as controls.

Results

[0595] Table 4 below shows the measured fluorescence for the *S. aureus* and *M. luteus* peptides (with amino termini) and substrates (with MurNAc termini) alone and after treatment with the amidases of SEQ ID NO: 6 or SEQ ID NO: 33, as well as for the amidases alone (negative control).

[0596] It can be seen that the MurNAc-peptide-MurNAc substrates (*S. aureus* substrate and *M. luteus* substrate) yield minimal OPA response until treated with the amidase of SEQ ID NO: 6 or SEQ ID NO: 33, where the fluorescent response increases significantly. The amidases appear to have no activity on the non-modified peptides (*S. aureus* peptide and *M. luteus* peptide), which was as expected.

[0597] MALDI-TOF MS analyses (data not shown) before and after treatment of the *S. aureus* and *M. luteus* substrates with the amidase of SEQ ID NO: 6 or SEQ ID NO: 33 confirmed that the OPA response is a result of enzymatic cleavage between the peptide and the MurNAc motifs to liberate the MurNAc motifs, yielding the free peptide N-termini.

TABLE 4

Peptide/substrate + enzyme	Fluorescence (RFU; 340, 455 nm)
SEQ ID NO: 6	29
SEQ ID NO: 33	27
<i>S. aureus</i> peptide	8420
<i>S. aureus</i> peptide + SEQ ID NO: 6	8240
<i>S. aureus</i> peptide + SEQ ID NO: 33	8547
<i>S. aureus</i> substrate	515
<i>S. aureus</i> substrate + SEQ ID NO: 6	7077
<i>S. aureus</i> substrate + SEQ ID NO: 33	5704
<i>M. luteus</i> peptide	3447
<i>M. luteus</i> peptide + SEQ ID NO: 6	3340
<i>M. luteus</i> peptide + SEQ ID NO: 33	3298
<i>M. luteus</i> substrate	381
<i>M. luteus</i> substrate + SEQ ID NO: 6	3166
<i>M. luteus</i> substrate + SEQ ID NO: 33	1853

Example 8: N-Acetylmuramyl-L-Alanine Amidase Assay, Test of Additional Amidases

[0598] Several other enzymes within the same family as the amidase of SEQ ID NO: 6 were tested against the *S. aureus* substrate (substrate 1) as described in Example 7. This revealed that the amidases of SEQ ID NOs: 3, 45, 24 and 12 had comparable activity towards the *S. aureus* substrate; see the results in Table 5 below, where the individual enzymes (without peptide or substrate) are included as negative controls.

TABLE 5

Peptide/substrate + enzyme	Fluorescence (RFU; 340, 455 nm)
<i>S. aureus</i> peptide	8458
<i>S. aureus</i> substrate	735
SEQ ID NO: 3	33
SEQ ID NO: 6	21
SEQ ID NO: 12	54
SEQ ID NO: 24	108
SEQ ID NO: 45	44
<i>S. aureus</i> substrate + SEQ ID NO: 3	6810
<i>S. aureus</i> substrate + SEQ ID NO: 6	7584

TABLE 5-continued

Peptide/substrate + enzyme	Fluorescence (RFU; 340, 455 nm)
S. aureus substrate + SEQ ID NO: 24	6903
S. aureus substrate + SEQ ID NO: 12	6602
S. aureus substrate + SEQ ID NO: 45	6851

[0599] The enzyme of SEQ ID NO: 105 was tested in a similar experiment and had comparable activity towards the S. aureus substrate; see Table 6.

TABLE 6

Peptide/substrate + enzyme	Fluorescence (RFU; 340, 455 nm)
SEQ ID NO: 105	37
S. aureus substrate	756
S. aureus substrate + SEQ ID NO: 105	6328

SEQUENCE LISTING

```

Sequence total quantity: 111
SEQ ID NO: 1      moltype = DNA length = 1380
FEATURE          Location/Qualifiers
sig_peptide      1..87
mat_peptide      88..1380
source           1..1380
mol_type = genomic DNA
organism = Hamadaea tsunoensis
CDS              1..1380
SEQUENCE: 1
atgacagtac cacctacacg tctgtctact ttcatgttag gagegtgtat cttagccgt 60
ggtagtgcgtc acccgccagc aagcgtcgt getgtccatc tagcgcctga cgcattaaaca 120
gtacgcgtcaa ctccacgcata aactgtgtc ttactgtct gttagtgcgtc tgacgcacaa 180
cgtagtgcgtt ttccacgtca cttattgtatc getattgtgtt acgctgaaac acacccgtat 240
ggacacgcacg gcaactccatc tgccagttgtt ggatatgtgtt ttatgtatc tactggcaat 300
ccggctgttc acatcttc tgaaggcttc egcttaactc gccttaaagg tagoacgtta 360
gagaataacc aagctgtcaa catccttgcgtt gcccgtcgcag ttttacgtctc ttacgtctgt 420
gatttggaaa ctgtcaacg tgactctgtca gacaatttgcgtt acgctgtgt agctcggttat 480
ggtagccgtca ctgtatccgtc tggtgcgtc ctttatgtctgt atacagggtt cgtatcttt 540
gccccacgggtt ccgtggatcc agcttgcgttcc ttccatgtgtt cagctgtgtc tgtagcacct 600
caacgtggta ctcttgcgtca tgccgtcgtca tcattgtact ctgcagacta cggctctgt 660
gcttgggctc cagcatctac atctaactac acagttgcaaa accgcggaaac agactataac 720
atcaattaca ttgttatcca cgtaactcaa ggatcttacg ctggctctat ttcttggttc 780
caaaatccatc cggetcgatc ttgtgtcat tacgttgcgtt gttcatctgtc tggtgcccatt 840
acgcgtctg ttcgtggaaa agatatcgtt tggcgcacgc gcaactggac atacaacacg 900
caagctatcg gcatcgaaaca tgaaggctat atcgacgacc cttcatgttt cactgacgca 960
atgtatcggtt cttcagcagc tcttacacgt tcacttacaa cgaaatacgc tattctctgt 1020
gaccgcacgc acatcatcggtt ccatatcgaa gttcccttctg caacgcacac ggtatctgtt 1080
cagtttgcgtt actggactta ccatatcgaa ttgttgcgtt ggtacacggg tattcgaaaca 1140
ggaacggtaa acgtatctgg tcttgcgtt attcgcgttgcgtt gttctgttactgcgtt 1200
gttgcgttgcgtt ctcttgcgtt cggagcgggaa gtttgcgtt actgcgttacg tacggcaccg 1260
acagtaacgg gtacttacgg cactagcaac atctgggacc gtatcggtac gaataagtat 1320
gttgcgtatcgtt gtttgcgtt gacggcttacatcgttaccacgttgcgtt 1380

SEQ ID NO: 2      moltype = AA length = 460
FEATURE          Location/Qualifiers
source           1..460
mol_type = protein
organism = Hamadaea tsunoensis
SEQUENCE: 2
MTVPPTRRAT FMLGALILAA GVAAPPASAA AAPVAPDAL VASTPASTGS LTAADFAAAT 60
RYGVPRDLLI AIGYAETHLD GHAGTPSAAG GYGVMLTGN PAVHTLAEAS RLTGLKASTL 120
ENNQAANILG AAVRLRSYAA DLKTAQRDSV DNWYAAVARY GGATDPSVAR LYADTVYDLL 180
ATGFGVPAKG VSVTARAVP QRGTLATAR SLDSADYGPA AWAPASTSNY TVANRETDYN 240
INYIVIHVTQ GSYAGSISWF QNPAAQVSLN YVVRSSDGAI TQSvrekdia WHAGNWTYNT 300
QAIIGIEHEGY IDDPFWFTDA MNYRSSAALT SLTTKYAIPR DRSHIIGHIE VPSATHDPG 360
QYWNWTYYMQ LVNGVTGIGT GTVNVSGLN IRSGPGTYGA VAGSLANGAG VSVYCQATGT 420
TVTGTGTSN IWDIGTNKY VADAYVLTGS DGFIPGVPRC 460

SEQ ID NO: 3      moltype = AA length = 431
FEATURE          Location/Qualifiers
source           1..431
mol_type = protein
organism = Hamadaea tsunoensis
SEQUENCE: 3
AAAPVAPDAL TVASTPASTG SLTAAFDAAA TRYGVPRDLL IAIGYAETHL DGHAGTPSAA 60
GGYGVMLTGT NPAVHTLAEV SRLTGLKAST LENNQAANIL GAAAVLRSYAA ADLKTAQRDS 120
VDNWYAAVAR YGGATDPSVA RLYADTVYDL LATGFGVPAK GVSVTARAVA PQRGTLATAR 180
ASLDSADYGPA AAWAPASTSN YTVANRETDY NINYIVIHVT QGSYAGSISWF FQNPAAQVSA 240
HYVVRSSDGAI TQSvrekdia WHAGNWTYNT QAIIGIEHEGY YIDDPFWFTD AMYRSSAALT 300

```

-continued

RSLTTKYAIP RDRSHIIGHI EVPSATHDTP GQYWNWTTYYM QLVNGVTGIG TGTNVSGSL	360
NIRSGPGTGY AVAGSLANGA GVSVYCQATG TTVTGTGTYGTS NIWDRTGNK YVADAYVLTG	420
SDGFIPGVPR C	431
 SEQ ID NO: 4 moltype = DNA length = 1548	
FEATURE Location/Qualifiers	
sig_peptide 1..90	
mat_peptide 91..1545	
source 1..1548	
mol_type = genomic DNA	
organism = Micromonospora maritima	
CDS 1..1545	
 SEQUENCE: 4	
gtgacgatttc ggagaccctc gcgtcggtt agtgtctcg ggggcgcatt gatccatcg 60	
atccggctga cggcccaagcc ggcccaggcc ggcctgcac accgcgcgca gcctctcgcc 120	
qcgcccttcg cgcaggccgc ggccgatcc qacgtcgccg ggcacctgtc cgccgcgtc 180	
gggtacgcg agacccgcct ggacggccac gggggcgccg ccagcgccctc cgggggttac 240	
ggcgtatgc acctgaccag caacccgaaat gtcgggacgc tcgaegaggc cgcgcgcgg 300	
acccggctgg accgcgttaccc gtcgttaccc cgggacgcggg cgaacgtggc cggcgcggcg 360	
gccccgtgtc gtccatcgc cgcaggccgc gggttcacggc cggcgcgcgg cgaacgcgtc 420	
aaccagtgtt acggcccgat cgcggctac gggggcgccg cgcacggggc caccggccgg 480	
ctgtacgcg actccgtata cgcgttgcgc gcccggggct tcatecgac caccggccgc 540	
ggcgagggtca cgttgacggg ccttcgggtt gacccgcggc gggggccgtt cgcgcacgtt 600	
gccccgtgtt gacccgggtt ctccggcacc cttagcaccg actacggccc ggcggccgtt 660	
gtccggccca actctgtccaa ctacacgggtt tccagccggc agtcgggtt cccgatcaac 720	
tacatcgatca tccacccatc gcaggccgtt tccggccgtt cgatcgtt gttccagaac 780	
gccccggccgcg gacccggccgc gcaacttcgtt ctcgttgcgtt cgcacgggtt ggttaccgg 840	
atgggtggccggg aaaggacat cgcctggcgc gcccggcaactt ggactacaaa caccggatcg 900	
atccggatcg agcacgggg gtaegtcacaa acggcccttc ggtacacccg cgcgtatgtt 960	
cggtcgtgtt cggcgtgtt cccgttaccc gtcgttacccg acggcatccc gaagaccgc 1020	
accaacatcg tccggccaccc cccgttacccg gggggccacgc acacccgacc gggtccggaaac 1080	
tggtaacttgcg cttactatcg cgcgttgcgtt accggccggca ccaacggccccc gccgacccgac 1140	
tggtcgacgc ttgtggacaa caccacccgc ggcgggttca cccgcggccgc caactggggc 1200	
accttcgtatcg actccggccgc ggcgttacccg ggcgttaccc ggttacccca ccccggtcg 1260	
gccccggccgcg cccgttacccg caagggttaccc gtcgttacccg cccgggttggag 1320	
gtcttggatcc cggccgtgtt cccgttacccg acctccgttgcgtt cgcgtatcg ggcgttacccg 1380	
agccggcaacc agacgggttgcgtt ggttacccg acggcgttgcgtt ggcgttacccg 1440	
ggcaccttca ccctggccgc cccgttacccg aacaagggttgcgtt gtcgttacccg 1500	
agccgggttgcgtt acgttgcgtt cccgttacccg cccgttacccg 1548	
 SEQ ID NO: 5 moltype = AA length = 515	
FEATURE Location/Qualifiers	
source 1..515	
mol_type = protein	
organism = Micromonospora maritima	
 SEQUENCE: 5	
VTRRPSRRV SLGGAMILM IGLTQPAQA APAHRAQPLA AAFAQAAADS DVPRDLAAL 60	
GYAETRLDGH GGAPSASGGY GVMHLTSNPK VRTLDEAARR TRLDRAELRT RDAANVAGAA 120	
AVLRSYADEA GLSAAQRDDV NQWYGPPIARY GGATDGATAR LYADSVYDLL ARGFIATTAG 180	
GEVSDGRPV APQRGRYADV APLGTGDFGT LSTDYGPAAW VPANSSNYTV SSRESAYPIN 240	
YIVIHTMQGS YAGSIISWFQNA AAAGTSAHYL LRSSDGAVTQ MVRDKDIAWH AGNWTYNTQS 300	
IGIEHEGYVD RSSAALTRYL CDKYGIPKTR TNIIGHNQVP GATHDPGPNN 360	
WNWTYMMQLV TGTTTPPPTD WSTIVDNTTA GRFTASANWG TSTYSAQRYG ADYRYANPVA 420	
ASDTAWYKVN IPATATYRVE VVYPAVAGYN TSTPYIVATT SGNQTVSVNQ TANGGGWRSL 480	
GTFTLAAGDA NKVGVSRWSG STGYVIADAI RVTRV 515	
 SEQ ID NO: 6 moltype = AA length = 485	
FEATURE Location/Qualifiers	
source 1..485	
mol_type = protein	
organism = Micromonospora maritima	
 SEQUENCE: 6	
APAHRAQPLA AAFAQAAADS DVPRDLAAL GYAETRLDGH GGAPSASGGY GVMHLTSNPK 60	
VRTLDEAARR TRLDRAELRT RDAANVAGAA AVLRSYADEA GLSAAQRDDV NQWYGPPIARY 120	
GGATDGATAR LYADSVYDLL ARGFIATTAG GEVSDGRPV APQRGRYADV APLGTGDFGT 180	
LSTDYGPAAW VPANSSNYTV SSRESAYPIN YIVIHTMQGS YAGSIISWFQNA AAAGTSAHYL 240	
LRSSDGAVTQ MVRDKDIAWH AGNWTYNTQS IGIEHEGYVD NASWTYMDAMY RSSAALTRYL 300	
CDKYGIPKTR TNIIGHNQVP GATHDPGPNN WNWTYMMQLV TGTTTPPPTD WSTIVDNTTA 360	
GRFTASANWG TSTYSAQRYG ADYRYANPVA ASDTAWYKVN IPATATYRVE VVYPAVAGYN 420	
TSTPYIVATT SGNQTVSVNQ TANGGGWRSL GTFTLAAGDA NKVGVSRWSG STGYVIADAI 480	
RVTRV 485	
 SEQ ID NO: 7 moltype = DNA length = 1527	
FEATURE Location/Qualifiers	
sig_peptide 1..78	
mat_peptide 79..1527	

-continued

```

source          1..1527
               mol_type = genomic DNA
               organism = Paenibacillus sp.

CDS            1..1527
SEQUENCE: 7
atgggaattc gtcgcgttcc tcgccttctt agcatctctc tttctgcata gtttcttctt 60
ccatttacag ttccagctgc atcatttgca gcagacgacg ctgcggatc agcgaactct 120
gcacatctcgac gaaaagggtt tcttcaaaaa gctttcgaag ccgcgtacca agatgttggc 180
gttccagtag agatccttct tggtcttago tacgctgaga ctcgcgtggaa cgaccacgag 240
ggaagacccc tcacaacttaa cggatatggc cttatgcacc ttgtctgagaa cccgaaaaaac 300
tettcaacttgc acacagtc tgagcaactt aaagttagaca aacaacttct taagacagac 360
aaacgcgtta acattcggcg atctgcgggt gtacttgcag gccttgc当地 ggcgaaaaaac 420
aacggaaaaac ttccggcttc tettgtctgc tggtatacga cagtagcagc gtattctgg 480
atcgacgacc ttccggcttc tgccgtttac gtcgacgagg tttcaaatgt tatcaacgag 540
ggaaaaaaacag cgtttagcgg cacagagatc ttccacccat accctacggc agttactccg 600
aattcgcgtg agtacacgcg agtactctt gtcgcgactt ctatggacta ccctgtgtgt 660
atctggaaacg ctgcgttactc tggcaactac tctgttaggt ctgcggccc aggagacatc 720
tctaatactcg taatccatac tacacaaagggt tcatatgtcg gcacaatcaa ctgggtccaa 780
gaccctgtcg ctgttgcg acgcgttacat gttgtcgca gtcgtcgagg ccagatcaca 840
caaatgtgtc gogacaaaaaa catgcatac catgctcgat ctcgc当地 gagac 900
ggcatcgagc atgagggtca tgtaactgtac cctgc当地 gggtt atactgactc aatgtatcg 960
tcatctcgac ctcttactcg ctggcttgc gaccgtatg gcatccccaa aacacgcaca 1020
gctatcaaaag gccattctgc gatgttgcgg aacgaccaca cagaccctgg cgc当地 actgg 1080
gactggactt attatgtc acttgcgttacat cttccgttacat cttgc当地 ggat ctcgtac 1140
aacgc当地 acag ctggcgctt cacggcgacg gcaacttggg gtacagotac ttggacact 1200
gagaagttatg gtcgtacta tgc当地 acaca acacccataa ctgtttc当地 aaaaaggcatgg 1260
ttccaaggcata caatccatc acgttgcgttacat gtc当地 acatcggt gccttcaac 1320
gctgc当地 gata acgacaaaaac gccgttacat atcgc当地 acat cttgc当地 aaaaaggcatgg 1380
aacgttacc acgacggctaa cttgttgc当地 tggatgttcc ttgttaatgta cactttaac 1440
agcggc当地 acgt ataacgttgc当地 tggatgttcc cttgttgc当地 cttgttcc 1500
ggc当地 acgttgc当地 tccgc当地 ttgttgc当地 aatcaaa 1527

SEQ ID NO: 8      moltype = AA length = 509
FEATURE          Location/Qualifiers
source           1..509
               mol_type = protein
               organism = Paenibacillus sp.

SEQUENCE: 8
MGIRRVSRLL SISLSAMLLL PFTVPAASFA ADDAAVSANS ASAGKGSQK AFEAASQEFG 60
VPVEILLGLS YAETRWNDHE GKPQLNNGY LMHLAENPKN SSLSTAAEQL KVDKQLLKTD 120
KAVNIRGSA VLAGLAKAKN NGKLPASLAD WYTVAAYSG IDDLPLARVY ADEVPKVINE 180
GKQALSGTEI LHLNPPTVTP NRAEYQTATL AATAMDYPGA IWNAAYSQNY SVGSRGPQDI 240
SNIVIHTTQG SYAGTINWPH DPAVPSVSAHY VVRSSDGQIT QMVRDKDIAY HARSANSTSL 300
GIEHEGYVTD PAWTDSMYR SSAALTRWLQ DQYGIPKTRT AIKGHSEMPG NDHTDPGSNW 360
DWTYYMSLNV PPVTTGIIVD NATAAGFTAS ANWGTATWNT EKYGSQDYRT TPQAVSDPAW 420
FQATIPTAGS YDVTYAWPSN AAYNDKTPFI ISTSTGNQTV NVNQQANGK WMLLGKYTLN 480
SGTYNVVGIS RWTSGTGNIF ADAIRLVIK 509

SEQ ID NO: 9      moltype = AA length = 483
FEATURE          Location/Qualifiers
source           1..483
               mol_type = protein
               organism = Paenibacillus sp.

SEQUENCE: 9
ASFAADDAAV SANSASAGKG SLQKAFEAAAS QEPGVPEIIL LGLSYAETRW NDHEGKPSQL 60
NGYGLMHLLAE NPKNSSLSTA AEQLVKDQL LKTDKAVNIR GSAAVLAGLA KAKNNGKLPA 120
SLADWYTTVA AYSGIDDLPL ARVYADEVFK VINEGKQALS GTEILHLPNT PVTPNRAEYT 180
QATLAATAMD YPGAIWNAAY SGNSVSGSRG PGDISNIVIH TTQGSYAGTI NWFKDPAAVV 240
SAHYVVRSQD QOITQMVRLDK DIAYHARSAN STSLGIEHEG VVTDPAWYTD SMYRSSAALT 300
RWLCDQYGIP KTRTAIKGHS EMPGNDHTDP GSNWDWTYYM SLVNPPVTGG IIVDNATAGA 360
FTASANWTA TWNTKEKYGSD YRYTTPQAVS DPAPWFQATIP TAGSYDVYAW WPSNAAYNDK 420
TPFIISTSTG NQTVNVNQQA NGGKWMLLGK YTLNSGTYNV VGISRWTSGT GNIFADAIRL 480
VIK 483

SEQ ID NO: 10     moltype = DNA length = 1479
FEATURE          Location/Qualifiers
sig_peptide      1..66
mat_peptide       67..1479
source           1..1479
               mol_type = genomic DNA
               organism = Nonomuraea sp.

CDS             1..1479
SEQUENCE: 10
atgagccgtc ttgc当地 gat ctttttgcgtt gtacttcttg ctttc当地 gggtt ttctc当地 ctgc当地 60
tacgc当地 gggc cagaccact tacagaagct ttgc当地 accgtc ctgc当地 ggctc tcacgc当地 gta 120
cctc当地 ctgc当地 acc ttcttgc当地 ttgttgc当地 ttgttgc当地 aacttacac ccacaacggc 180

```

-continued

gaaccatctg	catcagggtgg	ctatggaatg	atgcacccctg	tttctaattcc	aacaacaaaaaa	240
gctcttgota	aagctccgca	acttacaggaa	ttacactgca	ctgaggtaac	tgctgacgat	300
gcagcgaaca	tcttaggtgg	tgcagcagta	cttcgttagcc	atgtctatgc	tcttggtttg	360
gacagaagcag	cacgttaaaa	tgctggccgt	tggtaccaa	cagttcgccgaa	atacgttaac	420
gcatctcac	cagagactgc	acgtctttat	gccccatgcg	tatacgaatt	ccttggccaaa	480
ggotttcagg	ctgcagggtgt	taaagtatgt	ccacaagaag	taactgcgcg	ccgttgtgcg	540
tacgctaaga	cacgcgagg	aacagctgcg	gctagccca	actacccgt	ccgcacatgg	600
gttgcgtgtt	tttcttctaa	cttactgtca	tcttcgcgc	catcaacta	ccgcgtatcgat	660
cgtgtgtaa	tccacgttaac	tcaggatca	tatgtgtgc	gcatcgtcg	gttcaaaaac	720
ccttctgtgt	gggtttctgc	acactacgt	attcggttctt	ctgtatgggc	tgttactcaa	780
atgggtgtgt	acaaggatgt	tgctggatca	gccccacta	ggggctataa	cacacgttct	840
atccggatcg	aacatgaaagg	atgggtatca	gatgtttctt	gggtcaacta	agctatgttat	900
cgtagctctg	gtgcattgtac	tcggttacatt	tgtgacaaat	acggcatccc	taaagatcgt	960
tcacacatca	ttgggtcacaa	ccaagtacca	ggagcgcact	atacagaccc	aggttagccat	1020
tgggatttgg	cgaagtataat	gtctttagtgg	aatgggtggaa	gaggaacacc	atcttgggtct	1080
gttactgtgt	acaactactac	acgcggaaa	ttcacagctt	cagcaactg	gggtacttct	1140
gcctattctg	gccaacgcga	tggtgctgac	taccgttcc	caactcctct	tgccgcacatct	1200
gatccctgtt	ggttcaaaagc	taactccct	tctgcagggt	tttatecggt	tgaagtttgg	1260
tatccgtctg	accctgtca	taactcttaca	gctcccttaca	tcgtatgcg	ttctggccgt	1320
aaccaaacag	tttctgtgt	tcaacgttca	ggagggcggt	gatggccgac	tcttggaaacg	1380
ttctcttgg	cggtggcga	acacgacgtt	gtaggagtt	gccccgtggac	atctggcagc	1440
ggctatgtgt	tagcagatgc	tgtacgcatt	tcacattta			1479

SEQ ID NO: 11	moltype = AA	length = 493				
FEATURE	Location/Qualifiers					
source	1..493					
	mol_type = protein					
	organism = Nonomuraea sp.					
SEQUENCE: 11						
MSRLAAIVFA	VLLAEGFSPA	YAAADPLTEA	FDRAAAAHDV	PRDLLVALAY	AETHLNHNG	60
EPSASGGYGM	MHLVSNPTTK	ALAKAAELTG	LPAAEELRAD	AANILGGAAV	LRSHADALGL	120
DEAARKDAGR	WYQAVAEYGN	ASTPETARLY	ADAVYEFGLK	GPEAAVGKVA	PQEVTADRG	180
YAKTRELTA	ASPDYPDGTV	VAASSSNYTA	SSRPSSYAI	RVVIHVTQGS	YAGSISWFQN	240
PSAGVSAHYV	IRSSSDGAVTQ	MVRNKKDVWAH	AGNWGYNTR	IGIEHEGWVS	DASWTEAMY	300
RSSGALTRYI	CDKYGIPKDR	SHIIHGHNQVP	GATHTDPGSH	WDWTKYMSSV	NNGGGTPWS	360
VTVDNTTAGK	FTASANWGTG	AYSGRHHGAD	YRFATPLAAS	DPAWFKANIP	SAGSYRVEVW	420
YPSDPGYNSS	APYIVAASGG	NQTVFVDQRS	GGGGWRTLGT	FSLTAGEHDV	VGVSRTWTS	480
GYVVADAVRI	SHL					493

SEQ ID NO: 12	moltype = AA	length = 471				
FEATURE	Location/Qualifiers					
source	1..471					
	mol_type = protein					
	organism = Nonomuraea sp.					
SEQUENCE: 12						
AADPLTEAFD	RAAAAHDVPR	DLLVALAYAE	THLNHGHN	SASGGYGM	LVSNPTTK	60
AKAAELTGLP	AAELRADDAA	NIKGAAVLR	SHADALGLDE	AARKDAGR	WYQAVAEYGN	120
TPETARLYAD	AVYEFLGKGF	EAAGVKVAPQ	EVTADRGAYA	KTRELTAAS	PDYPDGTVWA	180
ASSSNYTA	RPSSSYAIDRV	VIHVTQGSYA	GSISWFQNP	AGVSAHYVIR	SSDGAVTQMV	240
RNKDVAWHAG	NWGYNTRSIG	IEHEGWVSDA	SWFTEAMYRS	SGALTRYICD	KYGIPKDRSH	300
IIGHNQVPG	THTDPGSHW	WTKYMSV	GGGTPSWSVT	VDNTTAGKFT	ASANWGT	360
SGQRHGADYR	SFTPLAASDP	AWFKANIPSA	GSYRVEVWY	SDPGYNSSAP	YIVASGGNQ	420
TVFVDQRS	GGWRTLGTFS	LTAGEHDV	VSRWTSGT	YVADAVRISH	L	471

SEQ ID NO: 13	moltype = DNA	length = 1920
FEATURE	Location/Qualifiers	
sig_peptide	1..117	
mat_peptide	118..1917	
source	1..1920	
	mol_type = genomic DNA	
	organism = Lysobacter antibioticus	
CDS	1..1917	

SEQUENCE: 13						
atgaacgaat	attccattgc	gcccattggg	gccggtaacc	gcgtgcgttc	gctgtcggt	60
tcgtcgat	tccgcctcg	ggcgcgtccc	gcccgtggg	ccgcgcaggc	ccaggccgca	120
cccgaaacc	ggcccttgc	ccaggccctg	ccatcgagg	aatcgatcga	acgcgtcgac	180
cgcgcgctgt	acgcggacta	cttcggccag	gcctatgcgc	gttaccgc	gatccggcc	240
ggcacccctgg	aatcgatcgc	ctacgtatgc	agccgctggc	agcaactgca	gccccggccc	300
gcccggggct	atggcgaaaca	gcacccggac	atggcgccgt	cgtacggccgt	catgggcctg	360
taccacggcg	agggtttcgc	cgatcaagt	agcgaaggcg	cgccgcgtat	cgccgtggcc	420
gccccggccg	tgcagcgcga	tccgcgtc	aatatcc	cctccggccgc	cttgcgtcgat	480
cgcgagatgc	gccccgacgg	ggtcgggtcc	aatgcggcga	tcgaagccac	gcgtccggcg	540
ctggagcgct	acgcgggtt	cgccggcaat	gccccgcaaga	gcgcgtatcca	ggatcacgccc	600
cgttccagg	tgccttcga	cgtgcgtcg	gccccggacaa	cgacccggcc	660	
atcgctgtgc	ccacgcgcgc	ggtcggctgg	gaacgcgcct	tcgtatgcgcg	caagctgg	720
cagctgcgcg	cgccgttcgt	cgccgtggac	gtgagccgcg	atccggtcga	ggccggccgc	780

-continued

tttggggacg	acggcgcggtt	cgcgcgtatcgt	ccgcgtcagcg	aaaccctgcg	cgcgcacatcg	840
ctgaccgggg	ccggaaaaaa	gaggaccgtat	tacggccccgg	cgctgtgggt	cgcttcgcct	900
taccactcca	cccgcacgtc	gtacgactcg	gtgaccatcc	acacgatgca	gggttattac	960
ggccggcagca	tctctgtgtt	ccagaacaaac	cccaacacg	tcagcgccga	ttacctgatc	1020
cgcagctccg	acggccagat	cacccagatg	gtgcgcgaga	accgcgcggc	ccatcacgtc	1080
ggcgtgcata	acaagaccac	gctcgccatc	gaggacacgaa	gcttcatcaa	caacgcgagt	1140
tggtacaccg	cggcgtatgt	caacgcctcg	cgccgcgttga	ccggcactt	ctgcgcgacc	1200
tacagcgcga	ttagctgcgt	gagcgcttc	aaggccccgg	ccggcagccg	catcaacgtg	1260
tttgcggcga	gcgtcaaggt	caaggccac	cagcaactaca	gcagccagac	ccacacccat	1320
ccgggcatac	actgggat	ggcgcgtatc	tacaacctgc	tcaatccggg	caatccggcc	1380
ggcggccgca	gcgtatgtca	cagtttgcga	agcgcgttgc	ggcatttgcga	caccggcccg	1440
gcgttattccg	gcagcaccac	cgccatcgcc	cgccgcgttc	tgagcgaacg	caactgcacc	1500
acgcgcgaaga	acggcgagt	ctcgctgcgg	ctgctgtga	aagacgatgc	cgccagcgcc	1560
gtatgcctgg	cggtgcgggt	gttgcgtggc	agcggcaatc	ccggcagccaa	cgccggccctg	1620
acgcgcgcac	acggcaaggt	cggtttctcg	gtcttcaccc	gcgcgacccg	gtatgcgcgc	1680
gcgcatecgca	tccgcacag	cgacggcacc	gaggcgtccg	tgagcgcgcg	gattgcgcgc	1740
aacacctgga	cctatctgga	gttggacccgt	accgacgacg	cgcagtggga	tgctgtggtc	1800
ggcggcgcaca	acggcgccat	caccgcgcgc	tcggtaacgc	tgcgtcggt	gtggttctac	1860
cgcgatcaga	cctcggtcga	cgtgaacgt	tacgtcgacg	atgtgcaggt	gaagaactga	1920

SEQ ID NO: 14	moltype = AA length = 639	
FEATURE	Location/Qualifiers	
source	1..639	
	mol_type = protein	
	organism = Lysobacter antibioticus	
SEQUENCE: 14		
MNEYSIARHG AGTGVRSLSW	SLTLALLALA APWAAQQAQAA PEDRALAQRL QIEESLQRVD	60
RALIYADYFRQ AYARYPSIPA	GTLESIAYVM SRWQQLQPGP AAGYGEQHQH MPRSYGVML	120
YHGEgefADQV SEGARLIGVP	AARVQRDPLS NILASAALL RELRADGVGA KSAIEATRPA	180
LERYAGFAGN AGKSAIQDHA	RSSFAFDVLL AQDKGVNDRG IVVPTRAVAW ERAFDARKLV	240
QLRAPFVRLL VSRDRVEAGA	LRDGGAFALD PLSETLRAPS LTAADEKSTD YGPALWVASP	300
YHSTRTSYDS VIIHTMCGYY	AGSISWFPQN PNSVSAHYLI RSSDGQTQMV VRENRAAHHV	360
GHVNKTTLGI EHEGFINNAS	WYTAAMYNA AALTRHFCAT YSAISCASAF KGPAGSGINV	420
LPASVKVKGH QHYSSQTHTD	PGINWDWARY YNLLNPGNPP GGGSVIDSFE STVGHFDTG	480
AYSGSTTGTIA ATSLSERNC	TRKNGECSLR LLLKDDAASA DAWAVRLLSG SGNPGSNAAL	540
TRANGKVCFW VFTGATGMSA	AIGIDDDSGT ERSVSRATAA NTWTYLEWSL TDDAQWDANV	600
GGANGAITAA SVKLDAAWFY	RDQTSFDVNV YVDDVQVKN	639

SEQ ID NO: 15	moltype = AA length = 600	
FEATURE	Location/Qualifiers	
source	1..600	
	mol_type = protein	
	organism = Lysobacter antibioticus	
SEQUENCE: 15		
APEDRALAQR LQIEESLQRV	DRALYADYFR QAYARYPSIP AGTLESIAYV MSRQQLQPG	60
PAAGYGEQHQ HMPRSYGVMG	LYHGEgefADQ VSEGARLIGV PAARVQRDPL SNILASAALL	120
DRELRADGVG AKSAIEATR	ALERYAGFAG NAGKSAIQDHA ARSSFAFDVLL LAQDKGVNDR	180
GIVVPTRTRA WERAFDARKL	VQLRAPEVRL DVSRDRVEAG ALRDDGAFAI DPLSETLRAP	240
SILTAADEKST DYGPALWVAS	PYHSTRTSYD SVIIHTMCGYY YAGSISWFPQN NPNSVSAHYL	300
IRSSDGQTQ MVRENRAAHV	GVHNKTTLGI IEHEGFINNA SWYTAAMYNA SAALTRHFC	360
TYSAISCASA FKGPAGSSG	VLPASVKVKG HOHYSSQTHD DPGINWDWAR YYNLLNPGNP	420
PGGGSVIDS ESTVGHFDTG	VLPASVKVKG HOHYSSQTHD DPGINWDWAR YYNLLNPGNP	480
ADAWAVRLLS GSGNPGSNAA	LTRANGKVGF WVTGATGMSA AIGIDDDSGT ERSVSRATAA	540
ANTWTYLEWS LTDDAQWDANV	ASVKLDAAWFV YRDQTSFDVNV YVDDVQVKN	600

SEQ ID NO: 16	moltype = DNA length = 1548					
FEATURE	Location/Qualifiers					
sig_peptide	1..93					
mat_peptide	94..1545					
source	1..1548					
	mol_type = genomic DNA					
	organism = Micromonospora sp.					
CDS	1..1545					
SEQUENCE: 16						
gtgactgttc	ggagaccctc	cgctcggtgt	agccaaatgc	tccgcggcgc	agcgatttgc	60
atgatcgccc	tgaccagcca	gccggccca	gcccgcgc	agcaggccgc	ggagacgtc	120
ggccgcgc	tgcaccaggc	ggccggccgc	tccgacgtgc	cgccgcac	gtctgcgcgc	180
ctcgggtatc	cgaggaccccg	gctggacgtt	cacaacgcgc	agcccacgc	ctccggccgg	240
tacggcgatc	tgcacccgt	cggcaaccccg	aagggtgcgg	ccctcgacga	ggccgcgcgc	300
cgtgcggcc	tggaccgcac	cgaactgcgc	accctgtac	cgccgcacgt	cgccggccgc	360
ggccgcgc	tccgtcgta	ccgcgtatcg	gcccggctca	ccgcgaacga	gcgcgacgc	420
gtcaaccatgt	ggtaacgcgtt	gateccccgc	tacggcggtt	cgtcggacaa	ggccacccgc	480
cggctgtatc	cgacgcgcgt	gtacgac	ctcgccgcgc	gtttcaggc	gaccacggcc	540
accggcgagg	tcacccgtgga	cgccgtcc	gtcgccgcgg	acgggggcga	ctacggccgc	600
gtggcgccgc	tgccgcgcgc	cgacatggc	accagagca	ccgactacgg	ccggcgcc	660
tgggtggccg	cgaaatcg	caactacacg	gcctccagcc	gcgactcg	gtacccgtc	720

-continued

aactacatca	tcatccacac	catgcaggc	agctacggcg	gctcgatcag	ctggttccag	780
aacgcagcgg	ccggcacca	cgcgcaactac	ctgtccgtt	cctcggacgg	cgcggttacc	840
cagatgttgt	gggacaagg	cgtcgcctt	cacgcgcga	actggactca	caaacccac	900
tcgtatcggt	tgcgacacg	ggctactcg	gacaacgcct	cctggatcac	cgacgcgtat	960
tacccgtctg	cgccgcgcgt	gacgcggcac	ctggccgaca	agtacggct	cccgaaagacc	1020
cgcagcaaca	tcatcggtca	caaccagg	ccgggcggca	cgcacaccga	ccgggttccg	1080
aactggtaa	ggacactta	catgcgcgtc	gtcacggca	ccacgcggcc	gcgcggcacc	1140
tggtcgacca	tctgtggacaa	caccacggc	ggccgggtca	ccgcgcggc	caactggagc	1200
acctcgctgt	actcgteca	gcgcgtacgg	ggcgtactcg	gtacatggca	ccatgttcgg	1260
gcacgcgacg	ccgcctggta	caaggtaac	atccccggca	ccgcacacca	ccgggtggag	1320
gtctgttacc	cgggccgtcg	cggttacaac	gccaccacgc	cgtacatcg	ggcgacccaggc	1380
agccgcacaa	agacggteca	cgtgaaccag	tcggccaaacg	tggtgttgg	ggcgctcgctg	1440
ggcaattca	ccctggccgc	cggggacgc	aacaaggatgg	gcatcagcc	ttggtccgg	1500
agcacccggct	acgtgtatcg	cgacgcgtatc	cgcatcacc	ggctcta		1548

SEQ ID NO: 17 moltype = AA length = 515
FEATURE Location/Qualifiers
source 1..515
mol_type = protein
organism = Micromonospora

SEQUENCE : 17						
VTVRPPRSRQ	SQLLGGAAIL	MIGLTSQPAQ	AAPQQGAETL	AAAFDQAAR	SDVPRDLLAA	60
LGYAETRLDG	HNGEPSASGG	YGMHHTSNP	KVRTLDEAAR	RARLDRTELR	TRDAANVAGA	120
AVAVLRYSYADQ	AGLTAKQRDD	VNQVYGLIAR	YGGSSDKATA	RLYADAVYDL	LGSGFRATTA	180
TGEVTVDGRP	VAPORGDYAA	VAPLGAADMG	TQSTDYGPA	WVAANNSNYT	ASSRESSYPI	240
NYIIIHTMQG	SYAGSISWFQ	NAAAGTSAHY	LLRSSDGAVT	QMVRDKDVW	HAGNWNTYNTQ	300
SIGIEHEGGYV	DNAWSYTDAM	YRSSLAAALRH	LADKYGIKPT	RSNIIGHNQV	PGATHDTPGP	360
NNWNWTYYMQL	VTGTTTTPPP	WSTIVDNTTA	GRFTSANSWS	TSSYSSQRYG	ADYRYANPVA	420
ASDAAWYKVN	IPATATYRVE	WVYPAVAGVN	ATTPYIVATS	SGNQTVNVNQ	SANGGGWRSL	480
GNFTLAAAGDA	NKVGISRWSG	STGYVIADAI	RITRV			515

SEQ ID NO: 18 moltype = AA length = 484
FEATURE Location/Qualifiers
source 1..484
mol_type = protein
organism = Micromonospora sp.

```

SEQUENCE : 18
APQQGAETLAA AFQDQAAARS DVPRDLAAL GYAETRLDGH NGEPSASGGY GVMHLSNPK 60
VRTLDEAARR ARLDRTTELRT RDAANVAGAA AVLRSYADQA GLTAKQRDDV NQWYGLIARY 120
GGSDDKATAR LYADATVYDIL GSGFRATTAT GEVTVDGRPV APQRQGDYAAV APLGAADMGT 180
QSTDYGPAAW VAANSSNYTA SSRESSYIPIN YIIIHTMQGS YAGSISWFQN AAAGTSAHYL 240
LRSSDGAVTQ MVRKDVAWH AGNWTYNTQS IGIHEHGIVD NASWYTDAMY RSSAALTRHL 300
ADKYGIPTRK SNIIGHNQV GATHDTPGPN WNWTYYMLQV TGTTTPPTW STIVDNTTAG 360
RFTASANWST SSYSSQRYGA DYRYANPVAAS DSAAWYKVNI PATATYRVEV WYPAVAGYNA 420
ITPYIVATSS GNQTVNVNQSG ANGGGWRSLG NFTLAAAGDAN KVGISRWSGS TGYVIADAIR 480
ITRV                                         484

```

```
SEQ ID NO: 19          moltype = DNA    length = 1533
FEATURE                  Location/Qualifiers
sig_peptide      1..90
mat_peptide       91..1530
source           1..1533
mol_type = genomic DNA
organism = Nomonuraea coxensis
CDS

```

CDS	1..1530				
SEQUENCE:	19				
atggaaactcg	cccgacacg	ccgcacccct	cgttcctcg	cggttccgtc	60
ctcgctcgca	ccccggccca	cgccgcgtcc	gcccggcccg	ccgcggaa	120
ggccgcgttc	ccaaaggccg	ggccgcgtac	gacgtgc	ccccggccgt	180
ggctacccgc	agaccggcc	cgacgggtac	gacggca	ccagccgg	240
ggcgctatgc	acccgggtac	caacccccc	aaccactcc	tggaga	300
accggccgt	ccacccggcg	actgcgc	gacgac	ccaa	360
gcccgtactcc	gctccacccg	cgacggcc	ggccgtcg	aaac	420
ggacgttgtt	accaggccgt	cgacggcc	gacggcc	gaagg	480
ctctacccgc	acgcggctta	cgagagcc	ggcaac	ggcc	540
gtcaagcccc	aggagggtac	cgccgaccc	ggcgagt	ccaa	600
gccaaggccg	acgcggccgt	cctcagc	gactac	ccgc	660
agctccacca	actacacccg	ctcagcc	ccgtcg	gatgt	720
atccacgt	cgcgggtt	gtacccgg	accatct	ccgc	780
caggctccg	cccaatact	ggtaaatt	tccaa	ccat	840
gagaaggacg	tcgtctggca	cgccgg	ttggacta	acacccgg	900
gaggcacgagg	gctacgtcaa	cgacgc	tggttac	cgatgt	960
ggggccctca	ccaaagaat	ctgcg	gagaag	ccaa	1020
atccggccaca	accagggtcc	ggccgc	ccacccg	ccgg	1080
accacgtaca	tgaatact	gacgggt	ggccgc	ctgg	1140
gacaacgc	cctccggca	gttaccc	ggccgc	ac	1200

-continued

aggcagcgct	acggctccga	ctaccgcttc	gccgaccgg	tctccgcacag	cgacgcggcg	1260
tgttactcg	ccgccccatccc	cagecgccgg	acctaccgc	tcgaggctcg	gtatccggcc	1320
gacgcggcgct	acaacagctc	ggcgcgtac	atcggtggca	cgtcaggcgg	caaccagacc	1380
gtttacgtcg	accaacgcag	cgccggccgg	tcttggaa	gcateggcac	gttctcgctg	1440
aacgcgggaa	cgtacaacgt	ggtcggaaatc	agccgggtgg	ccgcggcac	cggctacgtc	1500
atcgccgacg	cggtccgcat	cagccgcgtc	tga			1533

SEQ ID NO: 20	moltype = AA	length = 510
FEATURE	Location/Qualifiers	
source	1..510	
	mol_type = protein	
	organism = Nonomuraea coxensis	
SEQUENCE: 20		
MELARTRLTA LATSFLAVLV LVATGRPALA APTAADGTLT AAFAKAAAAY DVPRDLLVAL	60	
GYAETHLGDH DGKPSASGGY GVMHLVSNPT NHSLEKAEL TGRSTGELRA DDAANVLGGA	120	
AVLRSHADAL GLDETARKDA GRWYQAVAKY GNATSPELAR LYADAVYESL GLGIDIRGVQ	180	
VKPQEVTADR GEYAKARDLN AKADAGVLST DYGPAAWVA SSSNYTASSR PSSYAIDRVI	240	
IHVTOQGSYAG TISWFQNPNSA QVSAYVVK SNGAITQMVR EKDVAWHAGN WTYNTRSIGI	300	
EHEGYVNNDAS WFTDAMYRAS AALTKNICEK YGIPKDRSHI IGHNVQPGAT HTDPGSNW	360	
TTYMNYVTGG CGTPSWTTI DNATSGQFTA SANWGTSTYS SQRYGSDYRF ADPVSASDAA	420	
WYSAAIPSAG TYRVEWYPA DAGYNSSAPY IVATSGGNQT VYVDQRSGGG SWKSIGTFSL	480	
NAGTYNVVGI SRWTAGTGYV IADAVRISRV	510	

SEQ ID NO: 21	moltype = AA	length = 480
FEATURE	Location/Qualifiers	
source	1..480	
	mol_type = protein	
	organism = Nonomuraea coxensis	
SEQUENCE: 21		

APTAADGTLT AAFAKAAAAY DVPRDLLVAL GYAETHLGDH DGKPSASGGY GVMHLVSNPT	60	
NHSLEKAEL TGRSTGELRA DDAANVLGGA AVLRSHADAL GLDETARKDA GRWYQAVAKY	120	
GNATSPELAR LYADAVYESL GLGIDIRGVQ VKPQEVTADR GEYAKARDLN AKADAGVLST	180	
DYGPAAWVA SSSNYTASSR PSSYAIDRVI IHVTOQGSYAG TISWFQNPNSA QVSAYVVK	240	
SNGAITQMVR EKDVAWHAGN WTYNTRSIGI EHEGYVNNDAS WFTDAMYRAS AALTKNICEK	300	
YGIPKDRSHI IGHNVQPGAT HTDPGSNW TTYYMNYVTGG GGTPSWTTI DNATSGQFTA	360	
SANWGTSTYS SQRYGSDYRF ADPVSASDAA WYSAAIPSAG TYRVEWYPA DAGYNSSAPY	420	
IVATSGGNQT VYVDQRSGGG SWKSIGTFSL NAGTYNVVGI SRWTAGTGYV IADAVRISRV	480	

SEQ ID NO: 22	moltype = DNA	length = 1548
FEATURE	Location/Qualifiers	
sig_peptide	1..93	
mat_peptide	94..1548	
source	1..1548	
	mol_type = genomic DNA	
	organism = Micromonospora fulvopurpurea	
CDS	1..1548	

SEQUENCE: 22		
atgacgatcc gtcgtccacc acgtcgccgt ttacacaccc taggaggaga aatgatttt	60	
atgattggat taactggta acctgcacag gctgcgcac tcacatggac tcaaccttt	120	
gctgccgcacat tcgaccgtgc agctgcgtca tcagatgttc ctgcgtacgt tcttgcggct	180	
cttggatatacg cggaaactcg ctggatgttgc catgggtggt agccgtttgt atcagggtgg	240	
tacggatatacg tgcataatccat atcaaaccatc aaagttcgta ctttagatga agctgcgcgt	300	
cgcacacacgtt tagaccgtgc agacccgtt actccgtacg ctgcqaaactg agctgqagct	360	
gctgcgtatc ttgcgttca cgcggatgaa gcggttctta cggctgtca gcgcgacgac	420	
gttaaccaggat ggtatggccca aattgcgttgc tatggcgaa gcaactgtgc tgcaactgt	480	
cgtctttatcg cagattctgtt atatgcgtt ctgcgcgtc gattcatcgc gactactgca	540	
ggttgcgcgaaat tttctgtatc tgccgtccg gttgcgcctc aacgtgttgc ttatgtctgt	600	
gtagcttccat ttggcacttgc tgatttcgtt actctttctta ctgattacgg tccagctgt	660	
tgggttccatcg cgaacacgtt taactacaca gtttcatctt gtgaacatcgc atacccgtatc	720	
aattacatcg ttatccatcatc tcatacgatgtt gtcatacgac gtcataatgc ttgggttccatcg	780	
aacgctgtgtt ctggcacatc tgctcaactt ctttttgttgc cttccatgttgcgggttact	840	
caaataatgttgc tgcacaaaga tattgcgttgc cacgtggca attggactt caaacatcg	900	
tctatcgaa tcgagcatga aggatatgtt gacaatcgatc cttggatgttgc acagcgtatc	960	
tatcgatccat ttgtcgatgtt tacacgttgc ttatgcgttgc agtatgttgc cccgaaatc	1020	
cgcactaaca ttatcgatgtt taatcgatgtt cttggatgttgc ttatgcgttgc ttatgcgttgc	1080	
aactgttgatc ggacgttata catgcacattt gttactgttgc gcacgcggcc accgccttac	1140	
acatgttgc tcaatcgatgttgc taatcgatgttgc gttactgttgc ttatgcgttgc ttatgcgttgc	1200	
tctatcgatgttgc catacagcgatc tcaacgttgc gttactgttgc ttatgcgttgc ttatgcgttgc	1260	
gtctgtatcg atacacgtatc ttatcgatgttgc ttatgcgttgc ttatgcgttgc ttatgcgttgc	1320	
gaagatgttgc atccacgtatc ttatcgatgttgc ttatgcgttgc ttatgcgttgc ttatgcgttgc	1380	
acaacgcggaa accaaacgttgc atctgttgc caaacatcgatc ttatgcgttgc ttatgcgttgc	1440	
tttagtactt tcacacttgc cgctggatgttgc gtcgttgc ttatgcgttgc ttatgcgttgc	1500	
ggatctacgttgc gatacgatc ttatgcgttgc ttatgcgttgc ttatgcgttgc ttatgcgttgc	1548	

SEQ ID NO: 23	moltype = AA	length = 516
FEATURE	Location/Qualifiers	

-continued

```

source          1..516
               mol_type = protein
               organism = Micromonospora fulvopurpurea
SEQUENCE: 23
MTIRRPPR RV SHLLGGAMIL MIGLTGQPAQ AAPAHGAQPL AAAFDRAAAS SDVPRDVLA 60
LGYAETRLDG HGEPSVSGG YGVMLHTSNP KVRLDEAAR RTRLDRADLR TRDAANVAGA 120
AAVLRSYADE AGLTAAQRDD VNQWYGPPIAR YGGSTDAAATA RLYADSVYDL LARGFIATTA 180
GGEVSVDGRP VAPQRGRYAA VAPLGTGDPG TLSTDYGPAA WVPANSSNYT VSSRESAYPI 240
NYIVIHTMQG SYAGSISWFQ NAAAGTSAHY LLRSSDGAVT QMVRDKDIW HAGNWTYNTQ 300
SIGIEHEGYV DNASWYTDAM YRSSAALTRY LCDKYGIPKT RTNIIIGHNQV PGATHDPGP 360
NWNTYIMQL VTCGTTTPPT TWSTVVDNTT AGRFTASANW STSTYSAQRY GTDYRYANPV 420
AASDTAWYKV NIPATATYRV EVWYPAVAGY NTSTPYIVATT TSGNQTVSVN QTANGTWRS 480
LGTFTLAAGD ANKVGVS RWS GSTGYVIADA IRVTRV 516

SEQ ID NO: 24      moltype = AA length = 485
FEATURE
source          1..485
               mol_type = protein
               organism = Micromonospora fulvopurpurea
SEQUENCE: 24
APAHGQAQPLA AAFDRAAASS DVPRDVLAAL GYAETRLDG HGEPSVSGGY GVMHLTSNPK 60
VRTLDEAARR TRLDRADLDR RDAANVAGAA AVLRSYADEA GLTAAQRDDV NQWYGPPIARY 120
GGSTDAAATR LYADSDVYDLL ARGFIATTAG GEVSVDGRPV APQRGRYAAV APLGTGDFGT 180
LSTDYGPAAW VPANSSNYTV SSRESAYPIN YIVIHTMQGS YAGSIISWFQN AAAGTSAHYL 240
LRSSDGAVTQ MVRDKDIW AGNWTYNTQS IIGIEHEGYV D NASWYTDAMY RSSAALTRYL 300
CDKYGIPKTR TNIIIGHNQV GATHDPGPW NWNTYIMQLV TGGTTTPPTT WSTVVDNTTA 360
GRFTASANW S TSTYSAQRY TGDRYANPVA ASDTAWYKV N IPATATYRVE VVWYPAVAGYN 420
TSTPYIVATT SGNQTVSVNQ TANGTWRSL GTFTLAAGDA NKVGVS RWSG STGYVIADAI 480
RVTRV

SEQ ID NO: 25      moltype = DNA length = 1560
FEATURE
sig_peptide    1..84
mat_peptide     85..1557
source          1..1560
               mol_type = genomic DNA
               organism = Alicyclobacillus sp.
CDS             1..1557
SEQUENCE: 25
atgaagaaaa cttgggttac ggtcttgcgacc accaccgcatt tgaccttcctc cgtcggcgca 60
agctacgcggaa ctccctcggtt tgcacgcggaaa tcggacgcgc agtcgcggaaac gaccgcacccg 120
gcgttggaca atgcgttacac cgcacggcg aaggaaattca aagtccggaa agatctgtcg 180
atgcgttacct cctacgcggaa atccctgtgg caaagtgcggg ctggagacggt cgcccgatgac 240
gaccatcgccg acggcaaaagg cttgtatgcgg ttgacggacactcgttcaaa aaagaacctg 300
agcgacacggc cgaaaggctt cttggatcggc gcaaggaaac tggaggacaa cgcagggtcg 360
aacatccgcg cggcgccgtt cctgtatgcggc aaaggcgcaac atgagctcgga caaaccgttc 420
tccgacaaacg tcaacgactgt gtacaaaggcg gtgcgttccctt ttaaggccgc ttcttgacaaag 480
agcgacacaaag tgcgttgcgc cgatgaaatgtcgttcatgcattc tgaaggacgg gacccgttt 540
gcacatcgacg gggcacccctt ctcgtatctc ccgaacaaaaa ccgtcgatccc ggtcaaaagg 600
caactgtcgcc acgttacacta cggcgatgcg accaaccgtt cggcgacccc ggactactcc 660
ggcgccatctt ggaatgcggc gaggacatcg aacttaccaaaatgg tggcgacccg tccgacttcc 720
aaccgcgatcc octacgttgtt catccacatc accggagggtt cttactcccg cagatcaac 780
tggttcaaaacg acccgacgcgc gcaatgttcg qcacactatg tgcgttgcgtt ttccqacggc 840
cagatcaccgc agatggtgca ggacaaggac atgcgttgcg atgcgtgtac cttcaacacg 900
aacggcatcg gcatacgacg tgaaggatataa gaaacgcggaa cccgggttgcg caccgcgcg 960
atgtacaccc acatggcgcc gttgacccgtt cggatctgcgg aaaaataatgg cattccgatg 1020
gaccgcgacc acatctccgg ccactccggaa ctgtggggcaatgaccacac cgatccggc 1080
gtgaactggg attggaaccaa atacatgacc aaagtccggc ggttctccaa gaactggacc 1140
gtcgatcgacg tccgttgcgac agacacggca tccggcgccct tcaccatgtt cggcgcttcg 1200
caataactggc acccggatctc cggatctgcg tgcgcacaaactt caccacggc 1260
aacggcgccgatcgatcataa acatggcgcc gttgacccgtt cggatccggc cggccggcaac 1320
tacgaagtca aagtgttgcgtt cccgttccaaatc accggggccg cgaccacggc gaagtatgaa 1380
atccactaca acggcgccgtt cgttaaccaaaatc accgttccgc aaaggcccta ctccaaaccaa 1440
tgggtatccgc ttggcaccta caacttcgcg accggccacccg gccggctacgtt caagttggc 1500
gacaacacccg cgcacaccaaaatc caccatcgcc ttccgtatcgca tccgttccat ggggtcaataa 1560

SEQ ID NO: 26      moltype = AA length = 519
FEATURE
source          1..519
               mol_type = protein
               organism = Alicyclobacillus sp.
SEQUENCE: 26
MKKTWVTLVA TTALTFPSVGA SYATPSFAAK SDAQSQTAP ALDNAFTAAA KEFKVPKDLL 60
MAISYAESRW QVPAETVADD DHAHKGLMH LTDNSFKKNL SDTAKGLGIT AKQLEDNAGL 120
NIRGGAYLLA KAQHELGKPL SDNVNDWYE AASFEGASDK SDKVLFADAEV YRILKDGTSL 180
AIDGGTLSIF PNKTAVPKGQLSDVTVGVT TNPSATPDYS GAIWNAASTS NYQVASRPTS 240

```

-continued

NPITYVVIHD	TEGSYSGTIN	WFKDPSAQVS	AHYVVRSRDG	QITQMVQDKD	IAWHARTFNT	300
NGIGIEHEGY	EAQTGWYTD	MYTQSAALTR	AICQKYGIPM	DRDHILGHSE	LWGNDHTDPG	360
VNWWDWNKYM	KVTGVSKNWT	VVDVDDKDTA	SGAFTMYGAS	QYWHPVSGYG	VHNEINYNTNG	420
NGATIINYAI	WKPTIPVAGN	YEVKVFVPSN	YAGTTSAKYE	IHYNGGVVTK	TVSQSAYSQ	480
WVSLGTYNFA	TGTGGYVKLG	DNTGDTNTIA	FDTIRFMG			519

SEQ ID NO: 27	moltype = AA	length = 491				
FEATURE	Location/Qualifiers					
source	1..491					
	mol_type = protein					
	organism = Alicyclobacillus sp.					
SEQUENCE: 27						
AKSDAQSO	AAKEFKVPKD	LLMAISYAES	RWQVPAETVA	DDDHAHGKGL	60	
MHLTDNSFKK	NLSDTAKGL	ITAKQLEDNA	GLNIRGGAYL	LAKAQHELGK	PLSDNVNDWY	120
EVAVASFEGAS	DKSDKVLFA	EVRILKGDT	SLAIDGGTL	IIFPNKTVAPV	KGQLSDVTVYG	180
VTTNPSATPD	YSGAIWNAAS	TSNYQVASRP	TSNPITYVVI	HDETEGSYGT	INWFKDPSAQ	240
VSAHYVVRSS	DGQITQMVQD	KDIAWHARTF	NTNGIGIEHE	GYEAQTGWT	DAMYTQSAAL	300
TRAICQKYG	PMDRDHILGH	SELWGNHD	PGVNWDWINKY	MTKVTVGSKN	WTVVVDVDDKD	360
TASGAFTMYG	ASQYWHPVSG	YGVHNEINYT	NGNGATIINY	AIWKPTIPVA	GNYEVKVFVP	420
SNYAGTTSAK	YEIHYNQVV	TKTQSQAYS	NQWVSLGTYN	FATGTGGYVK	LGDNTGDTNT	480
IAFDTIRFMG	Q					491

SEQ ID NO: 28	moltype = DNA	length = 927				
FEATURE	Location/Qualifiers					
sig_peptide	1..57					
mat_peptide	58..924					
source	1..927					
	mol_type = genomic DNA					
	organism = Halomonas sp.					
CDS	1..924					
SEQUENCE: 28						
gtgctgcgcc	attggaccgc	cgtgatgggc	atcgccatgg	caagtgcata	gctggccggc	60
tgcgcctccc	cggaacac	ggagcgacgc	gacggctacg	tggtgatca	cactcac	120
tcgcgcgtgc	acaccaggcc	ggtgcggcc	tggtgatgc	actacaccg	cgtcgacgag	180
gcccgcgtgc	tgccgcgtgc	cacggcgtc	cacgtcgtc	ccccactacgt	actgcgcgtt	240
ccgcgcgcgg	agcgtcgagg	cctgcgcgt	gtctatc	tcgtcgacg	ggagcgcgc	300
gcttggcgc	ccggcgccag	cgcgtggaaa	ggccgcgc	atatacgc	cacttcgatc	360
ggcatcgaga	tcgtcaatac	cggggccgac	cgaccctaca	tcgagggtg	gcgggtgt	420
gaaggggc	ccggaggcgc	cgtggaa	aactgggcac	tttacccaa	cgcgcagatc	480
gaggcgctg	ttgcgcgtgc	gcgcgc	atcgagcgc	acgacatcc	ccccacccgac	540
gttgtcgc	actccgacat	cgcgcgc	cgcgcgc	ccccggccc	acgcttccc	600
tggcgc	caaac	tctaccaggc	aggcatcg	gtctggcgg	aggaggaa	660
tggcgc	aggcgtc	gttgcaggc	agacgacta	ccgcgcgca	ccgcgcgtc	720
gcctggg	gttgcaggc	ggcgcggc	gagctggac	gcgcgc	ccgcgcgt	780
cgcgcc	ttcc	cgatcg	ccgcgcgt	gactaccgc	gcgcgc	840
gcccgc	atcgatcg	ccgcgcgt	gtctggcgg	tatcgcccc	tgcagtcgaa	900
ggagcgt	cgac	ggagcgt	gctggaa	acggctcgaa		927

SEQ ID NO: 29	moltype = AA	length = 308				
FEATURE	Location/Qualifiers					
source	1..308					
	mol_type = protein					
	organism = Halomonas sp.					
SEQUENCE: 29						
VLRHWTAVMG	IAMASAWLAG	CASPEHLERR	DGYVVDHTHL	SPSHTSRVRH	LVMHYTDVDE	60
AESLAVLTGP	HVSAYHVPL	PPRERRGLP	VYQLVDEER	AWHAGASA	WKRPHINDTSI	120
GIEIVNVTGP	RPYIEVERLL	EGHPEDAVEV	NWAPYPDAQI	EEALIALSRD	IERHDIHPTD	180
VVAHSIDIAP	RKIDPGPRFP	WRKLYQAGIG	VWPSEEAVSH	WQARFEAEQL	PLATLQQALR	240
ANGYPLEATG	ELDRQTRAVL	RAFQMRFRPA	DYRGKPDAE	AAILWALLE	YRPLELERL	300
GAMTQPES						308

SEQ ID NO: 30	moltype = AA	length = 289				
FEATURE	Location/Qualifiers					
source	1..289					
	mol_type = protein					
	organism = Halomonas sp.					
SEQUENCE: 30						
GCASPEHLER	RDGYVVDHTH	LSPSHTSRVR	HLVMHYTDV	EAESLAVLTG	PHVSAHYVLP	60
LPPRERRGLP	LVYQLVDEER	RAWHAGASA	WKRPHINDTS	IGIEIVNVTGP	DRPYIEVERL	120
LEGHPEDAVE	VNWAPYPDAQ	EEALIALSRD	IIERHDIHPTD	DVVAHSIDIAP	TRKIDPGPRF	180
PWRKLYQAGI	GWPEEEAVS	HWQARFEAEQ	LPLATLQQAL	RAWGYPLEAT	GELDRQTRAV	240
LRAFQMRFRP	ADYRGKPDAE	SAILWALLE	AYRPLELERL	EGAMTQPES		289

SEQ ID NO: 31	moltype = DNA	length = 783
FEATURE	Location/Qualifiers	
sig_peptide	1..45	

-continued

```

mat_peptide      46..780
source          1..783
mol_type = genomic DNA
organism = Pseudomonas peli
CDS             1..780
SEQUENCE: 31
atgagaattc ttgtcttgc cctgtgtac accctgttga ctgcgtcac cagcgccctg 60
ccccatcgaca cccgtatga ggccgtatgg cagaacaccc gggtgcgtt catcatcttg 120
caactacacct cggcaaacct gcagcactcc ctggagctgc tgaccagg cgagggtgagc 180
agccattacc tgatecgccgaa gacccggccg accatctacc gcctgggtga tgagaatcg 240
cgcgcgttgc atgcgggggt cagtgtgg cagggacgca cttggctcaa tggcaccagc 300
atcggtatcg aactggtaa ccagggttc tatgtggcc ccaatggccg ctactggcag 360
ccctatcgcc cggcgccagat tgatgcgtg atcctctgc tcaaggacat catgcagcgt 420
catgagctgc ccctggccag catatcggtt catagcgata tcggccccca ggcgaaggc 480
gatccggccc ctgttatccc ctggccgggg cgggatgtt accctggccg 540
gaagccgtt cagtggccg ccacggcc gtgtacgac agcaactggc tgatgtggcc 600
tggtttgcg acgaactggc cagccacggc tacgagggtgc ccagccatgg cgagctggat 660
caggccacgc gcaatgttat ccggcccttc cagatgaat accggccagc caactatgac 720
ggcgagccgg acagcgaaac tggccgttgc ctctgggtgc taaaatag cgccagccgc 780
tga                                         783

SEQ ID NO: 32          moltype = AA  length = 260
FEATURE
source          1..260
mol_type = protein
organism = Pseudomonas peli
SEQUENCE: 32
MRILALALLI TLLTACTSGL PIDTRYEALG QNSRVQYIIL HYTSTNLQHS LELLTQGEVS 60
SHYLIGENPP TIYRLVDENR RAWHAGVSQW QRGTWLNGTS IGIELVNQGF YDGPNGRYWQ 120
PYAPAQIDAL ILLLKDIMQR HELPLGSIIG HSDIAPQRKV DPGPLFPWQR LAEAGLIPWP 180
EAGAVARQQA VYEQQLPDVA WFQQQLASHG YEVPSHGEDL QATRNVIAAF QMKYRFQANYD 240
GEPDSETGAL LWVLNNNSASR                                         260

SEQ ID NO: 33          moltype = AA  length = 245
FEATURE
source          1..245
mol_type = protein
organism = Pseudomonas peli
SEQUENCE: 33
CTSGGLPIDTR YEALGQNSRV QYIILHYTST NLQHSLELLT QGEVSSHYLI GENPPTIYRL 60
VDENRRRAWHA GVSQWQGRWT LNGTSIGIEL VNQGFYDGPW GRYWQPYAPA QIDALILLK 120
DIMQRHELPL GSIIIGHSDIA PQRKVDPGPFL FPWQRLABAG LIPWPEAGAV ARQQAVYEQQ 180
LPDVAWFQQQ LASHGYEVPS HGELDQATRN VIAAFQMKYR QANYDGEPS ETGALLWVNL 240
NSASR                                         245

SEQ ID NO: 34          moltype = DNA  length = 900
FEATURE
sig_peptide    1..57
mat_peptide     58..897
source          1..900
mol_type = genomic DNA
organism = Halomonas sp.
CDS             1..897
SEQUENCE: 34
atgtggcggaa agcgtgttgtt cgttgcattcc ctgaccctgc tgctcaactgc ctgtgcgggg 60
ccccggccacc gggaaacaacg caatggttat gtgggtggacc acacccatgt ggcaccttcc 120
cacaacaccc ggtacggca cctggatgtt cactacacgg atgtggatga agccggatgt 180
ctcgccgtgc tcacccggcc ccaggtcagc agccactacg tgctggccgtt accggccacgg 240
gagcatcgccg gccacggccgtt ggttacccgg ctgcgtcgac aggagccggccg ccgcctggcac 300
ggccggggccca ggcgttggaa ggcgcggccaa aatatacgg atacgttccat ccggcatcgag 360
atcgtaacaat ccggcccccga tcggccctac ggcggatgtt agccggatgtt ggagccacgg 420
cccgaggccgaa cgggtggatgtt ccgttggccca ccctaccccg aggacacat ccaggccgtt 480
atcgccctgtt cgcggatata catcgacgcg cacaatattt atcccaacggc cgtgtggcc 540
cactcggttata ttcgtcgccg ggcacggatcc gacccggggcc gggcggttcc ctggcatgcc 600
ctttacgacgg cgggttatecg cgtatggccca gaagaggccca cgggtggccg ctatcgccgac 660
cggttcgacc accgcgttcc cggatctcc acgtgtccgg cggcacttca tgccctggcc 720
tatccgttgg tggtaagcgaa cgaactggat tcaacagactc ggcgggtact tcggcccttc 780
cagatgcgtt ttcggccac cggactatcg cggctggccg atgcccggac ccggccaaatc 840
ctctgggcac ttctggcac cttatcgaccc gatgtactca ccggcgttggc gccccgatag 900

SEQ ID NO: 35          moltype = AA  length = 299
FEATURE
source          1..299
mol_type = protein
organism = Halomonas sp.
SEQUENCE: 35

```

-continued

MWRKRVVVAS	LTLTTACAG	PGHREQRNGY	VVDHTHVAPS	HNSRVRHLVM	HYTDVDEAES	60
LAVLTGPQVS	SHYVPLPAP	EHRGQPLVYQ	LVEERRAWH	AGASAWKRRT	NINDTSIGIE	120
IVNTGPDRPY	AEVERLLEQH	PEATEIGWA	PYPEAQIQL	IALSRDIIER	HNIHPTDVVA	180
HSDISPTRKI	DPGPAFPWHA	LYEAGIGVWP	EEATVARYRD	RFDQALPELS	TLQAALHAWG	240
YPLVVSDEL	SQTRAVLRAF	QMFRFRPTDYR	GLPDAETAAI	LWALLARYRP	DELTALEPR	299
 SEQ ID NO: 36		moltype = AA	length = 280			
FEATURE		Location/Qualifiers				
source		1..280				
		mol_type = protein				
		organism = Halomonas sp.				
SEQUENCE: 36						
GPGHREQRNG	YVVDHTHVAP	SHNSRVRHLV	MHYTDVDEAE	SLAVLTGPQV	SSHYVPLPAP	60
REHRGQPLVY	QLVDEERRAWH	HAGASAWKRRT	TNINDTSIGIE	EIVNTGPDRP	YAEVERLLEQH	120
HPEATVIGWA	APYPEAQIQL	LIALSRDIIER	RHNIHPTDVVA	AHSIDSPTRK	IDPGPAFPWHA	180
ALYEAGIGVW	PEEAATVARYR	DRFDQALPELS	STLQAALHAWG	GYPLVVSDEL	DSQTRAVLRA	240
FQMRFRPTDY	RGLPDAETAA	ILWALLARYRP	PDELTALEPR			280
 SEQ ID NO: 37		moltype = DNA	length = 783			
FEATURE		Location/Qualifiers				
sig_peptide		1..66				
mat_peptide		67..780				
source		1..783				
		mol_type = genomic DNA				
		organism = Pseudomonas pseudoalcaligenes				
CDS		1..780				
SEQUENCE: 37						
atgaagtctc	tttgccttc	cctcgccctt	gttctgcttg	ccgggttgcac	cggtgggtcta	60
cgtatcgatg	acagccacac	ggcgaccggc	cagaacagtgc	gtgtcaata	cgtcggtctg	120
caactacacct	ccgtctgaccc	gcagcgctcg	ctcgacccgc	tgacgcagac	cgagggtgagc	180
agccactacc	tgtatcgggga	tgccatcgcc	acggcttacc	gcctgttggaa	tgagaacccgt	240
cggcgcctgc	acgtgggtgt	cagcggatgg	aaggggcgca	cctggctcaa	cagcaccacg	300
atcggcatcg	agctggtaaa	ccagggttac	taccagacgc	cgccggcccg	ctactggcag	360
cctttcgccg	cgcagcagat	cgataccctg	atcggtctgc	tcaaggacat	cgtcaagcgt	420
caccaggctc	cgctgggtctc	gatcatcgcc	cacagcgatc	tggcgccggca	gcgaagggtc	480
gatccggggcc	ttttgttccc	cttggaaat	ctggccggacg	aggggctgtgt	gccctggccg	540
aacgaggaggc	ccgtggcgcc	ccagcaggcg	ctgtttcgaaa	ccagcctggc	cagcgtgcag	600
ttgttccagg	agcagtggc	gcaaaacggc	tacacggtgc	cgcagcatgg	cgagctggat	660
gaggcaggccg	gcaatgtcat	tgccgttccc	catatgtaaa	atcggtccggc	caactacacg	720
ggccaggccgg	acgcggaaac	tgccggcgcc	ttgttgggtgc	tcaatctgca	ggccggcgagg	780
tag						783
 SEQ ID NO: 38		moltype = AA	length = 260			
FEATURE		Location/Qualifiers				
source		1..260				
		mol_type = protein				
		organism = Pseudomonas pseudoalcaligenes				
SEQUENCE: 38						
MKSCLCLALAL	VLLAGCTGG	RIDDSHTATG	QNSRVQYVVL	HYTSADLQRS	LDLLTQTEVS	60
SHYLIGDAPP	TVYRLVDENR	RAWHVGVSEW	KGRTWLNSTT	IGIELVNQGY	YQTPAGRYWQ	120
PFAPQQIDTL	IVLLKDIVK	HQLPLGSIIA	HSDVAPQRKV	DPGPLFWKWR	LADEGLVPWP	180
NEDAVARQQA	LFSTSLPSVQ	WFQEQLAQNQ	YTVPQHGELD	EATRNVIAAF	QMKYRPANYD	240
GQPDAAETAA	LLVNLQAAAG					260
 SEQ ID NO: 39		moltype = AA	length = 238			
FEATURE		Location/Qualifiers				
source		1..238				
		mol_type = protein				
		organism = Pseudomonas pseudoalcaligenes				
SEQUENCE: 39						
DDSHTATGQN	SRVQYVVLHY	TSADLQRSLD	LLTQTEVSSH	YLIGDAPPV	YRLVDENRR	60
WHVGVSEWK	RTWLNSTTIG	IELVNQGYQQ	TPAGRQYWQPF	APQQIDTLIV	LLKDIVKRHQ	120
LPLGSIIAHS	DVAPQRKVDP	GPLFPWKRLA	DECLVPWPNE	DAVARQOALF	STSLSVQWF	180
QBQLAQNGYT	VPQHGEDEA	TRNVIAAFQM	KYRPANYDQG	PDAETAARLL	VNLQAAAG	238
 SEQ ID NO: 40		moltype = DNA	length = 1566			
FEATURE		Location/Qualifiers				
sig_peptide		1..69				
mat_peptide		70..1563				
source		1..1566				
		mol_type = genomic DNA				
		organism = Tumebacillus sp.				
CDS		1..1563				
SEQUENCE: 40						
atgaacaaaa	cgtgggtatc	ggtctcgcc	accacccgcac	tgaccctgtc	ggtcagcagc	60
gtgtatgcgc	aaccaacgc	tgcagccaaa	ctcgacaacc	aaacggctgc	gacagcaccg	120

-continued

gttttggaaa	gcacccctcag	ctctgctcg	aaggaaatttg	gcgttccgaa	ggaactgctg	180
atggcgatct	cctcagcgg	atcgccgtgg	caagatcgcc	cagaggaaac	acatctcacc	240
gctgagccgg	aaaaaaccaa	cgccaaaggc	ctgatgcacc	tcaacgcacaa	ctcccttc当地	300
aaaggccctga	gogatgctgc	aaaagcgctc	ggcgctccca	agaaacagat	ggaagacgat	360
gtgcaactga	acatcccgccg	cgggtcttac	ctgctcgca	aggcacaaa	agacccggc	420
aaggcgctta	cattccaaacgt	caacgatgg	tatgaagcgg	ttgtctccct	tgaagggtgcc	480
aaggacaagg	acgttgcgc	cttgggttgc	gatgaaggct	accgtgtgt	acaagaagga	540
acccgactgg	cgatcgagg	cgccacgctg	accctcgacc	cgaaactccaa	agtctgatccg	600
agcaaaaggc	tctacgcagg	cttgaccaac	ggcgccacca	actatggact	gactccggac	660
tactccggc	cgatctggaa	ccccggcggc	acgttccaact	atgcccgtcgc	ctctccggcc	720
acttcgaaacc	cgatcaacc	ggtcatacatc	catgacacccg	agggttccca	ctccgggtcg	780
atcaacttgt	tcaaaagaccc	ggccgcacaa	gtttccgcac	actacatcgt	ccgttccccc	840
gatggccaaa	tcacccagtt	ggtacaggac	aaagacatcg	catggcatgc	acgcgcgttc	900
aacaccaacgc	gaatcgcat	cgAACACGAA	ggctatcgcc	cacaaacccg	ctgggtacacc	960
gacgcgtatgt	acacccgc	ggccggcgtc	accctgtcgc	tctgcctcaa	atacaacatc	1020
cccatggacc	gggaccacat	cctcgctc	tccgactgt	ggggcaatga	ccacccgat	1080
ccggggcgtga	actgggattg	gaacaaatac	atgagcaaa	tgaccgggt	gacgaaaaac	1140
tacgcggccg	tactggtcg	caacccgc	gcacccgtcc	gttccacgt	gggtggcccg	1200
tcccaataact	ggcaccggc	cgcagggtac	ggcataccaca	accagatgac	gtacacgatg	1260
ggcaacggca	ccaaacccat	cttcaactac	gacacgttgc	ggccgactgt	1320	
ggcaactacc	aagtcaaa	cttcatcccg	tccaaacttc	cagcgaccac	caacgcgaag	1380
tatgaardtcc	actacaacgg	tggcgctatc	acccaaaacga	tctcccaacg	agcctactcc	1440
aaccaatggg	tgagccttgg	cacgtacago	ttcgccagcg	gcaccgcagg	ctacgtaaaa	1500
ctcggtgaca	acacccggcga	cacggcgatc	gtccggcatcg	acggcatcg	tttctcgct	1560
caataaa						1566

SEQ ID NO: 41	moltype = AA	length = 521
FEATURE	Location/Qualifiers	
source	1..521	
	mol_type = protein	
	organism = Tumebacillus sp.	
SEQUENCE: 41		
MNKTVWSVLA TTATLTSVSS	VYAQPHTAAK LDNQTVTAP VLESTFSSAA KEFGVPKELL	60
MAISYSERW QIAPEETHLT	AEPDKNNKGK LMHLNDNSFK KGLSDAAKAL GVSKKQMEDD	120
VQLNIRGGAY LLAKAQKD LG	KALTDIRKNDW YEAVASFEGA KDKDVAALFA DEVYRVLQEG	180
TALAIIEGGTL TLDPNKVDP	SKGVYAGLTN GGTNYGLTPD YSGAIWNPAS TSNYAVASRP	240
TSNPINSVII HDTEGSYS GS	INWFKDPAAQ VSAHYIVRSS DGQITQLVQD KDIAWHAR SF	300
NTNGIGIEHE GYAAQTGWYT	DAMYTASAAL TRAVCLKYNI PMDRDHILAH SELWGNHDHT	360
PGVNWDWNKY MSKVTVTKN	YAAWLNVDNT ASSGFTLGGP SQYWHPTAGY GIHNQMTYTM	420
GNGTNPISNY ATWKPTIPTA	GNYQVVFIP SNFAATTNAK YEIHYNNGVI TKTISQAAYS	480
NQNVSLGTYS FAAGTAGYVK	LGDNTGDTAY VGIDGMRFIA Q	521

SEQ ID NO: 42	moltype = AA	length = 498
FEATURE	Location/Qualifiers	
source	1..498	
	mol_type = protein	
	organism = Tumebacillus sp.	
SEQUENCE: 42		
QPTHAALKDN QTATVATAPVLE	STFSSAAKEF GVPKELLMAI SYSESRRQIA PEETHLTAEP	60
DKNNKGKLMH LNDNSFKKGL	SDAAKALGVS KKQMEDDVQI NIRGGAYLLA KAQKDLGKAL	120
TSNVNDWYE A	VASFEGAKD DVAALFADEV YRVLQEGTAL AIEGGTLTD PNSKVDP SKG	180
VYAGLTNGGT NYGLPTDYS G	AIWNPASTSN YAVASRPTSN PINSVIIHDT EGYSGSINW	240
FKDPAAOVSA HYIVRSSDQ	I TQLVQDKDI AWHARFSFTN GIGIEHEGYA AQTGWT DAM	300
YTASAALTRA VCLKYNIPMD RDHILAHSEL WGNDHTDPVG NWDWNKYM SK	VTGVTKNYAA 360	
VILDNTDA S GTLGGPSV WHPTAGYGIH NQMTYTMGNG TNPISNYATW KPTIPTAGNY	420	
QVKVFIPSNF AATTNAKYEI HYNGGVITKT ISQAAYSNOQ VSLGTYSF AA GTAGYVKLG D	480	
NTGDTAYVGI DGMRFIA Q		498

SEQ ID NO: 43	moltype = DNA	length = 1506
FEATURE	Location/Qualifiers	
sig_peptide	1..75	
mat_peptide	76..1503	
source	1..1506	
	mol_type = genomic DNA	
	organism = Pseudomonas pseudoalcaligenes	
CDS	1..1503	
SEQUENCE: 43		
atgactcgat tagccgtct	tgtcgctca gccctctccg ccctcctcat cctcgccgt	60
caccccccgcg ccccgccaccg	ggcgaccccg ctccggcccg ctttcgacaa ggccgcggcc	120
gcccaggacg tccccctgt	cttgcgtccg cgcgtcgcc acgcgcgac ccacccgtc	180
ggtcacaaacg gcgaggccag	cgccacggcc ggctacgggt tgatgcacct ggtagcaac	240
ccaccacgcg acacccttgg	gaaggccgc gagctcacgg ggctgeccgc ggagaagct	300
cgcggccgaca ccgaggccaa	catctcgcc ggcggccggcc tcctcgcc tc catcgccgac	360
gggctcgcc tcgacgaggc	cgccaggaaag gaggaggccg gctggatcga ggccgtcgcc	420
acgtacggca acgcctctc	gcccggatcg acgcgcgacg cgtctacag	480
ctcggttggcc tcggcttcaa	ggccaaaggc ctgcgtgtgg ccccccggca ggtcaccggcc	540

-continued

gacaggggag	tgtacgcagg	ggccaggagc	ctgaacgccaa	aggactccaa	cgcctggcc	600
gcccggccgc	ctgactaccc	gaacggccago	tgggtgcccc	ccagttcgag	caactacacc	660
gtgtcgagcc	gtccttcgag	ctacgcctatc	gaccgggtgg	tcatccacgt	gaccaggggc	720
tcc tacgcgc	ggtccatctc	ctggttccag	aacccgagcc	cccaggcttc	cgcgcactac	780
gtgtatccgtt	ccttcggacgg	cgccatcacc	cagatggtcc	gtgagaagga	cgtcgatgg	840
cacgcgggca	actggagcta	caacaccccg	tccgtcgccg	tgcagcacga	gggttcgtc	900
aacgcacgccc	cctggttcac	cgacgcgatg	taccgcgcgt	ccgcgcct	gaccgcac	960
atttgcgaca	agtacggcat	ccccaaggac	cgtagccaca	tcatcgccca	cgtggagggtc	1020
cccggtctca	cgcacaccga	ccccggcccg	cactggaaact	ggaacaccta	catgtcgatc	1080
gtgaccgggt	ggggcgccgg	cctcggttgc	accacgggtc	acaacacgg	cgcgttccac	1140
gcgagcggca	actggggcac	tcccaagtc	tccggccagg	gtaacggcgc	cgactacccg	1200
ttcgccaaacc	cggtggccgc	cagegacccc	gcttggtacc	gggcgaaact	gccccggca	1260
ggcagctacc	gggtcgaggt	cttgttaccc	tccgaccccg	gctacaacag	ctcgcccccc	1320
tacatecgctg	ccgcctcggg	cggaaaccc	acggtgatcg	tgcacccgg	atccggccgc	1380
ggtggtcgcc	gcacatcggt	cacccatcc	ctcaacgcgg	gtgacccgg	cgtcggtgg	1440
gtcagcggct	ggaccccggt	cacccggta	gtcgtcgcc	acgcgtccg	cataccgc	1500
ctgtaa						1506

SEQ ID NO: 44 moltype = AA length = 501
FEATURE Location/Qualifiers

source 1..501
mol_type = protein
organism = Nonomuraea dietziae

SEQUENCE: 44

MTRLAALVAS	ALSALLILAG	QPAAADRATP	LGAAPFDAAA	AQDVPDRLLA	AIAYAETHLD	60
GHNGEPEPSASG	GYGVMLHVLVSN	PTTHTLEKAA	ELTGLPAEKL	RADTEANILG	GAAVLRSIAD	120
GLGLDEARK	BEGRNYEAVA	TYGNASSPEL	ARLYADAVYE	LLGLGFKAKG	LRVAPREVTA	180
DRGVYAGARD	LNAKDSNALA	AAGPDYPNAS	WVPASSSNYT	VSSRPSSYAI	DRVVIHVETQG	240
SYAGSISWFQ	NPSAQVSAHY	VIRSSDGAI	QMREKDVAW	HAGNWSYNT	SVGIEHEGFV	300
NDASWFTDAM	YRASAALTRN	ICDKYGIPKD	RSHIIGHVEV	PGSTHTDPGP	HWNWNNTYMSY	360
VTGGGGGSWS	TTVDNTGAFT	ASGNWGTSSY	SAQRYGADYR	FANPVAASDP	AWYRANLPST	420
GSYRVEWYWP	SDPGYNSSAP	IYIAASGGNQ	TVVVDQRSGG	GWRTIGTFT	LNAGDRDVVG	480
VSRWTSGTGY	VVADAVRITR	L				501

SEQ ID NO: 45 moltype = AA length = 476
FEATURE Location/Qualifiers

source 1..476
mol_type = protein
organism = Nonomuraea dietziae

SEQUENCE: 45

DRATPLGAAF	DKAAAAQDVP	RDLLAAIAYA	ETHLDGHNGE	PSASGGYGV	HLVSNPTHT	60
LEKAAELTGL	PAEKLRADTE	ANILGGAABL	RSIADGLGLD	EAARKEEGRW	YEAVATYGN	120
SSPELARLYA	DAVYELLGLG	FKAKGLRVP	REVTADRGVY	AGARDLNAKD	SNALAAAGPD	180
YPNASWVPAS	SSNYTVSSRP	SSYAIIDRVVI	HVTQGSYAGS	ISWFQNPSAQ	VSAHYVIRSS	240
DGAITQMVRE	KDVAWHAGNW	SYNTRSGVIE	HEGFVNDAW	FTDAMYRASA	ALTRNICDKY	300
GIPKDRSHII	GHVEVPGSTH	TDPGPHWNWN	TYMSYVTGG	GGSWSTTVDN	TGAFTASGNW	360
GTSYSQAQRY	GADYRFANPV	AASDPAWYRA	NLPSTGSYRV	EVWYPSDPG	NSSAPYIVAA	420
SGGNQTVVVD	QRSGGGGWRT	IGTFTLNAGD	RDVVGVSERWT	SCTGYVVADA	VRITRL	476

SEQ ID NO: 46 moltype = DNA length = 1509

FEATURE Location/Qualifiers
sig_peptide 1..84
mat_peptide 85..1506
source 1..1509
mol_type = genomic DNA
organism = Laceyella sacchari
CDS 1..1506

SEQUENCE: 46

ttgagaaaacg	gtttgtctc	tttgtttagt	atttgcgtc	tgcactct	gcctttcct	60
tcagctccac	cgccccgttc	agccgaggaa	cagccgtctt	tgtcccatgt	cttcgagatg	120
gcccggccag	agtttggatgg	gcccgttcaa	gttgggttgg	ctatggctt	tgccgagacg	180
aggtggatgg	accatcagggg	ccaacccago	cagctcaacg	gataccggat	tatgcatttg	240
gccgaaaacc	ccaccaatga	ctcattggta	caagccagcc	gattgttgg	catagataaa	300
caagtgtca	cccgaggatc	cccgcttac	atccgtggcc	eggcagccgt	gttgcagcaa	360
atctccaaag	aacaaaacca	ggggcagggt	cgaaaaaaac	tggccgtatgg	gtacacttgt	420
gtacggaaat	acagcggact	atccagccaa	caaaatccaa	catggatgc	cgatgtatgt	480
tatgctctga	tcaaccgggg	cgtctctgt	gttatcaacg	gccaagaggt	gcgattagaa	540
cccacacccg	tcacacccaa	ccgcggggaa	tacggtaac	ctcgcgatcc	gtccggccaa	600
gccacacccg	attatccga	agcgcgtctg	gtggccggat	ccagtgccaa	ctatactgccc	660
gccaacacgg	aatccgacgg	caatgcctac	aactacgtga	tcatccacac	cacgcaaggc	720
tcttataatg	ggacgtatcg	ttgggttcaa	aatccctctg	cccaagtgg	cgcacattat	780
gtcatttcgc	ccagtgatgg	gcaagtgacc	caaatggtgc	agaacaaaga	categcttgg	840
catgcgggca	actgggatta	caatgtccac	tccgtgggaa	tgcagcatga	agggtatgtc	900
aatgtatccg	cctggatcac	tgtatccatg	taccgcgcct	ctgcaactgt	gaccggctgg	960
tttgtcaaca	ggtacggat	tcccaaaag	cgcaagtaca	ttatcgccca	taaccaagtt	1020
ccaggcgcaca	cccacacccg	ccccggcccc	aatttggat	ggaactat	catgagctt	1080

-continued

gtcaatcagt	cgggccgcgg	tgccgatttg	gtcaactgata	acgccacttc	gaaccgcettc	1140
actgcgcacgc	ccaaatgggc	gataggcgcg	accaatgcgc	aaaaatacgg	agcggattac	1200
cgcgtatgcgc	agectgaaac	gatcagtgc	gcagcttggg	acaagaataaa	cctccccacc	1260
tcttggaaattt	atgatgtata	tgctttgggg	ccgtcaggct	ccatctacaa	tgatcggaca	1320
cctttagtgc	tcacacccac	cageggtagc	cagaccgtcc	acgtttccca	acaatccagc	1380
ggagggtgtct	ggaaccatct	gggaaccttt	aactttgcgg	cgggcgatgc	caacccgatt	1440
gcccgtgtgc	gatggacgac	aggcacccgt	tatgtcatcg	ctgtatgtgt	caaattcgta	1500
aaaagatga						1509

SEQ ID NO: 47	moltype = AA	length = 502	
FEATURE	Location/Qualifiers		
source	1..502		
	mol_type = protein		
	organism = Laceyella sacchari		
SEQUENCE: 47			
LRKRLLSWLA	ICCLLTLPLFL	SAPPVAAEQQPSLSHVPEM AAAEFEVPM VLLAIGYAET	60
RWMDHQGQPS	QLNGYGINHL	AENPTNDLSV QASRLLGIDK QVLTRDIQAN IRGAAAVLQQ	120
ISKEQNQGV	PKKLADWYTV	VAEYSGLSSQ QTKAWYADDV YALINRGVSR VINGQEVRL	180
PTPVTNPNGE	YGEPRDPSQ	ATPDYPEARW VAASSANYTA ANRESDGNAI NYVIHTTQG	240
SYNGTISWFQ	NPSAQVSAHY	VIRSSDGQVTF QMVQNNDIAW HAGNWVDYVH SVGIBHEGYV	300
NDPAWYTADAM	YRASAKLTRW	LCNRGIPKD RSHIIGHNQV PGATHTDPGP NWDWNYYMSL	360
VNQSGGGADL	VIDDNATSNRF	TASANWAIGT TNAQKYGADY RYAKPETISD AAWYKVNLPT	420
SGSYDVYAWW	PSGSIYNDRT	PYVINTTSGS QTWHVSQOSS GGVWNHLGTF NFAAGDANRI	480
AVSRWTTGTG	YVIADAVKFV	KR	502

SEQ ID NO: 48	moltype = AA	length = 474	
FEATURE	Location/Qualifiers		
source	1..474		
	mol_type = protein		
	organism = Laceyella sacchari		
SEQUENCE: 48			
EQQPSLSHVF	EMAAAEEFEP	VEVLLAIGYA ETRWMDHQQ PSQSLNGYGIN HLAENPTND	60
LVQASRLLGI	DKQVLTRDIQ	ANIRGAAAVL QQISKEQNQG QVPKKLADWY TVVAEYSGLS	120
SQQTAKWYAD	DVYALINRGV	SRVINGQEVR LEPTPVTPNR GEYGEPRDPS GQATPDYPEA	180
RWVAASSANY	TAANRESDGN	AINYVIIHTT QGSYNGTISW FQNPNSAQVSA HYVIRSSDGQ	240
VTQMVNQKDI	AWHAGNWVDYN	VVNDPAWYTD AMYRASAKLT RWLCNRGIP	300
KDRSHIIGHN	QVPGATHTD	GPNWDWNYYM SLVNQSGGGA DLVTDNATSN RFTASANWAI	360
GTITNAQKYGA	DYRYAKPETI	SDAAWYKVNL PTSGSYDVYA WWPSSGSIYND RTPVINTTS	420
GSQTVHVSQO	SSGGVWNHLG	TFNFAAGDAN RIAVSRWTTG TGYVIADAVK FVKR	474

SEQ ID NO: 49	moltype = DNA	length = 1506	
FEATURE	Location/Qualifiers		
sig_peptide	1..87		
mat_peptide	88..1506		
source	1..1506		
	mol_type = genomic DNA		
	organism = Thermostaphylospora chromogena		
CDS	1..1506		
SEQUENCE: 49			
atgcgccttc	gtttatggc	ggtattggcg tgcgcttca cagttttgtt tcttactgt	60
ggcccaacaa	caggccacgc	acgtgcta cctcttgc acgcgttgc agaagccgt	120
gcagcgcatg	acgttccacg	cgacgttta gtacgcgttgc cttacgtga ttactgttta	180
gatgtatcgc	atgggttac	tgacgcgttgc qgaggatatq gtgttatgtca tttagttt	240
aaccctacaa	atcaactttt	atcaacttgc gcaagacttta ctggcttgc ttgtgaaaaa	300
cttcgtggcg	atacgcgc	taacatcatg ggttgtgttgc ctgttttacg tgccatgtct	360
gatgaatttag	gtcttgatga	ggctgcacgt aaagacccaa gtcgttggta cactgtgtt	420
gcccgtttagt	gtggcgcttc	agatctgttgc tgacgcgttgc ttacgcggta tgccgttatt	480
gaattgtttg	gattggcat	tgacgcgttgc ggctgttttttgc tagcaccaca agaagtaacg	540
gttgacccgt	gtgaatacgc	tgtatgttgc gactttaaacgc tcgcgttttgc	600
tctgcagatt	atccgcgttgc	tgcacatggta gctgcacaca gcgcaatata caccggctac	660
tcttcgttctt	tttcttatgc	tatcgacgtt gttatcttgc acgttactca aggttcttac	720
gtctggacta	tctcttggtt	ccaaaaccct tcagcgttgc tatctgttca ctatgttatt	780
cgttcttctg	acggaggcagt	aactcaaattgttgc gttacgttgc ttggcatgtt	840
ggaaatgttgc	attacaacac	acgttcttgc gttatgttgc atgaagggttgc gttgtataac	900
ccatcttgcgt	tcatgttgcgc	tcatgttgcgttgc gctgttgcacgc tcacatttgc	960
gacaaggatcg	gtatccaaa	agacccgttgc catatcttgc gtcataacca agttccagg	1020
gcgactcaca	ctgtatccggg	acctaattgg gattggaaacc gttcatgttgc atacgttact	1080
ggtaatggcg	gaaatccgcac	ttggcagggtt actgttagata acgttgcgttgc tggcaagg	1140
acagcttcgt	aaaactgggg	cacttcttgc tggcgttgc acgttgcgttgc agtgcgttac	1200
cggttttgcgt	cgcccgatct	tgcacatgttgc cctgcgttgc gttcatgttgc aatcccttgc	1260
gccccgttgcgt	accgtatcgat	ccttcgttgcgttgc gttcatgttgc tggcgttacaa ttcatcttgc	1320
cgttatatca	tcgcgcgttc	ttcaggtaac cgactgttgc atgttgcacca gctgttgcgtt	1380
ggtggcgcgt	ggcgcgcgtt	tggtactttt acgttgcgttgc cggcgttgcgttgc gttcatgttgc	1440
gtgttatcgc	gttggacatc	tggaacaggcgttgc acgttgcgttgc gttcatgttgc	1500
cgttac			1506

-continued

SEQ ID NO: 50	moltype = AA length = 502
FEATURE	Location/Qualifiers
source	1..502
	mol_type = protein
	organism = Thermostaphylospora chromogena
SEQUENCE: 50	
MRSRRLMAVLA CAFTVLFLTA APQAGHARAN PLADAFAEA AAHDVPRDLL VALAYAETRL	60
DDHDGEPSAS CGYGVMMHLVS NPTNHSLERA AELTGLPVEK LRGDTAAINM GGAAVLRAHA	120
DELGLDEEAR KDPGRWYTAV ARYGGASDPR VARLYADAVF ELLGLGIDAA GVTVAPOEV	180
VDRGEYADVE DLNAPKARVL SADYPPAAWV AAHSNTYAS SRPSSYAIADR VIIHTQGSY	240
AGTISWFQNP SANVSAHYVI RSSDGAVTQM VREKDVAWHA GNWNNTNRSI GIEHEGWVDN	300
PSWFTDAMYR ASAALTRHIC DKYGIPKDRT HIIGHNQVPG ATHTDPGPNW DWNRPMYEYVT	360
GNGGTPTWQV TVDNATAGKF TASENWGTST WSSQRYGADY RFATPVLASD PAWFRATIPS	420
AGEYRIEYVY PSDPGYNST PYIIATSSGN RTVYVDQRSG GGTWRSLSGT SLNAGDQNVV	480
AVSRWTSGT YVIADAVRIT	502
SEQ ID NO: 51	moltype = AA length = 473
FEATURE	Location/Qualifiers
source	1..473
	mol_type = protein
	organism = Thermostaphylospora chromogena
SEQUENCE: 51	
NPLADAFAEA AAAHDVPRDL LVALAYAETR LDDHDGEPSA SGYYGVMHLV SNPTNHSLER	60
AELTGLPVE KLKGDTAAANI MGGAAVLRH ADELGLDEAA RKDPGRWYTA VARYGGASDP	120
RVARLYADAV FELLGLGIDA AGVTVAPQEV TVDRGEYADV EDLNAPKARV LSADYPPAAW	180
VAAHSSNTA SSRPSSYAIID RVIIHTQGS YAGTISWPQON PSANVSAHYV IRSSDGAVTQ	240
MVREKDVAWHA AGNWNYNTRS IGIHEGWVD NPNSWFTDAMYR RASAALTRHI CDKYGIPKDR	300
THIIGHNQVP GATHDPGPBN WDWNRFMEYV TGNGGTPTWQ TVDNATAGKF FTASENWGT	360
TWSSQRYGAD YRFATPVLAS DPAWFRATIP SAGEYRIEYV YPSDGYNNS TPYIIATSSG	420
RTVYVDQRS GGGTWRSLGT FSLNAGDQN VAVSRWTSGT GYVIADAVRI TRY	473
SEQ ID NO: 52	moltype = DNA length = 1320
FEATURE	Location/Qualifiers
sig_peptide	1..75
mat_peptide	76..1317
source	1..1320
	mol_type = genomic DNA
	organism = Kribbella aluminosa
CDS	1..1317
SEQUENCE: 52	
atgtcccgat tagcaaagct gtgegcagec ctggccgtcg ggcgcgtcgc gctgaccgcc	60
ctcccgagca acgcggcatc gcccacccgc ggctctacc tcgcccaggc cttcacgacc	120
gcccggcgcga agtacggacgt accgcgggaa gtgtcggtcg gtgtcggtcg cgccgaaacc	180
catatccgcgacgtacggc cgcgcgago cagggcaactc ggtacggcgt gatgcacactg	240
ggcggacaaaca acgttaacaa gacgtgtcc gaggcaaca aactgacccg cgtccggc	300
gccaaggctgt ccaaggacga cgcgtcgaaac gtctccggc cgcggcgggt cctcgactcc	360
tacgcggcggc aggccaaacgt caaagaccgg gcagacccgt gcaagtggta cggcggtatc	420
gcggaaactgtccgcgcgacgtacccgc accgcggcgtcgttacaccga cgaggctc	480
cgaatcatgtt cccgggggtgt ccgcggccgc gggtctcgaa ccgacccggaa gccggtcac	540
ccggacccgcg cgcgtacgc gaaggccgtt ccgcgtcgaa ccgcggcgtt cgactacccg	600
agcgcgcatctt ggaacccggc gaccggcggc aactacccgc tggccggac cgcggcgtatc	660
accacatcgatccgtc tcatccacgt caccggcggc tctgtacccgc gcaaccatcg ctggttcaag	720
aacccgtccgc cgcggatccgtac ccgcgtactc gtgtccggc cggacccggc cgaggctcacc	780
cagatggttccgcgagaaggc caccggcgtgg cacgtccggc cggagaaccc gtacacgtatc	840
ggcatcggcgc accgaagggtt cgtcgaccatc ccgtcgatgtt tcaccgtatc gatgtacccg	900
tctgtcgccgcg cgcgtccggc caacatcgcc gaccggcggc gcatccggaa ggacccggcc	960
cacatcaacgg gccacaacgcg gatgcggaaac aacgaccaca ccgacccggg accgaacttgg	1020
aactgggact actacacgcgacgtgtgtac ggcggcggacc cgaacccggc ggagtacaa	1080
tccaccacgtt ggggttgggg cgtacacgtc cgtcgccgc cgaactgttc cgcgtcggtc	1140
gtccaccacgcg tccccggccgc gaccggcgtt ttcgtcgatc gccagggttca gggcgacacc	1200
gtgacggcggc ggggttgggg cacaactgg tggccggacca gcaacgggtac	1260
atgaccaaca tctatcgatc cgcggatccgtac cagaactgttc caggcgatcc ggactgttag	1320
SEQ ID NO: 53	moltype = AA length = 439
FEATURE	Location/Qualifiers
source	1..439
	mol_type = protein
	organism = Kribbella aluminosa
SEQUENCE: 53	
MSRLAKLCAA LAVGALALTA LPSNAASPPA GSHLAEAAFTT AAAKYDVPRE VLVGVGFAET	60
HLDGHGDTGPS QANGYGVML ASNNVNKTMS EASKLTGVPP AKLSKDDASN VLGAIAVLD	120
YAEQAKLKDAR ADLGKWWYVII AKYSHSADAS TARLYTDEVY RIIARGVRAA GVSTDPKPVS	180
PDRGAYAKAA PLGTAADVYP SAIWNPASTS NYRVGRATAI TTIVIHTQG SYAGTISWFK	240
NPSAQVSAHY VVRSSDGETV OMVAEKDTAW HVRTENPYTI GIEHEGYVDQ PSWFTDAMYR	300
SSAALTRNIA DRRGIPKDR AHIKGNEMPN NDHTDPGPNW NWYDYYTQLVN GGDPNPPEYN	360
FTTWGEGVNV RSAPKLSASV VTTLPGPTRV FVECQVQGDT VTAGGYTNW WAKLRDQHGY	420

-continued

MTNIYIDDPN QKLPGPVDC	439
SEQ ID NO: 54	moltype = AA length = 414
FEATURE	Location/Qualifiers
source	1..414
	mol_type = protein
	organism = Kribbella aluminosa
SEQUENCE: 54	
ASPPAGSHLA EAFTTAAAKY DVPREVLVGV GFAETHLDGH DGTPSQANGY GVMHLASNNV	60
NKTMSEASKL TGVPVAKLSK DDASNVLGAA AVLDSYABQA KLKDRAVLGK WYGVIAKYSH	120
SADASTARL DEVYRIIAR GVRAGVSTD PKPVSPDRGA YAKAAPLGTA AVDYPSSAIWN	180
PASTSNYRVG RTAAITIVI HVTQGSYACT ISWFKNPSAQ VSAHYVURSS DGEVTQMVAE	240
KDTAWHVRTE NPYTIGIEHE GYVDQPSWFT DAMYRSSAAL TRNIADRRGI PKDRAHIKGH	300
NEMPNNDHTD PGPNWNWDYY TQLVNNGDPN PPEYNFTTWG EGVNVRSAPK LSASVTTLP	360
GPTRVFVECQ VQGDTVTAGG YTNNWWAKLR DQHGYMTNIY IDDPNQKLPG VPDC	414
SEQ ID NO: 55	moltype = DNA length = 1332
FEATURE	Location/Qualifiers
sig_peptide	1..93
mat_peptide	94..1329
source	1..1332
	mol_type = genomic DNA
	organism = Streptomyces griseus
CDS	1..1329
SEQUENCE: 55	
atgacgtcgca agcagaggat gagactcgcg ctcgcactga ccgcggccgg ggcgtgagc	60
gtggcgctcc ttcggccggc cgccggccggc gccggacaccg tacgacccgga atgcggccgg	120
tccctggcct ggcactgggt ccccgccggc taccagcaga ccggagatcc ggaggacaag	180
gacacctacg gcaactacg caccggcgaa cggcccgaca gcaacgcgtt caagttcatc	240
gtcctgcacg acaccggactt cgactacgac accacccttca agatcttcca gaacccggcc	300
aaccaggatc cggccggactt cgtgttgcgc tccggccgttgc ggcacgttac acagatgttg	360
aagaacaagg acgtcgccgt gcaggccgggg aacttgttacc tcaacaccca ctccatccgg	420
atcgagcagg agggcgctgc agccggagggt gccacgttgcg acaccccttca gatgtacccg	480
tcgaccgcgc ggcctggcgc gtacccgttgcg gccaaggatcg acatcccgct cgaccggcaa	540
cacatccctcg ggcacggacgg ttgtccggcc accagccggc ccggaaacggaa gaacatgcac	600
tgggaccggg gaccctactg ggcacttgcg cgttactatgg cgctacttgc cgcggccacc	660
ggcccccaacgc ccccaaaacgc cagccggactt gtcaccgttca ggcgggactt cgcggaggaa	720
cacggaggat tcccgacttgcg cggaaaaggac gtcgacccccc cccggcggagg gggcggcg	780
gtcccttcgc acacggggac gtcggccggac ggcggcccttc ttcggccacc ggggtgtcat	840
ccggacggct cggccggggac gaaacttgcgc gctgacttggc gcaaggatcg cagtgcgacc	900
cacccggccgc tcgtccggca ccgggttaccgc ggttggggcgg egatctgttgc ttcggggag	960
aaggcttggt tcaacttcc gcccggttaccgc agggttaccgc ccccgaccgg cggcgtgttg	1020
gtccggccgc accccggggac gtcggaaatgg ctgttgcgttgc ggcggccactt ccccgaggaa	1080
cccgaggatcc ccccgaggatcc cgttgcggcc accgttggggc ccggccgttgc ttcaccatc	1140
aaggccgggtt accccgttccgc cggccggccgc gaggccggccca ccggccactt ctcggccacc	1200
acgatcgaca ctcgaagcc gtcggccaccgc acgttacttgc gtttgcgcga gaagtacgttgc	1260
acgggttccgc tccggccaccgc catggccgttgc gtcaggccgttccgcgttgc gtcggccgc	1320
ccggccgttgcat ga	1332
SEQ ID NO: 56	moltype = AA length = 443
FEATURE	Location/Qualifiers
source	1..443
	mol_type = protein
	organism = Streptomyces griseus
SEQUENCE: 56	
MTSKQRMRILA LALTAAGALS VALLSPAAAG ADTVRPECPR SLACDWVPAAY YQQTGDPEDK	60
DTYGNYDTAN RPDSNAVKFI VLHDETEVDYD TTLKIFQNPAQ NQTSAHVVVR SADGHVTQMV	120
KNKDVAWQAG NWYLNTHSIG IEQEGVAAEG ATWYTSEMYR STARLVRYLA AKYDIPLDRQ	180
HILGHGDGVPP TSAAGTKNMH WDGPYWDWN RFMALLGAPT APSAPKRSEL VTVSADFARN	240
QQEFRDCEKN VDLPRQGSSA VPLHTEPSAD APLFSDPGLH PDGSPGTNCA ADWGSKISAT	300
QQAVVADRVPW GWTAIWWYGE KAWFSTPPGT RVITPTGRSV VRPKPGTSEV LVYGVAYPEK	360
AEPYPTDFVKP TVGTPLVYTI KAGQAFPGGG EAPTGYYYAP TIDTSKPYDH TYFGGAQKYV	420
TVQIGHRIGF VKASDVDDVR AGS	443
SEQ ID NO: 57	moltype = AA length = 412
FEATURE	Location/Qualifiers
source	1..412
	mol_type = protein
	organism = Streptomyces griseus
SEQUENCE: 57	
DTRPPECPRS LACDWVPAAY QQTGDPEDKD TYGNYDTANR PDSNAVKFIV LHDTEVDYDT	60
TLKIFQNPAQ QTSAHVVRS ADGHVTQMV NKDVAWQAGN WYLNTHSIGI EQEGVAAEGA	120
TWYTSEMYR TARLVRYLA KYDIPLDROH ILGHGDGVPT SAAGTKNMHW DPGPYWDWR	180
FMALLGAPTA PSAPKRSEL TVSADFARNQ QEPRDCEKNV DLPRQGSSAV PLHTEPSADA	240
PLFSDPGLHP DGSPGTNCAA DWGSKISATQ QAVVADRVPW WTAIMWWYGEK AWFSTPPGTR	300
VTTPTGRSVV RPKPGTSEVL VYGVAYPEKA EYPTDFVKP VTGTPLVYTI AGQAFPGGG	360

-continued

APTGYYYAPT IDTSKPYDHT YFGGAQKYVT VQIGHRIGFV KASDVVVRA GS 412

SEQ ID NO: 58 moltype = DNA length = 2019
 FEATURE Location/Qualifiers
 sig_peptide 1..105
 mat_peptide 106..2016
 source 1..2019
 mol_type = genomic DNA
 organism = Micromonospora peucetia
 CDS 1..2016
 SEQUENCE: 58
 atgcacccgt cagcacaac gaggagcaga cgcgcttcgc tggccaccgc cgtggccgc 60
 gtcatggtgg cgacgcgct caccgcgcg ggatccgcg ccgcgcacc ggcgaccgac 120
 cggcagcage agtacgcgcg cgccgcgcg gactacggcg tgccggagag cgtctctgc 180
 ggcgtctccat atacatgcg cgcgtggac accaacgcgcg geacgcggag caccagcgc 240
 ggctacggat cgatcaccc caccgcgcg qgacacgtcg cgcgcctggc cgggggcacc 300
 caccacgacg agggcaccga ggacccgcgc ggcgacgact cccgcgcgtc cctggcgag 360
 ggcgcgagc cggcgcgcg ggctccgcg gaggcggcgc tccggacgt cgacgcgcgc 420
 gcggactca cggcgcgcg cgaggagcg ctgcggacgg acgtcacgcg gaacatccgg 480
 ggccggcgcg cgctgtggc cgctaccccg aaggagatcg gtgcggccgt cggtgcgcag 540
 accgaccggc cggcctggta cggcgcgcgt gcccgcgtact cggcgcgcga caccacccgac 600
 gccgcggcgg ctttcgccaa cgagggtgtac gccaccatcg ccacgcgcgcg caccgcactg 660
 accgcacgcg ggcagcgggt cacccgcgcg gcccgcggagg tccagecgga ggcgttcctgg 720
 ctggacccgc tgggcgtcgca aacgtcgcc cggccgcgcg ggctggatgc cccgagcgac 780
 atccgtcgca atggatcccc ggcgcctac cagaactacg gaaccacccct cggegcgtac 840
 ggaaccacacg acctggctga cggccgcgcg cagcagaaga tcgagtagat cgtcatccac 900
 gacacccgagg gtacttgtgg gcccgcgtg aactctgttgca aggacccgaa gcccgggtgg 960
 tggcaactaca cccctgcgtc ggtggacggc cacatcgccc agcacatcaa gacaagaaac 1020
 gtccggctggc acggccgcgcg ctggtaatcg aactctccatg ccacatggcct tgagcacgag 1080
 ggttcggcgg yacacggcgcg ctggtaatccacc gaggcgttgat accgcacccgc cgcacaactg 1140
 gtccgcaccc tggcggggcg gtacacatcg ccgctggacc gcaaccacat catgggcac 1200
 gacaacgtcc cggcgcgcgt cgccgcgcg acgtgggtggca tgcactggca cggccggccgc 1260
 tactgggact ggtcgacta cttegacccgt ctgaaaggcgc cgttctggc gaccgcac 1320
 caccggaccg gacttgtcac catcgaccgc gacttcgcgc ccaaccagcc gcagttcacc 1380
 ggtgcacacc ggcagcgcgcg ggccgtgcg aaccgcgcgc cgcgcacggc tccctgcgcgc 1440
 ctgcgcgcgt ctgcgcgcgt cgcctgcac aacgcgcgcg gccaggacgc gccgcgtgtc 1500
 aacgcacatcg cgctggggcc cgacggcacc cccaaacccatc tgcactgttc cgaccacccg 1560
 gcccgggtct cggcaggaca gacgtacgcg ctggccgagg tgccgggggtga ctggacggcg 1620
 atctggattcc tggcggagaa ggccgtgttc cacaacccgg cctcgccgcg gaccgcac 1680
 tggccgtcg cgcttgtcgcc caccggcaga gcaaggcaga ccacatccc ggtgtacggc 1740
 cggcgcgtacc cggaggaggc ggcttacccg gccggcgtgc cgtaaccagac gatctgcgcgc 1800
 ctccagtaca cgctctcgcc cggtgagccg tacgcgtcg gcaaccatgt ccccgccgag 1860
 tactaccggg ccaccacgtt cgacccgcgtt gccccgggtg accggacccgt catccgcgc 1920
 gagaacaagaat acgtcgatccatc ccaatccggcatac tgcactgtcaaa cctggccgac 1980
 gtgaacctgc tggccctcgcc gctggccgcg ccccgctga 2019

SEQ ID NO: 59 moltype = AA length = 672
 FEATURE Location/Qualifiers
 source 1..672
 mol_type = protein
 organism = Micromonospora peucetia
 SEQUENCE: 59
 MHLSATRSR RVLLATAVAA VMVATPLTAA GSAAAAPATD RQQYAAAAA EYGVPESTVLL 60
 GVSYLSQSRWD TNAGTPSTSA GYGPMLHTDA EHVAALPGGT HHDEGTEDPR GDDSRPSLAE 120
 AREPAEPAPA EAALRTLDAA AGLTGASEAA LRITDVTANIR GGAALLAAYQ KEIGAPVGAE 180
 TDPAAWYGV ARYSGADTTA AAAAFANEVY ATIATGDTRL TDDGQRVTLA AREVQPERSW 240
 LDRLGLRKLA RPDGLECPSD ISCEWIPAPY QNYGTTLGY GNHDLADRPA QQKIBYIVIH 300
 DTEGYFGPSV NLVKDPKRVG WHYTLRSVDG HIAQHIKTKN VGHAGNWYV NSKSIGLEHE 360
 GFAHGHTWYT EAMYRTSAKL VRHLARQYNI PLDRNHIGH DNVPGTVAAN VRGMHWDAGP 420
 YWDWSHYFDL TLKAPFWSTGT HRTGLVTIDP DFATNQPQFT GCNRQPPGVP NPPPTAPCP 480
 LRGSSALPLH NAPSQDAPLV NDIALRPDTG PNTMYVSDHG ARVSAQOTYA LAEVRGDWTA 540
 IWYLGQKAWF HNPASARTAK WSVGLVATPK AGKTTIPVYV RAYPEEAAYP AGVPYQTISP 600
 LQYTLSAGER YAVGNLLPGE YYRATTFDGS APGDRTVIRG ENKYVQIQFG HRIMYVNLD 660
 VNLLPSPLGA PR 672

SEQ ID NO: 60 moltype = AA length = 637
 FEATURE Location/Qualifiers
 source 1..637
 mol_type = protein
 organism = Micromonospora peucetia
 SEQUENCE: 60
 APATDRQQY AAAAEYGVP ESVLLGVSYL QSRWDTNAGT PSTSAGYGPMLHTDAEHVAA 60
 LPGGTHHDEG TEDPRGDDSR PSLAEAREPA EPAPAEALR TLDAAGLTG ASEELRTDV 120
 TANIRGGAAL LAAYQKEIGA PVGAETDPAA WYGAVALYSSG ADTTDAAAAT ANEVYATIAT 180
 GDTRLTDDGQ RVTLAAREVQ PERSWLDRLG LRKLARPDLG ECPSDISCEW IPAPYQNYGT 240
 TLGAYGNHDL ADRPAQOKIE YIVIHDTEGY FGPSVNLVLD PKRVGWHTL RSVGDGHIAQH 300

-continued

IKTKNKGWHA	GNWYVNSKSI	GLEHEGFAGH	GTWYTEAMYR	TSAKLVRHLA	RQYNIPLDRN	360
HIIGHDNVPG	TVAANVRGMH	WDAGPYWDWS	HYPDLLKAPF	WSTGTHRTGL	VTIDPPDFATN	420
QPQFTGCNRQ	PPGVPNPPPP	TAPCPLRGSS	ALPLHNAPSQ	DAPLVNDIAL	RPDGTPNTMY	480
VSDHGRVSA	QOTYALAEVR	GDTAIWYLG	QKAWFHNPS	ARTAKWSVGL	VATPKAGKTT	540
IPVYGRAYPE	EAAYPAGVPY	QTISPLQYTL	SAGERYAVGN	LLPGEYYRAT	TFDGSAPGDR	600
TIVRGENKYV	QIQFGHRIMY	VNLADVNLLP	SPLGAPR			637

SEQ ID NO: 61	moltype = DNA	length = 1899				
FEATURE	Location/Qualifiers					
sig_peptide	1..99					
mat_peptide	100..1896					
source	1..1899					
	mol_type = genomic DNA					
	organism = <i>Bacillus</i> sp.					
CDS	1..1896					
SEQUENCE: 61						
ttgggattta	aaaagctatc	atcagccatt	ttaacgttct	ccttaaccgc	aagccttttg	60
gtstatccccc	ctgactttac	accaaggcga	acttctgcag	cctcaacaga	aaacagcaat	120
gaagcgcacc	acctgcaaaa	ggcttttgaa	acagcggcga	aggaatttgg	agtacctgaa	180
tctgtccctc	tcgcgtcgc	ttataaccag	tcacgcgtgg	agcaccatga	aggccatagt	240
gaggctcgag	gctatggcat	tatgaatctt	gcagactgc	cagccgacat	gagcgcagg	300
ggcaaggatc	acgacggat	cattgcggat	ttggataatg	aaaatagcat	gcttaaaaaca	360
gcccgc当地	cttcaaatga	agatccggaa	gccttaaaa	aaagccctga	acaaaatatac	420
cggggccccgg	cagcttttt	acgcagat	gcacgc当地	cgacagggg	acttcctcc	480
gatgaagcag	actggtaggg	tgccgtcgtt	aaatacagcg	gaacagatca	ggaagtcatc	540
gctaaggact	ttgcagatc	agtttttag	accattcagc	aaggtagtgc	cagaaaaaac	600
cttgcgtgac	aaggatcg	attaaacgc	aaggaaat	caccaatataa	gactacag	660
ggcactatcc	ctcttcgca	caccaataac	acaatattcc	actgtccaaa	tggccttgat	720
tgcactttca	ttcctgtctc	ttataagca	ttttcgcgac	gcacaatgaa	ttacggcaac	780
tacgatatacg	ccatcgcc	aaaggacgt	ttagatattat	gctatattat	tattcatgt	840
attgaggcga	eggctgaa	cgccatccat	atccgtccat	cgtagtgca	900	
cactatgtc	tagattcaga	gacccggaaa	atcacccaga	tggtagtccc	tgaagatgt	960
ccatggcat	caggaaactg	gtatTTAA	atgcattcga	tcggatttga	gcatgaa	1020
tatgcgtcag	aaggcgctga	ctggtagt	gagcaatgt	atcgctctac	cgcaaaactt	1080
gtaagatacc	tttcaagacc	atthaacat	cctttggac	gacagcacat	tatcggccat	1140
gatgagatc	ctggcttac	aaacagcaaa	cataggac	tgcaactgg	tccggccgt	1200
tattgggatt	gggggactt	tttcgac	cttggagctt	ccattaatcc	aaggacgg	1260
gacaaagaca	gtaatatcg	cacaatccgc	ccaaatttca	atacaaatca	gccagactt	1320
acgtatagag	gaattaaaca	ggaaatgg	tcttcga	tgatttcat	atacagcgaa	1380
cccagcttgc	aggcaccatt	ggtagtgc	ccctgttcc	atccctgggg	caccagcaca	1440
agaatataat	atgactgggg	caataaagct	gcaatgggac	agatgttca	taaagccgg	1500
caggaaggcgc	atggcagac	tatatactac	gccggccaa	aaggctgg	ctataatcc	1560
acaatataaa	atagcgcc	aggcagccgg	accctcatcc	cgccaaa	agggtttgat	1620
tccataatctg	tatatggtgc	cgcctatcc	gacgacgc	cttacga	ggccgaa	1680
gcccgaatggg	caagaggaaa	agcacagtt	ctataccaga	tgccggctgg	ccaaatctat	1740
acagcaacag	caccaattca	gtccgattac	tatcatgoga	agtattataa	tgaccgg	1800
acaatataag	ttgttaaagg	gaatgtat	tactatcaga	ttttttacaa	tcatcgct	1860
ggattcgtga	agaaaagcga	tgtagaatgt	gtaaattaa			1899

SEQ ID NO: 62	moltype = AA	length = 632				
FEATURE	Location/Qualifiers					
source	1..632					
	mol_type = protein					
	organism = <i>Bacillus</i> sp.					
SEQUENCE: 62						
LGFKKLSSAI	LTFSLTASLL	AIPADFTPSA	TSAASTENS	EAHHLQKAFE	TAKEFGVPE	60
SVLLAVAYNQ	SRWEHHHEGHS	EVGGYGINML	ADLPADMRS	GKHDDGIIAA	LDNENSLMLKT	120
AANLLNEDPE	ALKKDPEQNI	RGGAALLAEF	ARQTTGELPS	DEADWYAVV	KYSGTDQEVI	180
AKDFADQVFE	TIQQGAARKN	LDGQRVVLNA	KEITPNKTTA	GTIPLRNTKV	TNTDCPNGLD	240
CTFIPAAKYQ	FSSSTSINYGN	YDIANRPKDD	LDIRYIIIH	IEGTAEASAIS	HFPQNPYVSA	300
HVVIDSETGK	ITQMRVPEDV	PWHAGNWYFN	MHSIGLEHEG	YAAEGADWYS	EQMYRSTAKL	360
VRYLSDRFNI	PLDRQHIIIGH	DEIPGLTTAK	HRSMHWDPGA	YWDWGHFFDL	LGASINPSSG	420
DKDSNIVTIR	PNFNTNQPDF	TYRGIKQEP	SSSLIHLYS	PSFEAPLVSD	PLLHPGGTST	480
RNINDWGNGKA	AMGQSFYKAG	QEGDWTAIYY	AGQKAWFYNP	NNKNNSVPGSG	TLITPKEGLD	540
SPVYGAAYP	DDAAYEEAGI	AEWARGKAQV	LYQMPAGQIY	TATAPIQSVDY	YHAKYYNDPA	600
TNKVVKGND	YYQIFYNHRL	GFVKKSDVEV	VN			632

SEQ ID NO: 63	moltype = AA	length = 599				
FEATURE	Location/Qualifiers					
source	1..599					
	mol_type = protein					
	organism = <i>Bacillus</i> sp.					
SEQUENCE: 63						
ASTENSNEAH	HLQKAFETAA	KEFGVPESVL	LAVAYNQSRW	EHHEGHSEVG	GYGIMNLADL	60
PADMSARGKH	DDGIIAALDN	ENSLMLKTAAN	LLNEDPEALK	KDPEQNIRGG	AALLAEFARQ	120
TTGELPSDEA	DWYGAVVVKYS	GTDQEVIAKD	FADQVFETIQ	QGAARKNL	DG QRVVLAKEI	180

-continued

TPNKTAGTI	PLRNTKYTNT	DCPNGLDCTF	IPAAKYQFSS	STSNYGNYDI	ANRPKDDLDI	240
RYIIIHIEG	TAESAISHFQ	NPSVYSAHV	IDSETGKITQ	MVRPEDPVWH	AGNWYFNMHS	300
IGLEHEGYAA	EGADWYSEQM	YRSTAKLVR	LSDRFNIPLD	RQHIIIGHDEI	PGLTTAKHRS	360
MHWDPGAYWD	WGFFFDLLGA	SINPSSGDKD	SNIVTIRPNF	NTNQPDFTYR	GIKQBPESSS	420
LIHLYSEPSF	EAPLVSDPLL	HPGGTSTRNI	NDWGNKAAMG	QSFYKAGQEG	DWTAIYYAGQ	480
KAWFYNPNNK	NSVPGSGTLI	TPKEGLDSIP	VYGAAYPDAA	AYEEAGIAEW	ARGKAQVLYQ	540
MPAGQIYTAT	APIQSDYYHA	KYYNDPATNK	VVKGNDEYYQ	IFYNHRLGFV	KKSDVEVVN	599

SEQ ID NO: 64	moltype = DNA	length = 1911
FEATURE	Location/Qualifiers	
sig_peptide	1..93	
mat_peptide	94..1908	
source	1..1911	
	mol_type = genomic DNA	
	organism = Bacillus sporothermodurans	
SEQUENCE: 64		
atgttattac gacgtttaaa aatcgata ttattgttca cattcatcct tatttttagc	60	
ttacttgtta tgccattcgg agtacgaaa gcaagtaaac attatacgat tgataacaat	120	
catcatttc ctgtcagca agcattact aaggctca aaggttca tgtcccgaaa	180	
agcttattaa tgcgttgc ctacaatgag tcacgttggc tagatcatca tggcagcca	240	
agcacatcg gtggcatgg aatctatcg ttaactgaag ccaagccctc acaaagtgg	300	
agtgtctaaag gaaacggaa agcacatca tctgttata atgtcaaca aatgtataccg	360	
ttgaaaacgg cagcttaact tctaggatca aaggacaatg tgataaaagt taacccggaa	420	
cagaacattc gcgggtgtgc tgcatctt ttgaaatatg ctgcgtatc ggttggccat	480	
ataccgaaat gtctcgctga ttgttatgg gcagttcta agtatacgcc ctcaacaaat	540	
caagttgtcg ctatgttatt tgcaagaccaat gtgtatgatc cgatcaaga aggtgcagaa	600	
gagggttggc acatcttgcgatccaaatccaaataaggat tccaaataaaa	660	
aagacaatg acaaactgaa gtttcaaaaa acgaaagaaa tggatgttata ttgcctaaa	720	
ggagtagatt gcaatgtat tccagcagca tataaaatc ttctctgt tacagattac	780	
ggaattatgc atcttgcac caggccaaatg gatggaaatg atattcgta tattttatc	840	
cacgatactg aaggcagctgatccaaatcgatc ttcaagatca gtcataatgc	900	
agtgctact atgttattcg ttctccgtat ggtcaatttca cagaatgggaaaacggag	960	
gatgttgcgatggcaacggcggcaactgttgcacatccatcgatattggatcatgc	1020	
gagggttgcgatccatcgatggctacttgcgatgttgcacatgtatcata tgcacatcgca	1080	
aaactagtaa atatatttgcgatggatccatcgatggatccatcgatgcacatatttc	1140	
ggccacgaca acgtccctgg tttaaacgcgc gcccggccaaatccgtatgcgttggatcc	1200	
gcagcttattt ggaactgggaaatccgttgcgatccatcgatggatccatcgatgc	1260	
aaaggaaatggaaatccgttgcgatccatcgatggatccatcgatgcacatccatcgat	1320	
ccatcaactt atcaaaatgcgatggatccatcgatggatccatcgatgcacatccatcgat	1380	
acggcaaccaatccgttgcgatggatccatcgatggatccatcgatgcacatccatcgat	1440	
cctggatcgatccatcgatggatccatcgatggatccatcgatgcacatccatcgat	1500	
gtatgtcgatccatcgatggatccatcgatggatccatcgatggatccatcgatgc	1560	
ttaacccggaaatccgttgcgatccatcgatggatccatcgatggatccatcgatgc	1620	
gggtctcgatccatcgatggatccatcgatggatccatcgatgcacatccatcgat	1680	
acaggccatccatcgatggatccatcgatggatccatcgatgcacatccatcgat	1740	
ggccaaatggatccatcgatggatccatcgatggatccatcgatgcacatccatcgat	1800	
aatccggatccatcgatggatccatcgatggatccatcgatgcacatccatcgat	1860	
aaccaccgtgtccatcgatggatccatcgatggatccatcgatgcacatccatcgat	1911	

SEQ ID NO: 65	moltype = AA	length = 636
FEATURE	Location/Qualifiers	
source	1..636	
	mol_type = protein	
	organism = Bacillus sporothermodurans	
SEQUENCE: 65		
MLLRRLKNT LLFTFILIFS LLVMPFGVSE ASKHYTIDTN HHSPLQQAFK KAAKEFHVP	60	
SLLMSVAYNE SRWLDDHHQGP STSGGYGIMH LTEAKPSQL SAKGNGIAHS SAINVQOMYT	120	
LKTAAKLLGV KDNVKVNPN QNIRGGAALL LEYARDTVGH IPRSLADWYG AVAKYSGSN	180	
QVVANDFADQ YVATIQEGAE EVLADQHVLW LKPNKVIPNK KTSDLKFQK TKEMDVDCPK	240	
GVDCRYIPAA YKQFSSLTDY GNYDLATRPK DGNDIRVIII HDTEGSYDSA INWFQDQSYA	300	
SAHYVIRSSD GQITEMVKPE DVAWQAGNWY FNAHSIGIEH EGYAVQGATW YSEQMYHASA	360	
KLVKYLAEKY HVPLDRAHIL GHNDVPGGLTP AAQTRMHWD P AAYWNWEHFF KKLGVPIHPT	420	
KGKKNRSIVT IAPKYLKNMP PLTYQNEQLE KOPANFVYL TEPSFSAPYI GDPALHADGS	480	
PGTTAINVWGT DKASTGDDWMW IYYGGKKAWF FNPKRKNTVS GKGLVTPKK	540	
GLDAIPVWGT AYPENSAYEG TGIPITGSECK ITPLQYTIAA QQVYVATNPV KADYYYAKLF	600	
NRLSENKVVK GNDEYYQIFF NHRVAFVKK DVEVKK	636	

SEQ ID NO: 66	moltype = AA	length = 605
FEATURE	Location/Qualifiers	
source	1..605	
	mol_type = protein	
	organism = Bacillus sporothermodurans	
SEQUENCE: 66		
SKHYTIDTNH HSPLQQAFK KAAKEFHVPES LLMSVAYNES RWLDHHQOPS TSGGYGMHL	60	
TEAKPSQSLSS AKGNGIAHS AINVQOMYTL KTAAKLLGVK DNVIKVNPEQ NIRGGAALL	120	

-continued

EYARDTVGHI	PRSLADWYGA	VAKYSGSNNQ	VVANDFADQV	YATIQEGAEEL	VLADGQLVL	180
KPNKVIPNKK	TSDKLKFQK	KEMDVDCPKG	VDCRYIPAAY	KQFSSLTDYG	NYDLATRPKD	240
GNDIRYPIIH	DTEGSYDSAI	NWFQDQSAYAS	AHYVIRSSDG	QITEMVKPED	VAWQAGNWYF	300
NAHSIGIEHE	GYAVQGATWY	SEQMYHASK	LKVYLAEKHY	VPLDRAHILG	HDNVPGLTPA	360
AQTRMHWDP	AYWNWEHFFK	KLGVPIHPTK	GKNSRIVTI	APKYLKNMPP	LTYQNEQLEK	420
QPANFVYLHT	EPSFSAPYIG	DPALHADGSP	GTTAINDWGD	KASTGOSFYV	ADHKGDWMAI	480
YYGGKKAWFF	NPKRKNTVSG	KGILVTPKKG	LDAIPVYGT	YPENSAYEGT	GIPTGSEGKI	540
TPLQYTIAG	QVYVATNPVK	ADYYYAKLFN	RLESENKVVKG	NDEYYQIFFN	HRVAFVKKSD	600
VEVKK						605

SEQ ID NO: 67	moltype = DNA	length = 1941
FEATURE	Location/Qualifiers	
sig_peptide	1..108	
mat_peptide	109..1938	
source	1..1941	
	mol_type = genomic DNA	
	organism = Paenibacillus pini	
CDS	1..1938	
SEQUENCE: 67		
ttgaaactac tgcgaacaat ccaatggaaa aagctgtcgc tcgcactcac agtcgcctca	60	
ctggcggtt ccggattcac accccgactt cctgatccat tcaaggccgt accttctgta	120	
tatgcggagc aagacaagac gaattcgttg caacaaggct tcgaatcagc ggctaaggag	180	
ttcggagtgc ctgtgagcat ttgtatgtcc gtttcttaca accttacaag gtggggagcat	240	
catccatggcc aaccaggatc ttctgggtga tacggatcatc tgccatggac cgacttggcc	300	
gtacaggata aagaagacca taacggAACC gacgacgaaag agaaccatc gacttggac	360	
gatcccggcgt ttcatccccat atctcgccgc gcacaacttat tgaatcttgc tccggactta	420	
ctgaaggcagg atccctgtgt caacatcgaa ggccggagocgc cattgtgtgc gaagtgacgt	480	
caggaaaccgc ttggtaaactt gacggccatcc gaaatccgattt ggtatgggg cgttgcacaa	540	
tacagcgtt ctcaagattt gggggccctt ctggagttt ccaaatatgtt atttgtatacg	600	
attcagcaggc gaataatcgcc gcaaaccatcg gaaaggacatca tgctacgttccatccaag	660	
gagggtgaaaccc ttaacatggaa tacggatccaa acgcttccatc tgctgtccatc gaaaccatcg	720	
aacgtcgagt gcccctcgaa tctccactgc agatctgttc tgccagccata tcagcagaac	780	
ggggatgacc ctgcggatttttcaattt gatcttgcgc accgtcccaa attttgtctt	840	
gatattcgtt atattgtcat tcatgatacc gaagaaacctt atcaggatatac gctcaatata	900	
tttaccaatc cgaatccatcgaa tgcggccatcc cactatgttcc tccgttgcgc cgacggccag	960	
atcacgcataa tggtcaagac aaaggatgttccatcgaa cctggccatgc caggccatcg gtatttcaat	1020	
atgcactcgat ttggcgtaga gcatgagggtt tttgtatggaa aaggagacaaatccatccatc	1080	
gagaggctt accgttcatc tgccggatggatccatc tggcggagaa atatgtatatttccatc	1140	
ccgcctcgat gggccatcatc tateggccatc gatggaaatccatc cgggttccatc tccagccatc	1200	
caagggttta tgcattcgaa tccggccctt tttggggatccatcgaa ctttgcgttccatc	1260	
gttggagocat cgatccatcgaa caaacatgttccatcgaa actaaagaca ttgtgacaaatccatc	1320	
tttaaaaacca atcaaccatcgaa tatcaatgttccatcgaa gcccatttttccatc	1380	
ttatataaag accggccatcttccatcgaa ctgattgttcatc tggcggccatc tggcggatccatc	1440	
aacaaggaaatccatcgaa accgggttccatcgaa aagggttccatcgaa tagggccaaatccatcgaa	1500	
ggccggccatcgaa accgggttccatcgaa tccatcgaa gacccatcgaa tccatcgaa	1560	
aatcccgaaatccatcgaa accgggttccatcgaa aagggttccatcgaa tagtccatccatcgaa	1620	
gcacgttccatcgaa accgggttccatcgaa tccatcgaa gacccatcgaa tccatcgaa	1680	
atcacgcataa tggtgcgttccatcgaa tacacttaccatcgaa cccatcgaa gtcgtatgttccatcgaa	1740	
gcgcgttccatcgaa accgggttccatcgaa tccatcgaa gacccatcgaa tccatcgaa	1800	
gcgcgttccatcgaa accgggttccatcgaa tccatcgaa gacccatcgaa tccatcgaa	1860	
ttccgttccatcgaa accgggttccatcgaa tccatcgaa gacccatcgaa tccatcgaa	1920	
acacgtcgatccatcgaa accgggttccatcgaa tccatcgaa gacccatcgaa tccatcgaa	1941	
SEQ ID NO: 68	moltype = AA	length = 646
FEATURE	Location/Qualifiers	
source	1..646	
	mol_type = protein	
	organism = Paenibacillus pini	
SEQUENCE: 68		
LKLLRTIQWK KLSLALTVAS LAVSGFTPGL PDPFKAVPSV YAEQDKTNSL QQAFESAAKE	60	
FGVPVSLIMVS VSYNLTRWEHH HGQGSTSTGG YGIMHLTDLV QVDKEDHNGT DDEENPSTD	120	
DPSVHTLSAA AQLLNLDPDL LKQDPVCNR GGAALLAKYA QETLGKLTAS ESDWYGGVAK	180	
YSGSQDGSAS LEFANNVFDT IQQGISRQTS EGQMLRLPSK EVKPNLDTVQ TLHRLPSKPD	240	
NVECPRNHLH RSVPAAYQQN GDDPSDYSNY DLADRPKFGP DIRYVIIHDT EETYQDTLNI	300	
FTNPNSNVSA HYVLRSSSDQI ITQMVKTKDV PWHAGNWWFN MHSIGVEHEG FAMEGATWFT	360	
ERLYRSSAAL VHYLABKYDI PLDRAHIIIGH DEIPGLTPAR QGVMHODPGP FWDWEHYMEL	420	
VGAPIHSKHG TKDIVTIKPG FKTNQPDIND APAQPSNFLY LYKEPDFNAE LIIDDPALVSQ	480	
NIKKDGFISIGA KATIGOTFSL AGKQGDWTAI WFGQQKAWFY NPKGKNTVSG KGMLVTPKAG	540	
AASIPVYGAAYPEAAAYPAD ITPNVLVPLQ YTISHGQSYV AVEKNKSDDY YAPVYTNPDY	600	
ATNKLIKSKE EFYRIYFNHR FAFVKASDVE KVRKQSVNET TRQDIP	646	
SEQ ID NO: 69	moltype = AA	length = 610
FEATURE	Location/Qualifiers	
source	1..610	
	mol_type = protein	
	organism = Paenibacillus pini	

-continued

SEQUENCE: 69
 VPSVYABQDK TNSLQQAFES AAKEFGVPVS ILMSVSYNLT RWEHHHGQPS TSGGYGIMHL 60
 TDLPVQDKED HNGTDDEENP STSDDPSVHT LSAAAQLLLN DPDLLKQDPV CNIRGGAIL 120
 AKYAQETLGLK LTASESDWYG GVAKYSGSQD SGASLEFANN VFDTIQQGIS RQTSEGQMLR 180
 LPSKEVKPNL DTQTLHLRP SKPDNVECP RLHCRSPAA YQONGDDPSD YSNYDLADRP 240
 KFGPDIFYIV IHDTEETYQD TLNIFTNPNS NVSAHYVLRS SDGQITQMVTL TKDVPWHAGN 300
 WYFNMHISGV EHEGFAMEGA TWFTERLYRS SAALVHYLAE KYDIPLDRAH IIGHDEIPGL 360
 TPARQGVMMHQ DPGPFWDWEI YMELVGAPIH SKHGTKDINT IKPGFKTNQP DINDAPAQPS 420
 NFLYLYKEPD FNAELIDDP A LVSNKKDGF SIGAKATIGQ TFSLAGKQGD WTAIWFGGQK 480
 AWFYNTPKGKN TVSGKGMLVT PKAGAASIPV YGAAYPEAAA YPADITPNVL VPLOYTISHG 540
 QSVVAVEKNK SDDYYAPVYT NDPYATNKLI KSKEEFYRIY FNHRFAFVKA SDVEKVRKQS 600
 VNETTTRQDIP 610

SEQ ID NO: 70 moltype = DNA length = 711
 FEATURE Location/Qualifiers
 sig_peptide 1..60
 mat_peptide 61..708
 source 1..711
 mol_type = genomic DNA
 organism = *Bacillus cohnii*
 CDS 1..708
 SEQUENCE: 70
 atgaaaatag tagcaacttt tttatgtta tttatttttgc tctgtgggtt tc当地aggct 60
 gaagtccaca atgtcgagag tgatgagaca atatcattag tt当地aaaaga agatgaatta 120
 acttataaaa agccagatac aaatccgagt gaatctttat atgttaacttc gtactattha 180
 cctaaccata attcgcgcac gagaacagca gaagttcacac atataatgtat tc当地acc 240
 agtaacccgcg caaggaaatcc acacaaaccgc tatgttaatggc agatattttc cgcaactgtt 300
 gaagaaatatg cgtgttcacg acatattattt attgtatcgcc aaggtaatatttcaatttt 360
 gtgtgatgaga gttagatggc gtttcatgca ggaaaaggaa acgattttaa ct当地ttggac 420
 taccggaaata acatgaatga atatccaatggtacgaaatggc当地ttggcaat tggaaacgaaa 480
 gaagaaatatg gc当地ttggaaatggc acaggaaatggc caataacgaaatcc accatata 540
 ggttatacag atgagcaata tc当地cttgc当地ttggaaatggc atgatgacgtt gtatgacgtt 600
 tattccaaagg tattaaaaaa cagagagaac gtatgacgtt ttgggttctg a 660
 cggaaatccatc ct当地cttgc当地ttggaaatggc ttggataaaaa ttgggttctg a 711

SEQ ID NO: 71 moltype = AA length = 236
 FEATURE Location/Qualifiers
 source 1..236
 mol_type = protein
 organism = *Bacillus cohnii*
 SEQUENCE: 71
 MKIVATFLCV FIFVCGCSKA EVTNVESDET ISLVKKEDEL TYKKPDTNPS ESLYVTSYLL 60
 PNDNSRRRTA EVTHIMIHYT SNAARNPQNP YVIEDIYALF EYGVSAHYI IDREGNIFQL 120
 VDESRAVFAH GKGNDLNFLD YRNMMNEYSI GIELMAIGTK EEMSLNLQEG QYELIPPSHI 180
 GYTDEQYHSL AKLLEDLYER YPKVLKNREN VVGHDEYAPV RKSDPGSLFD WNKIGF 236

SEQ ID NO: 72 moltype = AA length = 216
 FEATURE Location/Qualifiers
 source 1..216
 mol_type = protein
 organism = *Bacillus cohnii*
 SEQUENCE: 72
 EVTNVESDET ISLVKKEDEL TYKKPDTNPS ESLYVTSYLL PNDNSRRRTA EVTHIMIHYT 60
 SNAARNPQNP YVIEDIYALF EYGVSAHYI IDREGNIFQL VDESRAVFAH GKGNDLNFLD 120
 YRNMMNEYSI GIELMAIGTK EEMSLNLQEG QYELIPPSHI GYTDEQYHSL AKLLEDLYER 180
 YPKVLKNREN VVGHDEYAPV RKSDPGSLFD WNKIGF 216

SEQ ID NO: 73 moltype = DNA length = 1356
 FEATURE Location/Qualifiers
 sig_peptide 1..78
 mat_peptide 79..1353
 source 1..1356
 mol_type = genomic DNA
 organism = *Kribbella* sp.
 CDS 1..1353
 SEQUENCE: 73
 atgagtcaca aagttccccag actggtcgcgtt gtcgtccggc cggcgccact ggccttcagg 60
 ggcgtccccc gcaacgcata cacggccgtc gagacccggca gcacccgtc gctgtccgg 120
 gcccggca gggccggcgc ccgtacgac gtaccggcgtt agctctgtt cggcatccgg 180
 tacggccagt cgcacccgtc cggccacgc ggtcagccca gccaggccaa cgggtacggc 240
 gtcacccgtt cggccggca cccggccactt cccggccactt cggaggccgc gaagtcacc 300
 ggcgtccccc tccggccggca gggccaggac gagacccggca acgtgtccgg cggccggcc 360
 gtacttcggc cgtacccgtc caaggccggc ctgcaaggccgaa acacccgtc cggcatccgg 420
 aagtggtaacg aggtcgctgc ccgtactcg cactccggc acggccggc cggccggcc 480
 tacaccggac aggtctaccg gatcgctggc ctcggccgtt cggccggca aggctccacc 540
 cagccggcata aggtgacccgc ggacccggc aagtacccgtc acgtccggcc cggccggcc 600

-continued

ccggacgcggg	cctcgatcca	ggccgtcgac	taccggggcg	cgatctggaa	cgcggccagc	660
accaggcaact	accgcgtcg	acgcacccctcc	gcgatcagcga	cgatcgat	ccacgtgacc	720
caaggcgtcg	acgcggcgcac	gatcagctgg	ttcaagaacg	cgtcggcgca	ggtcagcgcg	780
cactacgtgg	tgcgttccag	cgacgggcag	atcacccaga	tggtggcga	gaaggacacc	840
gcctggcagc	cccgcagcgc	gaacccgtac	tcggtcggca	tcgagcacga	gggctgggtc	900
gaccgcgcgt	cggtggtcac	cgacgcgtat	tacccgcgt	ccgcggcgct	gaccggcaac	960
atcgcgcacc	ggcgcggcat	ccgaaagacc	cgagatc	tcagggcca	cagcggatg	1020
cccgacaca	accacaccga	ccccgggtcg	aacttggaa	ggacactata	catcgactg	1080
gtgaacggca	gcaacccgaa	cccgcgcagc	tacaacttca	ccacgtacgg	cagtgggtc	1140
cgggtccgcgt	cgacgcgcga	gctgaccgcg	tcacatcgta	ccacccgtcc	cggccgcagc	1200
cagggtttcg	tcacatcgca	gaagcaggcg	gacttgttca	ccggcgagg	caccagcaac	1260
aactgggtgt	ccaaatcg	cgacccggc	ggctacatca	ccaaatctca	catcgaccac	1320
cccgacgc	ccgcgcggg	cgccccgtc	tgctgt			1356

SEQ ID NO: 74 moltype = AA length = 451
 FEATURE Location/Qualifiers
 source 1..451
 mol_type = protein
 organism = Kribbella sp.

SEQUENCE: 74
 MSHKVPRLVA VLAAGALAFS ALPSNASTPV ETGSTSTLSE AFKTAATQYD VPRELLVGIG 60
 YAESHLDGHG QOPSQANGVY VMHLASNPNSN PTMSEAALKT GLPVEKLAKD ESANVLGAAA 120
 VLDAYADKAG LQGQTRDDIG KWYEVVAQYS HSADGPTARL YTDEVYRIVG LGVGAEGVST 180
 QPKVKTDRKG QYANVAPLGT RTPASIQAVD YPGAIWNAAS TSNYRVGRTS AISTIVIHVT 240
 QGSYAGTISW FKNASAQVSA HYVVRSSDQQ ITQMVAEKDT AWHARSANPY SVGIEHEGVW 300
 DQPSWFTDAM YRASAAALTRN IADRRGIPKT RTYIKGHSEM PDNDHDPGP NWNNWTYYMQL 360
 VNGSNNPNPPT YNFNTTYGSGV RVRSDAKLT A SIVTTLPGPT QVFVTCQKQG DLVTAEGTSN 420
 NWWSKLRLDQG GYMTNIYIDH PDAKLPGPVPC 451

SEQ ID NO: 75 moltype = AA length = 425
 FEATURE Location/Qualifiers
 source 1..425
 mol_type = protein
 organism = Kribbella sp.

SEQUENCE: 75
 STPVETGSTS TLSEAFKTAQ TQYDVPRELL VGIGYAESHL DGHGDQPSQA NGYGVMLAS 60
 NPSNPTMSEA AKLTGLPVEK LAKDESANVL GAAAVALDAYA DKAGLQGQTR DDIGKWYEVV 120
 AQYSHSADGP TARLYTDEVY RIVGLGVGA GVSTQPVKVT PDRGKYANVA PLGTRTPASI 180
 QAVDYPGAIW NAATSNSYRV GRITSQSYAG TISWFKNASA QVSAYHVRS 240
 SDGQITQMV A EKDTAWHARS ANPYSVGIEH EGWVQDQPSWF TDAMYRASAA LTRNIADRRG 300
 IPKTRRTYIKG HSEMPNDHT DPGPNWNWYT YMQLVNGSNP NPPTYNFTTY GSGVVRVRSDA 360
 KLTASIVTTL PGPTQVFVTC QKQGDLVTAE GTSNNWWSKL RDQGGYMTNI YIDHPDAKLP 420
 GVPVC 425

SEQ ID NO: 76 moltype = DNA length = 990
 FEATURE Location/Qualifiers
 sig_peptide 1..75
 mat_peptide 76..987
 source 1..990
 mol_type = genomic DNA
 organism = Bacillus sp.
 CDS 1..987

SEQUENCE: 76
 atgaaaaggc tcgttcttgt attagtatac attggcgatc tttttatgag catttctcc 60
 gttcatacag ttgcagaaaa ccatacgatc ctgtatgtat tgagatccgg agatacatta 120
 tggaaatcgcc ccaataataa cggatcatct gtccaaatataa taaaagaaac aaatggattg 180
 caatctgttattttgtatgttgcggatc tttttgttc caatggatc tgaatcgat 240
 gctggagata cactttggaa gctttcaaga gcatataact cttccgttca agcgataaaa 300
 gcaacaaatg gacttgcatac ggtatgttgcg tacataggcgg aaaagtggaa aattccctcc 360
 aagaaatattac ctatggatgg tcgtatgtt ctcatgcgcg gagggaaatt taaagactgg 420
 ttatataacc atgaattc acgaaacata agccttcattc aacagcacca cacgtggatc 480
 ccggctttagt gacatattaa tggccaaaat cactttcgat tgcttaagg gatggat 540
 tattcatacga aagaatgtggg ctggaaaaac attgcccaga acattacaac attccagac 600
 ggaaaaatag ccgtatctcg accatattaaac agtgcttcgt acggctccgtat tggtccaaag 660
 gcaaaattctg ttgggttaaa catgcacatc gttggaaat tggacttaagg caatgatcaa 720
 atgactgcgc aacataggaa aacgattatc tatcttacgg cattgttgcgat tattttttt 780
 gggtttaactc cttctgttgc cagcatcaca tatcatcgat ggtggatataa gaacacaaag 840
 gagagagatgt tggatcgaag tgaaggagtt tctgtaaaaa catgcccagg aacgggat 900
 ttccggagggaa atacaacaga aagtgcggaa aataattttt atcctttatgt gtcacgtaaa 960
 atgcaagaga ttagggatc catgaattaa 990

SEQ ID NO: 77 moltype = AA length = 329
 FEATURE Location/Qualifiers
 source 1..329
 mol_type = protein
 organism = Bacillus sp.

-continued

SEQUENCE: 77
 MKRLVLFMSIPI AVTVAENHSN LYDVRSGDTL WKIANKYGTS VQNLKETNGL 60
 QSDLLLVLVQR LFVPMRYEVV AGDTLWKL SR AYNSSVQAIC ATNGLTSVLY YIGQKLKIPP 120
 KKLPMDCQYV LMTREEFKDW LFNHEFTRNI SLIQQQHHTWS PAYGHFNGKN HFSLLKGMEY 180
 YHTKEVGWEN IAQNITTTFPD GKIAVS RPFN SAPDGSIGPK ANSVGLNIEH VGNFDLGNDQ 240
 MTAEHRETII YLTALLCMKF GLTPSVDSIT YHRWWDMNTK ERVLDRSEGV SVKTCPGTGF 300
 FGGNTTESAK NNFYPLVSRK MQEIRASMN 329

SEQ ID NO: 78 moltype = AA length = 304
 FEATURE Location/Qualifiers
 source 1..304
 mol_type = protein
 organism = *Bacillus* sp.

SEQUENCE: 78
 ENHSNLYDVR SGDTLWKIAN KYGTSVQNLK ETNGLQSDL LVGQRLFVPM RYEVVAGDTL 60
 WKLRSRAYNS VQAICATNGL TSDVLYIGOK LKIPPKLPM DGQYVLMTR EFKDWLFNHE 120
 FTRNISLIQO HHTWSPAYGH FNGKNHFSLL KGMEEYYHTKE VGWENIAQNI TTFPDGKIAV 180
 SRPFNSAPDG SIGPKANSVG LNIIEHVGPNF LGNDQMTAEH RETIILYLTA LCMKPLTPS 240
 VDSITYHRWW DMNTKERVLD RSEGVSVKTC PGTGFFGGNT TESAKNNFYP LVSRKMQEIR 300
 ASMN 304

SEQ ID NO: 79 moltype = DNA length = 993
 FEATURE Location/Qualifiers
 sig_peptide 1..72
 mat_peptide 73..990
 source 1..993
 mol_type = genomic DNA
 organism = *Bacillus* sp.
 CDS 1..990

SEQUENCE: 79
 atgaagaaaa accttgcctt cattttgtat ttaatcccaa tcataattcat gaatatcctt 60
 ctctgttcacg cgatttcaaa taaccatagc aacctttatg tagtaaaaagc tggagataca 120
 ttacactgaaa ttgcacataa attcgatact accatagagg agttgaagct aacaaatgg 180
 ttgcacatccg attctctatt ttgttgcacaa aaatttatggg ttccctattat gcatgaagtt 240
 gttagcaggaa aacacactgca ggacatttgc tcaacttacc attcttcaat agaaaaccata 300
 aaaaaggccaa atggactcgt ttcttgatgatgatcataatggcggcaatattt aaaaaggtaact 360
 cctaaaaaaa tgatcatgca aggtcaacat atccttgcataa caaaggaaatgatcataatgg 420
 tgggtgttta acaaccaatt taatcgatcatttccaaaca tcacacatgg 480
 ttacattcttta aaaaaaaaaaaatggatcataa aaccattttc aatatttttcaatggatcataatgg 540
 aatatttcata aaaaaaaaaatggatcataa aaccatggcc aaaaatataac gacccccc 600
 gatggaaaaat tagcaatcataatggatcataatggcc cagaaggatc aatggatcataatgg 660
 aaggcgaatt cagtagggct aaccatcgaa aatattggta actttgatcataatggatcataatgg 720
 gtaatgcacca aaaaaacacgca ggatcataatggatcataatggcc cttgtatcataatgg 780
 ttccggcttta ccccttcaat tgacatgttacttattatcataatggatcataatggatcataatgg 840
 aaggaaagat tattatcataatggatcataatggcc cggatcataatggatcataatggatcataatgg 900
 tttttccggat gcaatgccac taacatgatcataatggatcataatggatcataatggatcataatgg 960
 aagatagaag aatattgtatcataatggatcataatggatcataatggatcataatggatcataatgg 993

SEQ ID NO: 80 moltype = AA length = 330
 FEATURE Location/Qualifiers
 source 1..330
 mol_type = protein
 organism = *Bacillus* sp.

SEQUENCE: 80
 MKKNLVLICL LILIIIFMNL PVHAISNNHS NLYVVKAGDT LPEIADKFDT TIEELKLTNG 60
 LQSDSLFVEQ LKWVPIMHEV VTGETLQDIA STYHSSIETI KKANGLVSDE LYAGQILKVT 120
 PKKMIMOCQH ILMTKEEFKD WLFFNNQFNRD IRIIQHHHTW LPSYKQFKGT NHFQMLQSM 180
 NFHKKEMGWH NIAQNITTTFP DGKAVASRPF NIAPEGSIGS KANSVGLTIE NIGNFDLGHD 240
 VMTKEQODTI VYITALLCIK FGLTPSIDSI TYHHWWNLQT KERVLDNGPD YNVKTCPGTN 300
 FFGGNATNDA KKHFYPLVSA KIEEIVATMD 330

SEQ ID NO: 81 moltype = AA length = 306
 FEATURE Location/Qualifiers
 source 1..306
 mol_type = protein
 organism = *Bacillus* sp.

SEQUENCE: 81
 ISNNHSNLYV VKAGDTLPEI ADKFDTTIEE LKLTNGLQSD SLFVEQKLWV PIMHEVVTGE 60
 TIQDIASTYH SSIETIKKAN GLVSDELYAG QILKVTPKMM IMQGQHILMT KEEFKDWLFN 120
 NQFNRDIRII QQHHTWLPSY KQFKGTNHFQ MLQSMENFH KEMGWHNIAQ NITTFPDGKV 180
 AVSRPFIAP EGGSIGSKANS VGLTIEENIGN FDLGHVDVMTK EQQDTIVYIT ALLC1KFLT 240
 PSIDSITYHH WWNLQTKERV LDNGPDYNVK TCPGTNFFGG NATNDAKKH YPLVSAKIEE 300
 IVATMD 306

SEQ ID NO: 82 moltype = DNA length = 990
 FEATURE Location/Qualifiers

-continued

sig_peptide	1..69	
mat_peptide	70..987	
source	1..990	
	mol_type = genomic DNA	
	organism = <i>Bacillus</i> sp.	
CDS	1..987	
SEQUENCE: 82		
atgaaaaggc tcgttcttgt agtagttta attgccatac tttttgttag catttcttct 60		
gtttctcgag ctgcggaaaa ccatacgaaat ctgttatgtg tgagatctgg agatacatta 120		
tggaaagatcg ccaataataa ttggatcatct gtccaaaat taaaagaaac aaatggactg 180		
caatctgtt gtcgtttagt ttggaaagaat ttgtttgttc caatgagcta cgaagtctgt 240		
tctggagata cactttggaa gcttccaaga gcatataat cttcagtccca agcaataaaa 300		
gaaacaaaatg gacttacatc ggatgtttagt tacatagggg aaaagttaaa aatccctcct 360		
aagaaattac ctatggatgg tcgttatgtt ctcatgacgc gagaggaaatt taaagatgg 420		
tttattttaacc atgaatattac gagaacatac aeccttattt aacagcacca cacgtggctg 480		
cccgccatgt gocatTTAA ttggaaacaat cactttctgt tacttaaggg aatggagat 540		
tatcatacga aagaagtggg ttggggaaat atagctcaga accttacaaac attcccccgt 600		
ggggagaatag cagtctctag gccatTTAA agtgctccgg atggtagtat tggaccaaaa 660		
gctaactcga taggattaaa catcgaaatc atcgggaaatt ttgatTTAGG taatgatcaa 720		
atgacagctg aacatcaga aacattatc tatcttacgg cttgtctatg tatgaatggc 780		
ggattaactc cttcttattga cagcatcaca tatcatcggtt ggtgggatatacaca 840		
gagcgtgtgt ttggatcgaag tgaaggagtt ttgtgtggaaat ttgtgtccagg tactggatt 900		
ttcggcggga atacgacaga aagtgtcaag agtaatTTT atcctttagt gtcacgtaaa 960		
atagaagaga tttagagcaac ttgtgtttaa 990		
SEQ ID NO: 83	moltype = AA length = 329	
FEATURE	Location/Qualifiers	
source	1..329	
	mol_type = protein	
	organism = <i>Bacillus</i> sp.	
SEQUENCE: 83		
MKRLVLVDSL IAIILFVSISP VSAAAENHSN LYDVRSGDTL WKIANKYGTS VQNLKETNGL 60		
QSDLLLVGQR LFVPMYSYEVV SGDTLWKLRSR AYNSSVQAIC ETNGLTSDVL YIGQKLKIPP 120		
KKLPMMDQYV LMTREEFKDW LFNHFEFTNRN SLIQQQHHTWS PAYGHFNGNN HFSLLKGMEY 180		
YHTKEVGVEN IAQNLTTFPD GRIAIVSRPFN SAPDGSIGPK ANSICLNIIEH IGNFDLGNQ 240		
MTAEHRETII YLTALLCMKF GLTPSIDSIT YHRWWDMNTK ERVLDLRSEGV SVKTCPTGTF 300		
FGGNTTESAK SNFYPLVSRK IEEIRATLN 329		
SEQ ID NO: 84	moltype = AA length = 306	
FEATURE	Location/Qualifiers	
source	1..306	
	mol_type = protein	
	organism = <i>Bacillus</i> sp.	
SEQUENCE: 84		
AZENHSNLYD VRSGDTLWKI ANKYGTSVQN LKETNGLQSD LLLVGQRLFV PMSYEVVSGD 60		
TLWLKLSRAYN SSVQAIKETN GLTSDVLVYIG QKLKIPPKKL PMDGQYVLMT REEFKDWLNFN 120		
HEEFTRNISLI QOHHTWSPAY GHFNGNNHFS LLKGMEYYHT KEVGWENIAQ NLTTFPDGRI 180		
AVSRPFPNSAP DGSIGPKANS IGLNIEHIGN FDLGNDQMTA EHRETIYL ALLCMKFGLT 240		
PSIDSITYHR WWDMNTKERV LDRSEGVSVK TCPGTGFFGG NTTESAKSNF YPLVSRKIEE 300		
IRATLN 306		
SEQ ID NO: 85	moltype = DNA length = 2004	
FEATURE	Location/Qualifiers	
sig_peptide	1..105	
mat_peptide	106..2001	
source	1..2004	
	mol_type = genomic DNA	
	organism = <i>Streptomyces</i> sp.	
CDS	1..2001	
SEQUENCE: 85		
atgaaaaggc cggtggggaa aattgtcgca agcacccgac tactcatttc ttgtgttttt 60		
agttcatcgat tagcatcagc acatcatcat caccatcatc cttagggacga cgacacccggc 120		
gtgtctccagg cggcggttcgc cgacccggcc gagcgctacc aggtggggaa ggaagtgtgt 180		
cttggcgctct cctatctccaa gtccggctgg gacggccacc gtggcgccggc gagcggtgacc 240		
ggggggctacg cggccatcgtca ttcgtacggac ggcgcacaccg cgtcgccggc ggaggccggc 300		
ggcggtggaca accacatct gcacccggggag gaggacccgc gggcgacga cggacgggtc 360		
cttgagatgc cggaggagga gatccccccg ttccggagcc gtcggaggt gcccggaaagg 420		
ctccagacgg tggaccgggc ggcggagctg accccggctcg accccggagga cctgcgggtcc 480		
agcaacccggc cgaacgtaca gggcgccggc ggcgtgtgttgg cgcggccgcgc ggcgcaccc 540		
ggcctggagc cgacgcacga cccggggacat ttgtacggcc cgtcgccctc ctacgcgggc 600		
tccgcctcgc gggaggccgc ggggttcttc gccgacgggg tttactcggt gataaacggag 660		
ggcgccggc acaccacccgg cgaggccggag gtggtggagcc tggccggccac cgagggtgacc 720		
ccgcgcacccg ggcaggcgtc cgcgtggcc ctggccggagca agccggcgca tccccgggtg 780		
gagtggccgc ccacgggttc tcgtcgatgg atccccgggg cctacggagga gtacggccgc 840		
ccgcacggctt cgggtacgtca cggcaaccac gacaaggccgg accggccggca cggcggccgg 900		
gtgcgttaca tcgtcatcca cgcacatggag ggctacttctt ggcggccat cggactgtgt 960		

-continued

cagaaccgaa	cctggcgctc	ctggcagta	actgcctccagg	cgteggacgg	gcacatcgcg	1020
cagcacatcc	tggccaagga	cgtcgctgg	caggccggca	actggtagct	caacggccacg	1080
tccatcgccc	tggagcacga	gggttctctg	cggggccccgg	acgcctggta	caccggagggt	1140
atgttaccgc	cctcgccgcg	gctggtgccg	tacctggccc	ggcagcacga	catcccgtcg	1200
gaccggcacc	acatcatcg	ccactacaac	gtggcgggca	tcggcaccgc	caacatcccc	1260
gggatgcaca	ccgaccggcg	tccgtactgg	gactggggcgc	actacttcgg	gtgtatggc	1320
gcgcgcgatca	cgcccgacgc	ccggccgcac	agcgcgcgtgg	tgacgtacgc	tcccgactac	1380
gacaaccacc	gcccggttgt	cacccgctgc	gacccggccgg	acgcgcgcgc	gccgtgcgcg	1440
ccgcacggct	ccagcgccgt	geggctgcac	gtggcgccga	gtcatgacgc	ggcgctgggt	1500
ccggacatcg	ggccatcccg	ggcagcggc	ggccgggtccg	gatctcgat	ctacgacatc	1560
ggccggcccg	cctcgaccgg	ccacgatcg	gccccggccgg	cgagtggacg	1620	
gegatctgtt	tcaacggcg	gaaggccgtg	ttccacgacc	eggccggca	gcccggctcg	1680
gtcccgagcc	ggggctggat	cgccaccccg	aaggaggccg	tggacccgggt	gcccgttac	1740
ggcgctggcg	acccggagcc	ggggactac	ccggccggccg	tgccggtgccg	ccgcgtcgcg	1800
ccgcgtcccg	accaggatc	ggccggtccg	tegtacggcg	ttggggcgccg	ccggcaggcg	1860
ttcgacgggg	agtttactc	ggcggcccg	ttcgcacccg	ttggcggccg	gggtatccgg	1920
gggcagcggt	actaccagat	ccagtcgc	cacccggacg	cgatgtgaa	ggcggaggac	1980
gtggacgtgg	tgcccggtcg	ctgaa				2004

SEQ ID NO: 86 moltype = AA length = 667

FEATURE Location/Qualifiers

source 1..667

mol_type = protein

organism = *Streptomyces* sp.

SEQUENCE: 86

MKKPLGKIVA	STALLISVAF	SSSIASAHHH	HHHPRDDDTG	VLIQAAFADAA	ERYQVPEEV	60
LGVSYLNQSRW	DGHRGAAASVT	GGYGPMLTD	AHTALSREAG	AVDNHHLHGE	EDPRGDDGRV	120
LEMPEEEIPP	VPERSEVPER	LQTVDRRAEL	TGLDPEDLRS	SNAANVQGGA	ALLAAAQRDL	180
GLEPSSDDPAD	WYAAVASYAG	SASREAARFF	ADEVYSVINE	GARHTTGEQQ	VVELPATEVT	240
PTRGQASALA	LPEQRRDPRV	ECPPTVSCEW	IPAAYEYEEYR	ADGSVTYGNH	DKGDRPDGQR	300
VRYIVIHDME	GYFWPSIGLV	QNPTWASWQY	SLQASDGHIA	QHILAKDVGW	QAGNWYVNAT	360
SIGLEHEGFL	RAPDAWYTEV	MRSSARLVR	YLARQHIDPL	DRHHIICHYN	VPGIGTANIP	420
GMHTDPGPYW	DWAHYFRLMG	APITPSARPH	SVLTIKPVDY	DNHRPVFTGC	DPADAAAPCA	480
PHGSSAVRLH	VAPSHPDAALV	PDIHGTHPGSG	GRSGISIYDI	GARASTGQQY	AVAERAGEWT	540
AIWFNGEKAW	FHDPARQRTS	VPSRGWIATP	KEGVDRVPVY	GVAYPEPEDY	PPGVPVRAFA	600
PLPYQFTAGQ	SYAVGRGGEA	FDGEFYSATR	FDTVGSQVIR	QGRYYQIQLG	HRHAYVKAED	660
VDVVPV						667

SEQ ID NO: 87 moltype = AA length = 632

FEATURE Location/Qualifiers

source 1..632

mol_type = protein

organism = *Streptomyces* sp.

SEQUENCE: 87

DDDTGVLQAA	FADAARYQV	PEEVLLGVSY	LQSRWDGHGR	AASVTGGYGP	MHLTDAHTAL	60
SREAGAVDNH	HLHGEEDPRG	DDGRVLEMPE	EEIPPVPER	EVPERLQTV	RAAELETGLDP	120
EDLRSSNAAN	VQGGAAALLAA	AQRDLGELPE	DDPADWYAAV	ASYAGSASRE	AARFFADEVY	180
SVINEGARHT	TGEQGVVLEP	ATEVTPTRGQ	ASALALPEQR	RDPRVECPPT	VSCEWIPAA	240
EHEYERADGSV	TYGNHDKGDR	PDGQRVRYIV	IHDMEGYFWP	SIGLVQNPWT	ASWQYSLQAS	300
DGHIAQHILA	KDVGWQAGNW	YVNATSIGLE	HEGFLRAPDA	WYTEVMYRSS	ARLVRYLARQ	360
HIDPLDRHII	IGHYNVPVG	TANIPGMHTD	PGPYWDWHAIG	FRLMGAPI	SARPHSALVT	420
IRPDYDNRH	VFTGCDPADA	AAPCPAGHSS	AVRLHVAPSH	DAALALVPIGT	HPGSGGRSGI	480
SIYDIGARAS	TGQQYAVAER	AGEWTAIWFN	GEKAWFHDPDA	RQRTSVPSRG	WIATPKEGVD	540
RVPVYGVAYP	EPEDYPGPV	VRAFAPLPYQ	FTAGQSYAVG	RGGEAFDGEF	YSATRFDTV	600
SQVIRGQRYY	QIQLGHRAY	VKAEDVDV	VR			632

SEQ ID NO: 88 moltype = DNA length = 723

FEATURE Location/Qualifiers

sig_peptide 1..72

mat_peptide 73..720

source 1..723

mol_type = genomic DNA

organism = *Bacillus* sp.

CDS 1..720

SEQUENCE: 88

atggtaagaa	acttaggaat	aatataactc	attgttaacct	tatTTTTAAT	aggatgcaca	60
acagctgaaa	atcccAACAC	gatcgaaaa	gacacattac	aagcaatgga	agattcgaa	120
atagagaaga	aggacttgat	gcttcagtcg	gccccggacaa	gaaacgataa	taatcccgt	180
gattatctc	taccaactgga	aaactccaaa	cccgccggacgg	aggcaatcac	ccatgtcatg	240
gttcatttta	taagcaatgc	tgcgagaaa	ccagaagatc	cttataatac	tattgtatc	300
tatTCATT	ttgttggata	tgggtgtca	gacattata	tgtatggaa	agatggacaa	360
gtgtttcggc	ttgttatcaga	agatcggtc	gcttatcatg	ctggggcagg	agagcttga	420
gattatctc	actatacgga	cagcttaat	gaattttcga	taggtattga	actcttgc	480
atcggacta	ggaaagagat	gtttctgt	ataccagta	gtgtctacaa	tgtatagat	540
ccaagat	taggtatac	agatgaacaa	tacgaatcg	ttaacgttt	attggatgt	600
atTTCCAGA	gaaaccatc	aataaaataga	gatagaaatc	atgtgatttg	gcatgtatgaa	660

-continued

```

taggcacactg gaagaaaagc tgatccaggo tcattatttg attggctaa actcggtta 720
tag                                              723

SEQ ID NO: 89          moltype = AA length = 240
FEATURE                Location/Qualifiers
source                 1..240
mol_type = protein
organism = Bacillus sp.

SEQUENCE: 89
MVRNLGINIL IVTFLFLIGCT TAENSQTIKG DTLQAMEDSK IEKKDLMQLQS AETRNDNNPV 60
DYLLPLENSK PRTEAITHVM VHFISNAARN PEDPYNTIDI YSIFVEYGVs AHYMIGRDGT 120
VFLVLVSEDRV AHAGAGELE DYPDYTDLSN EFSIGIELLA IGTREEMFPA IPVRYVNVID 180
PRLVGYTDEQ YESLNVLDD IFQRNPSINR DRNHVIGHDE YAPGRKADPG SLFDWSKLGL 240

SEQ ID NO: 90          moltype = AA length = 216
FEATURE                Location/Qualifiers
source                 1..216
mol_type = protein
organism = Bacillus sp.

SEQUENCE: 90
SQTIGKDTLQ AMEDSKIEKK DLMLQSAETR NDNNPVDYLL PLENSKPRTE AITHVMVHFI 60
SNARNPDPD YNTIDIYSIF VEYVSAHYM IGRDGTVERL VSEDRVAYHA GAGELEDYPD 120
YTDSLNEFSI GIELLAIGTR EEMFPAAIPVr VYNVIDPRLV GYTDEQYESL NVLDDIFQR 180
NPSINRDRNH VIGHDEYAPG RKADPGSLFD WSKLGL 216

SEQ ID NO: 91          moltype = DNA length = 1002
FEATURE                Location/Qualifiers
sig_peptide           1..81
mat_peptide           82..999
source                 1..1002
mol_type = genomic DNA
organism = Bacillus sp.
CDS                   1..999

SEQUENCE: 91
atggtagatggatgtat agccgtttttt atttggtttc ttatgtatgac aggttttttg 60
aatttaccac aagcccaagc aatagcgcac aatcatagca acatttatga catcaaatca 120
ggtgatacat tggaaaaat agctaaaggc tatgggacaa ctgtgaaaga tttaaagcaa 180
acgaacggat taacctccga ttactttta ataggtaaa ggttggctgt acctatgaga 240
tatgaagtgc tctctggaga tacgatgttgg aaatttgcac agcaatacaa ctccacagta 300
ccgtcaaatca aatttgcacaa cggtttacca tcagatcatg ttatcatagg aaaaagggtg 360
aaaatccac aacgaaagtt acgaaatggat ggccaacatg tttaatgac aaaaaggag 420
tttagggcgt ggctatttaa tcaaaaaatc aaccgtataa ttctatcat ccaagaacac 480
cacacttgtt taccatgtt tagtgcgtt aatgaaacaa accatttcca actacttaaa 540
ggaatggatgatgtt gcatgaaatg ggttggagta acattgcaca gaataatcag 600
accttcccg atggaaacgtt ggcgttctt cgtccactaa acgtgcctcc agacggttct 660
attggaaattt acgcgaactc tatttgcatac aacattgaaa gctttaggaaa ttgcacata 720
ggaacatgc aatgttcaca ggcacaaaaaa gaaacatcatac tctatgttac tgcttctca 780
tcaattaaac taggcatttac gccatctt gacaccatca catatcacca ctggtggat 840
atgcgttacatg gttaaagatg gtttgcataa aacgaaatggat ttccgttcaaa aacatgc 900
gggacacatg tctttggcgg caatgcaca aaaatgtccca aaacaaactt ttatccactt 960
gtatctaaga aatagagaaa acaatggattt ag 1002

SEQ ID NO: 92          moltype = AA length = 333
FEATURE                Location/Qualifiers
source                 1..333
mol_type = protein
organism = Bacillus sp.

SEQUENCE: 92
MVRGICIAVF ICFLSMTGFL NLPQAQAIAH NHNSNIYDIKS GDTLWKIAQS YGTTVKDLQ 60
TNGLTSDELLL QHQRLFVPMR GLPQDMIYIG QKLKIPQRKL RMDGQHVLMT KEEFRGWLNF 120
KIPQRKLRMD QOHVLMTKER FRGWLFLNQKI NRNISIIQEH HTWLPDYSRF NETNHFQLLK 180
GMEYFHVHEM GWSNIAQNIT TFPDGTVAVS RPLNVPPDGs IGNYANSIGI NIESVGNFDI 240
GNDQMSQAQK ETILYVTTALL SIKLGLTPSI DTITYHHWWD MRTGKRVLDN NEGYSVKTCP 300
GTAFFGGNST KSAKTNFYPL VSKKIEEIKK TMD 333

SEQ ID NO: 93          moltype = AA length = 306
FEATURE                Location/Qualifiers
source                 1..306
mol_type = protein
organism = Bacillus sp.

SEQUENCE: 93
IAHNHSNIYD IKSGDTLWKI AQSYGTTVKD LKQTNGLTD LLLIGQRLFV PMRYEVVSGD 60
TLWKLSQLQYNT STVPSIKLAN GLPSDMIYIG QKLKIPQRKL RMDGQHVLMT KEEFRGWLNF 120
QKINRNISII QEHTWLPDY SRFNETNHQFQ LLKGMEYFHv HEMGWSNIAQ NITTFPDGTv 180
AVSRPLNVPP DGSIGNYANS IGINIESVGN FDIGNDQMSQ AKETILYVT ALLSIKLGt 240
PSIDTITYHH WWDMRTGKRV LDNNNEGYSVK TCPGTAFFGG NSTKSAKTNF YPLVSKKIEE 300

```

-continued

IKKTMD

306

```

SEQ ID NO: 94      moltype = DNA length = 1449
FEATURE          Location/Qualifiers
sig_peptide      1..87
mat_peptide      88..1446
source           1..1449
mol_type = genomic DNA
organism = Nonomuraea guangzhouensis
CDS              1..1446
SEQUENCE: 94
ttgaaggccc gactccgcca ttccggcggc ctgtggccgc ggcgcgtcat cccctctcg 60
ctgtctcgag ggcagccggc cggagccga tccgtgtatc ccatgagcga cgcgttcgcc 120
cgtgcggcoca ccacgtacga ggtggccgc gacctgtctgg ttcgtctcgc ctacgcggaa 180
accgcacccgg acggacaccg cggcgaaccc agegcgagcg ggggtacagg ggtgtatgcac 240
ctgtcaqca accccgtcqac gcacacgtc gacgcgcgcg ccaacgtqac gaagcagccc 300
gtctcggtt tgaaggcggc cgacgcggc aacatcacgg ggggcgcgc cgtgtgcgc 360
gcctacgcgc acggactcgg actggacgc gggggccgc aggaacgcgg caagtggat 420
caggcgggtt ccaagtacgg cggcgccttc tccggggacg tggccgggtt gtacccggac 480
accgtctacg accgtctgc ccaaggatc aaggtaacca cggccggccgg tgagacctc 540
acggcgacgc cgccggccgt ccagccccacg cggggctct acggcaaggc acaggagctg 600
ggcaagacca atacgtcgc ggcggcactgt gactaccgtt cggcggcgtg ggcggcggcg 660
cacagccaca actacgcgtt ctccaaaccc cccgaccatc cccgatcgtca ccgcacatc 720
atccacgtgg cccaggccac gtacgcgggg acgtatcgtact gttccagac cggggccagg 780
ccgaacccca cctgtcgca ctacgtcgcc cgttgcgtgg acggcgccgt caccaggatg 840
gtcagggaga aggacccggc ctteccacgcg ggcgactcca acaggcgctc ggtcggcatc 900
gacgacgggg gtcgggttgc gcacgcgttcc tgggttccacgg acacgtatgtt cccgttccctcg 960
ggccgcgtga cccgcaacat cccgcacagg tacggcatcc ccaaggaccc cacccacatc 1020
atccgcaca gggaggctcc cggggccagc cacaccgacc cccgttccggaa ctggaaactgg 1080
accaagtata tgcagtacgtt cacaacccgcg agcgggtggc gcaccaaccc gcacacccggc 1140
gagtccgtgt gggggccgtt ctteccacggg atcgtactcg cggcccttggg gacggcggcgc 1200
aacgtctacc tgcgtacaa ctccggcacc ggcggccaaatc ggcggccac gatcaactgt 1260
accaacccgcg acacggccac ggccaccaggc gccttccctgg aggtggaggcc cccagacacgc 1320
gtcaccgaca gcggttaactt cggctactac gcccggccgg tgccggccag cgcggccgac 1380
aagtgcgtct actggggccgg caaggccgtt acggccacctt acaacacccc cctcgaaacac 1440
tgccggtaa 1449

```

```

SEQ ID NO: 95      moltype = AA length = 482
FEATURE          Location/Qualifiers
source           1..482
mol_type = protein
organism = Nonomuraea guangzhouensis
SEQUENCE: 95
LKARLRHSAA LLAGALIPLS LLAGCPAGAA SADPMSDAFA RAATTYEVPR DLLVSLAYAE 60
THLDGHRGEPS SASGGYGVNMH LVSNPVRHTL ERAATLTQK VSALKADAA NITGAAVLR 120
AYADEGLDA AARKDAGKWW QAVAKYGGAS SADVARLYAD TVYDQLSQGI KVTPPAGETL 180
TATPRTVQPD RGSYAKAQEL GKTNTLAAA VDPSAAWAAA HSTNYAVSNR PTSDAIDRII 240
IIHVAQGTAG RSTDFWTGPRN PNPSSHYVV RSSDGAVTOM VREKDRAFHGA GDSNRRSVGI 300
EHEGWVEQAS WFTDTMYRSS AALTRNIADR YGIPKDRTHI IGHSEAPGAS HTDPGPWNW 360
TKYMQYVTNG SGGGTNPHTA ESVCGTGFTV IDSAPLGTAG NVYLTYNSGT GANCVATIKL 420
TNLGTATATS AYLEVEGQTR VTDGNGFYY AGPVVRASAAD KCVYWGKAG TATYNPLEH 480
CG 482

```

```

SEQ ID NO: 96      moltype = AA length = 453
FEATURE          Location/Qualifiers
source           1..453
mol_type = protein
organism = Nonomuraea guangzhouensis
SEQUENCE: 96
ASADPMSDAF ARAATTYEVPR RDLLVSLAYA ETHLDGHRGE PSASGGYGVNM HLVSNPVRHT 60
LERAATLTQK PVSAKADAA ANITGGAVAL RAYADEGLID AAARKDAGKWW YQAVAKYGGAA 120
SSADVARLYA DTVDQQLSQGK IKVTTTPAGET LTATPRTVQPD DRGSYAKAQEL LGKNTLAAA 180
VDYPSAAWAA AHSTNYAVSN RPTSDAIDRI IIHVAQGTAG GTIDWFQTGP RPNPTSSHYV 240
VRSSDGAVTQ MVREKDRAFH AGDSNRRSVG IEHEGWVEQA SWFTDTMYRS SAALTRNIAD 300
RYGIPKDRTHI IIGHSEAPGAS SHTDPGPWNW TWTQYVQVTN GSAGGTNPHT AESVCGTGFT 360
VIDSAPLGTAA GNVYLTYNNG TGANCVATIKL LTNLGTATAT SAYLEVEGQTT RVTDSGNFGY 420
YAGPVVRASAAD DKCVYWGKAG GTATYNPLEH HCG 453

```

```

SEQ ID NO: 97      moltype = DNA length = 1509
FEATURE          Location/Qualifiers
sig_peptide      1..87
mat_peptide      88..1506
source           1..1509
mol_type = genomic DNA
organism = Nonomuraea guangzhouensis
CDS              1..1506

```

-continued

SEQUENCE: 97

```

atgtcactct cccccaagcg attaacatct ctgcgtctttt ccgttcctcgc cgccctcctg 60
gtcttcgcgg gccagccccgc catcgccgc aaggacacac cgctatccga cgcttcgc 120
cgccgcgcgc cggccccagga catccccccgc gacctgtctg tcgcgtctcgc ctacgcgc 180
accacatgg acggccacaa cgccgcgcgc agccgcacgg cgggctacgg tttgtatgcac 240
ctggtcacca acccccacac gaaagcgctg gagaaggcgt cggggctcac cgggctgc 300
gtcaagaagt tgccgcggc aacatccctgg cggccgcgc actgtgcgc 360
gccaacgcgc accgatctgg cctggacgag gcccggcggg aggacccccc cccgtggta 420
gagtcgtgg ccaagttacgg caacgcgcgc tcggcccgatc ctacgcgcac 480
ggccgtctacg acgtgtctgg cctggacgatc cggcccaacgg acgtgtcggt ggccacccaa 540
gagggtgaccc cggacccggg caagttacggc gacacacccctt cgcttaaggc cgagggtggcc 600
agcccccaactt acccgacgc cgcctgggtt cccgcgaactt cggcgaacta caccgcctcc 660
agccggccgtt cgagatctacgc catcgaccgc gtatcatcc acgtggcgca gggctcgatc 720
ggccggacca tttccctgtt ccggaaacccgg agccggcaacgg ttcggcccca ctacgtgtc 780
aagtctgtt acggggccgtt caccggacgg agggccggc ctggcgcaca aggacgtcgcc 840
ggcaactgtt cttttttttt cttttttttt cttttttttt cttttttttt cttttttttt cttttttttt 900
gcctctgtgtt tcacggacgc gatgtaccgc tcctcgccgc cgctgacccaa gtatctgc 960
gacaagttacgc gatccctggaa ggccggcgcg cccatcatcc gccacacccaa ggtggccggc 1020
ggccacccacca cggacccggg tccggacttg aactggacca cgtatcatggaa ctacgtgacc 1080
gggtggccggc gacgcgcgtc gtggaccacc acggctcgaca acggccaccc cggacaggatc 1140
acccggacgc gaaactgggg cacccacccatc tactccaccc acgtgtacgg cgccggactac 1200
cggttgcgcg accccgtgtc cggccgtgtc gccggctgtt atcaggccgc cctcccccgc 1260
ggccggccatctt accggcggtt ggtctgtt ccggacgcac cgggttaccaa cagtcggcg 1320
ccctatcatcg tccggccctc cggccgcaccc cggacgggtt acgtggacca acgtccggc 1380
ggccggccatctt ggcacacgtt gggcaatttcc ttccctcaaccc cggggccaccgc caacgtgtt 1440
ggagtcaaccc ggtggccctc cggccacccggc ctcgttcatcc cggacggccgtt ccgcatacgc 1500
aagggtctga 1509

```

SEQ ID NO: 98 moltype = AA length = 502

FEATURE Location/Qualifiers
source 1..502
mol_type = protein
organism = Nonomuraea guangzhouensis

SEQUENCE: 98

```

MSLSPKRLTA LVSSVLAALL VFAGQPAIAA KDTPLSDAFA RAAAAQDIPR DLLVALAYAE 60
THLDGHNCEP SASGGYGVNMH LVSNPTTKAL EKASGLTGLP VKKLRADTE NILGAAALLR 120
ANADEGLDDE AARKDPGRWY ESVAKYGNAA SPQLARVYAD AVYELLGLGI QAKDVRVAPQ 180
EVTPADRGKYA DTPSLKAEV SPDYPDAAWV PANSGNYTAS SRPSSYAIIDR VIIHVAQGSY 240
AGTISWPQNP SANVSAYHVV KSSNGAVTQT VRDKDVWAHTV GNWSYNTRSI GIEHEGFVNNE 300
ASWFTDAMYR SSAALTKYIC DKYGIPKDR HIIIGHNQVPG ATHTDPGPNW NWTTYMNYVT 360
GGGGTPSWTT TVDNATSGQF TASANWGTST YSTQRYGADY RFADPVSASD AAWYQATLPS 420
AGTYRVEWY PDDAGYNSSA PYIVAASSGN QTVYVDQRSG GGSWHSLGNF SLNAGTANVV 480
GVSRWTSGT LVIADAVRIS KV 502

```

SEQ ID NO: 99 moltype = AA length = 473

FEATURE Location/Qualifiers
source 1..473
mol_type = protein
organism = Nonomuraea guangzhouensis

SEQUENCE: 99

```

AKDTPLSDAF RAAAAAQDIP RDLLVALAYA ETHLDGHNGE PSASGGYGVNM HLVSNPTTKA 60
LEKASGLTGL PVKKLRADTE ANILGAAALL RANADELGLD EAARKDPGRW YESVAKYGNAA 120
ASPLARVYDA VDYEGLGLG IQAKDVRVAP QEVTDGRKY ADTPSLKAEV ASPDYPDAAW 180
VPANSGNYTA SSRPSSYAIID RVIIHVAQGS YAGTISWPQNF PSANVSAYHVV VKSSNGAVTQ 240
TVRDKDVAWH AGNWSYNTRS IGEHEGFVN EASWFTDAMYR RSSAALTKYI CDKYGIPKDR 300
THIIGHNQVPG GATHTDPGPN WNWTTYMNYV TGGGGTPSWTT TVDNATSGQ FTASANWGT 360
TYSTQRYGAD YRFADPVSAS DAAWYQATLPS SAGTYRVEWY YPDAGYNNSS APYIVAASSG 420
NQTVYVDQRS GGGSWHSLGN FSLNAGTANV VGVSRTSGT GLVIADAVRI SKV 473

```

SEQ ID NO: 100 moltype = DNA length = 711

FEATURE Location/Qualifiers
sig_peptide 1..81
mat_peptide 82..708
source 1..711
mol_type = genomic DNA
organism = Bacillus cohnii
CDS 1..708

SEQUENCE: 100

```

atggaaaaaa tagcaactat cttatgtgtc gttatgttag tcaacgggtt ttcaaacgtt 60
ggaatccaa atgttgagag aaatggacca gtttcattttt tttaaaataaa agatgtatcc 120
acttataaaa agccaaatccaa atatccggatc gaaatcttac atgtatccctt ctactatcc 180
cctgacggaa attcggacgc aagaactgtca gaagtttacac atgtatgtat tcattttttt 240
agtaatgtcg agagaatccaa agagaatccaa tatgtttagt aagacattttt ctcgtgtttt 300
gaagaatatgt gctgttctgc acattatattt atgtatccggg aaggactat ctttcaattt 360
gtatgtatccaa gtagatgtac gtttcatccaa ggaaaaggaa tggatccaa ctacccatccaa 420
tacccaaatccaa gcatgtatccaa atattccaaatccaa ggtatccgtt ccgtttttttt 480

```

-continued

```

gaagaaaatga atttaaatgg gcaggaaagg caatacgaac taataccggc atccatatata 540
gggtatacag atgagaata tcacttatta gcaaaaactgt tagaagacct gtatgaggcg 600
tatccaaag tatttagaaaa cagagagaac gtatgaggc atgatgaata cgcacctgtt 660
cgaaaatcg acccttggaaag tttatggac ttggggaaaaaa ttgggttcgt a 711

SEQ ID NO: 101      moltype = AA length = 236
FEATURE           Location/Qualifiers
source            1..236
                  mol_type = protein
                  organism = Bacillus cohnii

SEQUENCE: 101
MKKIATILCV VMLVNGCSNV GITNVERNET VSLVKNKDEL TYKKPNTNPS ESLHVTPYYL 60
PDENSRRRTA EVTHVMYHT SNAARNPENP YVLEDIYSLF EEWGVSAHYI IDREGTIFQL 120
VDESRVAFHA GKGMDLNLYQ YRNSMNEYSI GIELMAITK EEMNLNLQEG QYELIPPSYI 180
GYTDEQYHSL AKLLEDLYER YPKVLRNREN VVGHDEYAPV RKSDPGSLFD WEKIGF 236

SEQ ID NO: 102      moltype = AA length = 209
FEATURE           Location/Qualifiers
source            1..209
                  mol_type = protein
                  organism = Bacillus cohnii

SEQUENCE: 102
NETVSLVKN DELTYKKPNT NPSESLHVT P YLDPDENSRR RTAEVTHVMI HYTSNAARNP 60
ENPVLEDIY SLFEYGVSA HYIIDREGTI FQLVDESRRVA FHAGKMDLN YLQYRNMSNE 120
YSIGIELMAI GTKEEMNLNL QEGQYELIPP SYIGYTDEQY HSLAKLLEDL YERYPKVLRN 180
RENVVGHDEY APVRKSDPGS LFDWEKIGF 209

SEQ ID NO: 103      moltype = DNA length = 918
FEATURE           Location/Qualifiers
sig_peptide       1..72
mat_peptide       73..915
source            1..918
                  mol_type = genomic DNA
                  organism = Halomonas sp.
CDS               1..915

SEQUENCE: 103
atgcgcgcgt ttttcgtcgt cactctcgcc atgctgggtc tgctggccgg ctgcgcac 60
ccggagcaat acgagccggcg tgacggctat gtgggtggacc acacccatgt gtgcgcctcc 120
cacaacaccc gggtaacggca tctgtgtat cactacccg atgtggacga ggccgaatcc 180
ctggcgaccc tgaccgtcc ccatgttcgcg agccactacg tgcgcgcgt accggcacgg 240
gcacatcgcc gggagccgcgt ggttacccag ctgcgtcgcg aggagccgcgg cgccgtggac 300
ggccggggcca ggcgcctggaa ggcgcgcacc aacatcaacg acacccatcat cggcatcgag 360
atcgatcaata cccggccgcg cccgcgcctac ggcggagggtgg agcgggggcgt ggaggagcac 420
ccggaaacgc atccgcgcat ccactggggc ccctacccccc aggacacat cgaggcgctg 480
atcgccctgt cgcggatata catcgcgcg aacaatattt accttacccga cgtgggtggcc 540
cactcgata ttcgcgcac ggcgaagatc gacccggggc cggcggtttcc ctggcatgcc 600
ctgtacaaag cgggtatccg cgtatggccc gaagcagccg cctgtggacacg ctatcgaccc 660
cgcttcgcgatc aggccgtccg cgaactcgcc accttcgcgg cggcgctcc ggcctggggc 720
tatccgtcgg cggtcagcga cgaactcgat tcacagactc ggcgcgtact ggcgcgcctc 780
cagatgcgcgt ttctggccgc cgaactatcgat ggccggccgg acgcgcgagac tgccggcgatc 840
ctctgggcac tgctggaaag atatcgcccc ctcgacccgttgg agccgggtcga gggggcgatc 900
gaagagccgg aggcatga 918

SEQ ID NO: 104      moltype = AA length = 305
FEATURE           Location/Qualifiers
source            1..305
                  mol_type = protein
                  organism = Halomonas sp.

SEQUENCE: 104
MARFFVVTLA MLVLLAGCAT PEQYERRDGY VVDHHTHVSPS HNSRVRHLVM HYTDVDEAES 60
LATLTGPHVS SHYVLPLPAR AHRGEPLVYQ LVDERRAWH AGASAWKRRT NINDTSIGIE 120
IVNTGPDRPY AEVERALEEH PESDPAIHWA PYPEAQIEAL IALSRSIIITR NNIHPTDVVA 180
HSDISPTRKI DPGPAPPWHA LYEAIGIVWP EAATVARYRT RFDQALPELA TLQAAQAWG 240
YPLAVSDELD SQTRAVLRAF QMRFRPADYR GRPDAETAAI LWALLERYRP LDLERFEGAM 300
EEPEA 305

SEQ ID NO: 105      moltype = AA length = 281
FEATURE           Location/Qualifiers
source            1..281
                  mol_type = protein
                  organism = Halomonas sp.

SEQUENCE: 105
ERRDGYVVDH THVSPSHNSR VRHLVMHYTD VDEAESLATL TGPHVSSHYV LPLPARAHG 60
EPLVYQLVDE ERRRAWHAGAS AWKRRTNIND TSIGIEIVNT GPDRPYAEVE RALEEHPESD 120
PAIHWAPYPE AQIEALIALS RDIITRNNIH PTDVVAHSID PTRKIDPGP AFPWHALYE 180
GIGVWPEAAT VARYRTRFDQ ALPELATLQA ALQAWGYPLA VSDELDSQTR AVLRAFQMRF 240

```

-continued

RPADYRGRPD	AETAAILWAL	LERYRPLDLE	RFEGAMEEPE	A	281
SEQ ID NO: 106		moltype = DNA	length = 1920		
FEATURE		Location/Qualifiers			
sig_peptide	1..171				
mat_peptide	172..1917				
source	1..1920				
		mol_type = genomic DNA			
		organism = Lysobacter capsici			
CDS	1..1917				
SEQUENCE: 106					
atgaacaaat atccactgc acgcccgtggg gtggtgaccg gctgttgttc gttgtcgcccc 60					
tctgtgaccg tcgtgtgct ggcgtcgcc gcgcattgg cccgcgcaggc gcaggcccg 120					
ccccaagac ggcgcctggc acacgcacctg cagatcgagg aatcgctgca acgcgtcgac 180					
cgcgcgtgtt acgcggacta ctccgcacg gctatcgccc gttaccgttc gatccggcc 240					
ggcacgtgg aatccatcgc ctacgtatg agccgtggc acaactgca gcccgcctcg 300					
gtcgccgcgtt acggcgaaca gcaccagcac atgcgcgtc cgtaacgggt catgggttg 360					
taccaacggc aagggttcgc cgtacaaatg ggcgaaggcg cgcgcgtgtat cgccgtccg 420					
gcgcgcgcgc tgcagcgca tccgttcgac aacatcctcg ctcgcggccg ctgtcgat 480					
cgcgagttgc ggcgcgacgg gateggcgcg aagtccggc tgcgacccac ggcgcggcg 540					
ctggagcggtt acgcgggtt cgccggcaat gcccccaaga gtgcgtatca ggatcaccc 600					
cgttccagggtt tccgttcgcg cgtgtgtgcg ggcgcaggaca aaggcgtcaa cgatcgccgc 660					
atcgctgtgc cgatgcgcgc ggtcggtgg gaacgcgcgtc cgacgcgcg caagctgttg 720					
cggctgcgcgc ggcgcgtgtt gcgcgtggac gtgagccgcg accgggtcga ggcgggttagc 780					
ttaaggacgc acggcgcggtt cgcgtcgac ccgtctcgac aaacctcgcc cgccgcggcg 840					
ctgaccgcgc cccgacaaaaa gaggcaccac tacggcccg cgctgtggt cgccctcgccc 900					
tatcactcgcg cgcgcacgcgc ctacgtactcg gtacccatc acacgtgca gggttatatac 960					
gccccgcacgc ttcctcggtt ccagaacaaac cccagcagcg tcacgcgcga ttacgtatc 1020					
cgcagttccgc acggccagat caccaggatgt gtgcgcgaga accgcgcggc ccatcactgc 1080					
ggcggtgcaca acaagaccac gctccgcata gaggcacaag gtttcatcaa caacgcgcac 1140					
tgttacaccgc cgcgcgtgtt caacgcgcgcg ggcgcgttgc cccgcgcactt ctgcgcgacc 1200					
taacgcgcgcg tcaactgcgc ggcgcgtgc agggggcccg cggcgcaggc catcaactgc 1260					
ctgcccgcoca ggcgtcaagggt caaggccac cagcattaca gcagccagac ccataccat 1320					
ccgggcgcata actgggattt ggcgcgttac tacaacccgc tcaacccggg caatccggcc 1380					
ggcgccgcgcg ggcgtatcgca cagtttcgaa agcgcgttgc ggcgcgttgc taccggcccg 1440					
gcgtactcggc gcgcgcaccc cggcgtcgcc ggcgcgtcgc tgacgcgcg caactgcacc 1500					
acgcgcgaaga acggcgactg ctcgtcgcc ctgttgcga aagacgcgcg ggcgcgcgc 1560					
ggcgccctggg cggtgaggctt gttgtcgccc agcggcaatc cgggcgcgaa cgcggccctt 1620					
acccgcgcaca acggcaagggtt cgggttcggc gtcttcaccc ggcgcacccg catagcgcgc 1680					
ggcggtcgca tcgacgcacag cgcgcgttgc tgcgcgcgc gatccggcc 1740					
aacacctgca cttacttgcg gttggacccgtt agcgcacgcg cgcgtggga tgcgtgggtt 1800					
ggcgccgcaca acggcgcgat caccggccgcg tcgggtgaacgc tcgacgcgtt gtgggttac 1860					
cgcgatcaga cttcggtcgat tgcgtatgtt atgtgcaggat gaagaactga 1920					
SEQ ID NO: 107		moltype = AA	length = 639		
FEATURE		Location/Qualifiers			
source	1..639				
		mol_type = protein			
		organism = Lysobacter capsici			
SEQUENCE: 107					
MNEYSTARQ VVTGVRSLSG SLTVAVLALA APLAAQAQAA PEDRALAQHL QIEESLQRVD 60					
RALYADYFRRQ AYARYPSIPA GTLESIAVYM SRWQQLQPSS VAAVGEHQH MPRSYVMGL 120					
YHGEFGFADQV GEGARLIGVP AARVORDPLS NILASAALLD RELRADIGA KSAVEATRPA 180					
LERYAGFAGN AGKSAIQDHA RSSFAFDVLL AQDKGVNDRG IVVPMRAVAW ERAFDARKLV 240					
RIRAPFVRDL VSRDRVEAGS LKDDGAFAD PLSETLRAPA LTAADEKSTD YGPALWVASP 300					
YHSARTSYDS VTIHTMQYY AGSISWQFNN PSSVSAHYLI RSSDGQTQM VRENRAAHHV 360					
GVHNKTTLGI EHEGFINNAS WYTAAMYNAS AALTRHFCA TYSIASCASAF RGPAGGSINV 420					
LPASVKVKGH QHYSSQTHTD PGINWDARY YNLLNPGNPNG GGGSVIDSFE STVGHFDTGP 480					
AYSGSTTGTIA ATSLSERNCNT TRKNGECLSR LLLKDDAASA GAWAVERLLSG SGNPGSNAAL 540					
TRANGKVGFV VFTGATGMSA AVGIDDSDGT ERSISRAIPA NTWTYLEWSL SDDAQWDAWV 600					
GGANGAITAA SVKLDAWVFY RDQTSFDNV YVDDVQVKN 639					
SEQ ID NO: 108		moltype = AA	length = 582		
FEATURE		Location/Qualifiers			
source	1..582				
		mol_type = protein			
		organism = Lysobacter capsici			
SEQUENCE: 108					
RVDRALYADY FRQAYARYPS IPAGTLESIA YVMSRWQQLQ PGSVAAVGEQ HQHMPPRSYGV 60					
MGLYHGEGFA DVQGEGEARLI GPVAAWRQD PLSNILASAA LLDRELRADG IGAKSAVEAT 120					
RPALERYAGF AGNAGKSAIQ DHARSSFAFD VLLAQDKGVN DRGIVVPMRA VAWERAFDAR 180					
KLVLRLRAPFV RLDVSRDRVE AGSLKDDGAF AIDPLSETLR APALTAADEK STDYGPALWV 240					
ASPYHSARTS YDSVTIHTMQ GYYAGSISWF QNNPSSVSAA YLIRSSDGQI TQMVRENRAA 300					
HHGVVHNKTT LGIEHEGFIN NASWYTAAMY NASAALTRHF CATYSAISCA SAFRGPAGSG 360					
INVLPAVKV KGHQHYSSQT HTDPGINWDW ARYYNLLNPG NPPGGGSVID SFESTVGHFD 420					
TGPAYSGSTT GIAATSLSER NCTTRKNGEC SLRLLLKDAA ASAGAWAVRL LSGSGNPGSN 480					

-continued

AALTRANGKV	GFWVFTGATG	MSAAVGIDDS	DGTERSISRA	IPANTWTYLE	WSLSDAQWD	540
AWGGANGAI	TAASVKLDAV	WFYRDQTSFD	VNVYVDDVQV	KN		582
 SEQ ID NO: 109						
FEATURE						
REGION						
source						
SEQUENCE: 109	MKKPLGKIVA	STALLISVAF	SSSIASA			27
 SEQ ID NO: 110						
FEATURE						
REGION						
source						
SEQUENCE: 110	HHHHHHPR					8
 SEQ ID NO: 111						
SEQUENCE: 111	000					

1. A cleaning composition comprising a peptidoglycan degradation enzyme, at least one surfactant, and at least one additional cleaning component selected from builders and bleach components.

2. The cleaning composition of claim 1, comprising a peptidoglycan degradation enzyme, at least 5 wt % anionic surfactants, and at least one additional cleaning component selected from at least one builder and at least one bleach component.

3. The cleaning composition according to claim 1, wherein the peptidoglycan degrading enzyme has N-acetyl-muramyl-L-alanine amidase activity.

4. The cleaning composition according to claim 1, wherein the peptidoglycan degrading enzyme has peptidoglycan lyase activity.

5. The cleaning composition according to claim 3, wherein the peptidoglycan degradation enzyme has N-acetyl muramyl-L-alanine amidase activity and peptidoglycan lyase activity.

6. The cleaning composition according to claim 1, wherein the peptidoglycan degradation enzyme comprises the motif N[IV]X[AG][GAS]A[AY][LV]L (SEQ ID NO: 111).

7. The cleaning composition of claim 6, wherein the peptidoglycan degradation enzyme is selected from the group consisting of: SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 9, SEQ ID NO: 12, SEQ ID NO: 15, SEQ ID NO: 18, SEQ ID NO: 21, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 42, SEQ ID NO: 45, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 60, SEQ ID NO: 63, SEQ ID NO: 66, SEQ ID NO: 69, SEQ ID NO: 75, SEQ ID NO: 87, SEQ ID NO: 96, SEQ ID NO: 99 and SEQ ID NO: 108, and polypeptides having at least at least 60% sequence identity thereto, and wherein the enzyme has peptidoglycan degradation activity.

8. A cleaning composition according to claim 1, comprising about 5 to about 60 wt % of at least one surfactant, and further comprising:

a. about 5 wt % to about 50 wt % of at least one builder ; and/or

b. about 1 wt % to about 20 wt % of at least one bleach component.

9. A cleaning composition according to claim 1, wherein the polypeptide having peptidoglycan degradation activity is selected from the group consisting of:

i. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 3,

ii. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 6,

iii. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 9,

iv. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 12,

v. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 15,

vi. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 18,

vii. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 21,

viii. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 24,

ix. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 27,

x. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 30,

xi. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 33,

xii. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 36,

xiii. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 39,

xiv. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 42,

xv. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 45,

xvi. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 48,

- xvii. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 51,
 - xviii. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 54,
 - xix. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 57,
 - xx. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 60,
 - xxi. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 63,
 - xxii. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 66,
 - xxiii. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 69,
 - xxiv. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 72,
 - xxv. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 75,
 - xxvi. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 78,
 - xxvii. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 81,
 - xxviii. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 84,
 - xxix. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 87
 - xxx. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 90,
 - xxxi. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 93,
 - xxxii. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 96,
 - xxxiii. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 99,
 - xxxiv. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 102,
 - xxxv. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 105, and
 - xxxvi. a polypeptide having at least at least 60% sequence identity to SEQ ID NO: 108.
- 10.** The cleaning composition according to claim 9, wherein the polypeptide has N-acetylmuramyl-L-alanine amidase and peptidoglycan lyase activity.
- 11-12.** (canceled)
- 13.** A method of cleaning on an item, comprising
- a) contacting the item with a solution comprising a peptidoglycan degradation enzyme having peptidoglycan lyase activity and N-acetylmuramyl-L-alanine amidase activity, and a cleaning component, wherein the cleaning component is selected from 5 to 60 wt % of at least one surfactant; 5 to 50 wt % of at least one builder; and 1 to 20 wt % of at least one bleach component, and optionally
 - b) rinsing the item;
- wherein the item is a textile.

* * * * *