

ANTIMICROBIAL AGENTS

The present invention relates to antimicrobial agents against Gram-positive bacteria, in particular to fusion proteins composed of an enzyme having the activity of degrading the cell wall of Gram-positive bacteria and an additional peptide stretch fused to the enzyme at the N- or C-terminus. Moreover, the present invention relates to nucleic acid molecules encoding said fusion protein, vectors comprising said nucleic acid molecules and host cells comprising either said nucleic acid molecules or said vectors. In addition, the present invention relates to said fusion protein for use as a medicament, in particular for the treatment or prevention of Gram-positive bacterial infections, as diagnostic means or as cosmetic substance. The present invention also relates to the treatment or prevention of Gram-positive bacterial contamination of foodstuff, of food processing equipment, of food processing plants, of surfaces coming into contact with foodstuff, of medical devices, of surfaces in hospitals and surgeries. Further, the present invention relates to a pharmaceutical composition comprising said fusion protein.

In contrast to Gram-negative bacteria, Gram-positive bacteria do not possess an outer membrane. The cytoplasmic membrane is surrounded by an up to 25 nm thick layer of peptidoglycan (which is only up to 5 nm for Gram-negative bacteria) which forms the cell wall. Main purpose of the cell wall of Gram-positives is to maintain bacterial shape and to counteract the internal bacterial cell pressure. Peptidoglycan, or murein, is a polymer consisting of sugars and amino acids. The sugar component consists of alternating residues of β -(1,4) linked N-acetylglucosamine and N-acetylmuramic acid residues compose the sugar components. A peptide chain of three to five amino acids is attached to the N-acetylmuramic acid. The peptide chain can be cross-linked to the peptide chain of another strand forming a 3D mesh-like layer. The peptide chain may contain D- and L- amino acid residues and the composition may vary for different bacteria.

A special situation is found in case of Mycobacteria which are usually considered Gram-positive. Mycobacteria were recently shown to possess an outer cell membrane. All Mycobacteria share a characteristic thick cell wall, which is hydrophobic, waxy, and rich in mycolic acids/mycolates. The cell wall consists of the hydrophobic mycolate layer and a peptidoglycan layer held together by arabinogalactan, a polysaccharide. To overcome the

thick cell wall of Mycobacteria a combined action of the new antimicrobial agents with a chitinase or a similar protein to disrupt the polysaccharide layer may be necessary.

Various types of agents having bactericidal or bacteriostatic activity are known, e.g. antibiotics, endolysins, antimicrobial peptides and defensins. Increasing microbial resistance to antibiotics, however, is creating difficulties in treating more and more infections caused by bacteria. Particular difficulties arise with infections caused by Gram-positive bacteria like *Staphylococcus aureus*, *Enterococci*, *Streptococci*, *Listeria monocytogenes* and *Clostridium difficile*, especially with e.g. Methicillin-resistant *Staphylococcus aureus* and Vancomycin-resistant *Enterococci*.

Endolysins are peptidoglycan hydrolases encoded by bacteriophages (or bacterial viruses). They are synthesized during late gene expression in the lytic cycle of phage multiplication and mediate the release of progeny virions from infected cells through degradation of the bacterial peptidoglycan. They are either $\beta(1,4)$ -glycosylases (lysozymes), transglycosylases, amidases or endopeptidases. Antimicrobial application of endolysins was already suggested in 1991 by Gasson (GB2243611). Although the killing capacity of endolysins has been known for a long time, the use of these enzymes as antibacterials was ignored due to the success and dominance of antibiotics. Only after the appearance of multiple antibiotic resistant bacteria this simple concept of combating human pathogens with endolysins received interest. A compelling need to develop totally new classes of antibacterial agents emerged and endolysins used as 'enzybiotics' - a hybrid term of 'enzymes' and 'antibiotics' - perfectly met this need. In 2001, Fischetti and coworkers demonstrated for the first time the therapeutic potential of bacteriophage C1 endolysin towards group A streptococci (Nelson et al., 2001). Since then many publications have established endolysins as an attractive and complementary alternative to control bacterial infections, particularly by Gram-positive bacteria. Subsequently different endolysins against other Gram-positive pathogens such as *Streptococcus pneumoniae* (Loeffler et al., 2001), *Bacillus anthracis* (Schuch et al., 2002), *S. agalactiae* (Cheng et al., 2005) and *Staphylococcus aureus* (Rashel et al., 2007) have proven their efficacy as enzybiotics. However, it is also known that endolysins can, under some conditions (e.g. high ionic strength), create stable protoplast, where the internal bacterial cell pressure is not sufficient to lead to a cell burst. Under these conditions the bacterial cell wall can regenerate and the bacteria will survive.

Antimicrobial peptides (AMPs) represent a wide range of short, cationic or amphipathic gene-encoded peptide antibiotics that can be found in virtually every organism. Different AMPs display different properties, and many peptides in this class are being intensively researched not only as antibiotics, but also as templates for cell-penetrating peptides. Despite sharing a few common features (e.g., cationicity, amphipathicity and short size), AMP sequences vary greatly, and at least four structural groups (α -helical, β -sheet, extended and looped) have been proposed to accommodate the diversity of the observed AMP conformations. Likewise, several modes of action as antibiotics have been proposed, and it was shown e.g. that the primary target of many of these peptides is the cell membrane whereas for other peptides the primary target is cytoplasmic invasion and disruption of core metabolic functions. AMPs may become concentrated enough to exhibit cooperative activity despite the absence of specific target binding; for example, by forming a pore in the membrane, as is the case for most AMPs. However, this phenomenon has only been observed in model phospholipid bilayers, and in some cases, AMP concentrations in the membrane that were as high as one peptide molecule per six phospholipid molecules were required for these events to occur. These concentrations are close to, if not at, full membrane saturation. As the minimum inhibitory concentration (MIC) for AMPs is typically in the low micromolar range, scepticism has understandably arisen regarding the relevance of these thresholds and their importance *in vivo* (Melo et al., Nature reviews, Microbiology, 2009, 245).

Defensins are a large family of small, cationic, cysteine- and arginine-rich antimicrobial peptides, found in both vertebrates and invertebrates. Defensins are divided into five groups according to the spacing pattern of cysteines: plant, invertebrate, α -, β -, and θ -defensins. The latter three are mostly found in mammals. α -defensins are proteins found in neutrophils and intestinal epithelia. β -defensins are the most widely distributed and are secreted by leukocytes and epithelial cells of many kinds. θ -defensins have been rarely found so far e.g. in leukocytes of rhesus macaques. Defensins are active against bacteria, fungi and many enveloped and nonenveloped viruses. However, the concentrations needed for efficient killing of bacteria are mostly high, i.e. in the μ -molar range. Activity of many peptides may be limited in presence of physiological salt conditions, divalent cations and serum. Depending on the content of hydrophobic amino acid residues Defensins also show haemolytic activity.

Thus, there is a need for new antimicrobial agents against Gram-positive bacteria.

This object is solved by the subject matter defined in the claims.

The term "protein" as used herein refers synonymously to the term "polypeptide". The term
5 "protein" as used herein refers to a linear polymer of amino acid residues linked by peptide
bonds in a specific sequence. The amino-acid residues of a protein may be modified by e.g.
covalent attachments of various groups such as carbohydrates and phosphate. Other
substances may be more loosely associated with the polypeptide chains, such as heme or lipid,
giving rise to the conjugated proteins which are also comprised by the term "protein" as used
10 herein. The various ways in which the polypeptide chains fold have been elucidated, in
particular with regard to the presence of alpha helices and beta-pleated sheets. The term
"protein" as used herein refers to all four classes of proteins being all-alpha, all-beta,
alpha/beta and alpha plus beta. Moreover, the term "protein" refers to a complex, wherein the
complex refers to a homomer.

15 The term "fusion protein" as used herein refers to an expression product resulting from the
fusion of two nucleic acid sequences. Such a protein may be produced, e.g., in recombinant
DNA expression systems. Moreover, the term "fusion protein" as used herein refers to a
fusion of a first amino acid sequence as e.g. an enzyme, with a second or further amino acid
20 sequence. The second or further amino acid sequence may define a domain or any kind of
peptide stretch. Preferably, said second and/or further amino acid sequence is foreign to and
not substantially homologous with any domain of the first amino acid sequence.

25 The term "peptide stretch" as used herein refers to any kind of peptide linked to a protein such
as an enzyme.

The term "peptide" as used herein refers to short polypeptides consisting of from about 2 to
about 100 amino acid residues, more preferably from about 4 to about 50 amino acid residues,
more preferably to about 5 to 30 amino acid residues, wherein the amino group of one amino
30 acid residue is linked to the carboxyl group of another amino acid residue by a peptide bond.
A peptide may have a specific function. A peptide can be a naturally occurring peptide or a
synthetically designed and produced peptide. The peptide can be, for example, derived or
removed from a native protein by enzymatic or chemical cleavage, or can be prepared using
conventional peptide synthesis techniques (e.g., solid phase synthesis) or molecular biology

techniques (see Sambrook, J. et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press, Cold Spring Harbor, N.Y. (1989)). Examples of naturally occurring peptides are antimicrobial peptides, defensins, sushi peptides. Examples of synthetically produced peptides are polycationic, amphiphatic or hydrophobic peptides. A peptide in the meaning of the present invention does not refer to His-tags, Strep-tags, thioredoxin or maltose binding proteins (MBP) or the like, which are used to purify or locate proteins.

The term “endolysin” as used herein refers to an enzyme which is suitable to hydrolyse bacterial cell walls. “Endolysins” comprise of at least one “enzymatically active domain” (EAD) having at least one of the following activities: endopeptidase, chitinase, T4 like muraminidase, lambda like muraminidase, N-acetyl-muramoyl-L-alanine-amidase (amidase), muramoyl-L-alanine-amidase, muramidase, lytic transglycosylase (C), lytic transglycosylase (M), N-acetyl-muramidase, N-acetyl-glucosaminidase (lysozyme) or transglycosylases as e.g. KZ144 and EL188. In addition, the endolysins may contain also regions which are enzymatically inactive, and bind to the cell wall of the host bacteria, the so-called CBDs (cell wall binding domains).

The term “CBD” as used herein refers to the cell wall binding domain of an endolysin. In endolysins being specific for Gram-positive bacteria the CBD is often found at the C-terminus, but may also be found N-terminal or somewhere else within the protein. Often CBD domains mediate binding of the endolysin to the bacterial cell wall but have no enzymatic activity in terms of hydrolyzing the cell wall.

The term “EAD” as used herein refers to the enzymatically active domain of an endolysin. The EAD is responsible for hydrolysing bacterial peptidoglycans. It exhibits at least one enzymatic activity of an endolysin. The EAD can also be composed of more than one enzymatically active module.

The term “autolysins” refers to enzymes related to endolysins but encoded by bacteria and involved in e.g. cell division. An overview of autolysins is can be found in “Bacterial peptidoglycan (murein) hydrolases. Vollmer W, Joris B, Charlier P, Foster S. *FEMS Microbiol Rev.* 2008 Mar;32(2):259-86”.

The term "bacteriocin" as used herein refers to protein-like, polypeptide-like or peptide-like substances which are able to inhibit the growth of other bacteria. Some bacteriocins are capable of degrading bacterial cell walls like Lysostaphin (degrading *Staphylococcus* cell walls), Mutanolysin (degrading *Streptococcus* cell walls) and Enterolysin (degrading *Enterococcus* cell walls). Preferably said inhibition is specifically by means of absorption of said other bacteria to specific receptors of the bacteriocin. In general, bacteriocins are produced by microorganisms. However, the term "bacteriocin" as used herein refers both to an isolated form produced by a microorganism or to a synthetically produced form, and refers also to variants which substantially retain the activities of their parent bacteriocins, but whose sequences have been altered by insertion or deletion of one or more amino acid residues.

The term, "antimicrobial peptide" (AMP) as used herein refers to any peptide that has microbicidal and/or microbistatic activity. Thus, the term "antimicrobial peptide" as used herein refers in particular to any peptide having anti-bacterial, anti-fungal, anti-mycotic, anti-parasitic, anti-protozoal, anti-viral, anti-infectious, anti-infective and/or germicidal, algicidal, amoebicidal, microbicidal, bactericidal, fungicidal, parasiticidal, protozoacidal, protozoicidal properties.

The term "defensin" as used herein refers to a peptide present within animals, preferably mammals, more preferably humans, wherein the defensin plays a role in the innate host defense system as the destruction of foreign substances such as infectious bacteria and/or infectious viruses and/or fungi. A defensin is non-antibody microbicidal and/or tumoricidal protein, peptide or polypeptide. Examples for "defensins" are "mammalian defensins," alpha-defensins, beta-defensins, indolicidin and magainins. The term "defensins" as used herein refers both to an isolated form from animal cells or to a synthetically produced form, and refers also to variants which substantially retain the cytotoxic activities of their parent proteins, but whose sequences have been altered by insertion or deletion of one or more amino acid residues.

The term "sushi peptide" as used herein refers to complement control proteins (CCP) having short consensus repeats. The sushi module of sushi peptides functions as a protein-protein interaction domain in many different proteins. Peptides containing a Sushi domain have been shown to have antimicrobial activities.

As used herein, the term "cationic peptide" refers to a peptide having positively charged amino acid residues. Preferably a cationic peptide has a pKa-value of 9.0 or greater. Typically, at least four of the amino acid residues of the cationic peptide can be positively charged, for example, lysine or arginine. "Positively charged" refers to the side chains of the amino acid residues which have a net positive charge at about physiological conditions. Examples of naturally occurring cationic peptides which can be recombinantly produced are defensins, magainins, melittin, and cecropins.

The term "polycationic peptide" as used herein refers to a synthetically produced peptide composed of mostly lysine and/or arginine residues.

The term "amphipathic peptide" as used herein refers to peptides having both hydrophilic and hydrophobic functional groups. Preferably, the term "amphipathic peptide" as used herein refers to a peptide having a defined arrangement of hydrophilic and hydrophobic groups e.g. amphipathic peptides may be e.g. alpha helical, having predominantly non polar side chains along one side of the helix and polar residues along the remainder of its surface.

The term "hydrophobic group" as used herein refers to chemical groups such as amino acid side chains which are substantially water insoluble, but soluble in an oil phase, with the solubility in the oil phase being higher than that in water or in an aqueous phase. In water, amino acids having a hydrophobic side chain interact with one another to generate a nonaqueous environment. Examples of amino acids with hydrophobic side chains are alanine, valine, leucine, isoleucine, phenylalanine, histidine, tryptophane and tyrosine.

The term "deletion" as used herein refers to the removal of 1, 2, 3, 4, 5 or more amino acid residues from the respective starting sequence.

The term "insertion" or "addition" as used herein refers to the insertion or addition of 1, 2, 3, 4, 5 or more amino acid residues to the respective starting sequence.

The term "substitution" as used herein refers to the exchange of an amino acid residue located at a certain position for a different one.

The present invention relates to new antibacterial agents against Gram-positive bacteria, in particular to fusion proteins composed of an enzyme having the activity of degrading the cell wall of Gram-positive bacteria and an additional peptide stretch fused to the enzyme at the N- or C-terminus or at both termini.

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The fusion proteins according to the present invention have the advantage that they may prevent the regeneration of stable protoplasts and thus, preventing the survival of the bacteria which should be eliminated. The regeneration of the protoplast by the bacteria occurs under some conditions (e.g. high ionic strength), where the internal bacterial cell pressure is not sufficient to lead to a cell burst and leads to the survival of the bacteria.

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In one aspect of the present invention the enzyme having the activity of degrading the cell wall of Gram-positive bacteria is an endolysine, autolysine and/or bacteriocin.

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In another aspect of the present invention the enzyme may contain also regions which are enzymatically inactive, and bind to the cell wall of the host bacteria, the so-called CBDs (cell wall binding domains).

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Preferred fusion proteins according to the present invention are depicted in SEQ ID NO:63 to 90. The fusion proteins according to SEQ ID NO:63 to 90 may comprise one or more additional amino acid residues on the N-terminus. Preferably the additional amino acid residue is methionine.

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Preferably, the endolysin is encoded by bacteriophages specific for Gram-positive bacteria such as Gram-positive bacteria of bacterial groups, families, genera or species comprising strains pathogenic for humans or animals as listed in the following table.

Table 1:

I. Phylum Actinobacteria

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Class: Actinobacteridae

Order Actinomycetales

Families:

Actinomycineae: Actinomycetaceae (Actinomyces, Mobiluncus)

Corynebacterineae: Mycobacteriaceae (Mycobacterium), Nocardiaceae,

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Corynebacteriaceae

Frankineae: Frankiaceae

- Micrococcineae: Brevibacteriaceae
- Propionibacteriaceae (Propionibacterium)
- Order: Bifidobacteriales
- Families:
- 5 Bifidobacteriaceae (Bifidobacterium, Falcivibrio, Gardnerella)
- Other subclasses: Acidimicrobidae, Coriobacteridae, Rubrobacteridae, Sphaerobacteridae
- II. Phylum Firmicutes
- 10 Class: Bacilli
- Order: Bacillales:
- Families:
- Bacillaceae (Bacillus), Listeriaceae (Listeria), Staphylococcaceae (Staphylococcus, Gemella, Jeotgalicoccus)
- 15 Order: Lactobacillales:
- Families: Enterococcaceae (Enterococcus), Lactobacillaceae (Lactobacillus, Pediococcus), Leuconostocaceae (Leuconostoc), Streptococcaceae (Lactococcus, Streptococcus)
- 20 Class: Clostridia
- Order: Clostridiales (Clostridium, Peptostreptococcus, Selenomonas)
- Order: Halanaerobiales
- Order: Thermoanaerobacterales
- 25 Class: Tenericutes/Mollicutes
- Order: Mycoplasmatales (Mycoplasma, Ureaplasma)
- Order: Entomoplasmatales (Spiroplasma)
- Order: Anaeroplasmatales (Erysipelothrix)
- Order: Acholeplasmatales (Acholeplasma)
- 30 Order: Haloplasmatales (Haloplasma)

Preferably, the autolysin is encoded by Gram-positive bacteria such as Gram-positive bacteria of bacterial groups, families, genera or species comprising strains pathogenic for humans or animals as listed in table 1.

35 Preferably, the bacteriocin is encoded by Gram-positive bacteria such as Gram-positive bacteria of bacterial groups, families, genera or species comprising strains pathogenic for humans or animals as listed in table 1.

40 The enzyme according to the present invention has cell wall degrading activity against Gram-positive bacteria of bacterial groups, families, genera or species comprising strains pathogenic for humans or animals like *Listeria monocytogenes*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Enterococcus faecium*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Streptococcus mutans*, *Streptococcus equi*, *Clostridium difficile*, *Clostridium botulinum*,

Clostridium tetani, *Clostridium perfringens*, *Bacillus anthracis*, *Bacillus cereus*, *Propionibacterium acnes*, *Mycobacterium avium*, *Mycobacterium tuberculosis*, *Corynebacterium diphtheriae*, *Mycoplasma pneumoniae*, *Actinomyces*.

- 5 Preferred endolysins are *Listeria* phage endolysins PlyA118, PlyA500, PlyPSA, PlyA511, PlyP35, PlyP40, Staph phage Phi 11, Phi MR11, LysK, *Clostridium perfringens* PlyS6, Ply3626, *Clostridium difficile*: CD27L endolysin, Streptococcus: B30 endolysin, phage Dp-1 Pal amidase, C1 endolysin, Cpl-1 endolysin, PlyGBS, Enterococcus: PlyV12, *Bacillus anthracis*: Phage gamma endolysin PlyG.

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Preferred autolysins are described in: Bacterial peptidoglycan (murein) hydrolases. Vollmer W, Joris B, Charlier P, Foster S. FEMS Microbiol Rev. 2008 Mar;32(2):259-86. Epub 2008 Feb 11. Review. An example of a preferred autolysin is the AtlA Autolysine.

- 15 Preferred bacteriocins are Lysostaphin (degrading *Staphylococcus* cell walls), Mutanolysin (degrading *Streptococcus* cell walls) and Enterolysin (degrading *Enterococcus* cell walls).

More preferably, the endolysin part is selected from the group consisting of Cpl-1 according to SEQ ID NO:57, Ply511 according to SEQ ID NO:58, LysK according to SEQ ID NO:59,

- 20 Lysostaphin according to SEQ ID NO:60 and PA6-gp20 according to SEQ ID NO:61.

In another preferred embodiment of the present invention the endolysins, autolysins and bacteriocins of the fusion protein according to the present invention comprise modifications and/or alterations of the amino acid sequences. Such alterations and/or modifications may

25 comprise mutations such as deletions, insertions and additions, substitutions or combinations thereof and/or chemical changes of the amino acid residues, e.g. biotinylation, acetylation, pegylation, chemical changes of the amino-, SH- or carboxyl- groups. Said endolysins, autolysins and bacteriocins of the fusion protein according to the present invention exhibit the lytic activity of the respective wild-type endolysin. However, said activity can be the same,

30 higher or lower as the activity of the respective wild-type endolysin. Said activity can be about 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190 or about 200 % of the activity of the respective wild-type endolysin or even more. The activity can be measured by assays well known in the art by a person skilled in the art as e.g. the plate lysis assay or the liquid lysis assay which are e.g. described in *Briers et al., J. Biochem.*

Biophys Methods 70: 531-533, (2007) or *Donovan DM, Lardeo M, Foster-Frey J. FEMS Microbiol Lett.* 2006 Dec;265(1) or similar publications.

Preferably, the peptide stretch of the fusion protein according to the invention is fused to the N-terminus and/or to the C-terminus of the endolysin. In a particular preferred embodiment said peptide stretch is only fused to the N-terminus of the enzyme. In another preferred embodiment the peptide stretch is only fused to the C-Terminus of the enzyme. However, also preferred are modified fusion proteins having a peptide stretch both on the N-terminus and on the C-terminus. Said peptide stretches on the N-terminus and on the C-terminus can be the same or distinct peptide stretches. The peptide stretch can be linked to the enzyme by additional amino acid residues e.g. due to cloning reasons. Preferably, said peptide stretch can be linked to the fusion protein by at least 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 additional amino acid residues. In a preferred embodiment the peptide stretch is linked to the enzyme by the additional amino acid residues glycine and/or serine (Gly-Ser). Moreover, the peptide stretch of the fusion protein according to the invention further comprises additional amino acids on its N-terminus. Preferably, the peptide stretch comprises the amino acid methionine (Met) or alanine, methionine and glycine (Ala-Met-Gly).

The peptide stretch of the fusion protein according to the present invention is preferably covalently bound to the enzyme. Preferably, said peptide stretch consists of at least 5, more preferably at least of 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or at least 100 amino acid residues. Especially preferred is a peptide stretch comprising about 5 to about 100 amino acid residues, about 5 to about 50 or about 5 to about 30 amino acid residues. More preferred is a peptide stretch comprising about 6 to about 42 amino acid residues, about 6 to about 39 amino acid residues, about 6 to about 38 amino acid residues, about 6 to about 31 amino acid residues, about 6 to about 25 amino acid residues, about 6 to about 24 amino acid residues, about 6 to about 22 amino acid residues, about 6 to about 21 amino acid residues, about 6 to about 20 amino acid residues, about 6 to about 19 amino acid residues, about 6 to about 16 amino acid residues, about 6 to about 14 amino acid residues, about 6 to about 12 amino acid residues, about 6 to about 10 amino acid residues or about 6 to about 9 amino acid residues.

Preferably, the peptide stretch is no tag such as a His₆-tag, Strep-tag, Avi-tag, Myc-tag, Gst-tag, JS-tag, cystein-tag, FLAG-tag or other tags known in the art and no thioredoxin or maltose binding proteins (MBP). However, the peptide stretch and/or the endolysin, autolysin or bacteriocin according to the present invention may comprise in addition such tag or tags.

More preferably the peptide stretch has the function to facilitate the burst of the bacterial cell via interaction of the fusion protein with: first the peptidoglycan layer, degrading the peptidoglycan and second the cytoplasmic membrane, destabilizing the cytoplasmic membrane.

In one aspect of the present invention the fused peptide stretch is a cationic peptide, more preferably a polycationic peptide. Preferably the cationic peptide comprises one or more of the positively charged amino acid residues of lysine, arginine and/or histidine. Preferably, more than about 60, 65, 70, 75, 80, 85, 90, 95 or about 100 %, of the amino acid residues in said peptide are positively charged amino acid residues. Advantageously, the cationic peptide is fused at the N-terminal and/or the C-terminal end of the enzyme having cell wall degrading activity, thus enhancing the cationicity of the fusion proteins and/or antimicrobial agents of the present invention. In another embodiment of the invention, the cationic peptide fused to the enzyme consists of at least 5, more preferably of at least 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 amino acid residues. Preferably at least about 60, 65, 70, 75, 80, 85, 90, 95 or about 100 %, of the amino acid residues of the cationic peptide are either arginine or lysine. In another embodiment of the present invention the cationic peptide comprises about 3 to about 50, more preferably about 5 to about 20, for instance about 5 to about 15 amino acid residues and the said amino acid residues are either arginine or lysine residues. Preferred cationic peptides are depicted in SEQ ID NOs:13 and 14.

Especially preferred are cationic and/or polycationic peptide stretches comprising at least one motive according to SEQ ID NO: 62 (KRKKRK). In particular cationic peptide stretches comprising at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16 or 17 motives according to SEQ ID NO: 62 (KRKKRK) are preferred. More preferred are cationic peptide stretches comprising at least one KRK motive (lys-arg-lys), preferable at least 2, 3, 4, 5, 6, 7, 8, 9, 10,

11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32 or 33 KRK motives.

In another preferred embodiment of the present invention the cationic peptide stretch
 5 comprises beside the positively charged amino acid residues, in particular lysine and/or arginine residues, neutrally charged amino acid residues, in particular glycine and/or serine residues. Preferred are cationic peptide stretches consisting of about 70 % to about 100 %, or about 80 % to about 95 %, or about 85 % to about 90 % positively charged amino acid residues, in particular lysine, arginine and/or histidine residues, more preferably lysine and/or
 10 arginine residues and of about 0 % to about 30 %, or about 5 % to about 20 %, or about 10 % to about 20 % neutrally charged amino acid residues, in particular glycine and/or serine residues. Preferred are polypeptide stretches consisting of about 4 % to about 8 % serine residues, of about 33 % to about 36 % arginine residues and of about 56 % to about 63 % lysine residues. Especially preferred are polypeptide stretches comprising at least one motive
 15 according to SEQ ID NO: 45 (KRXKR), wherein X is any other amino acid than lysine, arginine and histidine. Especially preferred are polypeptide stretches comprising at least one motive according to SEQ ID NO: 46 (KRSKR). More preferred are cationic stretches comprising at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or about 20 motives according to SEQ ID NO: 45 (KRXKR) or SEQ ID NO: 46 (KRSKR).

20 Also preferred are polypeptide stretches consisting of about 9 to about 16 % glycine residues, of about 4 to about 11 % serine residues, of about 26 to about 32 % arginine residues and of about 47 to about 55 % lysine residues. Especially preferred are polypeptide stretches comprising at least one motive according to SEQ ID NO: 47 (KRGSG). More preferred are
 25 cationic stretches comprising at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or about 20 motives according to SEQ ID NO: 47 (KRGSG).

In another preferred embodiment of the present invention the cationic peptide stretch
 30 comprises beside the positively charged amino acid residues, in particular lysine and/or arginine residues, hydrophobic amino acid residues, in particular valine, isoleucine, leucine, methionine, phenylalanine, tryptophan, cysteine, alanine, tyrosine, histidine, threonin, serine, proline and glycine residues, more preferably alanine, valine, leucine, isoleucine, phenylalanine, and/or tryptophan residues. Preferred are cationic peptide stretches consisting of about 70 % to about 100 %, or about 80 % to about 95 %, or about 85 % to about 90 %

positively charged amino acid residues, in particular lysine and/or arginine residues and of about 0 % to about 30 %, or about 5 % to about 20 %, or about 10 % to about 20 % hydrophobic amino acid residues, valine, isoleucine, leucine, methionine, phenylalanine, tryptophan, cysteine, alanine, tyrosine, histidine, threonine, serine, proline and glycine residues, more preferably alanine, valine, leucine, isoleucine, phenylalanine, and/or tryptophan residues.

Especially preferred are peptide stretches selected from the group consisting of the following sequences:

Table 2:

peptide stretch	length	SEQ ID NO:
KRKKRK	6	SEQ ID NO:24
KRKKRKKRK	9	SEQ ID NO:13
RRRRRRRRR	9	SEQ ID NO:25
KKKKKKKK	8	SEQ ID NO:26
KRKKRKKRKK	10	SEQ ID NO:27
KRKKRKKRKKRK	12	SEQ ID NO:28
KRKKRKKRKKRKKR	14	SEQ ID NO:29
KKKKKKKKKKKKKKKK	16	SEQ ID NO:30
KRKKRKKRKKRKKRKKRK	18	SEQ ID NO:31
KRKKRKKRKKRKKRKKRKK	19	SEQ ID NO:32
RRRRRRRRRRRRRRRRRR	19	SEQ ID NO:33
KKKKKKKKKKKKKKKKKK	19	SEQ ID NO:34
KRKKRKKRKRKRKKRKKRK	20	SEQ ID NO:35
KRKKRKKRKRKRKKRKKRKK	21	SEQ ID NO:36
KRKKRKKRKKRKKRKKRKKRK	21	SEQ ID NO:37
KRKKRKKRKRGSGRKKRKKRK	22	SEQ ID NO:38
KRKKRKKRKRGSGRKKRKKRK	24	SEQ ID NO:39
KRKKRKKRKKRKKRKKRKKRKK	25	SEQ ID NO:40
KRKKRKKRKRKRKKRKKRKRKRKKRKKRKK	31	SEQ ID NO:41
KRKKRKKRKRGSGRKKRKKRKRGSGRKKRKKRK	38	SEQ ID NO:42
KRKKRKKRKKRKKRKKRKKRKKRKKRKKRKKRKKRKKRKK	39	SEQ ID NO:43
KRKKRKKRKRKRKKRKKRKRKRKRKKRKRKRKRKRKRKKRKKRKK	42	SEQ ID NO:44

In a further aspect of the present invention the fused peptide stretch is an amphipatic peptide, which comprises one or more of the positively charged amino acid residues of lysine, arginine and/or histidine, combined to one or more of the hydrophobic amino acid residues of valine, isoleucine, leucine, methionine, phenylalanine, tryptophan, cysteine, alanine, tyrosine,

histidine, threonine, serine, proline and/or glycine. Side chains of the amino acid residues are oriented in order that cationic and hydrophobic surfaces are clustered at opposite sides of the peptide. Preferably, more than about 30, 40, 50, 60 or 70% of the amino acids in said peptide are positively charged amino acids. Preferably, more than about 30, 40, 50, 60 or 70%, of the amino acid residues in said peptide are hydrophobic amino acid residues. Advantageously, the amphipathic peptide is fused at the N-terminal and/or the C-terminal end of the enzyme having cell wall degrading activity, thus enhancing the amphipathicity of the latter proteins.

In another embodiment of the invention, the amphipathic peptide fused to the enzyme consists of at least 5, more preferably at least of 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 amino acid residues. In a preferred embodiment at least about 30, 40, 50, 60 or 70% of the said amino acid residues of the amphipathic peptide are either arginine or lysine residues and/or at least about 30, 40, 50, 60 or 70% of the said amino acid residues of the amphipathic peptide are of the hydrophobic amino acids valine, isoleucine, leucine, methionine, phenylalanine, tryptophan, cysteine, alanine, tyrosine, histidine, threonine, serine, proline and/or glycine.

Preferred amphipathic peptides are Pleurocidin according to SEQ ID NO:1, Cecropin P1 according to SEQ ID NO:2, Buforin II according to SEQ ID NO:3, Buforin I according to SEQ ID NO:23 and Magainin according to SEQ ID NO:4. Further preferred amphipathic peptides are Cathelidicine e.g. LL-37 according to SEQ ID NO:5, Nigrocin 2 according to SEQ ID NO: 48 and Ascaphine 5 according to SEQ ID NO:49.

In a further aspect of the present invention the fused peptide stretch is an antimicrobial peptide, which comprises a positive net charge and around 50% hydrophobic amino acids. The antimicrobial peptides are amphipathic, with a length of about 12 to about 50 amino acid residues.

Examples for antimicrobial peptides are listed in the following table.

Table 3:

Peptid	Sequenz	
LL-37	LLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLPRTES	SEQ ID NO:5
SMAP-29	RGLRRLGRKIAHG VKKYGPTVLRRIIRIAG	SEQ ID NO:6

Indolicidin	ILPWKWPWWPWRR	SEQ ID NO:7
Protegrin	RGGRLCYCRRRFCVCVGR	SEQ ID NO:8
Cecropin P1	SWLSKTAKKLENSAKKRISGIAIAIQGGPR	SEQ ID NO:2
Magainin	GIGKFLHSAKKFGKAFVGEIMNS	SEQ ID NO:4
Pleurocidin	GWGSFFKKAHVKGKVGKAALTHYL	SEQ ID NO:1
Cecropin A (A.aegypti)	GGLKKLGKKLEGAGKRVFNAAEKALPVVAGAKALRK	SEQ ID NO:9
Cecropin A (D.melanogaster)	GWLKKIGKKIERVGGQHTRDATIQGLGIPQQAANVAATARG	SEQ ID NO:10
Buforin II	TRSSRAGLQFPVGRVHRLLRK	SEQ ID NO:3
Sarcotoxin IA	GWLKKIGKKIERVGGQHTRDATIQGLGIAQQAANVAATAR	SEQ ID NO:11
Apidaecine	ANRPVYIPPPRPPHPRL	SEQ ID NO:50
Ascaphine 5	GKDWIKGAACKLIKTVASHIANQ	SEQ ID NO:49
Nigrocine 2	GLLSKVLGVGKKVLCGVSGSLVC	SEQ ID NO:48
Pseudin 1	GLNTLKKVFQGLHEAIKLINNHVQ	SEQ ID NO:51
Ranalexin	FLGGLIVPAMICAVTKKC	SEQ ID NO:52
Melittin	GIGAVLKVLTTGLPALISWIKRKRQQ	SEQ ID NO:53

In a further aspect of the present invention the fused peptide stretch is a sushi peptide which is described by Ding JL, Li P, Ho B Cell Mol Life Sci. 2008 Apr;65(7-8):1202-19. The Sushi peptides: structural characterization and mode of action against Gram-negative bacteria. Especially preferred is the sushi 1 peptide according to SEQ ID NO:54.

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Preferred sushi peptides are sushi peptides S1 and S3 and multiples thereof; FASEB J. 2000 Sep;14(12):1801-13.

In a further aspect of the present invention the fused peptide stretch is a defensin, preferably Cathelicidine, Cecropin P1, Cecropin A or Magainin II.

In a further aspect of the present invention the fused peptide stretch is a hydrophobic peptide e.g. Apidaecine having the amino acid sequence according to SEQ ID NO: 50, WLBU2-Variant having the amino acid sequence according to SEQ ID NO: 55 and Walmagh1 having the amino acid sequence according to SEQ ID NO: 56. The hydrophobic peptide having the amino acid sequence Phe-Phe-Val-Ala-Pro (SEQ ID NO: 12) is not part of the present invention.

In another preferred embodiment of the present invention the peptide stretches of the fusion protein according to the present invention comprise modifications and/or alterations of the amino acid sequences. Such alterations and/or modifications may comprise mutations such as deletions, insertions and additions, substitutions or combinations thereof and/or chemical

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changes of the amino acid residues, e.g. biotinylation, acetylation, pegylation, chemical changes of the amino-, SH- or carboxyl- groups.

Especially preferred are fusion proteins according to the SEQ ID NOs: 63 to 90 and the fusion proteins selected from the group consisting of the following fusion proteins:

Table 4:

Fusion protein	Fusion protein	Enzyme part	Peptide stretch (N-terminal unless otherwise indicated)
P1-E1	SEQ ID NO: 63	Cpl-1 (SEQ ID NO: 57)	Ascaphine 5 (SEQ ID NO:49)
P2-E1	SEQ ID NO: 64	Cpl-1 (SEQ ID NO: 57)	Apiadaecine (SEQ ID NO:50)
P3-E1	SEQ ID NO: 65	Cpl-1 (SEQ ID NO: 57)	Nigrocine 2 (SEQ ID NO:48)
P4-E1	SEQ ID NO: 66	Cpl-1 (SEQ ID NO: 57)	Pseudin 1 (SEQ ID NO:51)
P7-E1	SEQ ID NO: 67	Cpl-1 (SEQ ID NO: 57)	Ranalexin (SEQ ID NO:52)
P8-E1	SEQ ID NO: 68	Cpl-1 (SEQ ID NO: 57)	WLBUE2-Variant (SEQ ID NO:55)
P9-E1	SEQ ID NO: 69	Cpl-1 (SEQ ID NO: 57)	Sushi 1 (SEQ ID NO:54)
P10-E1	SEQ ID NO: 70	Cpl-1 (SEQ ID NO: 57)	Melittin (SEQ ID NO:53)
P11-E1	SEQ ID NO: 71	Cpl-1 (SEQ ID NO: 57)	LL-37 (SEQ ID NO:5)
P12-E1	SEQ ID NO: 72	Cpl-1 (SEQ ID NO: 57)	Indolicidin (SEQ ID NO:7)
P13-E1	SEQ ID NO: 73	Cpl-1 (SEQ ID NO: 57)	SMAP-29 (SEQ ID NO:6)
P14-E1	SEQ ID NO: 74	Cpl-1 (SEQ ID NO: 57)	Protegrin (SEQ ID NO:8)
P15-E1	SEQ ID NO: 75	Cpl-1 (SEQ ID NO: 57)	Cecropin P1 (SEQ ID NO:2)
P16-E1	SEQ ID NO: 76	Cpl-1 (SEQ ID NO: 57)	Magainin (SEQ ID NO:4)
P17-E1	SEQ ID NO: 77	Cpl-1 (SEQ ID NO: 57)	Pleurocidin (SEQ ID NO:1)
P18-E1	SEQ ID NO: 78	Cpl-1 (SEQ ID NO:57)	Cecropin A (A. aegypti) (SEQ ID NO:9)
P19-E1	SEQ ID NO: 79	Cpl-1 (SEQ ID NO:57)	Cecropin A (D. melanogaster) (SEQ ID NO:10)
P20-E1	SEQ ID NO: 80	Cpl-1	Buforin II

		(SEQ ID NO:57)	(SEQ ID NO:3)
P21-E1	SEQ ID NO: 81	Cpl-1 (SEQ ID NO:57)	Sarcotoxin IA (SEQ ID NO:11)
P5-E1	SEQ ID NO: 82	Cpl-1 (SEQ ID NO:57)	PK (SEQ ID NO:13)
P22-E2	SEQ ID NO: 83	Ply511 (SEQ ID NO:58)	Pentapeptid (SEQ ID NO:12)
P5-E7	SEQ ID NO: 84	LysK (SEQ ID NO:59)	PK (N-terminal) (SEQ ID NO:13)
P6-E7	SEQ ID NO: 85	LysK (SEQ ID NO:59)	PK2 (SEQ ID NO:31)
P5-E8	SEQ ID NO: 86	Lysostaphin (SEQ ID NO:60)	PK (C-terminal) (SEQ ID NO:13)
P6-E8	SEQ ID NO: 87	Lysostaphin (SEQ ID NO:60)	PK2 (SEQ ID NO:31)
P23-E9	SEQ ID NO: 88	PA6-gp20 (SEQ ID NO:61)	Walmagh1 (SEQ ID NO:56)
P5-E7	SEQ ID NO: 89	LysK (SEQ ID NO:59)	PK (C-terminal) (SEQ ID NO:13)
P5-E8	SEQ ID NO: 90	Lysostaphin (SEQ ID NO:60)	PK (N-terminal) (SEQ ID NO:13)

The fusion protein according to the present invention, and thus in particular the especially preferred fusion proteins according to SEQ ID NO:63 to 90, may additional comprise a methionine on the N-terminus.

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The fusion protein according to the present invention, and thus in particular the especially preferred fusion proteins according to SEQ ID NO:63 to 90, may additional comprise a tag e.g. for purification. Preferred is a His₆-tag, preferably at the C-terminus of the fusion protein. Said tag can be linked to the fusion protein by additional amino acid residues e.g. due to cloning reasons. Preferably said tag can be linked to the fusion protein by at least 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 additional amino acid residues. In a preferred embodiment the fusion protein comprises a His₆-tag at its C-terminus linked to the fusion protein by the additional amino acid residues lysine and glycine (Lys-Gly) or leucine and glutamic acid (Leu-Glu). In another preferred embodiment the fusion protein comprises a His₆-tag at its N-terminus linked to the fusion protein by the additional amino acid residues lysine and glycine (Lys-Gly) or leucine and glutamic acid (Leu-Glu). In a more preferred embodiment the fusion protein comprises a His₆-tag at its N-terminus linked to the fusion protein by the additional amino acid residues leucine and glutamic acid (Leu-Glu). In another preferred embodiment the fusion protein

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comprises a His₆-tag at its C-terminus linked to the fusion protein by the additional amino acid residues leucine and glutamic acid (Leu-Glu).

In a more preferred embodiment the fusion protein comprises a His₆-tag at its C-terminus
 5 linked to the fusion protein by the additional amino acid residues leucine and glutamic acid (Leu-Glu) and the peptide stretch of the fusion protein according to the invention is linked to the N-terminus of the enzyme by the additional amino acid residues glycine and serine (Gly-Ser). In another preferred embodiment the fusion protein comprises a His₆-tag at its C-terminus linked to the fusion protein by the additional amino acid residues leucine and
 10 glutamic acid (Leu-Glu) and the peptide stretch of the fusion protein according to the invention is linked to the N-terminus of the enzyme by the additional amino acid residues glycine and serine (Gly-Ser) and the fusion protein comprises on the N-terminus the additional amino acid residues methionine (Met) or methionine and glycine (Met-Gly) or alanine, methionine and glycine (Ala-Met-Gly). Preferably the fusion proteins are according
 15 to SEQ ID NO: 108 to 123.

In another preferred embodiment the fusion protein comprises a His₆-tag at its N-terminus, wherein the His₆-tag further comprises on its N-terminus the additional amino acids serine and serine (Ser-Ser) or methionine and glycine (Met-Gly) or methionine, glycine, serine and
 20 serine (Met-Gly-Ser-Ser).

In another preferred embodiment the fusion protein comprises a His₆-tag at its N-terminus linked to the fusion protein by the additional amino acid residues serine, serine, glycine, leucine, valine, proline, arginine, glycine, serine and histidine (Ser-Ser-Gly-Leu-Val-Pro-Arg-
 25 Gly-Ser-His). In another preferred embodiment the fusion protein comprises a His₆-tag at its N-terminus linked to the fusion protein by the additional amino acid residues serine, serine, glycine, leucine, valine, proline, arginine, glycine, serine, histidine and methionine (Ser-Ser-Gly-Leu-Val-Pro-Arg-Gly-Ser-His-Met). In another preferred embodiment the fusion protein comprises a His₆-tag at its N-terminus linked to the fusion protein by the additional amino
 30 acid residues serine, serine, glycine, leucine, valine, proline, arginine, glycine, serine and histidine (Ser-Ser-Gly-Leu-Val-Pro-Arg-Gly-Ser-His) or serine, serine, glycine, leucine, valine, proline, arginine, glycine, serine, histidine and methionine (Ser-Ser-Gly-Leu-Val-Pro-Arg-Gly-Ser-His-Met) and the peptide stretch of the fusion protein according to the invention is linked to the C-terminus of the enzyme by the additional amino acid residue serine. In

another preferred embodiment the fusion protein comprises a His₆-tag at its N-terminus linked to the fusion protein by the additional amino acid residues serine, serine, glycine, leucine, valine, proline, arginine, glycine, serine and histidine (Ser-Ser-Gly-Leu-Val-Pro-Arg-Gly-Ser-His) or serine, serine, glycine, leucine, valine, proline, arginine, glycine, serine, histidine and methionine (Ser-Ser-Gly-Leu-Val-Pro-Arg-Gly-Ser-His-Met) and the peptide stretch of the fusion protein according to the invention is linked to the C-terminus of the enzyme by the additional amino acid residue serine and the His₆-tag comprises on the N-terminus the additional amino acid residues serine and serine (Ser-Ser) or methionine, glycine, serine and serine (Met-Gly-Ser-Ser) or methionine and serine (Met-Ser). Preferably the fusion proteins are according to SEQ ID NO: 122 and 123.

Fusion proteins are constructed by linking at least two nucleic acid sequences using standard cloning techniques as described e.g. by Sambrook et al. 2001, Molecular Cloning: A Laboratory Manual. Such a protein may be produced, e.g., in recombinant DNA expression systems. Such fusion proteins according to the present invention can be obtained by fusing the nucleic acids for endolysin and the respective peptide stretch.

The fusion proteins according to the present invention may be fused or linked to other additional proteins. Example for this other additional protein is thioredoxin.

The present invention further relates to an isolated nucleic acid molecule encoding the fusion protein according to the present invention. The present invention further relates to a vector comprising the nucleic acid molecule according to the present invention. Said vector may provide for the constitutive or inducible expression of said fusion protein according to the present invention.

The invention also relates to a method for obtaining said fusion proteins from a micro-organism, such as a genetically modified suitable host cell which expresses said fusion proteins. Said host cell may be a micro-organism such as bacteria or yeast or an animal cell as e.g. a mammalian cell, in particular a human cell. In one embodiment of the present invention the host cell is a *Pichia pastoris* cell. The host may be selected due to mere biotechnological reasons, e.g. yield, solubility, costs, etc. but may be also selected from a medical point of view, e.g. a non-pathological bacteria or yeast, human cells. Another aspect of the present invention is related to a method for genetically transforming a suitable host cell in order to

obtain the expression of the fusion proteins according to the invention wherein the host cell is genetically modified by the introduction of a genetic material encoding said fusion proteins into the host cell and obtain their translation and expression by genetic engineering methods well known by the man skilled in the art.

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In a further aspect the present invention relates to a composition, preferably a pharmaceutical composition, comprising a fusion protein according to the present invention and/or a host transformed with a nucleic acid molecule or a vector comprising a nucleotide sequence encoding a fusion protein according to the present invention.

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The present invention also relates to a fusion protein according to the present invention and/or a host transformed with a nucleic acid comprising a nucleotide sequence encoding a fusion protein according to the present invention for use as a medicament. In a further aspect the present invention relates to the use of a fusion protein according to the present invention

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and/or a host transformed with a vector comprising a nucleic acid molecule comprising a nucleotide sequence encoding a modified, fusion protein according to the present invention in the manufacture of a medicament for the treatment and/or prevention of a disorder, disease or condition associated with Gram-positive bacteria. In particular the treatment and/or prevention of the disorder, disease or condition may be caused by Gram-positive bacteria of

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bacterial groups, families, genera or species comprising strains pathogenic for humans or animals like *Listeria monocytogenes*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Enterococcus faecium*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Streptococcus mutans*, *Streptococcus equi*, *Clostridium difficile*, *Clostridium botulinum*, *Clostridium tetani*, *Clostridium perfringens*, *Bacillus anthracis*, *Bacillus cereus*, *Propionibacterium acnes*,
25 *Mycobacterium avium*, *Mycobacterium tuberculosis*, *Corynebacterium diphtheriae*, *Mycoplasma pneumoniae*, *Actinomyces*.

The present invention further relates to a medicament comprising a fusion protein according to the present invention and/or a host transformed with a nucleic acid comprising a nucleotide sequence encoding a fusion protein according to the present invention.

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In a further aspect the present invention relates to a method of treating a disorder, disease or condition in a subject in need of treatment and/or prevention, which method comprises administering to said subject an effective amount of a fusion protein according to the present

invention and/or an effective amount of a host transformed with a nucleic acid comprising a nucleotide sequence encoding a fusion protein according to the present invention or a composition according to the present invention. The subject may be a human or an animal.

- 5 In particular said method of treatment may be for the treatment and/or prevention of infections of the skin, of soft tissues, the respiratory system, the lung, the digestive tract, the eye, the ear, the teeth, the nasopharynx, the mouth, the bones, the vagina, of wounds of bacteraemia and/or endocarditis caused by Gram-positive bacteria, in particular by the Gram-positive bacteria as listed above.

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The dosage and route of administration used in a method of treatment (or prophylaxis) according to the present invention depends on the specific disease/site of infection to be treated. The route of administration may be for example oral, topical, nasopharyngeal, parenteral, intravenous, rectal or any other route of administration.

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For application of a fusion protein according to the present invention and/or an effective amount of a host transformed with a nucleic acid comprising a nucleotide sequence encoding a fusion protein according to the present invention or a composition according to the present invention to a site of infection (or site endangered to be infected) a formulation may be used

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that protects the active compounds from environmental influences such as proteases, oxidation, immune response etc., until it reaches the site of infection. Therefore, the formulation may be capsule, dragee, pill, powder, suppository, emulsion, suspension, gel, lotion, cream, salve, injectable solution, syrup, spray, inhalant or any other medical reasonable galenic formulation. Preferably, the galenic formulation may comprise suitable

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carriers, stabilizers, flavourings, buffers or other suitable reagents. . For example, for topical application the formulation may be a lotion, cream, gel, salve or plaster, for nasopharyngeal application the formulation may be saline solution to be applied via a spray to the nose. For oral administration in case of the treatment and/or prevention of a specific infection site e.g. in the intestine, it can be necessary to protect a fusion protein according to the present

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invention from the harsh digestive environment of the gastrointestinal tract until the site of infection is reached. Thus, bacteria as carrier, which survive the initial steps of digestion in the stomach and which secret later on a fusion protein according to the present invention into the intestinal environment can be used.

In a specific embodiment of the present invention the use of a fusion protein according to the present invention and/or a host transformed with a vector comprising a nucleic acid molecule comprising a nucleotide sequence encoding a fusion protein according to the present invention in the manufacture of a medicament for the treatment and/or prevention of a disorder, disease or condition caused by *Listeria monocytogenes*, in particular Granulomatosis infantiseptica (listeriosis of newborns), mononucleosis, conjunctivitis, meningitis, granulomatosis septica and the listeriosis of pregnant women.

In another specific embodiment of the present invention the disorder, disease or condition is caused by *Staphylococcus aureus*, in particular infections of the skin like pyoderma, particularly folliculitis, furuncle, carbuncle, abscesses of the sweat glands and pemphigus, and like scaled skin syndrome. The scaled skin syndrome can appear in three clinical pictures: dermatitis exfoliativa, impetigo bullosa and scarlatiniform erythroderma. Moreover the disorder, disease or condition caused by *Staphylococcus aureus* is *Staphylococcus* pneumonia, hospitalism, in particular surgical wound infections, mastitis puerperalis and enterokolitis, and food poisonings.

In another specific embodiment of the present invention the disorder, disease or condition is caused by *Streptococcus pyogenes*, in particular tonsillitis, pharyngitis, scarlet, erysipelas, rheumatic fever and acute glomerulonephritis.

In another specific embodiment of the present invention the disorder, disease or condition is caused by *Streptococcus pneumoniae*, in particular pneumonia, ulcer serpens corneae, otitis media, meningitis, peritonitis, mastoiditis and osteomyelitis.

In another specific embodiment of the present invention the disorder, disease or condition is caused by *Clostridium perfringens*, in particular gas gangrene, enteritis necroticans ulcerosa and food poisonings.

In another specific embodiment of the present invention the disorder, disease or condition is caused by *Clostridium botulinum*, in particular botulism.

In another specific embodiment of the present invention the disorder, disease or condition is caused by *Clostridium difficile*, in particular pseudomembranous enterokolitis.

In another specific embodiment of the present invention the disorder, disease or condition is caused by *Bacillus anthracis*, in particular cutaneous anthrax, inhalation anthrax, and gastrointestinal anthrax.

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In another specific embodiment of the present invention the disorder, disease or condition is caused by *Enterococcus faecalis* or *E. faecium*, like nosokomial infections, and endokarditis.

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In another specific embodiment of the present invention the disorder, disease or condition is caused by *Bacillus cereus*, in particular food poisonings, bronchial pneumonia, septicaemia and meningitis.

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In another specific embodiment of the present invention the disorder, disease or condition is caused by *Mycobacterium avium*, *Mycobacterium paratuberculosis* and *Mycobacterium tuberculosis*, in particular tuberculosis.

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In another specific embodiment of the present invention the disorder, disease or condition is caused by *Mycoplasma pneumoniae*, in particular pneumonia, diseases of the upper respiratory tract and inflammations of the ear drum.

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In another specific embodiment of the present invention the disorder, disease or condition is caused by *Actinomyces*, in particular actinomycosis in human, cattle, cat and dog.

In another specific embodiment of the present invention the disorder, disease or condition is caused by *Corynebacterium diphtheriae*, in particular localized diphtheria of the tonsils, the nose, the nasopharynx or the middle ear, progressive diphtheria of the larynx, the trachea and the bronchi, toxic or malignant diphtheria, skin and wound diphtheria.

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Preferably, a fusion protein according to the present invention is used for medical treatment, if the infection to be treated (or prevented) is caused by multiresistant bacterial strains, in particular by strains resistant against one or more of the following antibiotics: streptomycin, tetracycline, cephalothin, penicillin, gentamicin, cefotaxime, cephalosporin, ceftazidime or imipenem. Furthermore, a fusion protein according to the present invention can be used in

methods of treatment by administering it in combination with conventional antibacterial agents, such as antibiotics, lantibiotics, bacteriocins or endolysins, etc.

The present invention also relates to a pharmaceutical pack comprising one or more compartments, wherein at least one compartment comprises one or more fusion protein according to the present invention and/or one or more hosts transformed with a nucleic acid comprising a nucleotide sequence encoding a fusion protein according to the present invention or a composition according to the present invention,

In another aspect the present invention relates to a process of preparation of a pharmaceutical composition, said process comprising admixing one or more fusion protein according to the present invention and/or one or more hosts transformed with a nucleic acid comprising a nucleotide sequence encoding a fusion protein according to the present invention with a pharmaceutically acceptable diluent, excipient or carrier.

In an even further aspect the composition according to the present invention is a cosmetic composition. Several bacterial species can cause irritations on environmentally exposed surfaces of the patient's body such as the skin. In order to prevent such irritations or in order to eliminate minor manifestations of said bacterial pathogens, special cosmetic preparations may be employed, which comprise sufficient amounts of the fusion protein according to the present invention in order to degrade already existing or freshly settling pathogenic Gram-positive bacteria.

In a further aspect the present invention relates to the fusion protein according to the present invention for use as diagnostic means in medicinal, food or feed or environmental diagnostics, in particular as a diagnostic means for the diagnostic of bacteria infection caused in particular by Gram-positive bacteria. In this respect the fusion protein according to the present invention may be used as a tool to specifically degrade pathogenic bacteria, in particular Gram-positive pathogenic bacteria. The degradation of the bacterial cells by the fusion protein according to the present invention can be supported by the addition of detergents like Triton X-100 or other additives which weaken the bacterial cell envelope like polymyxin B. Specific cell degradation is needed as an initial step for subsequent specific detection of bacteria using nucleic acid based methods like PCR, nucleic acid hybridization or NASBA (Nucleic Acid Sequence Based Amplification), immunological methods like IMS, immunofluorescence or

ELISA techniques, or other methods relying on the cellular content of the bacterial cells like enzymatic assays using proteins specific for distinct bacterial groups or species (e.g. β -galactosidase for enterobacteria, coagulase for coagulase positive strains).

- 5 In a further aspect the present invention relates to the use of the fusion protein according to the present invention for the treatment or prevention of Gram-positive bacterial contamination of foodstuff, of food processing equipment, of food processing plants, of surfaces coming into contact with foodstuff such as shelves and food deposit areas and in all other situations, where pathogenic, facultative pathogenic or other undesirable bacteria can potentially infest food
10 material, of medical devices and of all kind of surfaces in hospitals and surgeries.

In particular, a fusion protein of the present invention may be used prophylactically as sanitizing agent. Said sanitizing agent may be used before or after surgery, or for example during hemodialysis. Moreover, premature infants and immunocompromised persons, or
15 those subjects with need for prosthetic devices may be treated with a fusion protein according to the present invention. Said treatment may be either prophylactically or during acute infection. In the same context, nosocomial infections, especially by antibiotic resistant strains like *Methicillin-resistant Staphylococcus aureus*, *Vancomycin-resistant Enterococcus faecalis*, *Vancomycin-resistant Enterococcus faecium*, *Streptococcus pneumoniae*, *Propionibacterium*
20 *acnes*, *multidrug-resistant Mycobacterium tuberculosis*, may be treated prophylactically or during acute phase with a fusion protein of the present invention. Therefore, a fusion protein according to the present invention may be used as a disinfectant also in combination with other ingredients useful in a disinfecting solution like detergents, tensids, solvents, antibiotics, lanthibiotics, or bacteriocins.

25 For the use of the fusion protein according to the present invention as a disinfectant e.g. in hospital, dental surgery, veterinary, kitchen or bathroom, the fusion protein can be prepared in a composition in form of e.g. a fluid, a powder, a gel, or an ingredient of a wet wipe or a disinfection sheet product. Said composition may additionally comprise suitable carrier,
30 additives, diluting agents and/or excipients for its respective use and form, respectively, - but also agents that support the antimicrobial activity like EDTA or agents enhance the antimicrobial activity of the fusion proteins. The fusion protein may also be used with common disinfectant agents like, Alcohols, Aldehydes, Oxidizing agents, Phenolics, Quaternary ammonium compounds or UV-light. For disinfecting for example surfaces,

objects and/or devices the fusion protein can be applied on said surfaces, objects and/or devices. The application may occur for instance by wetting the disinfecting composition with any means such as a cloth or rag, by spraying, pouring. The fusion proteins may be used in varying concentration depending on the respective application and the „reaction time“ intended to obtain full antimicrobial activity.

Further scope of applicability of the present invention will become apparent from the detailed description given hereinafter, however, it should be understood that the detailed description and specific examples, while indicating preferred embodiments of the invention, are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description. It is to be understood that both the foregoing general description and the following detailed description are exemplary and explanatory only and are not restrictive of the invention, as claimed.

The following examples explain the present invention but are not considered to be limiting. Unless indicated differently, molecular biological standard methods were used, as e.g., described by Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York.

EXAMPLE 1: Cloning, expression and purification of Cpl-1, Ply511, LysK, Lysostaphin (Lss) and PA6-gp20 enzymes modified with various peptide stretches on the N-terminus or the C-terminus.

Enzymes

Cpl-1 according to SEQ ID NO: 57 is an endolysin originating from *Streptococcus pneumoniae* phage Cpl-1. The endolysin Cpl-1 is encoded by the nucleic acid molecule according to SEQ ID NO: 91. The nucleic acid molecule according to SEQ ID NO: 91 was synthetically produced with a BamH I (5'-GGA TCC-3') restriction site at the 5'-end of the nucleic acid molecule and an Xho I (5'-CTC GAG-3') restriction site at the 3'-end of the nucleic acid molecule.

Ply511 according to SEQ ID NO: 58 is an endolysin originating from *Listeria monocytogenes* phage A511. The endolysin Ply511 is encoded by the nucleic acid molecule according to SEQ

ID NO: 92. The nucleic acid molecule according to SEQ ID NO: 92 was synthetically produced with a BamH I (5'-GGA TCC-3') restriction site at the 5'-end of the nucleic acid molecule and an Xho I (5'-CTC GAG-3') restriction site at the 3'-end of the nucleic acid molecule.

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LysK according to SEQ ID NO: 59 is an endolysin originating from *Staphylococcus aureus* phage K. The endolysin LysK is encoded by the nucleic acid molecule according to SEQ ID NO: 93. The nucleic acid molecule according to SEQ ID NO: 93 was synthetically produced with a BamH I (5'-GGA TCC-3') restriction site at the 5'-end of the nucleic acid molecule and an Xho I (5'-CTC GAG-3') restriction site at the 3'-end of the nucleic acid molecule.

10

Lysostaphin (Lss) according to SEQ ID NO: 60 is a bacteriocin originating from *Staphylococcus simulans*. The bacteriocin Lss is encoded by the nucleic acid molecule according to SEQ ID NO: 94. The nucleic acid molecule according to SEQ ID NO: 94 was synthetically produced with a BamH I (5'-GGA TCC-3') restriction site at the 5'-end of the nucleic acid molecule and an Xho I (5'-CTC GAG-3') restriction site at the 3'-end of the nucleic acid molecule.

15

PA6-gp20 according to SEQ ID NO: 61 is an endolysin originating from *Propionibacterium acnes* phage. The endolysin PA6-gp20 is encoded by the nucleic acid molecule according to SEQ ID NO: 123. The nucleic acid molecule according to SEQ ID NO: 123 was synthetically produced with a BamH I (5'-GGA TCC-3') restriction site at the 5'-end of the nucleic acid molecule and an Xho I (5'-CTC GAG-3') restriction site at the 3'-end of the nucleic acid molecule.

20

25

The following peptide stretches in table 5 were used for production of fusion proteins with the enzymes Cpl-1, Ply511, LysK, Lysostaphin (Lss) and PA6-gp20:

Table 5 :

Peptide stretch	Nucleic acid molecule encoding the peptide stretch
Pseudin 1 (SEQ ID NO:51)	SEQ ID NO: 95
WLBU2-Variant	SEQ ID NO: 96

(SEQ ID NO:55)	
LL-37 (SEQ ID NO: 5)	SEQ ID NO: 97
Indolicidin (SEQ ID NO: 7)	SEQ ID NO: 98
Magainin (SEQ ID NO:4)	SEQ ID NO: 99
Pleurocidin (SEQ ID NO:1)	SEQ ID NO: 100
Cecropin A (A. aegypti) (SEQ ID NO:9)	SEQ ID NO:101
Buforin II (SEQ ID NO:3)	SEQ ID NO: 102
Sarcotoxin IA (SEQ ID NO:11)	SEQ ID NO: 103
PK (SEQ ID NO:13)	SEQ ID NO:104
Pentapeptide (SEQ ID NO:12)	SEQ ID NO:105
PK2 (SEQ ID NO: 31)	SEQ ID NO:106

The nucleic acid molecules encoding the respective peptide stretches were synthetically produced with a Nde I (5'-CAT ATG-3') restriction site at the 5'-end of the nucleic acid molecule and a BamH I (5'-GGA TCC-3') restriction site at the 3'-end of the nucleic acid molecule, except the nucleic acid molecule encoding the PK and PK2 for ligation with the bacteriocin Lss, which was produced with a Nco I restriction site plus two additional nucleotides (5'-CCA TGG GC-3') at the 5'-end of the nucleic acid molecule.

Fusion proteins are constructed by linking at least two nucleic acid sequences using standard cloning techniques as described e.g. by Sambrook et al. 2001, Molecular Cloning: A Laboratory Manual. Therefore the nucleic acid molecules encoding the peptide stretches were cleaved in a digest with the respective restriction enzymes Nde I and BamH I and in case of the nucleic acid molecule encoding the peptide stretch PK and PK2 for ligation with the Lss the digest was performed with the restriction enzymes Nco I and BamH I. Subsequently the cleaved nucleic acids encoding the peptide stretches were ligated into the pET21 b expression vector (Novagen, Darmstadt, Germany), which was also cleaved in a digest with the respective restriction enzymes Nde I and BamH I before. The cleaved nucleic acid molecule

encoding the peptide stretch PK and PK2 for ligation with Lss was ligated into a modified pET32 b expression vector (unmodified vector obtainable from Novagen, Darmstadt, Germany), which was also cleaved in a digest with the respective restriction enzymes Nco I and BamH I before. The modification of the pET32b expression vector refers to the deletion of the sequence encoding a S-tag and the central His₆-tag.

Afterwards, the nucleic acid molecules encoding the enzymes Cpl-1, Ply511, PA6-gp20, LysK and Lss were cleaved in a digest with the restriction enzyme BamH I and Xho I, so that the endolysin could be ligated into the pET21b expression vector (Novagen, Darmstadt, Germany) and the modified pET32 b expression vector, respectively, which were also cleaved in a digest with the respective restriction enzymes BamH I and Xho I before.

In the case of the peptide stretch PK, which was ligated to the C-terminus of the Lysostaphin and the LysK, the resulting fusion protein has a His₆-tag on the N-terminus, wherein the His₆-tag is linked to the N-terminus by a linker. For the cloning of the respective nucleic acid molecules the pET32 b expression vector (Novagen, Darmstadt, Germany) was used.

Thus, the nucleic acid molecule encoding the peptide stretch is ligated into the respective vector at the 5'-end of the nucleic acid molecule encoding the respective enzyme. Moreover, the nucleic acid molecule encoding the respective enzyme is ligated into the respective plasmid, so that a nucleic acid molecule encoding a His₆-tag consisting of six histidine residues is associated at the 3'-end of the nucleic acid molecule encoding the endolysin.

As some fusion proteins may either be toxic upon expression in bacteria, or not homogenous due to protein degradation, the strategy might be to express these fusion proteins fused or linked to other additional proteins. Example for these other additional protein is thioredoxin, which was shown to mediate expression of toxic antimicrobial peptides in *E.coli* (TrxA mediating fusion expression of antimicrobial peptide CM4 from multiple joined genes in *Escherichia coli*. Zhou L, Zhao Z, Li B, Cai Y, Zhang S. Protein Expr Purif. 2009 Apr;64(2):225-230). In the case of the fusion protein consisting of the N-terminal PK or PK2 peptide and the bacteriocin Lss, the peptide was ligated into the modified pET32 b expression vector, so that an additional thioredoxin is associated at the 5'-end of the peptide. The thioredoxin could be removed from the expressed fusion protein by the use of enterokinase,

therefore between the nucleic acid molecule encoding the peptide and the one encoding the thioredoxin is an enterokinase restriction site introduced.

The sequence of the endolysin-peptide-fusions was controlled via DNA-sequencing and correct clones were transformed into *E.coli* BL21(DE3) and in *E. coli* BL21 (DE3) pLysS cells (Novagen, Darmstadt, Germany) for protein expression.

Recombinant expression of the fusion proteins according to SEQ ID NO: 107 to 122 and 124 is performed in *E. coli* BL21 (DE3) and *E. coli* BL21 (DE3) pLysS cells (Novagen, Darmstadt, Germany). The cells were growing until an optical density of OD_{600nm} of 0.5-0.8 was reached. Then the expression of the fusion protein was induced with 1 mM IPTG (isopropylthiogalactoside) and the expression was performed at 37°C for a period of 4 hours.

E.coli BL21 cells were harvested by centrifugation for 20 min at 6000g and disrupted via sonication on ice. Soluble and insoluble fraction of the *E.coli* crude extract were separated by centrifugation (Sorvall, SS34, 30 min, 15 000 rpm). All proteins were purified by Ni²⁺ affinity chromatography (Akta FPLC, GE Healthcare) using the C-terminal His₆-tag, encoded by the pET21b or pET32b vectors.

Some proteins were expressed using a modified pET32b vector (S-tag and central His₆-tag deleted) as described above, which fuses thioredoxin on the N-terminus of the proteins of interest. The vector also contains an enterokinase cleavage site right before the protein of interest. This site allows the proteolytic cleavage between thioredoxin and the protein of interest, which can purified via the remaining C-terminal His₆-tag. For antimicrobial function of the fusion protein it may be necessary to remove the thioredoxin by proteolytic cleavage. Therefore the fusion protein was cleaved with 2-4 units/mg recombinant enterokinase (Novagen, Darmstadt, Germany) to remove the thioredoxin following the protocol provided by the manufacturer. After enterokinase cleavage the fusion protein was purified via His₆-tag purification as described below.

The Ni²⁺ affinity chromatography is performed in 4 subsequent steps, all at room temperature:

1. *Equilibration* of the *Histrap FF 5 ml* column (GE Healthcare) with up to 10 column volumes of Washing Buffer (20 mM imidazole, 1 M NaCl and 20 mM Hepes on pH 7.4) at a flow rate of 3-5 ml/min.
2. *Loading* of the total lysate (with wanted fusion protein) on the *Histrap FF 5 ml* column at a flow rate of 3-5 ml/min.
3. Washing of the column with up to 10 column volumes of Washing Buffer to remove unbound sample followed by a second washing step with 10% Elution buffer (500 mM imidazole, 0.5 M NaCl and 20 mM Hepes on pH 7.4) at a flow rate of 3-5 ml/min.
4. Elution of bounded fusion proteins from the column with a linear gradient of 4 column volumes of Elution Buffer (500 mM imidazole, 0.5 M NaCl and 20 mM Hepes on pH 7.4) to 100% at a flow rate of 3-5 ml/min.

Purified stock solutions of fusion proteins in Elution Buffer (20 mM Hepes pH 7.4; 0.5 M NaCl; 500 mM imidazole) were at least 90% pure as determined visually on SDS-PAGE gels (data not shown).

EXAMPLE 2: Antimicrobial activity of Cpl-1 enzymes modified with various peptide stretches on the N-terminus.

The fusion proteins Cpl 1 with the N-terminal peptide stretches Pseudin 1, WLBU2-Variant, LL-37, Indolicidin, Magainin, Pleurocidin, Cecropin A (*A. aegypti*), Buforin II, Sarcotoxin IA and PK were produced as described in example 1. The antimicrobial activity of said fusion protein against *Streptococcus pneumoniae* DSMZ 11967 and *Streptococcus pneumoniae* DSMZ 14378 were tested by using the plating test described below. The measured activity of the fusion protein is shown in Table 6.

The results presented in Table 6 show high antimicrobial activity of all fusion proteins against *Streptococcus pneumoniae* DSMZ 11967 and *Streptococcus pneumoniae* DSMZ 14378.

Plating assay:

Exponentially growing cells of e.g. Streptococci, Listeria, Propionibacteria or Staphylococci were taken (1ml) cooled on ice and washed with distilled water. The bacteria were

resuspended in 20mM Tris pH 7.0, 1 mM MgCl₂, 0.5 M Saccharose. Fusion proteins were diluted in resuspension buffer, adding sucrose to a final concentration of 0.5 M and incubated (final concentration of the fusion protein about 10µg/ml) with the respective bacteria for 60 minutes at room temperature. After that bacteria were plated on appropriated agar plates (e.g. Streptococci: Columbia blood agar) containing 0.5 M sucrose and the resulting colonies were counted after incubation.

The residual colonies were counted after an overnight incubation at 37°C. Based on the counted cell numbers the antibacterial activity as logarithmic units ($=\log_{10}N_0/N_i$ with N_0 = number of untreated cells and N_i = number of treated cells) was calculated. All samples were replicated at least in four fold.

Table 6:

Fusion protein	Enzyme part	Peptide stretch (N-terminal unless otherwise indicated)	Activity against <i>Streptococcus pneumoniae</i> DSMZ 11967	Activity against <i>Streptococcus pneumoniae</i> DSMZ 14378
SEQ ID NO:107	Cpl-1 (SEQ ID NO:57)	Pseudin 1 (SEQ ID NO:51)	+++	+++
SEQ ID NO:108	Cpl-1 (SEQ ID NO:57)	WLB2-Variant (SEQ ID NO:55)	++	++
SEQ ID NO:109	Cpl-1 (SEQ ID NO:57)	LL-37 (SEQ ID NO:5)	+++	+++
SEQ ID NO:110	Cpl-1 (SEQ ID NO:57)	Indolicidin (SEQ ID NO:7)	+++	+++
SEQ ID NO:111	Cpl-1 (SEQ ID NO:57)	Magainin (SEQ ID NO:4)	+++	+++
SEQ ID NO:112	Cpl-1 (SEQ ID NO:57)	Pleurocidin (SEQ ID NO:1)	+++	+++
SEQ ID NO:113	Cpl-1 (SEQ ID NO:57)	Cecropin A (A. aegypti) (SEQ ID NO:9)	+++	+++
SEQ ID NO:114	Cpl-1 (SEQ ID NO:57)	Buforin II (SEQ ID NO:3)	+++	+++
SEQ ID NO:115	Cpl-1 (SEQ ID NO:57)	Sarcotoxin IA (SEQ ID NO:11)	+++	+++
SEQ ID NO:116	Cpl-1 (SEQ ID NO:57)	PK (SEQ ID NO:13)	+++	+++

Abbreviations: +: 1 log; ++: 2-3 log; +++: 4 or more logs.

EXAMPLE 3: Antimicrobial activity of Ply511 enzyme modified with the pentapeptide on the N-terminus.

The fusion protein Ply511 with the N-terminal peptide stretch pentapeptide according to SEQ ID NO: 12 was produced as described in example 1. The antimicrobial activity of said fusion protein against *Listeria monocytogenes* DSMZ 15675 and *Listeria monocytogenes* DSMZ 20600 was tested by using the plating test described in example 2. The measured activity of the fusion protein is shown in Table 7.

The results presented in Table 7 show high antimicrobial activity of the fusion protein pentapeptide: Ply511 against *Listeria monocytogenes* DSMZ 15675 and *Listeria monocytogenes* DSMZ 20600.

Table 7:

Fusion protein	Enzyme part	Peptide stretch (N-terminal unless otherwise indicated)	Activity against <i>Listeria monocytogenes</i> DSMZ 15675	Activity against <i>Listeria monocytogenes</i> DSMZ 20600
SEQ ID NO:117	Ply511 (SEQ ID NO:58)	Pentapeptid (SEQ ID NO:12)	+++	+++

Abbreviations: +: 1 log; ++: 2-3 log; +++: 4 or more logs.

EXAMPLE 4: Antimicrobial activity of Lss and LysK enzyme modified with polycationic peptides on the N-terminus or C-terminus.

The fusion proteins Lss and LysK, respectively, with the N-terminal peptide stretch PK according to SEQ ID NO: 13, the fusion protein Lss with the N-terminal peptide stretch PK2 according to SEQ ID NO:31, as well as the fusion proteins Lss and LysK, respectively, with the C-terminal peptide stretch PK were produced as described in example 1. The antimicrobial activity of said fusion proteins against *Staphylococcus aureus* DSMZ 346 and

Staphylococcus epidermidis DSMZ 20041 was tested by using the plating test described in example 2, as well as by using the lysis test as described in the following.

Lysis test

- 5 The Lysis test was used for the modified LysK and Lysostaphins to examine the antimicrobial effect of these fusion proteins.

10 Staphylococcal cells were grown in BHI medium until and optical density at 600nm of 0.7-1 was reached indicating exponential growth. Cells were harvested by centrifugation and resuspended in lysis buffer (20 mM Tris-HCl (pH 7.4), 60 mM NaCl, 2 mM CaCl₂). Cells were resuspended at an optical density at 600nm of 1.0 and incubated with fusion proteins. Activity was measured spectrophotometrically at 600nm.

The measured activity of the fusion protein is shown in Table 8.

15 The results presented in Table 8 show high antimicrobial activity of the fusion proteins Lss with the N-terminal peptide PK or PK2 against *Staphylococcus aureus* DSMZ 346 and *Staphylococcus epidermidis* DSMZ 20041. But also the other fusion proteins show antimicrobial activity against the two tested bacterial strains.

20

Table 8

Fusion protein	Enzyme part	Peptide stretch (N-terminal unless otherwise indicated)	Activity against <i>Staphylococcus aureus</i> DSMZ 346	Activity against <i>Staphylococcus epidermidis</i> DSMZ 20041
SEQ ID NO:118	LysK (SEQ ID NO:59)	PK (SEQ ID NO:13)	+	+
SEQ ID NO:119	Lysostaphin (SEQ ID NO:60)	PK (SEQ ID NO:13)	+++	+++
SEQ ID NO:120	Lysostaphin (SEQ ID NO:60)	PK2 (SEQ ID NO:31)	+++	+++
SEQ ID NO:121	LysK (SEQ ID NO:59)	PK (C-terminal) (SEQ ID NO:13)	+	+
SEQ ID NO:122	Lysostaphin (SEQ ID NO:60)	PK (C-terminal) (SEQ ID NO:13)	+	+

Abbreviations: +: 1 log; ++: 2-3 log; +++: 4 or more logs.

EXAMPLE 5: Antimicrobial activity of PA6-gp20 enzyme modified with the hydrophobic peptide stretch Walmagh 1

The fusion protein PA6-gp20 with the N-terminal peptide stretch Walmagh 1 according to SEQ ID NO: 56 was produced as described in example 1. The antimicrobial activity of said fusion protein against *Propionibacterium acnes* DSMZ 1897 and *Propionibacterium acnes* DSMZ 16379 was tested by using the plating test described in example 2. The measured activity of the fusion protein is shown in Table 9.

The results presented in Table 9 show antimicrobial activity of the fusion protein against both bacterial strains of *Propionibacterium acnes*.

Table 9:

Fusion protein	Enzyme part	Peptide stretch (N-terminal unless otherwise indicated)	Activity against <i>Propionibacterium acnes</i> DSMZ 1897	Activity against <i>Propionibacterium acnes</i> DSMZ 16379
SEQ ID NO: 124	PA6-gp20 (SEQ ID NO:61)	Walmagh 1 (SEQ ID NO:56)	++	++

Abbreviations: ++: 2-3 log;

The fusion proteins in Table 6 to 9 without any tag and linker were also tested with the activity assays described above. They all showed antimicrobial activity against the used bacterial strains in Table 6 to 9.

CLAIMS

1. A fusion protein composed of an enzyme having the activity of degrading the cell wall of Gram-positive bacteria and a peptide stretch fused to the enzyme at the N- or C-terminus or at both termini.
2. The fusion protein according to claim 1, wherein said fusion protein comprises an additional amino acid residue on the N-terminus.
3. The fusion protein according to claim 1 or 2, wherein said fusion protein exhibits an amino acid sequence according to SEQ ID NO: 63 to 90.
4. The fusion protein according to any of the preceding claims, wherein said fusion protein comprises a tag or additional protein on the C- and/or N-terminus.
5. The fusion protein according to claim 4, wherein said tag or additional protein is linked to the fusion protein by one or more additional amino acid residues.
6. The fusion protein according to any of the preceding claims, wherein the peptide stretch is linked to the fusion protein by one or more additional amino acid residues.
7. The fusion protein according to claim 1, wherein the enzyme is an endolysin, autolysin or a bacteriocin.
8. The fusion protein according to claim 7, wherein the enzyme exhibits an amino acid sequence according to SEQ ID NO: 57 to 61.
9. The fusion protein according to any of the preceding claims, wherein the Gram-positive bacteria are selected from the group consisting of the bacteria listed in table 1.
10. The fusion protein according to any one of the preceding claims, wherein the peptide stretch is a cationic, more preferably a polycationic peptide, amphipathic peptide, sushi peptide, defensin, hydrophobic peptide or an antimicrobial peptide.

11. The fusion protein according to claim 10, wherein the sushi peptide exhibits an amino acid sequence according to SEQ ID NO: 54.
- 5 12. The fusion protein according to claim 10, wherein the cationic peptide comprises at least one amino acid residue selected out of the group consisting of arginine, histidine and lysine residues.
13. The fusion protein according to claim 10, wherein the antimicrobial peptide exhibits an amino acid sequence according to SEQ ID NO:1 to 11 or 48 to 53.
- 10 14. The fusion protein according to claim 10, wherein the hydrophobic peptide exhibits an amino acid sequence according to SEQ ID NO: 12, 50, 55 or 56.
- 15 15. The fusion protein according to claim 10, wherein at least about 70% of the amino acid residues comprised in said cationic peptide are either arginine, histidine or lysine residues, or wherein at least about 70% of the amino acid residues comprised in said peptide are either arginine or lysine, or wherein the amino acid residues comprised in said peptide are either arginine or lysine residues.
- 20 16. The fusion protein according to claim 15, wherein the cationic peptide exhibits an amino acid sequence according to SEQ ID NO: 13 or 24 to 44.
- 25 17. The fusion protein according to claim 10, wherein the amphipatic peptide comprises at least one positively charged amino acid residues selected out of the group consisting of lysine, arginine and histidine residues, combined to at least one hydrophobic amino acid residue selected out of the group consisting of valine, isoleucine, leucine, methionine, phenylalanine, tryptophan, cysteine, alanine, tyrosine, histidine, threonin, serine, proline and glycine residues.
- 30 18. The fusion protein according to claim 17, wherein at least about 70% of the said amino acid residues in said amphipatic peptide are either arginine or lysine residues and at least about 30% of the said amino acid residues in said amphipatic peptide are valine, isoleucine, leucine, methionine, phenylalanine, tryptophan, cysteine, alanine, tyrosine, histidine, threonin, serine, proline or glycine residues.

19. The fusion protein according to claim 18, wherein the amphipatic peptide exhibits an amino acid sequence according to SEQ ID NO: 1 to 5, 23, 48 or 49.
- 5 20. The fusion protein according to any one of claims 1 to 19, wherein the peptide stretch comprises about 5 to about 100 amino acid residues, in particular about 5 to 50 amino acid residues, in particular about 5 to 30 amino acid residues.
- 10 21. An isolated nucleic acid molecule encoding a fusion protein according to any of claims 1 to 19.
22. A vector comprising the nucleic acid molecule according to claim 21.
- 15 23. A host cell comprising the nucleic acid molecule according to claim 21 or the vector according to claim 122.
24. A host cell according to claim 23, wherein the cell is a bacterial cell or a yeast cell.
- 20 25. A host cell according to claim 24, wherein the yeast cell is *Pichia pastoris* cell.
26. The fusion protein according to any one of claims 1 to 20 for use as a medicament, diagnostic means or cosmetic substance.
- 25 27. The fusion protein according to any one of claims 1 to 20 for use as a medicament for treatment or prevention of Gram-positive bacterial infections.
28. The fusion protein according to any one of the claims 1 to 20 for use as a disinfectant.
- 30 29. The use of the fusion protein according to any one of claims 1 to 20 for the treatment or prevention of Gram-positive bacterial contamination of foodstuff, of food processing equipment, of food processing plants, of surfaces coming into contact with foodstuff, of medical devices, of surfaces in hospitals and surgeries.

30. The use of the fusion protein according to any one of claims 1 to 20 as a diagnostic means in medicinal, food or feed or environmental diagnostics.

31. Pharmaceutical composition comprising a fusion protein according to any one of claims 1 to 20.

5

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 <213> Unknown

<220>
 <223> Putative Lysin Staphylococcus phage K

<400> 16

Met Gly Ser Lys Arg Lys Lys Arg Lys Lys Arg Lys Arg Ser Lys Arg
 1 5 10 15

Lys Lys Arg Lys Lys Arg Lys Arg Ser Lys Arg Lys Lys Arg Lys Lys
 20 25 30

Arg Lys Ala Lys Thr Gln Ala Glu Ile Asn Lys Arg Leu Asp Ala Tyr
 35 40 45

Ala Lys Gly Thr Val Asp Ser Pro Tyr Arg Val Lys Lys Ala Thr Ser
 50 55 60

Tyr Asp Pro Ser Phe Gly Val Met Glu Ala Gly Ala Ile Asp Ala Asp

65					70						75				80
Gly	Tyr	Tyr	His	Ala	Gln	Cys	Gln	Asp	Leu	Ile	Thr	Asp	Tyr	Val	Leu
				85					90					95	
Trp	Leu	Thr	Asp	Asn	Lys	Val	Arg	Thr	Trp	Gly	Asn	Ala	Lys	Asp	Gln
			100					105					110		
Ile	Lys	Gln	Ser	Tyr	Gly	Thr	Gly	Phe	Lys	Ile	His	Glu	Asn	Lys	Pro
		115					120					125			
Ser	Thr	Val	Pro	Lys	Lys	Gly	Trp	Ile	Ala	Val	Phe	Thr	Ser	Gly	Ser
	130					135					140				
Tyr	Glu	Gln	Trp	Gly	His	Ile	Gly	Ile	Val	Tyr	Asp	Gly	Gly	Asn	Thr
145					150					155					160
Ser	Thr	Phe	Thr	Ile	Leu	Glu	Gln	Asn	Trp	Asn	Gly	Tyr	Ala	Asn	Lys
				165					170					175	
Lys	Pro	Thr	Lys	Arg	Val	Asp	Asn	Tyr	Tyr	Gly	Leu	Thr	His	Phe	Ile
			180					185					190		
Glu	Ile	Pro	Val	Lys	Ala	Gly	Thr	Thr	Val	Lys	Lys	Glu	Thr	Ala	Lys
		195					200					205			
Lys	Ser	Ala	Ser	Lys	Thr	Pro	Ala	Pro	Lys	Lys	Lys	Ala	Thr	Leu	Lys
	210					215					220				
Val	Ser	Lys	Asn	His	Ile	Asn	Tyr	Thr	Met	Asp	Lys	Arg	Gly	Lys	Lys
225					230					235					240
Pro	Glu	Gly	Met	Val	Ile	His	Asn	Asp	Ala	Gly	Arg	Ser	Ser	Gly	Gln
				245					250					255	
Gln	Tyr	Glu	Asn	Ser	Leu	Ala	Asn	Ala	Gly	Tyr	Ala	Arg	Tyr	Ala	Asn
			260					265					270		
Gly	Ile	Ala	His	Tyr	Tyr	Gly	Ser	Glu	Gly	Tyr	Val	Trp	Glu	Ala	Ile
		275					280					285			
Asp	Ala	Lys	Asn	Gln	Ile	Ala	Trp	His	Thr	Gly	Asp	Gly	Thr	Gly	Ala
	290					295					300				
Asn	Ser	Gly	Asn	Phe	Arg	Phe	Ala	Gly	Ile	Glu	Val	Cys	Gln	Ser	Met
305					310					315					320

Ser Ala Ser Asp Ala Gln Phe Leu Lys Asn Glu Gln Ala Val Phe Gln
325 330 335

Phe Thr Ala Glu Lys Phe Lys Glu Trp Gly Leu Thr Pro Asn Arg Lys
340 345 350

Thr Val Arg Leu His Met Glu Phe Val Pro Thr Ala Cys Pro His Arg
355 360 365

Ser Met Val Leu His Thr Gly Phe Asn Pro Val Thr Gln Gly Arg Pro
370 375 380

Ser Gln Ala Ile Met Asn Lys Leu Lys Asp Tyr Phe Ile Lys Gln Ile
385 390 395 400

Lys Asn Tyr Met Asp Lys Gly Thr Ser Ser Ser Thr Val Val Lys Asp
405 410 415

Gly Lys Thr Ser Ser Ala Ser Thr Pro Ala Thr Arg Pro Val Thr Gly
420 425 430

Ser Trp Lys Lys Asn Gln Tyr Gly Thr Trp Tyr Lys Pro Glu Asn Ala
435 440 445

Thr Phe Val Asn Gly Asn Gln Pro Ile Val Thr Arg Ile Gly Ser Pro
450 455 460

Phe Leu Asn Ala Pro Val Gly Gly Asn Leu Pro Ala Gly Ala Thr Ile
465 470 475 480

Val Tyr Asp Glu Val Cys Ile Gln Ala Gly His Ile Trp Ile Gly Tyr
485 490 495

Asn Ala Tyr Asn Gly Asn Arg Val Tyr Cys Pro Val Arg Thr Cys Gln
500 505 510

Gly Val Pro Pro Asn Gln Ile Pro Gly Val Ala Trp Gly Val Phe Lys
515 520 525

<210> 17
<211> 505
<212> PRT
<213> Unknown

<220>
<223> Putative Lysin Staphylococcus phage K

<400> 17

Met Ala Lys Thr Gln Ala Glu Ile Asn Lys Arg Leu Asp Ala Tyr Ala

1		5		10		15													
Lys	Gly	Thr	Val	Asp	Ser	Pro	Tyr	Arg	Val	Lys	Lys	Ala	Thr	Ser	Tyr				
			20					25					30						
Asp	Pro	Ser	Phe	Gly	Val	Met	Glu	Ala	Gly	Ala	Ile	Asp	Ala	Asp	Gly				
		35					40					45							
Tyr	Tyr	His	Ala	Gln	Cys	Gln	Asp	Leu	Ile	Thr	Asp	Tyr	Val	Leu	Trp				
	50					55					60								
Leu	Thr	Asp	Asn	Lys	Val	Arg	Thr	Trp	Gly	Asn	Ala	Lys	Asp	Gln	Ile				
65					70				75						80				
Lys	Gln	Ser	Tyr	Gly	Thr	Gly	Phe	Lys	Ile	His	Glu	Asn	Lys	Pro	Ser				
				85					90					95					
Thr	Val	Pro	Lys	Lys	Gly	Trp	Ile	Ala	Val	Phe	Thr	Ser	Gly	Ser	Tyr				
			100					105					110						
Glu	Gln	Trp	Gly	His	Ile	Gly	Ile	Val	Tyr	Asp	Gly	Gly	Asn	Thr	Ser				
		115					120					125							
Thr	Phe	Thr	Ile	Leu	Glu	Gln	Asn	Trp	Asn	Gly	Tyr	Ala	Asn	Lys	Lys				
	130					135					140								
Pro	Thr	Lys	Arg	Val	Asp	Asn	Tyr	Tyr	Gly	Leu	Thr	His	Phe	Ile	Glu				
145					150					155					160				
Ile	Pro	Val	Lys	Ala	Gly	Thr	Thr	Val	Lys	Lys	Glu	Thr	Ala	Lys	Lys				
				165					170					175					
Ser	Ala	Ser	Lys	Thr	Pro	Ala	Pro	Lys	Lys	Lys	Ala	Thr	Leu	Lys	Val				
			180					185					190						
Ser	Lys	Asn	His	Ile	Asn	Tyr	Thr	Met	Asp	Lys	Arg	Gly	Lys	Lys	Pro				
		195					200					205							
Glu	Gly	Met	Val	Ile	His	Asn	Asp	Ala	Gly	Arg	Ser	Ser	Gly	Gln	Gln				
	210					215					220								
Tyr	Glu	Asn	Ser	Leu	Ala	Asn	Ala	Gly	Tyr	Ala	Arg	Tyr	Ala	Asn	Gly				
225					230					235					240				
Ile	Ala	His	Tyr	Tyr	Gly	Ser	Glu	Gly	Tyr	Val	Trp	Glu	Ala	Ile	Asp				
				245					250					255					

Ala Lys Asn Gln Ile Ala Trp His Thr Gly Asp Gly Thr Gly Ala Asn
 260 265 270

Ser Gly Asn Phe Arg Phe Ala Gly Ile Glu Val Cys Gln Ser Met Ser
 275 280 285

Ala Ser Asp Ala Gln Phe Leu Lys Asn Glu Gln Ala Val Phe Gln Phe
 290 295 300

Thr Ala Glu Lys Phe Lys Glu Trp Gly Leu Thr Pro Asn Arg Lys Thr
 305 310 315 320

Val Arg Leu His Met Glu Phe Val Pro Thr Ala Cys Pro His Arg Ser
 325 330 335

Met Val Leu His Thr Gly Phe Asn Pro Val Thr Gln Gly Arg Pro Ser
 340 345 350

Gln Ala Ile Met Asn Lys Leu Lys Asp Tyr Phe Ile Lys Gln Ile Lys
 355 360 365

Asn Tyr Met Asp Lys Gly Thr Ser Ser Ser Thr Val Val Lys Asp Gly
 370 375 380

Lys Thr Ser Ser Ala Ser Thr Pro Ala Thr Arg Pro Val Thr Gly Ser
 385 390 395 400

Trp Lys Lys Asn Gln Tyr Gly Thr Trp Tyr Lys Pro Glu Asn Ala Thr
 405 410 415

Phe Val Asn Gly Asn Gln Pro Ile Val Thr Arg Ile Gly Ser Pro Phe
 420 425 430

Leu Asn Ala Pro Val Gly Gly Asn Leu Pro Ala Gly Ala Thr Ile Val
 435 440 445

Tyr Asp Glu Val Cys Ile Gln Ala Gly His Ile Trp Ile Gly Tyr Asn
 450 455 460

Ala Tyr Asn Gly Asn Arg Val Tyr Cys Pro Val Arg Thr Cys Gln Gly
 465 470 475 480

Val Pro Pro Asn Gln Ile Pro Gly Val Ala Trp Gly Val Phe Lys Ser
 485 490 495

Lys Arg Lys Lys Arg Lys Lys Arg Lys
 500 505

<210> 18
 <211> 527
 <212> PRT
 <213> Unknown

<220>
 <223> Putative Lysin Staphylococcus phage K

<400> 18

Met Ala Lys Thr Gln Ala Glu Ile Asn Lys Arg Leu Asp Ala Tyr Ala
 1 5 10 15

Lys Gly Thr Val Asp Ser Pro Tyr Arg Val Lys Lys Ala Thr Ser Tyr
 20 25 30

Asp Pro Ser Phe Gly Val Met Glu Ala Gly Ala Ile Asp Ala Asp Gly
 35 40 45

Tyr Tyr His Ala Gln Cys Gln Asp Leu Ile Thr Asp Tyr Val Leu Trp
 50 55 60

Leu Thr Asp Asn Lys Val Arg Thr Trp Gly Asn Ala Lys Asp Gln Ile
 65 70 75 80

Lys Gln Ser Tyr Gly Thr Gly Phe Lys Ile His Glu Asn Lys Pro Ser
 85 90 95

Thr Val Pro Lys Lys Gly Trp Ile Ala Val Phe Thr Ser Gly Ser Tyr
 100 105 110

Glu Gln Trp Gly His Ile Gly Ile Val Tyr Asp Gly Gly Asn Thr Ser
 115 120 125

Thr Phe Thr Ile Leu Glu Gln Asn Trp Asn Gly Tyr Ala Asn Lys Lys
 130 135 140

Pro Thr Lys Arg Val Asp Asn Tyr Tyr Gly Leu Thr His Phe Ile Glu
 145 150 155 160

Ile Pro Val Lys Ala Gly Thr Thr Val Lys Lys Glu Thr Ala Lys Lys
 165 170 175

Ser Ala Ser Lys Thr Pro Ala Pro Lys Lys Lys Ala Thr Leu Lys Val
 180 185 190

Ser Lys Asn His Ile Asn Tyr Thr Met Asp Lys Arg Gly Lys Lys Pro
 195 200 205

Glu Gly Met Val Ile His Asn Asp Ala Gly Arg Ser Ser Gly Gln Gln
 210 215 220

Tyr Glu Asn Ser Leu Ala Asn Ala Gly Tyr Ala Arg Tyr Ala Asn Gly
 225 230 235 240

Ile Ala His Tyr Tyr Gly Ser Glu Gly Tyr Val Trp Glu Ala Ile Asp
 245 250 255

Ala Lys Asn Gln Ile Ala Trp His Thr Gly Asp Gly Thr Gly Ala Asn
 260 265 270

Ser Gly Asn Phe Arg Phe Ala Gly Ile Glu Val Cys Gln Ser Met Ser
 275 280 285

Ala Ser Asp Ala Gln Phe Leu Lys Asn Glu Gln Ala Val Phe Gln Phe
 290 295 300

Thr Ala Glu Lys Phe Lys Glu Trp Gly Leu Thr Pro Asn Arg Lys Thr
 305 310 315 320

Val Arg Leu His Met Glu Phe Val Pro Thr Ala Cys Pro His Arg Ser
 325 330 335

Met Val Leu His Thr Gly Phe Asn Pro Val Thr Gln Gly Arg Pro Ser
 340 345 350

Gln Ala Ile Met Asn Lys Leu Lys Asp Tyr Phe Ile Lys Gln Ile Lys
 355 360 365

Asn Tyr Met Asp Lys Gly Thr Ser Ser Ser Thr Val Val Lys Asp Gly
 370 375 380

Lys Thr Ser Ser Ala Ser Thr Pro Ala Thr Arg Pro Val Thr Gly Ser
 385 390 395 400

Trp Lys Lys Asn Gln Tyr Gly Thr Trp Tyr Lys Pro Glu Asn Ala Thr
 405 410 415

Phe Val Asn Gly Asn Gln Pro Ile Val Thr Arg Ile Gly Ser Pro Phe
 420 425 430

Leu Asn Ala Pro Val Gly Gly Asn Leu Pro Ala Gly Ala Thr Ile Val
 435 440 445

Tyr Asp Glu Val Cys Ile Gln Ala Gly His Ile Trp Ile Gly Tyr Asn
 450 455 460

Ala Tyr Asn Gly Asn Arg Val Tyr Cys Pro Val Arg Thr Cys Gln Gly
465 470 475 480

Val Pro Pro Asn Gln Ile Pro Gly Val Ala Trp Gly Val Phe Lys Ser
485 490 495

Lys Arg Lys Lys Arg Lys Lys Arg Lys Arg Ser Lys Arg Lys Lys Arg
500 505 510

Lys Lys Arg Lys Arg Ser Lys Arg Lys Lys Arg Lys Lys Arg Lys
515 520 525

<210> 19
<211> 255
<212> PRT
<213> Unknown

<220>
<223> Lysostaphin

<400> 19

Met Gly Ser Lys Arg Lys Lys Arg Lys Lys Arg Lys His Glu His Ser
1 5 10 15

Ala Gln Trp Leu Asn Asn Tyr Lys Lys Gly Tyr Gly Tyr Gly Pro Tyr
20 25 30

Pro Leu Gly Ile Asn Gly Gly Met His Tyr Gly Val Asp Phe Phe Met
35 40 45

Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser Gly Lys Ile Val Glu
50 55 60

Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln Ile Gly Leu Ile Glu
65 70 75 80

Asn Asp Gly Val His Arg Gln Trp Tyr Met His Leu Ser Lys Tyr Asn
85 90 95

Val Lys Val Gly Asp Tyr Val Lys Ala Gly Gln Ile Ile Gly Trp Ser
100 105 110

Gly Ser Thr Gly Tyr Ser Thr Ala Pro His Leu His Phe Gln Arg Met
115 120 125

Val Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp Pro Met Pro Phe Leu
130 135 140

Lys Ser Ala Gly Tyr Gly Lys Ala Gly Gly Thr Val Thr Pro Thr Pro
145 150 155 160

Asn Thr Gly Trp Lys Thr Asn Lys Tyr Gly Thr Leu Tyr Lys Ser Glu
165 170 175

Ser Ala Ser Phe Thr Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly
180 185 190

Pro Phe Arg Ser Met Pro Gln Ser Gly Val Leu Lys Ala Gly Gln Thr
195 200 205

Ile His Tyr Asp Glu Val Met Lys Gln Asp Gly His Val Trp Val Gly
210 215 220

Tyr Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp
225 230 235 240

Asn Lys Ser Thr Asn Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
245 250 255

<210> 20
<211> 277
<212> PRT
<213> Unknown

<220>
<223> Lysostaphin

<400> 20

Met Gly Ser Lys Arg Lys Lys Arg Lys Lys Arg Lys Arg Ser Lys Arg
1 5 10 15

Lys Lys Arg Lys Lys Arg Lys Arg Ser Lys Arg Lys Lys Arg Lys Lys
20 25 30

Arg Lys His Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys Gly
35 40 45

Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His Tyr
50 55 60

Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser
65 70 75 80

Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn
85 90 95

Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr Met
100 105 110

His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly
115 120 125

Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His
130 135 140

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

Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly Gly
165 170 175

Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr Gly
180 185 190

Thr Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp Ile
195 200 205

Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly Val
210 215 220

Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln Asp
225 230 235 240

Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile Tyr
245 250 255

Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val Leu
260 265 270

Trp Gly Thr Ile Lys
275

<210> 21
<211> 254
<212> PRT
<213> Unknown

<220>
<223> Lysostaphin

<400> 21

Met His Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys Gly Tyr
1 5 10 15

Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His Tyr Gly
20 25 30

Val Asp Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser
35 40 45

Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln
50 55 60

Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr Met His
65 70 75 80

Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly Gln
85 90 95

Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His Leu
100 105 110

His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp
115 120 125

Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly Gly Thr
130 135 140

Val Thr Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr Gly Thr
145 150 155 160

Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp Ile Ile
165 170 175

Thr Arg Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly Val Leu
180 185 190

Lys Ala Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln Asp Gly
195 200 205

His Val Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu
210 215 220

Pro Val Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val Leu Trp
225 230 235 240

Gly Thr Ile Lys Ser Lys Arg Lys Lys Arg Lys Lys Arg Lys
245 250

<210> 22
<211> 276

<212> PRT
<213> Unknown

<220>
<223> Lysostaphin

<400> 22

Met His Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys Gly Tyr
1 5 10 15

Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His Tyr Gly
20 25 30

Val Asp Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser
35 40 45

Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln
50 55 60

Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr Met His
65 70 75 80

Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly Gln
85 90 95

Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His Leu
100 105 110

His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp
115 120 125

Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly Gly Thr
130 135 140

Val Thr Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr Gly Thr
145 150 155 160

Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp Ile Ile
165 170 175

Thr Arg Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly Val Leu
180 185 190

Lys Ala Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln Asp Gly
195 200 205

His Val Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu
210 215 220

Pro Val Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val Leu Trp
 225 230 235 240

Gly Thr Ile Lys Ser Lys Arg Lys Lys Arg Lys Lys Arg Lys Arg Ser
 245 250 255

Lys Arg Lys Lys Arg Lys Lys Arg Lys Arg Ser Lys Arg Lys Lys Arg
 260 265 270

Lys Lys Arg Lys
 275

<210> 23
 <211> 39
 <212> PRT
 <213> Unknown

<220>
 <223> Buforin I

<400> 23

Ala Gly Arg Gly Lys Gln Gly Gly Lys Val Arg Ala Lys Ala Lys Thr
 1 5 10 15

Arg Ser Ser Arg Ala Gly Leu Gln Phe Pro Val Gly Arg Val His Arg
 20 25 30

Leu Leu Arg Lys Gly Asn Tyr
 35

<210> 24
 <211> 6
 <212> PRT
 <213> Unknown

<220>
 <223> peptide stretch

<400> 24

Lys Arg Lys Lys Arg Lys
 1 5

<210> 25
 <211> 9
 <212> PRT
 <213> Unknown

<220>
 <223> peptide stretch

<400> 25

Arg Arg Arg Arg Arg Arg Arg Arg Arg
1 5

<210> 26
<211> 8
<212> PRT
<213> Unknown

<220>
<223> peptide stretch

<400> 26

Lys Lys Lys Lys Lys Lys Lys Lys
1 5

<210> 27
<211> 10
<212> PRT
<213> Unknown

<220>
<223> peptide stretch

<400> 27

Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys
1 5 10

<210> 28
<211> 12
<212> PRT
<213> Unknown

<220>
<223> peptide stretch

<400> 28

Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys
1 5 10

<210> 29
<211> 14
<212> PRT
<213> Unknown

<220>
<223> peptide stretch

<400> 29

Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg
1 5 10

<210> 30
<211> 16

<212> PRT
<213> Unknown

<220>
<223> peptide stretch

<400> 30

Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
1 5 10 15

<210> 31
<211> 18
<212> PRT
<213> Unknown

<220>
<223> peptide stretch

<400> 31

Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys
1 5 10 15

Arg Lys

<210> 32
<211> 19
<212> PRT
<213> Unknown

<220>
<223> peptide stretch

<400> 32

Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys
1 5 10 15

Arg Lys Lys

<210> 33
<211> 19
<212> PRT
<213> Unknown

<220>
<223> peptide stretch

<400> 33

Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg
1 5 10 15

Arg Arg Arg

<210> 34
<211> 19
<212> PRT
<213> Unknown

<220>
<223> peptide stretch

<400> 34

Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
1 5 10 15

Lys Lys Lys

<210> 35
<211> 20
<212> PRT
<213> Unknown

<220>
<223> peptide stretch

<400> 35

Lys Arg Lys Lys Arg Lys Lys Arg Lys Arg Ser Lys Arg Lys Lys Arg
1 5 10 15

Lys Lys Arg Lys
20

<210> 36
<211> 21
<212> PRT
<213> Unknown

<220>
<223> peptide stretch

<400> 36

Lys Arg Lys Lys Arg Lys Lys Arg Lys Arg Ser Lys Arg Lys Lys Arg
1 5 10 15

Lys Lys Arg Lys Lys
20

<210> 37
<211> 21
<212> PRT
<213> Unknown

<220>
 <223> peptide stretch
 <400> 37
 Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys
 1 5 10 15
 Arg Lys Lys Arg Lys
 20
 <210> 38
 <211> 22
 <212> PRT
 <213> Unknown
 <220>
 <223> peptide stretch
 <400> 38
 Lys Arg Lys Lys Arg Lys Lys Arg Lys Arg Gly Ser Gly Lys Arg Lys
 1 5 10 15
 Lys Arg Lys Lys Arg Lys
 20
 <210> 39
 <211> 24
 <212> PRT
 <213> Unknown
 <220>
 <223> peptide stretch
 <400> 39
 Lys Arg Lys Lys Arg Lys Lys Arg Lys Arg Gly Ser Gly Ser Gly Lys
 1 5 10 15
 Arg Lys Lys Arg Lys Lys Arg Lys
 20
 <210> 40
 <211> 25
 <212> PRT
 <213> Unknown
 <220>
 <223> peptide stretch
 <400> 40
 Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys
 1 5 10 15

Arg Lys Lys Arg Lys Lys Arg Lys Lys
20 25

<210> 41
<211> 31
<212> PRT
<213> Unknown

<220>
<223> peptide stretch

<400> 41

Lys Arg Lys Lys Arg Lys Lys Arg Lys Arg Ser Lys Arg Lys Lys Arg
1 5 10 15

Lys Lys Arg Lys Arg Ser Lys Arg Lys Lys Arg Lys Lys Arg Lys
20 25 30

<210> 42
<211> 38
<212> PRT
<213> Unknown

<220>
<223> peptide stretch

<400> 42

Lys Arg Lys Lys Arg Lys Lys Arg Lys Arg Gly Ser Gly Ser Gly Lys
1 5 10 15

Arg Lys Lys Arg Lys Lys Arg Lys Gly Ser Gly Ser Gly Lys Arg Lys
20 25 30

Lys Arg Lys Lys Arg Lys
35

<210> 43
<211> 39
<212> PRT
<213> Unknown

<220>
<223> peptide stretch

<400> 43

Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys
1 5 10 15

Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg
20 25 30

Lys Lys Arg Lys Lys Arg Lys
35

<210> 44
<211> 42
<212> PRT
<213> Unknown

<220>
<223> peptide stretch

<400> 44

Lys Arg Lys Lys Arg Lys Lys Arg Lys Arg Ser Lys Arg Lys Lys Arg
1 5 10 15

Lys Lys Arg Lys Arg Ser Lys Arg Lys Lys Arg Lys Lys Arg Lys Arg
20 25 30

Ser Lys Arg Lys Lys Arg Lys Lys Arg Lys
35 40

<210> 45
<211> 5
<212> PRT
<213> Unknown

<220>
<223> motif for polypeptide stretches, wherein X is any other amino
acid than lysine, arginine and histidine

<220>
<221> misc_feature
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<400> 45

Lys Arg Xaa Lys Arg
1 5

<210> 46
<211> 5
<212> PRT
<213> Unknown

<220>
<223> motif for polypeptide stretches

<400> 46

Lys Arg Ser Lys Arg
1 5

<210> 47
<211> 5

<212> PRT
<213> Unknown

<220>
<223> motif for polypeptide stretches

<400> 47

Lys Arg Gly Ser Gly
1 5

<210> 48
<211> 22
<212> PRT
<213> Unknown

<220>
<223> Nigrocine 2

<400> 48

Gly Leu Leu Ser Lys Val Leu Gly Val Gly Lys Lys Val Leu Cys Gly
1 5 10 15

Val Ser Gly Leu Val Cys
20

<210> 49
<211> 24
<212> PRT
<213> Unknown

<220>
<223> Ascaphine 5

<400> 49

Gly Ile Lys Asp Trp Ile Lys Gly Ala Ala Lys Lys Leu Ile Lys Thr
1 5 10 15

Val Ala Ser His Ile Ala Asn Gln
20

<210> 50
<211> 17
<212> PRT
<213> Unknown

<220>
<223> Apidaecine

<400> 50

Ala Asn Arg Pro Val Tyr Ile Pro Pro Pro Arg Pro Pro His Pro Arg
1 5 10 15

Leu

<210> 51
<211> 24
<212> PRT
<213> Unknown

<220>
<223> Pseudin 1

<400> 51

Gly Leu Asn Thr Leu Lys Lys Val Phe Gln Gly Leu His Glu Ala Ile
1 5 10 15

Lys Leu Ile Asn Asn His Val Gln
20

<210> 52
<211> 18
<212> PRT
<213> Unknown

<220>
<223> Ranalexin

<400> 52

Phe Leu Gly Gly Leu Ile Val Pro Ala Met Ile Cys Ala Val Thr Lys
1 5 10 15

Lys Cys

<210> 53
<211> 26
<212> PRT
<213> Unknown

<220>
<223> Melittin

<400> 53

Gly Ile Gly Ala Val Leu Lys Val Leu Thr Thr Gly Leu Pro Ala Leu
1 5 10 15

Ile Ser Trp Ile Lys Arg Lys Arg Gln Gln
20 25

<210> 54
<211> 34
<212> PRT
<213> Unknown

<220>

<223> Sushi 1 peptide

<400> 54

Gly Phe Lys Leu Lys Gly Met Ala Arg Ile Ser Cys Leu Pro Asn Gly
1 5 10 15

Gln Trp Ser Asn Phe Pro Pro Lys Cys Ile Arg Glu Cys Ala Met Val
20 25 30

Ser Ser

<210> 55

<211> 27

<212> PRT

<213> Unknown

<220>

<223> WLBW2-Variant

<400> 55

Lys Arg Trp Val Lys Arg Val Lys Arg Val Lys Arg Trp Val Lys Arg
1 5 10 15

Val Val Arg Val Val Lys Arg Trp Val Lys Arg
20 25

<210> 56

<211> 18

<212> PRT

<213> Unknown

<220>

<223> Walmagh1

<400> 56

Gly Phe Phe Ile Pro Ala Val Ile Leu Pro Ser Ile Ala Phe Leu Ile
1 5 10 15

Val Pro

<210> 57

<211> 339

<212> PRT

<213> Unknown

<220>

<223> Cpl-1

<400> 57

Met Val Lys Lys Asn Asp Leu Phe Val Asp Val Ser Ser His Asn Gly

1	5	10	15
Tyr	Asp	Ile	Thr
	20		
Gly	Ile	Leu	Glu
			25
Gln	Met	Gly	Thr
			Thr
Asn	Thr	Ile	
	30		
Ile	Lys	Ile	Ser
	35		
Glu	Ser	Thr	Thr
			40
Tyr	Leu	Asn	Pro
			Cys
			45
Gln	Val	Glu	Gln
	50		
Ser	Asn	Pro	Ile
			55
Gly	Phe	Tyr	His
			60
Phe	Ala	Arg	Phe
Gly	Gly	Asp	Val
	65		
Ala	Glu	Ala	Glu
			70
Arg	Glu	Ala	Gln
			75
Phe	Phe	Leu	Asp
			80
Asn	Val	Pro	Met
			85
Gln	Val	Lys	Tyr
			90
Leu	Val	Leu	Asp
			Tyr
Glu	Asp	Asp	
			95
Pro	Ser	Gly	Asp
			100
Ala	Gln	Ala	Asn
			105
Thr	Asn	Ala	Cys
			Leu
Arg	Phe	Met	
			110
Gln	Met	Ile	Ala
			115
Asp	Ala	Gly	Tyr
			120
Lys	Pro	Ile	Tyr
			125
Tyr	Ser	Tyr	Lys
Pro	Phe	Thr	His
			130
Asp	Asn	Val	Asp
			135
Tyr	Gln	Gln	Ile
			140
Leu	Ala	Gln	Phe
Pro	Asn	Ser	Leu
			145
Trp	Ile	Ala	Gly
			150
Tyr	Gly	Leu	Asn
			155
Asp	Gly	Thr	Ala
			160
Asn	Phe	Glu	Tyr
			165
Phe	Pro	Ser	Met
			170
Asp	Gly	Ile	Arg
			175
Trp	Trp	Gln	Tyr
Ser	Ser	Asn	Pro
			180
Phe	Asp	Lys	Asn
			185
Ile	Val	Leu	Leu
			190
Asp	Asp	Glu	Glu
Asp	Asp	Lys	Pro
			195
Lys	Thr	Ala	Gly
			200
Thr	Trp	Lys	Gln
			205
Asp	Ser	Lys	Gly
Trp	Trp	Phe	Arg
			210
Arg	Asn	Asn	Gly
			215
Ser	Phe	Pro	Tyr
			220
Asn	Lys	Trp	Glu
Lys	Ile	Gly	Gly
			225
Val	Trp	Tyr	Tyr
			230
Phe	Asp	Ser	Lys
			235
Gly	Tyr	Cys	Leu
			240
Thr	Ser	Glu	Trp
			245
Leu	Lys	Asp	Asn
			Glu
Lys	Trp	Tyr	Tyr
			250
Leu	Lys	Asp	
			255

Asn Gly Ala Met Ala Thr Gly Trp Val Leu Val Gly Ser Glu Trp Tyr
260 265 270

Tyr Met Asp Asp Ser Gly Ala Met Val Thr Gly Trp Val Lys Tyr Lys
275 280 285

Asn Asn Trp Tyr Tyr Met Thr Asn Glu Arg Gly Asn Met Val Ser Asn
290 295 300

Glu Phe Ile Lys Ser Gly Lys Gly Trp Tyr Phe Met Asn Thr Asn Gly
305 310 315 320

Glu Leu Ala Asp Asn Pro Ser Phe Thr Lys Glu Pro Asp Gly Leu Ile
325 330 335

Thr Val Ala

<210> 58
<211> 341
<212> PRT
<213> Unknown

<220>
<223> Ply511

<400> 58

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

Gly Lys Leu Lys Gly Ala Asn Phe Val Ile Ala His Glu Thr Ala Asn
20 25 30

Ser Lys Ser Thr Ile Asp Asn Glu Val Ser Tyr Met Thr Arg Asn Trp
35 40 45

Lys Asn Ala Phe Val Thr His Phe Val Gly Gly Gly Gly Arg Val Val
50 55 60

Gln Val Ala Asn Val Asn Tyr Val Ser Trp Gly Ala Gly Gln Tyr Ala
65 70 75 80

Asn Ser Tyr Ser Tyr Ala Gln Val Glu Leu Cys Arg Thr Ser Asn Ala
85 90 95

Thr Thr Phe Lys Lys Asp Tyr Glu Val Tyr Cys Gln Leu Leu Val Asp
100 105 110

Leu Ala Lys Lys Ala Gly Ile Pro Ile Thr Leu Asp Ser Gly Ser Lys
115 120 125

Thr Ser Asp Lys Gly Ile Lys Ser His Lys Trp Val Ala Asp Lys Leu
130 135 140

Gly Gly Thr Thr His Gln Asp Pro Tyr Ala Tyr Leu Ser Ser Trp Gly
145 150 155 160

Ile Ser Lys Ala Gln Phe Ala Ser Asp Leu Ala Lys Val Ser Gly Gly
165 170 175

Gly Asn Thr Gly Thr Ala Pro Ala Lys Pro Ser Thr Pro Ala Pro Lys
180 185 190

Pro Ser Thr Pro Ser Thr Asn Leu Asp Lys Leu Gly Leu Val Asp Tyr
195 200 205

Met Asn Ala Lys Lys Met Asp Ser Ser Tyr Ser Asn Arg Asp Lys Leu
210 215 220

Ala Lys Gln Tyr Gly Ile Ala Asn Tyr Ser Gly Thr Ala Ser Gln Asn
225 230 235 240

Thr Thr Leu Leu Ser Lys Ile Lys Gly Gly Ala Pro Lys Pro Ser Thr
245 250 255

Pro Ala Pro Lys Pro Ser Thr Ser Thr Ala Lys Lys Ile Tyr Phe Pro
260 265 270

Pro Asn Lys Gly Asn Trp Ser Val Tyr Pro Thr Asn Lys Ala Pro Val
275 280 285

Lys Ala Asn Ala Ile Gly Ala Ile Asn Pro Thr Lys Phe Gly Gly Leu
290 295 300

Thr Tyr Thr Ile Gln Lys Asp Arg Gly Asn Gly Val Tyr Glu Ile Gln
305 310 315 320

Thr Asp Gln Phe Gly Arg Val Gln Val Tyr Gly Ala Pro Ser Thr Gly
325 330 335

Ala Val Ile Lys Lys
340

<210> 59
<211> 495

<212> PRT
<213> Unknown

<220>
<223> LysK

<400> 59

Met Ala Lys Thr Gln Ala Glu Ile Asn Lys Arg Leu Asp Ala Tyr Ala
1 5 10 15

Lys Gly Thr Val Asp Ser Pro Tyr Arg Val Lys Lys Ala Thr Ser Tyr
20 25 30

Asp Pro Ser Phe Gly Val Met Glu Ala Gly Ala Ile Asp Ala Asp Gly
35 40 45

Tyr Tyr His Ala Gln Cys Gln Asp Leu Ile Thr Asp Tyr Val Leu Trp
50 55 60

Leu Thr Asp Asn Lys Val Arg Thr Trp Gly Asn Ala Lys Asp Gln Ile
65 70 75 80

Lys Gln Ser Tyr Gly Thr Gly Phe Lys Ile His Glu Asn Lys Pro Ser
85 90 95

Thr Val Pro Lys Lys Gly Trp Ile Ala Val Phe Thr Ser Gly Ser Tyr
100 105 110

Glu Gln Trp Gly His Ile Gly Ile Val Tyr Asp Gly Gly Asn Thr Ser
115 120 125

Thr Phe Thr Ile Leu Glu Gln Asn Trp Asn Gly Tyr Ala Asn Lys Lys
130 135 140

Pro Thr Lys Arg Val Asp Asn Tyr Tyr Gly Leu Thr His Phe Ile Glu
145 150 155 160

Ile Pro Val Lys Ala Gly Thr Thr Val Lys Lys Glu Thr Ala Lys Lys
165 170 175

Ser Ala Ser Lys Thr Pro Ala Pro Lys Lys Lys Ala Thr Leu Lys Val
180 185 190

Ser Lys Asn His Ile Asn Tyr Thr Met Asp Lys Arg Gly Lys Lys Pro
195 200 205

Glu Gly Met Val Ile His Asn Asp Ala Gly Arg Ser Ser Gly Gln Gln
210 215 220

Tyr Glu Asn Ser Leu Ala Asn Ala Gly Tyr Ala Arg Tyr Ala Asn Gly
 225 230 235 240
 Ile Ala His Tyr Tyr Gly Ser Glu Gly Tyr Val Trp Glu Ala Ile Asp
 245 250 255
 Ala Lys Asn Gln Ile Ala Trp His Thr Gly Asp Gly Thr Gly Ala Asn
 260 265 270
 Ser Gly Asn Phe Arg Phe Ala Gly Ile Glu Val Cys Gln Ser Met Ser
 275 280 285
 Ala Ser Asp Ala Gln Phe Leu Lys Asn Glu Gln Ala Val Phe Gln Phe
 290 295 300
 Thr Ala Glu Lys Phe Lys Glu Trp Gly Leu Thr Pro Asn Arg Lys Thr
 305 310 315 320
 Val Arg Leu His Met Glu Phe Val Pro Thr Ala Cys Pro His Arg Ser
 325 330 335
 Met Val Leu His Thr Gly Phe Asn Pro Val Thr Gln Gly Arg Pro Ser
 340 345 350
 Gln Ala Ile Met Asn Lys Leu Lys Asp Tyr Phe Ile Lys Gln Ile Lys
 355 360 365
 Asn Tyr Met Asp Lys Gly Thr Ser Ser Ser Thr Val Val Lys Asp Gly
 370 375 380
 Lys Thr Ser Ser Ala Ser Thr Pro Ala Thr Arg Pro Val Thr Gly Ser
 385 390 395 400
 Trp Lys Lys Asn Gln Tyr Gly Thr Trp Tyr Lys Pro Glu Asn Ala Thr
 405 410 415
 Phe Val Asn Gly Asn Gln Pro Ile Val Thr Arg Ile Gly Ser Pro Phe
 420 425 430
 Leu Asn Ala Pro Val Gly Gly Asn Leu Pro Ala Gly Ala Thr Ile Val
 435 440 445
 Tyr Asp Glu Val Cys Ile Gln Ala Gly His Ile Trp Ile Gly Tyr Asn
 450 455 460
 Ala Tyr Asn Gly Asn Arg Val Tyr Cys Pro Val Arg Thr Cys Gln Gly

465 470 475 480
 Val Pro Pro Asn Gln Ile Pro Gly Val Ala Trp Gly Val Phe Lys
 485 490 495

 <210> 60
 <211> 245
 <212> PRT
 <213> Unknown

 <220>
 <223> Lysostaphin

 <400> 60

 Met Ala His Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys Gly
 1 5 10 15

 Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His Tyr
 20 25 30

 Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser
 35 40 45

 Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn
 50 55 60

 Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr Met
 65 70 75 80

 His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly
 85 90 95

 Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His
 100 105 110

 Leu His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala Gln
 115 120 125

 Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly Gly
 130 135 140

 Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr Gly
 145 150 155 160

 Thr Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp Ile
 165 170 175

 Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly Val
 180 185 190

Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln Asp
195 200 205

Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile Tyr
210 215 220

Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val Leu
225 230 235 240

Trp Gly Thr Ile Lys
245

<210> 61
<211> 286
<212> PRT
<213> Unknown

<220>
<223> PA6-gp20

<400> 61

Met Val Arg Tyr Ile Pro Ala Ala His His Ser Ala Gly Ser Asn Asn
1 5 10 15

Pro Val Asn Arg Val Val Ile His Ala Thr Cys Pro Asp Val Gly Phe
20 25 30

Pro Ser Ala Ser Arg Lys Gly Arg Ala Val Ser Thr Ala Asn Tyr Phe
35 40 45

Ala Ser Pro Ser Ser Gly Gly Ser Ala His Tyr Val Cys Asp Ile Gly
50 55 60

Glu Thr Val Gln Cys Leu Ser Glu Ser Thr Ile Gly Trp His Ala Pro
65 70 75 80

Pro Asn Pro His Ser Leu Gly Ile Glu Ile Cys Ala Asp Gly Gly Ser
85 90 95

His Ala Ser Phe Arg Val Pro Gly His Ala Tyr Thr Arg Glu Gln Trp
100 105 110

Leu Asp Pro Gln Val Trp Pro Ala Val Glu Arg Ala Ala Val Leu Cys
115 120 125

Arg Arg Leu Cys Asp Lys Tyr Asn Val Pro Lys Arg Lys Leu Ser Ala
130 135 140

Ala Asp Leu Lys Ala Gly Arg Arg Gly Val Cys Gly His Val Asp Val
 145 150 155 160

Thr Asp Ala Trp His Gln Ser Asp His Asp Asp Pro Gly Pro Trp Phe
 165 170 175

Pro Trp Asp Lys Phe Met Ala Val Val Asn Gly Gly Ser Gly Asp Ser
 180 185 190

Gly Glu Leu Thr Val Ala Asp Val Lys Ala Leu His Asp Gln Ile Lys
 195 200 205

Gln Leu Ser Ala Gln Leu Thr Gly Ser Val Asn Lys Leu His His Asp
 210 215 220

Val Gly Val Val Gln Val Gln Asn Gly Asp Leu Gly Lys Arg Val Asp
 225 230 235 240

Ala Leu Ser Trp Val Lys Asn Pro Val Thr Gly Lys Leu Trp Arg Thr
 245 250 255

Lys Asp Ala Leu Trp Ser Val Trp Tyr Tyr Val Leu Glu Cys Arg Ser
 260 265 270

Arg Leu Asp Arg Leu Glu Ser Ala Val Asn Asp Leu Lys Lys
 275 280 285

<210> 62

<211> 6

<212> PRT

<213> Unknown

<220>

<223> cationic peptide

<400> 62

Lys Arg Lys Lys Arg Lys
 1 5

<210> 63

<211> 362

<212> PRT

<213> Unknown

<220>

<223> Ascaphine5-Cpl1

<400> 63

Gly Ile Lys Asp Trp Ile Lys Gly Ala Ala Lys Lys Leu Ile Lys Thr

1	5	10	15
Val	Ala	Ser	His
	20		
Ile	Ala	Asn	Gln
		25	
Val	Lys	Lys	Asn
			30
Asp	Leu	Phe	Val
Asp	Val	Ser	Ser
	35		
His	Asn	Gly	Tyr
		40	
Asp	Ile	Thr	Gly
			45
Ile	Leu	Glu	Gln
Met	Gly	Thr	Thr
	50		
Asn	Thr	Ile	Ile
		55	
Lys	Ile	Ser	Glu
			60
Ser	Thr	Thr	Tyr
Leu	Asn	Pro	Cys
	65		
Leu	Ser	Ala	Gln
	70		
Val	Glu	Gln	Ser
		75	
Asn	Pro	Ile	Gly
			80
Phe	Tyr	His	Phe
		85	
Arg	Phe	Gly	Gly
		90	
Asp	Val	Ala	Glu
			95
Ala	Glu	Ala	Glu
			95
Arg			
Glu	Ala	Gln	Phe
		100	
Phe	Leu	Asp	Asn
			105
Val	Pro	Met	Gln
			110
Lys	Tyr	Leu	
Val	Leu	Asp	Tyr
	115		
Glu	Asp	Asp	Pro
			120
Ser	Gly	Asp	Ala
			125
Gln	Ala	Asn	Thr
Asn	Ala	Cys	Leu
	130		
Arg	Phe	Met	Gln
		135	
Met	Ile	Ala	Asp
			140
Ala	Gly	Tyr	Lys
Pro	Ile	Tyr	Tyr
	145		
Ser	Tyr	Lys	Pro
	150		
Phe	Thr	His	Asp
		155	
Asn	Val	Asp	Tyr
			160
Gln	Gln	Ile	Leu
		165	
Ala	Gln	Phe	Pro
			170
Asn	Ser	Leu	Trp
			175
Ile	Ala	Gly	Tyr
Gly	Leu	Asn	Asp
	180		
Gly	Thr	Ala	Asn
		185	
Phe	Glu	Tyr	Phe
			190
Pro	Ser	Met	Asp
Gly	Ile	Arg	Trp
	195		
Trp	Gln	Tyr	Ser
			200
Ser	Ser	Asn	Pro
			205
Phe	Asp	Lys	Asn
			210
Ile	Val	Thr	Ala
			215
Gly	Glu	Asp	Asp
			220
Lys	Pro	Lys	Thr
Trp	Lys	Gln	Asp
	225		
Ser	Lys	Gly	Trp
	230		
Trp	Phe	Arg	Arg
		235	
Asn	Asn	Gly	Ser
			240
Phe	Pro	Tyr	Asn
	245		
Lys	Trp	Glu	Lys
			250
Ile	Gly	Gly	Val
			255
Trp	Tyr	Tyr	Phe

Asp Ser Lys Gly Tyr Cys Leu Thr Ser Glu Trp Leu Lys Asp Asn Glu
260 265 270

Lys Trp Tyr Tyr Leu Lys Asp Asn Gly Ala Met Ala Thr Gly Trp Val
275 280 285

Leu Val Gly Ser Glu Trp Tyr Tyr Met Asp Asp Ser Gly Ala Met Val
290 295 300

Thr Gly Trp Val Lys Tyr Lys Asn Asn Trp Tyr Tyr Met Thr Asn Glu
305 310 315 320

Arg Gly Asn Met Val Ser Asn Glu Phe Ile Lys Ser Gly Lys Gly Trp
325 330 335

Tyr Phe Met Asn Thr Asn Gly Glu Leu Ala Asp Asn Pro Ser Phe Thr
340 345 350

Lys Glu Pro Asp Gly Leu Ile Thr Val Ala
355 360

<210> 64
<211> 355
<212> PRT
<213> Unknown

<220>
<223> Apidaecine-Cpl1

<400> 64

Ala Asn Arg Pro Val Tyr Ile Pro Pro Pro Arg Pro Pro His Pro Arg
1 5 10 15

Leu Val Lys Lys Asn Asp Leu Phe Val Asp Val Ser Ser His Asn Gly
20 25 30

Tyr Asp Ile Thr Gly Ile Leu Glu Gln Met Gly Thr Thr Asn Thr Ile
35 40 45

Ile Lys Ile Ser Glu Ser Thr Thr Tyr Leu Asn Pro Cys Leu Ser Ala
50 55 60

Gln Val Glu Gln Ser Asn Pro Ile Gly Phe Tyr His Phe Ala Arg Phe
65 70 75 80

Gly Gly Asp Val Ala Glu Ala Glu Arg Glu Ala Gln Phe Phe Leu Asp
85 90 95

Asn Val Pro Met Gln Val Lys Tyr Leu Val Leu Asp Tyr Glu Asp Asp
 100 105 110

Pro Ser Gly Asp Ala Gln Ala Asn Thr Asn Ala Cys Leu Arg Phe Met
 115 120 125

Gln Met Ile Ala Asp Ala Gly Tyr Lys Pro Ile Tyr Tyr Ser Tyr Lys
 130 135 140

Pro Phe Thr His Asp Asn Val Asp Tyr Gln Gln Ile Leu Ala Gln Phe
 145 150 155 160

Pro Asn Ser Leu Trp Ile Ala Gly Tyr Gly Leu Asn Asp Gly Thr Ala
 165 170 175

Asn Phe Glu Tyr Phe Pro Ser Met Asp Gly Ile Arg Trp Trp Gln Tyr
 180 185 190

Ser Ser Asn Pro Phe Asp Lys Asn Ile Val Leu Leu Asp Asp Glu Glu
 195 200 205

Asp Asp Lys Pro Lys Thr Ala Gly Thr Trp Lys Gln Asp Ser Lys Gly
 210 215 220

Trp Trp Phe Arg Arg Asn Asn Gly Ser Phe Pro Tyr Asn Lys Trp Glu
 225 230 235 240

Lys Ile Gly Gly Val Trp Tyr Tyr Phe Asp Ser Lys Gly Tyr Cys Leu
 245 250 255

Thr Ser Glu Trp Leu Lys Asp Asn Glu Lys Trp Tyr Tyr Leu Lys Asp
 260 265 270

Asn Gly Ala Met Ala Thr Gly Trp Val Leu Val Gly Ser Glu Trp Tyr
 275 280 285

Tyr Met Asp Asp Ser Gly Ala Met Val Thr Gly Trp Val Lys Tyr Lys
 290 295 300

Asn Asn Trp Tyr Tyr Met Thr Asn Glu Arg Gly Asn Met Val Ser Asn
 305 310 315 320

Glu Phe Ile Lys Ser Gly Lys Gly Trp Tyr Phe Met Asn Thr Asn Gly
 325 330 335

Glu Leu Ala Asp Asn Pro Ser Phe Thr Lys Glu Pro Asp Gly Leu Ile
 340 345 350

Thr Val Ala
355

<210> 65
<211> 360
<212> PRT
<213> Unknown

<220>
<223> Nigrocine2-Cpl1

<400> 65

Gly Leu Leu Ser Lys Val Leu Gly Val Gly Lys Lys Val Leu Cys Gly
1 5 10 15

Val Ser Gly Leu Val Cys Val Lys Lys Asn Asp Leu Phe Val Asp Val
20 25 30

Ser Ser His Asn Gly Tyr Asp Ile Thr Gly Ile Leu Glu Gln Met Gly
35 40 45

Thr Thr Asn Thr Ile Ile Lys Ile Ser Glu Ser Thr Thr Tyr Leu Asn
50 55 60

Pro Cys Leu Ser Ala Gln Val Glu Gln Ser Asn Pro Ile Gly Phe Tyr
65 70 75 80

His Phe Ala Arg Phe Gly Gly Asp Val Ala Glu Ala Glu Arg Glu Ala
85 90 95

Gln Phe Phe Leu Asp Asn Val Pro Met Gln Val Lys Tyr Leu Val Leu
100 105 110

Asp Tyr Glu Asp Asp Pro Ser Gly Asp Ala Gln Ala Asn Thr Asn Ala
115 120 125

Cys Leu Arg Phe Met Gln Met Ile Ala Asp Ala Gly Tyr Lys Pro Ile
130 135 140

Tyr Tyr Ser Tyr Lys Pro Phe Thr His Asp Asn Val Asp Tyr Gln Gln
145 150 155 160

Ile Leu Ala Gln Phe Pro Asn Ser Leu Trp Ile Ala Gly Tyr Gly Leu
165 170 175

Asn Asp Gly Thr Ala Asn Phe Glu Tyr Phe Pro Ser Met Asp Gly Ile
180 185 190

Arg Trp Trp Gln Tyr Ser Ser Asn Pro Phe Asp Lys Asn Ile Val Leu
195 200 205

Leu Asp Asp Glu Glu Asp Asp Lys Pro Lys Thr Ala Gly Thr Trp Lys
210 215 220

Gln Asp Ser Lys Gly Trp Trp Phe Arg Arg Asn Asn Gly Ser Phe Pro
225 230 235 240

Tyr Asn Lys Trp Glu Lys Ile Gly Gly Val Trp Tyr Tyr Phe Asp Ser
245 250 255

Lys Gly Tyr Cys Leu Thr Ser Glu Trp Leu Lys Asp Asn Glu Lys Trp
260 265 270

Tyr Tyr Leu Lys Asp Asn Gly Ala Met Ala Thr Gly Trp Val Leu Val
275 280 285

Gly Ser Glu Trp Tyr Tyr Met Asp Asp Ser Gly Ala Met Val Thr Gly
290 295 300

Trp Val Lys Tyr Lys Asn Asn Trp Tyr Tyr Met Thr Asn Glu Arg Gly
305 310 315 320

Asn Met Val Ser Asn Glu Phe Ile Lys Ser Gly Lys Gly Trp Tyr Phe
325 330 335

Met Asn Thr Asn Gly Glu Leu Ala Asp Asn Pro Ser Phe Thr Lys Glu
340 345 350

Pro Asp Gly Leu Ile Thr Val Ala
355 360

<210> 66
<211> 362
<212> PRT
<213> Unknown

<220>
<223> Pseudin1-Cpl1

<400> 66

Gly Leu Asn Thr Leu Lys Lys Val Phe Gln Gly Leu His Glu Ala Ile
1 5 10 15

Lys Leu Ile Asn Asn His Val Gln Val Lys Lys Asn Asp Leu Phe Val
20 25 30

Asp Val Ser Ser His Asn Gly Tyr Asp Ile Thr Gly Ile Leu Glu Gln
 35 40 45
 Met Gly Thr Thr Asn Thr Ile Ile Lys Ile Ser Glu Ser Thr Thr Tyr
 50 55 60
 Leu Asn Pro Cys Leu Ser Ala Gln Val Glu Gln Ser Asn Pro Ile Gly
 65 70 75 80
 Phe Tyr His Phe Ala Arg Phe Gly Gly Asp Val Ala Glu Ala Glu Arg
 85 90 95
 Glu Ala Gln Phe Phe Leu Asp Asn Val Pro Met Gln Val Lys Tyr Leu
 100 105 110
 Val Leu Asp Tyr Glu Asp Asp Pro Ser Gly Asp Ala Gln Ala Asn Thr
 115 120 125
 Asn Ala Cys Leu Arg Phe Met Gln Met Ile Ala Asp Ala Gly Tyr Lys
 130 135 140
 Pro Ile Tyr Tyr Ser Tyr Lys Pro Phe Thr His Asp Asn Val Asp Tyr
 145 150 155 160
 Gln Gln Ile Leu Ala Gln Phe Pro Asn Ser Leu Trp Ile Ala Gly Tyr
 165 170 175
 Gly Leu Asn Asp Gly Thr Ala Asn Phe Glu Tyr Phe Pro Ser Met Asp
 180 185 190
 Gly Ile Arg Trp Trp Gln Tyr Ser Ser Asn Pro Phe Asp Lys Asn Ile
 195 200 205
 Val Leu Leu Asp Asp Glu Glu Asp Asp Lys Pro Lys Thr Ala Gly Thr
 210 215 220
 Trp Lys Gln Asp Ser Lys Gly Trp Trp Phe Arg Arg Asn Asn Gly Ser
 225 230 235 240
 Phe Pro Tyr Asn Lys Trp Glu Lys Ile Gly Gly Val Trp Tyr Tyr Phe
 245 250 255
 Asp Ser Lys Gly Tyr Cys Leu Thr Ser Glu Trp Leu Lys Asp Asn Glu
 260 265 270
 Lys Trp Tyr Tyr Leu Lys Asp Asn Gly Ala Met Ala Thr Gly Trp Val
 275 280 285

Leu Val Gly Ser Glu Trp Tyr Tyr Met Asp Asp Ser Gly Ala Met Val
 290 295 300

Thr Gly Trp Val Lys Tyr Lys Asn Asn Trp Tyr Tyr Met Thr Asn Glu
 305 310 315 320

Arg Gly Asn Met Val Ser Asn Glu Phe Ile Lys Ser Gly Lys Gly Trp
 325 330 335

Tyr Phe Met Asn Thr Asn Gly Glu Leu Ala Asp Asn Pro Ser Phe Thr
 340 345 350

Lys Glu Pro Asp Gly Leu Ile Thr Val Ala
 355 360

<210> 67
 <211> 356
 <212> PRT
 <213> Unknown

<220>
 <223> Ranalexin-Cpl1

<400> 67

Phe Leu Gly Gly Leu Ile Val Pro Ala Met Ile Cys Ala Val Thr Lys
 1 5 10 15

Lys Cys Val Lys Lys Asn Asp Leu Phe Val Asp Val Ser Ser His Asn
 20 25 30

Gly Tyr Asp Ile Thr Gly Ile Leu Glu Gln Met Gly Thr Thr Asn Thr
 35 40 45

Ile Ile Lys Ile Ser Glu Ser Thr Thr Tyr Leu Asn Pro Cys Leu Ser
 50 55 60

Ala Gln Val Glu Gln Ser Asn Pro Ile Gly Phe Tyr His Phe Ala Arg
 65 70 75 80

Phe Gly Gly Asp Val Ala Glu Ala Glu Arg Glu Ala Gln Phe Phe Leu
 85 90 95

Asp Asn Val Pro Met Gln Val Lys Tyr Leu Val Leu Asp Tyr Glu Asp
 100 105 110

Asp Pro Ser Gly Asp Ala Gln Ala Asn Thr Asn Ala Cys Leu Arg Phe
 115 120 125

Met Gln Met Ile Ala Asp Ala Gly Tyr Lys Pro Ile Tyr Tyr Ser Tyr
 130 135 140

Lys Pro Phe Thr His Asp Asn Val Asp Tyr Gln Gln Ile Leu Ala Gln
 145 150 155 160

Phe Pro Asn Ser Leu Trp Ile Ala Gly Tyr Gly Leu Asn Asp Gly Thr
 165 170 175

Ala Asn Phe Glu Tyr Phe Pro Ser Met Asp Gly Ile Arg Trp Trp Gln
 180 185 190

Tyr Ser Ser Asn Pro Phe Asp Lys Asn Ile Val Leu Leu Asp Asp Glu
 195 200 205

Glu Asp Asp Lys Pro Lys Thr Ala Gly Thr Trp Lys Gln Asp Ser Lys
 210 215 220

Gly Trp Trp Phe Arg Arg Asn Asn Gly Ser Phe Pro Tyr Asn Lys Trp
 225 230 235 240

Glu Lys Ile Gly Gly Val Trp Tyr Tyr Phe Asp Ser Lys Gly Tyr Cys
 245 250 255

Leu Thr Ser Glu Trp Leu Lys Asp Asn Glu Lys Trp Tyr Tyr Leu Lys
 260 265 270

Asp Asn Gly Ala Met Ala Thr Gly Trp Val Leu Val Gly Ser Glu Trp
 275 280 285

Tyr Tyr Met Asp Asp Ser Gly Ala Met Val Thr Gly Trp Val Lys Tyr
 290 295 300

Lys Asn Asn Trp Tyr Tyr Met Thr Asn Glu Arg Gly Asn Met Val Ser
 305 310 315 320

Asn Glu Phe Ile Lys Ser Gly Lys Gly Trp Tyr Phe Met Asn Thr Asn
 325 330 335

Gly Glu Leu Ala Asp Asn Pro Ser Phe Thr Lys Glu Pro Asp Gly Leu
 340 345 350

Ile Thr Val Ala
 355

<210> 68
 <211> 365
 <212> PRT

<213> Unknown

<220>

<223> WLBU2-Variant-Cpl1

<400> 68

Lys Arg Trp Val Lys Arg Val Lys Arg Val Lys Arg Trp Val Lys Arg
1 5 10 15

Val Val Arg Val Val Lys Arg Trp Val Lys Arg Val Lys Lys Asn Asp
20 25 30

Leu Phe Val Asp Val Ser Ser His Asn Gly Tyr Asp Ile Thr Gly Ile
35 40 45

Leu Glu Gln Met Gly Thr Thr Asn Thr Ile Ile Lys Ile Ser Glu Ser
50 55 60

Thr Thr Tyr Leu Asn Pro Cys Leu Ser Ala Gln Val Glu Gln Ser Asn
65 70 75 80

Pro Ile Gly Phe Tyr His Phe Ala Arg Phe Gly Gly Asp Val Ala Glu
85 90 95

Ala Glu Arg Glu Ala Gln Phe Phe Leu Asp Asn Val Pro Met Gln Val
100 105 110

Lys Tyr Leu Val Leu Asp Tyr Glu Asp Asp Pro Ser Gly Asp Ala Gln
115 120 125

Ala Asn Thr Asn Ala Cys Leu Arg Phe Met Gln Met Ile Ala Asp Ala
130 135 140

Gly Tyr Lys Pro Ile Tyr Tyr Ser Tyr Lys Pro Phe Thr His Asp Asn
145 150 155 160

Val Asp Tyr Gln Gln Ile Leu Ala Gln Phe Pro Asn Ser Leu Trp Ile
165 170 175

Ala Gly Tyr Gly Leu Asn Asp Gly Thr Ala Asn Phe Glu Tyr Phe Pro
180 185 190

Ser Met Asp Gly Ile Arg Trp Trp Gln Tyr Ser Ser Asn Pro Phe Asp
195 200 205

Lys Asn Ile Val Leu Leu Asp Asp Glu Glu Asp Asp Lys Pro Lys Thr
210 215 220

Ala Gly Thr Trp Lys Gln Asp Ser Lys Gly Trp Trp Phe Arg Arg Asn
225 230 235 240

Asn Gly Ser Phe Pro Tyr Asn Lys Trp Glu Lys Ile Gly Gly Val Trp
245 250 255

Tyr Tyr Phe Asp Ser Lys Gly Tyr Cys Leu Thr Ser Glu Trp Leu Lys
260 265 270

Asp Asn Glu Lys Trp Tyr Tyr Leu Lys Asp Asn Gly Ala Met Ala Thr
275 280 285

Gly Trp Val Leu Val Gly Ser Glu Trp Tyr Tyr Met Asp Asp Ser Gly
290 295 300

Ala Met Val Thr Gly Trp Val Lys Tyr Lys Asn Asn Trp Tyr Tyr Met
305 310 315 320

Thr Asn Glu Arg Gly Asn Met Val Ser Asn Glu Phe Ile Lys Ser Gly
325 330 335

Lys Gly Trp Tyr Phe Met Asn Thr Asn Gly Glu Leu Ala Asp Asn Pro
340 345 350

Ser Phe Thr Lys Glu Pro Asp Gly Leu Ile Thr Val Ala
355 360 365

<210> 69
<211> 372
<212> PRT
<213> Unknown

<220>
<223> Sushi1-Cpl1

<400> 69

Gly Phe Lys Leu Lys Gly Met Ala Arg Ile Ser Cys Leu Pro Asn Gly
1 5 10 15

Gln Trp Ser Asn Phe Pro Pro Lys Cys Ile Arg Glu Cys Ala Met Val
20 25 30

Ser Ser Val Lys Lys Asn Asp Leu Phe Val Asp Val Ser Ser His Asn
35 40 45

Gly Tyr Asp Ile Thr Gly Ile Leu Glu Gln Met Gly Thr Thr Asn Thr
50 55 60

Ile Ile Lys Ile Ser Glu Ser Thr Thr Tyr Leu Asn Pro Cys Leu Ser

65					70						75				80
Ala	Gln	Val	Glu	Gln	Ser	Asn	Pro	Ile	Gly	Phe	Tyr	His	Phe	Ala	Arg
				85					90					95	
Phe	Gly	Gly	Asp	Val	Ala	Glu	Ala	Glu	Arg	Glu	Ala	Gln	Phe	Phe	Leu
			100					105					110		
Asp	Asn	Val	Pro	Met	Gln	Val	Lys	Tyr	Leu	Val	Leu	Asp	Tyr	Glu	Asp
		115					120					125			
Asp	Pro	Ser	Gly	Asp	Ala	Gln	Ala	Asn	Thr	Asn	Ala	Cys	Leu	Arg	Phe
	130					135					140				
Met	Gln	Met	Ile	Ala	Asp	Ala	Gly	Tyr	Lys	Pro	Ile	Tyr	Tyr	Ser	Tyr
145					150					155					160
Lys	Pro	Phe	Thr	His	Asp	Asn	Val	Asp	Tyr	Gln	Gln	Ile	Leu	Ala	Gln
				165					170					175	
Phe	Pro	Asn	Ser	Leu	Trp	Ile	Ala	Gly	Tyr	Gly	Leu	Asn	Asp	Gly	Thr
			180					185					190		
Ala	Asn	Phe	Glu	Tyr	Phe	Pro	Ser	Met	Asp	Gly	Ile	Arg	Trp	Trp	Gln
		195					200					205			
Tyr	Ser	Ser	Asn	Pro	Phe	Asp	Lys	Asn	Ile	Val	Leu	Leu	Asp	Asp	Glu
	210					215					220				
Glu	Asp	Asp	Lys	Pro	Lys	Thr	Ala	Gly	Thr	Trp	Lys	Gln	Asp	Ser	Lys
225					230					235					240
Gly	Trp	Trp	Phe	Arg	Arg	Asn	Asn	Gly	Ser	Phe	Pro	Tyr	Asn	Lys	Trp
				245					250					255	
Glu	Lys	Ile	Gly	Gly	Val	Trp	Tyr	Tyr	Phe	Asp	Ser	Lys	Gly	Tyr	Cys
			260					265					270		
Leu	Thr	Ser	Glu	Trp	Leu	Lys	Asp	Asn	Glu	Lys	Trp	Tyr	Tyr	Leu	Lys
		275					280					285			
Asp	Asn	Gly	Ala	Met	Ala	Thr	Gly	Trp	Val	Leu	Val	Gly	Ser	Glu	Trp
	290					295					300				
Tyr	Tyr	Met	Asp	Asp	Ser	Gly	Ala	Met	Val	Thr	Gly	Trp	Val	Lys	Tyr
305					310					315					320

Lys Asn Asn Trp Tyr Tyr Met Thr Asn Glu Arg Gly Asn Met Val Ser
325 330 335

Asn Glu Phe Ile Lys Ser Gly Lys Gly Trp Tyr Phe Met Asn Thr Asn
340 345 350

Gly Glu Leu Ala Asp Asn Pro Ser Phe Thr Lys Glu Pro Asp Gly Leu
355 360 365

Ile Thr Val Ala
370

<210> 70
<211> 364
<212> PRT
<213> Unknown

<220>
<223> Melittin-Cpl1

<400> 70

Gly Ile Gly Ala Val Leu Lys Val Leu Thr Thr Gly Leu Pro Ala Leu
1 5 10 15

Ile Ser Trp Ile Lys Arg Lys Arg Gln Gln Val Lys Lys Asn Asp Leu
20 25 30

Phe Val Asp Val Ser Ser His Asn Gly Tyr Asp Ile Thr Gly Ile Leu
35 40 45

Glu Gln Met Gly Thr Thr Asn Thr Ile Ile Lys Ile Ser Glu Ser Thr
50 55 60

Thr Tyr Leu Asn Pro Cys Leu Ser Ala Gln Val Glu Gln Ser Asn Pro
65 70 75 80

Ile Gly Phe Tyr His Phe Ala Arg Phe Gly Gly Asp Val Ala Glu Ala
85 90 95

Glu Arg Glu Ala Gln Phe Phe Leu Asp Asn Val Pro Met Gln Val Lys
100 105 110

Tyr Leu Val Leu Asp Tyr Glu Asp Asp Pro Ser Gly Asp Ala Gln Ala
115 120 125

Asn Thr Asn Ala Cys Leu Arg Phe Met Gln Met Ile Ala Asp Ala Gly
130 135 140

Tyr Lys Pro Ile Tyr Tyr Ser Tyr Lys Pro Phe Thr His Asp Asn Val
 145 150 155 160

Asp Tyr Gln Gln Ile Leu Ala Gln Phe Pro Asn Ser Leu Trp Ile Ala
 165 170 175

Gly Tyr Gly Leu Asn Asp Gly Thr Ala Asn Phe Glu Tyr Phe Pro Ser
 180 185 190

Met Asp Gly Ile Arg Trp Trp Gln Tyr Ser Ser Asn Pro Phe Asp Lys
 195 200 205

Asn Ile Val Leu Leu Asp Asp Glu Glu Asp Asp Lys Pro Lys Thr Ala
 210 215 220

Gly Thr Trp Lys Gln Asp Ser Lys Gly Trp Trp Phe Arg Arg Asn Asn
 225 230 235 240

Gly Ser Phe Pro Tyr Asn Lys Trp Glu Lys Ile Gly Gly Val Trp Tyr
 245 250 255

Tyr Phe Asp Ser Lys Gly Tyr Cys Leu Thr Ser Glu Trp Leu Lys Asp
 260 265 270

Asn Glu Lys Trp Tyr Tyr Leu Lys Asp Asn Gly Ala Met Ala Thr Gly
 275 280 285

Trp Val Leu Val Gly Ser Glu Trp Tyr Tyr Met Asp Asp Ser Gly Ala
 290 295 300

Met Val Thr Gly Trp Val Lys Tyr Lys Asn Asn Trp Tyr Tyr Met Thr
 305 310 315 320

Asn Glu Arg Gly Asn Met Val Ser Asn Glu Phe Ile Lys Ser Gly Lys
 325 330 335

Gly Trp Tyr Phe Met Asn Thr Asn Gly Glu Leu Ala Asp Asn Pro Ser
 340 345 350

Phe Thr Lys Glu Pro Asp Gly Leu Ile Thr Val Ala
 355 360

<210> 71
 <211> 375
 <212> PRT
 <213> Unknown

<220>
 <223> LL-37-Cpl1

<400> 71

Leu Leu Gly Asp Phe Phe Arg Lys Ser Lys Glu Lys Ile Gly Lys Glu
1 5 10 15

Phe Lys Arg Ile Val Gln Arg Ile Lys Asp Phe Leu Arg Asn Leu Val
20 25 30

Pro Arg Thr Glu Ser Val Lys Lys Asn Asp Leu Phe Val Asp Val Ser
35 40 45

Ser His Asn Gly Tyr Asp Ile Thr Gly Ile Leu Glu Gln Met Gly Thr
50 55 60

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

Cys Leu Ser Ala Gln Val Glu Gln Ser Asn Pro Ile Gly Phe Tyr His
85 90 95

Phe Ala Arg Phe Gly Gly Asp Val Ala Glu Ala Glu Arg Glu Ala Gln
100 105 110

Phe Phe Leu Asp Asn Val Pro Met Gln Val Lys Tyr Leu Val Leu Asp
115 120 125

Tyr Glu Asp Asp Pro Ser Gly Asp Ala Gln Ala Asn Thr Asn Ala Cys
130 135 140

Leu Arg Phe Met Gln Met Ile Ala Asp Ala Gly Tyr Lys Pro Ile Tyr
145 150 155 160

Tyr Ser Tyr Lys Pro Phe Thr His Asp Asn Val Asp Tyr Gln Gln Ile
165 170 175

Leu Ala Gln Phe Pro Asn Ser Leu Trp Ile Ala Gly Tyr Gly Leu Asn
180 185 190

Asp Gly Thr Ala Asn Phe Glu Tyr Phe Pro Ser Met Asp Gly Ile Arg
195 200 205

Trp Trp Gln Tyr Ser Ser Asn Pro Phe Asp Lys Asn Ile Val Leu Leu
210 215 220

Asp Asp Glu Glu Asp Asp Lys Pro Lys Thr Ala Gly Thr Trp Lys Gln
225 230 235 240

Asp Ser Lys Gly Trp Trp Phe Arg Arg Asn Asn Gly Ser Phe Pro Tyr
245 250 255

Asn Lys Trp Glu Lys Ile Gly Gly Val Trp Tyr Tyr Phe Asp Ser Lys
260 265 270

Gly Tyr Cys Leu Thr Ser Glu Trp Leu Lys Asp Asn Glu Lys Trp Tyr
275 280 285

Tyr Leu Lys Asp Asn Gly Ala Met Ala Thr Gly Trp Val Leu Val Gly
290 295 300

Ser Glu Trp Tyr Tyr Met Asp Asp Ser Gly Ala Met Val Thr Gly Trp
305 310 315 320

Val Lys Tyr Lys Asn Asn Trp Tyr Tyr Met Thr Asn Glu Arg Gly Asn
325 330 335

Met Val Ser Asn Glu Phe Ile Lys Ser Gly Lys Gly Trp Tyr Phe Met
340 345 350

Asn Thr Asn Gly Glu Leu Ala Asp Asn Pro Ser Phe Thr Lys Glu Pro
355 360 365

Asp Gly Leu Ile Thr Val Ala
370 375

<210> 72
<211> 351
<212> PRT
<213> Unknown

<220>
<223> Indolicidin-Cpl1

<400> 72

Ile Leu Pro Trp Lys Trp Pro Trp Trp Pro Trp Arg Arg Val Lys Lys
1 5 10 15

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

Gly Ile Leu Glu Gln Met Gly Thr Thr Asn Thr Ile Ile Lys Ile Ser
35 40 45

Glu Ser Thr Thr Tyr Leu Asn Pro Cys Leu Ser Ala Gln Val Glu Gln
50 55 60

Ser Asn Pro Ile Gly Phe Tyr His Phe Ala Arg Phe Gly Gly Asp Val

65					70						75				80
Ala	Glu	Ala	Glu	Arg	Glu	Ala	Gln	Phe	Phe	Leu	Asp	Asn	Val	Pro	Met
				85					90					95	
Gln	Val	Lys	Tyr	Leu	Val	Leu	Asp	Tyr	Glu	Asp	Asp	Pro	Ser	Gly	Asp
			100					105					110		
Ala	Gln	Ala	Asn	Thr	Asn	Ala	Cys	Leu	Arg	Phe	Met	Gln	Met	Ile	Ala
		115					120					125			
Asp	Ala	Gly	Tyr	Lys	Pro	Ile	Tyr	Tyr	Ser	Tyr	Lys	Pro	Phe	Thr	His
	130					135					140				
Asp	Asn	Val	Asp	Tyr	Gln	Gln	Ile	Leu	Ala	Gln	Phe	Pro	Asn	Ser	Leu
145					150					155					160
Trp	Ile	Ala	Gly	Tyr	Gly	Leu	Asn	Asp	Gly	Thr	Ala	Asn	Phe	Glu	Tyr
				165					170					175	
Phe	Pro	Ser	Met	Asp	Gly	Ile	Arg	Trp	Trp	Gln	Tyr	Ser	Ser	Asn	Pro
			180					185					190		
Phe	Asp	Lys	Asn	Ile	Val	Leu	Leu	Asp	Asp	Glu	Glu	Asp	Asp	Lys	Pro
		195					200					205			
Lys	Thr	Ala	Gly	Thr	Trp	Lys	Gln	Asp	Ser	Lys	Gly	Trp	Trp	Phe	Arg
	210					215					220				
Arg	Asn	Asn	Gly	Ser	Phe	Pro	Tyr	Asn	Lys	Trp	Glu	Lys	Ile	Gly	Gly
225					230					235					240
Val	Trp	Tyr	Tyr	Phe	Asp	Ser	Lys	Gly	Tyr	Cys	Leu	Thr	Ser	Glu	Trp
				245					250					255	
Leu	Lys	Asp	Asn	Glu	Lys	Trp	Tyr	Tyr	Leu	Lys	Asp	Asn	Gly	Ala	Met
			260					265					270		
Ala	Thr	Gly	Trp	Val	Leu	Val	Gly	Ser	Glu	Trp	Tyr	Tyr	Met	Asp	Asp
		275					280					285			
Ser	Gly	Ala	Met	Val	Thr	Gly	Trp	Val	Lys	Tyr	Lys	Asn	Asn	Trp	Tyr
	290					295					300				
Tyr	Met	Thr	Asn	Glu	Arg	Gly	Asn	Met	Val	Ser	Asn	Glu	Phe	Ile	Lys
305					310					315					320

Ser Gly Lys Gly Trp Tyr Phe Met Asn Thr Asn Gly Glu Leu Ala Asp
325 330 335

Asn Pro Ser Phe Thr Lys Glu Pro Asp Gly Leu Ile Thr Val Ala
340 345 350

<210> 73
<211> 367
<212> PRT
<213> Unknown

<220>
<223> SMAP-29-Cpl1

<400> 73

Arg Gly Leu Arg Arg Leu Gly Arg Lys Ile Ala His Gly Val Lys Lys
1 5 10 15

Tyr Gly Pro Thr Val Leu Arg Ile Ile Arg Ile Ala Gly Val Lys Lys
20 25 30

Asn Asp Leu Phe Val Asp Val Ser Ser His Asn Gly Tyr Asp Ile Thr
35 40 45

Gly Ile Leu Glu Gln Met Gly Thr Thr Asn Thr Ile Ile Lys Ile Ser
50 55 60

Glu Ser Thr Thr Tyr Leu Asn Pro Cys Leu Ser Ala Gln Val Glu Gln
65 70 75 80

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

Ala Glu Ala Glu Arg Glu Ala Gln Phe Phe Leu Asp Asn Val Pro Met
100 105 110

Gln Val Lys Tyr Leu Val Leu Asp Tyr Glu Asp Asp Pro Ser Gly Asp
115 120 125

Ala Gln Ala Asn Thr Asn Ala Cys Leu Arg Phe Met Gln Met Ile Ala
130 135 140

Asp Ala Gly Tyr Lys Pro Ile Tyr Tyr Ser Tyr Lys Pro Phe Thr His
145 150 155 160

Asp Asn Val Asp Tyr Gln Gln Ile Leu Ala Gln Phe Pro Asn Ser Leu
165 170 175

Trp Ile Ala Gly Tyr Gly Leu Asn Asp Gly Thr Ala Asn Phe Glu Tyr
180 185 190

Phe Pro Ser Met Asp Gly Ile Arg Trp Trp Gln Tyr Ser Ser Asn Pro
195 200 205

Phe Asp Lys Asn Ile Val Leu Leu Asp Asp Glu Glu Asp Asp Lys Pro
210 215 220

Lys Thr Ala Gly Thr Trp Lys Gln Asp Ser Lys Gly Trp Trp Phe Arg
225 230 235 240

Arg Asn Asn Gly Ser Phe Pro Tyr Asn Lys Trp Glu Lys Ile Gly Gly
245 250 255

Val Trp Tyr Tyr Phe Asp Ser Lys Gly Tyr Cys Leu Thr Ser Glu Trp
260 265 270

Leu Lys Asp Asn Glu Lys Trp Tyr Tyr Leu Lys Asp Asn Gly Ala Met
275 280 285

Ala Thr Gly Trp Val Leu Val Gly Ser Glu Trp Tyr Tyr Met Asp Asp
290 295 300

Ser Gly Ala Met Val Thr Gly Trp Val Lys Tyr Lys Asn Asn Trp Tyr
305 310 315 320

Tyr Met Thr Asn Glu Arg Gly Asn Met Val Ser Asn Glu Phe Ile Lys
325 330 335

Ser Gly Lys Gly Trp Tyr Phe Met Asn Thr Asn Gly Glu Leu Ala Asp
340 345 350

Asn Pro Ser Phe Thr Lys Glu Pro Asp Gly Leu Ile Thr Val Ala
355 360 365

<210> 74
<211> 356
<212> PRT
<213> Unknown

<220>
<223> Protegrin-Cpl1

<400> 74

Arg Gly Gly Arg Leu Cys Tyr Cys Arg Arg Arg Phe Cys Val Cys Val
1 5 10 15

Gly Arg Val Lys Lys Asn Asp Leu Phe Val Asp Val Ser Ser His Asn

20					25					30					
Gly	Tyr	Asp	Ile	Thr	Gly	Ile	Leu	Glu	Gln	Met	Gly	Thr	Thr	Asn	Thr
		35					40					45			
Ile	Ile	Lys	Ile	Ser	Glu	Ser	Thr	Thr	Tyr	Leu	Asn	Pro	Cys	Leu	Ser
50						55					60				
Ala	Gln	Val	Glu	Gln	Ser	Asn	Pro	Ile	Gly	Phe	Tyr	His	Phe	Ala	Arg
65					70					75					80
Phe	Gly	Gly	Asp	Val	Ala	Glu	Ala	Glu	Arg	Glu	Ala	Gln	Phe	Phe	Leu
				85					90					95	
Asp	Asn	Val	Pro	Met	Gln	Val	Lys	Tyr	Leu	Val	Leu	Asp	Tyr	Glu	Asp
		100						105					110		
Asp	Pro	Ser	Gly	Asp	Ala	Gln	Ala	Asn	Thr	Asn	Ala	Cys	Leu	Arg	Phe
		115				120						125			
Met	Gln	Met	Ile	Ala	Asp	Ala	Gly	Tyr	Lys	Pro	Ile	Tyr	Tyr	Ser	Tyr
130						135				140					
Lys	Pro	Phe	Thr	His	Asp	Asn	Val	Asp	Tyr	Gln	Gln	Ile	Leu	Ala	Gln
145					150				155						160
Phe	Pro	Asn	Ser	Leu	Trp	Ile	Ala	Gly	Tyr	Gly	Leu	Asn	Asp	Gly	Thr
				165					170					175	
Ala	Asn	Phe	Glu	Tyr	Phe	Pro	Ser	Met	Asp	Gly	Ile	Arg	Trp	Trp	Gln
		180						185				190			
Tyr	Ser	Ser	Asn	Pro	Phe	Asp	Lys	Asn	Ile	Val	Leu	Leu	Asp	Asp	Glu
		195				200						205			
Glu	Asp	Asp	Lys	Pro	Lys	Thr	Ala	Gly	Thr	Trp	Lys	Gln	Asp	Ser	Lys
210						215				220					
Gly	Trp	Trp	Phe	Arg	Arg	Asn	Asn	Gly	Ser	Phe	Pro	Tyr	Asn	Lys	Trp
225					230				235						240
Glu	Lys	Ile	Gly	Gly	Val	Trp	Tyr	Tyr	Phe	Asp	Ser	Lys	Gly	Tyr	Cys
				245				250						255	
Leu	Thr	Ser	Glu	Trp	Leu	Lys	Asp	Asn	Glu	Lys	Trp	Tyr	Tyr	Leu	Lys
		260						265				270			

Asp Asn Gly Ala Met Ala Thr Gly Trp Val Leu Val Gly Ser Glu Trp
275 280 285

Tyr Tyr Met Asp Asp Ser Gly Ala Met Val Thr Gly Trp Val Lys Tyr
290 295 300

Lys Asn Asn Trp Tyr Tyr Met Thr Asn Glu Arg Gly Asn Met Val Ser
305 310 315 320

Asn Glu Phe Ile Lys Ser Gly Lys Gly Trp Tyr Phe Met Asn Thr Asn
325 330 335

Gly Glu Leu Ala Asp Asn Pro Ser Phe Thr Lys Glu Pro Asp Gly Leu
340 345 350

Ile Thr Val Ala
355

<210> 75
<211> 369
<212> PRT
<213> Unknown

<220>
<223> Cecropin P1-Cpl1

<400> 75

Ser Trp Leu Ser Lys Thr Ala Lys Lys Leu Glu Asn Ser Ala Lys Lys
1 5 10 15

Arg Ile Ser Glu Gly Ile Ala Ile Ala Ile Gln Gly Gly Pro Arg Val
20 25 30

Lys Lys Asn Asp Leu Phe Val Asp Val Ser Ser His Asn Gly Tyr Asp
35 40 45

Ile Thr Gly Ile Leu Glu Gln Met Gly Thr Thr Asn Thr Ile Ile Lys
50 55 60

Ile Ser Glu Ser Thr Thr Tyr Leu Asn Pro Cys Leu Ser Ala Gln Val
65 70 75 80

Glu Gln Ser Asn Pro Ile Gly Phe Tyr His Phe Ala Arg Phe Gly Gly
85 90 95

Asp Val Ala Glu Ala Glu Arg Glu Ala Gln Phe Phe Leu Asp Asn Val
100 105 110

Pro Met Gln Val Lys Tyr Leu Val Leu Asp Tyr Glu Asp Asp Pro Ser

115					120					125					
Gly	Asp	Ala	Gln	Ala	Asn	Thr	Asn	Ala	Cys	Leu	Arg	Phe	Met	Gln	Met
	130					135					140				
Ile	Ala	Asp	Ala	Gly	Tyr	Lys	Pro	Ile	Tyr	Tyr	Ser	Tyr	Lys	Pro	Phe
145					150					155					160
Thr	His	Asp	Asn	Val	Asp	Tyr	Gln	Gln	Ile	Leu	Ala	Gln	Phe	Pro	Asn
				165					170					175	
Ser	Leu	Trp	Ile	Ala	Gly	Tyr	Gly	Leu	Asn	Asp	Gly	Thr	Ala	Asn	Phe
			180					185					190		
Glu	Tyr	Phe	Pro	Ser	Met	Asp	Gly	Ile	Arg	Trp	Trp	Gln	Tyr	Ser	Ser
		195					200					205			
Asn	Pro	Phe	Asp	Lys	Asn	Ile	Val	Leu	Leu	Asp	Asp	Glu	Glu	Asp	Asp
	210					215					220				
Lys	Pro	Lys	Thr	Ala	Gly	Thr	Trp	Lys	Gln	Asp	Ser	Lys	Gly	Trp	Trp
225					230					235					240
Phe	Arg	Arg	Asn	Asn	Gly	Ser	Phe	Pro	Tyr	Asn	Lys	Trp	Glu	Lys	Ile
			245						250					255	
Gly	Gly	Val	Trp	Tyr	Tyr	Phe	Asp	Ser	Lys	Gly	Tyr	Cys	Leu	Thr	Ser
		260						265					270		
Glu	Trp	Leu	Lys	Asp	Asn	Glu	Lys	Trp	Tyr	Tyr	Leu	Lys	Asp	Asn	Gly
		275					280					285			
Ala	Met	Ala	Thr	Gly	Trp	Val	Leu	Val	Gly	Ser	Glu	Trp	Tyr	Tyr	Met
	290					295					300				
Asp	Asp	Ser	Gly	Ala	Met	Val	Thr	Gly	Trp	Val	Lys	Tyr	Lys	Asn	Asn
305					310					315					320
Trp	Tyr	Tyr	Met	Thr	Asn	Glu	Arg	Gly	Asn	Met	Val	Ser	Asn	Glu	Phe
				325					330					335	
Ile	Lys	Ser	Gly	Lys	Gly	Trp	Tyr	Phe	Met	Asn	Thr	Asn	Gly	Glu	Leu
			340					345					350		
Ala	Asp	Asn	Pro	Ser	Phe	Thr	Lys	Glu	Pro	Asp	Gly	Leu	Ile	Thr	Val
		355					360					365			

Ala

<210> 76
<211> 361
<212> PRT
<213> Unknown

<220>
<223> Magainin-Cpl1

<400> 76

Gly Ile Gly Lys Phe Leu His Ser Ala Lys Lys Phe Gly Lys Ala Phe
1 5 10 15

Val Gly Glu Ile Met Asn Ser Val Lys Lys Asn Asp Leu Phe Val Asp
20 25 30

Val Ser Ser His Asn Gly Tyr Asp Ile Thr Gly Ile Leu Glu Gln Met
35 40 45

Gly Thr Thr Asn Thr Ile Ile Lys Ile Ser Glu Ser Thr Thr Tyr Leu
50 55 60

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

Tyr His Phe Ala Arg Phe Gly Gly Asp Val Ala Glu Ala Glu Arg Glu
85 90 95

Ala Gln Phe Phe Leu Asp Asn Val Pro Met Gln Val Lys Tyr Leu Val
100 105 110

Leu Asp Tyr Glu Asp Asp Pro Ser Gly Asp Ala Gln Ala Asn Thr Asn
115 120 125

Ala Cys Leu Arg Phe Met Gln Met Ile Ala Asp Ala Gly Tyr Lys Pro
130 135 140

Ile Tyr Tyr Ser Tyr Lys Pro Phe Thr His Asp Asn Val Asp Tyr Gln
145 150 155 160

Gln Ile Leu Ala Gln Phe Pro Asn Ser Leu Trp Ile Ala Gly Tyr Gly
165 170 175

Leu Asn Asp Gly Thr Ala Asn Phe Glu Tyr Phe Pro Ser Met Asp Gly
180 185 190

Ile Arg Trp Trp Gln Tyr Ser Ser Asn Pro Phe Asp Lys Asn Ile Val
195 200 205

Leu Leu Asp Asp Glu Glu Asp Asp Lys Pro Lys Thr Ala Gly Thr Trp
210 215 220

Lys Gln Asp Ser Lys Gly Trp Trp Phe Arg Arg Asn Asn Gly Ser Phe
225 230 235 240

Pro Tyr Asn Lys Trp Glu Lys Ile Gly Gly Val Trp Tyr Tyr Phe Asp
245 250 255

Ser Lys Gly Tyr Cys Leu Thr Ser Glu Trp Leu Lys Asp Asn Glu Lys
260 265 270

Trp Tyr Tyr Leu Lys Asp Asn Gly Ala Met Ala Thr Gly Trp Val Leu
275 280 285

Val Gly Ser Glu Trp Tyr Tyr Met Asp Asp Ser Gly Ala Met Val Thr
290 295 300

Gly Trp Val Lys Tyr Lys Asn Asn Trp Tyr Tyr Met Thr Asn Glu Arg
305 310 315 320

Gly Asn Met Val Ser Asn Glu Phe Ile Lys Ser Gly Lys Gly Trp Tyr
325 330 335

Phe Met Asn Thr Asn Gly Glu Leu Ala Asp Asn Pro Ser Phe Thr Lys
340 345 350

Glu Pro Asp Gly Leu Ile Thr Val Ala
355 360

<210> 77
<211> 363
<212> PRT
<213> Unknown

<220>
<223> Pleurocidin-Cpl1

<400> 77

Gly Trp Gly Ser Phe Phe Lys Lys Ala Ala His Val Gly Lys His Val
1 5 10 15

Gly Lys Ala Ala Leu Thr His Tyr Leu Val Lys Lys Asn Asp Leu Phe
20 25 30

Val Asp Val Ser Ser His Asn Gly Tyr Asp Ile Thr Gly Ile Leu Glu

35	40	45																	
Gln	Met	Gly	Thr	Thr	Asn	Thr	Ile	Ile	Lys	Ile	Ser	Glu	Ser	Thr	Thr				
	50					55					60								
Tyr	Leu	Asn	Pro	Cys	Leu	Ser	Ala	Gln	Val	Glu	Gln	Ser	Asn	Pro	Ile				
65					70					75					80				
Gly	Phe	Tyr	His	Phe	Ala	Arg	Phe	Gly	Gly	Asp	Val	Ala	Glu	Ala	Glu				
				85					90					95					
Arg	Glu	Ala	Gln	Phe	Phe	Leu	Asp	Asn	Val	Pro	Met	Gln	Val	Lys	Tyr				
			100					105					110						
Leu	Val	Leu	Asp	Tyr	Glu	Asp	Asp	Pro	Ser	Gly	Asp	Ala	Gln	Ala	Asn				
		115					120					125							
Thr	Asn	Ala	Cys	Leu	Arg	Phe	Met	Gln	Met	Ile	Ala	Asp	Ala	Gly	Tyr				
	130					135					140								
Lys	Pro	Ile	Tyr	Tyr	Ser	Tyr	Lys	Pro	Phe	Thr	His	Asp	Asn	Val	Asp				
145					150					155					160				
Tyr	Gln	Gln	Ile	Leu	Ala	Gln	Phe	Pro	Asn	Ser	Leu	Trp	Ile	Ala	Gly				
				165					170					175					
Tyr	Gly	Leu	Asn	Asp	Gly	Thr	Ala	Asn	Phe	Glu	Tyr	Phe	Pro	Ser	Met				
			180					185					190						
Asp	Gly	Ile	Arg	Trp	Trp	Gln	Tyr	Ser	Ser	Asn	Pro	Phe	Asp	Lys	Asn				
		195					200					205							
Ile	Val	Leu	Leu	Asp	Asp	Glu	Glu	Asp	Asp	Lys	Pro	Lys	Thr	Ala	Gly				
	210					215					220								
Thr	Trp	Lys	Gln	Asp	Ser	Lys	Gly	Trp	Trp	Phe	Arg	Arg	Asn	Asn	Gly				
225					230					235					240				
Ser	Phe	Pro	Tyr	Asn	Lys	Trp	Glu	Lys	Ile	Gly	Gly	Val	Trp	Tyr	Tyr				
				245					250					255					
Phe	Asp	Ser	Lys	Gly	Tyr	Cys	Leu	Thr	Ser	Glu	Trp	Leu	Lys	Asp	Asn				
			260					265					270						
Glu	Lys	Trp	Tyr	Tyr	Leu	Lys	Asp	Asn	Gly	Ala	Met	Ala	Thr	Gly	Trp				
		275					280					285							

Val Leu Val Gly Ser Glu Trp Tyr Tyr Met Asp Asp Ser Gly Ala Met
 290 295 300

Val Thr Gly Trp Val Lys Tyr Lys Asn Asn Trp Tyr Tyr Met Thr Asn
 305 310 315 320

Glu Arg Gly Asn Met Val Ser Asn Glu Phe Ile Lys Ser Gly Lys Gly
 325 330 335

Trp Tyr Phe Met Asn Thr Asn Gly Glu Leu Ala Asp Asn Pro Ser Phe
 340 345 350

Thr Lys Glu Pro Asp Gly Leu Ile Thr Val Ala
 355 360

<210> 78
 <211> 374
 <212> PRT
 <213> Unknown

<220>
 <223> Cecropin A (A.aegypti)-Cpl1

<400> 78

Gly Gly Leu Lys Lys Leu Gly Lys Lys Leu Glu Gly Ala Gly Lys Arg
 1 5 10 15

Val Phe Asn Ala Ala Glu Lys Ala Leu Pro Val Val Ala Gly Ala Lys
 20 25 30

Ala Leu Arg Lys Val Lys Lys Asn Asp Leu Phe Val Asp Val Ser Ser
 35 40 45

His Asn Gly Tyr Asp Ile Thr Gly Ile Leu Glu Gln Met Gly Thr Thr
 50 55 60

Asn Thr Ile Ile Lys Ile Ser Glu Ser Thr Thr Tyr Leu Asn Pro Cys
 65 70 75 80

Leu Ser Ala Gln Val Glu Gln Ser Asn Pro Ile Gly Phe Tyr His Phe
 85 90 95

Ala Arg Phe Gly Gly Asp Val Ala Glu Ala Glu Arg Glu Ala Gln Phe
 100 105 110

Phe Leu Asp Asn Val Pro Met Gln Val Lys Tyr Leu Val Leu Asp Tyr
 115 120 125

Glu Asp Asp Pro Ser Gly Asp Ala Gln Ala Asn Thr Asn Ala Cys Leu

130		135		140
Arg Phe Met Gln Met Ile Ala Asp Ala Gly Tyr Lys Pro Ile Tyr Tyr				
145		150		155
Ser Tyr Lys Pro Phe Thr His Asp Asn Val Asp Tyr Gln Gln Ile Leu				
	165		170	175
Ala Gln Phe Pro Asn Ser Leu Trp Ile Ala Gly Tyr Gly Leu Asn Asp				
	180		185	190
Gly Thr Ala Asn Phe Glu Tyr Phe Pro Ser Met Asp Gly Ile Arg Trp				
	195		200	205
Trp Gln Tyr Ser Ser Asn Pro Phe Asp Lys Asn Ile Val Leu Leu Asp				
	210		215	220
Asp Glu Glu Asp Asp Lys Pro Lys Thr Ala Gly Thr Trp Lys Gln Asp				
225		230		235
Ser Lys Gly Trp Trp Phe Arg Arg Asn Asn Gly Ser Phe Pro Tyr Asn				
	245		250	255
Lys Trp Glu Lys Ile Gly Gly Val Trp Tyr Tyr Phe Asp Ser Lys Gly				
	260		265	270
Tyr Cys Leu Thr Ser Glu Trp Leu Lys Asp Asn Glu Lys Trp Tyr Tyr				
	275		280	285
Leu Lys Asp Asn Gly Ala Met Ala Thr Gly Trp Val Leu Val Gly Ser				
	290		295	300
Glu Trp Tyr Tyr Met Asp Asp Ser Gly Ala Met Val Thr Gly Trp Val				
305		310		315
Lys Tyr Lys Asn Asn Trp Tyr Tyr Met Thr Asn Glu Arg Gly Asn Met				
	325		330	335
Val Ser Asn Glu Phe Ile Lys Ser Gly Lys Gly Trp Tyr Phe Met Asn				
	340		345	350
Thr Asn Gly Glu Leu Ala Asp Asn Pro Ser Phe Thr Lys Glu Pro Asp				
	355		360	365
Gly Leu Ile Thr Val Ala				
370				

<210> 79
 <211> 378
 <212> PRT
 <213> Unknown

<220>
 <223> Cecropin A (D.melanogaster)-Cpl1

<400> 79

Gly Trp Leu Lys Lys Ile Gly Lys Lys Ile Glu Arg Val Gly Gln His
 1 5 10 15

Thr Arg Asp Ala Thr Ile Gln Gly Leu Gly Ile Pro Gln Gln Ala Ala
 20 25 30

Asn Val Ala Ala Thr Ala Arg Gly Val Lys Lys Asn Asp Leu Phe Val
 35 40 45

Asp Val Ser Ser His Asn Gly Tyr Asp Ile Thr Gly Ile Leu Glu Gln
 50 55 60

Met Gly Thr Thr Asn Thr Ile Ile Lys Ile Ser Glu Ser Thr Thr Tyr
 65 70 75 80

Leu Asn Pro Cys Leu Ser Ala Gln Val Glu Gln Ser Asn Pro Ile Gly
 85 90 95

Phe Tyr His Phe Ala Arg Phe Gly Gly Asp Val Ala Glu Ala Glu Arg
 100 105 110

Glu Ala Gln Phe Phe Leu Asp Asn Val Pro Met Gln Val Lys Tyr Leu
 115 120 125

Val Leu Asp Tyr Glu Asp Asp Pro Ser Gly Asp Ala Gln Ala Asn Thr
 130 135 140

Asn Ala Cys Leu Arg Phe Met Gln Met Ile Ala Asp Ala Gly Tyr Lys
 145 150 155 160

Pro Ile Tyr Tyr Ser Tyr Lys Pro Phe Thr His Asp Asn Val Asp Tyr
 165 170 175

Gln Gln Ile Leu Ala Gln Phe Pro Asn Ser Leu Trp Ile Ala Gly Tyr
 180 185 190

Gly Leu Asn Asp Gly Thr Ala Asn Phe Glu Tyr Phe Pro Ser Met Asp
 195 200 205

Gly Ile Arg Trp Trp Gln Tyr Ser Ser Asn Pro Phe Asp Lys Asn Ile
 210 215 220

Val Leu Leu Asp Asp Glu Glu Asp Asp Lys Pro Lys Thr Ala Gly Thr
 225 230 235 240

Trp Lys Gln Asp Ser Lys Gly Trp Trp Phe Arg Arg Asn Asn Gly Ser
 245 250 255

Phe Pro Tyr Asn Lys Trp Glu Lys Ile Gly Gly Val Trp Tyr Tyr Phe
 260 265 270

Asp Ser Lys Gly Tyr Cys Leu Thr Ser Glu Trp Leu Lys Asp Asn Glu
 275 280 285

Lys Trp Tyr Tyr Leu Lys Asp Asn Gly Ala Met Ala Thr Gly Trp Val
 290 295 300

Leu Val Gly Ser Glu Trp Tyr Tyr Met Asp Asp Ser Gly Ala Met Val
 305 310 315 320

Thr Gly Trp Val Lys Tyr Lys Asn Asn Trp Tyr Tyr Met Thr Asn Glu
 325 330 335

Arg Gly Asn Met Val Ser Asn Glu Phe Ile Lys Ser Gly Lys Gly Trp
 340 345 350

Tyr Phe Met Asn Thr Asn Gly Glu Leu Ala Asp Asn Pro Ser Phe Thr
 355 360 365

Lys Glu Pro Asp Gly Leu Ile Thr Val Ala
 370 375

<210> 80
 <211> 359
 <212> PRT
 <213> Unknown

<220>
 <223> BuforinII-Cpl1

<400> 80

Thr Arg Ser Ser Arg Ala Gly Leu Gln Phe Pro Val Gly Arg Val His
 1 5 10 15

Arg Leu Leu Arg Lys Val Lys Lys Asn Asp Leu Phe Val Asp Val Ser
 20 25 30

Ser His Asn Gly Tyr Asp Ile Thr Gly Ile Leu Glu Gln Met Gly Thr
 35 40 45

Thr Asn Thr Ile Ile Lys Ile Ser Glu Ser Thr Thr Tyr Leu Asn Pro
 50 55 60

Cys Leu Ser Ala Gln Val Glu Gln Ser Asn Pro Ile Gly Phe Tyr His
 65 70 75 80

Phe Ala Arg Phe Gly Gly Asp Val Ala Glu Ala Glu Arg Glu Ala Gln
 85 90 95

Phe Phe Leu Asp Asn Val Pro Met Gln Val Lys Tyr Leu Val Leu Asp
 100 105 110

Tyr Glu Asp Asp Pro Ser Gly Asp Ala Gln Ala Asn Thr Asn Ala Cys
 115 120 125

Leu Arg Phe Met Gln Met Ile Ala Asp Ala Gly Tyr Lys Pro Ile Tyr
 130 135 140

Tyr Ser Tyr Lys Pro Phe Thr His Asp Asn Val Asp Tyr Gln Gln Ile
 145 150 155 160

Leu Ala Gln Phe Pro Asn Ser Leu Trp Ile Ala Gly Tyr Gly Leu Asn
 165 170 175

Asp Gly Thr Ala Asn Phe Glu Tyr Phe Pro Ser Met Asp Gly Ile Arg
 180 185 190

Trp Trp Gln Tyr Ser Ser Asn Pro Phe Asp Lys Asn Ile Val Leu Leu
 195 200 205

Asp Asp Glu Glu Asp Asp Lys Pro Lys Thr Ala Gly Thr Trp Lys Gln
 210 215 220

Asp Ser Lys Gly Trp Trp Phe Arg Arg Asn Asn Gly Ser Phe Pro Tyr
 225 230 235 240

Asn Lys Trp Glu Lys Ile Gly Gly Val Trp Tyr Tyr Phe Asp Ser Lys
 245 250 255

Gly Tyr Cys Leu Thr Ser Glu Trp Leu Lys Asp Asn Glu Lys Trp Tyr
 260 265 270

Tyr Leu Lys Asp Asn Gly Ala Met Ala Thr Gly Trp Val Leu Val Gly
 275 280 285

Ser Glu Trp Tyr Tyr Met Asp Asp Ser Gly Ala Met Val Thr Gly Trp
 290 295 300

Val Lys Tyr Lys Asn Asn Trp Tyr Tyr Met Thr Asn Glu Arg Gly Asn
 305 310 315 320

Met Val Ser Asn Glu Phe Ile Lys Ser Gly Lys Gly Trp Tyr Phe Met
 325 330 335

Asn Thr Asn Gly Glu Leu Ala Asp Asn Pro Ser Phe Thr Lys Glu Pro
 340 345 350

Asp Gly Leu Ile Thr Val Ala
 355

<210> 81
 <211> 377
 <212> PRT
 <213> Unknown

<220>
 <223> Sarcotoxin IA-Cpl1

<400> 81

Gly Trp Leu Lys Lys Ile Gly Lys Lys Ile Glu Arg Val Gly Gln His
 1 5 10 15

Thr Arg Asp Ala Thr Ile Gln Gly Leu Gly Ile Ala Gln Gln Ala Ala
 20 25 30

Asn Val Ala Ala Thr Ala Arg Val Lys Lys Asn Asp Leu Phe Val Asp
 35 40 45

Val Ser Ser His Asn Gly Tyr Asp Ile Thr Gly Ile Leu Glu Gln Met
 50 55 60

Gly Thr Thr Asn Thr Ile Ile Lys Ile Ser Glu Ser Thr Thr Tyr Leu
 65 70 75 80

Asn Pro Cys Leu Ser Ala Gln Val Glu Gln Ser Asn Pro Ile Gly Phe
 85 90 95

Tyr His Phe Ala Arg Phe Gly Gly Asp Val Ala Glu Ala Glu Arg Glu
 100 105 110

Ala Gln Phe Phe Leu Asp Asn Val Pro Met Gln Val Lys Tyr Leu Val
 115 120 125

Leu Asp Tyr Glu Asp Asp Pro Ser Gly Asp Ala Gln Ala Asn Thr Asn
130 135 140

Ala Cys Leu Arg Phe Met Gln Met Ile Ala Asp Ala Gly Tyr Lys Pro
145 150 155 160

Ile Tyr Tyr Ser Tyr Lys Pro Phe Thr His Asp Asn Val Asp Tyr Gln
165 170 175

Gln Ile Leu Ala Gln Phe Pro Asn Ser Leu Trp Ile Ala Gly Tyr Gly
180 185 190

Leu Asn Asp Gly Thr Ala Asn Phe Glu Tyr Phe Pro Ser Met Asp Gly
195 200 205

Ile Arg Trp Trp Gln Tyr Ser Ser Asn Pro Phe Asp Lys Asn Ile Val
210 215 220

Leu Leu Asp Asp Glu Glu Asp Asp Lys Pro Lys Thr Ala Gly Thr Trp
225 230 235 240

Lys Gln Asp Ser Lys Gly Trp Trp Phe Arg Arg Asn Asn Gly Ser Phe
245 250 255

Pro Tyr Asn Lys Trp Glu Lys Ile Gly Gly Val Trp Tyr Tyr Phe Asp
260 265 270

Ser Lys Gly Tyr Cys Leu Thr Ser Glu Trp Leu Lys Asp Asn Glu Lys
275 280 285

Trp Tyr Tyr Leu Lys Asp Asn Gly Ala Met Ala Thr Gly Trp Val Leu
290 295 300

Val Gly Ser Glu Trp Tyr Tyr Met Asp Asp Ser Gly Ala Met Val Thr
305 310 315 320

Gly Trp Val Lys Tyr Lys Asn Asn Trp Tyr Tyr Met Thr Asn Glu Arg
325 330 335

Gly Asn Met Val Ser Asn Glu Phe Ile Lys Ser Gly Lys Gly Trp Tyr
340 345 350

Phe Met Asn Thr Asn Gly Glu Leu Ala Asp Asn Pro Ser Phe Thr Lys
355 360 365

Glu Pro Asp Gly Leu Ile Thr Val Ala

370

375

<210> 82
 <211> 347
 <212> PRT
 <213> Unknown

<220>
 <223> PK-Cpl1

<400> 82

Lys Arg Lys Lys Arg Lys Lys Arg Lys Val Lys Lys Asn Asp Leu Phe
 1 5 10 15

Val Asp Val Ser Ser His Asn Gly Tyr Asp Ile Thr Gly Ile Leu Glu
 20 25 30

Gln Met Gly Thr Thr Asn Thr Ile Ile Lys Ile Ser Glu Ser Thr Thr
 35 40 45

Tyr Leu Asn Pro Cys Leu Ser Ala Gln Val Glu Gln Ser Asn Pro Ile
 50 55 60

Gly Phe Tyr His Phe Ala Arg Phe Gly Gly Asp Val Ala Glu Ala Glu
 65 70 75 80

Arg Glu Ala Gln Phe Phe Leu Asp Asn Val Pro Met Gln Val Lys Tyr
 85 90 95

Leu Val Leu Asp Tyr Glu Asp Asp Pro Ser Gly Asp Ala Gln Ala Asn
 100 105 110

Thr Asn Ala Cys Leu Arg Phe Met Gln Met Ile Ala Asp Ala Gly Tyr
 115 120 125

Lys Pro Ile Tyr Tyr Ser Tyr Lys Pro Phe Thr His Asp Asn Val Asp
 130 135 140

Tyr Gln Gln Ile Leu Ala Gln Phe Pro Asn Ser Leu Trp Ile Ala Gly
 145 150 155 160

Tyr Gly Leu Asn Asp Gly Thr Ala Asn Phe Glu Tyr Phe Pro Ser Met
 165 170 175

Asp Gly Ile Arg Trp Trp Gln Tyr Ser Ser Asn Pro Phe Asp Lys Asn
 180 185 190

Ile Val Leu Leu Asp Asp Glu Glu Asp Asp Lys Pro Lys Thr Ala Gly
 195 200 205

Thr Trp Lys Gln Asp Ser Lys Gly Trp Trp Phe Arg Arg Asn Asn Gly
 210 215 220

Ser Phe Pro Tyr Asn Lys Trp Glu Lys Ile Gly Gly Val Trp Tyr Tyr
 225 230 235 240

Phe Asp Ser Lys Gly Tyr Cys Leu Thr Ser Glu Trp Leu Lys Asp Asn
 245 250 255

Glu Lys Trp Tyr Tyr Leu Lys Asp Asn Gly Ala Met Ala Thr Gly Trp
 260 265 270

Val Leu Val Gly Ser Glu Trp Tyr Tyr Met Asp Asp Ser Gly Ala Met
 275 280 285

Val Thr Gly Trp Val Lys Tyr Lys Asn Asn Trp Tyr Tyr Met Thr Asn
 290 295 300

Glu Arg Gly Asn Met Val Ser Asn Glu Phe Ile Lys Ser Gly Lys Gly
 305 310 315 320

Trp Tyr Phe Met Asn Thr Asn Gly Glu Leu Ala Asp Asn Pro Ser Phe
 325 330 335

Thr Lys Glu Pro Asp Gly Leu Ile Thr Val Ala
 340 345

<210> 83
 <211> 345
 <212> PRT
 <213> Unknown

<220>
 <223> Pentapeptid-Ply511

<400> 83

Phe Phe Val Ala Pro Val Lys Tyr Thr Val Glu Asn Lys Ile Ile Ala
 1 5 10 15

Gly Leu Pro Lys Gly Lys Leu Lys Gly Ala Asn Phe Val Ile Ala His
 20 25 30

Glu Thr Ala Asn Ser Lys Ser Thr Ile Asp Asn Glu Val Ser Tyr Met
 35 40 45

Thr Arg Asn Trp Lys Asn Ala Phe Val Thr His Phe Val Gly Gly Gly
 50 55 60

Gly Arg Val Val Gln Val Ala Asn Val Asn Tyr Val Ser Trp Gly Ala
 65 70 75 80

Gly Gln Tyr Ala Asn Ser Tyr Ser Tyr Ala Gln Val Glu Leu Cys Arg
 85 90 95

Thr Ser Asn Ala Thr Thr Phe Lys Lys Asp Tyr Glu Val Tyr Cys Gln
 100 105 110

Leu Leu Val Asp Leu Ala Lys Lys Ala Gly Ile Pro Ile Thr Leu Asp
 115 120 125

Ser Gly Ser Lys Thr Ser Asp Lys Gly Ile Lys Ser His Lys Trp Val
 130 135 140

Ala Asp Lys Leu Gly Gly Thr Thr His Gln Asp Pro Tyr Ala Tyr Leu
 145 150 155 160

Ser Ser Trp Gly Ile Ser Lys Ala Gln Phe Ala Ser Asp Leu Ala Lys
 165 170 175

Val Ser Gly Gly Gly Asn Thr Gly Thr Ala Pro Ala Lys Pro Ser Thr
 180 185 190

Pro Ala Pro Lys Pro Ser Thr Pro Ser Thr Asn Leu Asp Lys Leu Gly
 195 200 205

Leu Val Asp Tyr Met Asn Ala Lys Lys Met Asp Ser Ser Tyr Ser Asn
 210 215 220

Arg Asp Lys Leu Ala Lys Gln Tyr Gly Ile Ala Asn Tyr Ser Gly Thr
 225 230 235 240

Ala Ser Gln Asn Thr Thr Leu Leu Ser Lys Ile Lys Gly Gly Ala Pro
 245 250 255

Lys Pro Ser Thr Pro Ala Pro Lys Pro Ser Thr Ser Thr Ala Lys Lys
 260 265 270

Ile Tyr Phe Pro Pro Asn Lys Gly Asn Trp Ser Val Tyr Pro Thr Asn
 275 280 285

Lys Ala Pro Val Lys Ala Asn Ala Ile Gly Ala Ile Asn Pro Thr Lys
 290 295 300

Phe Gly Gly Leu Thr Tyr Thr Ile Gln Lys Asp Arg Gly Asn Gly Val
 305 310 315 320

Tyr Glu Ile Gln Thr Asp Gln Phe Gly Arg Val Gln Val Tyr Gly Ala
325 330 335

Pro Ser Thr Gly Ala Val Ile Lys Lys
340 345

<210> 84
<211> 503
<212> PRT
<213> Unknown

<220>
<223> PK-LysK (PK N-terminal)

<400> 84

Lys Arg Lys Lys Arg Lys Lys Arg Lys Ala Lys Thr Gln Ala Glu Ile
1 5 10 15

Asn Lys Arg Leu Asp Ala Tyr Ala Lys Gly Thr Val Asp Ser Pro Tyr
20 25 30

Arg Val Lys Lys Ala Thr Ser Tyr Asp Pro Ser Phe Gly Val Met Glu
35 40 45

Ala Gly Ala Ile Asp Ala Asp Gly Tyr Tyr His Ala Gln Cys Gln Asp
50 55 60

Leu Ile Thr Asp Tyr Val Leu Trp Leu Thr Asp Asn Lys Val Arg Thr
65 70 75 80

Trp Gly Asn Ala Lys Asp Gln Ile Lys Gln Ser Tyr Gly Thr Gly Phe
85 90 95

Lys Ile His Glu Asn Lys Pro Ser Thr Val Pro Lys Lys Gly Trp Ile
100 105 110

Ala Val Phe Thr Ser Gly Ser Tyr Glu Gln Trp Gly His Ile Gly Ile
115 120 125

Val Tyr Asp Gly Gly Asn Thr Ser Thr Phe Thr Ile Leu Glu Gln Asn
130 135 140

Trp Asn Gly Tyr Ala Asn Lys Lys Pro Thr Lys Arg Val Asp Asn Tyr
145 150 155 160

Tyr Gly Leu Thr His Phe Ile Glu Ile Pro Val Lys Ala Gly Thr Thr
165 170 175

Val Lys Lys Glu Thr Ala Lys Lys Ser Ala Ser Lys Thr Pro Ala Pro
 180 185 190

Lys Lys Lys Ala Thr Leu Lys Val Ser Lys Asn His Ile Asn Tyr Thr
 195 200 205

Met Asp Lys Arg Gly Lys Lys Pro Glu Gly Met Val Ile His Asn Asp
 210 215 220

Ala Gly Arg Ser Ser Gly Gln Gln Tyr Glu Asn Ser Leu Ala Asn Ala
 225 230 235 240

Gly Tyr Ala Arg Tyr Ala Asn Gly Ile Ala His Tyr Tyr Gly Ser Glu
 245 250 255

Gly Tyr Val Trp Glu Ala Ile Asp Ala Lys Asn Gln Ile Ala Trp His
 260 265 270

Thr Gly Asp Gly Thr Gly Ala Asn Ser Gly Asn Phe Arg Phe Ala Gly
 275 280 285

Ile Glu Val Cys Gln Ser Met Ser Ala Ser Asp Ala Gln Phe Leu Lys
 290 295 300

Asn Glu Gln Ala Val Phe Gln Phe Thr Ala Glu Lys Phe Lys Glu Trp
 305 310 315 320

Gly Leu Thr Pro Asn Arg Lys Thr Val Arg Leu His Met Glu Phe Val
 325 330 335

Pro Thr Ala Cys Pro His Arg Ser Met Val Leu His Thr Gly Phe Asn
 340 345 350

Pro Val Thr Gln Gly Arg Pro Ser Gln Ala Ile Met Asn Lys Leu Lys
 355 360 365

Asp Tyr Phe Ile Lys Gln Ile Lys Asn Tyr Met Asp Lys Gly Thr Ser
 370 375 380

Ser Ser Thr Val Val Lys Asp Gly Lys Thr Ser Ser Ala Ser Thr Pro
 385 390 395 400

Ala Thr Arg Pro Val Thr Gly Ser Trp Lys Lys Asn Gln Tyr Gly Thr
 405 410 415

Trp Tyr Lys Pro Glu Asn Ala Thr Phe Val Asn Gly Asn Gln Pro Ile

420 425 430
 Val Thr Arg Ile Gly Ser Pro Phe Leu Asn Ala Pro Val Gly Gly Asn
 435 440 445
 Leu Pro Ala Gly Ala Thr Ile Val Tyr Asp Glu Val Cys Ile Gln Ala
 450 455 460
 Gly His Ile Trp Ile Gly Tyr Asn Ala Tyr Asn Gly Asn Arg Val Tyr
 465 470 475 480
 Cys Pro Val Arg Thr Cys Gln Gly Val Pro Pro Asn Gln Ile Pro Gly
 485 490 495
 Val Ala Trp Gly Val Phe Lys
 500
 <210> 85
 <211> 512
 <212> PRT
 <213> Unknown
 <220>
 <223> PK2-LysK
 <400> 85
 Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys
 1 5 10 15
 Arg Lys Ala Lys Thr Gln Ala Glu Ile Asn Lys Arg Leu Asp Ala Tyr
 20 25 30
 Ala Lys Gly Thr Val Asp Ser Pro Tyr Arg Val Lys Lys Ala Thr Ser
 35 40 45
 Tyr Asp Pro Ser Phe Gly Val Met Glu Ala Gly Ala Ile Asp Ala Asp
 50 55 60
 Gly Tyr Tyr His Ala Gln Cys Gln Asp Leu Ile Thr Asp Tyr Val Leu
 65 70 75 80
 Trp Leu Thr Asp Asn Lys Val Arg Thr Trp Gly Asn Ala Lys Asp Gln
 85 90 95
 Ile Lys Gln Ser Tyr Gly Thr Gly Phe Lys Ile His Glu Asn Lys Pro
 100 105 110
 Ser Thr Val Pro Lys Lys Gly Trp Ile Ala Val Phe Thr Ser Gly Ser

115					120					125					
Tyr	Glu	Gln	Trp	Gly	His	Ile	Gly	Ile	Val	Tyr	Asp	Gly	Gly	Asn	Thr
130						135					140				
Ser	Thr	Phe	Thr	Ile	Leu	Glu	Gln	Asn	Trp	Asn	Gly	Tyr	Ala	Asn	Lys
145					150					155					160
Lys	Pro	Thr	Lys	Arg	Val	Asp	Asn	Tyr	Tyr	Gly	Leu	Thr	His	Phe	Ile
				165					170					175	
Glu	Ile	Pro	Val	Lys	Ala	Gly	Thr	Thr	Val	Lys	Lys	Glu	Thr	Ala	Lys
			180					185					190		
Lys	Ser	Ala	Ser	Lys	Thr	Pro	Ala	Pro	Lys	Lys	Lys	Ala	Thr	Leu	Lys
		195					200					205			
Val	Ser	Lys	Asn	His	Ile	Asn	Tyr	Thr	Met	Asp	Lys	Arg	Gly	Lys	Lys
210						215					220				
Pro	Glu	Gly	Met	Val	Ile	His	Asn	Asp	Ala	Gly	Arg	Ser	Ser	Gly	Gln
225						230					235				240
Gln	Tyr	Glu	Asn	Ser	Leu	Ala	Asn	Ala	Gly	Tyr	Ala	Arg	Tyr	Ala	Asn
				245					250					255	
Gly	Ile	Ala	His	Tyr	Tyr	Gly	Ser	Glu	Gly	Tyr	Val	Trp	Glu	Ala	Ile
			260					265					270		
Asp	Ala	Lys	Asn	Gln	Ile	Ala	Trp	His	Thr	Gly	Asp	Gly	Thr	Gly	Ala
		275					280					285			
Asn	Ser	Gly	Asn	Phe	Arg	Phe	Ala	Gly	Ile	Glu	Val	Cys	Gln	Ser	Met
290						295					300				
Ser	Ala	Ser	Asp	Ala	Gln	Phe	Leu	Lys	Asn	Glu	Gln	Ala	Val	Phe	Gln
305						310					315				320
Phe	Thr	Ala	Glu	Lys	Phe	Lys	Glu	Trp	Gly	Leu	Thr	Pro	Asn	Arg	Lys
				325					330					335	
Thr	Val	Arg	Leu	His	Met	Glu	Phe	Val	Pro	Thr	Ala	Cys	Pro	His	Arg
			340					345					350		
Ser	Met	Val	Leu	His	Thr	Gly	Phe	Asn	Pro	Val	Thr	Gln	Gly	Arg	Pro
		355					360					365			

Ser Gln Ala Ile Met Asn Lys Leu Lys Asp Tyr Phe Ile Lys Gln Ile
370 375 380

Lys Asn Tyr Met Asp Lys Gly Thr Ser Ser Ser Thr Val Val Lys Asp
385 390 395 400

Gly Lys Thr Ser Ser Ala Ser Thr Pro Ala Thr Arg Pro Val Thr Gly
405 410 415

Ser Trp Lys Lys Asn Gln Tyr Gly Thr Trp Tyr Lys Pro Glu Asn Ala
420 425 430

Thr Phe Val Asn Gly Asn Gln Pro Ile Val Thr Arg Ile Gly Ser Pro
435 440 445

Phe Leu Asn Ala Pro Val Gly Gly Asn Leu Pro Ala Gly Ala Thr Ile
450 455 460

Val Tyr Asp Glu Val Cys Ile Gln Ala Gly His Ile Trp Ile Gly Tyr
465 470 475 480

Asn Ala Tyr Asn Gly Asn Arg Val Tyr Cys Pro Val Arg Thr Cys Gln
485 490 495

Gly Val Pro Pro Asn Gln Ile Pro Gly Val Ala Trp Gly Val Phe Lys
500 505 510

<210> 86
<211> 259
<212> PRT
<213> Unknown

<220>
<223> PK-Lss

<400> 86

Lys Arg Lys Lys Arg Lys Lys Arg Lys Ala His Glu His Ser Ala Gln
1 5 10 15

Trp Leu Asn Asn Tyr Lys Lys Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu
20 25 30

Gly Ile Asn Gly Gly Met His Tyr Gly Val Asp Phe Phe Met Asn Ile
35 40 45

Gly Thr Pro Val Lys Ala Ile Ser Ser Gly Lys Ile Val Glu Ala Gly
50 55 60

Trp Ser Asn Tyr Gly Gly Gly Asn Gln Ile Gly Leu Ile Glu Asn Asp

65		70		75		80									
Gly	Val	His	Arg	Gln	Trp	Tyr	Met	His	Leu	Ser	Lys	Tyr	Asn	Val	Lys
				85					90					95	
Val	Gly	Asp	Tyr	Val	Lys	Ala	Gly	Gln	Ile	Ile	Gly	Trp	Ser	Gly	Ser
			100					105					110		
Thr	Gly	Tyr	Ser	Thr	Ala	Pro	His	Leu	His	Phe	Gln	Arg	Met	Val	Asn
			115				120					125			
Ser	Phe	Ser	Asn	Ser	Thr	Ala	Gln	Asp	Pro	Met	Pro	Phe	Leu	Lys	Ser
	130					135					140				
Ala	Gly	Tyr	Gly	Lys	Ala	Gly	Gly	Thr	Val	Thr	Pro	Thr	Pro	Asn	Thr
145					150					155					160
Gly	Trp	Lys	Thr	Asn	Lys	Tyr	Gly	Thr	Leu	Tyr	Lys	Ser	Glu	Ser	Ala
				165					170					175	
Ser	Phe	Thr	Pro	Asn	Thr	Asp	Ile	Ile	Thr	Arg	Thr	Thr	Gly	Pro	Phe
			180					185					190		
Arg	Ser	Met	Pro	Gln	Ser	Gly	Val	Leu	Lys	Ala	Gly	Gln	Thr	Ile	His
		195					200					205			
Tyr	Asp	Glu	Val	Met	Lys	Gln	Asp	Gly	His	Val	Trp	Val	Gly	Tyr	Thr
	210					215					220				
Gly	Asn	Ser	Gly	Gln	Arg	Ile	Tyr	Leu	Pro	Val	Arg	Thr	Trp	Asn	Lys
225					230					235					240
Ser	Thr	Asn	Thr	Leu	Gly	Val	Leu	Trp	Gly	Thr	Ile	Lys	Leu	Val	Pro
				245					250					255	

Arg Gly Ser

<210> 87
 <211> 268
 <212> PRT
 <213> Unknown

<220>
 <223> PK2-Lss

<400> 87

Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys

1	5	10	15																
Arg	Lys	Ala	His	Glu	His	Ser	Ala	Gln	Trp	Leu	Asn	Asn	Tyr	Lys	Lys				
			20					25					30						
Gly	Tyr	Gly	Tyr	Gly	Pro	Tyr	Pro	Leu	Gly	Ile	Asn	Gly	Gly	Met	His				
		35					40					45							
Tyr	Gly	Val	Asp	Phe	Phe	Met	Asn	Ile	Gly	Thr	Pro	Val	Lys	Ala	Ile				
	50					55					60								
Ser	Ser	Gly	Lys	Ile	Val	Glu	Ala	Gly	Trp	Ser	Asn	Tyr	Gly	Gly	Gly				
65					70				75						80				
Asn	Gln	Ile	Gly	Leu	Ile	Glu	Asn	Asp	Gly	Val	His	Arg	Gln	Trp	Tyr				
				85					90					95					
Met	His	Leu	Ser	Lys	Tyr	Asn	Val	Lys	Val	Gly	Asp	Tyr	Val	Lys	Ala				
			100					105					110						
Gly	Gln	Ile	Ile	Gly	Trp	Ser	Gly	Ser	Thr	Gly	Tyr	Ser	Thr	Ala	Pro				
		115					120					125							
His	Leu	His	Phe	Gln	Arg	Met	Val	Asn	Ser	Phe	Ser	Asn	Ser	Thr	Ala				
	130					135					140								
Gln	Asp	Pro	Met	Pro	Phe	Leu	Lys	Ser	Ala	Gly	Tyr	Gly	Lys	Ala	Gly				
145					150					155					160				
Gly	Thr	Val	Thr	Pro	Thr	Pro	Asn	Thr	Gly	Trp	Lys	Thr	Asn	Lys	Tyr				
				165					170					175					
Gly	Thr	Leu	Tyr	Lys	Ser	Glu	Ser	Ala	Ser	Phe	Thr	Pro	Asn	Thr	Asp				
		180						185					190						
Ile	Ile	Thr	Arg	Thr	Thr	Gly	Pro	Phe	Arg	Ser	Met	Pro	Gln	Ser	Gly				
		195					200					205							
Val	Leu	Lys	Ala	Gly	Gln	Thr	Ile	His	Tyr	Asp	Glu	Val	Met	Lys	Gln				
	210					215					220								
Asp	Gly	His	Val	Trp	Val	Gly	Tyr	Thr	Gly	Asn	Ser	Gly	Gln	Arg	Ile				
225					230					235					240				
Tyr	Leu	Pro	Val	Arg	Thr	Trp	Asn	Lys	Ser	Thr	Asn	Thr	Leu	Gly	Val				
				245					250					255					

Leu Trp Gly Thr Ile Lys Leu Val Pro Arg Gly Ser
 260 265

<210> 88
 <211> 303
 <212> PRT
 <213> Unknown

<220>
 <223> Walmagh1-PA6gp20

<400> 88

Gly Phe Phe Ile Pro Ala Val Ile Leu Pro Ser Ile Ala Phe Leu Ile
 1 5 10 15

Val Pro Val Arg Tyr Ile Pro Ala Ala His His Ser Ala Gly Ser Asn
 20 25 30

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

Phe Pro Ser Ala Ser Arg Lys Gly Arg Ala Val Ser Thr Ala Asn Tyr
 50 55 60

Phe Ala Ser Pro Ser Ser Gly Gly Ser Ala His Tyr Val Cys Asp Ile
 65 70 75 80

Gly Glu Thr Val Gln Cys Leu Ser Glu Ser Thr Ile Gly Trp His Ala
 85 90 95

Pro Pro Asn Pro His Ser Leu Gly Ile Glu Ile Cys Ala Asp Gly Gly
 100 105 110

Ser His Ala Ser Phe Arg Val Pro Gly His Ala Tyr Thr Arg Glu Gln
 115 120 125

Trp Leu Asp Pro Gln Val Trp Pro Ala Val Glu Arg Ala Ala Val Leu
 130 135 140

Cys Arg Arg Leu Cys Asp Lys Tyr Asn Val Pro Lys Arg Lys Leu Ser
 145 150 155 160

Ala Ala Asp Leu Lys Ala Gly Arg Arg Gly Val Cys Gly His Val Asp
 165 170 175

Val Thr Asp Ala Trp His Gln Ser Asp His Asp Asp Pro Gly Pro Trp
 180 185 190

Phe Pro Trp Asp Lys Phe Met Ala Val Val Asn Gly Gly Ser Gly Asp

195	200	205
Ser Gly Glu Leu Thr Val Ala Asp Val Lys Ala Leu His Asp Gln Ile		
210	215	220
Lys Gln Leu Ser Ala Gln Leu Thr Gly Ser Val Asn Lys Leu His His		
225	230	235 240
Asp Val Gly Val Val Gln Val Gln Asn Gly Asp Leu Gly Lys Arg Val		
245	250	255
Asp Ala Leu Ser Trp Val Lys Asn Pro Val Thr Gly Lys Leu Trp Arg		
260	265	270
Thr Lys Asp Ala Leu Trp Ser Val Trp Tyr Tyr Val Leu Glu Cys Arg		
275	280	285
Ser Arg Leu Asp Arg Leu Glu Ser Ala Val Asn Asp Leu Lys Lys		
290	295	300
<210> 89		
<211> 503		
<212> PRT		
<213> Unknown		
<220>		
<223> LysK-PK (PK C-terminal)		
<400> 89		
Ala Lys Thr Gln Ala Glu Ile Asn Lys Arg Leu Asp Ala Tyr Ala Lys		
1	5	10 15
Gly Thr Val Asp Ser Pro Tyr Arg Val Lys Lys Ala Thr Ser Tyr Asp		
20	25	30
Pro Ser Phe Gly Val Met Glu Ala Gly Ala Ile Asp Ala Asp Gly Tyr		
35	40	45
Tyr His Ala Gln Cys Gln Asp Leu Ile Thr Asp Tyr Val Leu Trp Leu		
50	55	60
Thr Asp Asn Lys Val Arg Thr Trp Gly Asn Ala Lys Asp Gln Ile Lys		
65	70	75 80
Gln Ser Tyr Gly Thr Gly Phe Lys Ile His Glu Asn Lys Pro Ser Thr		
85	90	95
Val Pro Lys Lys Gly Trp Ile Ala Val Phe Thr Ser Gly Ser Tyr Glu		
100	105	110

Gln Trp Gly His Ile Gly Ile Val Tyr Asp Gly Gly Asn Thr Ser Thr
 115 120 125

Phe Thr Ile Leu Glu Gln Asn Trp Asn Gly Tyr Ala Asn Lys Lys Pro
 130 135 140

Thr Lys Arg Val Asp Asn Tyr Tyr Gly Leu Thr His Phe Ile Glu Ile
 145 150 155 160

Pro Val Lys Ala Gly Thr Thr Val Lys Lys Glu Thr Ala Lys Lys Ser
 165 170 175

Ala Ser Lys Thr Pro Ala Pro Lys Lys Lys Ala Thr Leu Lys Val Ser
 180 185 190

Lys Asn His Ile Asn Tyr Thr Met Asp Lys Arg Gly Lys Lys Pro Glu
 195 200 205

Gly Met Val Ile His Asn Asp Ala Gly Arg Ser Ser Gly Gln Gln Tyr
 210 215 220

Glu Asn Ser Leu Ala Asn Ala Gly Tyr Ala Arg Tyr Ala Asn Gly Ile
 225 230 235 240

Ala His Tyr Tyr Gly Ser Glu Gly Tyr Val Trp Glu Ala Ile Asp Ala
 245 250 255

Lys Asn Gln Ile Ala Trp His Thr Gly Asp Gly Thr Gly Ala Asn Ser
 260 265 270

Gly Asn Phe Arg Phe Ala Gly Ile Glu Val Cys Gln Ser Met Ser Ala
 275 280 285

Ser Asp Ala Gln Phe Leu Lys Asn Glu Gln Ala Val Phe Gln Phe Thr
 290 295 300

Ala Glu Lys Phe Lys Glu Trp Gly Leu Thr Pro Asn Arg Lys Thr Val
 305 310 315 320

Arg Leu His Met Glu Phe Val Pro Thr Ala Cys Pro His Arg Ser Met
 325 330 335

Val Leu His Thr Gly Phe Asn Pro Val Thr Gln Gly Arg Pro Ser Gln
 340 345 350

Ala Ile Met Asn Lys Leu Lys Asp Tyr Phe Ile Lys Gln Ile Lys Asn
355 360 365

Tyr Met Asp Lys Gly Thr Ser Ser Ser Thr Val Val Lys Asp Gly Lys
370 375 380

Thr Ser Ser Ala Ser Thr Pro Ala Thr Arg Pro Val Thr Gly Ser Trp
385 390 395 400

Lys Lys Asn Gln Tyr Gly Thr Trp Tyr Lys Pro Glu Asn Ala Thr Phe
405 410 415

Val Asn Gly Asn Gln Pro Ile Val Thr Arg Ile Gly Ser Pro Phe Leu
420 425 430

Asn Ala Pro Val Gly Gly Asn Leu Pro Ala Gly Ala Thr Ile Val Tyr
435 440 445

Asp Glu Val Cys Ile Gln Ala Gly His Ile Trp Ile Gly Tyr Asn Ala
450 455 460

Tyr Asn Gly Asn Arg Val Tyr Cys Pro Val Arg Thr Cys Gln Gly Val
465 470 475 480

Pro Pro Asn Gln Ile Pro Gly Val Ala Trp Gly Val Phe Lys Lys Arg
485 490 495

Lys Lys Arg Lys Lys Arg Lys
500

<210> 90
<211> 252
<212> PRT
<213> Unknown

<220>
<223> Lss-PK (PK C-terminal)

<400> 90

His Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys Gly Tyr Gly
1 5 10 15

Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His Tyr Gly Val
20 25 30

Asp Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser Gly
35 40 45

Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln Ile

50 55 60
 Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr Met His Leu
 65 70 75 80
 Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly Gln Ile
 85 90 95
 Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His Leu His
 100 105 110
 Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp Pro
 115 120 125
 Met Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly Gly Thr Val
 130 135 140
 Thr Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr Gly Thr Leu
 145 150 155 160
 Tyr Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp Ile Ile Thr
 165 170 175
 Arg Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly Val Leu Lys
 180 185 190
 Ala Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln Asp Gly His
 195 200 205
 Val Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu Pro
 210 215 220
 Val Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val Leu Trp Gly
 225 230 235 240
 Thr Ile Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys
 245 250

<210> 91
 <211> 1017
 <212> DNA
 <213> Unknown

<220>
 <223> Cpl-1

<400> 91
 atggtgaaaa aaaacgatct gttcgttgac gtgtcttccc acaacggtta cgatatcact 60
 ggcatctctgg aacagatggg caccaccaac accattatca aaatctccga aagcacgacc 120

tatctgaacc cgtgtctgtc tgcccaggta gaacagtcta acccaattgg cttctaccat	180
ttcgcacgtt tcggtggtga tgtagccgaa gcggaacgtg aagcgcagtt ctttctggat	240
aacgtgccga tgcaggttaa atacctggtt ctggactatg aagacgatcc gtctggtgac	300
gcacaggcaa acaccaacgc gtgcctgcgt ttcattgcaga tgattgcaga cgctggctac	360
aaaccgatct attactctta caaacggtc acccacgata acgtcgatta ccagcagatt	420
ctggcgcagt ttccgaactc tctgtggatc gcaggttatg gcctgaacga cggctactgcg	480
aactttgagt atttcccaag catggacggc atccgctggt ggcagtattc ctccaacccg	540
ttcgacaaaa acatcgtact gctggacgac gaagaggacg acaaaccgaa aactgctggt	600
acctggaaac aggatagcaa aggctggtgg tttcgtcgt acaacggttc ttttccgtac	660
aacaaatggg aaaaaatcgg tgggtgtttg tattacttcg actccaaagg ctactgcctg	720
acgagcgaat ggctgaaaga taacgagaaa tgggtactatc tcaaagacaa cggtgccatg	780
gctactggtt gggttctggt tggttctgag tgggtactaca tggacgattc tggtgctatg	840
gttaccggct gggtgaaata caaaaacaac tgggtattaca tgacgaacga acgcggtaac	900
atggtgagca acgaattcat caaatccggc aaaggctggt acttcatgaa cactaacggt	960
gaactggcgg ataaccgctc tttcaccaaa gaaccggatg gcctgatcac cgctcgct	1017

<210> 92
 <211> 1023
 <212> DNA
 <213> Unknown

<220>
 <223> Ply511

<400> 92	
atggtgaaat acaccgtgga aaacaaaatc atcgcaggcc tgccgaaagg caaactgaaa	60
ggcgcgaact tcgttattgc tcatgaaacc gcaaactcca aatccaccat cgacaacgaa	120
gtcagctata tgactcgcaa ctggaaaaac gcgtttgtga ctcactttgt aggtggcggt	180
ggccgtgtcg tacaggtagc gaacgttaac tacgtaagct ggggtgcagg tcagtatgct	240
aacagctatt cctacgcgca ggtagaactg tgtcgtacgt ctaacgcgac cacgttcaaa	300
aaagactacg aggtttattg ccagctgctg gttgacctgg caaaaaagc tggatatcca	360
atcacctggt attctggctc caaaacctct gacaaaggca tcaaattcca caaatggggt	420
gctgacaaac tgggcggtac cactcaccag gacctgatg cttacctgtc ttcttggggc	480
atttctaaag ccagttcgc ctctgatctg gctaaagttt ctggcggtgg taacaccggt	540
actgctccag caaaaccgtc tactccggca caaaaccgt ctactccgtc tactaacctg	600
gacaaactgg gcctggtgga ttacatgaac gcgaaaaaaa tggatagcag ctactccaac	660

cgtgacaaac	tggcgaaaca	gtacggtatc	gcaaactata	gcggtaccgc	ctctcagaac	720
accaccctgc	tctctaaaat	caaaggcggt	gcacaaaaac	caagcactcc	agcgccaaaa	780
ccgtctacct	ccacggctaa	aaaaatctac	ttcccgccga	acaaaggtaa	ctgggtccgta	840
tacccgacca	acaaagctcc	ggtgaaagcc	aacgcaattg	gtgctatcaa	cccgaccaaa	900
ttcgggtggc	tgacctatac	gattcagaaa	gatcgcggca	acggtgtgta	cgaaattcag	960
accgatcagt	tcggtcgtgt	tcagggtttac	ggtgctccgt	ctaccggtgc	ggttatcaaa	1020
aaa						1023

<210> 93
 <211> 1485
 <212> DNA
 <213> Unknown

<220>
 <223> LysK

<400> 93	
atggccaaaa	cccaggctga aatcaacaaa cgtctggacg cgtacgctaa aggcactggt 60
gattctccgt	accgtgtgaa aaaagccacc tcctatgata cgtcttttgg tgtaatggaa 120
gcgggcgcta	ttgacgctga cggctattac catgcccagt gccaggatct gatcacggac 180
tatgttctgt	ggctgaccga caacaaagtt cgtacctggg gtaacgcgaa agatcagatc 240
aaacagtcct	acggcaccgg ttcaaaaatc cagcagaaca aaccgtccac cgttccgaaa 300
aaagggttga	tcgctgtctt cacctctggc tcctatgaac agtgggggtca catcggtatc 360
gtgtacgatg	gtggtaacac cagcacgttc accatcctgg aacagaactg gaacggttac 420
gcgaacaaaa	aaccgaccaa acgtgtggat aactactacg gcctgacgca cttcattgaa 480
atcccgggtga	aagctggtac taccgtgaaa aaagagacgg cgaaaaaatc tgcctctaaa 540
actccggcac	cgaaaaaaaa agccaccctg aaagtctcta aaaaccacat caactacacg 600
atggacaaac	gcggtaaaaa accggaaggc atgggtcattc acaacgatgc tggtcgctct 660
tccggccagc	agtatgaaaa cagcctggct aacgcagggt acgcacgtta cgcaaacggt 720
attgcgcact	actacggttc tgaaggctat gtgtgggaag ctatcgacgc gaaaaaccag 780
attgcgtggc	acaccggcga cgggtaccggc gctaactctg gcaacttccg ctttgcaggc 840
attgaggtat	gtcagtctat gtccgcgtct gatgcgcagt tcctgaaaaa cgaacaggct 900
gtcttccagt	tactgcgga gaaattcaaa gaatgggggtc tgactccgaa ccgcaaaact 960
gtacgcctgc	acatggaatt tgttccgact gcatgtccgc atcgtagcat ggttctgcac 1020
actggcttta	acccggttac tcagggtcgt ccgagccagg cgatcatgaa caaactgaaa 1080
gactacttta	tcaaacagat caaaaactac atggataaag gcaccagctc cagcaccgta 1140

gttaaagatg gcaaaacttc tagcgcgctcc actccggcaa cccgtccggt tactggttct	1200
tggaaaaaaa accagtatgg tacctggtac aaaccggaaa acgccacctt cgtaaacggc	1260
aaccagccga ttgtaactcg tatcggttct ccgtttctga acgcgccggt tggcggcaac	1320
ctgccggcag gtgctacgat tgtgtacgac gaagtttgca ttcaggcagg ccacatttgg	1380
atcggctaca acgcgtataa cggtaacgc gtttactgcc cgggtacgtac ctgtcaggggt	1440
gttccgccga accagattcc gggcgtggca tggggtgttt tcaaa	1485

<210> 94
 <211> 735
 <212> DNA
 <213> Unknown

<220>
 <223> Lss

<400> 94	
atggcccatg agcattcagc ccaatggctc aataattata aaaaaggata tgggtatggt	60
ccttatccct tggggattaa tgggtggtatg cattatgggg tcgacttttt tatgaacatt	120
ggtacccccg ttaaagcaat ctcatctggg aaaatagttg aagctggatg gtcaaactac	180
ggtggcggca atcagattgg cctgatagaa aatgacggag ttcaccgtca gtggtacatg	240
cacctttcga agtataacgt caaggtaggc gactatgtaa aggctgggtca aattatcgggt	300
tggtcaggaa gtacaggata tagtaccgcg cccacctcc atttccagcg gatggtgaac	360
tcattctcga actctaccgc acaggatccg atgccgttcc tgaaaagtgc aggctatggc	420
aaagctgggg gcacagtaac tcccaccccg aacaccggat ggaagacaaa taagtacgggt	480
acactttaca aaagcgagtc agcatcattt acaccgaata cggacatcat cacacgtact	540
acaggaccgt tcaggtcgat gcctcaatct ggggtcctca aggctggaca gacgatacac	600
tacgacgagg tcatgaagca ggacgggcat gtctgggtcg ggtacactgg aaactctgga	660
caacgaattt atcttccggt tcgaacatgg aacaaatcaa cgaatacatt gggcgtgcta	720
tgggggacca taaag	735

<210> 95
 <211> 528
 <212> DNA
 <213> Unknown

<220>
 <223> Pseudin 1

<400> 95	
aacccgatta tcgatggcat tatcgcgctg gaaggaggtt acgtctttta tccgaaagat	60
aagggtggag caacacattg gggattaca gaagcgacgg caccagcaca tggttatgca	120
ggagacatgc gtgatctaac tcatgccgaa gcctacgcaa tacttgagga ggattactgg	180

atcaaaccgg gttttgatgt tatctcaacg ctgtcgtggc ctgtgagctt tgaattgtgt	240
gatgcagcgg ttaacatagg tgcataccac cctagtgcct ggttacagag atggcttaac	300
gtgttcaatc acgaaggcaa acgctatcca gacattcatg tagacggcaa cattgggtccc	360
aggacttttag cagccttaga acattacttg gcttggagag ggcaagaagg tgaagctgta	420
ctggtgaaag ctctgaattg cagccaaggg acctactatc taaacgtcgc tgagaagaac	480
cacaacaacg aacagttcat ctacggttgg atcaagaatc gtgtgacc	528

<210> 96
 <211> 81
 <212> DNA
 <213> Unknown

<220>
 <223> WLB2-Variant

<400> 96	
aaacgctggg ttaaacgcgt gaaacgtgtc aaacgttggg tcaaacgtgt tgtccgtgta	60
gtgaaacggt gggtgaaacg c	81

<210> 97
 <211> 111
 <212> DNA
 <213> Unknown

<220>
 <223> LL-37

<400> 97	
ctcctgggtg acttctttcg caaatccaaa gagaaaatcg gcaaagagtt caaacgtatc	60
gtgcagcgca ttaaagactt tctgcgtaac ctggttccgc gtaccgaatc t	111

<210> 98
 <211> 39
 <212> DNA
 <213> Unknown

<220>
 <223> Indolicidin

<400> 98	
atcctgccgt ggaaatggcc gtggtggcca tggcgtcgc	39

<210> 99
 <211> 69
 <212> DNA
 <213> Unknown

<220>
 <223> Magainin

<400> 99

ggatcggca aattcctgca ctccgcaaaa aaattcggca aagctttcgt gggcgaaatt 60
atgaactct 69

<210> 100
<211> 75
<212> DNA
<213> Unknown

<220>
<223> Pleurocidin

<400> 100
ggctgggggtt ctttctttaa aaaagcggct cacgttggca aacatgtagg taaagcagct 60
ctgaccact atctg 75

<210> 101
<211> 108
<212> DNA
<213> Unknown

<220>
<223> Cecropin A (A. aegypti)

<400> 101
ggcggcctga aaaaactggg caaaaaactg gaaggtgccg gcaaactgtg gttcaacgct 60
gcagaaaaag cactgccggt tgtagctggt gctaaagctc tccgtaaa 108

<210> 102
<211> 120
<212> DNA
<213> Unknown

<220>
<223> Cecropin A (D. melanogaster)

<400> 102
ggctggctga aaaaaattgg caaaaaaatc gaacgcgtgg gccagcacac gcgtgatgca 60
accatccagg gtctgggtat cccacagcag gcagctaacg tagccgcgac tgctcgtggt 120

<210> 103
<211> 117
<212> DNA
<213> Unknown

<220>
<223> Sarcotoxin IA

<400> 103
ggatggctca aaaagattgg caagaaaatc gagcgagtcg gtcagcatac gcgtgatgca 60
actatccagg gtttaggtat cgcacagcaa gcagctaattg tagcagctac tgctcgg 117

<210> 104
<211> 27

<212> DNA
 <213> Unknown

 <220>
 <223> PK

 <400> 104
 aagcgtaaga aacgcaaaaa acgcaaa 27

<210> 105
 <211> 15
 <212> DNA
 <213> Unknown

 <220>
 <223> Pentapeptide

 <400> 105
 ttctttgtgg cgccg 15

<210> 106
 <211> 54
 <212> DNA
 <213> Unknown

 <220>
 <223> PK2

 <400> 106
 aagcgtaaga aacgcaaaaa acgcaaaaaa cgcaaaaaac gcaagaaaag aaaa 54

<210> 107
 <211> 373
 <212> PRT
 <213> Unknown

 <220>
 <223> Pseudin1-Cpl1

 <400> 107

 Met Gly Leu Asn Thr Leu Lys Lys Val Phe Gln Gly Leu His Glu Ala
 1 5 10 15

 Ile Lys Leu Ile Asn Asn His Val Gln Gly Ser Val Lys Lys Asn Asp
 20 25 30

 Leu Phe Val Asp Val Ser Ser His Asn Gly Tyr Asp Ile Thr Gly Ile
 35 40 45

 Leu Glu Gln Met Gly Thr Thr Asn Thr Ile Ile Lys Ile Ser Glu Ser
 50 55 60

 Thr Thr Tyr Leu Asn Pro Cys Leu Ser Ala Gln Val Glu Gln Ser Asn
 65 70 75 80

Pro Ile Gly Phe Tyr His Phe Ala Arg Phe Gly Gly Asp Val Ala Glu
 85 90 95

Ala Glu Arg Glu Ala Gln Phe Phe Leu Asp Asn Val Pro Met Gln Val
 100 105 110

Lys Tyr Leu Val Leu Asp Tyr Glu Asp Asp Pro Ser Gly Asp Ala Gln
 115 120 125

Ala Asn Thr Asn Ala Cys Leu Arg Phe Met Gln Met Ile Ala Asp Ala
 130 135 140

Gly Tyr Lys Pro Ile Tyr Tyr Ser Tyr Lys Pro Phe Thr His Asp Asn
 145 150 155 160

Val Asp Tyr Gln Gln Ile Leu Ala Gln Phe Pro Asn Ser Leu Trp Ile
 165 170 175

Ala Gly Tyr Gly Leu Asn Asp Gly Thr Ala Asn Phe Glu Tyr Phe Pro
 180 185 190

Ser Met Asp Gly Ile Arg Trp Trp Gln Tyr Ser Ser Asn Pro Phe Asp
 195 200 205

Lys Asn Ile Val Leu Leu Asp Asp Glu Glu Asp Asp Lys Pro Lys Thr
 210 215 220

Ala Gly Thr Trp Lys Gln Asp Ser Lys Gly Trp Trp Phe Arg Arg Asn
 225 230 235 240

Asn Gly Ser Phe Pro Tyr Asn Lys Trp Glu Lys Ile Gly Gly Val Trp
 245 250 255

Tyr Tyr Phe Asp Ser Lys Gly Tyr Cys Leu Thr Ser Glu Trp Leu Lys
 260 265 270

Asp Asn Glu Lys Trp Tyr Tyr Leu Lys Asp Asn Gly Ala Met Ala Thr
 275 280 285

Gly Trp Val Leu Val Gly Ser Glu Trp Tyr Tyr Met Asp Asp Ser Gly
 290 295 300

Ala Met Val Thr Gly Trp Val Lys Tyr Lys Asn Asn Trp Tyr Tyr Met
 305 310 315 320

Thr Asn Glu Arg Gly Asn Met Val Ser Asn Glu Phe Ile Lys Ser Gly
 325 330 335

Lys Gly Trp Tyr Phe Met Asn Thr Asn Gly Glu Leu Ala Asp Asn Pro
340 345 350

Ser Phe Thr Lys Glu Pro Asp Gly Leu Ile Thr Val Ala Leu Glu His
355 360 365

His His His His His
370

<210> 108
<211> 376
<212> PRT
<213> Unknown

<220>
<223> WLBU2-Variant-Cpl1

<400> 108

Met Lys Arg Trp Val Lys Arg Val Lys Arg Val Lys Arg Trp Val Lys
1 5 10 15

Arg Val Val Arg Val Val Lys Arg Trp Val Lys Arg Gly Ser Val Lys
20 25 30

Lys Asn Asp Leu Phe Val Asp Val Ser Ser His Asn Gly Tyr Asp Ile
35 40 45

Thr Gly Ile Leu Glu Gln Met Gly Thr Thr Asn Thr Ile Ile Lys Ile
50 55 60

Ser Glu Ser Thr Thr Tyr Leu Asn Pro Cys Leu Ser Ala Gln Val Glu
65 70 75 80

Gln Ser Asn Pro Ile Gly Phe Tyr His Phe Ala Arg Phe Gly Gly Asp
85 90 95

Val Ala Glu Ala Glu Arg Glu Ala Gln Phe Phe Leu Asp Asn Val Pro
100 105 110

Met Gln Val Lys Tyr Leu Val Leu Asp Tyr Glu Asp Asp Pro Ser Gly
115 120 125

Asp Ala Gln Ala Asn Thr Asn Ala Cys Leu Arg Phe Met Gln Met Ile
130 135 140

Ala Asp Ala Gly Tyr Lys Pro Ile Tyr Tyr Ser Tyr Lys Pro Phe Thr
145 150 155 160

His Asp Asn Val Asp Tyr Gln Gln Ile Leu Ala Gln Phe Pro Asn Ser
165 170 175

Leu Trp Ile Ala Gly Tyr Gly Leu Asn Asp Gly Thr Ala Asn Phe Glu
180 185 190

Tyr Phe Pro Ser Met Asp Gly Ile Arg Trp Trp Gln Tyr Ser Ser Asn
195 200 205

Pro Phe Asp Lys Asn Ile Val Leu Leu Asp Asp Glu Glu Asp Asp Lys
210 215 220

Pro Lys Thr Ala Gly Thr Trp Lys Gln Asp Ser Lys Gly Trp Trp Phe
225 230 235 240

Arg Arg Asn Asn Gly Ser Phe Pro Tyr Asn Lys Trp Glu Lys Ile Gly
245 250 255

Gly Val Trp Tyr Tyr Phe Asp Ser Lys Gly Tyr Cys Leu Thr Ser Glu
260 265 270

Trp Leu Lys Asp Asn Glu Lys Trp Tyr Tyr Leu Lys Asp Asn Gly Ala
275 280 285

Met Ala Thr Gly Trp Val Leu Val Gly Ser Glu Trp Tyr Tyr Met Asp
290 295 300

Asp Ser Gly Ala Met Val Thr Gly Trp Val Lys Tyr Lys Asn Asn Trp
305 310 315 320

Tyr Tyr Met Thr Asn Glu Arg Gly Asn Met Val Ser Asn Glu Phe Ile
325 330 335

Lys Ser Gly Lys Gly Trp Tyr Phe Met Asn Thr Asn Gly Glu Leu Ala
340 345 350

Asp Asn Pro Ser Phe Thr Lys Glu Pro Asp Gly Leu Ile Thr Val Ala
355 360 365

Leu Glu His His His His His His
370 375

<210> 109
<211> 386
<212> PRT
<213> Unknown

<220>

<223> LL-37-Cpl1

<400> 109

Met Leu Leu Gly Asp Phe Phe Arg Lys Ser Lys Glu Lys Ile Gly Lys
1 5 10 15

Glu Phe Lys Arg Ile Val Gln Arg Ile Lys Asp Phe Leu Arg Asn Leu
20 25 30

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

Asp Val Ser Ser His Asn Gly Tyr Asp Ile Thr Gly Ile Leu Glu Gln
50 55 60

Met Gly Thr Thr Asn Thr Ile Ile Lys Ile Ser Glu Ser Thr Thr Tyr
65 70 75 80

Leu Asn Pro Cys Leu Ser Ala Gln Val Glu Gln Ser Asn Pro Ile Gly
85 90 95

Phe Tyr His Phe Ala Arg Phe Gly Gly Asp Val Ala Glu Ala Glu Arg
100 105 110

Glu Ala Gln Phe Phe Leu Asp Asn Val Pro Met Gln Val Lys Tyr Leu
115 120 125

Val Leu Asp Tyr Glu Asp Asp Pro Ser Gly Asp Ala Gln Ala Asn Thr
130 135 140

Asn Ala Cys Leu Arg Phe Met Gln Met Ile Ala Asp Ala Gly Tyr Lys
145 150 155 160

Pro Ile Tyr Tyr Ser Tyr Lys Pro Phe Thr His Asp Asn Val Asp Tyr
165 170 175

Gln Gln Ile Leu Ala Gln Phe Pro Asn Ser Leu Trp Ile Ala Gly Tyr
180 185 190

Gly Leu Asn Asp Gly Thr Ala Asn Phe Glu Tyr Phe Pro Ser Met Asp
195 200 205

Gly Ile Arg Trp Trp Gln Tyr Ser Ser Asn Pro Phe Asp Lys Asn Ile
210 215 220

Val Leu Leu Asp Asp Glu Glu Asp Asp Lys Pro Lys Thr Ala Gly Thr
225 230 235 240

Trp Lys Gln Asp Ser Lys Gly Trp Trp Phe Arg Arg Asn Asn Gly Ser
245 250 255

Phe Pro Tyr Asn Lys Trp Glu Lys Ile Gly Gly Val Trp Tyr Tyr Phe
260 265 270

Asp Ser Lys Gly Tyr Cys Leu Thr Ser Glu Trp Leu Lys Asp Asn Glu
275 280 285

Lys Trp Tyr Tyr Leu Lys Asp Asn Gly Ala Met Ala Thr Gly Trp Val
290 295 300

Leu Val Gly Ser Glu Trp Tyr Tyr Met Asp Asp Ser Gly Ala Met Val
305 310 315 320

Thr Gly Trp Val Lys Tyr Lys Asn Asn Trp Tyr Tyr Met Thr Asn Glu
325 330 335

Arg Gly Asn Met Val Ser Asn Glu Phe Ile Lys Ser Gly Lys Gly Trp
340 345 350

Tyr Phe Met Asn Thr Asn Gly Glu Leu Ala Asp Asn Pro Ser Phe Thr
355 360 365

Lys Glu Pro Asp Gly Leu Ile Thr Val Ala Leu Glu His His His His
370 375 380

His His
385

<210> 110
<211> 362
<212> PRT
<213> Unknown

<220>
<223> Indolicidin-Cpl1

<400> 110

Met Ile Leu Pro Trp Lys Trp Pro Trp Trp Pro Trp Arg Arg Gly Ser
1 5 10 15

Val Lys Lys Asn Asp Leu Phe Val Asp Val Ser Ser His Asn Gly Tyr
20 25 30

Asp Ile Thr Gly Ile Leu Glu Gln Met Gly Thr Thr Asn Thr Ile Ile
35 40 45

Lys Ile Ser Glu Ser Thr Thr Tyr Leu Asn Pro Cys Leu Ser Ala Gln
 50 55 60

Val Glu Gln Ser Asn Pro Ile Gly Phe Tyr His Phe Ala Arg Phe Gly
 65 70 75 80

Gly Asp Val Ala Glu Ala Glu Arg Glu Ala Gln Phe Phe Leu Asp Asn
 85 90 95

Val Pro Met Gln Val Lys Tyr Leu Val Leu Asp Tyr Glu Asp Asp Pro
 100 105 110

Ser Gly Asp Ala Gln Ala Asn Thr Asn Ala Cys Leu Arg Phe Met Gln
 115 120 125

Met Ile Ala Asp Ala Gly Tyr Lys Pro Ile Tyr Tyr Ser Tyr Lys Pro
 130 135 140

Phe Thr His Asp Asn Val Asp Tyr Gln Gln Ile Leu Ala Gln Phe Pro
 145 150 155 160

Asn Ser Leu Trp Ile Ala Gly Tyr Gly Leu Asn Asp Gly Thr Ala Asn
 165 170 175

Phe Glu Tyr Phe Pro Ser Met Asp Gly Ile Arg Trp Trp Gln Tyr Ser
 180 185 190

Ser Asn Pro Phe Asp Lys Asn Ile Val Leu Leu Asp Asp Glu Glu Asp
 195 200 205

Asp Lys Pro Lys Thr Ala Gly Thr Trp Lys Gln Asp Ser Lys Gly Trp
 210 215 220

Trp Phe Arg Arg Asn Asn Gly Ser Phe Pro Tyr Asn Lys Trp Glu Lys
 225 230 235 240

Ile Gly Gly Val Trp Tyr Tyr Phe Asp Ser Lys Gly Tyr Cys Leu Thr
 245 250 255

Ser Glu Trp Leu Lys Asp Asn Glu Lys Trp Tyr Tyr Leu Lys Asp Asn
 260 265 270

Gly Ala Met Ala Thr Gly Trp Val Leu Val Gly Ser Glu Trp Tyr Tyr
 275 280 285

Met Asp Asp Ser Gly Ala Met Val Thr Gly Trp Val Lys Tyr Lys Asn
 290 295 300

Asn Trp Tyr Tyr Met Thr Asn Glu Arg Gly Asn Met Val Ser Asn Glu
 305 310 315 320

Phe Ile Lys Ser Gly Lys Gly Trp Tyr Phe Met Asn Thr Asn Gly Glu
 325 330 335

Leu Ala Asp Asn Pro Ser Phe Thr Lys Glu Pro Asp Gly Leu Ile Thr
 340 345 350

Val Ala Leu Glu His His His His His His
 355 360

<210> 111
 <211> 372
 <212> PRT
 <213> Unknown

<220>
 <223> Magainin-Cpl1

<400> 111

Met Gly Ile Gly Lys Phe Leu His Ser Ala Lys Lys Phe Gly Lys Ala
 1 5 10 15

Phe Val Gly Glu Ile Met Asn Ser Gly Ser Val Lys Lys Asn Asp Leu
 20 25 30

Phe Val Asp Val Ser Ser His Asn Gly Tyr Asp Ile Thr Gly Ile Leu
 35 40 45

Glu Gln Met Gly Thr Thr Asn Thr Ile Ile Lys Ile Ser Glu Ser Thr
 50 55 60

Thr Tyr Leu Asn Pro Cys Leu Ser Ala Gln Val Glu Gln Ser Asn Pro
 65 70 75 80

Ile Gly Phe Tyr His Phe Ala Arg Phe Gly Gly Asp Val Ala Glu Ala
 85 90 95

Glu Arg Glu Ala Gln Phe Phe Leu Asp Asn Val Pro Met Gln Val Lys
 100 105 110

Tyr Leu Val Leu Asp Tyr Glu Asp Asp Pro Ser Gly Asp Ala Gln Ala
 115 120 125

Asn Thr Asn Ala Cys Leu Arg Phe Met Gln Met Ile Ala Asp Ala Gly
 130 135 140

Tyr Lys Pro Ile Tyr Tyr Ser Tyr Lys Pro Phe Thr His Asp Asn Val
 145 150 155 160

Asp Tyr Gln Gln Ile Leu Ala Gln Phe Pro Asn Ser Leu Trp Ile Ala
 165 170 175

Gly Tyr Gly Leu Asn Asp Gly Thr Ala Asn Phe Glu Tyr Phe Pro Ser
 180 185 190

Met Asp Gly Ile Arg Trp Trp Gln Tyr Ser Ser Asn Pro Phe Asp Lys
 195 200 205

Asn Ile Val Leu Leu Asp Asp Glu Glu Asp Asp Lys Pro Lys Thr Ala
 210 215 220

Gly Thr Trp Lys Gln Asp Ser Lys Gly Trp Trp Phe Arg Arg Asn Asn
 225 230 235 240

Gly Ser Phe Pro Tyr Asn Lys Trp Glu Lys Ile Gly Gly Val Trp Tyr
 245 250 255

Tyr Phe Asp Ser Lys Gly Tyr Cys Leu Thr Ser Glu Trp Leu Lys Asp
 260 265 270

Asn Glu Lys Trp Tyr Tyr Leu Lys Asp Asn Gly Ala Met Ala Thr Gly
 275 280 285

Trp Val Leu Val Gly Ser Glu Trp Tyr Tyr Met Asp Asp Ser Gly Ala
 290 295 300

Met Val Thr Gly Trp Val Lys Tyr Lys Asn Asn Trp Tyr Tyr Met Thr
 305 310 315 320

Asn Glu Arg Gly Asn Met Val Ser Asn Glu Phe Ile Lys Ser Gly Lys
 325 330 335

Gly Trp Tyr Phe Met Asn Thr Asn Gly Glu Leu Ala Asp Asn Pro Ser
 340 345 350

Phe Thr Lys Glu Pro Asp Gly Leu Ile Thr Val Ala Leu Glu His His
 355 360 365

His His His His
 370

<210> 112
 <211> 374

<212> PRT
<213> Unknown

<220>
<223> Pleurocidin-Cpl1

<400> 112

Met Gly Trp Gly Ser Phe Phe Lys Lys Ala Ala His Val Gly Lys His
1 5 10 15

Val Gly Lys Ala Ala Leu Thr His Tyr Leu Gly Ser Val Lys Lys Asn
20 25 30

Asp Leu Phe Val Asp Val Ser Ser His Asn Gly Tyr Asp Ile Thr Gly
35 40 45

Ile Leu Glu Gln Met Gly Thr Thr Asn Thr Ile Ile Lys Ile Ser Glu
50 55 60

Ser Thr Thr Tyr Leu Asn Pro Cys Leu Ser Ala Gln Val Glu Gln Ser
65 70 75 80

Asn Pro Ile Gly Phe Tyr His Phe Ala Arg Phe Gly Gly Asp Val Ala
85 90 95

Glu Ala Glu Arg Glu Ala Gln Phe Phe Leu Asp Asn Val Pro Met Gln
100 105 110

Val Lys Tyr Leu Val Leu Asp Tyr Glu Asp Asp Pro Ser Gly Asp Ala
115 120 125

Gln Ala Asn Thr Asn Ala Cys Leu Arg Phe Met Gln Met Ile Ala Asp
130 135 140

Ala Gly Tyr Lys Pro Ile Tyr Tyr Ser Tyr Lys Pro Phe Thr His Asp
145 150 155 160

Asn Val Asp Tyr Gln Gln Ile Leu Ala Gln Phe Pro Asn Ser Leu Trp
165 170 175

Ile Ala Gly Tyr Gly Leu Asn Asp Gly Thr Ala Asn Phe Glu Tyr Phe
180 185 190

Pro Ser Met Asp Gly Ile Arg Trp Trp Gln Tyr Ser Ser Asn Pro Phe
195 200 205

Asp Lys Asn Ile Val Leu Leu Asp Asp Glu Glu Asp Asp Lys Pro Lys
210 215 220

Thr Ala Gly Thr Trp Lys Gln Asp Ser Lys Gly Trp Trp Phe Arg Arg
 225 230 235 240

Asn Asn Gly Ser Phe Pro Tyr Asn Lys Trp Glu Lys Ile Gly Gly Val
 245 250 255

Trp Tyr Tyr Phe Asp Ser Lys Gly Tyr Cys Leu Thr Ser Glu Trp Leu
 260 265 270

Lys Asp Asn Glu Lys Trp Tyr Tyr Leu Lys Asp Asn Gly Ala Met Ala
 275 280 285

Thr Gly Trp Val Leu Val Gly Ser Glu Trp Tyr Tyr Met Asp Asp Ser
 290 295 300

Gly Ala Met Val Thr Gly Trp Val Lys Tyr Lys Asn Asn Trp Tyr Tyr
 305 310 315 320

Met Thr Asn Glu Arg Gly Asn Met Val Ser Asn Glu Phe Ile Lys Ser
 325 330 335

Gly Lys Gly Trp Tyr Phe Met Asn Thr Asn Gly Glu Leu Ala Asp Asn
 340 345 350

Pro Ser Phe Thr Lys Glu Pro Asp Gly Leu Ile Thr Val Ala Leu Glu
 355 360 365

His His His His His His
 370

<210> 113
 <211> 385
 <212> PRT
 <213> Unknown

<220>
 <223> Cecropin A (A.aegypti)-Cpl1

<400> 113

Met Gly Gly Leu Lys Lys Leu Gly Lys Lys Leu Glu Gly Ala Gly Lys
 1 5 10 15

Arg Val Phe Asn Ala Ala Glu Lys Ala Leu Pro Val Val Ala Gly Ala
 20 25 30

Lys Ala Leu Arg Lys Gly Ser Val Lys Lys Asn Asp Leu Phe Val Asp
 35 40 45

Val Ser Ser His Asn Gly Tyr Asp Ile Thr Gly Ile Leu Glu Gln Met
 50 55 60

Gly Thr Thr Asn Thr Ile Ile Lys Ile Ser Glu Ser Thr Thr Tyr Leu
 65 70 75 80

Asn Pro Cys Leu Ser Ala Gln Val Glu Gln Ser Asn Pro Ile Gly Phe
 85 90 95

Tyr His Phe Ala Arg Phe Gly Gly Asp Val Ala Glu Ala Glu Arg Glu
 100 105 110

Ala Gln Phe Phe Leu Asp Asn Val Pro Met Gln Val Lys Tyr Leu Val
 115 120 125

Leu Asp Tyr Glu Asp Asp Pro Ser Gly Asp Ala Gln Ala Asn Thr Asn
 130 135 140

Ala Cys Leu Arg Phe Met Gln Met Ile Ala Asp Ala Gly Tyr Lys Pro
 145 150 155 160

Ile Tyr Tyr Ser Tyr Lys Pro Phe Thr His Asp Asn Val Asp Tyr Gln
 165 170 175

Gln Ile Leu Ala Gln Phe Pro Asn Ser Leu Trp Ile Ala Gly Tyr Gly
 180 185 190

Leu Asn Asp Gly Thr Ala Asn Phe Glu Tyr Phe Pro Ser Met Asp Gly
 195 200 205

Ile Arg Trp Trp Gln Tyr Ser Ser Asn Pro Phe Asp Lys Asn Ile Val
 210 215 220

Leu Leu Asp Asp Glu Glu Asp Asp Lys Pro Lys Thr Ala Gly Thr Trp
 225 230 235 240

Lys Gln Asp Ser Lys Gly Trp Trp Phe Arg Arg Asn Asn Gly Ser Phe
 245 250 255

Pro Tyr Asn Lys Trp Glu Lys Ile Gly Gly Val Trp Tyr Tyr Phe Asp
 260 265 270

Ser Lys Gly Tyr Cys Leu Thr Ser Glu Trp Leu Lys Asp Asn Glu Lys
 275 280 285

Trp Tyr Tyr Leu Lys Asp Asn Gly Ala Met Ala Thr Gly Trp Val Leu
 290 295 300

Val Gly Ser Glu Trp Tyr Tyr Met Asp Asp Ser Gly Ala Met Val Thr
 305 310 315 320

Gly Trp Val Lys Tyr Lys Asn Asn Trp Tyr Tyr Met Thr Asn Glu Arg
 325 330 335

Gly Asn Met Val Ser Asn Glu Phe Ile Lys Ser Gly Lys Gly Trp Tyr
 340 345 350

Phe Met Asn Thr Asn Gly Glu Leu Ala Asp Asn Pro Ser Phe Thr Lys
 355 360 365

Glu Pro Asp Gly Leu Ile Thr Val Ala Leu Glu His His His His His
 370 375 380

His
 385

<210> 114
 <211> 370
 <212> PRT
 <213> Unknown

<220>
 <223> BuforinII-Cpl1

<400> 114

Met Thr Arg Ser Ser Arg Ala Gly Leu Gln Phe Pro Val Gly Arg Val
 1 5 10 15

His Arg Leu Leu Arg Lys Gly Ser Val Lys Lys Asn Asp Leu Phe Val
 20 25 30

Asp Val Ser Ser His Asn Gly Tyr Asp Ile Thr Gly Ile Leu Glu Gln
 35 40 45

Met Gly Thr Thr Asn Thr Ile Ile Lys Ile Ser Glu Ser Thr Thr Tyr
 50 55 60

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

Phe Tyr His Phe Ala Arg Phe Gly Gly Asp Val Ala Glu Ala Glu Arg
 85 90 95

Glu Ala Gln Phe Phe Leu Asp Asn Val Pro Met Gln Val Lys Tyr Leu
 100 105 110

Val Leu Asp Tyr Glu Asp Asp Pro Ser Gly Asp Ala Gln Ala Asn Thr
 115 120 125

Asn Ala Cys Leu Arg Phe Met Gln Met Ile Ala Asp Ala Gly Tyr Lys
 130 135 140

Pro Ile Tyr Tyr Ser Tyr Lys Pro Phe Thr His Asp Asn Val Asp Tyr
 145 150 155 160

Gln Gln Ile Leu Ala Gln Phe Pro Asn Ser Leu Trp Ile Ala Gly Tyr
 165 170 175

Gly Leu Asn Asp Gly Thr Ala Asn Phe Glu Tyr Phe Pro Ser Met Asp
 180 185 190

Gly Ile Arg Trp Trp Gln Tyr Ser Ser Asn Pro Phe Asp Lys Asn Ile
 195 200 205

Val Leu Leu Asp Asp Glu Glu Asp Asp Lys Pro Lys Thr Ala Gly Thr
 210 215 220

Trp Lys Gln Asp Ser Lys Gly Trp Trp Phe Arg Arg Asn Asn Gly Ser
 225 230 235 240

Phe Pro Tyr Asn Lys Trp Glu Lys Ile Gly Gly Val Trp Tyr Tyr Phe
 245 250 255

Asp Ser Lys Gly Tyr Cys Leu Thr Ser Glu Trp Leu Lys Asp Asn Glu
 260 265 270

Lys Trp Tyr Tyr Leu Lys Asp Asn Gly Ala Met Ala Thr Gly Trp Val
 275 280 285

Leu Val Gly Ser Glu Trp Tyr Tyr Met Asp Asp Ser Gly Ala Met Val
 290 295 300

Thr Gly Trp Val Lys Tyr Lys Asn Asn Trp Tyr Tyr Met Thr Asn Glu
 305 310 315 320

Arg Gly Asn Met Val Ser Asn Glu Phe Ile Lys Ser Gly Lys Gly Trp
 325 330 335

Tyr Phe Met Asn Thr Asn Gly Glu Leu Ala Asp Asn Pro Ser Phe Thr
 340 345 350

Lys Glu Pro Asp Gly Leu Ile Thr Val Ala Leu Glu His His His His
 355 360 365

His His
370

<210> 115
<211> 388
<212> PRT
<213> Unknown

<220>
<223> Sarcotoxin IA-Cpl1

<400> 115

Met Gly Trp Leu Lys Lys Ile Gly Lys Lys Ile Glu Arg Val Gly Gln
1 5 10 15

His Thr Arg Asp Ala Thr Ile Gln Gly Leu Gly Ile Ala Gln Gln Ala
20 25 30

Ala Asn Val Ala Ala Thr Ala Arg Gly Ser Val Lys Lys Asn Asp Leu
35 40 45

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

Glu Gln Met Gly Thr Thr Asn Thr Ile Ile Lys Ile Ser Glu Ser Thr
65 70 75 80

Thr Tyr Leu Asn Pro Cys Leu Ser Ala Gln Val Glu Gln Ser Asn Pro
85 90 95

Ile Gly Phe Tyr His Phe Ala Arg Phe Gly Gly Asp Val Ala Glu Ala
100 105 110

Glu Arg Glu Ala Gln Phe Phe Leu Asp Asn Val Pro Met Gln Val Lys
115 120 125

Tyr Leu Val Leu Asp Tyr Glu Asp Asp Pro Ser Gly Asp Ala Gln Ala
130 135 140

Asn Thr Asn Ala Cys Leu Arg Phe Met Gln Met Ile Ala Asp Ala Gly
145 150 155 160

Tyr Lys Pro Ile Tyr Tyr Ser Tyr Lys Pro Phe Thr His Asp Asn Val
165 170 175

Asp Tyr Gln Gln Ile Leu Ala Gln Phe Pro Asn Ser Leu Trp Ile Ala
180 185 190

Gly Tyr Gly Leu Asn Asp Gly Thr Ala Asn Phe Glu Tyr Phe Pro Ser
195 200 205

Met Asp Gly Ile Arg Trp Trp Gln Tyr Ser Ser Asn Pro Phe Asp Lys
210 215 220

Asn Ile Val Leu Leu Asp Asp Glu Glu Asp Asp Lys Pro Lys Thr Ala
225 230 235 240

Gly Thr Trp Lys Gln Asp Ser Lys Gly Trp Trp Phe Arg Arg Asn Asn
245 250 255

Gly Ser Phe Pro Tyr Asn Lys Trp Glu Lys Ile Gly Gly Val Trp Tyr
260 265 270

Tyr Phe Asp Ser Lys Gly Tyr Cys Leu Thr Ser Glu Trp Leu Lys Asp
275 280 285

Asn Glu Lys Trp Tyr Tyr Leu Lys Asp Asn Gly Ala Met Ala Thr Gly
290 295 300

Trp Val Leu Val Gly Ser Glu Trp Tyr Tyr Met Asp Asp Ser Gly Ala
305 310 315 320

Met Val Thr Gly Trp Val Lys Tyr Lys Asn Asn Trp Tyr Tyr Met Thr
325 330 335

Asn Glu Arg Gly Asn Met Val Ser Asn Glu Phe Ile Lys Ser Gly Lys
340 345 350

Gly Trp Tyr Phe Met Asn Thr Asn Gly Glu Leu Ala Asp Asn Pro Ser
355 360 365

Phe Thr Lys Glu Pro Asp Gly Leu Ile Thr Val Ala Leu Glu His His
370 375 380

His His His His
385

<210> 116
<211> 358
<212> PRT
<213> Unknown

<220>
<223> PK-Cpl1

<400> 116

Met Lys Arg Lys Lys Arg Lys Lys Arg Lys Gly Ser Val Lys Lys Asn
 1 5 10 15
 Asp Leu Phe Val Asp Val Ser Ser His Asn Gly Tyr Asp Ile Thr Gly
 20 25 30
 Ile Leu Glu Gln Met Gly Thr Thr Asn Thr Ile Ile Lys Ile Ser Glu
 35 40 45
 Ser Thr Thr Tyr Leu Asn Pro Cys Leu Ser Ala Gln Val Glu Gln Ser
 50 55 60
 Asn Pro Ile Gly Phe Tyr His Phe Ala Arg Phe Gly Gly Asp Val Ala
 65 70 75 80
 Glu Ala Glu Arg Glu Ala Gln Phe Phe Leu Asp Asn Val Pro Met Gln
 85 90 95
 Val Lys Tyr Leu Val Leu Asp Tyr Glu Asp Asp Pro Ser Gly Asp Ala
 100 105 110
 Gln Ala Asn Thr Asn Ala Cys Leu Arg Phe Met Gln Met Ile Ala Asp
 115 120 125
 Ala Gly Tyr Lys Pro Ile Tyr Tyr Ser Tyr Lys Pro Phe Thr His Asp
 130 135 140
 Asn Val Asp Tyr Gln Gln Ile Leu Ala Gln Phe Pro Asn Ser Leu Trp
 145 150 155 160
 Ile Ala Gly Tyr Gly Leu Asn Asp Gly Thr Ala Asn Phe Glu Tyr Phe
 165 170 175
 Pro Ser Met Asp Gly Ile Arg Trp Trp Gln Tyr Ser Ser Asn Pro Phe
 180 185 190
 Asp Lys Asn Ile Val Leu Leu Asp Asp Glu Glu Asp Asp Lys Pro Lys
 195 200 205
 Thr Ala Gly Thr Trp Lys Gln Asp Ser Lys Gly Trp Trp Phe Arg Arg
 210 215 220
 Asn Asn Gly Ser Phe Pro Tyr Asn Lys Trp Glu Lys Ile Gly Gly Val
 225 230 235 240
 Trp Tyr Tyr Phe Asp Ser Lys Gly Tyr Cys Leu Thr Ser Glu Trp Leu
 245 250 255

Lys Asp Asn Glu Lys Trp Tyr Tyr Leu Lys Asp Asn Gly Ala Met Ala
260 265 270

Thr Gly Trp Val Leu Val Gly Ser Glu Trp Tyr Tyr Met Asp Asp Ser
275 280 285

Gly Ala Met Val Thr Gly Trp Val Lys Tyr Lys Asn Asn Trp Tyr Tyr
290 295 300

Met Thr Asn Glu Arg Gly Asn Met Val Ser Asn Glu Phe Ile Lys Ser
305 310 315 320

Gly Lys Gly Trp Tyr Phe Met Asn Thr Asn Gly Glu Leu Ala Asp Asn
325 330 335

Pro Ser Phe Thr Lys Glu Pro Asp Gly Leu Ile Thr Val Ala Leu Glu
340 345 350

His His His His His His
355

<210> 117
<211> 356
<212> PRT
<213> Unknown

<220>
<223> Pentapeptid-Ply511

<400> 117

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

Ile Ile Ala Gly Leu Pro Lys Gly Lys Leu Lys Gly Ala Asn Phe Val
20 25 30

Ile Ala His Glu Thr Ala Asn Ser Lys Ser Thr Ile Asp Asn Glu Val
35 40 45

Ser Tyr Met Thr Arg Asn Trp Lys Asn Ala Phe Val Thr His Phe Val
50 55 60

Gly Gly Gly Gly Arg Val Val Gln Val Ala Asn Val Asn Tyr Val Ser
65 70 75 80

Trp Gly Ala Gly Gln Tyr Ala Asn Ser Tyr Ser Tyr Ala Gln Val Glu
85 90 95

Leu Cys Arg Thr Ser Asn Ala Thr Thr Phe Lys Lys Asp Tyr Glu Val
 100 105 110

Tyr Cys Gln Leu Leu Val Asp Leu Ala Lys Lys Ala Gly Ile Pro Ile
 115 120 125

Thr Leu Asp Ser Gly Ser Lys Thr Ser Asp Lys Gly Ile Lys Ser His
 130 135 140

Lys Trp Val Ala Asp Lys Leu Gly Gly Thr Thr His Gln Asp Pro Tyr
 145 150 155 160

Ala Tyr Leu Ser Ser Trp Gly Ile Ser Lys Ala Gln Phe Ala Ser Asp
 165 170 175

Leu Ala Lys Val Ser Gly Gly Gly Asn Thr Gly Thr Ala Pro Ala Lys
 180 185 190

Pro Ser Thr Pro Ala Pro Lys Pro Ser Thr Pro Ser Thr Asn Leu Asp
 195 200 205

Lys Leu Gly Leu Val Asp Tyr Met Asn Ala Lys Lys Met Asp Ser Ser
 210 215 220

Tyr Ser Asn Arg Asp Lys Leu Ala Lys Gln Tyr Gly Ile Ala Asn Tyr
 225 230 235 240

Ser Gly Thr Ala Ser Gln Asn Thr Thr Leu Leu Ser Lys Ile Lys Gly
 245 250 255

Gly Ala Pro Lys Pro Ser Thr Pro Ala Pro Lys Pro Ser Thr Ser Thr
 260 265 270

Ala Lys Lys Ile Tyr Phe Pro Pro Asn Lys Gly Asn Trp Ser Val Tyr
 275 280 285

Pro Thr Asn Lys Ala Pro Val Lys Ala Asn Ala Ile Gly Ala Ile Asn
 290 295 300

Pro Thr Lys Phe Gly Gly Leu Thr Tyr Thr Ile Gln Lys Asp Arg Gly
 305 310 315 320

Asn Gly Val Tyr Glu Ile Gln Thr Asp Gln Phe Gly Arg Val Gln Val
 325 330 335

Tyr Gly Ala Pro Ser Thr Gly Ala Val Ile Lys Lys Leu Glu His His
 340 345 350

His His His His
355

<210> 118
<211> 514
<212> PRT
<213> Unknown

<220>
<223> PK-LysK

<400> 118

Met Lys Arg Lys Lys Arg Lys Lys Arg Lys Gly Ser Ala Lys Thr Gln
1 5 10 15

Ala Glu Ile Asn Lys Arg Leu Asp Ala Tyr Ala Lys Gly Thr Val Asp
20 25 30

Ser Pro Tyr Arg Val Lys Lys Ala Thr Ser Tyr Asp Pro Ser Phe Gly
35 40 45

Val Met Glu Ala Gly Ala Ile Asp Ala Asp Gly Tyr Tyr His Ala Gln
50 55 60

Cys Gln Asp Leu Ile Thr Asp Tyr Val Leu Trp Leu Thr Asp Asn Lys
65 70 75 80

Val Arg Thr Trp Gly Asn Ala Lys Asp Gln Ile Lys Gln Ser Tyr Gly
85 90 95

Thr Gly Phe Lys Ile His Glu Asn Lys Pro Ser Thr Val Pro Lys Lys
100 105 110

Gly Trp Ile Ala Val Phe Thr Ser Gly Ser Tyr Glu Gln Trp Gly His
115 120 125

Ile Gly Ile Val Tyr Asp Gly Gly Asn Thr Ser Thr Phe Thr Ile Leu
130 135 140

Glu Gln Asn Trp Asn Gly Tyr Ala Asn Lys Lys Pro Thr Lys Arg Val
145 150 155 160

Asp Asn Tyr Tyr Gly Leu Thr His Phe Ile Glu Ile Pro Val Lys Ala
165 170 175

Gly Thr Thr Val Lys Lys Glu Thr Ala Lys Lys Ser Ala Ser Lys Thr
180 185 190

Pro Ala Pro Lys Lys Lys Ala Thr Leu Lys Val Ser Lys Asn His Ile
 195 200 205

Asn Tyr Thr Met Asp Lys Arg Gly Lys Lys Pro Glu Gly Met Val Ile
 210 215 220

His Asn Asp Ala Gly Arg Ser Ser Gly Gln Gln Tyr Glu Asn Ser Leu
 225 230 235 240

Ala Asn Ala Gly Tyr Ala Arg Tyr Ala Asn Gly Ile Ala His Tyr Tyr
 245 250 255

Gly Ser Glu Gly Tyr Val Trp Glu Ala Ile Asp Ala Lys Asn Gln Ile
 260 265 270

Ala Trp His Thr Gly Asp Gly Thr Gly Ala Asn Ser Gly Asn Phe Arg
 275 280 285

Phe Ala Gly Ile Glu Val Cys Gln Ser Met Ser Ala Ser Asp Ala Gln
 290 295 300

Phe Leu Lys Asn Glu Gln Ala Val Phe Gln Phe Thr Ala Glu Lys Phe
 305 310 315 320

Lys Glu Trp Gly Leu Thr Pro Asn Arg Lys Thr Val Arg Leu His Met
 325 330 335

Glu Phe Val Pro Thr Ala Cys Pro His Arg Ser Met Val Leu His Thr
 340 345 350

Gly Phe Asn Pro Val Thr Gln Gly Arg Pro Ser Gln Ala Ile Met Asn
 355 360 365

Lys Leu Lys Asp Tyr Phe Ile Lys Gln Ile Lys Asn Tyr Met Asp Lys
 370 375 380

Gly Thr Ser Ser Ser Thr Val Val Lys Asp Gly Lys Thr Ser Ser Ala
 385 390 395 400

Ser Thr Pro Ala Thr Arg Pro Val Thr Gly Ser Trp Lys Lys Asn Gln
 405 410 415

Tyr Gly Thr Trp Tyr Lys Pro Glu Asn Ala Thr Phe Val Asn Gly Asn
 420 425 430

Gln Pro Ile Val Thr Arg Ile Gly Ser Pro Phe Leu Asn Ala Pro Val
 435 440 445

Gly Gly Asn Leu Pro Ala Gly Ala Thr Ile Val Tyr Asp Glu Val Cys
 450 455 460

Ile Gln Ala Gly His Ile Trp Ile Gly Tyr Asn Ala Tyr Asn Gly Asn
 465 470 475 480

Arg Val Tyr Cys Pro Val Arg Thr Cys Gln Gly Val Pro Pro Asn Gln
 485 490 495

Ile Pro Gly Val Ala Trp Gly Val Phe Lys Leu Glu His His His His
 500 505 510

His His

<210> 119
 <211> 272
 <212> PRT
 <213> Unknown

<220>
 <223> PK-Lss

<400> 119

Ala Met Gly Lys Arg Lys Lys Arg Lys Lys Arg Lys Gly Ser Ala His
 1 5 10 15

Glu His Ser Ala Gln Trp Leu Asn Asn Tyr Lys Lys Gly Tyr Gly Tyr
 20 25 30

Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His Tyr Gly Val Asp
 35 40 45

Phe Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser Gly Lys
 50 55 60

Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln Ile Gly
 65 70 75 80

Leu Ile Glu Asn Asp Gly Val His Arg Gln Trp Tyr Met His Leu Ser
 85 90 95

Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly Gln Ile Ile
 100 105 110

Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His Leu His Phe
 115 120 125

Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp Pro Met
 130 135 140

Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly Gly Thr Val Thr
 145 150 155 160

Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr Gly Thr Leu Tyr
 165 170 175

Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp Ile Ile Thr Arg
 180 185 190

Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly Val Leu Lys Ala
 195 200 205

Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln Asp Gly His Val
 210 215 220

Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu Pro Val
 225 230 235 240

Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu Gly Val Leu Trp Gly Thr
 245 250 255

Ile Lys Leu Val Pro Arg Gly Ser Leu Glu His His His His His His
 260 265 270

<210> 120
 <211> 281
 <212> PRT
 <213> Unknown

<220>
 <223> PK2-Lss

<400> 120

Ala Met Gly Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys Arg Lys Lys
 1 5 10 15

Arg Lys Lys Arg Lys Gly Ser Ala His Glu His Ser Ala Gln Trp Leu
 20 25 30

Asn Asn Tyr Lys Lys Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile
 35 40 45

Asn Gly Gly Met His Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr
 50 55 60

Pro Val Lys Ala Ile Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser
65 70 75 80

Asn Tyr Gly Gly Gly Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val
85 90 95

His Arg Gln Trp Tyr Met His Leu Ser Lys Tyr Asn Val Lys Val Gly
100 105 110

Asp Tyr Val Lys Ala Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly
115 120 125

Tyr Ser Thr Ala Pro His Leu His Phe Gln Arg Met Val Asn Ser Phe
130 135 140

Ser Asn Ser Thr Ala Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly
145 150 155 160

Tyr Gly Lys Ala Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp
165 170 175

Lys Thr Asn Lys Tyr Gly Thr Leu Tyr Lys Ser Glu Ser Ala Ser Phe
180 185 190

Thr Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser
195 200 205

Met Pro Gln Ser Gly Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp
210 215 220

Glu Val Met Lys Gln Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn
225 230 235 240

Ser Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr
245 250 255

Asn Thr Leu Gly Val Leu Trp Gly Thr Ile Lys Leu Val Pro Arg Gly
260 265 270

Ser Leu Glu His His His His His His
275 280

<210> 121
<211> 525
<212> PRT
<213> Unknown

<220>

<223> LysK-PK (PK C-terminal)

<400> 121

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
1 5 10 15

Arg Gly Ser His Met Ala Lys Thr Gln Ala Glu Ile Asn Lys Arg Leu
20 25 30

Asp Ala Tyr Ala Lys Gly Thr Val Asp Ser Pro Tyr Arg Val Lys Lys
35 40 45

Ala Thr Ser Tyr Asp Pro Ser Phe Gly Val Met Glu Ala Gly Ala Ile
50 55 60

Asp Ala Asp Gly Tyr Tyr His Ala Gln Cys Gln Asp Leu Ile Thr Asp
65 70 75 80

Tyr Val Leu Trp Leu Thr Asp Asn Lys Val Arg Thr Trp Gly Asn Ala
85 90 95

Lys Asp Gln Ile Lys Gln Ser Tyr Gly Thr Gly Phe Lys Ile His Glu
100 105 110

Asn Lys Pro Ser Thr Val Pro Lys Lys Gly Trp Ile Ala Val Phe Thr
115 120 125

Ser Gly Ser Tyr Glu Gln Trp Gly His Ile Gly Ile Val Tyr Asp Gly
130 135 140

Gly Asn Thr Ser Thr Phe Thr Ile Leu Glu Gln Asn Trp Asn Gly Tyr
145 150 155 160

Ala Asn Lys Lys Pro Thr Lys Arg Val Asp Asn Tyr Tyr Gly Leu Thr
165 170 175

His Phe Ile Glu Ile Pro Val Lys Ala Gly Thr Thr Val Lys Lys Glu
180 185 190

Thr Ala Lys Lys Ser Ala Ser Lys Thr Pro Ala Pro Lys Lys Lys Ala
195 200 205

Thr Leu Lys Val Ser Lys Asn His Ile Asn Tyr Thr Met Asp Lys Arg
210 215 220

Gly Lys Lys Pro Glu Gly Met Val Ile His Asn Asp Ala Gly Arg Ser
225 230 235 240

Ser Gly Gln Gln Tyr Glu Asn Ser Leu Ala Asn Ala Gly Tyr Ala Arg
 245 250 255
 Tyr Ala Asn Gly Ile Ala His Tyr Tyr Gly Ser Glu Gly Tyr Val Trp
 260 265 270
 Glu Ala Ile Asp Ala Lys Asn Gln Ile Ala Trp His Thr Gly Asp Gly
 275 280 285
 Thr Gly Ala Asn Ser Gly Asn Phe Arg Phe Ala Gly Ile Glu Val Cys
 290 295 300
 Gln Ser Met Ser Ala Ser Asp Ala Gln Phe Leu Lys Asn Glu Gln Ala
 305 310 315 320
 Val Phe Gln Phe Thr Ala Glu Lys Phe Lys Glu Trp Gly Leu Thr Pro
 325 330 335
 Asn Arg Lys Thr Val Arg Leu His Met Glu Phe Val Pro Thr Ala Cys
 340 345 350
 Pro His Arg Ser Met Val Leu His Thr Gly Phe Asn Pro Val Thr Gln
 355 360 365
 Gly Arg Pro Ser Gln Ala Ile Met Asn Lys Leu Lys Asp Tyr Phe Ile
 370 375 380
 Lys Gln Ile Lys Asn Tyr Met Asp Lys Gly Thr Ser Ser Ser Thr Val
 385 390 395 400
 Val Lys Asp Gly Lys Thr Ser Ser Ala Ser Thr Pro Ala Thr Arg Pro
 405 410 415
 Val Thr Gly Ser Trp Lys Lys Asn Gln Tyr Gly Thr Trp Tyr Lys Pro
 420 425 430
 Glu Asn Ala Thr Phe Val Asn Gly Asn Gln Pro Ile Val Thr Arg Ile
 435 440 445
 Gly Ser Pro Phe Leu Asn Ala Pro Val Gly Gly Asn Leu Pro Ala Gly
 450 455 460
 Ala Thr Ile Val Tyr Asp Glu Val Cys Ile Gln Ala Gly His Ile Trp
 465 470 475 480
 Ile Gly Tyr Asn Ala Tyr Asn Gly Asn Arg Val Tyr Cys Pro Val Arg
 485 490 495

Thr Cys Gln Gly Val Pro Pro Asn Gln Ile Pro Gly Val Ala Trp Gly
500 505 510

Val Phe Lys Ser Lys Arg Lys Lys Arg Lys Lys Arg Lys
515 520 525

<210> 122
<211> 274
<212> PRT
<213> Unknown

<220>
<223> Lss-PK (PK C-terminal)

<400> 122

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
1 5 10 15

Arg Gly Ser His Met His Glu His Ser Ala Gln Trp Leu Asn Asn Tyr
20 25 30

Lys Lys Gly Tyr Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly
35 40 45

Met His Tyr Gly Val Asp Phe Phe Met Asn Ile Gly Thr Pro Val Lys
50 55 60

Ala Ile Ser Ser Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly
65 70 75 80

Gly Gly Asn Gln Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln
85 90 95

Trp Tyr Met His Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val
100 105 110

Lys Ala Gly Gln Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr
115 120 125

Ala Pro His Leu His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser
130 135 140

Thr Ala Gln Asp Pro Met Pro Phe Leu Lys Ser Ala Gly Tyr Gly Lys
145 150 155 160

Ala Gly Gly Thr Val Thr Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn
165 170 175

Lys Tyr Gly Thr Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn
180 185 190

Thr Asp Ile Ile Thr Arg Thr Thr Gly Pro Phe Arg Ser Met Pro Gln
195 200 205

Ser Gly Val Leu Lys Ala Gly Gln Thr Ile His Tyr Asp Glu Val Met
210 215 220

Lys Gln Asp Gly His Val Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln
225 230 235 240

Arg Ile Tyr Leu Pro Val Arg Thr Trp Asn Lys Ser Thr Asn Thr Leu
245 250 255

Gly Val Leu Trp Gly Thr Ile Lys Ser Lys Arg Lys Lys Arg Lys Lys
260 265 270

Arg Lys

<210> 123
<211> 858
<212> DNA
<213> unknown

<220>
<223> PA6gp20

<400> 123
atggtacgct acatcccagc agcgcatacac tctgcaggct ctaacaaccc ggtgaaccgt 60
gtagtgatcc acgcgacctg tccggatgta ggcttcccg ctgcttcccg taaaggctgt 120
gcggtttcca ctgcgaacta cttcgcgtct ccgtcctctg gcggttctgc aactacgtg 180
tgcgatatcg gtgagaccgt gcagtgcctg tccgaaagca ctattggttg gcacgctccg 240
ccgaaccac atagcctggg tatcgaaatc tgtgtgacg gtggctccca cgcttctttc 300
cgtgtcccag gtcacgtta cactcgcgaa cagtggctgg atccacaggt ttggccagcc 360
gtagaacgtg ctgcagttct gtgtcgtcgc ctgtgcgaca aatataacgt cccgaaacgc 420
aaactgtctg cagcggacct gaaagcaggt cgtcgtggtg tttgcggtca cgttgacgta 480
accgacgcct ggcaccagtc tgatcacgac gatccgggtc cgtgggtttcc gtgggacaaa 540
ttcatggcag tggttaacgg tggcagcggg gattctggcg aactgaccgt tgccgacgtc 600
aaagcgtgc acgaccagat taaacagctc tctgctcagc tgaccggtag cgtgaacaaa 660
ctgcaccatg acgtaggcgt tgtccaggtt cagaacggtg atctgggcaa acgcgttgat 720
gctctgagct ggggtgaaaaa cccggtgacg ggtaaactgt ggcgtaccaa agatgcgctg 780

tggtccgttt ggtactatgt tctggaatgc cgtagccgtc tggaccgtct ggaatctgcc 840
 gtgaacgacc tgaaaaaa 858

<210> 124
 <211> 314
 <212> PRT
 <213> unknown

<220>
 <223> Walmagh1-PA6gp20

<400> 124

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

Ile Val Pro Gly Ser Val Arg Tyr Ile Pro Ala Ala His His Ser Ala
 20 25 30

Gly Ser Asn Asn Pro Val Asn Arg Val Val Ile His Ala Thr Cys Pro
 35 40 45

Asp Val Gly Phe Pro Ser Ala Ser Arg Lys Gly Arg Ala Val Ser Thr
 50 55 60

Ala Asn Tyr Phe Ala Ser Pro Ser Ser Gly Gly Ser Ala His Tyr Val
 65 70 75 80

Cys Asp Ile Gly Glu Thr Val Gln Cys Leu Ser Glu Ser Thr Ile Gly
 85 90 95

Trp His Ala Pro Pro Asn Pro His Ser Leu Gly Ile Glu Ile Cys Ala
 100 105 110

Asp Gly Gly Ser His Ala Ser Phe Arg Val Pro Gly His Ala Tyr Thr
 115 120 125

Arg Glu Gln Trp Leu Asp Pro Gln Val Trp Pro Ala Val Glu Arg Ala
 130 135 140

Ala Val Leu Cys Arg Arg Leu Cys Asp Lys Tyr Asn Val Pro Lys Arg
 145 150 155 160

Lys Leu Ser Ala Ala Asp Leu Lys Ala Gly Arg Arg Gly Val Cys Gly
 165 170 175

His Val Asp Val Thr Asp Ala Trp His Gln Ser Asp His Asp Asp Pro
 180 185 190

Gly Pro Trp Phe Pro Trp Asp Lys Phe Met Ala Val Val Asn Gly Gly
195 200 205

Ser Gly Asp Ser Gly Glu Leu Thr Val Ala Asp Val Lys Ala Leu His
210 215 220

Asp Gln Ile Lys Gln Leu Ser Ala Gln Leu Thr Gly Ser Val Asn Lys
225 230 235 240

Leu His His Asp Val Gly Val Val Gln Val Gln Asn Gly Asp Leu Gly
245 250 255

Lys Arg Val Asp Ala Leu Ser Trp Val Lys Asn Pro Val Thr Gly Lys
260 265 270

Leu Trp Arg Thr Lys Asp Ala Leu Trp Ser Val Trp Tyr Tyr Val Leu
275 280 285

Glu Cys Arg Ser Arg Leu Asp Arg Leu Glu Ser Ala Val Asn Asp Leu
290 295 300

Lys Lys Leu Glu His His His His His His
305 310

12