

Antimicrobial Agents

The present invention relates to antimicrobial agents against Gram-negative bacteria, in particular to fusion proteins composed of an enzyme having the activity of degrading the cell wall of Gram-negative bacteria and an additional peptide stretch fused to the enzyme on 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-negative bacterial infections, as diagnostic means or as cosmetic substance. The present invention also relates to the treatment or prevention of Gram-negative 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. Furthermore, the present invention relates to pharmaceutical or cosmetic compositions comprising said fusion protein.

Gram-negative bacteria possess an outer membrane, with its characteristic asymmetric bilayer as a hallmark. The outer membrane bilayer consists of an inner monolayer containing phospholipids (primarily phosphatidyl ethanolamine) and an outer monolayer that is mainly composed of a single glycolipid, lipopolysaccharide (LPS). There is an immense diversity of LPS structures in the bacterial kingdom and the LPS structure may be modified in response to prevailing environmental conditions. The stability of the LPS layer and interaction between different LPS molecules is mainly achieved by the electrostatic interaction of divalent ions (Mg^{2+} , Ca^{2+}) with the anionic components of the LPS molecule (phosphate groups in the lipid A and the inner core and carboxyl groups of KDO). Furthermore, the dense and ordered packing of the hydrophobic moiety of lipid A, favored by the absence of unsaturated fatty acids, forms a rigid structure with high viscosity. This makes it less permeable for lipophilic molecules and confers additional stability to the outer membrane (OM).

Various types of agents having bactericidal or bacteriostatic activity are known, e.g. antibiotics, endolysins, antimicrobial peptides and defensins. Increasingly 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-negative bacteria like *Pseudomonas aeruginosa* and Enterobacteriaceae.

Endolysins are peptidoglycan hydrolases encoded by bacteriophages (or bacterial viruses).

5 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
10 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 'enzymiotics' - a hybrid term of 'enzymes' and 'antibiotics' - perfectly met
15 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
20 *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 enzymiotics. Nowadays, the most important challenge of endolysin therapy lies in the insensitivity of Gram-negative bacteria towards the exogenous action of endolysins, since the outer membrane shields the access of endolysins from the peptidoglycan. This
25 currently prevents the expansion of the range of effective endolysins to important Gram-negative pathogens.

Antimicrobial peptides (AMPs) represent a wide range of short, cationic, gene encoded peptide antibiotics that can be found in virtually every organism. Different AMPs display
30 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 are 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.

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 "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 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.

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 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.

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 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.

5 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.
 10 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 “EAD” as used herein refers to the enzymatically active domain of an endolysin.
 15 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 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”.

25 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. 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 by a microorganism or to a synthetically produced form, and refers also to variants which substantially retain the
 30 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 microbiocidal and/or microbiostatic 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, microbiocidal, bacteriocidal, 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 a 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-negative bacteria, in particular to fusion proteins composed of an enzyme having the activity of degrading the cell wall of Gram-negative bacteria and a peptide stretch fused to the enzyme on the N- or C-terminus or at both termini.

In one aspect of the present invention the enzyme having the activity of degrading the cell wall of Gram-negative bacteria is an endolysin, autolysin or bacteriocin.

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

- 5 Preferred fusion proteins according to the present invention are depicted in SEQ ID NO:36 to 63. The fusion proteins according to SEQ ID NO:36 to 63 may comprise one or more additional amino acid residues on the N-terminus. Preferably the additional amino acid residue is methionine.
- 10 Preferably, the endolysin is encoded by bacteriophages specific for Gram-negative bacteria such as Gram-negative bacteria of bacterial groups, families, genera or species comprising strains pathogenic for humans or animals like *Enterobacteriaceae* (*Escherichia*, especially *E. coli*, *Salmonella*, *Shigella*, *Citrobacter*, *Edwardsiella*, *Enterobacter*, *Hafnia*, *Klebsiella*, especially *K. pneumoniae*, *Morganella*, *Proteus*, *Providencia*, *Serratia*, *Yersinia*),
- 15 *Pseudomonadaceae* (*Pseudomonas*, especially *P. aeruginosa*, *Burkholderia*, *Stenotrophomonas*, *Shewanella*, *Sphingomonas*, *Comamonas*), *Neisseria*, *Moraxella*, *Vibrio*, *Aeromonas*, *Brucella*, *Francisella*, *Bordetella*, *Legionella*, *Bartonella*, *Coxiella*, *Haemophilus*, *Pasteurella*, *Mannheimia*, *Actinobacillus*, *Gardnerella*, *Spirochaetaceae* (*Treponema* and *Borrelia*), *Leptospiraceae*, *Campylobacter*, *Helicobacter*, *Spirillum*,
- 20 *Streptobacillus*, *Bacteroidaceae* (*Bacteroides*, *Fusobacterium*, *Prevotella*, *Porphyromonas*), *Acinetobacter*, especially *A. baumannii*.

- Preferably, the autolysin is encoded by Gram-negative bacteria such as Gram-negative bacteria of bacterial groups, families, genera or species comprising strains pathogenic for
- 25 humans or animals like *Enterobacteriaceae* (*Escherichia*, especially *E. coli*, *Salmonella*, *Shigella*, *Citrobacter*, *Edwardsiella*, *Enterobacter*, *Hafnia*, *Klebsiella*, especially *K. pneumoniae*, *Morganella*, *Proteus*, *Providencia*, *Serratia*, *Yersinia*), *Pseudomonadaceae* (*Pseudomonas*, especially *P. aeruginosa*, *Burkholderia*, *Stenotrophomonas*, *Shewanella*, *Sphingomonas*, *Comamonas*), *Neisseria*, *Moraxella*, *Vibrio*, *Aeromonas*, *Brucella*,
- 30 *Francisella*, *Bordetella*, *Legionella*, *Bartonella*, *Coxiella*, *Haemophilus*, *Pasteurella*, *Mannheimia*, *Actinobacillus*, *Gardnerella*, *Spirochaetaceae* (*Treponema* and *Borrelia*), *Leptospiraceae*, *Campylobacter*, *Helicobacter*, *Spirillum*, *Streptobacillus*, *Bacteroidaceae*

(*Bacteroides*, *Fusobacterium*, *Prevotella*, *Porphyromonas*), *Acinetobacter*, especially *A. baumannii*.

The bacteriocin is preferably specific for Gram-negative bacteria as listed above, but may also be less specific.

The enzyme according to the present invention has cell wall degrading activity against Gram-negative bacteria of bacterial groups, families, genera or species comprising strains pathogenic for humans or animals like *Enterobacteriaceae* (*Escherichia*, especially *E. coli*, *Salmonella*, *Shigella*, *Citrobacter*, *Edwardsiella*, *Enterobacter*, *Hafnia*, *Klebsiella*, especially *K. pneumoniae*, *Morganella*, *Proteus*, *Providencia*, *Serratia*, *Yersinia*), *Pseudomonadaceae* (*Pseudomonas*, especially *P. aeruginosa*, *Burkholderia*, *Stenotrophomonas*, *Shewanella*, *Sphingomonas*, *Comamonas*), *Neisseria*, *Moraxella*, *Vibrio*, *Aeromonas*, *Brucella*, *Francisella*, *Bordetella*, *Legionella*, *Bartonella*, *Coxiella*, *Haemophilus*, *Pasteurella*, *Mannheimia*, *Actinobacillus*, *Gardnerella*, *Spirochaetaceae* (*Treponema* and *Borrelia*), *Leptospiraceae*, *Campylobacter*, *Helicobacter*, *Spirillum*, *Streptobacillus*, *Bacteroidaceae* (*Bacteroides*, *Fusobacterium*, *Prevotella*, *Porphyromonas*), *Acinetobacter*, especially *A. baumannii*.

Specific examples of an endolysin part derived from a phage or that is a wild type endolysin are depicted in the following table:

Table 1:

phage	publication	Wild type endolysin	predicted function of the endolysin
ΦV10	Perry, L.L. and Applegate, B.M.	PhiV10p30	chitinase
FELS-1	McClelland, M. and Wilson, R.K.	STM0907.Fels0	chitinase
ε15	Kropinski, A.M. and McConnel, M.R.	epsilon15p25	chitinase
YUA	Ceyssens, P. (Laboratory for Gene technology)	YuA20	lytic transglycosylase (C) / 1 transmembranair domain (N)
B3	Braid, M.D. and Kitts, C.L.	ORF23	lytic transglycosylase (C) / 2 transmembranair domains (N)
BCEPμ	Summer, E.J. and Young, R.	BcepMu22	lytic transglycosylase (M) / 1 transmembranair domain (N)
F116	Byrne, M. and Kropinski, A.M.	F116p62	muraminidase (T4-like)
FELS-2	McClelland, M. and Wilson, R.K.	STM2715.S.Fels2	muraminidase (T4-like)
ES18	Casjens, S.R. and Hendrix, R.W.	gp76	muraminidase (T4-like)
SETP3	De Lappe, N and Cormican, M.	SPSV3_gp23	muraminidase (T4-like)

ΦECO32	Savalia, D and Severinov, K	phi32_17	muraminidase (T4-like)
HK022	Juhala , R and Hendrix, R.W.	HK022p54	muraminidase (lambdalike)
HK97	Juhala , R and Hendrix, R.W.	HK97p58	muraminidase (lambdalike)
HK620	Clark, A.J. and Dhillon, T.S.	HK620p36	muraminidase (lambdalike)
E1	Pickard, D. and Dougan, G	VIP0007	muraminidase (lambdalike)
SF6	Casjens, S and Clark, A.J.	Sf6p62	muraminidase (lambdalike)
SFV	Allison, G.E. and Verma, N.K.	R (SfVp40)	muraminidase (lambdalike)
BCEPC6B	Summer, EJ and Young, R.	gp22	muraminidase (lambdalike)
BCEPNAZGUL	Summer, EJ and Young, R.	Nazgul38	muraminidase (lambdalike)
P2	Christie, G.E. and Calender, R.	K (P2p09)	muraminidase (lambdalike)
WΦ	Christie, G.E. and Esposito, D.	K (Wphi09)	muraminidase (lambdalike)
RV5	Kropinski, A.M. and Johnson	rv5_gp085	muraminidase (lambdalike)
JS98	Zuber, S and Denou, E.	EpJS98_gp116	muraminidase (T4-like)
13A	Savalia, D and Molineux, I.	gp3.5	muramoyl-L-alanine amidase
BA14	Savalia, D and Molineux, I.	gp3.5	muramoyl-L-alanine amidase
ECODS1	Savalia, D and Molineux, I.	gp3.5	muramoyl-L-alanine amidase
K1F	Scholl, D and Merril, C	CKV1F_gp16	muramoyl-L-alanine amidase
T3	Pajunen, M.I. and Mollieux, I.J.	T3p18	muramoyl-L-alanine amidase
GH-1	Kropinski, A.M. and Kovalyova, I.V.	gh-1p12	muramoyl-L-alanine amidase
K11	Molineux, I. and Savalia, D.	gp3.5	muramoyl-L-alanine amidase
ΦCTX	Nakayama, K and Hayashi, T.	ORF12	PG-binding domain (N) / muramidase (C)
BCEP43	Summer, EJ and Young, R.	Bcep43-27	PG-binding domain (N) / muramidase (C)
BCEP781	Summer, EJ and Young, R.	Bcep781-27	PG-binding domain (N) / muramidase (C)
BCEP1	Summer, EJ and Young, R.	Bcep1-28	PG-binding domain (N) / muramidase (C)
BCEPNY3	Summer, EJ and Young, R.	BcepNY3gene26	PG-binding domain (N) / muramidase (C)
ΦE12-2	DeShazer, D and Nierman, W.C.	gp45	PG-binding domain (N) / muramidase (C)
Φ52237	DeShazer, D and Nierman, W.C.	gp28	PG-binding domain (N) / muramidase (C)
ΦP27	Recktenwald, J and Schmidt, H.	P27p30	endopeptidase
RB49	Monod, C and Krisch, H.M.	RB49p102	endopeptidase
Φ1	Arbiol, C. and Comeau, A.M.	phi1-p102	endopeptidase
T5	Pankova, N.V. and Ksenzenko, V.N.	lys (T5.040)	endopeptidase
201phi2-1	Thomas <i>et al.</i> , 2008		PG-binding domain (N) / unknown catalytic domain (C)
Aeh1	Monod, C and Krisch, H.M.	Aeh1p339	muraminidase (T4-like)
YYZ-2008	Kropinski, A.M.	YYZgp45	muraminidase (lambda-like)

Also preferred is the endolysin part deriving from endolysins of the *Pseudomonas aeruginosa* phages Φ KZ and EL, of the *Pseudomonas putida* phage, of the *E. coli* phage N4, of the phage LUZ24, gp61 muramidase, STM0016 endolysin and PSP3 endolysin.

- 5 Further examples for the endolysin part is selected from the group consisting of phiKZgp144 according to SEQ ID NO:1, ELgp188 according to SEQ ID NO:2, *Salmonella* endolysin according to SEQ ID NO:3, Enterobacteria phage T4 endolysin according to SEQ ID NO:4, *Acinetobacter baumannii* endolysin according to SEQ ID NO:5, *E.coli* Phage K1F endolysin according to SEQ ID NO:18, OBPgpLYS according to SEQ ID NO:34, PSP3 *Salmonella*
- 10 endolysin (PSP3gp10) according to SEQ ID NO:20, *E.coli* Phage P2 endolysin (P2gp09) according to SEQ ID NO:21, *Salmonella typhimurium* phage muramidase STM0016 according to SEQ ID NO:22, *E.coli* Phage N4 muramidase N4-gp61 according to SEQ ID NO:23 and N4-gp61 trunc. according to SEQ ID NO:24, KZ144 according to SEQ ID NO:25.
- 15 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 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,
- 20 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, autolysin and bacteriocins. However, said activity can be the same, 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,
- 25 160, 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.

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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, autolysin or bacteriocin. 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 serine (Gly-Ser) or leucine and glutamic acid (Leu-Glu). 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), alanine and methionine and glycine (Ala-Met-Gly-Ser) or alanine and methionine and glycine and serine (Ala-Met-Gly-Ser).

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 His-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 lead the fusion protein through the outer membrane but may have activity or may have no or only low activity when administered without being fused to the enzyme. The function to lead the fusion protein through the outer membrane of Gram-negative bacteria is caused by the potential of the outer membrane or LPS disrupting or permeabilising or destabilizing activity of said peptide stretch.

In one aspect of the present invention the fused peptide stretch is an amphipathic 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 preferably 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 acid residues in said peptide are positively charged amino acid. 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 to 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 amphipatic peptides are Pleurocidin according to SEQ ID NO:6, Cecropin P1 according to SEQ ID NO:7, Buforin II according to SEQ ID NO:8, Buforin I according to SEQ ID NO:19 and Magainin according to SEQ ID NO:9. Further preferred amphipatic peptides are Cathelidicine e.g. LL-37 according to SEQ ID NO:10, Nigrocine 2 according to SEQ ID NO:26 and Ascaphine 5 according to SEQ ID NO:27.

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.

Specific examples of antimicrobial peptides according to the present invention are listed in the following table.

Table 2:

Peptid	Sequenz	
LL-37	LLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLPRTES	SEQ ID NO:10
SMAP-29	RGLRRLGRKIAHG VKKYGPTVLRIRIAG	SEQ ID NO:11
Indolicidin	ILPWKWPWWPWRR	SEQ ID NO:12
Protegrin	RGGRLCYCRRRFCVCVGR	SEQ ID NO:13
Cecropin P1	SWLSKTAKKLENSAKKRISegIAIAIQGGPR	SEQ ID NO:7
Magainin	GIGKFLHSAKKFGKAFVGEIMNS	SEQ ID NO:9
Pleurocidin	GWGSFFKKAHVGHVGHVGAALHYL	SEQ ID NO:6
Cecropin A (A.aegypti)	GGLKKLGKKLEGAGKRVFNAAEKALPVVAGAKALRK	SEQ ID NO:14
Cecropin A (D. melanogaster)	GWLKKIGKKIERVGGHTRDATIQGLGIPQQAANVAATARG	SEQ ID NO:15
Buforin II	TRSSRAGLQFPVGRVHRLLRK	SEQ ID NO:8
Sarcotoxin IA	GWLKKIGKKIERVGGHTRDATIQGLGIAQQAANVAATAR	SEQ ID NO:16
Apidaecin	ANRPVYIPPPRPPHPRL	SEQ ID NO:28
Ascaphine 5	GKDWIKGAACKLIKTVASHIANQ	SEQ ID NO:27
Nigrocine 2	GLLSKVLGVGKKVLCGVSGSLVC	SEQ ID NO:26
Pseudin 1	GLNTLKKVFQGLHEAIKLNNHVQ	SEQ ID NO:29
Ranalexin	FLGGLIVPAMICAVTKKC	SEQ ID NO:30
Melittin	GIGAVLKVLTTGLPALISWIKRKRQQ	SEQ ID NO:31

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:32.

5 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.

10 In a further aspect of the present invention the fused peptide stretch is a hydrophobic peptidee.g. Apidaecine having the amino acid sequence according to SEQ ID NO:28, WLBU2-Variant having the amino acid sequence according to SEQ ID NO:33 and Walmagh1 having the amino acid sequence according to SEQ ID NO:35. The hydrophobic peptide having the amino acid sequence Phe-Phe-Val-Ala-Pro (SEQ ID NO:17) is not part of the
15 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
20 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.

Specific examples of fusion proteins according to the present invention are listed in the
25 following table:

Table 3:

Fusion protein	Fusion protein	Enzyme part	Peptide stretch (N-terminal unless otherwise indicated)
P1-E6	SEQ ID NO: 36	KZ144 (SEQ ID NO:25)	Ascaphine 5 (SEQ ID NO:27)
P2-E6	SEQ ID NO: 37	KZ144 (SEQ ID NO:25)	Apiadaecine (SEQ ID NO:28)
P3-E6	SEQ ID NO: 38	KZ144	Nigrocine 2

		(SEQ ID NO:25)	(SEQ ID NO:26)
P4-E6	SEQ ID NO: 39	KZ144 (SEQ ID NO:25)	Pseudin 1 (SEQ ID NO:29)
P7-E6	SEQ ID NO: 40	KZ144 (SEQ ID NO:25)	Ranalexin (SEQ ID NO:30)
P8-E6	SEQ ID NO: 41	KZ144 (SEQ ID NO:25)	WLBU2-Variant (SEQ ID NO:33)
P9-E6	SEQ ID NO: 42	KZ144 (SEQ ID NO:25)	Sushi 1 (SEQ ID NO:32)
P10-E6	SEQ ID NO: 43	KZ144 (SEQ ID NO:25)	Melittin (SEQ ID NO:31)
P11-E6	SEQ ID NO: 44	KZ144 (SEQ ID NO:25)	LL-37 (SEQ ID NO:10)
P12-E6	SEQ ID NO: 45	KZ144 (SEQ ID NO:25)	Indolicidin (SEQ ID NO:12)
P13-E6	SEQ ID NO: 46	KZ144 (SEQ ID NO:25)	SMAP-29 (SEQ ID NO:11)
P14-E6	SEQ ID NO: 47	KZ144 (SEQ ID NO:25)	Protegrin (SEQ ID NO:13)
P15-E6	SEQ ID NO: 48	KZ144 (SEQ ID NO:25)	Cecropin P1 (SEQ ID NO:7)
P16-E6	SEQ ID NO: 49	KZ144 (SEQ ID NO:25)	Magainin (SEQ ID NO:9)
P17-E6	SEQ ID NO: 50	KZ144 (SEQ ID NO:25)	Pleurocidin (SEQ ID NO:6)
P18-E6	SEQ ID NO: 51	KZ144 (SEQ ID NO:25)	Cecropin A (A. aegypti) (SEQ ID NO:14)
P19-E6	SEQ ID NO: 52	KZ144 (SEQ ID NO:25)	Cecropin A (A. melanogaster) (SEQ ID NO:15)
P20-E6	SEQ ID NO: 53	KZ144 (SEQ ID NO:25)	Buforin II (SEQ ID NO:8)

P21-E6	SEQ ID NO: 54	KZ144 (SEQ ID NO:25)	Sarcotoxin IA (SEQ ID NO:16)
P1-E3	SEQ ID NO: 55	STM0016 (SEQ ID NO:22)	Ascapphine 5 (SEQ ID NO:27)
	SEQ ID NO: 56	STM0016 (SEQ ID NO:22)	Nigrocline 2 (SEQ ID NO:26)
	SEQ ID NO: 57	STM0016 (SEQ ID NO:22)	SMAP-29 (SEQ ID NO:11)
	SEQ ID NO: 58	STM0016 (SEQ ID NO:22)	Sarcotoxin IA (SEQ ID NO:16)
P10-E4	SEQ ID NO: 59	N4-gp61 (SEQ ID NO:23)	Melittin (SEQ ID NO:31)
	SEQ ID NO: 60	N4-gp61 (SEQ ID NO:23)	SMAP-29 (SEQ ID NO:11)
P10-E5	SEQ ID NO: 61	N4-gp61 trunc. (SEQ ID NO:24)	Melittin (SEQ ID NO:31)
	SEQ ID NO: 62	N4-gp61 trunc. (SEQ ID NO:24)	Cecropin P1 (SEQ ID NO:7)
	SEQ ID NO: 63	N4-gp61 trunc. (SEQ ID NO:24)	SMAP-29 (SEQ ID NO:11)

The fusion protein according to the present invention, and thus in particular the especially preferred fusion proteins according to SEQ ID NO: 36 to 63, may additionally comprise a methionine on the N-terminus.

The fusion protein according to the present invention, and thus in particular the especially preferred fusion proteins according to SEQ ID NO: 36 to 63 may additionally comprise a tag e.g. for purification. Preferred is a His₆-tag, preferably at the C-terminus and/or the N-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 another preferred
5 embodiment the fusion protein comprises a His₆-tag at its N- and 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 a more preferred embodiment the fusion protein comprises a His₆-tag at its C-terminus
10 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. 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 glutamic acid (Leu-
15 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 alanine, methionine and glycine (Ala-Met-Gly) or alanine, methionine, glycine and serine (Ala-Met-Gly-Ser). Preferably the fusion proteins are according to SEQ ID
20 NO: 77 to 90.

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
25 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.

30 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.

5 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
10 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
15 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.

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
20 transformed with a nucleic acid molecule or a vector comprising a nucleotide sequence encoding a fusion protein according to the present invention.

In a preferred embodiment of the present invention the composition comprises additionally agents permeabilizing the outer membrane of Gram-negative bacteria such metal chelators as
25 e.g. EDTA, TRIS, lactic acid, lactoferrin, polymyxin, citric acid and/or other substances as described e.g. by Vaara (Agents that increase the permeability of the outer membrane. Vaara M. Microbiol. Rev. 1992 Sep; 56 (3):395-441). Also preferred are compositions comprising combinations of the above mentioned permeabilizing agents. Especially preferred is a composition comprising about 10 μ M to about 100 mM EDTA, more preferably about 50 μ M
30 to about 10 mM EDTA, more preferably about 0.5 mM to about 10 mM EDTA, more preferably about 0.5 mM to about 2 mM EDTA, more preferably about 0.5 mM to 1 mM EDTA. However, also compositions comprising about 10 μ M to about 0.5 mM EDTA are

preferred. Also preferred is a composition comprising about 0.5 mM to about 2 mM EDTA, more preferably about 1 mM EDTA and additionally about 10 to about 100 mM TRIS.

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 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-negative bacteria. In particular the treatment and/or prevention of the disorder, disease or condition may be caused by Gram-negative bacteria of bacterial groups, families, genera or species comprising strains pathogenic for humans or animals like *Enterobacteriaceae* (*Escherichia*, especially *E. coli*, *Salmonella*, *Shigella*, *Citrobacter*, *Edwardsiella*, *Enterobacter*, *Hafnia*, *Klebsiella*, especially *K. pneumoniae*, *Morganella*, *Proteus*, *Providencia*, *Serratia*, *Yersinia*), *Pseudomonadaceae* (*Pseudomonas*, especially *P. aeruginosa*, *Burkholderia*, *Stenotrophomonas*, *Shewanella*, *Sphingomonas*, *Comamonas*), *Neisseria*, *Moraxella*, *Vibrio*, *Aeromonas*, *Brucella*, *Francisella*, *Bordetella*, *Legionella*, *Bartonella*, *Coxiella*, *Haemophilus*, *Pasteurella*, *Mannheimia*, *Actinobacillus*, *Gardnerella*, *Spirochaetaceae* (*Treponema* and *Borrelia*), *Leptospiraceae*, *Campylobacter*, *Helicobacter*, *Spirillum*, *Streptobacillus*, *Bacteroidaceae* (*Bacteroides*, *Fusobacterium*, *Prevotella*, *Porphyromonas*), *Acinetobacter*, especially *A. baumannii*.

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.

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.

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 bacteriaemia and/or endocarditis caused by Gram-negative bacteria, in particular by the Gram-negative bacteria as listed above.

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.

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 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 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 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 secrete 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 *Pseudomonas*, particularly by *Pseudomonas aeruginosa* in particular intestinal affections, in particular in infants, infections of the meninges, e.g. meningitis haemorrhagica, infections of the middle ear, the skin (Ecthyma gangraenosum), in particular burns, the urinary tract, rhinitis, bacteremic pneumonia, in particular wherein the patient is suffering from cystic fibrosis or hematologic malignancies such as leukemia, or with neutropenia from immunosuppressive therapy, septicemia, in particular because of long-term intravenous or urinary catheterization, invasive surgical procedures and severe burns, endocarditis, in particular wherein the patient is a intravenous drug user or a patient with complications from open heart surgery, highly destructive ocular infections, in particular after the use of contaminated ophthalmologic solutions or severe facial burns, osteochondritis, in particular as a result of severe trauma or puncture wounds through contaminated clothing.

In another specific embodiment of the present invention the disorder, disease or condition is caused by *Burkholderia pseudomallei*, in particular Whitmore's Disease, chronic pneumonia, septicemia, in particular wherein the patient has a traumatized skin lesion.

In another specific embodiment of the present invention the disorder, disease or condition is caused by *Salmonella thyphimurium* and *Salmonella enteritidis*, in particular acute gastroenteritis and local purulent processes, particularly osteomyelitis, endocarditis, cholecystitis and especially caused by *Salmonella thyphimurium* meningitis, in particular wherein the patient is less than two years old.

In another specific embodiment of the present invention the disorder, disease or condition is caused by *Salmonella typhi*, in particular typus.

In another specific embodiment of the present invention the disorder, disease or condition is caused by *Salmonell paratyphi*, in particular paratyphus.

In another specific embodiment of the present invention the disorder, disease or condition is caused by *Acinetobacter baumannii*, in particular bronchitis, pneumonia, wound infections and septicemia, in particular as a result of intravenous catheterization.

- 5 In another specific embodiment of the present invention the disorder, disease or condition is caused by *Escherichia coli*, in particular extra intestinal infections, particularly appendicitis, purulent cholecystitis, peritonitis, purulent meningitis and infection of the urinary tract, intrainestinal *E. coli* infections, particularly epidemic enteritis, and infectious disease similar to dysentery, septicemia, enterotoxemia, mastitis and dysentery.

10

In another specific embodiment of the present invention the disorder, disease or condition is caused by *Klebsiella pneumoniae*, in particular pneumonia, bacteremia, meningitis and infections of the urinary tract.

- 15 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, gentamicin, cefotaxime, cephalosporin, ceftazidime or imipenem. Furthermore, a fusion protein according to the present invention can be used in methods of
20 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
25 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
30 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-negative 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-negative 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-negative 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).

In a further aspect the present invention relates to the use of the fusion protein according to the present invention for the treatment, removal, reduction or prevention of Gram-negative 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 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 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 *Pseudomonas aeruginosa* (FQRP), *Acinetobacter* species and Enterobacteriaceae such as *E.coli*, *Salmonella*, *Shigella*, *Citrobacter*, *Edwardsiella*, *Enterobacter*, *Hafnia*, *Klebsiella*, *Morganella*, *Proteus*, *Providencia*, *Serratia* and *Yersinia* species 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.

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, 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.

Another aspect of the present invention is that the invention can be used like a tool box, i.e. any peptide stretch disclosed above may be fused to any endolysin, autolysin or bacteriocin disclosed herein. Thus, it is possible to combine the respective peptide stretch, which enables the binding of the fusion protein to the respective bacteria and the endolysin, autolysin or

bacteriocin, which inhibit the growth of the respective bacteria. Consequently, it is possible to construct a suitable fusion protein for any bacteria which should be eliminated.

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 gp144 and gp188 modified with an amphipathic peptide.

As a proof of principle, the potential of the LPS disrupting activity of amphipathic peptides to lead gp144 and gp188 through the outer membrane and the consequent antibacterial activity against Gram-negative bacteria is demonstrated. Gp144 and gp188 are modular endolysins originating from *Pseudomonas aeruginosa* phages ϕ KZ and EL with an N-terminal peptidoglycan binding and C-terminal catalytic domain (Briers et al., 2007).

To extend the 5' end of the open reading frame encoding gp144 or gp188 with a gene fragment encoding the amphipathic α 4 helix of T4 lysozyme (aa 143-155: Pro-Asn-Arg-Ala-Lys-Arg-Val-Ile-Thr-Thr-Phe-Arg-Thr according to SEQ ID NO: 92) a tail PCR with an extended 5' primer and standard 3' primer was applied. The PCR product was cloned in the pEXP5CT/TOPO® expression vector (Invitrogen, Carlsbad, CA, USA).

Expression of all constructs was performed in *E. coli* BL21 (DE3) pLysS cells. All proteins were purified by Ni^{2+} affinity chromatography using the C-terminal 6xHis-tag. The yields for different purifications are shown in table 4. Remarkably, $\alpha 4$ -KZ144 production was not toxic for the host, in contrast to KZ144, resulting in a significant higher yield.

5

Purified stock solutions were ~90% pure. All gp144 derivatives showed multimer formation which could be converted to monomers by addition of β -mercapto-ethanol, indicating that interdisulfide bonds cause multimerization.

Table 4 - Yields of recombinant purification of endolysins modified with an amphipathic peptide*.

Fusion	Endolysin	
	gp144	gp188
α 4 helix	179 mg	38 mg

* The total yield of purified recombinant protein per liter E. coli expression culture is shown. This value was determined by spectrophotometric measurement of the protein concentration and the total volume of the purified stock solution. The purification of gp188 derivatives was performed under more stringent conditions (65 mM imidazole) compared to gp144 derivatives (50mM imidazole) to ensure high purity.

Characterization of gp144 and gp188 modified with an amphipathic peptide

1.A. Enzymatic activity of gp144 and gp188 modified with an amphipathic peptide

To assess the influence of the modification on the enzymatic activity of gp144 or gp188, the specific activity of the variants was measured on chloroform-permeabilized *Pseudomonas aeruginosa* cells and compared to the corresponding unmodified endolysin. Different incremental amounts of all modified endolysins were tested to determine the corresponding saturation curve. The slope of the linear regression of the linear region of this curve is a measure for the specific activity and was expressed relatively to the slope of unmodified gp144 or gp188 (Table 5).

Table 5 - Enzymatic activity of gp144 or gp188 modified with an amphipathic peptide*.

Fusion	Endolysin	
	gp144	gp188
α 4 helix	23%	146%

* The specific enzymatic activity of the different variants was determined and expressed relatively to the specific activity of the corresponding original endolysin (=100%), which was tested simultaneously. The buffer conditions of the assay were the optimal conditions of the corresponding endolysins ($\text{KH}_2\text{PO}_4/\text{K}_2\text{HPO}_4$ I = 120 mM pH 6.2 and I = 80 mM pH 7.3 for gp144 and gp188, respectively).

1.B. Antibacterial activity of gp144 and gp188 modified with an amphipathic peptide

Exponential ($\sim 10^6$ /ml) *P. aeruginosa* PAO1 cells were incubated at room temperature with unmodified and modified gp144/gp188. After 1 hour, cell suspensions were diluted and plated. The residual colonies were counted after an overnight incubation (Table 6). Unmodified gp144 gp188 does not reduce cell numbers significantly compared to the negative control. This observation illustrates the efficacy of the outer membrane as a barrier. Fusion proteins with the amphipathic α 4-helix inactivate exponential cells with 50 ± 11 and 34 ± 11 % for α 4-KZ144 and α 4-EL188, respectively. When stationary cells with a 100-fold higher density are used, these values are similar (35 ± 18 and $32 \pm 17\%$, respectively). Despite the rather high variability between different replicates, these values differ significantly from the untreated cells ($\alpha = 0.05$). In general, modified gp144 derivatives tend to have a higher antibacterial activity than gp188 derivatives.

Table 6 - Antibacterial effect of endolysins gp144 and gp188 and their derivatives*.

Exponentially growing cells	Endolysins			
	gp144		gp188	
Fusion	%	log	%	log
unmodified	0 ± 15	0.00 ± 0.06	10 ± 13	0.05 ± 0.06
α 4 helix	50 ± 11	0.31 ± 0.09	34 ± 11	0.19 ± 0.07

* Exponentially growing *P. aeruginosa* PAO1 cells were 100 x diluted and incubated (final density was $\sim 10^6$ /ml) with 10 μ g undialyzed protein (final concentration 100 μ g/ml, buffer: 20 mM NaH_2PO_4 -NaOH pH7.4; 0.5 M NaCl; 0.5 M imidazole) for 1 hour at room temperature. Aliquots are diluted and plated. The antibacterial activity is expressed as the relative inactivation (%) ($=100-(N_i/N_0)*100$ with N_0 = number of untreated cells and N_i = number of treated cells) and in logarithmic units ($=\log_{10}N_0/N_i$). All samples were replicated in six fold. Averages/standard deviations are represented. Statistical analysis was performed using a student's t-test.

EXAMPLE 2. Cloning, expression and purification of gp144 and gp188 modified with a hydrophobic peptide.

As a proof of principle, the potential of the LPS disrupting activity of a hydrophobic pentapeptides to lead gp144 and gp188 through the outer membrane and the consequent antibacterial activity against Gram-negative bacteria is demonstrated. Gp144 and gp188 are modular endolysins originating from *Pseudomonas aeruginosa* phages ϕ KZ and EL with an N-terminal peptidoglycan binding and C-terminal catalytic domain (Briers et al., 2007).

To extend the 5' end of the open reading frame encoding gp144 or gp188 with a gene fragment encoding 5 hydrophobic residues (Phe-Phe-Val-Ala-Pro) a tail PCR with an extended 5' primer and standard 3' primer was applied. The PCR product was cloned in the pEXP5CT/TOPO® expression vector (Invitrogen, Carlsbad, CA, USA).

5

Expression of all constructs was performed in E. coli BL21 (DE3) pLysS cells. All proteins were purified by Ni²⁺ affinity chromatography using the C-terminal 6xHis-tag. The yields for different purifications are shown in table 7.

- 10 Purified stock solutions were ~90% pure. All gp144 derivatives showed multimer formation which could be converted to monomers by addition of β -mercapto-ethanol, indicating that interdisulfide bonds cause multimerization.

Table 7 - Yields of recombinant purification of endolysin derivatives.*

15

Fusion	Endolysin	
	gp144	gp188
Phe-Phe-Val-Ala-Pro	25 mg	85 mg

- 20 * The total yield of purified recombinant protein per liter E. coli expression culture is shown. This value was determined by spectrophotometric measurement of the protein concentration and the total volume of the purified stock solution. The purification of gp188 derivatives was performed under more stringent conditions (65 mM imidazole) compared to gp144 derivatives (50mM imidazole) to ensure high purity.

25

Characterization of gp144 and gp188 modified with a hydrophobic pentapeptide

2.A. Enzymatic activity of gp144 and gp188 modified with a hydrophobic pentapeptide

- 30 To assess the influence of the modifications on the enzymatic activity of gp144 or gp188, the specific activity of the variants was measured on chloroform-permeabilized *Pseudomonas aeruginosa* cells and compared to the corresponding unmodified endolysin. Different incremental amounts of all modified endolysins were tested to determine the corresponding saturation curve. The slope of the linear regression of the linear region of this curve is a
- 35 measure for the specific activity and was expressed relatively to the slope of unmodified gp144 or gp188 (Table 8).

Table 8 - Enzymatic activity of gp144 or gp188 modified with a hydrophobic peptide*.

Fusion	Endolysin	
	gp144	gp188
Hydrophobic pentapeptide	150%	100%

* The specific enzymatic activity of the different variants was determined and expressed relatively to the specific activity of the corresponding original endolysin (=100%), which was tested simultaneously. The buffer conditions of the assay were the optimal conditions of the corresponding endolysins ($\text{KH}_2\text{PO}_4/\text{K}_2\text{HPO}_4$ I = 120 mM pH 6.2 and I = 80 mM pH 7.3 for gp144 and gp188, respectively).

2.B. Antibacterial activity of gp144 and gp188 modified with a hydrophobic pentapeptide

Exponential ($\sim 10^6/\text{ml}$) *P. aeruginosa* PAO1 cells were incubated at room temperature with unmodified and modified gp144/gp188. After 1 hour, cell suspensions were diluted and plated. The residual colonies were counted after an overnight incubation (Table 9). Unmodified gp144 gp188 does not reduce cell numbers significantly compared to the negative control. This observation illustrates the efficacy of the outer membrane as a barrier. Incubation with the hydrophobic pentapeptide fusion proteins causes a significant reduction ($\alpha = 0.05$) of the bacterial cell number (83 ± 7 and $69 \pm 21\%$ for modified gp144 and gp188, respectively). In general, modified gp144 derivatives tend to have a higher antibacterial activity than gp188 derivatives.

Table 9 - Antibacterial effect of endolysins gp144 and gp188 and their derivatives*.

Exponentially growing cells	Endolysins			
	gp144		gp188	
Fusion	%	log	%	log
unmodified	0 ± 15	0.00 ± 0.06	10 ± 13	0.05 ± 0.06
Hydrophobic pentapeptide	83 ± 7	0.9 ± 0.2	69 ± 21	0.7 ± 0.3

* Exponentially growing *P. aeruginosa* PAO1 cells were 100 x diluted and incubated (final density was $\sim 10^6/\text{ml}$) with 10 μg undialyzed protein (final concentration 100 $\mu\text{g}/\text{ml}$, buffer: 20 mM NaH_2PO_4 -NaOH pH7.4; 0.5 M NaCl; 0.5 M imidazole) for 1 hour at room temperature. Aliquots are diluted and plated. The antibacterial activity is expressed as the relative inactivation (%) ($=100-(N_i/N_0)*100$ with N_0 = number of untreated cells and N_i = number of treated cells) and in logarithmic units ($=\log_{10}N_0/N_i$). All samples were replicated in six fold. Averages/standard deviations are represented. Statistical analysis was performed using a student's t-test.

EXAMPLE 3: Cloning, expression and purification of KZ144 and STM0016 modified with various peptide stretches on the N-terminus of the endolysin.

5 KZ144 according to SEQ ID NO: 25 is a modular endolysin originating from *Pseudomonas aeruginosa* phage ϕ KZ with an N-terminal peptidoglycan binding and C-terminal catalytic domain (Briers et al., 2007). The endolysin KZ144 is encoded by the nucleic acid molecule according to SEQ ID NO: 64. The nucleic acid molecule according to SEQ ID NO: 64 was synthetically produced with a BamH I (5'-GGA TCC-3') restriction site at the 5'-end of the
10 nucleic acid molecule and an Xho I (5'-CTC GAG-3') restriction site at the 3'-end of the nucleic acid molecule.

STM0016 is a hypothetical protein with homology to the *E. coli* phage N4 endolysin N4-gp61. The endolysin STM0016 is encoded by the nucleic acid molecule according to SEQ ID
15 NO: 65. The nucleic acid molecule according to SEQ ID NO: 65 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.

N4-gp61 is an *E. coli* N4 phage endolysin. The endolysin is encoded by the nucleic acid
20 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.

25 The following peptide stretches in table 10 were used for production of fusion proteins with the endolysin KZ144 or STM0016:

Table 10:

Peptide stretch	Nucleic acid molecule encoding the peptide stretch
Pseudin 1 (SEQ ID NO:29)	SEQ ID NO: 66
Ranalexin	SEQ ID NO: 67

(SEQ ID NO:30)	
Sushi 1 (SEQ ID NO:32)	SEQ ID NO: 68
WLBU2-Variant (SEQ ID NO:33)	SEQ ID NO:69
Melittin (SEQ ID NO:31)	SEQ ID NO:70
SMAP-29 (SEQ ID NO:11)	SEQ ID NO:71
Pleurocidin (SEQ ID NO: 6)	SEQ ID NO: 72
Cecropin A (A. aegypti) (SEQ ID NO:14)	SEQ ID NO:73
Cecropin A (A. melanogaster) (SEQ ID NO:15)	SEQ ID NO:74
Buforin II (SEQ ID NO:8)	SEQ ID NO:75
Sarcotoxin IA (SEQ ID NO:16)	SEQ ID NO:76

- 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 Sushi 1 peptide, 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.
- 10 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 Sushi 1 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 Sushi I 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 His-tag.

Afterwards, the nucleic acid molecule encoding the endolysin KZ144 was 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. The nucleic acid molecule encoding the endolysin STM0016 and the nucleic acid molecule encoding the endolysin N4gp61 were cleaved in a digest with the restriction enzyme BamH I and Xho I, so that the respective endolysin could be ligated into the pET21b expression vector (Novagen, Darmstadt, Germany).

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 endolysin KZ144 or STM0016. Moreover, the nucleic acid molecule encoding the endolysin KZ144 or STM0016 is ligated into the respective plasmid, so that a nucleic acid molecule encoding a His-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 Sushi 1 peptide and the endolysin KZ144, the Sushi 1 peptide is ligated into the modified pET32 b expression vector, so that an additional thioredoxin is associated at the 5'-end of the Sushi 1 peptide. The thioredoxin could be removed from the expressed fusion protein by the use of enterokinase, therefore between the nucleic acid molecule encoding the Sushi 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) (Novagen, Darmstadt, Germany) for protein expression.

Recombinant expression of the fusion proteins according to SEQ ID NO: 77 to 90 is performed in *E. coli* BL21 (DE3) pLysS and *E. coli* BL21 (DE3) 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 6xHis-tag, encoded by the pET21b or pET32b vectors.

As described above, some of the fusion proteins were expressed using a modified pET32b vector (S-tag and central His-tag deleted), 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 His-tag. For antimicrobial function of the fusion protein Sushi 1-KZ144 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 His-tag purification as described below.

5 The Ni^{2+} 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 4: Antimicrobial activity of the endolysin KZ144 modified with various peptide stretches on the N-terminus.

The fusion protein consisting of KZ144 and the peptide stretch $\alpha 4$ helix was constructed as described in example 1. The other fusion proteins consisting of KZ144 and the respective peptide stretches were constructed as described in example 3.

E. coli DSMZ 11753, *Acinetobacter baumannii* DSMZ 30007 and *Pseudomonas aeruginosa* PAO1p cells (Burn wound isolate, Queen Astrid Hospital, Brussels; Pirnay JP et al. (2003), *J*

Clin Microbiol., 41(3):1192-1202) were used as test strains. Overnight cultures were diluted 10-fold in fresh LB medium and grown to OD₆₀₀=0.6. The culture was spun down and diluted 10-fold in dilution buffer (10 mM HEPES, 0.5 mM EDTA; pH 7.4). Bacteria were incubated at room temperature with each 10 µg undialyzed fusion protein at a final concentration of 100 µg/ml in buffer (20 mM NaH₂P0₄-NaOH pH 7.4; 0.5 M NaCl; 0.5 M imidazole). After 1 hour cell dilution series were made in PBS and plated on LB. Additionally, a negative control was plated using buffer (20 mM NaH₂P0₄-NaOH pH 7.4; 0.5 M NaCl; 0.5 M imidazole). 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 (Table 11). All samples were replicated at least in four fold.

The antimicrobial activity of these fusion proteins is given in the following table.

Table 11: Antimicrobial activity of KZ144 modified with various peptide stretches against gram-negative bacteria

Fusion protein	Enzyme part	Peptide stretch (N-terminal unless otherwise indicated)	Activity against <i>Pseudomonas</i> <i>aeruginosa</i>	Activity against <i>E.</i> <i>coli</i> DSMZ 11753	Activity against <i>Acinetobacter</i> <i>baumannii</i> DSMZ 30007
SEQ ID NO: 77	KZ144 (SEQ ID NO:25)	Pseudin 1 (SEQ ID NO:29)	+	n.d.	n.d.
SEQ ID NO: 78	KZ144 (SEQ ID NO:25)	Ranalexin (SEQ ID NO:30)	+	n.d.	n.d.
SEQ ID NO: 79	KZ144 (SEQ ID NO:25)	Sushi 1 (SEQ ID NO:32)	+	n.d.	++
SEQ ID NO: 80	KZ144 (SEQ ID NO:25)	WLBU2-Variant (SEQ ID NO:33)	n.d.	+	n.d.
SEQ ID NO: 81	KZ144 (SEQ ID NO:25)	Melittin (SEQ ID NO:31)	+	n.d.	n.d.
SEQ ID NO: 82	KZ144 (SEQ ID NO:25)	SMAP-29 (SEQ ID NO:11)	+++	+++	n.d.
SEQ ID NO: 83	KZ144 (SEQ ID NO:25)	Cecropin A (<i>A.</i> <i>aegypti</i>) (SEQ ID NO:14)	++	+	++
SEQ ID NO: 84	KZ144 (SEQ ID NO:25)	Pleurocidin (SEQ ID NO: 6)	+	n.d.	n.d.
SEQ ID NO: 85	KZ144	Cecropin A (<i>A.</i>	+	n.d.	n.d.

	(SEQ ID NO:25)	melanogaster) (SEQ ID NO:15)			
SEQ ID NO: 86	KZ144 (SEQ ID NO:25)	Buforin II (SEQ ID NO:8)	+	n.d.	n.d.
SEQ ID NO: 87	KZ144 (SEQ ID NO:25)	Sarcotoxin IA (SEQ ID NO:16)	++	++	++
SEQ ID NO: 93	KZ144 (SEQ ID NO:25)	α 4 helix (SEQ ID NO:92)	$\pm$	n.d.	n.d.

Abbreviations: $\pm$ < 1 log; +: 1 log; ++: 2-3 log; +++: 4 or more logs; n.d. means that this strain was not tested with the respective fusion protein.

5

Example 5: Antimicrobial activity of the endolysin STM0016 modified with various peptide stretches on the N-terminus

The fusion proteins consisting of STM0016 and the peptide stretch Sarcotoxin IA or SMAP-29 was constructed as described in example 3.

E. coli DSMZ 11753, *Salmonella typhimurium* DSMZ 17058 and *Pseudomonas aeruginosa* PAO1p cells (Burn wound isolate, Queen Astrid Hospital, Brussels; Pirnay JP et al. (2003), *J Clin Microbiol.*, 41(3):1192-1202) were used as test strains. The antimicrobial activity of the fusion proteins consisting of the endolysin STM0016 and the peptide Sarcotoxin IA or SMAP-29 was examined as described in example 4. The antimicrobial activity of these fusion proteins is given in the following table.

Table 12:

Fusion protein	Enzyme part	Peptide stretch (N-terminal unless otherwise indicated)	Activity against <i>Pseudomonas</i> <i>aeruginosa</i>	Activity against <i>E.</i> <i>coli</i> DSMZ 11753	Activity against <i>Salmonella</i> <i>typhimurium</i> DSMZ 17058
SEQ ID NO: 88	STM0016 (SEQ ID NO: 22)	Sarcotoxin IA (SEQ ID NO:16)	+	n.d.	+
SEQ ID NO: 89	STM0016 (SEQ ID NO: 22)	SMAP-29 (SEQ ID NO: 11)	+	+	+

Abbreviations: +: 1 log; n.d. means that this strain was not tested with the respective fusion protein.

20

Example 6: Antimicrobial activity of the endolysin N4gp61 modified with a peptide stretch on the N-terminus

The fusion protein consisting of N4gp61 and the peptide stretch SMAP-29 was constructed as described in example 3.

E. coli DSMZ 11753, *Salmonella typhimurium* DSMZ 17058 and *Pseudomonas aeruginosa* PAO1p cells (Burn wound isolate, Queen Astrid Hospital, Brussels; Pirnay JP et al. (2003), *J Clin Microbiol.*, 41(3):1192-1202) were used as test strains. The antimicrobial activity of the fusion protein consisting of the endolysin N4gp61 and the peptide SMAP-29 was examined as described in example 4. The antimicrobial activity of this fusion protein is given in the following table.

Table 13:

Fusion protein	Enzyme part	Peptide stretch (N-terminal unless otherwise indicated)	Activity against <i>Pseudomonas aeruginosa</i>	Activity against <i>E. coli</i> DSMZ 11753	Activity against <i>Salmonella typhimurium</i> DSMZ 17058
SEQ ID NO: 90	N4-gp61 (SEQ ID NO:23)	SMAP-29 (SEQ ID NO: 11)	+	+	+

Abbreviations: +: 1 log; n.d. means that this strain was not tested with the respective fusion protein.

Example 7: Antimicrobial activity of the endolysin gp188 modified with a peptide stretch on the N-terminus

The fusion proteins consisting of the endolysin gp188 and the peptide stretches α 4 helix, SMAP-29 or Sarcotoxin IA were constructed as described in example 1. *E. coli* DSMZ 11753, *Acinetobacter baumannii* DSMZ 30007 and *Pseudomonas aeruginosa* PAO1p cells (Burn wound isolate, Queen Astrid Hospital, Brussels; Pirnay JP et al. (2003), *J Clin Microbiol.*, 41(3):1192-1202) were used as test strains. The antimicrobial activity of the

fusion proteins consisting of the endolysin gp188 and the respective peptide stretches was examined as described in example 4. The antimicrobial activity of these fusion proteins is given in the following table.

5 Table 14:

Fusion protein	Enzyme part	Peptide stretch (N-terminal unless otherwise indicated)	Activity against <i>Pseudomonas</i> <i>aeruginosa</i>	Activity against <i>E.</i> <i>coli</i> DSMZ 11753	Activity against <i>Acinetobacter</i> <i>baumannii</i> DSMZ 30007
SEQ ID NO: 94	gp188 (SEQ ID NO:2)	α 4 helix (SEQ ID NO: 92)	$\pm$	n.d.	n.d.
SEQ ID NO: 95	gp188 (SEQ ID NO:2)	SMAP-29 (SEQ ID NO: 11)	++	++	++
SEQ ID NO: 96	gp188 (SEQ ID NO:2)	Sarcotoxin IA (SEQ ID NO: 16)	+	+	+

Abbreviations: $\pm$ < 1 log; +: 1 log; ++: 2-3 log; n.d. means that this strain was not tested with the respective fusion protein.

10 Example 8: Antimicrobial activity of the *Salmonella* endolysin modified with the peptide stretch SMAP-29 on the N-terminus

The fusion proteins consisting of the *Salmonella* endolysin having an amino acid sequence according to SEQ ID NO: 3 and the peptide stretch SMAP-29 were constructed analogous to
 15 example 3. *E. coli* DSMZ 11753 and *Salmonella typhimurium* DSMZ 17058 were used as test strains. The antimicrobial activity of the fusion protein was examined as described in example 4. The antimicrobial activity of this fusion protein is given in the following table.

Table 15:

Fusion protein	Enzyme part	Peptide stretch (N-terminal unless otherwise indicated)	Activity against <i>E. coli</i> DSMZ 11753	Activity against <i>Salmonella</i> <i>typhimurium</i> DSMZ 17058
SEQ ID NO: 97	Salmonella endolysin (SEQ ID NO:3)	SMAP-29 (SEQ ID NO: 11)	+	+

Abbreviations: +: 1 log;

5 Example 9: Antimicrobial activity of the *Acinetobacter baumannii* endolysin modified with various peptide stretches on the N-terminus

The fusion proteins consisting of the *Acinetobacter baumannii* endolysin having an amino acid sequence according to SEQ ID NO: 5 and the peptide stretches SMAP-29, Pseudin 1 and Sushi 1 were constructed analogous to example 3. *Acinetobacter baumannii* DSMZ 30007 and *Pseudomonas aeruginosa* PAO1p cells (Burn wound isolate, Queen Astrid Hospital, Brussels; Pirnay JP et al. (2003), *J Clin Microbiol.*, 41(3):1192-1202) were used as test strains. The antimicrobial activity of the fusion proteins was examined as described in example 4. The antimicrobial activity of these fusion proteins is given in the following table.

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Table 16:

Fusion protein	Enzyme part	Peptide stretch (N-terminal unless otherwise indicated)	Activity against <i>Pseudomonas</i> <i>aeruginosa</i>	Activity against <i>Acinetobacter</i> <i>baumannii</i> DSMZ 30007
SEQ ID NO: 98	<i>Acinetobacter</i>	Pseudin 1	±	n.d.

	<i>baumannii</i> endolysin (SEQ ID NO:5)	(SEQ ID NO: 29)		
SEQ ID NO: 99	<i>Acinetobacter</i> <i>baumannii</i> endolysin (SEQ ID NO:5)	SMAP-29 (SEQ ID NO: 11)	++	++
SEQ ID NO: 100	<i>Acinetobacter</i> <i>baumannii</i> endolysin (SEQ ID NO:5)	Sushi 1 (SEQ ID NO: 32)	+	+

Abbreviations: $\pm$ < 1 log; +: 1 log; ++: 2-3 log; n.d. means that this strain was not tested with the respective fusion protein.

- 5 The fusion proteins in Table 11 to 16 without any tag and linker were also tested with the activity assays described above. They all showed antimicrobial activity against the used bacterial strains (data not shown).

CLAIMS

1. A fusion protein composed of an enzyme having the activity of degrading the cell wall of Gram-negative bacteria and a peptide stretch fused to the enzyme at the N- or C-terminus or at both termini, wherein the peptide stretch is an amphipatic peptide, sushi peptide, defensin, hydrophobic peptide or an antimicrobial peptide.
2. The fusion protein according to claim 1, wherein said fusion protein exhibits an amino acid sequence according to SEQ ID NO: 63 to 90.
3. The fusion protein according to claim 1 or 2, wherein said fusion protein exhibits an additional amino acid residue on the N-terminus.
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: 22-25.
9. The fusion protein according to claim 1, wherein the antimicrobial peptide exhibits an amino acid sequence according to SEQ ID NO: 6 to 16 or 26 to 31.
10. The fusion protein according to claim 1, wherein the sushi peptide exhibits an amino acid sequence according to SEQ ID NO: 32.

11. The fusion protein according to claim 1, wherein the hydrophobic peptide exhibits an amino acid sequence according to SEQ ID NO: 28, 33 or 35.

12. The fusion protein according to any of the preceding claims, wherein the Gram-negative bacteria are selected from the group consisting of
 - Enterobacteriaceae,
 in particular Escherichia, Salmonella, Shigella, Citrobacter, Edwardsiella, Enterobacter, Hafnia, Klebsiella, Morganella, Proteus, Providencia, Serratia, and Yersinia,
 - Pseudomonadaceae,
 in particular Pseudomonas, Burkholderia, Stenotrophomonas, Shewanella, Sphingomonas and Comamonas,
 - Neisseria, Moraxella, Vibrio, Aeromonas, Brucella, Francisella, Bordetella, Legionella, Bartonella, Coxiella, Haemophilus, Pasteurella, Mannheimia, Actinobacillus, Gardnerella, Spirochaetaceae,
 in particular Treponema and Borrelia,
 - Leptospiraceae, Campylobacter, Helicobacter, Spirillum, Streptobacillus, Bacteroidaceae,
 in particular Bacteroides, Fusobacterium, Prevotella and Porphyromonas, and Acinetobacter,
 in particular A. baumannii.

13. The fusion protein according to claim 1, wherein the amphipatic peptide comprises at least one positively charged amino acid residue 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.

14. The fusion protein according to claim 1, 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.

- 5 15. The fusion protein according to any of the preceding claims, 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 16. An isolated nucleic acid molecule encoding a fusion protein according to any of claims 1 to 15.
17. A vector comprising the nucleic acid molecule according to claim 16.
18. A host cell comprising the nucleic acid molecule according to claim 16 or the vector according to claim 17.
- 15 19. A host cell according to claim 18, wherein the cell is a bacterial cell or a yeast cell.
- 20 20. The fusion protein according to any one of claims 1 to 15 for use as a medicament, diagnostic means or cosmetic substance.
21. The fusion protein according to any one of claims 1 to 15 for use as a medicament for treatment or prevention of Gram-negative bacterial infections.
- 25 22. The fusion protein according to any one of claims 1 to 15 for use as a disinfectant.
23. The use of the fusion protein according to any one of claims 1 to 15 for the treatment or prevention of Gram-negative bacterial contamination of foodstuff, of food processing equipment, of food processing plants, of surfaces coming into contact with foodstuff, of
30 medical devices, of surfaces in hospitals and surgeries.
24. The use of the fusion protein according to any one of claims 1 to 15 as a diagnostic means in medicinal, food or feed or environmental diagnostics.

25. Pharmaceutical composition comprising a fusion protein according to any one of claims 1 to 15.

SEQUENCE LISTING

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<120> ANTIMICROBIAL AGENTS

<130> LYS-002 PCT

<140> unknown

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<160> 100

<170> PatentIn version 3.3

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Gln Thr Leu Leu Asn Leu Cys Gly Tyr Asp Val Gly Lys Pro Asp Gly
20 25 30

Ile Phe Gly Asn Asn Thr Phe Asn Gln Val Val Lys Phe Gln Lys Asp
35 40 45

Asn Cys Leu Asp Ser Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu
50 55 60

Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met
65 70 75 80

Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala
85 90 95

Val Glu Asn Ala Thr Gly Val Arg Ser Gln Leu Leu Leu Thr Phe Ala
100 105 110

Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser

115 120 125
 Ala Thr Gly Trp Phe Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile
 130 135 140
 Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala
 145 150 155 160
 Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile
 165 170 175
 Lys Glu Asn Met Asn Ile Leu Arg Pro Val Leu Lys Arg Glu Pro Thr
 180 185 190
 Asp Thr Asp Leu Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg
 195 200 205
 Arg Phe Leu Thr Thr Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro
 210 215 220
 Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser
 225 230 235 240
 Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala
 245 250 255
 Ala His Arg Lys
 260

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<220>
 <223> ELgp188

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Met Asn Phe Arg Thr Lys Asn Gly Tyr Arg Asp Leu Gln Ala Leu Val
 1 5 10 15

Lys Glu Leu Gly Leu Tyr Thr Gly Gln Ile Asp Gly Val Trp Gly Lys
 20 25 30

Gly Thr Ser Ser Ser Thr Glu Thr Leu Leu Arg Gly Tyr Ala Glu Val

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

Thr Leu Tyr Thr Thr Tyr Tyr Lys Gly Leu Leu Pro Glu Asn Arg His
 275 280 285

Val Ile Ser Tyr
 290

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<220>
 <223> Salmonella endolysin

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Gly Tyr Val Asn His Pro Asp Asp Lys Gly Gly Pro Thr Lys Trp Gly
 20 25 30

Ile Thr Glu Lys Val Ala Arg Ala His Gly Tyr Arg Gly Asp Met Arg
 35 40 45

Asn Leu Thr Arg Gly Gln Ala Leu Glu Ile Leu Glu Thr Asp Tyr Trp
 50 55 60

Tyr Gly Pro Arg Phe Asp Arg Val Ala Lys Ala Ser Pro Asp Val Ala
 65 70 75 80

Ala Glu Leu Cys Asp Thr Gly Val Asn Met Gly Pro Ser Val Ala Ala
 85 90 95

Lys Met Leu Gln Arg Trp Leu Asn Val Phe Asn Gln Gly Gly Arg Leu
 100 105 110

Tyr Pro Asp Met Asp Thr Asp Gly Arg Ile Gly Pro Arg Thr Leu Asn
 115 120 125

Ala Leu Arg Val Tyr Leu Glu Lys Arg Gly Lys Asp Gly Glu Arg Val
 130 135 140

Leu Leu Val Ala Leu Asn Cys Thr Gln Gly Glu Arg Tyr Leu Glu Leu
 145 150 155 160

Ala Glu Lys Arg Glu Ala Asp Glu Ser Phe Val Tyr Gly Trp Met Lys
165 170 175

Glu Arg Val Leu Ile
180

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<220>
<223> Enterobacteria phage T4 endolysin

<400> 4

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

Ile Tyr Lys Asp Thr Glu Gly Tyr Tyr Thr Ile Gly Ile Gly His Leu
20 25 30

Leu Thr Lys Ser Pro Ser Leu Asn Ala Ala Lys Ser Glu Leu Asp Lys
35 40 45

Ala Ile Gly Arg Asn Cys Asn Gly Val Ile Thr Lys Asp Glu Ala Glu
50 55 60

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

Asn Ala Lys Leu Lys Pro Val Tyr Asp Ser Leu Asp Ala Val Arg Arg
85 90 95

Cys Ala Leu Ile Asn Met Val Phe Gln Met Gly Glu Thr Gly Val Ala
100 105 110

Gly Phe Thr Asn Ser Leu Arg Met Leu Gln Gln Lys Arg Trp Asp Glu
115 120 125

Ala Ala Val Asn Leu Ala Lys Ser Arg Trp Tyr Asn Gln Thr Pro Asn
130 135 140

Arg Ala Lys Arg Val Ile Thr Thr Phe Arg Thr Gly Thr Trp Asp Ala
145 150 155 160

Tyr Lys Asn

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<211> 280
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<213> unknown

<220>
<223> *Acinetobacter baumanii* endolysin

<400> 5

Met Glu Tyr Asp Met Ile Leu Lys Phe Gly Ser Lys Gly Asp Ala Val
1 5 10 15

Ala Thr Leu Gln Lys Gln Leu Ala Lys Met Gly Tyr Lys Gly Val Lys
20 25 30

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

Ala Val Ile Gln Leu Gln Arg Lys Phe Gly Leu Val Ala Asp Gly Lys
50 55 60

Val Gly Asp Lys Thr Arg Gln Ala Leu Ala Gly Asp Ser Val Ser Lys
65 70 75 80

Phe Leu Lys Asp Glu Asp Tyr Lys Lys Ala Ala Ile Arg Leu Lys Val
85 90 95

Pro Glu Leu Val Ile Arg Val Phe Gly Ala Val Glu Gly Leu Gly Val
100 105 110

Gly Phe Leu Pro Asn Gly Lys Ala Lys Ile Leu Phe Glu Arg His Arg
115 120 125

Met Tyr Phe Tyr Leu Cys Gln Ala Leu Gly Lys Thr Phe Ala Asn Ser
130 135 140

Gln Val Lys Ile Thr Pro Asn Ile Val Asn Thr Leu Thr Gly Gly Tyr
145 150 155 160

Lys Gly Asp Ala Ala Glu Tyr Thr Arg Leu Ser Met Ala Ile Asn Ile
165 170 175

His Lys Glu Ser Ala Leu Met Ser Thr Ser Trp Gly Gln Phe Gln Ile
180 185 190

Met Gly Glu Asn Trp Lys Asp Leu Gly Tyr Ser Ser Val Gln Glu Phe
195 200 205

Val Asp Gln Gln Gln Leu Asn Glu Gly Asn Gln Leu Glu Ala Phe Ile
210 215 220

Arg Phe Ile Glu Trp Lys Pro Gly Leu Leu Glu Ala Leu Arg Lys Gln
225 230 235 240

Asp Trp Asp Thr Val Phe Thr Leu Tyr Asn Gly Lys Asn Tyr Lys Lys
245 250 255

Leu Gly Tyr Gln Ala Lys Phe Gln Lys Glu Trp Asp His Leu Glu Pro
260 265 270

Ile Tyr Arg Glu Lys Thr Ala Ala
275 280

<210> 6
<211> 25
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<220>
<223> amphipatic peptide Pleurocidin

<400> 6

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
20 25

<210> 7
<211> 31
<212> PRT
<213> unknown

<220>
<223> amphipatic peptide Cecropin P1

<400> 7

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
20 25 30

<210> 8
<211> 21
<212> PRT
<213> unknown

<220>
<223> amphipatic peptide Buforin II

<400> 8

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
20

<210> 9
<211> 23
<212> PRT
<213> unknown

<220>
<223> amphipatic peptide Magainin

<400> 9

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
20

<210> 10
<211> 37
<212> PRT
<213> unknown

<220>
<223> amphipatic peptides Cathelidicine LL-37

<400> 10

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
 35

<210> 11
 <211> 29
 <212> PRT
 <213> unknown

<220>
 <223> SMAP-29

<400> 11

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
 20 25

<210> 12
 <211> 13
 <212> PRT
 <213> unknown

<220>
 <223> Indolicidin

<400> 12

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

<210> 13
 <211> 18
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 <213> unknown

<220>
 <223> Protegrin

<400> 13

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

Gly Arg

<210> 14
<211> 36
<212> PRT
<213> unknown

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

<400> 14

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
35

<210> 15
<211> 40
<212> PRT

<213> unknown

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

<400> 15

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
35 40

<210> 16
<211> 39
<212> PRT
<213> unknown

<220>
<223> Sarcotoxin IA

<400> 16

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
 35

<210> 17
 <211> 5
 <212> PRT
 <213> unknown

<220>
 <223> Pentapeptide

<400> 17

Phe Phe Val Ala Pro
 1 5

<210> 18
 <211> 152
 <212> PRT
 <213> unknown

<220>
 <223> E. coli phage K1F

<400> 18

Met Val Ser Lys Val Gln Phe Asn Pro Arg Ser Arg Thr Asp Ala Ile
 1 5 10 15

Phe Val His Cys Ser Ala Thr Lys Pro Glu Met Asp Ile Gly Val Glu
 20 25 30

Thr Ile Arg Met Trp His Lys Gln Gln Ala Trp Leu Asp Val Gly Tyr
 35 40 45

His Phe Ile Ile Lys Arg Asp Gly Thr Val Glu Glu Gly Arg Pro Val
 50 55 60

Asn Val Val Gly Ser His Val Lys Asp Trp Asn Ser Arg Ser Val Gly
 65 70 75 80

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

Phe Thr Pro Ala Gln Met Asn Ser Leu Arg Asn Lys Leu Asp Asp Leu
100 105 110

Lys Val Met Tyr Pro Gln Ala Glu Ile Arg Ala His His Asp Val Ala
115 120 125

Pro Lys Ala Cys Pro Ser Phe Asp Leu Gln Arg Trp Leu Ser Thr Asn
130 135 140

Glu Leu Val Thr Ser Asp Arg Gly
145 150

<210> 19
<211> 39
<212> PRT
<213> unknown

<220>
<223> Buforin I

<400> 19

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> 20
<211> 165
<212> PRT
<213> unknown

<220>
<223> PSP3 gp10 Salmonella endolysin

<400> 20

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

Gly Tyr Asp Val Ile Val Thr Gly Phe Asp Gly Ser Pro Glu Ile Phe
35 40 45

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

Phe Asn Arg Arg Gly Glu Lys Ser Thr Ala Ser Gly Arg Tyr Gln Gln
65 70 75 80

Leu Tyr Ile Phe Trp Pro His Tyr Lys Lys Gln Leu Ala Leu Pro Asp
85 90 95

Phe Ser Pro Leu Ser Gln Asp Lys Leu Ala Ile Gln Leu Ile Arg Glu
100 105 110

Arg Gly Ala Ile Asp Asp Ile Arg Ala Gly Arg Ile Glu Arg Ala Val
115 120 125

Ser Arg Cys Arg Asn Ile Trp Ala Ser Leu Pro Gly Ala Gly Tyr Gly
130 135 140

Gln Arg Glu His Ser Leu Glu Lys Leu Val Thr Val Trp Arg Thr Ala
145 150 155 160

Gly Gly Val Met Ala
165

<210> 21
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<220>
<223> E. coli phage endolysin P2gp09

<400> 21

Met Pro Val Ile Asn Thr His Gln Asn Ile Ala Ala Phe Leu Asp Met
1 5 10 15

Leu Ala Val Ser Glu Gly Thr Ala Asn His Pro Leu Thr Lys Asn Arg
20 25 30

Gly Tyr Asp Val Ile Val Thr Gly Leu Asp Gly Lys Pro Glu Ile Phe
35 40 45

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

Phe Asn Arg Arg Gly Glu Lys Ser Thr Ala Ser Gly Arg Tyr Gln Gln
 65 70 75 80

Leu Tyr Leu Phe Trp Pro His Tyr Arg Lys Gln Leu Ala Leu Pro Asp
 85 90 95

Phe Ser Pro Leu Ser Gln Asp Arg Leu Ala Ile Gln Leu Ile Arg Glu
 100 105 110

Arg Gly Ala Leu Asp Asp Ile Arg Ala Gly Arg Ile Glu Arg Ala Ile
 115 120 125

Ser Arg Cys Arg Asn Ile Trp Ala Ser Leu Pro Gly Ala Gly Tyr Gly
 130 135 140

Gln Arg Glu His Ser Leu Glu Lys Leu Val Thr Val Trp Arg Thr Ala
 145 150 155 160

Gly Gly Val Pro Ala
 165

<210> 22
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<220>
 <223> STM0016

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 1 5 10 15

Asn Pro Lys Asp Lys Gly Gly Ala Thr His Trp Gly Ile Thr Glu Ala
 20 25 30

Thr Ala Arg Ala His Gly Tyr Ala Gly Asp Met Arg Asp Leu Thr His
 35 40 45

Ala Glu Ala Tyr Ala Ile Leu Glu Glu Asp Tyr Trp Ile Lys Pro Gly
 50 55 60

Phe Asp Val Ile Ser Thr Leu Ser Trp Pro Val Ser Phe Glu Leu Cys
65 70 75 80

Asp Ala Ala Val Asn Ile Gly Ala Tyr His Pro Ser Ala Trp Leu Gln
85 90 95

Arg Trp Leu Asn Val Phe Asn His Glu Gly Lys Arg Tyr Pro Asp Ile
100 105 110

His Val Asp Gly Asn Ile Gly Pro Arg Thr Leu Ala Ala Leu Glu His
115 120 125

Tyr Leu Ala Trp Arg Gly Gln Glu Gly Glu Ala Val Leu Val Lys Ala
130 135 140

Leu Asn Cys Ser Gln Gly Thr Tyr Tyr Leu Asn Val Ala Glu Lys Asn
145 150 155 160

His Asn Asn Glu Gln Phe Ile Tyr Gly Trp Ile Lys Asn Arg Val Thr
165 170 175

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<211> 208
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<220>
<223> E.coli Phage N4 muramidase N4-gp61

<400> 23

Met Ala Ile Ser Lys Lys Lys Val Gly Gly Val Gly Gly Val Ile Ala
1 5 10 15

Ala Ile Ile Ala Ala Val Phe Ala Val Glu Gly Gly Tyr Val Asn Asp
20 25 30

Pro Lys Asp Pro Gly Gly Glu Thr Asn His Gly Val Thr Ile Gln Val
35 40 45

Ala Gln Lys His Lys Gln Glu Leu Glu Ser Met Tyr Asn Trp Asp Gly
50 55 60

Ser Met Lys Asn Leu Thr Gln Glu Met Ala Ser Ser Ile Tyr Tyr Asn
65 70 75 80

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

Ala Val Thr Glu Lys Leu Val Asp Ala Gly Val Asn Thr Gly Pro Ala
100 105 110

Arg Pro Ser Arg Trp Leu Gln Glu Ser Leu Asn Ala Phe Ser Arg Asn
115 120 125

Gly Lys Asp Tyr Pro Lys Ile Gln Val Asp Gly Lys Val Gly Ser Gly
130 135 140

Thr Leu Ser Ala Tyr Lys Ser Leu Gln Asn Lys Arg Gly Lys Val Glu
145 150 155 160

Ala Cys Lys Leu Ile Leu Lys Ser Leu Asp Gly Lys Gln Leu Asn Tyr
165 170 175

Tyr Leu Ser Leu Asn Met Pro Glu Tyr Thr Thr Gly Trp Ile Ala Asn
180 185 190

Arg Ile Gly Asn Val Pro Leu Glu Arg Cys Asn Glu Asp Ile Val Asn
195 200 205

<210> 24
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<212> PRT
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<223> 24 N4-gp61 trunc.

<400> 24

Val Glu Gly Gly Tyr Val Asn Asp Pro Lys Asp Pro Gly Gly Glu Thr
1 5 10 15

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

Glu Ser Met Tyr Asn Trp Asp Gly Ser Met Lys Asn Leu Thr Gln Glu
35 40 45

Met Ala Ser Ser Ile Tyr Tyr Asn Asp Tyr Ile Leu Lys Pro Gly Phe
50 55 60

Val Lys Phe Ala Asp Val Ser Pro Ala Val Thr Glu Lys Leu Val Asp
65 70 75 80

Ala Gly Val Asn Thr Gly Pro Ala Arg Pro Ser Arg Trp Leu Gln Glu
85 90 95

Ser Leu Asn Ala Phe Ser Arg Asn Gly Lys Asp Tyr Pro Lys Ile Gln
100 105 110

Val Asp Gly Lys Val Gly Ser Gly Thr Leu Ser Ala Tyr Lys Ser Leu
115 120 125

Gln Asn Lys Arg Gly Lys Val Glu Ala Cys Lys Leu Ile Leu Lys Ser
130 135 140

Leu Asp Gly Lys Gln Leu Asn Tyr Tyr Leu Ser Leu Asn Met Pro Glu
145 150 155 160

Tyr Thr Thr Gly Trp Ile Ala Asn Arg Ile Gly Asn Val Pro Leu Glu
165 170 175

Arg Cys Asn Glu Asp Ile Val Asn
180

<210> 25
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<220>
<223> E.coli phage KZ144

<400> 25

Lys Val Leu Arg Lys Gly Asp Arg Gly Asp Glu Val Cys Gln Leu Gln
1 5 10 15

Thr Leu Leu Asn Leu Cys Gly Tyr Asp Val Gly Lys Pro Asp Gly Ile
20 25 30

Phe Gly Asn Asn Thr Phe Asn Gln Val Val Lys Phe Gln Lys Asp Asn
35 40 45

Cys Leu Asp Ser Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu
50 55 60

Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro
65 70 75 80

Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val
85 90 95

Glu Asn Ala Thr Gly Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser
100 105 110

Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala
115 120 125

Thr Gly Trp Phe Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu
130 135 140

Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu
145 150 155 160

Arg Lys Asp Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys
165 170 175

Glu Asn Met Asn Ile Leu Arg Pro Val Leu Lys Arg Glu Pro Thr Asp
180 185 190

Thr Asp Leu Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg
195 200 205

Phe Leu Thr Thr Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys
210 215 220

Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro
225 230 235 240

Lys Thr Ile Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala
245 250 255

His Arg Lys

<210> 26
<211> 22
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<223> Nigrocine 2

<400> 26

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
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<210> 27

<211> 24

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<223> Ascaphine 5

<400> 27

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> 28

<211> 17

<212> PRT

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<220>

<223> Apidaecin

<400> 28

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

Leu

<210> 29

<211> 24

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<400> 29

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> 30
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<220>
<223> Ranalexin

<400> 30

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

Lys Cys

<210> 31
<211> 26
<212> PRT
<213> unknown

<220>
<223> Melittin

<400> 31

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> 32
<211> 34
<212> PRT
<213> unknown

<220>
<223> Sushi 1

<400> 32

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> 33
 <211> 27
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 <223> WLUB2 variant

<400> 33

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> 34
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<220>
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<400> 34

Met Gly Ser Lys Asn Ser Glu Lys Asn Ala Ser Ile Ile Met Ser Ile
 1 5 10 15

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

Leu Phe Gly Glu Lys Cys Arg Gly Ala Ile Ile Leu Met Leu Asn Lys
 35 40 45

Val Tyr Pro Asn Phe Ser Thr Asn Lys Leu Pro Ser Asn Thr Tyr Glu
 50 55 60

Ala Glu Ser Val Phe Thr Phe Leu Gln Thr Ala Leu Ala Gly Val Gly
 65 70 75 80

Leu Tyr Thr Ile Thr Ile Asp Gly Lys Trp Gly Gly Thr Ser Gln Gly
 85 90 95

Ala Ile Asp Ala Leu Val Lys Ser Tyr Arg Gln Ile Thr Glu Ala Glu
 100 105 110

Arg Ala Gly Ser Thr Leu Pro Leu Gly Leu Ala Thr Val Met Ser Lys
 115 120 125

His Met Ser Ile Glu Gln Leu Arg Ala Met Leu Pro Thr Asp Arg Gln
 130 135 140

Gly Tyr Ala Glu Val Tyr Ile Asp Pro Leu Asn Glu Thr Met Asp Ile
 145 150 155 160

Phe Glu Ile Asn Thr Pro Leu Arg Ile Ala His Phe Met Ala Gln Ile
 165 170 175

Leu His Glu Thr Ala Cys Phe Lys Tyr Thr Glu Glu Leu Ala Ser Gly
 180 185 190

Lys Ala Tyr Glu Gly Arg Ala Asp Leu Gly Asn Thr Arg Pro Gly Asp
 195 200 205

Gly Pro Leu Phe Lys Gly Arg Gly Leu Leu Gln Ile Thr Gly Arg Leu
 210 215 220

Asn Tyr Val Lys Cys Gln Val Tyr Leu Arg Glu Lys Leu Lys Asp Pro
 225 230 235 240

Thr Phe Asp Ile Thr Ser Ser Val Thr Cys Ala Gln Gln Leu Ser Glu
 245 250 255

Ser Pro Leu Leu Ala Ala Leu Ala Ser Gly Tyr Phe Trp Arg Phe Ile
 260 265 270

Lys Pro Lys Leu Asn Glu Thr Ala Asp Lys Asp Asp Ile Tyr Trp Val
 275 280 285

Ser Val Tyr Val Asn Gly Tyr Ala Lys Gln Ala Asn Pro Tyr Tyr Pro
 290 295 300

Asn Arg Asp Lys Glu Pro Asn His Met Lys Glu Arg Val Gln Met Leu
 305 310 315 320

Ala Val Thr Lys Lys Ala Leu Gly Ile Val Lys Gly
 325 330

<210> 35
 <211> 18
 <212> PRT
 <213> unknown

<220>
 <223> 35 Walmagh1

<400> 35

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

Val Pro

<210> 36
 <211> 283
 <212> PRT
 <213> unknown

<220>
 <223> Ascaphine5-KZ144

<400> 36

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 Lys Val Leu Arg Lys Gly Asp Arg
 20 25 30

Gly Asp Glu Val Cys Gln Leu Gln Thr Leu Leu Asn Leu Cys Gly Tyr
 35 40 45

Asp Val Gly Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln
 50 55 60

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

Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile
 85 90 95

Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala Ala
 100 105 110

Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly Val Arg Ser
115 120 125

Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu
130 135 140

Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr
145 150 155 160

Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val
165 170 175

Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala
180 185 190

Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg Pro
195 200 205

Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His Phe
210 215 220

Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu
225 230 235 240

Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile
245 250 255

Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn
260 265 270

Leu Met Asp Gly Lys Val Ala Ala His Arg Lys
275 280

<210> 37
<211> 276
<212> PRT
<213> unknown

<220>
<223> Apidaecine-KZ144

<400> 37

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

Leu Lys Val Leu Arg Lys Gly Asp Arg Gly Asp Glu Val Cys Gln Leu
 20 25 30

Gln Thr Leu Leu Asn Leu Cys Gly Tyr Asp Val Gly Lys Pro Asp Gly
 35 40 45

Ile Phe Gly Asn Asn Thr Phe Asn Gln Val Val Lys Phe Gln Lys Asp
 50 55 60

Asn Cys Leu Asp Ser Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu
 65 70 75 80

Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met
 85 90 95

Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala
 100 105 110

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

Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser
 130 135 140

Ala Thr Gly Trp Phe Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile
 145 150 155 160

Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala
 165 170 175

Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile
 180 185 190

Lys Glu Asn Met Asn Ile Leu Arg Pro Val Leu Lys Arg Glu Pro Thr
 195 200 205

Asp Thr Asp Leu Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg
 210 215 220

Arg Phe Leu Thr Thr Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro
 225 230 235 240

Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser
245 250 255

Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala
260 265 270

Ala His Arg Lys
275

<210> 38
<211> 281
<212> PRT
<213> unknown

<220>
<223> Nigrocine2-KZ144

<400> 38

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 Lys Val Leu Arg Lys Gly Asp Arg Gly Asp
20 25 30

Glu Val Cys Gln Leu Gln Thr Leu Leu Asn Leu Cys Gly Tyr Asp Val
35 40 45

Gly Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln Val Val
50 55 60

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

Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr
85 90 95

Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr
100 105 110

Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly Val Arg Ser Gln Leu
115 120 125

Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys
130 135 140

Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr Gly Thr
 145 150 155 160

Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr
 165 170 175

Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu Met
 180 185 190

Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg Pro Val Leu
 195 200 205

Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His Phe Phe Gly
 210 215 220

Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu Leu Ala
 225 230 235 240

Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr
 245 250 255

Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu Met
 260 265 270

Asp Gly Lys Val Ala Ala His Arg Lys
 275 280

<210> 39
 <211> 283
 <212> PRT
 <213> unknown

<220>
 <223> Pseudin1-KZ144

<400> 39

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 Lys Val Leu Arg Lys Gly Asp Arg
 20 25 30

Gly Asp Glu Val Cys Gln Leu Gln Thr Leu Leu Asn Leu Cys Gly Tyr
 35 40 45

Asp Val Gly Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln
 50 55 60

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

Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile
 85 90 95

Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala Ala
 100 105 110

Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly Val Arg Ser
 115 120 125

Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu
 130 135 140

Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr
 145 150 155 160

Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val
 165 170 175

Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala
 180 185 190

Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg Pro
 195 200 205

Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His Phe
 210 215 220

Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu
 225 230 235 240

Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile
 245 250 255

Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn
 260 265 270

Leu Met Asp Gly Lys Val Ala Ala His Arg Lys
 275 280

<210> 40
 <211> 277
 <212> PRT
 <213> unknown

<220>
 <223> Rana lexin-KZ144

<400> 40

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

Lys Cys Lys Val Leu Arg Lys Gly Asp Arg Gly Asp Glu Val Cys Gln
 20 25 30

Leu Gln Thr Leu Leu Asn Leu Cys Gly Tyr Asp Val Gly Lys Pro Asp
 35 40 45

Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln Val Val Lys Phe Gln Lys
 50 55 60

Asp Asn Cys Leu Asp Ser Asp Gly Ile Val Gly Lys Asn Thr Trp Ala
 65 70 75 80

Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro
 85 90 95

Met Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn
 100 105 110

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

Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser
 130 135 140

Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr Gly Thr Trp Lys Thr Met
 145 150 155 160

Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly
 165 170 175

Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu
 180 185 190

Ile Lys Glu Asn Met Asn Ile Leu Arg Pro Val Leu Lys Arg Glu Pro
195 200 205

Thr Asp Thr Asp Leu Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala
210 215 220

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

Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly
245 250 255

Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val
260 265 270

Ala Ala His Arg Lys
275

<210> 41
<211> 286
<212> PRT
<213> unknown

<220>
<223> WLB02-Variant-KZ144

<400> 41

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 Lys Val Leu Arg Lys
20 25 30

Gly Asp Arg Gly Asp Glu Val Cys Gln Leu Gln Thr Leu Leu Asn Leu
35 40 45

Cys Gly Tyr Asp Val Gly Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr
50 55 60

Phe Asn Gln Val Val Lys Phe Gln Lys Asp Asn Cys Leu Asp Ser Asp
65 70 75 80

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

Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser
100 105 110

Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly
115 120 125

Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe
130 135 140

Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln
145 150 155 160

Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys
165 170 175

Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg
180 185 190

Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile
195 200 205

Leu Arg Pro Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu
210 215 220

Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly
225 230 235 240

Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn
245 250 255

Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu
260 265 270

Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys
275 280 285

<210> 42
<211> 293
<212> PRT
<213> unknown

<220>
<223> Sushi1-KZ144

<400> 42

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 Lys Val Leu Arg Lys Gly Asp Arg Gly Asp Glu Val Cys Gln
35 40 45

Leu Gln Thr Leu Leu Asn Leu Cys Gly Tyr Asp Val Gly Lys Pro Asp
50 55 60

Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln Val Val Lys Phe Gln Lys
65 70 75 80

Asp Asn Cys Leu Asp Ser Asp Gly Ile Val Gly Lys Asn Thr Trp Ala
85 90 95

Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro
100 105 110

Met Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn
115 120 125

Ala Val Glu Asn Ala Thr Gly Val Arg Ser Gln Leu Leu Leu Thr Phe
130 135 140

Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser
145 150 155 160

Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr Gly Thr Trp Lys Thr Met
165 170 175

Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly
180 185 190

Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu
195 200 205

Ile Lys Glu Asn Met Asn Ile Leu Arg Pro Val Leu Lys Arg Glu Pro
210 215 220

Thr Asp Thr Asp Leu Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala
 225 230 235 240

Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu Leu Ala Ala Thr His Phe
 245 250 255

Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly
 260 265 270

Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val
 275 280 285

Ala Ala His Arg Lys
 290

<210> 43
 <211> 285
 <212> PRT
 <213> unknown

<220>
 <223> Melttin-KZ144

<400> 43

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 Lys Val Leu Arg Lys Gly
 20 25 30

Asp Arg Gly Asp Glu Val Cys Gln Leu Gln Thr Leu Leu Asn Leu Cys
 35 40 45

Gly Tyr Asp Val Gly Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe
 50 55 60

Asn Gln Val Val Lys Phe Gln Lys Asp Asn Cys Leu Asp Ser Asp Gly
 65 70 75 80

Ile Val Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro
 85 90 95

Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg
 100 105 110

Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly Val
115 120 125

Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp
130 135 140

Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe
145 150 155 160

Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr
165 170 175

Gly Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile
180 185 190

Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu
195 200 205

Arg Pro Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala
210 215 220

His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln
225 230 235 240

Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro
245 250 255

Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val
260 265 270

Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys
275 280 285

<210> 44
<211> 296
<212> PRT
<213> unknown

<220>
<223> LL-37-KZ144

<400> 44

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

Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn
260 265 270

Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu Met Asp
275 280 285

Gly Lys Val Ala Ala His Arg Lys
290 295

<210> 45
<211> 272
<212> PRT
<213> unknown

<220>
<223> Indolicidin-KZ144

<400> 45

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

Arg Lys Gly Asp Arg Gly Asp Glu Val Cys Gln Leu Gln Thr Leu Leu
20 25 30

Asn Leu Cys Gly Tyr Asp Val Gly Lys Pro Asp Gly Ile Phe Gly Asn
35 40 45

Asn Thr Phe Asn Gln Val Val Lys Phe Gln Lys Asp Asn Cys Leu Asp
50 55 60

Ser Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys
65 70 75 80

Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn
85 90 95

Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala
100 105 110

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

Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp
130 135 140

Phe Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly
 145 150 155 160

Met Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp
 165 170 175

Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met
 180 185 190

Asn Ile Leu Arg Pro Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu
 195 200 205

Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr
 210 215 220

Thr Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln
 225 230 235 240

Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile
 245 250 255

Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys
 260 265 270

<210> 46
 <211> 288
 <212> PRT
 <213> unknown

<220>
 <223> SMAP-29-KZ144

<400> 46

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 Lys Val Leu
 20 25 30

Arg Lys Gly Asp Arg Gly Asp Glu Val Cys Gln Leu Gln Thr Leu Leu
 35 40 45

Asn Leu Cys Gly Tyr Asp Val Gly Lys Pro Asp Gly Ile Phe Gly Asn
 50 55 60

Asn Thr Phe Asn Gln Val Val Lys Phe Gln Lys Asp Asn Cys Leu Asp
 65 70 75 80

Ser Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys
 85 90 95

Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn
 100 105 110

Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala
 115 120 125

Thr Gly Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser
 130 135 140

Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp
 145 150 155 160

Phe Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly
 165 170 175

Met Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp
 180 185 190

Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met
 195 200 205

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

Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr
 225 230 235 240

Thr Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln
 245 250 255

Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile
 260 265 270

Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys
 275 280 285

<210> 47
 <211> 277
 <212> PRT
 <213> unknown

<220>
 <223> Protegrin-KZ144

<400> 47

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

Gly Arg Lys Val Leu Arg Lys Gly Asp Arg Gly Asp Glu Val Cys Gln
 20 25 30

Leu Gln Thr Leu Leu Asn Leu Cys Gly Tyr Asp Val Gly Lys Pro Asp
 35 40 45

Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln Val Val Lys Phe Gln Lys
 50 55 60

Asp Asn Cys Leu Asp Ser Asp Gly Ile Val Gly Lys Asn Thr Trp Ala
 65 70 75 80

Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro
 85 90 95

Met Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn
 100 105 110

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

Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser
 130 135 140

Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr Gly Thr Trp Lys Thr Met
 145 150 155 160

Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly
 165 170 175

Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu
 180 185 190

Ile Lys Glu Asn Met Asn Ile Leu Arg Pro Val Leu Lys Arg Glu Pro
195 200 205

Thr Asp Thr Asp Leu Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala
210 215 220

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

Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly
245 250 255

Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val
260 265 270

Ala Ala His Arg Lys
275

<210> 48
<211> 290
<212> PRT
<213> unknown

<220>
<223> Cecropin P1-KZ144

<400> 48

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 Lys
20 25 30

Val Leu Arg Lys Gly Asp Arg Gly Asp Glu Val Cys Gln Leu Gln Thr
35 40 45

Leu Leu Asn Leu Cys Gly Tyr Asp Val Gly Lys Pro Asp Gly Ile Phe
50 55 60

Gly Asn Asn Thr Phe Asn Gln Val Val Lys Phe Gln Lys Asp Asn Cys
65 70 75 80

Leu Asp Ser Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu Phe
85 90 95

Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr
100 105 110

Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu
115 120 125

Asn Ala Thr Gly Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser Ile
130 135 140

Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr
145 150 155 160

Gly Trp Phe Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn
165 170 175

Tyr Gly Met Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu Arg
180 185 190

Lys Asp Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu
195 200 205

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

Asp Leu Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe
225 230 235 240

Leu Thr Thr Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu
245 250 255

Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys
260 265 270

Thr Ile Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His
275 280 285

Arg Lys
290

<210> 49

<211> 282

<212> PRT

<213> unknown

<220>

<223> Magainin-KZ144

<400> 49

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 Lys Val Leu Arg Lys Gly Asp Arg Gly
20 25 30

Asp Glu Val Cys Gln Leu Gln Thr Leu Leu Asn Leu Cys Gly Tyr Asp
35 40 45

Val Gly Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln Val
50 55 60

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

Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro
85 90 95

Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala
100 105 110

Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly Val Arg Ser Gln
115 120 125

Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile
130 135 140

Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr Gly
145 150 155 160

Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu
165 170 175

Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu
180 185 190

Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg Pro Val
195 200 205

Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His Phe Phe
210 215 220

Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu Leu
 225 230 235 240

Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe
 245 250 255

Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu
 260 265 270

Met Asp Gly Lys Val Ala Ala His Arg Lys
 275 280

<210> 50

<211> 284

<212> PRT

<213> unknown

<220>

<223> Pleurocidin-KZ144

<400> 50

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 Lys Val Leu Arg Lys Gly Asp
 20 25 30

Arg Gly Asp Glu Val Cys Gln Leu Gln Thr Leu Leu Asn Leu Cys Gly
 35 40 45

Tyr Asp Val Gly Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe Asn
 50 55 60

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

Val Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro
 85 90 95

Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala
 100 105 110

Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly Val Arg
 115 120 125

Ser Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp Tyr
130 135 140

Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu
145 150 155 160

Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly
165 170 175

Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser
180 185 190

Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg
195 200 205

Pro Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His
210 215 220

Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn
225 230 235 240

Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser
245 250 255

Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr
260 265 270

Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys
275 280

<210> 51

<211> 295

<212> PRT

<213> unknown

<220>

<223> Cecropin A (A.aegypti)-KZ144

<400> 51

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 Lys Val Leu Arg Lys Gly Asp Arg Gly Asp Glu Val
 35 40 45

Cys Gln Leu Gln Thr Leu Leu Asn Leu Cys Gly Tyr Asp Val Gly Lys
 50 55 60

Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln Val Val Lys Phe
 65 70 75 80

Gln Lys Asp Asn Cys Leu Asp Ser Asp Gly Ile Val Gly Lys Asn Thr
 85 90 95

Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys Thr
 100 105 110

Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro Val
 115 120 125

Met Asn Ala Val Glu Asn Ala Thr Gly Val Arg Ser Gln Leu Leu Leu
 130 135 140

Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala Lys
 145 150 155 160

Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr Gly Thr Trp Lys
 165 170 175

Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr Asp Pro
 180 185 190

Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu Met Gly Ala
 195 200 205

Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg Pro Val Leu Lys Arg
 210 215 220

Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His Phe Phe Gly Pro Gly
 225 230 235 240

Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu Leu Ala Ala Thr
 245 250 255

His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn Lys
260 265 270

Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu Met Asp Gly
275 280 285

Lys Val Ala Ala His Arg Lys
290 295

<210> 52
<211> 299
<212> PRT
<213> unknown

<220>
<223> Cecropin A (D.melanogaster)-KZ144

<400> 52

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 Lys Val Leu Arg Lys Gly Asp Arg
35 40 45

Gly Asp Glu Val Cys Gln Leu Gln Thr Leu Leu Asn Leu Cys Gly Tyr
50 55 60

Asp Val Gly Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln
65 70 75 80

Val Val Lys Phe Gln Lys Asp Asn Cys Leu Asp Ser Asp Gly Ile Val
85 90 95

Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile
100 105 110

Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala Ala
115 120 125

Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly Val Arg Ser
130 135 140

Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu
145 150 155 160

Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr
165 170 175

Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val
180 185 190

Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala
195 200 205

Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg Pro
210 215 220

Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His Phe
225 230 235 240

Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu
245 250 255

Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile
260 265 270

Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn
275 280 285

Leu Met Asp Gly Lys Val Ala Ala His Arg Lys
290 295

<210> 53
<211> 280
<212> PRT
<213> unknown

<220>
<223> BuforinII-KZ144

<400> 53

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 Lys Val Leu Arg Lys Gly Asp Arg Gly Asp Glu
20 25 30

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

Gly Lys Val Ala Ala His Arg Lys
 275 280

<210> 54
 <211> 298
 <212> PRT
 <213> unknown

<220>
 <223> Sarcotoxin IA-KZ144

<400> 54

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 Lys Val Leu Arg Lys Gly Asp Arg Gly
 35 40 45

Asp Glu Val Cys Gln Leu Gln Thr Leu Leu Asn Leu Cys Gly Tyr Asp
 50 55 60

Val Gly Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln Val
 65 70 75 80

Val Lys Phe Gln Lys Asp Asn Cys Leu Asp Ser Asp Gly Ile Val Gly
 85 90 95

Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro
 100 105 110

Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala
 115 120 125

Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly Val Arg Ser Gln
 130 135 140

Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile
 145 150 155 160

Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr Gly
 165 170 175

Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu
180 185 190

Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu
195 200 205

Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg Pro Val
210 215 220

Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His Phe Phe
225 230 235 240

Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu Leu
245 250 255

Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe
260 265 270

Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu
275 280 285

Met Asp Gly Lys Val Ala Ala His Arg Lys
290 295

<210> 55
<211> 200
<212> PRT
<213> unknown

<220>
<223> Ascaphine 5-STM0016

<400> 55

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 Asn Pro Ile Ile Asp Gly Ile Ile
20 25 30

Ala Leu Glu Gly Gly Tyr Val Phe Asn Pro Lys Asp Lys Gly Gly Ala
35 40 45

Thr His Trp Gly Ile Thr Glu Ala Thr Ala Arg Ala His Gly Tyr Ala
50 55 60

Gly Asp Met Arg Asp Leu Thr His Ala Glu Ala Tyr Ala Ile Leu Glu
65 70 75 80

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

Trp Pro Val Ser Phe Glu Leu Cys Asp Ala Ala Val Asn Ile Gly Ala
100 105 110

Tyr His Pro Ser Ala Trp Leu Gln Arg Trp Leu Asn Val Phe Asn His
115 120 125

Glu Gly Lys Arg Tyr Pro Asp Ile His Val Asp Gly Asn Ile Gly Pro
130 135 140

Arg Thr Leu Ala Ala Leu Glu His Tyr Leu Ala Trp Arg Gly Gln Glu
145 150 155 160

Gly Glu Ala Val Leu Val Lys Ala Leu Asn Cys Ser Gln Gly Thr Tyr
165 170 175

Tyr Leu Asn Val Ala Glu Lys Asn His Asn Asn Glu Gln Phe Ile Tyr
180 185 190

Gly Trp Ile Lys Asn Arg Val Thr
195 200

<210> 56
<211> 198
<212> PRT
<213> unknown

<220>
<223> Nigrocine2-STM0016

<400> 56

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

Glu Gly Gly Tyr Val Phe Asn Pro Lys Asp Lys Gly Gly Ala Thr His
35 40 45

Trp Gly Ile Thr Glu Ala Thr Ala Arg Ala His Gly Tyr Ala Gly Asp
50 55 60

Met Arg Asp Leu Thr His Ala Glu Ala Tyr Ala Ile Leu Glu Glu Asp
65 70 75 80

Tyr Trp Ile Lys Pro Gly Phe Asp Val Ile Ser Thr Leu Ser Trp Pro
85 90 95

Val Ser Phe Glu Leu Cys Asp Ala Ala Val Asn Ile Gly Ala Tyr His
100 105 110

Pro Ser Ala Trp Leu Gln Arg Trp Leu Asn Val Phe Asn His Glu Gly
115 120 125

Lys Arg Tyr Pro Asp Ile His Val Asp Gly Asn Ile Gly Pro Arg Thr
130 135 140

Leu Ala Ala Leu Glu His Tyr Leu Ala Trp Arg Gly Gln Glu Gly Glu
145 150 155 160

Ala Val Leu Val Lys Ala Leu Asn Cys Ser Gln Gly Thr Tyr Tyr Leu
165 170 175

Asn Val Ala Glu Lys Asn His Asn Asn Glu Gln Phe Ile Tyr Gly Trp
180 185 190

Ile Lys Asn Arg Val Thr
195

<210> 57
<211> 205
<212> PRT
<213> unknown

<220>
<223> SMAP-29-STM0016

<400> 57

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 Asn Pro Ile
20 25 30

Ile Asp Gly Ile Ile Ala Leu Glu Gly Gly Tyr Val Phe Asn Pro Lys
35 40 45

Asp Lys Gly Gly Ala Thr His Trp Gly Ile Thr Glu Ala Thr Ala Arg
50 55 60

Ala His Gly Tyr Ala Gly Asp Met Arg Asp Leu Thr His Ala Glu Ala
65 70 75 80

Tyr Ala Ile Leu Glu Glu Asp Tyr Trp Ile Lys Pro Gly Phe Asp Val
85 90 95

Ile Ser Thr Leu Ser Trp Pro Val Ser Phe Glu Leu Cys Asp Ala Ala
100 105 110

Val Asn Ile Gly Ala Tyr His Pro Ser Ala Trp Leu Gln Arg Trp Leu
115 120 125

Asn Val Phe Asn His Glu Gly Lys Arg Tyr Pro Asp Ile His Val Asp
130 135 140

Gly Asn Ile Gly Pro Arg Thr Leu Ala Ala Leu Glu His Tyr Leu Ala
145 150 155 160

Trp Arg Gly Gln Glu Gly Glu Ala Val Leu Val Lys Ala Leu Asn Cys
165 170 175

Ser Gln Gly Thr Tyr Tyr Leu Asn Val Ala Glu Lys Asn His Asn Asn
180 185 190

Glu Gln Phe Ile Tyr Gly Trp Ile Lys Asn Arg Val Thr
195 200 205

<210> 58

<211> 215

<212> PRT

<213> unknown

<220>

<223> Sarcotoxin IA-STM0016

<400> 58

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 Asn Pro Ile Ile Asp Gly Ile Ile Ala
35 40 45

Leu Glu Gly Gly Tyr Val Phe Asn Pro Lys Asp Lys Gly Gly Ala Thr
50 55 60

His Trp Gly Ile Thr Glu Ala Thr Ala Arg Ala His Gly Tyr Ala Gly
65 70 75 80

Asp Met Arg Asp Leu Thr His Ala Glu Ala Tyr Ala Ile Leu Glu Glu
85 90 95

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

Pro Val Ser Phe Glu Leu Cys Asp Ala Ala Val Asn Ile Gly Ala Tyr
115 120 125

His Pro Ser Ala Trp Leu Gln Arg Trp Leu Asn Val Phe Asn His Glu
130 135 140

Gly Lys Arg Tyr Pro Asp Ile His Val Asp Gly Asn Ile Gly Pro Arg
145 150 155 160

Thr Leu Ala Ala Leu Glu His Tyr Leu Ala Trp Arg Gly Gln Glu Gly
165 170 175

Glu Ala Val Leu Val Lys Ala Leu Asn Cys Ser Gln Gly Thr Tyr Tyr
180 185 190

Leu Asn Val Ala Glu Lys Asn His Asn Asn Glu Gln Phe Ile Tyr Gly
195 200 205

Trp Ile Lys Asn Arg Val Thr
210 215

<210> 59
<211> 233
<212> PRT
<213> unknown

<220>

<223> Melittin-N4gp61

<400> 59

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 Ala Ile Ser Lys Lys Lys
20 25 30

Val Gly Gly Val Gly Gly Val Ile Ala Ala Ile Ile Ala Ala Val Phe
35 40 45

Ala Val Glu Gly Gly Tyr Val Asn Asp Pro Lys Asp Pro Gly Gly Glu
50 55 60

Thr Asn His Gly Val Thr Ile Gln Val Ala Gln Lys His Lys Gln Glu
65 70 75 80

Leu Glu Ser Met Tyr Asn Trp Asp Gly Ser Met Lys Asn Leu Thr Gln
85 90 95

Glu Met Ala Ser Ser Ile Tyr Tyr Asn Asp Tyr Ile Leu Lys Pro Gly
100 105 110

Phe Val Lys Phe Ala Asp Val Ser Pro Ala Val Thr Glu Lys Leu Val
115 120 125

Asp Ala Gly Val Asn Thr Gly Pro Ala Arg Pro Ser Arg Trp Leu Gln
130 135 140

Glu Ser Leu Asn Ala Phe Ser Arg Asn Gly Lys Asp Tyr Pro Lys Ile
145 150 155 160

Gln Val Asp Gly Lys Val Gly Ser Gly Thr Leu Ser Ala Tyr Lys Ser
165 170 175

Leu Gln Asn Lys Arg Gly Lys Val Glu Ala Cys Lys Leu Ile Leu Lys
180 185 190

Ser Leu Asp Gly Lys Gln Leu Asn Tyr Tyr Leu Ser Leu Asn Met Pro
195 200 205

Glu Tyr Thr Thr Gly Trp Ile Ala Asn Arg Ile Gly Asn Val Pro Leu
 210 215 220

Glu Arg Cys Asn Glu Asp Ile Val Asn
 225 230

<210> 60
 <211> 236
 <212> PRT
 <213> unknown

<220>
 <223> SMAP-29-N4gp61

<400> 60

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 Ala Ile Ser
 20 25 30

Lys Lys Lys Val Gly Gly Val Gly Gly Val Ile Ala Ala Ile Ile Ala
 35 40 45

Ala Val Phe Ala Val Glu Gly Gly Tyr Val Asn Asp Pro Lys Asp Pro
 50 55 60

Gly Gly Glu Thr Asn His Gly Val Thr Ile Gln Val Ala Gln Lys His
 65 70 75 80

Lys Gln Glu Leu Glu Ser Met Tyr Asn Trp Asp Gly Ser Met Lys Asn
 85 90 95

Leu Thr Gln Glu Met Ala Ser Ser Ile Tyr Tyr Asn Asp Tyr Ile Leu
 100 105 110

Lys Pro Gly Phe Val Lys Phe Ala Asp Val Ser Pro Ala Val Thr Glu
 115 120 125

Lys Leu Val Asp Ala Gly Val Asn Thr Gly Pro Ala Arg Pro Ser Arg
 130 135 140

Trp Leu Gln Glu Ser Leu Asn Ala Phe Ser Arg Asn Gly Lys Asp Tyr
 145 150 155 160

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

Tyr Lys Ser Leu Gln Asn Lys Arg Gly Lys Val Glu Ala Cys Lys Leu
180 185 190

Ile Leu Lys Ser Leu Asp Gly Lys Gln Leu Asn Tyr Tyr Leu Ser Leu
195 200 205

Asn Met Pro Glu Tyr Thr Thr Gly Trp Ile Ala Asn Arg Ile Gly Asn
210 215 220

Val Pro Leu Glu Arg Cys Asn Glu Asp Ile Val Asn
225 230 235

<210> 61
<211> 210
<212> PRT
<213> unknown

<220>
<223> Melittin-N4gp61trunc

<400> 61

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 Glu Gly Gly Tyr Val
20 25 30

Asn Asp Pro Lys Asp Pro Gly Gly Glu Thr Asn His Gly Val Thr Ile
35 40 45

Gln Val Ala Gln Lys His Lys Gln Glu Leu Glu Ser Met Tyr Asn Trp
50 55 60

Asp Gly Ser Met Lys Asn Leu Thr Gln Glu Met Ala Ser Ser Ile Tyr
65 70 75 80

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

Ser Pro Ala Val Thr Glu Lys Leu Val Asp Ala Gly Val Asn Thr Gly
100 105 110

Pro Ala Arg Pro Ser Arg Trp Leu Gln Glu Ser Leu Asn Ala Phe Ser
115 120 125

Arg Asn Gly Lys Asp Tyr Pro Lys Ile Gln Val Asp Gly Lys Val Gly
130 135 140

Ser Gly Thr Leu Ser Ala Tyr Lys Ser Leu Gln Asn Lys Arg Gly Lys
145 150 155 160

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

Asn Tyr Tyr Leu Ser Leu Asn Met Pro Glu Tyr Thr Thr Gly Trp Ile
180 185 190

Ala Asn Arg Ile Gly Asn Val Pro Leu Glu Arg Cys Asn Glu Asp Ile
195 200 205

Val Asn
210

<210> 62
<211> 215
<212> PRT
<213> unknown

<220>
<223> Cecropin P1-N4gp61trunc

<400> 62

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

Glu Gly Gly Tyr Val Asn Asp Pro Lys Asp Pro Gly Gly Glu Thr Asn
35 40 45

His Gly Val Thr Ile Gln Val Ala Gln Lys His Lys Gln Glu Leu Glu
50 55 60

Ser Met Tyr Asn Trp Asp Gly Ser Met Lys Asn Leu Thr Gln Glu Met
65 70 75 80

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

Lys Phe Ala Asp Val Ser Pro Ala Val Thr Glu Lys Leu Val Asp Ala
100 105 110

Gly Val Asn Thr Gly Pro Ala Arg Pro Ser Arg Trp Leu Gln Glu Ser
115 120 125

Leu Asn Ala Phe Ser Arg Asn Gly Lys Asp Tyr Pro Lys Ile Gln Val
130 135 140

Asp Gly Lys Val Gly Ser Gly Thr Leu Ser Ala Tyr Lys Ser Leu Gln
145 150 155 160

Asn Lys Arg Gly Lys Val Glu Ala Cys Lys Leu Ile Leu Lys Ser Leu
165 170 175

Asp Gly Lys Gln Leu Asn Tyr Tyr Leu Ser Leu Asn Met Pro Glu Tyr
180 185 190

Thr Thr Gly Trp Ile Ala Asn Arg Ile Gly Asn Val Pro Leu Glu Arg
195 200 205

Cys Asn Glu Asp Ile Val Asn
210 215

<210> 63
<211> 213
<212> PRT
<213> unknown

<220>
<223> SMAP-29-N4gp61trunc

<400> 63

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 Glu Gly
20 25 30

Gly Tyr Val Asn Asp Pro Lys Asp Pro Gly Gly Glu Thr Asn His Gly
35 40 45

Val Thr Ile Gln Val Ala Gln Lys His Lys Gln Glu Leu Glu Ser Met
50 55 60

Tyr Asn Trp Asp Gly Ser Met Lys Asn Leu Thr Gln Glu Met Ala Ser
65 70 75 80

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

Ala Asp Val Ser Pro Ala Val Thr Glu Lys Leu Val Asp Ala Gly Val
100 105 110

Asn Thr Gly Pro Ala Arg Pro Ser Arg Trp Leu Gln Glu Ser Leu Asn
115 120 125

Ala Phe Ser Arg Asn Gly Lys Asp Tyr Pro Lys Ile Gln Val Asp Gly
130 135 140

Lys Val Gly Ser Gly Thr Leu Ser Ala Tyr Lys Ser Leu Gln Asn Lys
145 150 155 160

Arg Gly Lys Val Glu Ala Cys Lys Leu Ile Leu Lys Ser Leu Asp Gly
165 170 175

Lys Gln Leu Asn Tyr Tyr Leu Ser Leu Asn Met Pro Glu Tyr Thr Thr
180 185 190

Gly Trp Ile Ala Asn Arg Ile Gly Asn Val Pro Leu Glu Arg Cys Asn
195 200 205

Glu Asp Ile Val Asn
210

<210> 64
<211> 777
<212> DNA
<213> unknown

<220>
<223> KZ144

<400> 64
aaagtattac gcaaaggcga taggggtgat gaggtatgtc aactccagac actcttaa 60
ttatgtggct atgatgttg aaagccagat ggtatTTTTT gaaataacac ctttaatacag 120
gtagttaaatt ttcaaaaaga taattgtcta gatagtgatg gtattgtagg taagaatact 180

tgggctgaat tattcagtaa atattctcca cctattcctt ataaaactat ccctatgcc	240
actgcaaata aatcacgtgc agctgcaact ccagttatga atgcagtaga aaatgctact	300
ggcgttcgta gccagttgct actaacattt gcttctattg aatcagcatt cgattacgaa	360
ataaaagcta agacttcata agctactggg tggttccaat tccttactgg aacatggaaa	420
acaatgattg aaaattatgg catgaagtat ggcgacttta ctgatccaac tggggcatta	480
cgtaaagatc cacgtataag tgctttaatg ggtgccgaac taattaaaga gaatatgaat	540
attcttcgtc ctgtccttaa acgtgaacca actgatactg atctttattt agctcacttc	600
tttgggcctg gtgcagcccg tcgtttcctg accactggcc agaatgaatt agctgctacc	660
catttcccaa aagaagctca ggcaaacca tctatTTTTT ataacaaga tgggtcacct	720
aaaaccattc aagaagtta taacttaatg gatggtaaag ttgcagcaca tagaaaa	777

<210> 65
 <211> 528
 <212> DNA
 <213> unknown

<220>
 <223> STM0016

<400> 65	
aacccgatta tcgatggcat tatcgcgctg gaaggagggtt acgtcttta tccgaaagat	60
aaggggtggag caacacattg ggggtattaca gaagcgacgg cacgagcaca tggttatgca	120
ggagacatgc gtgatctaac tcatgccgaa gcctacgcaa tacttgagga ggattactgg	180
atcaaaccgg gttttgatgt tatctcaacg ctgtcgtggc ctgtgagctt tgaattgtgt	240
gatgcagcgg ttaacatagg tgcataccac cctagtgcct gggtacagag atggcttaac	300
gtgttcaatc acgaaggcaa acgctatcca gacattcatg tagacggcaa cattgggtccc	360
aggactttag cagccttaga acattacttg gcttggagag ggcaagaagg tgaagctgta	420
ctggtgaaag ctctgaattg cagccaaggg acctactatc taaacgtcgc tgagaagaac	480
cacaacaacg aacagttcat ctacggttgg atcaagaatc gtgtgacc	528

<210> 66
 <211> 528
 <212> DNA
 <213> unknown

<220>
 <223> Pseudin 1

<400> 66
 aacccgatta tcgatggcat tatcgcgctg gaaggagggtt acgtcttta tccgaaagat 60
 aaggggtggag caacacattg ggggtattaca gaagcgacgg cacgagcaca tggttatgca 120
 ggagacatgc gtgatctaac tcatgccgaa gcctacgcaa tacttgagga ggattactgg 180
 atcaaaccgg gttttgatgt tatctcaacg ctgtcgtggc ctgtgagctt tgaattgtgt 240
 gatgcagcgg ttaacatagg tgcataccac cctagtgctt ggttacagag atggcttaac 300
 gtgttcaatc acgaaggcaa acgctatcca gacattcatg tagacggcaa cattgggtccc 360
 aggacttttag cagccttaga acattacttg gcttgagag ggcaagaagg tgaagctgta 420
 ctggtgaaag ctctgaattg cagccaaggg acctactatc taaacgtcgc tgagaagaac 480
 cacaacaacg aacagttcat ctacggttgg atcaagaatc gtgtgacc 528

<210> 67
 <211> 54
 <212> DNA
 <213> unknown

<220>
 <223> Ranalexin

<400> 67
 ttcttgggcg gtctgattgt tccagctatg atctgtgcgg tgaccaaaaa atgc 54

<210> 68
 <211> 102
 <212> DNA
 <213> unknown

<220>
 <223> Sushi 1

<400> 68
 ggcttcaaac tgaaaggat ggctcgatc tcctgtctgc caaacgggtca gtgggtctaac 60
 tttccaccga aatgcatccg tgaatgcgcg atgggttagct ct 102

<210> 69
 <211> 81
 <212> DNA
 <213> unknown

<220>
 <223> WLB2-Variant

<400> 69
 aaacgctggg ttaaaccgct gaaacgtgtc aaacgttggg tcaaacgtgt tgtccgtgta 60
 gtgaaacgtt ggggtgaaacg c 81

<210> 70
 <211> 78
 <212> DNA
 <213> unknown

<220>
 <223> Melittin

<400> 70
 ggtatcggtg ctgtgctgaa agttctgacc actgggtctgc cggcactgat ttcttggatc 60
 aaacgcaaac gtcagcag 78

<210> 71
 <211> 87
 <212> DNA
 <213> unknown

<220>
 <223> SMAP-29

<400> 71
 cgtgggtctgc gtcgcctggg tcgcaaaatt gcgcacggcg tcaaaaaata cggcccgcacc 60
 gtgctgcgca ttatccgcat cgctggt 87

<210> 72
 <211> 75
 <212> DNA
 <213> unknown

<220>
 <223> Pleurocidin

<400> 72
 ggctgggggtt ctttctttaa aaaagcggct cacgttggca aacatgtagg taaagcagct 60
 ctgaccact atctg 75

<210> 73
 <211> 108
 <212> DNA
 <213> unknown

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

<400> 73
 ggcggcctga aaaaactggg caaaaaactg gaagggtccg gcaaactgtg gttcaacgct 60
 gcagaaaaag cactgccggt tgtagctggt gctaaagctc tccgtaaa 108

<210> 74
 <211> 120
 <212> DNA
 <213> unknown

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

<400> 74
 ggctggctga aaaaaattgg caaaaaaatc gaacgcgtgg gccagcacac gcgtgatgca 60
 accatccagg gtctgggtat cccacagcag gcagctaacg tagccgcgac tgctcgtggt 120

<210> 75
 <211> 63
 <212> DNA
 <213> unknown

<220>
 <223> Buforin II

<400> 75
 acccgtagct ctcgtgctgg cctgcagttt ccggttggtc gcgtgcaccg tctgctccgc 60
 aaa 63

<210> 76
 <211> 117
 <212> DNA
 <213> unknown

<220>
 <223> Sarcotoxin IA

<400> 76
 ggatggctca aaaagattgg caagaaaatc gagcgagtcg gtcagcatat gcgtgatgca 60
 actatccagg gtttaggtat cgcacagcaa gcagctaattg tagcagctac tgctcgg 117

<210> 77
 <211> 294
 <212> PRT
 <213> unknown

<220>
 <223> Pseudin 1-KZ144

<400> 77

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 Lys Val Leu Arg Lys
 20 25 30

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

Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu
260 265 270

Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys Leu Glu
275 280 285

His His His His His His
290

<210> 78
<211> 288
<212> PRT
<213> unknown

<220>
<223> Ranalexin-KZ144

<400> 78

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

Lys Lys Cys Gly Ser Lys Val Leu Arg Lys Gly Asp Arg Gly Asp Glu
20 25 30

Val Cys Gln Leu Gln Thr Leu Leu Asn Leu Cys Gly Tyr Asp Val Gly
35 40 45

Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln Val Val Lys
50 55 60

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

Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys
85 90 95

Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro
100 105 110

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

Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala
130 135 140

Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr Gly Thr Trp
 145 150 155 160

Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr Asp
 165 170 175

Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu Met Gly
 180 185 190

Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg Pro Val Leu Lys
 195 200 205

Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His Phe Phe Gly Pro
 210 215 220

Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu Leu Ala Ala
 225 230 235 240

Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn
 245 250 255

Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu Met Asp
 260 265 270

Gly Lys Val Ala Ala His Arg Lys Leu Glu His His His His His His
 275 280 285

<210> 79
 <211> 306
 <212> PRT
 <213> unknown

<220>
 <223> Sushi1-KZ144

<400> 79

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

Pro Asn Gly Gln Trp Ser Asn Phe Pro Pro Lys Cys Ile Arg Glu Cys
 20 25 30

Ala Met Val Ser Ser Gly Ser Lys Val Leu Arg Lys Gly Asp Arg Gly
 35 40 45

Asp Glu Val Cys Gln Leu Gln Thr Leu Leu Asn Leu Cys Gly Tyr Asp
 50 55 60

Val Gly Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln Val
 65 70 75 80

Val Lys Phe Gln Lys Asp Asn Cys Leu Asp Ser Asp Gly Ile Val Gly
 85 90 95

Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro
 100 105 110

Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala
 115 120 125

Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly Val Arg Ser Gln
 130 135 140

Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile
 145 150 155 160

Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr Gly
 165 170 175

Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu
 180 185 190

Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu
 195 200 205

Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg Pro Val
 210 215 220

Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His Phe Phe
 225 230 235 240

Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu Leu
 245 250 255

Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe
 260 265 270

Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu
 275 280 285

Met Asp Gly Lys Val Ala Ala His Arg Lys Leu Glu His His His His
 290 295 300

His His
 305

<210> 80
 <211> 297
 <212> PRT
 <213> unknown

<220>
 <223> WLBUE2-Variant-KZ144

<400> 80

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 Lys Val
 20 25 30

Leu Arg Lys Gly Asp Arg Gly Asp Glu Val Cys Gln Leu Gln Thr Leu
 35 40 45

Leu Asn Leu Cys Gly Tyr Asp Val Gly Lys Pro Asp Gly Ile Phe Gly
 50 55 60

Asn Asn Thr Phe Asn Gln Val Val Lys Phe Gln Lys Asp Asn Cys Leu
 65 70 75 80

Asp Ser Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser
 85 90 95

Lys Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala
 100 105 110

Asn Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn
 115 120 125

Ala Thr Gly Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu
 130 135 140

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

Trp Phe Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr
165 170 175

Gly Met Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys
180 185 190

Asp Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn
195 200 205

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

Leu Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu
225 230 235 240

Thr Thr Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala
245 250 255

Gln Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr
260 265 270

Ile Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His Arg
275 280 285

Lys Leu Glu His His His His His His
290 295

<210> 81
<211> 296
<212> PRT
<213> unknown

<220>
<223> Melttin-KZ144

<400> 81

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

Leu Ile Ser Trp Ile Lys Arg Lys Arg Gln Gln Gly Ser Lys Val Leu
20 25 30

Arg Lys Gly Asp Arg Gly Asp Glu Val Cys Gln Leu Gln Thr Leu Leu
35 40 45

Asn Leu Cys Gly Tyr Asp Val Gly Lys Pro Asp Gly Ile Phe Gly Asn
 50 55 60

Asn Thr Phe Asn Gln Val Val Lys Phe Gln Lys Asp Asn Cys Leu Asp
 65 70 75 80

Ser Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys
 85 90 95

Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn
 100 105 110

Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala
 115 120 125

Thr Gly Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser
 130 135 140

Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp
 145 150 155 160

Phe Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly
 165 170 175

Met Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp
 180 185 190

Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met
 195 200 205

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

Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr
 225 230 235 240

Thr Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln
 245 250 255

Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile
 260 265 270

Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys
 275 280 285

Leu Glu His His His His His His
 290 295

<210> 82
 <211> 299
 <212> PRT
 <213> unknown

<220>
 <223> SMAP-29-KZ144

<400> 82

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

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

Lys Val Leu Arg Lys Gly Asp Arg Gly Asp Glu Val Cys Gln Leu Gln
 35 40 45

Thr Leu Leu Asn Leu Cys Gly Tyr Asp Val Gly Lys Pro Asp Gly Ile
 50 55 60

Phe Gly Asn Asn Thr Phe Asn Gln Val Val Lys Phe Gln Lys Asp Asn
 65 70 75 80

Cys Leu Asp Ser Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu
 85 90 95

Phe Ser Lys Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro
 100 105 110

Thr Ala Asn Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val
 115 120 125

Glu Asn Ala Thr Gly Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser
 130 135 140

Ile Glu Ser Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala
 145 150 155 160

Thr Gly Trp Phe Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu
165 170 175

Asn Tyr Gly Met Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu
180 185 190

Arg Lys Asp Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys
195 200 205

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

Thr Asp Leu Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg
225 230 235 240

Phe Leu Thr Thr Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys
245 250 255

Glu Ala Gln Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro
260 265 270

Lys Thr Ile Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala
275 280 285

His Arg Lys Leu Glu His His His His His
290 295

<210> 83
<211> 306
<212> PRT
<213> unknown

<220>
<223> Cecropin A (A.aegypti)-KZ144

<400> 83

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 Lys Val Leu Arg Lys Gly Asp Arg Gly
35 40 45

Asp Glu Val Cys Gln Leu Gln Thr Leu Leu Asn Leu Cys Gly Tyr Asp
 50 55 60

Val Gly Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln Val
 65 70 75 80

Val Lys Phe Gln Lys Asp Asn Cys Leu Asp Ser Asp Gly Ile Val Gly
 85 90 95

Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile Pro
 100 105 110

Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala Ala Ala
 115 120 125

Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly Val Arg Ser Gln
 130 135 140

Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu Ile
 145 150 155 160

Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr Gly
 165 170 175

Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val Leu
 180 185 190

Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala Leu
 195 200 205

Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg Pro Val
 210 215 220

Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His Phe Phe
 225 230 235 240

Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu Leu
 245 250 255

Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile Phe
 260 265 270

Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn Leu
 275 280 285

Met Asp Gly Lys Val Ala Ala His Arg Lys Leu Glu His His His His
 290 295 300

His His
 305

<210> 84
 <211> 295
 <212> PRT
 <213> unknown

<220>
 <223> Pleurocidin-KZ144

<400> 84

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 Lys Val Leu Arg
 20 25 30

Lys Gly Asp Arg Gly Asp Glu Val Cys Gln Leu Gln Thr Leu Leu Asn
 35 40 45

Leu Cys Gly Tyr Asp Val Gly Lys Pro Asp Gly Ile Phe Gly Asn Asn
 50 55 60

Thr Phe Asn Gln Val Val Lys Phe Gln Lys Asp Asn Cys Leu Asp Ser
 65 70 75 80

Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr
 85 90 95

Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys
 100 105 110

Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr
 115 120 125

Gly Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala
 130 135 140

Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe
 145 150 155 160

Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met
165 170 175

Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro
180 185 190

Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn
195 200 205

Ile Leu Arg Pro Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr
210 215 220

Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr
225 230 235 240

Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala
245 250 255

Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln
260 265 270

Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys Leu
275 280 285

Glu His His His His His
290 295

<210> 85
<211> 310
<212> PRT
<213> unknown

<220>
<223> Cecropin A (D.melanogaster)-KZ144

<400> 85

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 Pro Gln Gln Ala
20 25 30

Ala Asn Val Ala Ala Thr Ala Arg Gly Gly Ser Lys Val Leu Arg Lys
35 40 45

Gly Asp Arg Gly Asp Glu Val Cys Gln Leu Gln Thr Leu Leu Asn Leu
 50 55 60

Cys Gly Tyr Asp Val Gly Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr
 65 70 75 80

Phe Asn Gln Val Val Lys Phe Gln Lys Asp Asn Cys Leu Asp Ser Asp
 85 90 95

Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser
 100 105 110

Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser
 115 120 125

Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly
 130 135 140

Val Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe
 145 150 155 160

Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln
 165 170 175

Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys
 180 185 190

Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg
 195 200 205

Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile
 210 215 220

Leu Arg Pro Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu
 225 230 235 240

Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly
 245 250 255

Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn
 260 265 270

Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu
275 280 285

Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys Leu Glu
290 295 300

His His His His His His
305 310

<210> 86
<211> 291
<212> PRT
<213> unknown

<220>
<223> BuforinII-KZ144

<400> 86

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 Lys Val Leu Arg Lys Gly Asp Arg
20 25 30

Gly Asp Glu Val Cys Gln Leu Gln Thr Leu Leu Asn Leu Cys Gly Tyr
35 40 45

Asp Val Gly Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe Asn Gln
50 55 60

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

Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys Tyr Ser Pro Pro Ile
85 90 95

Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg Ala Ala
100 105 110

Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly Val Arg Ser
115 120 125

Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp Tyr Glu
130 135 140

Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe Leu Thr
 145 150 155 160

Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr Gly Val
 165 170 175

Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile Ser Ala
 180 185 190

Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu Arg Pro
 195 200 205

Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu Tyr Leu Ala His Phe
 210 215 220

Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln Asn Glu
 225 230 235 240

Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro Ser Ile
 245 250 255

Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val Tyr Asn
 260 265 270

Leu Met Asp Gly Lys Val Ala Ala His Arg Lys Leu Glu His His His
 275 280 285

His His His
 290

<210> 87
 <211> 309
 <212> PRT
 <213> unknown

<220>
 <223> Sarcotoxin IA-KZ144

<400> 87

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 Lys Val Leu Arg Lys Gly
 35 40 45

Asp Arg Gly Asp Glu Val Cys Gln Leu Gln Thr Leu Leu Asn Leu Cys
 50 55 60

Gly Tyr Asp Val Gly Lys Pro Asp Gly Ile Phe Gly Asn Asn Thr Phe
 65 70 75 80

Asn Gln Val Val Lys Phe Gln Lys Asp Asn Cys Leu Asp Ser Asp Gly
 85 90 95

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

Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn Lys Ser Arg
 115 120 125

Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala Thr Gly Val
 130 135 140

Arg Ser Gln Leu Leu Leu Thr Phe Ala Ser Ile Glu Ser Ala Phe Asp
 145 150 155 160

Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp Phe Gln Phe
 165 170 175

Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly Met Lys Tyr
 180 185 190

Gly Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp Pro Arg Ile
 195 200 205

Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met Asn Ile Leu
 210 215 220

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

His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr Thr Gly Gln
 245 250 255

Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln Ala Asn Pro
 260 265 270

Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile Gln Glu Val
275 280 285

Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys Leu Glu His
290 295 300

His His His His His
305

<210> 88
<211> 226
<212> PRT
<213> unknown

<220>
<223> Sarcotoxin IA-STM0016

<400> 88

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 Asn Pro Ile Ile Asp Gly
35 40 45

Ile Ile Ala Leu Glu Gly Gly Tyr Val Phe Asn Pro Lys Asp Lys Gly
50 55 60

Gly Ala Thr His Trp Gly Ile Thr Glu Ala Thr Ala Arg Ala His Gly
65 70 75 80

Tyr Ala Gly Asp Met Arg Asp Leu Thr His Ala Glu Ala Tyr Ala Ile
85 90 95

Leu Glu Glu Asp Tyr Trp Ile Lys Pro Gly Phe Asp Val Ile Ser Thr
100 105 110

Leu Ser Trp Pro Val Ser Phe Glu Leu Cys Asp Ala Ala Val Asn Ile
115 120 125

Gly Ala Tyr His Pro Ser Ala Trp Leu Gln Arg Trp Leu Asn Val Phe
130 135 140

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

Gly Pro Arg Thr Leu Ala Ala Leu Glu His Tyr Leu Ala Trp Arg Gly
 165 170 175

Gln Glu Gly Glu Ala Val Leu Val Lys Ala Leu Asn Cys Ser Gln Gly
 180 185 190

Thr Tyr Tyr Leu Asn Val Ala Glu Lys Asn His Asn Asn Glu Gln Phe
 195 200 205

Ile Tyr Gly Trp Ile Lys Asn Arg Val Thr Leu Glu His His His His
 210 215 220

His His
 225

<210> 89
 <211> 216
 <212> PRT
 <213> unknown

<220>
 <223> SMAP-29-STM0016

<400> 89

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

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

Asn Pro Ile Ile Asp Gly Ile Ile Ala Leu Glu Gly Gly Tyr Val Phe
 35 40 45

Asn Pro Lys Asp Lys Gly Gly Ala Thr His Trp Gly Ile Thr Glu Ala
 50 55 60

Thr Ala Arg Ala His Gly Tyr Ala Gly Asp Met Arg Asp Leu Thr His
 65 70 75 80

Ala Glu Ala Tyr Ala Ile Leu Glu Glu Asp Tyr Trp Ile Lys Pro Gly
 85 90 95

Phe Asp Val Ile Ser Thr Leu Ser Trp Pro Val Ser Phe Glu Leu Cys
100 105 110

Asp Ala Ala Val Asn Ile Gly Ala Tyr His Pro Ser Ala Trp Leu Gln
115 120 125

Arg Trp Leu Asn Val Phe Asn His Glu Gly Lys Arg Tyr Pro Asp Ile
130 135 140

His Val Asp Gly Asn Ile Gly Pro Arg Thr Leu Ala Ala Leu Glu His
145 150 155 160

Tyr Leu Ala Trp Arg Gly Gln Glu Gly Glu Ala Val Leu Val Lys Ala
165 170 175

Leu Asn Cys Ser Gln Gly Thr Tyr Tyr Leu Asn Val Ala Glu Lys Asn
180 185 190

His Asn Asn Glu Gln Phe Ile Tyr Gly Trp Ile Lys Asn Arg Val Thr
195 200 205

Leu Glu His His His His His His
210 215

<210> 90
<211> 247
<212> PRT
<213> unknown

<220>
<223> SMAP-29-N4gp61

<400> 90

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

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

Ala Ile Ser Lys Lys Lys Val Gly Gly Val Gly Gly Val Ile Ala Ala
35 40 45

Ile Ile Ala Ala Val Phe Ala Val Glu Gly Gly Tyr Val Asn Asp Pro
50 55 60

Lys Asp Pro Gly Gly Glu Thr Asn His Gly Val Thr Ile Gln Val Ala
65 70 75 80

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

Met Lys Asn Leu Thr Gln Glu Met Ala Ser Ser Ile Tyr Tyr Asn Asp
100 105 110

Tyr Ile Leu Lys Pro Gly Phe Val Lys Phe Ala Asp Val Ser Pro Ala
115 120 125

Val Thr Glu Lys Leu Val Asp Ala Gly Val Asn Thr Gly Pro Ala Arg
130 135 140

Pro Ser Arg Trp Leu Gln Glu Ser Leu Asn Ala Phe Ser Arg Asn Gly
145 150 155 160

Lys Asp Tyr Pro Lys Ile Gln Val Asp Gly Lys Val Gly Ser Gly Thr
165 170 175

Leu Ser Ala Tyr Lys Ser Leu Gln Asn Lys Arg Gly Lys Val Glu Ala
180 185 190

Cys Lys Leu Ile Leu Lys Ser Leu Asp Gly Lys Gln Leu Asn Tyr Tyr
195 200 205

Leu Ser Leu Asn Met Pro Glu Tyr Thr Thr Gly Trp Ile Ala Asn Arg
210 215 220

Ile Gly Asn Val Pro Leu Glu Arg Cys Asn Glu Asp Ile Val Asn Leu
225 230 235 240

Glu His His His His His His
245

<210> 91
<211> 624
<212> DNA
<213> unknown

<220>
<223> N4gp61

<400> 91
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 gcagtatttg ccgttgaagg tggatacggt aatgacccga aagatccagg aggtgaaaca 120
 aaccatggtg taactattca ggtcgcacaa aaacacaagc aagaacttga gtcgatgtat 180
 aactgggacg ggtcaatgaa gaatctgaca caggagatgg cctcaagtat atattacaac 240
 gattatatcc tcaagcctgg ctttgtgaaa tttgcggatg taagtccagc ggttacggaa 300
 aaacttgtgg atgctggagt aaatacaggt ccagcaagac caagccgttg gttacaagaa 360
 tccttgaatg ctttctcacg caacggcaaa gattatccga aaatccaagt tgacgggaaa 420
 gtaggttctg gaactttgag tgcttacaaa agcctgcaga ataagcgagg aaaagtggaa 480
 gcctgcaaat taatactgaa gtctctggat ggcaagcagc taaactacta tctgagcctc 540
 aatatgcctg agtataccac aggttggatt gcgaatcgta ttggaaatgt gcctttggaa 600
 cgctgtaatg aagatatcgt caac 624

<210> 92
 <211> 13
 <212> PRT
 <213> unknown

<220>
 <223> beta 4 helix

<400> 92

Pro Asn Arg Ala Lys Arg Val Ile Thr Thr Phe Arg Thr
 1 5 10

<210> 93
 <211> 272
 <212> PRT
 <213> unknown

<220>
 <223> beta 4 helix:KZ144

<400> 93

Pro Asn Arg Ala Lys Arg Val Ile Thr Thr Phe Arg Thr Lys Val Leu
 1 5 10 15

Arg Lys Gly Asp Arg Gly Asp Glu Val Cys Gln Leu Gln Thr Leu Leu
 20 25 30

Asn Leu Cys Gly Tyr Asp Val Gly Lys Pro Asp Gly Ile Phe Gly Asn
 35 40 45

Asn Thr Phe Asn Gln Val Val Lys Phe Gln Lys Asp Asn Cys Leu Asp
 50 55 60

Ser Asp Gly Ile Val Gly Lys Asn Thr Trp Ala Glu Leu Phe Ser Lys
 65 70 75 80

Tyr Ser Pro Pro Ile Pro Tyr Lys Thr Ile Pro Met Pro Thr Ala Asn
 85 90 95

Lys Ser Arg Ala Ala Ala Thr Pro Val Met Asn Ala Val Glu Asn Ala
 100 105 110

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

Ala Phe Asp Tyr Glu Ile Lys Ala Lys Thr Ser Ser Ala Thr Gly Trp
 130 135 140

Phe Gln Phe Leu Thr Gly Thr Trp Lys Thr Met Ile Glu Asn Tyr Gly
 145 150 155 160

Met Lys Tyr Gly Val Leu Thr Asp Pro Thr Gly Ala Leu Arg Lys Asp
 165 170 175

Pro Arg Ile Ser Ala Leu Met Gly Ala Glu Leu Ile Lys Glu Asn Met
 180 185 190

Asn Ile Leu Arg Pro Val Leu Lys Arg Glu Pro Thr Asp Thr Asp Leu
 195 200 205

Tyr Leu Ala His Phe Phe Gly Pro Gly Ala Ala Arg Arg Phe Leu Thr
 210 215 220

Thr Gly Gln Asn Glu Leu Ala Ala Thr His Phe Pro Lys Glu Ala Gln
 225 230 235 240

Ala Asn Pro Ser Ile Phe Tyr Asn Lys Asp Gly Ser Pro Lys Thr Ile
 245 250 255

Gln Glu Val Tyr Asn Leu Met Asp Gly Lys Val Ala Ala His Arg Lys
 260 265 270

<210> 94
 <211> 304
 <212> PRT
 <213> unknown

<220>
 <223> beta 4 helix:gp188

<400> 94

Pro Asn Arg Ala Lys Arg Val Ile Thr Thr Phe Arg Thr Asn Phe Arg
 1 5 10 15

Thr Lys Asn Gly Tyr Arg Asp Leu Gln Ala Leu Val Lys Glu Leu Gly
 20 25 30

Leu Tyr Thr Gly Gln Ile Asp Gly Val Trp Gly Lys Gly Thr Ser Ser
 35 40 45

Ser Thr Glu Thr Leu Leu Arg Gly Tyr Ala Glu Val Val Gly Lys Asn
 50 55 60

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

Val Ile Thr Ala Leu Gln Arg Asn Leu Ala Phe Leu Gly Leu Tyr Ser
 85 90 95

Leu Thr Val Asp Gly Ile Trp Gly Asn Gly Thr Leu Ser Gly Leu Asp
 100 105 110

Lys Ala Phe Glu Val Tyr Lys Glu Arg Tyr Arg Thr Pro Thr Tyr Asp
 115 120 125

Ile Ala Trp Ser Gly Lys Val Ser Pro Ala Phe Thr Ala Lys Val Lys
 130 135 140

Asp Trp Cys Gly Val His Val Pro Asn His Arg Ala Pro His Trp Leu
 145 150 155 160

Met Ala Cys Met Ala Phe Glu Thr Gly Gln Thr Phe Ser Pro Ser Ile
 165 170 175

Lys Asn Ala Ala Gly Ser Glu Ala Tyr Gly Leu Ile Gln Phe Met Ser
 180 185 190

Pro Ala Ala Asn Asp Leu Asn Val Pro Leu Ser Val Ile Arg Ser Met
 195 200 205

Asp Gln Leu Thr Gln Leu Asp Leu Val Phe Lys Tyr Phe Glu Met Trp
 210 215 220

Met Lys Arg Gly Lys Arg Tyr Thr Gln Leu Glu Asp Phe Tyr Leu Thr
 225 230 235 240

Ile Phe His Pro Ala Ser Val Gly Lys Lys Ala Asp Glu Val Leu Phe
 245 250 255

Leu Gln Gly Ser Lys Ala Tyr Leu Gln Asn Lys Gly Phe Asp Val Asp
 260 265 270

Lys Asp Gly Lys Ile Thr Leu Gly Glu Ile Ser Ser Thr Leu Tyr Thr
 275 280 285

Thr Tyr Tyr Lys Gly Leu Leu Pro Glu Asn Arg His Val Ile Ser Tyr
 290 295 300

<210> 95
 <211> 320
 <212> PRT
 <213> unknown

<220>
 <223> SMAP-29:gp188

<400> 95

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 Asn Phe Arg
 20 25 30

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

Leu Tyr Thr Gly Gln Ile Asp Gly Val Trp Gly Lys Gly Thr Ser Ser
 50 55 60

Ser Thr Glu Thr Leu Leu Arg Gly Tyr Ala Glu Val Val Gly Lys Asn
 65 70 75 80

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

Val Ile Thr Ala Leu Gln Arg Asn Leu Ala Phe Leu Gly Leu Tyr Ser
 100 105 110

Leu Thr Val Asp Gly Ile Trp Gly Asn Gly Thr Leu Ser Gly Leu Asp
 115 120 125

Lys Ala Phe Glu Val Tyr Lys Glu Arg Tyr Arg Thr Pro Thr Tyr Asp
 130 135 140

Ile Ala Trp Ser Gly Lys Val Ser Pro Ala Phe Thr Ala Lys Val Lys
 145 150 155 160

Asp Trp Cys Gly Val His Val Pro Asn His Arg Ala Pro His Trp Leu
 165 170 175

Met Ala Cys Met Ala Phe Glu Thr Gly Gln Thr Phe Ser Pro Ser Ile
 180 185 190

Lys Asn Ala Ala Gly Ser Glu Ala Tyr Gly Leu Ile Gln Phe Met Ser
 195 200 205

Pro Ala Ala Asn Asp Leu Asn Val Pro Leu Ser Val Ile Arg Ser Met
 210 215 220

Asp Gln Leu Thr Gln Leu Asp Leu Val Phe Lys Tyr Phe Glu Met Trp
 225 230 235 240

Met Lys Arg Gly Lys Arg Tyr Thr Gln Leu Glu Asp Phe Tyr Leu Thr
 245 250 255

Ile Phe His Pro Ala Ser Val Gly Lys Lys Ala Asp Glu Val Leu Phe
 260 265 270

Leu Gln Gly Ser Lys Ala Tyr Leu Gln Asn Lys Gly Phe Asp Val Asp
 275 280 285

Lys Asp Gly Lys Ile Thr Leu Gly Glu Ile Ser Ser Thr Leu Tyr Thr
 290 295 300

Thr Tyr Tyr Lys Gly Leu Leu Pro Glu Asn Arg His Val Ile Ser Tyr
 305 310 315 320

<210> 96
 <211> 330
 <212> PRT
 <213> unknown

<220>
 <223> Sarcotoxin IA:gp188

<400> 96

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 Asn Phe Arg Thr Lys Asn Gly Tyr Arg
 35 40 45

Asp Leu Gln Ala Leu Val Lys Glu Leu Gly Leu Tyr Thr Gly Gln Ile
 50 55 60

Asp Gly Val Trp Gly Lys Gly Thr Ser Ser Ser Thr Glu Thr Leu Leu
 65 70 75 80

Arg Gly Tyr Ala Glu Val Val Gly Lys Asn Thr Gly Gly Ile Gly Leu
 85 90 95

Pro Thr Thr Ser Asp Ala Ser Gly Tyr Asn Val Ile Thr Ala Leu Gln
 100 105 110

Arg Asn Leu Ala Phe Leu Gly Leu Tyr Ser Leu Thr Val Asp Gly Ile
 115 120 125

Trp Gly Asn Gly Thr Leu Ser Gly Leu Asp Lys Ala Phe Glu Val Tyr
 130 135 140

Lys Glu Arg Tyr Arg Thr Pro Thr Tyr Asp Ile Ala Trp Ser Gly Lys
 145 150 155 160

Val Ser Pro Ala Phe Thr Ala Lys Val Lys Asp Trp Cys Gly Val His
 165 170 175

Val Pro Asn His Arg Ala Pro His Trp Leu Met Ala Cys Met Ala Phe
 180 185 190

Glu Thr Gly Gln Thr Phe Ser Pro Ser Ile Lys Asn Ala Ala Gly Ser
195 200 205

Glu Ala Tyr Gly Leu Ile Gln Phe Met Ser Pro Ala Ala Asn Asp Leu
210 215 220

Asn Val Pro Leu Ser Val Ile Arg Ser Met Asp Gln Leu Thr Gln Leu
225 230 235 240

Asp Leu Val Phe Lys Tyr Phe Glu Met Trp Met Lys Arg Gly Lys Arg
245 250 255

Tyr Thr Gln Leu Glu Asp Phe Tyr Leu Thr Ile Phe His Pro Ala Ser
260 265 270

Val Gly Lys Lys Ala Asp Glu Val Leu Phe Leu Gln Gly Ser Lys Ala
275 280 285

Tyr Leu Gln Asn Lys Gly Phe Asp Val Asp Lys Asp Gly Lys Ile Thr
290 295 300

Leu Gly Glu Ile Ser Ser Thr Leu Tyr Thr Thr Tyr Tyr Lys Gly Leu
305 310 315 320

Leu Pro Glu Asn Arg His Val Ile Ser Tyr
325 330

<210> 97
<211> 209
<212> PRT
<213> unknown

<220>
<223> SMAP-29:Salmonella endolysin

<400> 97

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 Lys Pro Lys
20 25 30

Asp Glu Ile Phe Asp Glu Ile Leu Gly Lys Glu Gly Gly Tyr Val Asn
35 40 45

His Pro Asp Asp Lys Gly Gly Pro Thr Lys Trp Gly Ile Thr Glu Lys
 50 55 60

Val Ala Arg Ala His Gly Tyr Arg Gly Asp Met Arg Asn Leu Thr Arg
 65 70 75 80

Gly Gln Ala Leu Glu Ile Leu Glu Thr Asp Tyr Trp Tyr Gly Pro Arg
 85 90 95

Phe Asp Arg Val Ala Lys Ala Ser Pro Asp Val Ala Ala Glu Leu Cys
 100 105 110

Asp Thr Gly Val Asn Met Gly Pro Ser Val Ala Ala Lys Met Leu Gln
 115 120 125

Arg Trp Leu Asn Val Phe Asn Gln Gly Gly Arg Leu Tyr Pro Asp Met
 130 135 140

Asp Thr Asp Gly Arg Ile Gly Pro Arg Thr Leu Asn Ala Leu Arg Val
 145 150 155 160

Tyr Leu Glu Lys Arg Gly Lys Asp Gly Glu Arg Val Leu Leu Val Ala
 165 170 175

Leu Asn Cys Thr Gln Gly Glu Arg Tyr Leu Glu Leu Ala Glu Lys Arg
 180 185 190

Glu Ala Asp Glu Ser Phe Val Tyr Gly Trp Met Lys Glu Arg Val Leu
 195 200 205

Ile

<210> 98
 <211> 303
 <212> PRT
 <213> unknown

<220>
 <223> Pseudin 1:Acinetobacter baumannii endolysin

<400> 98

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 Glu Tyr Asp Met Ile Leu Lys Phe
 20 25 30

Gly Ser Lys Gly Asp Ala Val Ala Thr Leu Gln Lys Gln Leu Ala Lys
 35 40 45

Met Gly Tyr Lys Gly Val Lys Asp Lys Pro Leu Ser Val Asp Gly His
 50 55 60

Phe Gly Glu Ser Thr Glu Phe Ala Val Ile Gln Leu Gln Arg Lys Phe
 65 70 75 80

Gly Leu Val Ala Asp Gly Lys Val Gly Asp Lys Thr Arg Gln Ala Leu
 85 90 95

Ala Gly Asp Ser Val Ser Lys Phe Leu Lys Asp Glu Asp Tyr Lys Lys
 100 105 110

Ala Ala Ile Arg Leu Lys Val Pro Glu Leu Val Ile Arg Val Phe Gly
 115 120 125

Ala Val Glu Gly Leu Gly Val Gly Phe Leu Pro Asn Gly Lys Ala Lys
 130 135 140

Ile Leu Phe Glu Arg His Arg Met Tyr Phe Tyr Leu Cys Gln Ala Leu
 145 150 155 160

Gly Lys Thr Phe Ala Asn Ser Gln Val Lys Ile Thr Pro Asn Ile Val
 165 170 175

Asn Thr Leu Thr Gly Gly Tyr Lys Gly Asp Ala Ala Glu Tyr Thr Arg
 180 185 190

Leu Ser Met Ala Ile Asn Ile His Lys Glu Ser Ala Leu Met Ser Thr
 195 200 205

Ser Trp Gly Gln Phe Gln Ile Met Gly Glu Asn Trp Lys Asp Leu Gly
 210 215 220

Tyr Ser Ser Val Gln Glu Phe Val Asp Gln Gln Gln Leu Asn Glu Gly
 225 230 235 240

Asn Gln Leu Glu Ala Phe Ile Arg Phe Ile Glu Trp Lys Pro Gly Leu
245 250 255

Leu Glu Ala Leu Arg Lys Gln Asp Trp Asp Thr Val Phe Thr Leu Tyr
260 265 270

Asn Gly Lys Asn Tyr Lys Lys Leu Gly Tyr Gln Ala Lys Phe Gln Lys
275 280 285

Glu Trp Asp His Leu Glu Pro Ile Tyr Arg Glu Lys Thr Ala Ala
290 295 300

<210> 99

<211> 308

<212> PRT

<213> unknown

<220>

<223> SMAP-29: *Acinetobacter baumannii* endolysin

<400> 99

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 Glu Tyr Asp
20 25 30

Met Ile Leu Lys Phe Gly Ser Lys Gly Asp Ala Val Ala Thr Leu Gln
35 40 45

Lys Gln Leu Ala Lys Met Gly Tyr Lys Gly Val Lys Asp Lys Pro Leu
50 55 60

Ser Val Asp Gly His Phe Gly Glu Ser Thr Glu Phe Ala Val Ile Gln
65 70 75 80

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

Thr Arg Gln Ala Leu Ala Gly Asp Ser Val Ser Lys Phe Leu Lys Asp
100 105 110

Glu Asp Tyr Lys Lys Ala Ala Ile Arg Leu Lys Val Pro Glu Leu Val
115 120 125

Ile Arg Val Phe Gly Ala Val Glu Gly Leu Gly Val Gly Phe Leu Pro
130 135 140

Asn Gly Lys Ala Lys Ile Leu Phe Glu Arg His Arg Met Tyr Phe Tyr
145 150 155 160

Leu Cys Gln Ala Leu Gly Lys Thr Phe Ala Asn Ser Gln Val Lys Ile
165 170 175

Thr Pro Asn Ile Val Asn Thr Leu Thr Gly Gly Tyr Lys Gly Asp Ala
180 185 190

Ala Glu Tyr Thr Arg Leu Ser Met Ala Ile Asn Ile His Lys Glu Ser
195 200 205

Ala Leu Met Ser Thr Ser Trp Gly Gln Phe Gln Ile Met Gly Glu Asn
210 215 220

Trp Lys Asp Leu Gly Tyr Ser Ser Val Gln Glu Phe Val Asp Gln Gln
225 230 235 240

Gln Leu Asn Glu Gly Asn Gln Leu Glu Ala Phe Ile Arg Phe Ile Glu
245 250 255

Trp Lys Pro Gly Leu Leu Glu Ala Leu Arg Lys Gln Asp Trp Asp Thr
260 265 270

Val Phe Thr Leu Tyr Asn Gly Lys Asn Tyr Lys Lys Leu Gly Tyr Gln
275 280 285

Ala Lys Phe Gln Lys Glu Trp Asp His Leu Glu Pro Ile Tyr Arg Glu
290 295 300

Lys Thr Ala Ala
305

<210> 100
<211> 313
<212> PRT
<213> unknown

<220>
<223> Sushi 1: *Acinetobacter baumannii* endolysin

<400> 100

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

Phe Val Asp Gln Gln Gln Leu Asn Glu Gly Asn Gln Leu Glu Ala Phe
245 250 255

Ile Arg Phe Ile Glu Trp Lys Pro Gly Leu Leu Glu Ala Leu Arg Lys
260 265 270

Gln Asp Trp Asp Thr Val Phe Thr Leu Tyr Asn Gly Lys Asn Tyr Lys
275 280 285

Lys Leu Gly Tyr Gln Ala Lys Phe Gln Lys Glu Trp Asp His Leu Glu
290 295 300

Pro Ile Tyr Arg Glu Lys Thr Ala Ala
305 310