

CLAIMS

1. A polypeptide comprising the amino acid sequence of a globular Gram-negative endolysin and the amino acid sequence of a cell wall binding domain of i) a modular Gram-negative endolysin or ii) a bacteriophage tail/baseplate protein.
2. The polypeptide according to claim 1, wherein the Gram-negative modular endolysin is selected from the group consisting of KZ144, EL188, OBPgpLYS, PVPSE1gp146, and 201φ2-1 endolysin.
3. The polypeptide according to claim 1, wherein the bacteriophage tail/baseplate protein is a bacteriophage tail/baseplate protein of a bacteriophage selected from the group consisting of Vibrio phage ICP1 and Vibrio phage RYC.
4. The polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence selected from the group of sequences consisting of SEQ ID Nos.: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 and 14, , and sequences having at least 80% sequence identity to any of these SEQ ID Nos..
5. The polypeptide according to any one of the preceding claims, wherein the globular endolysin is a endopeptidase, chitinase, T4 like muraminidase, lambda like muraminidase, N-acetyl-muramoyl-L-alanine-amidase, muramoyl-L-alanine-amidase, muramidase, lytic transglycosylase (C), lytic transglycosylase (M), N-acetyl-muramidase, N-acetyl-glucosaminidase or transglycosylase.
6. The polypeptide according to any one of the preceding claims, wherein the globular endolysin is an endolysin deriving from a bacteriophage infecting bacteria of the genus selected from the group consisting of: *Acinetobacter*, *Aeromonas*, *Aggregatibacter*, *Azospirillum*, *Bacteroides*, *Burkholderia*, *Campylobacter*, *Candidatus*, *Caulobacter*, *Clavibacter*, *Cronobacter*, *Delftia*, *Enterobacter*, *Erwinia*, *Escherichia*, *Flavobacterium*, *Haemophilus*, *Iodobacteria*, *Klebsiella*, *Kluyvera*, *Mannheimia*, *Morganella*, *Neisseria*, *Pantoea*, *Pasteurella*, *Planktothrix*, *Pseudoalteromonas*, *Pseudomonas*, *Ralstonia*, *Salmonella*, *Shigella*, *Sinorhizobium*, *Sodalis*,

Synechococcus, *Thalassomonas*, *Thermus*, *Vibrio*, *Xanthomonas*, *Xylella*, and *Yersinia*.

7. The polypeptide according to any one of the preceding claims, wherein the globular endolysin is deriving from the group of endolysins listed in table 1.
8. The polypeptide according to claim 7, wherein the globular endolysin is selected from the group consisting of Lys68, ABgp46 and Lys394 endolysin, in particular wherein the globular endolysin is Lys68 endolysin.
9. The polypeptide according to any one of the preceding claims, wherein the polypeptide comprises an amino acid sequence selected from the group of sequences consisting of SEQ ID Nos.: 18, 19, 20, 21, 22, 23, 24, 25, 27 and 28.
10. The polypeptide according to any one of the preceding claims, wherein the polypeptide does not comprise the amino acid sequence of a Gram-negative modular endolysin.
11. The polypeptide according to any one of the preceding claims, wherein the polypeptide does not comprise an enzymatically active domain (EAD) of a Gram-negative modular endolysin.
12. The polypeptide according to any one of the preceding claims, wherein the enzymatic activity of the globular endolysin is the only enzymatic activity of the polypeptide.
13. The polypeptide according to any one of the preceding claims, wherein the amino acid sequence of the globular endolysin exhibits less than 90% sequence identity with the amino acid sequence of an enzymatically active domain of any modular endolysin.
14. The polypeptide according to any one of the preceding claims, wherein the amino acid sequence of the globular endolysin and the amino acid sequence of the cell wall binding domain are either linked directly to each other or via an intermediate linker sequence, the linker sequence preferably not exceeding more than 50 amino acids in length.

15. The polypeptide according to any one of the preceding claims, wherein the polypeptide degrades peptidoglycan of at least one Gram-negative bacterial species.
16. The polypeptide according to any one of the preceding claims, wherein the polypeptide binds to peptidoglycan of at least one Gram-negative bacterial species.
17. The polypeptide according to any one of the preceding claims wherein the polypeptide comprises an amino acid sequence selected from the group of sequences consisting of SEQ ID NOs: 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39 and 40, wherein SEQ ID NO: 40 is preferred.
18. The polypeptide according to any one of the preceding claims, wherein the polypeptide comprises additionally at least one amino acid sequence selected from the group consisting of amphipathic peptide, cationic peptide, polycationic peptide, hydrophobic peptide, naturally occurring antimicrobial peptide, sushi peptide and defensin.
19. The polypeptide according to claim 18, wherein the additional amino acid sequence is present at the N- or C-terminus of the polypeptide.
20. The polypeptide according to claim 18, wherein the polypeptide comprises at least one additional amino acid sequence stretch selected from the group consisting of: KRK and SEQ ID NOs: 41 - 115.
21. The polypeptide according to claim 18, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO: 116.
22. The polypeptide according to any one of the preceding claims, wherein the polypeptide comprises additionally a tag sequence.
23. Nucleic acid encoding a polypeptide according to any one of claims 1 to 22.
24. Vector comprising a nucleic acid according to claim 23.

25. Host cell comprising a polypeptide according to any one of claims 1 to 22, a nucleic acid according to claim 23, and/or a vector according to claim 24.
26. Composition comprising a polypeptide according to any one of claims 1 to 22, a nucleic acid according to claim 23, a vector according to claim 24 and/or a host cell according to claim 25.
27. Composition according to claim 26, wherein the composition is a pharmaceutical composition comprising a pharmaceutical acceptable diluent, excipient or carrier.
28. The polypeptide according to any one of claims 1 to 22, the nucleic acid according to claim 23, the vector according to claim 24, the host cell according to claim 25 and/or the composition according to claim 26 or 27 for use in a method for treatment of the human or animal body by surgery or therapy or for use in diagnostic methods practised on the human or animal body.
29. The polypeptide, nucleic acid, vector, host cell, or composition for use according to claim 28, wherein the method is a method for preventing or treating bacterial infections of the human or animal body.
30. The polypeptide, nucleic acid, vector, host cell, or composition for use according to claim 29, wherein the method is a method for preventing or treating bacterial infections caused by Gram negative bacteria.
31. Use of polypeptide according to any one of claims 1 to 22 and/or the composition according to claim 26 or 27 as non-therapeutic disinfectant.
32. A method for treatment of the human or animal body by surgery or therapy, wherein the method comprises administering an efficient amount of the polypeptide according to any one of claims 1 to 22, the nucleic acid according to claim 23, the vector according to claim 24, the host cell according to claim 25 and/or the composition according to claim 26 or 27.

33. The method according to claim 32, wherein the method is a method for preventing or treating bacterial infections of the human or animal body, in particular wherein the method is a method for preventing or treating bacterial infections caused by Gram negative bacteria.