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 derived 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 derived 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 and /or does not comprise an enzymatically active domain (EAD) of a Gram-negative modular endolysin.

11. 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.

12. The polypeptide according to any one of the preceding claims, wherein the polypeptide degrades and/or binds to peptidoglycan of at least one Gram-negative bacterial species.

13. 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.

14. 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.

15. The polypeptide according to claim 14, 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.

16. The polypeptide according to claim 14, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO: 116.

17. Nucleic acid encoding ~~a~~ the polypeptide ~~according to~~as defined in any one of claims 1 to 16.

18. Host cell comprising ~~a~~ the polypeptide ~~according to~~as defined in any one of claims 1 to 16, and/or ~~a~~ the nucleic acid ~~according to~~as defined in claim 17.

19. Use of ~~a~~ the polypeptide ~~according to~~as defined in any one of claims 1 to 16, ~~the nucleic acid according to claim 17,~~ the host cell ~~according to~~as defined in claim 18 in the manufacture of a medicament for preventing or treating bacterial infections caused by Gram negative bacteria.

20. Use of the polypeptide ~~according to~~as defined in any one of claims 1 to 16 as non-therapeutic disinfectant against Gram-negative bacteria.