dotted/semi-solid line; SEQ ID NO: 32) and His-tag (underlined with dotted line; SEQ ID NO: 135).

SEQ ID NO: 141 Fusion protein of SMAP-29 (underlined with solid line; SEQ ID NO: 76), modified KZ144 without N-terminal methionine and with T82I, A206V, S232T, I122M; A160T, C14S and C50S (underlined with semi-dotted/semi-solid line; SEQ ID NO: 33) and His-tag (underlined with dotted line; SEQ ID NO: 135).

SEQ ID NO: 142 Fusion protein of SMAP-29 (underlined with solid line; SEQ ID NO: 76), modified KZ144 without N-terminal methionine and with T82I, A206N, S232T, I122M; A160T C14S and C50S (underlined with semi-dotted/semi-solid line; SEQ ID NO: 49) and His-tag (underlined with dotted line; SEQ ID NO: 135).

SEQ ID NO: 151 Fusion protein of SMAP-29 (underlined with solid line; SEQ ID NO: 76), KZ144 without N-terminal methionine (underlined with semi-dotted/semi-solid line; SEQ ID NO: 2) and His-tag (underlined with dotted line; SEQ ID NO: 135).

In a first aspect the present ~~invention~~ disclosure relates to a polypeptide comprising an amino acid sequence exhibiting at least about 90% sequence identity with the sequence of SEQ ID NO: 1, wherein SEQ ID NO: 1 is characterized by

X1 may be absent or any amino acid, in particular M,

X14 may be any amino acid, preferably S, R or N, more preferably S or R

X23 may be any amino acid, preferably S, R or N, more preferably S

X50 may be any amino acid, preferably S, R or N, more preferably S or N

X82 may be any amino acid, preferably T or I

X122 may be any amino acid, preferably I or M

X149 may be any amino acid, preferably M or P

X154 may be any amino acid, preferably L or T

X160 may be any amino acid, preferably A or T

Campylobacter bacteria. In particular, the polypeptide according to the present invention is preferably capable of degrading the peptidoglycan of *Pseudomonas aeroginosa*, in particular *Pseudomonas aeroginosa* PAO1, *Campylobacter jejuni* and/or *Campylobacter coli*.

The peptidoglycan degrading activity on gram negative bacteria can be measured by assays well known in the art, e.g. by muralytic assays in which the outer membrane of gram negative bacteria is permeabilized or removed (e.g. with chloroform) to allow the putative enzyme access to the peptidoglycan layer. If the enzyme is active, degradation of the peptidoglycan layer will lead to a drop of turbidity, which can be measured photometrically (see for example *Briers et al., J. Biochem. Biophys Methods 70: 531-533, (2007)*.

In ~~a further aspect~~an embodiment, the present invention relates to a nucleic acid encoding a polypeptide according to the present invention. A person skilled in the art, having the degeneracy of the genetic code in mind, will be aware of means to generate such nucleic acid.

In ~~a further aspect~~an embodiment, the present invention relates to a vector, such as an expression or cloning vector, which comprises a nucleic acid according to the present invention.

In ~~a further aspect~~an embodiment, the present invention relates to a host cell comprising a polypeptide according to the present invention, a nucleic acid according to the present invention, and/or a vector according to the present invention.

In ~~a further aspect~~an embodiment, the present invention relates to composition comprising a polypeptide according to the present invention, a nucleic acid according to the present invention, a vector according to the present invention, and/or a host cell according to the present invention. Preferably, said composition is a pharmaceutical composition comprising a pharmaceutical acceptable diluent, excipient or carrier.

As set out above, a polypeptide according to the present invention comprises an amino acid sequence exhibiting at least about 90% sequence identity with the sequence of SEQ ID NO: 1, wherein the polypeptide does neither comprise the amino acid sequence of SEQ ID NO: 2, nor of SEQ ID NO: 3, nor of SEQ ID NO: 4. However, in a further ~~aspect~~embodiment, and slightly distinct from the above mentioned polypeptides of the invention, the present invention also relates additionally to a polypeptide comprising an amino acid sequence exhibiting at least

about 90% sequence identity with the sequence of SEQ ID NO: 1, wherein the polypeptide does neither comprise the amino acid sequence of SEQ ID NO: 2, nor of SEQ ID NO: 152, nor of SEQ ID NO: 4. Optionally, said polypeptide of this additional ~~aspect~~ embodiment does also not comprise the amino acid sequence of SEQ ID NO: 3. All embodiments and combinations disclosed above, in the examples or in the claims for the polypeptide of the invention, and respective nucleic acids, vectors, host cells and compositions, are specifically contemplated for this further ~~aspect~~ embodiment as well.

X212 is T or N
X224 is P or Q
X230 is N or Y
X232 is S or T.

4. The polypeptide according to any one of the preceding claims 2 to 3, wherein the sequence exhibiting at least about 90% sequence identity with the sequence of SEQ ID NO: 1 deviates from the sequence of SEQ ID NO: 1 as defined in claims 2 to 3 only at one or more residues selected from X1, X14, X23, X50, X82, X122, X149, X154, X160, X167, X179, X180, X186, X206, X212, X224, X230 and/or X232.

5. The polypeptide according to any one of the preceding claims, wherein the polypeptide exhibits in the amino acid sequence exhibiting at least about 90% sequence identity with the sequence of SEQ ID NO: 1 a glutamic acid residue at position 115.

6. The polypeptide according to any one of the preceding claims, wherein the polypeptide exhibits at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, at least about 99,5% or even 100% sequence identity with the sequence of SEQ ID NO: 1.

7. The polypeptide according to any one of the preceding claims, wherein the polypeptide comprises the sequence of SEQ ID NO: 1.

8. The polypeptide according to any one of the preceding claims, wherein X14 is not C.

9. The polypeptide according to any one of the preceding claims, wherein X23 is not C.

10. The polypeptide according to any one of the preceding claims, wherein X50 is not C.

11. The polypeptide according to any one of the preceding claims, wherein X14 and X23 are not C.

12. The polypeptide according to any one of the preceding claims, wherein X14 and X50 are not C.

13. The polypeptide according to any one of the preceding claims, wherein X23 and X50 are not C.

14. The polypeptide according to any one of the preceding claims, wherein neither X14 nor X23 nor X50 are C.

15. The polypeptide according to any one of the preceding claims, wherein X14 is S.

16. The polypeptide according to any one of the preceding claims 1 to 14, wherein X14 is R.

17. The polypeptide according to any one of the preceding claims, wherein X23 is S.

18. The polypeptide according to any one of the preceding claims, wherein X50 is S.

19. The polypeptide according to any one of the preceding claims 1 to 17 , wherein X50 is N.

20. The polypeptide according to any one of the preceding claims 1 to 15 and 17 to 19, wherein X14 and X23 are S.

21. The polypeptide according to any one of the preceding claims 1 to 15, 17 and 18, wherein X14 and X50 are S.

22. The polypeptide according to any one of the preceding claims 1 to 18, wherein X23 and X50 are S.

23. The polypeptide according to any one of the preceding claims 1 to 15, 17 and 18, wherein X14, X23 and X50 are S.

24. The polypeptide according to claim 16 , wherein X14 is R and X50 is S.

25. The polypeptide according to claim 15 , wherein X14 is S and X50 is N.

26. The polypeptide according to claim 16 , wherein X14 is R and X50 is N.

27. The polypeptide according to claim 16, wherein X149 is P.

28. The polypeptide according to claim 27, wherein X160 is T.

29. The polypeptide according to any one of the preceding claims, wherein X82 is I.

30. The polypeptide according to any one of the preceding claims, wherein X122 is M.

31. The polypeptide according to any one of the preceding claims, wherein X149 is P.

32. The polypeptide according to any one of the preceding claims, wherein X154 is T.

33. The polypeptide according to any one of the preceding claims, wherein X160 is T.

34. The polypeptide according to any one of the preceding claims, wherein X167 is L.

35. The polypeptide according to any one of the preceding claims, wherein X179 is F.

36. The polypeptide according to any one of the preceding claims, wherein X180 is E.

37. The polypeptide according to any one of the preceding claims, wherein X186 is Y.

38. The polypeptide according to any one of the preceding claims, wherein X206 is V.

39. The polypeptide according to any one of the preceding claims, wherein X206 is N.

40. The polypeptide according to any one of the preceding claims, wherein X212 is N.

41. The polypeptide according to any one of the preceding claims, wherein X224 is Q.

42. The polypeptide according to any one of the preceding claims, wherein X230 is Y.

43. The polypeptide according to any one of the preceding claims, wherein X232 is T.

44. The polypeptide according to any one of the preceding claims, wherein X122 is M and X160 is T.

45. The polypeptide according to any one of the preceding claims, wherein X82 is I, X206 is V and X232 is T.

46. The polypeptide according to claim 27, wherein X160 is A.

47. The polypeptide according to claim 45, wherein X122 is M and X160 is T.

48. The polypeptide according to claim 45, wherein, wherein X122 is M.

49. The polypeptide according to claim 21, wherein X122 is M and X160 is T.

50. The polypeptide according to claim 47, wherein X14 is S and X50 is S.

51. The polypeptide according to claim 49, wherein X82 is I, X206 is N and X232 is T.

52. The polypeptide according to claim 51, wherein X149 is P.

53. The polypeptide according to claim 51, wherein M180 is E.

54. The polypeptide according to claim 51, wherein X186 is Y.

55. The polypeptide according to claim 51, wherein X230 is Y.

56. The polypeptide according to claim 24, wherein X82 is I, X122 is M, X206 is V, and X232 is T.

57. The polypeptide according to claim 56, wherein X160 is T.

58. The polypeptide according to claim 56 or claim 57, wherein X149 is P.

59. The polypeptide according to claim 24, wherein X82 is I, X122 is M, X160 is T, X206 is V, and X232 is T.

60. The polypeptide according to claim 25, wherein X82 is I, X122 is M, X160 is T, X206 is V, and X232 is T.

61. The polypeptide according to claim 26, wherein X82 is I, X122 is M, X149 is P, X206 is V, and X232 is T.

62. The polypeptide according to claim 61, wherein X167 is L.

63. The polypeptide according to claim 61, wherein X179 is F.

64. The polypeptide according to claim 61, wherein X212 is N.

65. The polypeptide according to claim 61, wherein X224 is Q

66. The polypeptide according to claim 61, wherein X154 is T.

67. The polypeptide according to any one of the preceding claims, wherein X1 is not M.

68. The polypeptide according to any one of the preceding claims, wherein SEQ ID NO: 1 is a sequence selected from the group consisting of SEQ ID NOs: 6-49.

69. The polypeptide according to any one of the preceding claims, wherein the polypeptide comprises a sequence selected from the group consisting of SEQ ID NOs: 6-49.

70. The polypeptide according to any one of the preceding claims, wherein the polypeptide comprises additionally at least one amino acid sequence stretch selected from the group consisting of amphiphatic peptide, cationic peptide, polycationic peptide, hydrophobic peptide, naturally occurring antimicrobial peptide, sushi peptide and defensin.

71. The polypeptide according to any one of the preceding claims, wherein the polypeptide comprises at least two distinct amino acid sequence stretches selected from the group of

amphiphatic peptide, cationic peptide, polycationic peptide, hydrophobic peptide, naturally occurring antimicrobial peptide, sushi peptide and defensin.

72. The polypeptide according to any one of claims 70 to 71, wherein the at least one amino acid sequence stretch is present at the N- or C-terminus of the polypeptide.

73. The polypeptide according to any one of the preceding claims 70 to 72, wherein the polypeptide comprises at least one additional amino acid sequence stretch selected from the group consisting of: KRK and SEQ ID NOs: 50 - 120.

74. The polypeptide according to any one of the preceding claims 70 to 73, wherein the polypeptide comprises at least one additional amino acid sequence stretch having the amino acid sequence of SMAP-29, SEQ ID NO: 76.

75. The polypeptide according to claim 74, wherein the sequence of SMAP-29, SEQ ID NO: 76, is located in the polypeptide N-terminally of the sequence exhibiting at least about 90% sequence identity with the sequence SEQ ID NO: 1.

76. The polypeptide according to any one of claims 70 to 75, wherein the polypeptide comprises an amino acid sequence exhibiting at least 91,5% sequence identity with an amino acid sequence selected from any of SEQ ID NOs: 121-134, wherein the polypeptide does neither comprise the amino acid sequence of SEQ ID NO: 2, nor SEQ ID NO: 3, nor SEQ ID NO: 4.

77. The polypeptide according to claim 76, wherein the polypeptide comprises an amino acid sequence exhibiting at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 98,5%, at least about 98,75%, at least about 99%, or at least about 99,5% sequence identity with an amino acid sequence selected from any of SEQ ID NOs: 121-134.

78. The polypeptide according to any one of the preceding claims, wherein the polypeptide comprises a sequence selected from from the group consisting of SEQ ID NOs: 121-134.

79. The polypeptide according to any one of the preceding claims, wherein the polypeptide comprises additionally a tag sequence.

80. The polypeptide according to claim 79, wherein the tag is located C-terminally of the amino acid sequence exhibiting at least 90% sequence identity with the sequence of SEQ ID NO: 1.

81. The polypeptide according to any one claims 79 to 80, wherein the tag is linked to the amino acid sequence exhibiting at least 90% sequence identity with the sequence of SEQ ID NO: 1 directly or via a short linker of 1 to 10 amino acid residues, preferably 1 to 5 amino acid residues, even more preferably 1 to 2 amino acids.

82. The polypeptide according to any one claims 79 to 81, wherein the polypeptide comprises a His-tag, preferably a His tag according to SEQ ID NO: 135.

83. The polypeptide according to any one of claims 79 to 82, wherein the polypeptide comprises an amino acid sequence exhibiting at least 91,5% sequence identity with an amino acid sequence selected from any of SEQ ID NOs: 136-149, wherein the polypeptide does neither comprise the amino acid sequence of SEQ ID NO: 2 nor SEQ ID NO: 3.

84. The polypeptide according to claim 83, wherein the polypeptide comprises an amino acid sequence exhibiting at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 98,5%, at least about 98,75%, at least about 99%, or at least about 99,5% sequence identity with an amino acid sequence selected from any of SEQ ID NOs: 136-149.

85. The polypeptide according to any one of the preceding claims, wherein the polypeptide has an overall length not exceeding about 320 amino acids, preferably not exceeding about 310 amino acids.

86. The polypeptide according to any one of the preceding claims, wherein the polypeptide comprises a sequence selected from the group consisting of SEQ ID NOs: 136-149.

87. The polypeptide according to any one of the preceding claims, wherein the polypeptide degrades the peptidoglycan of Gram-negative bacteria, in particular of Pseudomonas and/or Campylobacter bacteria.

88. Nucleic acid encoding a polypeptide according to any one of claims 1 to 87.

89. Vector comprising a nucleic acid according to claim 88.

90. Host cell comprising a polypeptide according to any one of claims 1 to 87, a nucleic acid according to claim 88, and/or a vector according to claim 89.

91. Composition comprising a polypeptide according to any one of claims 1 to 87, a nucleic acid according to claim 88, a vector according to claim 89 and/or a host cell according to claim 90.

92. Composition according to claim 91, wherein the composition is a pharmaceutical composition comprising a pharmaceutical acceptable diluent, excipient or carrier.

X212 is T or N

X224 is P or Q

X230 is N or Y

X232 is S or T.

4. The polypeptide according to any one of the preceding claims 2 to 3, wherein the sequence exhibiting at least about 90% sequence identity with the sequence of SEQ ID NO: 1 deviates from the sequence of SEQ ID NO: 1 as defined in claims 2 to 3 only at one or more residues selected from X1, X14, X23, X50, X82, X122, X149, X154, X160, X167, X179, X180, X186, X206, X212, X224, X230 and/or X232.

5. The polypeptide according to any one of the preceding claims, wherein the polypeptide exhibits in the amino acid sequence exhibiting at least about 90% sequence identity with the sequence of SEQ ID NO: 1 a glutamic acid residue at position 115.

6. The polypeptide according to any one of the preceding claims, wherein the polypeptide comprises the sequence of SEQ ID NO: 1.

7. The polypeptide according to any one of the preceding claims, wherein X14, X23 and/or X50 is not C.

8. The polypeptide according to any one of the preceding claims, wherein SEQ ID NO: 1 is a sequence selected from the group consisting of SEQ ID NOs: 6-49.

9. The polypeptide according to any one of the preceding claims, wherein the polypeptide comprises a sequence selected from the group consisting of SEQ ID NOs: 6-49.

10. The polypeptide according to any one of the preceding claims, wherein the polypeptide comprises at least one additional amino acid sequence stretch selected from the group consisting of: KRK and SEQ ID NOs: 50 - 120.

11. The polypeptide according to any one of the preceding claims, wherein the polypeptide comprises at least one additional amino acid sequence stretch having the amino acid sequence of SMAP-29, SEQ ID NO: 76.

12. The polypeptide according to any one of the preceding claims, wherein the polypeptide comprises an amino acid sequence exhibiting at least 91,5% sequence identity with an amino acid sequence selected from any of SEQ ID NOs: 121-134, wherein the polypeptide does neither comprise the amino acid sequence of SEQ ID NO: 2, nor SEQ ID NO: 3, nor SEQ ID NO: 4.

13. The polypeptide according to any one of the preceding claims, wherein the polypeptide comprises a sequence selected from the group consisting of SEQ ID NOs: 121-134 or comprises a sequence selected from the group consisting of SEQ ID NOs: 136-149.

14. The polypeptide according to any one of the preceding claims, wherein the polypeptide degrades the peptidoglycan of Gram-negative bacteria, in particular of Pseudomonas and/or Campylobacter bacteria.