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 one aspect the present 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

X167 may be any amino acid, preferably I or L

X179 may be any amino acid, preferably N or F

X180 may be any amino acid, preferably M or E

X186 may be any amino acid, preferably V or Y

X206 may be any amino acid, preferably A, N or V

X212 may be any amino acid, preferably T or N

X224 may be any amino acid, preferably P or Q

X230 may be any amino acid, preferably N or Y

X232 may be any amino acid, preferably S or T;

and 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.

In another aspect, there is provided 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,

X14 may be any amino acid,

X23 may be any amino acid,

X50 may be any amino acid,

X82 may be any amino acid,

X122 may be any amino acid,

X149 may be any amino acid,

X154 may be any amino acid,

X160 may be any amino acid,

X167 may be any amino acid,

X179 may be any amino acid,

X180 may be any amino acid,

X186 may be any amino acid,

X206 may be any amino acid,

X212 may be any amino acid,

X224 may be any amino acid,

X230 may be any amino acid,

X232 may be any amino acid;

and wherein the polypeptide exhibits in the amino acid sequence exhibiting at least about 90% sequence identity with the sequence of SEQ ID NO: 1 at least one of the following:

X14	is not C;
X23	is not C;
X50	is not C;
X82	is I
X122	is M
X149	is P
X154	is T
X160	is T
X167	is L
X179	is F
X180	is E
X186	is Y
X206	is N or V
X212	is N
X224	is Q
X230	is Y and/or
X232	is T,

and 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.

The term "polypeptide" as used herein refers in particular to a polymer of amino acid residues linked by peptide bonds in a specific sequence. The amino acid residues of a polypeptide 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, such as heme or lipid, giving rise to conjugated polypeptides which are also comprised by the term "polypeptide" as used herein. The term as used herein is intended to encompass also proteins. Thus, the term "polypeptide" also encompasses for example complexes of two or more amino acid polymer chains. The term "polypeptide " does encompass embodiments of polypeptides which exhibit optionally modifications typically used in the art, e.g. biotinylation, acetylation,

pegylation, chemical changes of the amino-, SH- or carboxyl-groups (e.g. protecting groups) etc.. As will become apparent from the description below, the polypeptide according to the present invention may also be a fusion protein, i.e. linkage of at least two amino acid sequences which do not occur in this combination in nature. The term " polypeptide " as used herein is not limited to a specific length of the amino acid polymer chain, but typically the polypeptide will exhibit a length of more than about 50 amino acids, more than about 100 amino acids or even more than about 150 amino acids. Usually, but not necessarily, a typical polypeptide of the present invention will not exceed about 750 amino acids in length.

As used herein, the term "% sequence identity", has to be understood as follows: Two sequences to be compared are aligned to give a maximum correlation between the sequences. This may include inserting "gaps" in either one or both sequences, to enhance the degree of alignment. A % identity may then be determined over the whole length of each of the

Claims

1. 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,
X14	may be any amino acid,
X23	may be any amino acid,
X50	may be any amino acid,
X82	may be any amino acid,
X122	may be any amino acid,
X149	may be any amino acid,
X154	may be any amino acid,
X160	may be any amino acid,
X167	may be any amino acid,
X179	may be any amino acid,
X180	may be any amino acid,
X186	may be any amino acid,
X206	may be any amino acid,
X212	may be any amino acid,
X224	may be any amino acid,
X230	may be any amino acid,
X232	may be any amino acid;

and wherein the polypeptide exhibits in the amino acid sequence exhibiting at least about 90% sequence identity with the sequence of SEQ ID NO: 1 at least one of the following:

X14 is not C;
X23 is not C;
X50 is not C;
X82 is I
X122 is M
X149 is P
X154 is T
X160 is T
X167 is L
X179 is F
X180 is E
X186 is Y
X206 is N or V
X212 is N
X224 is Q
X230 is Y and/or
X232 is T,

and 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.

2. Polypeptide according to claim 1, wherein:

X14 is S, R or N,
X23 is S, R or N,
X50 is S, R or N,
X82 is T or I
X122 is I or M
X149 is M or P
X154 is L or T
X160 is A or T
X167 is I or L
X179 is N or F
X180 is M or E
X186 is V or Y
X206 is A, N or V

X212 is T or N

X224 is P or Q

X230 is N or Y

X232 is S or T.

3. The polypeptide according to any one of the preceding claims, 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 claim 1 or 2 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.

4. 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.

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

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

7. 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.

8. 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.

9. 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.

10. 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.

11. 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.

12. 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.

13. 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.