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Készítmények Staphylococcus aureus elleni immunizálásra

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(54) **Compositions for immunising against Staphylococcus aureus**

Zusammensetzungen zur Immunisierung gegen Staphylococcus aureus

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WO-A2-02/094868

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- **DATABASE Geneseq [Online] 20 November 2003 (2003-11-20), XP002601982, retrieved from EBI accession no. GSP:ABM72354 Database accession no. ABM72354**

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Description**TECHNICAL FIELD**

5 [0001] This invention relates to antigens derived from *S.aureus* and to their use in immunisation.

BACKGROUND ART

10 [0002] *Staphylococcus aureus* is a Gram-positive spherical bacterium. Annual US mortality exceeds that of any other infectious disease, including HIV/AIDS, and *S.aureus* is the leading cause of bloodstream, lower respiratory tract, skin & soft tissue infections. There is currently no authorised vaccine. A vaccine based on a mixture of surface polysaccharides from bacterial types 5 and 8, StaphVAX™, failed to reduce infections when compared to the placebo group in a phase III clinical trial in 2005.

15 [0003] Reference 1 reports that the "V710" vaccine from Merck and InterCell is undergoing a phase 2/3 trial on patients undergoing cardiothoracic surgery. The V710 vaccine is based on a single antigen, IsdB [2], a conserved iron-sequestering cell-surface protein.

[0004] WO 02/094868 discloses 5642 proteins, one of them being sta006, for use as a vaccine.

20 [0005] *S.aureus* causes a range of illnesses from minor skin infections to life-threatening diseases such as pneumonia, meningitis, osteomyelitis, bacteremia, endocarditis, toxic shock syndrome, organ abscesses and septicemia. The bacterium has multiple virulence factors which are differentially expressed during different phases of its life cycle, and so a vaccine which can prevent one disease might not prevent another. For instance, the V710 vaccine may be effective against hematic spread of the *S.aureus*, but may be ineffective against pneumonia and may not elicit any opsonic activity. One aim of the invention is to provide vaccines which can protect against hematic spread and pneumonia, and which may also elicit an opsonic response.

25 [0006] Thus there remains a need to identify further and improved antigens for use in *S.aureus* vaccines, and in particular for vaccines which are useful against multiple *S.aureus* pathologies.

DISCLOSURE OF THE INVENTION

30 [0007] The inventors have identified various *S.aureus* polypeptides that are useful for immunisation, either alone or in combination. These polypeptides may be combined with *S.aureus* saccharides or other *S.aureus* polypeptides. The antigens are useful in *S.aureus* vaccines but may also be used as components in vaccines for immunising against multiple pathogens.

35 [0008] The inventors have identified the following 36 polypeptides: clfA, clfB, coA, eap, ebhA, ebpS, efb, emp, esaC, esxA, esxB, FnBA, FnBB, Hla, hlgB, hlgC, isdA, isdB, isdC, isdG, isdH, isdI, lukD, lukE, lukF, lukS, nuc, sasA, sasB, sasC, sasD, sasF, sdrC, sdrD, spa, and sdrE2. This set of antigens is referred to herein as the first antigen group'. Thus the invention provides an immunogenic composition comprising a combination of antigens, said combination comprising two or more (*i.e.* 2, 3, 4, 5, 6 or more) antigens selected from the group consisting of: (1) a clfA antigen; (2) a clfB antigen; (3) a coA antigen; (4) a eap antigen; (5) a ebhA antigen; (6) a ebpS antigen; (7) a efb antigen; (8) a emp antigen; (9) a esaC antigen; (10) a esxA antigen; (11) a esxB antigen; (12) a FnBA antigen; (13) a FnBB antigen; (14) a Hla antigen; (15) a hlgB antigen; (16) a hlgC antigen; (17) a isdA antigen; (18) a isdB antigen; (19) a isdC antigen; (20) a isdG antigen; (21) a isdH antigen; (22) a isdI antigen; (23) a lukD antigen; (24) a lukE antigen; (25) a lukF antigen; (26) a lukS antigen; (27) a nuc antigen; (28) a sasA antigen; (29) a sasB antigen; (30) a sasC antigen; (31) a sasD antigen; (32) a sasF antigen; (33) a sdrC antigen; (34) a sdrD antigen; (35) a spa antigen; (36) a sdrE2 antigen.

45 [0009] Within the first antigen group, antigens are preferably selected from a subset of 16 of the 36 polypeptides, namely: clfA, clfB, emp, esaC, esxA, esxB, hla, isdA, isdB, isdC, sasD, sasF, sdrC, sdrD, spa, and sdrE2. Thus the invention provides an immunogenic composition comprising a combination of antigens, said combination comprising two or more (*i.e.* 2, 3, 4, 5, 6 or more) antigens selected from the group consisting of these sixteen antigens.

50 [0010] The inventors have also identified the following 128 polypeptides: sta001, sta002, sta003, sta004, sta005, sta006, sta007, sta008, sta009, sta010, sta011, sta012, sta013, sta014, sta015, sta016, sta017, sta018, sta019, sta020, sta021, sta022, sta023, sta024, sta025, sta026, sta027, sta028, sta029, sta030, sta031, sta032, sta033, sta034, sta035, sta036, sta037, sta038, sta039, sta040, sta041, sta042, sta043, sta044, sta045, sta046, sta047, sta048, sta049, sta050, sta051, sta052, sta053, sta054, sta055, sta056, sta057, sta058, sta059, sta060, sta061, sta062, sta063, sta064, sta065, sta066, sta067, sta068, sta069, sta070, sta071, sta072, sta073, sta074, sta075, sta076, sta077, sta078, sta079, sta080, sta081, sta082, sta083, sta084, sta085, sta086, sta087, sta088, sta089, sta090, sta091, sta092, sta093, sta094, sta095, sta096, sta097, sta098, sta099, sta100, sta101, sta102, sta103, sta104, sta105, sta106, sta107, sta108, sta109, sta110, sta111, sta112, sta113, sta114, sta115, sta116, sta117, sta118, sta119, sta 120, NW 6, NW_9, NW_10, NW_7, NW_8, NW_2, NW_1, and NW_5. This set of antigens is referred to herein as 'the second antigen group'. Thus the invention

provides an immunogenic composition comprising a combination of antigens, said combination comprising two or more (*i.e.* 2, 3, 4, 5, 6 or more) antigens selected from the group consisting of: (1) a sta001 antigen; (2) a sta002 antigen; (3) a sta003 antigen; (4) a sta004 antigen; (5) a sta005 antigen; (6) a sta006 antigen; (7) a sta007 antigen; (8) a sta008 antigen; (9) a sta009 antigen; (10) a sta010 antigen; (11) a sta011 antigen; (12) a sta012 antigen; (13) a sta013 antigen; (14) a sta014 antigen; (15) a sta015 antigen; (16) a sta016 antigen; (17) a sta017 antigen; (18) a sta018 antigen; (19) a sta019 antigen; (20) a sta020 antigen; (21) a sta021 antigen; (22) a sta022 antigen; (23) a sta023 antigen; (24) a sta024 antigen; (25) a sta025 antigen; (26) a sta026 antigen; (27) a sta027 antigen; (28) a sta028 antigen; (29) a sta029 antigen; (30) a sta030 antigen; (31) a sta031 antigen; (32) a sta032 antigen; (33) a sta033 antigen; (34) a sta034 antigen; (35) a sta035 antigen; (36) a sta036 antigen; (37) a sta037 antigen; (38) a sta038 antigen; (39) a sta039 antigen; (40) a sta040 antigen; (41) a sta041 antigen; (42) a sta042 antigen; (43) a sta043 antigen; (44) a sta044 antigen; (45) a sta045 antigen; (46) a sta046 antigen; (47) a sta047 antigen; (48) a sta048 antigen; (49) a sta049 antigen; (50) a sta050 antigen; (51) a sta051 antigen; (52) a sta052 antigen; (53) a sta053 antigen; (54) a sta054 antigen; (55) a sta055 antigen; (56) a sta056 antigen; (57) a sta057 antigen; (58) a sta058 antigen; (59) a sta059 antigen; (60) a sta060 antigen; (61) a sta061 antigen; (62) a sta062 antigen; (63) a sta063 antigen; (64) a sta064 antigen; (65) a sta065 antigen; (66) a sta066 antigen; (67) a sta067 antigen; (68) a sta068 antigen; (69) a sta069 antigen; (70) a sta070 antigen; (71) a sta071 antigen; (72) a sta072 antigen; (73) a sta073 antigen; (74) a sta074 antigen; (75) a sta075 antigen; (76) a sta076 antigen; (77) a sta077 antigen; (78) a sta078 antigen; (79) a sta079 antigen; (80) a sta080 antigen; (81) a sta081 antigen; (82) a sta082 antigen; (83) a sta083 antigen; (84) a sta084 antigen; (85) a sta085 antigen; (86) a sta086 antigen; (87) a sta087 antigen; (88) a sta088 antigen; (89) a sta089 antigen; (90) a sta090 antigen; (91) a sta091 antigen; (92) a sta092 antigen; (93) a sta093 antigen; (94) a sta094 antigen; (95) a sta095 antigen; (96) a sta096 antigen; (97) a sta097 antigen; (98) a sta098 antigen; (99) a sta099 antigen; (100) a sta100 antigen; (101) a sta101 antigen; (102) a sta102 antigen; (103) a sta103 antigen; (104) a sta104 antigen; (105) a sta105 antigen; (106) a sta106 antigen; (107) a sta107 antigen; (108) a sta108 antigen; (109) a sta109 antigen; (110) a sta110 antigen; (111) a sta111 antigen; (112) a sta112 antigen; (113) a sta113 antigen; (114) a sta114 antigen; (115) a sta115 antigen; (116) a sta116 antigen; (117) a sta117 antigen; (118) a sta118 antigen; (119) a sta119 antigen; (120) a sta120 antigen; (121) a NW_6 antigen; (122) a NW_9 antigen; (123) a NW_10 antigen; (124) a NW_7 antigen; (125) a NW_8 antigen; (126) a NW_2 antigen; (127) a NW_1 antigen; and (128) a NW_5 antigen.

[0011] Within the second antigen group of 128 antigens, a preferred subset of 113 antigens omits (81) and (107) to (120) from this list.

[0012] Within the second antigen group, a subset of 27 of the 128 polypeptides is referred to herein as 'the third antigen group', namely: sta001, sta002, sta003, sta004, sta005, sta006, sta007, sta008, sta009, sta010, sta019, sta028, sta040, sta049, sta057, sta064, sta073, sta095, sta098, sta101, sta105, NW_1, NW_6, NW_7, NW_8, NW_9 and NW_10. The invention provides an immunogenic composition comprising a combination of antigens, said combination comprising two or more (*i.e.* 2, 3, 4, 5, 6 or more) antigens selected from the third antigen group.

[0013] The 101 antigens that are in the second antigen group but not in the third antigen group are referred to herein as 'the fourth antigen group'. Within the fourth antigen group of 101 antigens, a preferred subset of 86 antigens omits (81) and (107) to (120) from the above list. The second antigen group thus consists of a combination of the third and fourth antigen groups.

[0014] Within the second antigen group, a subset of 8 of the 128 polypeptides is referred to herein as 'the fifth antigen group', namely: sta004, sta006, sta007, sta011, sta028, sta060, sta098 and sta112. The invention provides an immunogenic composition comprising a combination of antigens, said combination comprising two or more (*i.e.* 2, 3, 4, 5, 6 or more) antigens selected from the fifth antigen group.

[0015] Within the 36 antigens of the first antigen group there are 630 possible pairs of different antigens. All such pairs are disclosed herein and are part of the invention. Thus the invention provides an immunogenic composition comprising a pair of antigens, wherein said pair is one of said 630 pairs.

[0016] Within the 128 antigens of the second antigen group there are 8128 possible pairs of different antigens. All such pairs are disclosed herein and are part of the invention. Thus the invention provides an immunogenic composition comprising a pair of antigens, wherein said pair is one of said 8128 pairs.

[0017] Within the preferred 113 antigens of the second antigen group there are 6328 possible pairs of different antigens. All such pairs are disclosed herein and are part of the invention. Thus the invention provides an immunogenic composition comprising a pair of antigens, wherein said pair is one of said 6328 pairs.

[0018] Within the preferred 27 antigens of the third antigen group there are 351 possible pairs of different antigens. All such pairs are disclosed herein and are part of the invention. Thus the invention provides an immunogenic composition comprising a pair of antigens, wherein said pair is one of said 351 pairs.

[0019] Within the 101 antigens of the fourth antigen group there are 5050 possible pairs of different antigens. All such pairs are disclosed herein and are part of the invention. Thus the invention provides an immunogenic composition comprising a pair of antigens, wherein said pair is one of said 5050 pairs.

[0020] Within the preferred 86 antigens of the fourth antigen group there are 3655 possible pairs of different antigens.

All such pairs are disclosed herein and are part of the invention. Thus the invention provides an immunogenic composition comprising a pair of antigens, wherein said pair is one of said 3655 pairs.

[0021] In one embodiment, a composition includes at least one antigen (*i.e.* 1, 2, 3, 4, 5, 6 or more) selected from the first antigen group and at least one antigen (*i.e.* 1, 2, 3, 4, 5, 6 or more) selected from the second antigen group. Antigens from the first antigen group may be selected from the preferred subset of 16 antigens, and antigens from the second antigen group may be selected from the third antigen group or the fifth antigen group.

[0022] The invention also provides an immunogenic composition comprising a combination of antigens, said combination comprising two or more (*i.e.* 2, 3, 4, 5, 6 or more) antigens selected from the group consisting of: (1) a *clfA* antigen; (2) a *clfB* antigen; (3) a *sdrE2* antigen; (4) a *sdrC* antigen; (5) a *SasF* antigen; (6) a *emp* antigen; (7) a *sdrD* antigen; (8) a *spa* antigen; (9) a *esaC* antigen; (10) a *esxA* antigen; (11) a *esxB* antigen; (12) a *sta006* antigen; (13) a *isdC* antigen; (14) a *hla* antigen; (15) a *sta011* antigen; (16) *isdA* antigen; (17) a *isdB* antigen; (18) a *sasF* antigen. This group of 18 antigens is sometimes referred to herein as the 'sixth antigen group'.

[0023] The invention also provides an immunogenic composition comprising a combination of antigens, said combination comprising two or more (*i.e.* 2, 3, 4 or 5) antigens selected from the group consisting of: (1) a *esxA* antigen; (2) a *esxB* antigen; (3) a *sta006* antigen; (4) a *hla* antigen; and/or (5) a *sta011* antigen. The composition may also include an adjuvant *e.g.* an aluminium hydroxide adjuvant.

[0024] Advantageous combinations of the invention are those in which two or more antigens act synergistically. Thus the protection against *S.aureus* disease achieved by their combined administration exceeds that expected by mere addition of their individual protective efficacy.

[0025] Specific combinations of interest include, but are not limited to:

(1) An immunogenic composition comprising a *sdrD* antigen, a *sdrE2* antigen and a *isdC* antigen. The *sdrD* and *sdrE2* antigens can usefully be combined as a hybrid polypeptide, as discussed below, *e.g.* an *SdrDE* hybrid with an *sdrE2* antigen downstream of a *sdrD* antigen.

(2) An immunogenic composition comprising a *sasD* antigen, a *clfB* antigen and a *sdrC* antigen.

(3) An immunogenic composition comprising a *sasD* antigen, a *clfB* antigen, a *sdrC* antigen and a *clfA* antigen.

(4) An immunogenic composition comprising a *sdrD* antigen, a *sdrE2* antigen, a *isdC* antigen and a *sta011* antigen. The *sdrD* and *sdrE2* antigens can usefully be combined as a hybrid polypeptide, as discussed below, *e.g.* a *SdrDE* hybrid with a *sdrE2* antigen downstream of a *sdrD* antigen.

(5) An immunogenic composition comprising a *sasD* antigen, a *clfB* antigen, a *sdrC* antigen and a *sta006* antigen.

(6) An immunogenic composition comprising a *sdrD* antigen, a *sdrE2* antigen, a *isdC* antigen and a *hla* antigen. The *sdrD* and *sdrE2* antigens can usefully be combined as a hybrid polypeptide, as discussed below, *e.g.* a *SdrDE* hybrid with a *sdrE2* antigen downstream of a *sdrD* antigen. The *Hla* antigen may be a detoxified mutant *e.g.* including a H35L mutation.

(7) An immunogenic composition comprising a *sasD* antigen, a *clfB* antigen, a *sdrC* antigen and a *esxA* antigen.

(8) An immunogenic composition comprising a *esxA* antigen, a *esxB* antigen, a *sta006* antigen and a *hla* antigen. The *esxA* and *esxB* antigens can usefully be combined as a hybrid polypeptide, as discussed below, *e.g.* a *EsxAB* hybrid with a *esxB* antigen downstream of a *esxA* antigen. The *Hla* antigen may be a detoxified mutant *e.g.* including a H35L mutation.

(9) An immunogenic composition comprising a *sdrD* antigen, a *sdrE2* antigen, a *isdC* antigen and a *esxA* antigen. The *sdrD* and *sdrE2* antigens can usefully be combined as a hybrid polypeptide, as discussed below, *e.g.* a *SdrDE* hybrid with a *sdrE2* antigen downstream of a *sdrD* antigen.

(10) An immunogenic composition comprising a *esxA* antigen, a *esxB* antigen, a *sta006* antigen and a *sta011* antigen. The *esxA* and *esxB* antigens may be combined as a hybrid polypeptide, as discussed below, *e.g.* an *EsxAB* hybrid.

(11) An immunogenic composition comprising a *esxA* antigen, a *esxB* antigen and a *sta011* antigen. The *esxA* and *esxB* antigens can usefully be combined as a hybrid polypeptide, as discussed below, *e.g.* a *EsxAB* hybrid with a *esxB* antigen downstream of a *esxA* antigen.

(12) An immunogenic composition comprising a sasD antigen, a clfB antigen, a sdrC antigen and a spa antigen.

(13) An immunogenic composition comprising a esxA antigen, a esxB antigen, a isdA antigen, a sta006 antigen, a sta011 antigen and a spa antigen. The esxA and esxB antigens may be combined as a hybrid polypeptide, as discussed below, e.g. an EsxAB hybrid. The isdA antigen may be a fragment of a full-length isdA antigen e.g. SEQ ID NO: 157. The spa antigen may be a fragment of a full-length spa antigen, such as a Spa(D) domain mutated to disrupt or decrease binding to IgG Fc.

(14) An immunogenic composition comprising a esxA antigen, a esxB antigen, a Hla antigen, a sta006 antigen and a sta011 antigen. The esxA and esxB antigens may be combined as a hybrid polypeptide, as discussed below, e.g. an EsxAB hybrid. The Hla antigen may be a detoxified mutant e.g. including a H35L mutation.

(15) An immunogenic composition comprising a sdrD antigen, a sdrE2 antigen, a isdC antigen and a sdrE2 antigen. The sdrD and sdrE2 antigens can usefully be combined as a hybrid polypeptide, as discussed below, e.g. a SdrDE hybrid with a sdrE2 antigen downstream of a sdrD antigen.

(16) An immunogenic composition comprising a esxA antigen, a esxB antigen and a hla antigen. The esxA and esxB antigens can usefully be combined as a hybrid polypeptide, as discussed below, e.g. a EsxAB hybrid with a esxB antigen downstream of a esxA antigen. The Hla antigen may be a detoxified mutant e.g. including a H35L mutation.

(17) An immunogenic composition comprising a hla antigen, a isdA antigen, a sta006 antigen and a sta011 antigen. The isdA antigen may be a fragment of a full-length isdA antigen e.g. SEQ ID NO: 157. The Hla antigen may be a detoxified mutant e.g. including a H35L mutation.

(18) An immunogenic composition comprising a esxA antigen, a esxB antigen, a sta006 antigen and a isdA antigen. The esxA and esxB antigens can usefully be combined as a hybrid polypeptide, as discussed below, e.g. a EsxAB hybrid with a esxB antigen downstream of a esxA antigen. The isdA antigen may be a fragment of a full-length isdA antigen e.g. SEQ ID NO: 157.

(19) An immunogenic composition comprising a sasD antigen, a clfB antigen, a sdrC antigen and a hla antigen. The Hla antigen may be a detoxified mutant e.g. including a H35L mutation.

(20) An immunogenic composition comprising a Hla antigen, a sta006 antigen and a sta011 antigen. The Hla antigen may be a detoxified mutant e.g. including a H35L mutation.

(21) An immunogenic composition comprising a esxA antigen and a esxB antigen. The esxA and esxB antigens can usefully be combined as a hybrid polypeptide, as discussed below, e.g. an EsxAB hybrid with an esxB antigen downstream of an esxA antigen.

(22) An immunogenic composition comprising a esxA antigen, a esxB antigen and a sta006 antigen. The esxA and esxB antigens can usefully be combined as a hybrid polypeptide, as discussed below, e.g. a EsxAB hybrid with a esxB antigen downstream of a esxA antigen.

(23) An immunogenic composition comprising a spa antigen, a sta006 antigen and a sta011 antigen. The spa antigen may be a fragment of a full-length spa antigen, such as a Spa(D) domain mutated to disrupt or decrease binding to IgG Fc.

(24) An immunogenic composition comprising a esxA antigen, a esxB antigen, a isdA antigen, a sta006 antigen and a sta011 antigen. The esxA and esxB antigens may be combined as a hybrid polypeptide, as discussed below, e.g. an EsxAB hybrid. The isdA antigen may be a fragment of a full-length isdA antigen e.g. SEQ ID NO: 157.

(25) An immunogenic composition comprising a sta006 antigen and a sta011 antigen.

(26) An immunogenic composition comprising a esxA antigen, a esxB antigen, a sta006 antigen, a isdA antigen and a clfB antigen. The esxA and esxB antigens can usefully be combined as a hybrid polypeptide, as discussed below, e.g. a EsxAB hybrid with a esxB antigen downstream of a esxA antigen. The isdA antigen may be a fragment of a full-length isdA antigen e.g. SEQ ID NO: 157. The clfB antigen may be a fragment of a full-length clfB antigen e.g.

SEQ ID NO: 163.

(27) An immunogenic composition comprising a sta006 antigen, a sta011 antigen and a sta019 antigen.

(28) An immunogenic composition comprising a esxA antigen, a esxB antigen, a sta006 antigen, a hla antigen and a clfB antigen. The esxA and esxB antigens can usefully be combined as a hybrid polypeptide, as discussed below, e.g. a EsxAB hybrid with a esxB antigen downstream of a esxA antigen. The clfB antigen may be a fragment of a full-length clfB antigen e.g. SEQ ID NO: 163. The Hla antigen may be a detoxified mutant e.g. including a H35L mutation.

(29) An immunogenic composition comprising a sta006 antigen, a sta011 antigen, a sta019 antigen, and a hla antigen. The Hla antigen may be a detoxified mutant e.g. including a H35L mutation.

(30) An immunogenic composition comprising a esxA antigen, a esxB antigen, a sta006 antigen, a sta011 antigen and a clfB antigen. The esxA and esxB antigens can usefully be combined as a hybrid polypeptide, as discussed below, e.g. a EsxAB hybrid with a esxB antigen downstream of a esxA antigen. The clfB antigen may be a fragment of a full-length clfB antigen e.g. SEQ ID NO: 163.

(31) An immunogenic composition comprising a spa antigen, a esxA antigen, a esxB antigen, a sta006 antigen and a sta011 antigen. The spa antigen may be a fragment of a full-length spa antigen, such as a Spa(D) domain mutated to disrupt or decrease binding to IgG Fc. The esxA and esxB antigens may be combined as a hybrid polypeptide, as discussed below, e.g. an EsxAB hybrid.

(32) An immunogenic composition comprising a sdrD antigen, a sdrE2 antigen, a isdC antigen and a esxB antigen. The sdrD and sdrE2 antigens can usefully be combined as a hybrid polypeptide, as discussed below, e.g. a SdrDE hybrid with a sdrE2 antigen downstream of a sdrD antigen.

(33) An immunogenic composition comprising a esxA antigen, a esxB antigen, a sta006 antigen, a sta011 antigen and a sta019 antigen. The esxA and esxB antigens can usefully be combined as a hybrid polypeptide, as discussed below, e.g. a EsxAB hybrid with a esxB antigen downstream of a esxA antigen.

(34) An immunogenic composition comprising a esxA antigen, a esxB antigen, a sta006 antigen, a isdA antigen and a sdrD antigen. The esxA and esxB antigens can usefully be combined as a hybrid polypeptide, as discussed below, e.g. a EsxAB hybrid with a esxB antigen downstream of a esxA antigen. The isdA antigen may be a fragment of a full-length isdA antigen e.g. SEQ ID NO: 157. The sdrD antigen may be a fragment of a full-length sdrD antigen e.g. SEQ ID NO: 156.

(35) An immunogenic composition comprising a esxA antigen, a esxB antigen, and a isdA antigen. The esxA and esxB antigens can usefully be combined as a hybrid polypeptide, as discussed below, e.g. a EsxAB hybrid with a esxB antigen downstream of a esxA antigen. The isdA antigen may be a fragment of a full-length isdA antigen e.g. SEQ ID NO: 157.

(36) An immunogenic composition comprising a sasD antigen, a clfB antigen, a sdrC antigen, a esxA antigen and a esxB antigen. The esxA and esxB antigens can usefully be combined as a hybrid polypeptide, as discussed below, e.g. an EsxAB hybrid with an esxB antigen downstream of an esxA antigen.

(37) An immunogenic composition comprising a Hla antigen, a spa antigen, a sta006 antigen and a sta011 antigen. The Hla antigen may be a detoxified mutant e.g. including a H35L mutation. The spa antigen may be a fragment of a full-length spa antigen, such as a Spa(D) domain mutated to disrupt or decrease binding to IgG Fc.

[0026] In some embodiments, any of these 37 compositions may include additional staphylococcal antigens, and these further antigens can be polypeptides and/or saccharides. For example, they can usefully also include one or more *S.aureus* capsular saccharide conjugate(s) e.g. against a serotype 5 and/or a serotype 8 strain. The inclusion of one or both such conjugates is particularly useful for combinations (8), (10), (20), (23), (25), (31) and (37).

[0027] In other embodiments, these 37 compositions include no additional staphylococcal polypeptide antigens. In other embodiments, these 37 compositions include no additional staphylococcal antigens. In other embodiments, these 37 compositions include no additional antigens.

[0028] The invention also provides a polypeptide comprising amino acid sequence (a) having 80% or more identity

(e.g. 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ-ID NO: 15-1; and/or (b) comprising a fragment of at least 'n' consecutive amino acids from amino acids 1-97 of SEQ ID NO: 151 and at least 'n' consecutive amino acids from amino acids 104-207 of SEQ ID NO: 151, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). The invention also provides a polypeptide comprising amino acid sequence (a) having 80% or more identity (e.g. 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 152; and/or (b) comprising a fragment of at least 'n' consecutive amino acids from amino acids 1-104 of SEQ ID NO: 152 and at least 'n' consecutive amino acids from amino acids 111-207 of SEQ ID NO: 152, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These polypeptides can elicit antibodies (e.g. when administered to a human) which recognise both the wild-type staphylococcal protein comprising SEQ ID NO: 10 and the wild-type staphylococcal protein comprising SEQ ID NO: 11. Thus the immune response will recognise both of antigens *esxA* and *esxB*. Preferred fragments of (b) provide an epitope from SEQ ID NO: 10 and an epitope from SEQ ID NO: 11. The invention also provides an immunogenic composition comprising a combination of such a protein and an adjuvant, such as an aluminium hydroxide adjuvant.

[0029] The invention also provides a polypeptide comprising amino acid sequence (a) having 80% or more identity (e.g. 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 241; and/or (b) comprising both a fragment of at least 'n' consecutive amino acids from amino acids 1-96 of SEQ ID NO: 241 and a fragment of at least 'n' consecutive amino acids from amino acids 103-205 of SEQ ID NO: 241, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These polypeptides (e.g. SEQ ID NO: 250) can elicit antibodies (e.g. when administered to a human) which recognise both the wild-type staphylococcal protein comprising SEQ ID NO: 10 and the wild-type staphylococcal protein comprising SEQ ID NO: 11. Thus the immune response will recognise both of antigens *esxA* and *esxB*. Preferred fragments of (b) provide an epitope from SEQ ID NO: 10 and an epitope from SEQ ID NO: 11. The invention also provides an immunogenic composition comprising a combination of such a protein and an adjuvant, such as an aluminium hydroxide adjuvant.

[0030] The invention also provides a polypeptide comprising a staphylococcal hemolysin sequence, wherein the sequence does not include a sequence having at least 90% identity to SEQ ID NO: 217 but can elicit antibodies which can kill staphylococci. The polypeptide may have a first sequence having 80% or more identity (e.g. 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 218 and a second sequence having 80% or more identity (e.g. 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 219, wherein the first and second sequences are either directly joined or are joined by an intervening amino acid sequence having fewer than 40 amino acids (e.g. ≤ 35 amino acids, ≤ 30 amino acids, ≤ 25 amino acids, ≤ 20 amino acids, ≤ 15 amino acids, ≤ 10 amino acids, ≤ 5 amino acids). SEQ ID NOs: 189 and 216 are examples of such polypeptides, in which the first and second sequences are joined by a tetrapeptide PSGS sequence (SEQ ID NO: 225).

[0031] The invention also provides an immunogenic composition comprising a Sta011 antigen and a Ca^{++} ion. The antigen and Ca^{++} ion may form a complex e.g. atoms in the antigen may coordinate the Ca^{++} ion. The immunogenic composition may also include an adjuvant.

[0032] The invention also provides a oligomer of a Sta011 antigen, and also immunogenic compositions comprising such oligomers. The oligomer can be a dimer, trimer, tetramer, pentamer, hexamer, heptamer, octamer or higher. An oligomer may comprise a Ca^{++} ion, and a composition comprising Sta011 oligomers may comprise 5-500mM Ca^{++} ions.

Further polypeptide antigens

[0033] In additions to antigens from the various antigen groups of the invention, immunogenic compositions may include one or more of the following *S.aureus* antigens (or antigens comprising immunogenic fragment(s) thereof) to enhance the efficacy against *S.aureus* of an immune response elicited by the composition [e.g. see references 3-10]:

- AhpC
- AhpF
- Autolysin amidase
- Autolysin glucosaminidase
- Collagen binding protein CAN
- EbhB

- GehD lipase
- Heparin binding protein HBP (17kDa)
- 5 • Laminin receptor
- MAP
- MntC (also known as SitC)
- 10 • MRPII
- Npase
- 15 • ORF0594
- ORF0657n
- ORF0826
- 20 • PBP4
- RAP (RNA III activating protein)
- 25 • Sai-1
- Sask
- SBI
- 30 • SdrG
- SdrH
- 35 • SSP-1
- SSP-2
- Vitronectin-binding protein

Combinations with saccharides

[0034] The individual antigens identified in the antigen groups of the invention may be used in combination with conjugated saccharide antigens. Thus the invention provides an immunogenic composition comprising a combination of:

- (1) one or more antigen(s) selected from the first, second, third or fourth antigen groups (as defined above); and
- (2) one or more conjugates of a *S.aureus* exopolysaccharide and a carrier protein.

[0035] A conjugate used in component (2) of this combination includes a saccharide moiety and a carrier moiety. The saccharide moiety is from the exopolysaccharide of *S.aureus*, which is a poly-N-acetylglucosamine (PNAG). The saccharide may be a polysaccharide having the size that arises during purification of the exopolysaccharide from bacteria, or it may be an oligosaccharide achieved by fragmentation of such a polysaccharide e.g. size can vary from over 400kDa to between 75 and 400kDa, or between 10 and 75kDa, or up to 30 repeat units. The saccharide moiety can have various degrees of N-acetylation and, as described in reference 11, the PNAG may be less than 40% N-acetylated (e.g. less than 35, 30, 20, 15, 10 or 5% N-acetylated; deacetylated PNAG is also known as dPNAG). Deacetylated epitopes of PNAG can elicit antibodies that are capable of mediating opsonic killing. The PNAG may or may not be O-succinylated e.g. it may be O-succinylated on fewer less than 25, 20, 15, 10, 5, 2, 1 or 0.1% of residues.

[0036] The invention also provides an immunogenic composition comprising a combination of:

- (1) one or more antigen(s) selected from the first, second, third or fourth antigen groups; and
- (2) one or more conjugates of a *S.aureus* capsular saccharide and a carrier protein.

[0037] A conjugate used in component (2) of this combination includes a saccharide moiety and a carrier moiety. The saccharide moiety is from the capsular saccharide of a *S.aureus*. The saccharide may be a polysaccharide having the size that arises during purification of capsular polysaccharide from bacteria, or it may be an oligosaccharide achieved by fragmentation of such a polysaccharide. Capsular saccharides may be obtained from any suitable strain of *S.aureus* (or any bacterium having a similar or identical saccharide), such as from a type 5 and/or a type 8 *S.aureus* strain and/or a type 336 *S.aureus* strain. Most strains of infectious *S.aureus* contain either Type 5 or Type 8 capsular saccharides. Both have FucNAcp in their repeat unit as well as ManNAcA which can be used to introduce a sulphydryl group for linkage. The repeating unit of the Type 5 saccharide is $\rightarrow 4$)- β -D-Man NAcA-(1 $\rightarrow$ 4)- α -L-FucNAc(3OAc)-(1 $\rightarrow$ 3)- β -D-FucNAc-(1 $\rightarrow$, whereas the repeating unit of the Type 8 saccharide is $\rightarrow 3$)- β -D-ManNAcA(4OAc)-(1 $\rightarrow$ 3)- α -L-FucNAc(1 $\rightarrow$ 3)- α -D-FucNAc(1 $\rightarrow$. The type 336 saccharide is a β -linked hexosamine with no O-acetylation [12,13] and is cross-reactive with antibodies raised against the 336 strain (ATCC 55804). A combination of a type 5 and a type 8 saccharide is typical, and a type 336 saccharide may be added to this pairing [14].

[0038] The invention also provides an immunogenic composition comprising a combination of:

- (1) one or more antigen(s) selected from the first, second, third or fourth antigen groups;
- (2) one or more conjugates of a *S.aureus* exopolysaccharide and a carrier protein; and
- (3) one or more conjugates of a *S.aureus* capsular saccharide and a carrier protein.

[0039] The carrier moiety in these conjugates will usually be a protein, but usually not one of the antigens of (1). Typical carrier proteins are bacterial toxins, such as diphtheria or tetanus toxins, or toxoids or mutants or fragments thereof. The CRM197 diphtheria toxin mutant [15] is useful. Other suitable carrier proteins include the *N.meningitidis* outer membrane protein complex [16], synthetic peptides [17,18], heat shock proteins [19,20], pertussis proteins [21,22], cytokines [23], lymphokines [23], hormones [23], growth factors [23], artificial proteins comprising multiple human CD4⁺ T cell epitopes from various pathogen-derived antigens [24] such as N19 [25], protein D from *H.influenzae* [26-28], pneumolysin [29] or its non-toxic derivatives [30], pneumococcal surface protein PspA [31], iron-uptake proteins [32], toxin A or B from *C.difficile* [33], recombinant *P.aeruginosa* exoprotein A (rEPA) [34], etc. In some embodiments the carrier protein is a *S.aureus* protein, such as an antigen selected from the first, second, third or fourth antigen groups.

[0040] Where a composition includes more than one conjugate, each conjugate may use the same carrier protein or a different carrier protein.

[0041] Conjugates may have excess carrier (w/w) or excess saccharide (w/w). In some embodiments, a conjugate may include substantially equal weights of each.

[0042] The carrier molecule may be covalently conjugated to the carrier directly or via a linker. Direct linkages to the protein may be achieved by, for instance, reductive amination between the saccharide and the carrier, as described in, for example, references 35 and 36. The saccharide may first need to be activated e.g. by oxidation. Linkages via a linker group may be made using any known procedure, for example, the procedures described in references 37 and 38. A preferred type of linkage is an adipic acid linker, which may be formed by coupling a free -NH₂ group (e.g. introduced to a glucan by amination) with adipic acid (using, for example, diimide activation), and then coupling a protein to the resulting saccharide-adipic acid intermediate [39,40]. Another preferred type of linkage is a carbonyl linker, which may be formed by reaction of a free hydroxyl group of a saccharide CDI [41, 42] followed by reaction with a protein to form a carbamate linkage. Other linkers include β -propionamido [43], nitrophenyl-ethylamine [44], haloacyl halides [45], glycosidic linkages [46], 6-aminocaproic acid [47], ADH [48], C₄ to C₁₂ moieties [49], etc. Carbodiimide condensation can also be used [50].

[0043] PNAG conjugates may be prepared in various ways e.g. by a process comprising: a) activating the PNAG by adding a linker comprising a maleimide group to form an activated PNAG; b) activating the carrier protein by adding a linker comprising a sulphydryl group to form an activated carrier protein; and c) reacting the activated PNAG and the activated carrier protein to form a PNAG-carrier protein conjugate; or by a process comprising a) activating the PNAG by adding a linker comprising a sulphydryl group to form an activated PNAG; b) activating the carrier protein by adding a linker comprising a maleimide group to form an activated carrier protein; and c) reacting the activated PNAG and the activated carrier protein to form a PNAG-carrier protein conjugate; or by a process comprising a) activating the PNAG by adding a linker comprising a sulphydryl group to form an activated PNAG; b) activating the carrier protein by adding a linker comprising a sulphydryl group to form an activated carrier protein; and c) reacting the activated PNAG and the activated carrier protein to form a PNAG-carrier protein conjugate.

[0044] The individual antigens identified in the antigen groups of the invention may be used as carrier proteins for

exopolysaccharides, to form a covalent conjugate. Thus the invention provides an immunogenic composition comprising a conjugate of (1) an antigen selected from the first, second, third and fourth antigen groups and (2) a *S.aureus* exopolysaccharide. The invention also provides an immunogenic composition comprising a conjugate of (1) an antigen selected from the first, second, third and fourth antigen groups and (2) a *S.aureus* capsular saccharide. Further characteristics of such conjugates are described above. These conjugates may be combined with any of the antigens disclosed herein.

Combinations with non-staphylococcal antigens

[0045] The individual antigens identified in the antigen groups of the invention may be used in combination with non-staphylococcal antigens, and in particular with antigens from bacteria associated with nosocomial infections. Thus the invention provides an immunogenic composition comprising a combination of:

- (1) one or more antigen(s) selected from the first, second, third and fourth antigen groups (as defined above); and
- (2) one or more antigen(s) selected from the group consisting of: *Clostridium difficile*; *Pseudomonas aeruginosa*; *Candida albicans*; and extraintestinal pathogenic *Escherichia coli*.

[0046] Further suitable antigens for use in combination with staphylococcal antigens of the invention are listed on pages 33-46 of reference 51.

First antigens group

clfA

[0047] The 'clfA' antigen is annotated as 'clumping factor A'. In the NCTC 8325 strain clfA is SAOUHSC_00812 and has amino acid sequence SEQ ID NO: 1 (GI:88194572). In the Newman strain it is nwmn_0756 (GI:151220968).

[0048] Useful clfA antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 1 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 1; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of (SEQ ID NO: 1, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more)). These clfA proteins include variants of SEQ ID NO: 1. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 1. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 1 while retaining at least one epitope of SEQ ID NO: 1. The final 368 C-terminal amino acids of SEQ ID NO: 1 can usefully be omitted. The first 39 N-terminal amino acids of SEQ ID NO: 1 can usefully be omitted. Other fragments omit one or more protein domains.

[0049] SEQ ID NO: 224 is a useful fragment of SEQ ID NO: 1 ('ClfA₄₀₋₅₅₉'). This fragment omits the long repetitive region towards the C-terminal of SEQ ID NO: 1.

clfB

[0050] The 'clfB' antigen is annotated as 'clumping factor B'. In the NCTC 8325 strain clfB is SAOUHSC_02963 and has amino acid sequence SEQ ID NO: 2 (GI:88196585). In the Newman strain it is nwmn_2529 (GI:151222741).

[0051] Useful clfB antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 2 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 2; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 2, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more)). These clfB proteins include variants of SEQ ID NO: 2. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 2. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 2 while retaining at least one epitope of SEQ ID NO: 2. The final 40 C-terminal amino acids of SEQ ID NO: 2 can usefully be omitted. The first 44 N-terminal amino acids of SEQ ID NO: 2 can usefully be omitted. Other fragments omit one or more protein domains. ClfB is naturally a long protein and so the use of fragments is helpful e.g. for purification, handling, fusion, expression, etc. SEQ ID NO: 163 is a useful fragment of SEQ ID NO: 2 ('ClfB₄₅₋₅₅₂'). This fragment includes the most exposed domain of ClfB and is more easily used at an industrial scale. It also reduces the antigen's similarity with human proteins. Other useful fragments, based on a 3-domain model of ClfB, include: ClfB₄₅₋₃₆₀ (also known as CLfB-N12; SEQ ID NO: 196); ClfB₂₁₂₋₅₄₂ (also known as CLfB-N23; SEQ ID NO: 197); and ClfB₃₆₀₋₅₄₂ (also known as CLfB-N3; SEQ ID NO: 198).

coA

[0052] The 'coA' antigen is annotated as 'coagulase Coa'. In the NCTC 8325 strain coA is SAOUHSC_00192 and has amino acid sequence SEQ ID NO: 3 (GI:88194002). In the Newman strain it is nwmn_0166 (GI: 151220378).

[0053] Useful coA antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 3 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 3; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 3, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50; 60, 70, 80, 90, 100, 150, 200, 250 or more). These coA proteins include variants of SEQ ID NO: 3. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 3. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 3 while retaining at least one epitope of SEQ ID NO: 3. The first 14 N-terminal amino acids of SEQ ID NO: 3 can usefully be omitted. Other fragments omit one or more protein domains.

eap

[0054] The 'eap' antigen is annotated as 'MHC class II analog protein'. In the NCTC 8325 strain eap is SAOUHSC_02161 and has amino acid sequence SEQ ID NO: 4 (GI:88195840). In the Newman strain it is nwmn_1872 (GI:151222084).

[0055] Useful eap antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 4 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 4; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 4, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These eap proteins include variants of SEQ ID NO: 4. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 4. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 4 while retaining at least one epitope of SEQ ID NO: 4. The first 17 N-terminal amino acids of SEQ ID NO: 4 can usefully be omitted. Other fragments omit one or more protein domains.

ebhA

[0056] The 'ebhA' antigen is annotated as 'Ebha'. In the NCTC 8325 strain ebhA is SAOUHSC_01447 and has amino acid sequence SEQ ID NO: 5 (GI:88195168).

[0057] Useful ebhA antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 5 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 5; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 5, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These ebhA proteins include variants of SEQ ID NO: 5. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 5. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 5 while retaining at least one epitope of SEQ ID NO: 5. The first 39 N-terminal amino acids of SEQ ID NO: 5 can usefully be omitted. Other fragments omit one or more protein domains.

ebpS

[0058] The 'ebpS' antigen is annotated as 'elastin binding protein EbpS'. In the NCTC 8325 strain ebpS is SAOUHSC_01501 and has amino acid sequence SEQ ID NO: 6 (GI:88195217). In the Newman strain it is nwmn_1389 (GI:151221601).

[0059] Useful ebpS antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 6 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 6; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 6, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These ebpS proteins include variants of SEQ ID NO: 6. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 6. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids

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(e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 6 while retaining at least one epitope of SEQ ID NO: 6. Other fragments omit one or more protein domains.

[0060] SEQ ID NO: 165 is a useful fragment of SEQ ID NO: 6 ('EbpS₁₋₁₉₈'), This fragment includes the most exposed domain of EbpS and is more easily used at an industrial scale. It also reduces the antigen's similarity with human proteins.

efb

[0061] The 'efb' antigen is annotated as 'fibrinogen-binding protein truncated'. In the NCTC 8325 strain efb is SAOUHSC_01114 and has amino acid sequence SEQ ID NO: 7 (GI:88194860). In the Newman strain it is nwmn_1069 (GI:151221281).

[0062] Useful efb antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 7 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 7; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 7, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150 or more). These efb proteins include variants of SEQ ID NO: 7. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 7. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 7 while retaining at least one epitope of SEQ ID NO: 7. The first 14 N-terminal amino acids of SEQ ID NO: 7 can usefully be omitted. Other fragments omit one or more protein domains.

emp

[0063] The 'emp' antigen is annotated as 'extracellular matrix and plasma binding protein'. In the NCTC 8325 strain emp is SAOUHSC_00816 and has amino acid sequence SEQ ID NO: 8 (GI:88194575). In the Newman strain it is nwmn_0758 (GI:151220970).

[0064] Useful emp antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 8 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 8; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 8, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These emp proteins include variants of SEQ ID NO: 8. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 8. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 8 while retaining at least one epitope of SEQ ID NO: 8. The first 26 N-terminal amino acids of SEQ ID NO: 8 can usefully be omitted. Other fragments omit one or more protein domains.

[0065] SEQ ID NOS: 190, 191, 192 and 193 are useful fragments of SEQ ID NO: 8 ('Emp₃₅₋₃₄₀', 'Emp₂₇₋₃₃₄', 'Emp₃₅₋₃₃₄' and 'Emp₂₇₋₁₄₇', respectively).

esaC

[0066] The 'esaC' antigen is annotated as 'esaC'. In the NCTC 8325 strain esaC is SAOUHSC_00264 and has amino acid sequence SEQ ID NO: 9 (GI:88194069).

[0067] Useful esaC antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 9 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 9; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 9, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These esaC proteins include variants of SEQ ID NO: 9. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 9. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 9 while retaining at least one epitope of SEQ ID NO: 9. Other fragments omit one or more protein domains.

esxA

[0068] The 'esxA' antigen is annotated as 'protein'. In the NCTC 8325 strain esxA is SAOUHSC_00257 and has amino acid sequence SEQ ID NO: 10 (GI:88194063).

[0069] Useful esxA antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO:

10 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 10; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 10, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90 or more). These *esxA* proteins include variants of SEQ ID NO: 10. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 10. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 10 while retaining at least one epitope of SEQ ID NO: 10. Other fragments omit one or more protein domains.

esxB

[0070] The '*esxB*' antigen is annotated as '*esxB*'. In the NCTC 8325 strain *esxB* is SAOUHSC_00265 and has amino acid sequence SEQ ID NO: 11 (GI:88194070).

[0071] Useful *esxB* antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 11 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 11; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 11, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These *esxB* proteins include variants of SEQ ID NO: 11. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 11. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 11 while retaining at least one epitope of SEQ ID NO: 11. Other fragments omit one or more protein domains.

FnBA

[0072] The '*FnBA*' antigen is annotated as 'fibronectin-binding protein A precursor *FnBPA*'. In the NCTC 8325 strain *FnBA* is SAOUHSC_02803 and has amino acid sequence SEQ ID NO: 12 (GI:88196438). In the Newman strain it is *nwmn_2399* (GI:151222611). Proteomic analysis has revealed that this protein is secreted or surface-exposed.

[0073] Useful *FnBA* antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 12 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 12; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 12, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These *FnBA* proteins include variants of SEQ ID NO: 12. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 12. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 12 while retaining at least one epitope of SEQ ID NO: 12. The final 37 C-terminal amino acids of SEQ ID NO: 12 can usefully be omitted. Other fragments omit one or more protein domains. *FnBA* is naturally a long protein and so the use of fragments is helpful e.g. for purification, handling, fusion, expression, etc.

[0074] SEQ ID NOS: 166 ('*FnBA*₁₋₅₁₁') and 167 ('*FnBA*₅₁₂₋₉₅₃') are useful fragments of SEQ ID NO: 12. These fragments are more easily used at an industrial scale.

FnBB

[0075] The '*FnBB*' antigen is annotated as 'fibronectin binding protein B *FnBPB*'. In the NCTC 8325 strain *FnBB* is SAOUHSC_02802 and has amino acid sequence SEQ ID NO: 13 (GI:88196437). In the Newman strain it is *nwmn_2397* (GI:151222609).

[0076] Useful *FnBB* antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 13 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 13; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 13, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These *FnBB* proteins include variants of SEQ ID NO: 13. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 13. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 13 while retaining at least one epitope of SEQ ID NO: 13. The final 37 C-terminal amino acids of SEQ ID NO: 13 can usefully be omitted. Other fragments omit one or more protein domains.

Hla

[0077] The 'Hla' antigen is the 'alpha-hemolysin precursor' also known as 'alpha toxin' or simply 'hemolysin'. In the NCTC 8325 strain Hla is SAOUHSC_01121 and has amino acid sequence SEQ ID NO: 14 (GI:88194865). In the Newman strain it is nwmn_1073 (GI:151221285). Hla is an important virulence determinant produced by most strains of *S.aureus*, having pore-forming and haemolytic activity. Anti-Hla antibodies can neutralise the detrimental effects of the toxin in animal models, and Hla is particularly useful for protecting against pneumonia.

[0078] Useful Hla antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 14 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 14; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 14, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These Hla proteins include variants of SEQ ID NO: 14. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 14. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 14 while retaining at least one epitope of SEQ ID NO: 14. The first 26 N-terminal amino acids of SEQ ID NO: 14 can usefully be omitted (e.g. to give SEQ ID NO: 231). Truncation at the C-terminus can also be used e.g. leaving only 50 amino acids (residues 27-76 of SEQ ID NO: 14) [52]. Other fragments omit one or more protein domains.

[0079] Hla's toxicity can be avoided in compositions of the invention by chemical inactivation (e.g. using formaldehyde, glutaraldehyde or other cross-linking reagents). Instead, however, it is preferred to use mutant forms of Hla which remove its toxic activity while retaining its immunogenicity. Such detoxified mutants are already known in the art. One useful Hla antigen has a mutation at residue 61 of SEQ ID NO: 14, which is residue 35 of the mature antigen (i.e. after omitting the first 26 N-terminal amino acids = residue 35 of SEQ ID NO: 231). Thus residue 61 may not be histidine, and may instead be e.g. Ile, Val or preferably Leu. A His-Arg mutation at this position can also be used. For example, SEQ ID NO: 150 is the mature mutant Hla-H35L sequence (i.e. SEQ ID NO: 231 with a H35L mutation) and a useful Hla antigen comprises (SEQ ID NO: 150. Another useful mutation replaces a long loop with a short sequence e.g. to replace the 39mer at residues 136-174 of SEQ ID NO: 14 with a tetramer such as PSGS (SEQ ID NO: 225), as in SEQ ID NO: 189 (which also includes the H35L mutation) and SEQ ID NO: 216 (which does not include the H35L mutation). Another useful mutation replaces residue Y101 e.g. with a leucine (SEQ ID NO: 242). Another useful mutation replaces residue D152 e.g. with a leucine (SEQ ID NO: 243). Another useful mutant replaces residues H35 and Y101 e.g. with a leucine (SEQ ID NO: 244). Another useful mutant replaces residues H35 and D152 e.g. with a leucine (SEQ ID NO: 245).

[0080] Further useful Hla antigens are disclosed in references 53 and 54.

[0081] SEQ ID NOs: 160, 161 & 194 are three useful fragments of SEQ ID NO: 14 ('Hla₂₇₋₇₆', 'Hla₂₇₋₈₉' and 'Hla₂₇₋₇₉', respectively). SEQ ID NOs: 158, 159 and 195 are the corresponding fragments from SEQ ID NO: 150.

[0082] One useful Hla sequence is SEQ ID NO: 232, which was used in the examples. It has a N-terminal Met, then an Ala-Ser dipeptide from the expression vector, then SEQ ID NO: 150 (from NCTC8325 strain). It is encoded by SEQ ID NO: 233.

hlgB

[0083] The 'hlgB' antigen is annotated as 'leukocidin f subunit precursor HlgB'. In the NCTC 8325 strain hlgB is SAOUHSC_02710 and has amino acid sequence SEQ ID NO: 15 (GI:88196350).

[0084] Useful hlgB antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 15 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 15; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 15, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These hlgB proteins include variants of SEQ ID NO: 15. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 15. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 15 while retaining at least one epitope of SEQ ID NO: 15. The first 26 N-terminal amino acids of SEQ ID NO: 15 can usefully be omitted. Other fragments omit one or more protein domains.

hlgC

[0085] The 'hlgC' antigen is annotated as 'leukocidin s subunit precursor HlgC'. In the NCTC 8325 strain hlgC is SAOUHSC_02709 and has amino acid sequence SEQ ID NO: 16 (GI:88196349).

[0086] Useful hlgC antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO:

16 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 16; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 16, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These hlgC proteins include variants of SEQ ID NO: 16. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 16. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 16 while retaining at least one epitope of SEQ ID NO: 16. The first 29 N-terminal amino acids of SEQ ID NO: 16 can usefully be omitted. Other fragments omit one or more protein domains.

isdA

[0087] The 'isdA' antigen is annotated as 'IsdA protein'. In the NCTC 8325 strain isdA is SAOUHSC_01081 and has amino acid sequence SEQ ID NO: 17 (GI:88194829). In the Newman strain it is nwmn_1041 (GI:151221253).

[0088] Useful isdA antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 17 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 17; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 17, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These isdA proteins include variants of SEQ ID NO: 17. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 17. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 17 while retaining at least one epitope of SEQ ID NO: 17. The final 38 C-terminal amino acids of SEQ ID NO: 17 can usefully be omitted. The first 46 N-terminal amino acids of SEQ ID NO: 17 can usefully be omitted. Truncation to exclude the C-terminal 38mer of SEQ ID NO: 17 (beginning with the LPKTG motif) is also useful. Other fragments omit one or more protein domains.

[0089] SEQ ID NO: 157 is a useful fragment of SEQ ID NO: 17 (amino acids 40-184 of SEQ ID NO: 17; 'IsdA₄₀₋₁₈₄') which includes the natural protein's heme binding site and includes the antigen's most exposed domain. It also reduces the antigen's similarity with human proteins. Other useful fragments are disclosed in references 55 and 56.

[0090] IsdA does not adsorb well to aluminium hydroxide adjuvants, so IsdA present in a composition may be unadsorbed or may be adsorbed to an alternative adjuvant e.g. to an aluminium phosphate.

[0091] Anti-IsdA antibodies protect mice against *S.aureus* abscess formation and lethal challenge [57].

isdB

[0092] The 'isdB' antigen is annotated as 'neurofilament protein isdB'. In the NCTC 8325 strain isdB is SAOUHSC_01079 and has amino acid sequence SEQ ID NO: 18 (GI:88194828). IsdB has been proposed for use as a vaccine antigen on its own [2], but this may not prevent pneumonia.

[0093] Useful isdB antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 18 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 18; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 18, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These isdB proteins include variants of SEQ ID NO: 18. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 18. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 18 while retaining at least one epitope of SEQ ID NO: 18. The final 36 C-terminal amino acids of SEQ ID NO: 18 can usefully be omitted. The first 40 N-terminal amino acids of SEQ ID NO: 18 can usefully be omitted. Other fragments omit one or more protein domains. Useful fragments of IsdB are disclosed in references 56 and 58 e.g. lacking 37 internal amino acids of SEQ ID NO: 18.

[0094] Anti-IsdB antibodies protect mice against *S.aureus* abscess formation and lethal challenge [57].

[0095] In some embodiments, compositions of the invention do not include an isdB antigen.

isdC

[0096] The 'isdC' antigen is annotated as 'protein'. In the NCTC 8325 strain isdC is SAOUHSC_01082 and has amino acid sequence SEQ ID NO: 19 (GI:88194830).

[0097] Useful isdC antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 19 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 19; and/or (b) comprising

a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 19, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 70, 80, 90, 100, 150, 200 or more). These *isdC* proteins include variants of SEQ ID NO: 19. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 19. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 19 while retaining at least one epitope of SEQ ID NO: 19. The final 39 C-terminal amino acids of SEQ ID NO: 19 can usefully be omitted. The first 28 N-terminal amino acids of SEQ ID NO: 19 can usefully be omitted. Other fragments omit one or more protein domains. Useful fragments of *IsdB* are disclosed in reference 56.

[0098] Reference 59 discloses antigens which usefully include epitopes from both *IsdB* and *IsdH*.

isdG

[0099] The '*isdG*' antigen is annotated as 'heme-degrading monooxygenase *IsdG*'. In the NCTC 8325 strain *isdG* is SAOUHSC_01089 and has amino acid sequence SEQ ID NO: 20 (GI:88194836).

[0100] Useful *isdG* antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 20 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 20; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 20, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These *isdG* proteins include variants of SEQ ID NO: 20. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 20. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 20 while retaining at least one epitope of SEQ ID NO: 20. Other fragments omit one or more protein domains.

isdH

[0101] The '*isdH*' antigen is annotated as '*isdH*'. In the NCTC 8325 strain *isdH* is SAOUHSC_01843 and has amino acid sequence SEQ ID NO: 21 (GI:88195542). In the Newman strain it is nwmn_1624 (GI:151221836). It has also been known as HarA.

[0102] Useful *isdH* antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 21 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 21; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 21, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These *isdH* proteins include, variants of SEQ ID NO: 21. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 21. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 21 while retaining at least one epitope of SEQ ID NO: 21. The final 35 C-terminal amino acids of SEQ ID NO: 21 can usefully be omitted. The first 40 N-terminal amino acids of SEQ ID NO: 21 can usefully be omitted. Other fragments omit one or more protein domains.

[0103] Reference 59 discloses antigens which usefully include epitopes from both *IsdB* and *IsdH*.

isdI

[0104] The '*isdI*' antigen is annotated as 'heme-degrading monooxygenase *IsdI*'. In the NCTC 8325' strain *isdI* is SAOUHSC_00130 and has amino acid sequence SEQ ID NO: 22 (GI:88193943).

[0105] Useful *isdI* antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 22 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 22; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 22, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These *isdI* proteins include variants of SEQ ID NO: 22. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 22. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 22 while retaining at least one epitope of SEQ ID NO: 22. Other fragments omit one or more protein domains.

lukD

[0106] The '*lukD*' antigen is annotated as 'leukotoxin *LukD*'. In the NCTC 8325 strain *lukD* is SAOUHSC_01954 and

has amino acid sequence SEQ ID NO: 23 (GI:88195647). In the Newman strain it is nwmn_1718 (GI:151221930).

[0107] Useful lukD antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 23 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 23; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 23, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These lukD proteins include variants of SEQ ID NO: 23. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 23. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 23 while retaining at least one epitope of SEQ ID NO: 23. The final 43 C-terminal amino acids of SEQ ID NO: 23 can usefully be omitted. The first 26 N-terminal amino acids of SEQ ID NO: 23 can usefully be omitted. Other fragments omit one or more protein domains.

lukE

[0108] The 'lukE' antigen is annotated as 'leukotoxin LukE'. In the NCTC 8325 strain lukE is SAOUHSC_01955 and has amino acid sequence SEQ ID-NO: 24 (GI:88195648).

[0109] Useful lukE antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 24 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 24; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 24, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These lukE proteins include variants of SEQ ID NO: 24. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 24. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 24 while retaining at least one epitope of SEQ ID NO: 24. Other fragments omit one or more protein domains.

lukF

[0110] The 'lukF' antigen is annotated as 'Leukocidin/Hemolysin toxin family LukF'. In the NCTC 8325 strain lukF is SAOUHSC_02241 and has amino acid sequence SEQ ID NO: 25 (GI:88195914). Useful lukF antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 25 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 25; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 25, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These lukF proteins include variants of SEQ ID NO: 25. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 25. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 25 while retaining at least one epitope of SEQ ID NO: 25. Other fragments omit one or more protein domains.

lukS

[0111] The 'lukS' antigen is annotated as 'probable leukocidin S subunit LukS'. In the NCTC 8325 strain lukS is SAOUHSC_02243 and has amino acid sequence SEQ ID NO: 26 (GI:88195915). In the Newman strain it is nwmn_1928 (GI:151222140).

[0112] Useful lukS antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 26 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 26; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 26, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These lukS proteins include variants of SEQ ID NO: 26. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 26. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 26 while retaining at least one epitope of SEQ ID NO: 26. The first 22 N-terminal amino acids of SEQ ID NO: 26 can usefully be omitted. Other fragments omit one or more protein domains.

nuc

[0113] The 'nuc' antigen is annotated as 'thermonuclease precursor'. In the NCTC 8325 strain *nuc* is SAOUHSC_01316 and has amino acid sequence SEQ ID NO: 27 (GI:88195046).

[0114] Useful *nuc* antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 27 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 27; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 27, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150 or more). These *nuc* proteins include variants of SEQ ID NO: 27. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 27. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 27 while retaining at least one epitope of SEQ ID NO: 27. The final 39 C-terminal amino acids of SEQ ID NO: 27 can usefully be omitted. The first 19 N-terminal amino acids of SEQ ID NO: 27 can usefully be omitted. Other fragments omit one or more protein domains.

sasA

[0115] The 'sasA' antigen is annotated as 'SasA'. In the NCTC 8325 strain *sasA* is SAOUHSC_02990 and has amino acid sequence SEQ ID NO: 28 (GI:88196609).

[0116] Useful *sasA* antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 28 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 28; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 28, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These *sasA* proteins include variants of SEQ ID NO: 28. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 28. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 28 while retaining at least one epitope of SEQ ID NO: 28. The final 43 C-terminal amino acids of SEQ ID NO: 28 can usefully be omitted. The first 90 N-terminal amino acids of SEQ ID NO: 28 can usefully be omitted. Other fragments omit one or more protein domains.

sasB

[0117] The 'sasB' antigen is annotated as 'fmtB protein; SasB'. In the NCTC 8325 strain *sasB* is SAOUHSC_02404 and has amino acid sequence SEQ ID NO: 29 (GI:88196065).

[0118] Useful *sasB* antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 29 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 29; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 29, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These *sasB* proteins include variants of SEQ ID NO: 29. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 29. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 29 while retaining at least one epitope of SEQ ID NO: 29. The final 39 C-terminal amino acids of SEQ ID NO: 29 can usefully be omitted. The first 38 N-terminal amino acids of SEQ ID NO: 29 can usefully be omitted. Other fragments omit one or more protein domains.

sasC

[0119] The 'sasC' antigen is annotated as 'Mrp protein; SasC'. In the NCTC 8325 strain *sasC* is SAOUHSC_01873 and has amino acid sequence SEQ ID NO: 30 (GI:88195570).

[0120] Useful *sasC* antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 30 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 30; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 30, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These *sasC* proteins include variants of SEQ ID NO: 30. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 30. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 30 while retaining at least one epitope of SEQ ID NO: 30. The final 36 C-terminal amino acids of SEQ ID NO: 30 can usefully be omitted. The first 37

N-terminal amino acids of SEQ ID NO: 30 can usefully be omitted. Other fragments omit one or more protein domains.

sasD

5 **[0121]** The 'sasD' antigen is annotated as 'SasD protein'. In the NCTC 8325 strain sasD is SAOUHSC_00094 and has amino acid sequence SEQ ID NO: 31 (GI:88193909).

[0122] Useful sasD antigens can elicit an antibody (e.g. when administered to a human) that recognises (SEQ ID NO: 31 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 31; and/or (b) comprising
10 a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 31, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150 or more). These sasD proteins include variants of SEQ ID NO: 31. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 31. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 31 while retaining at least one epitope
15 of SEQ ID NO: 31. The first 28 N-terminal amino acids of SEQ ID NO: 31 can usefully be omitted. Other fragments omit one or more protein domains.

sasF

20 **[0123]** The 'sasF' antigen is annotated as 'sasF protein'. In the NCTC 8325 strain sasF is SAOUHSC_02982 and has amino acid sequence SEQ ID NO: 32 (GI:88196601).

[0124] Useful sasF antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 32 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 32; and/or (b) comprising
25 a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 32, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sasF proteins include variants of SEQ ID NO: 32. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 32. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 32 while retaining at least one
30 epitope of SEQ ID NO: 32. The final 39 C-terminal amino acids of SEQ ID NO: 32 can usefully be omitted. The first 37 N-terminal amino acids of SEQ ID NO: 32 can usefully be omitted. Other fragments omit one or more protein domains.

sdrC

35 **[0125]** The 'sdrC' antigen is annotated as 'sdrC protein'. In the NCTC 8325 strain sdrC is SAOUHSC_00544 and has amino acid sequence SEQ ID NO: 33 (GI:88194324).

[0126] Useful sdrC antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 33 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 33; and/or (b) comprising
40 a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 33, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sdrC proteins include variants of SEQ ID NO: 33. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 33. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 33 while retaining at least one
45 epitope of SEQ ID NO: 33. The final 38 C-terminal amino acids of SEQ ID NO: 33 can usefully be omitted. The first 50 N-terminal amino acids of SEQ ID NO: 33 can usefully be omitted. Other fragments omit one or more protein domains. SdrC is naturally a long protein and so the use of fragments is helpful e.g. for purification, handling, fusion, expression, etc.
[0127] SEQ ID NO: 164 is a useful fragment of SEQ ID NO: 33 ('SdrC₁₋₅₁₈'). This fragment includes the most exposed domain of SdrC and is more easily used at an industrial scale. It also reduces the antigen's similarity with human proteins.
50

sdrD

[0128] The 'sdrD' antigen is annotated as 'sdrD protein'. In the NCTC 8325 strain sdrD is SAOUHSC_00545 and has amino acid sequence SEQ ID NO: 34 (GI:88194325).

55 **[0129]** Useful sdrD antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 34 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 34; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 34, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18,

20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sdrD proteins include variants of SEQ ID NO: 34. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 34. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 34 while retaining at least one epitope of SEQ ID NO: 34. The final 38 C-terminal amino acids of SEQ ID NO: 34 can usefully be omitted. The first 52 N-terminal amino acids of SEQ ID NO: 34 can usefully be omitted. Other fragments omit one or more protein domains. SdrD is naturally a long protein and so the use of fragments is very helpful e.g. for purification, handling, fusion, expression, etc.

[0130] SEQ ID NO: 156 is a useful fragment of SEQ ID NO: 34 ('SdrD₅₃₋₅₉₂'). This fragment includes the most exposed domain of SdrD and is more easily used at an industrial scale. It also reduces the antigen's similarity with human proteins. Another useful fragment, with the same C-terminus residue, is SdrD₃₉₄₋₅₉₂ (also known as SdrD-N3; SEQ ID NO: 199). Another useful fragment is SEQ ID NO: 236 (amino acids 593-1123 of SEQ ID NO: 34), referred to herein as 'SdrD_{CnaB}'.

sdrE2

[0131] The 'sdrE2' antigen is annotated as 'Ser-Asp rich fibrinogen/bone sialoprotein-binding protein SdrE'. In the Newman strain sdrE2 is NWMN_0525 and has amino acid sequence SEQ ID NO: 35 (GI:151220737).

[0132] Useful sdrE2 antigens can elicit an antibody (e.g. when administered to a human) that recognise SEQ ID NO: 35 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 35; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 35, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sdrE2 proteins include variants of SEQ ID NO: 35. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 35. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 35 while retaining at least one epitope of SEQ ID NO: 35. The final 38 C-terminal amino acids of SEQ ID NO: 35 can usefully be omitted. The first 52 N-terminal amino acids of SEQ ID NO: 35 can usefully be omitted. Other fragments omit one or more protein domains. SdrE2 is naturally a long protein and so the use of fragments is very helpful e.g. for purification, handling, fusion, expression, etc.

[0133] SEQ ID NO: 155 is a useful fragment of SEQ ID NO: 35 ('SdrE₅₃₋₆₃₂'). This fragment includes the most exposed domain of SdrE2 and is more easily used at an industrial scale. It also reduces the antigen's similarity with human proteins.

spa

[0134] The 'spa' antigen is annotated as 'protein A' or 'SpA'. In the NCTC 8325 strain spa is SAOUHSC_00069 and has amino acid sequence SEQ ID NO: 36 (GI:88193885). In the Newman strain it is nwmn_0055 (GI:151220267). All *S.aureus* strains express the structural gene for spa, a well characterized virulence factor whose cell wall-anchored surface protein product has five highly homologous immunoglobulin binding domains designated E, D, A, B, and C [60]. These domains display ~80% identity at the amino acid level, are 56 to 61 residues in length, and are organized as tandem repeats [61]. SpA is synthesized as a precursor protein with an N-terminal signal peptide and a C-terminal sorting signal [62,63]. Cell wall-anchored spa is displayed in great abundance on the staphylococcal surface [64,65]. Each of its immunoglobulin binding domains is composed of antiparallel α -helices that assemble into a three helix bundle and can bind the Fc domain of immunoglobulin G (IgG) [66,67], the VH3 heavy chain (Fab) of IgM (i.e. the B cell receptor) [68], the von Willebrand factor at its A1 domain [69] and/or the TNF- α receptor I (TNFRI) [70], which is displayed on surfaces of airway epithelia.

[0135] Useful spa antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 36 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 36; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 36, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These spa proteins include variants of SEQ ID NO: 36. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 36. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 36 while retaining at least one epitope of SEQ ID NO: 36. The final 35 C-terminal amino acids of SEQ ID NO: 36 can usefully be omitted. The first 36 N-terminal amino acids of SEQ ID NO: 36 can usefully be omitted. Other fragments omit one or more protein domains. Reference 71 suggests that individual IgG-binding domains might be useful immunogens, alone or in combination.

[0136] SEQ ID NO: 162 is a useful fragment of SEQ ID NO: 36 ('SpA₃₇₋₃₂₅'). This fragment contains all the five SpA Ig-binding domains (which are naturally arranged from N- to C-terminus in the order E, D, A, B, C) and includes the most

exposed domain of SpA. It also reduces the antigen's similarity with human proteins. Other useful fragments may omit 1, 2, 3 or 4 of the natural A, B, C, D and/or E domains to prevent the excessive B cell expansion and then apoptosis which might occur if spa functions as a B cell superantigen. As reported in reference 71, other useful fragments may include only 1, 2, 3 or 4 of the natural A, B, C, D and/or E domains *e.g.* comprise only the SpA(A) domain but not B to E, or comprise only the SpA(D) domain but not A, B, C or E, *etc.* Thus a spa antigen useful with the invention may include 1, 2, 3, 4 or 5 IgG-binding domains, but ideally has 4 or fewer

[0137] If an antigen includes only one type of spa domain (*e.g.* only the SpA(A) or SpA(D) domain), it may include more than one copy of this domain *e.g.* multiple SpA(D) domains in a single polypeptide chain.

[0138] An individual domain within the antigen may be mutated at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more amino acids relative to SEQ ID NO: 36 (*e.g.* see ref. 71, disclosing mutations at residues 3 and/or 24 of domain D, at residue 46 and/or 53 of domain A, *etc.*). Such mutants should not remove the antigen's ability to elicit an antibody that recognises SEQ ID NO: 36, but may remove the antigen's binding to IgG and/or other human proteins (such as human blood proteins).

[0139] In certain aspects a spa antigen includes a substitution at (a) one or more amino acid substitution in an IgG Fc binding sub-domain of SpA domain A, B, C, D and/or E that disrupts or decreases binding to IgG Fc, and (b) one or more amino acid substitution in a V_H3 binding sub-domain of SpA domain A, B, C, D, and/or E that disrupts or decreases binding to V_H3. In certain embodiments, a variant SpA comprises at least or at most 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more variant SpA domain D peptide.

Second antigen group

sta001

[0140] The 'sta001' antigen is annotated as '5'-nucleotidase family protein'. In the NCTC 8325 strain sta001 is SAOUHSC_00025 and has amino acid sequence SEQ ID NO: 37 (GI:88193846). In the Newman strain it is nwmn_0022 (GI:151220234). It has also been referred to as AdsA and SasH and SA0024.

[0141] Useful sta001 antigens can elicit an antibody (*e.g.* when administered to a human) that recognises SEQ ID NO: 37 and/or may comprise an amino acid sequence: (a) having 50% or more identity (*e.g.* 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 37; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 37, wherein 'n' is 7 or more (*e.g.* 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta001 proteins include variants of SEQ ID NO: 37. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 37. Other preferred fragments lack one or more amino acids (*e.g.* 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (*e.g.* 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 37 while retaining at least one epitope of SEQ ID NO: 37. The final 34 C-terminal amino acids of SEQ ID NO: 37 can usefully be omitted. The first 38 N-terminal amino acids of SEQ ID NO: 37 can usefully be omitted. Other fragments omit one or more protein domains.

sta002

[0142] The 'sta002' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta002 is SAOUHSC_00356 and has amino acid sequence SEQ ID NO: 38 (GI:88194155). In the Newman strain it is nwmn_0364 (GI:151220576).

[0143] Useful sta002 antigens can elicit an antibody (*e.g.* when administered to a human) that recognises SEQ ID NO: 38 and/or may comprise an amino acid sequence: (a) having 50% or more identity (*e.g.* 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 38; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 38, wherein 'n' is 7 or more (*e.g.* 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150 or more). These sta002 proteins include variants of SEQ ID NO: 38. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 38. Other preferred fragments lack one or more amino acids (*e.g.* 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (*e.g.* 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 38 while retaining at least one epitope of SEQ ID NO: 38. The first 18 N-terminal amino acids of SEQ ID NO: 38 can usefully be omitted. Other fragments omit one or more protein domains.

[0144] SEQ ID NOs: 153 ('sta002₁₉₋₁₈₇') and 154 ('sta002₁₉₋₁₂₄') are two useful fragments of SEQ ID NO: 38 which reduce the antigen's similarity with human proteins.

sta003

[0145] The 'sta003' antigen is annotated as 'surface protein'. In the NCTC 8325 strain sta003 is SAOUHSC_00400 and has amino acid sequence SEQ ID NO: 39 (GI:88194195). In the Newman strain it is nwmn_0401 (GI:151220613).

[0146] Useful sta003 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 39 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 39; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 39, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta003 proteins include variants of SEQ ID NO: 39. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 39. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 39 while retaining at least one epitope of SEQ ID NO: 39. The first 32 N-terminal amino acids of SEQ ID NO: 39 can usefully be omitted. Other fragments omit one or more protein domains.

sta004

[0147] The 'sta004' antigen is annotated as 'Siderophore binding protein FatB'. In the NCTC 8325 strain sta004 is SAOUHSC_00749 and has amino acid sequence SEQ ID NO: 40 (GI:88194514). In the Newman strain it is nwmn_0705 (GI:151220917).

[0148] Useful sta004 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 40 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 40; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 40, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta004 proteins include variants of SEQ ID NO: 40. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 40. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 40 while retaining at least one epitope of SEQ ID NO: 40. The first 18 N-terminal amino acids of SEQ ID NO: 40 can usefully be omitted. Other fragments omit one or more protein domains.

sta005

[0149] The 'sta005' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta005 is SAOUHSC_01127 and has amino acid sequence SEQ ID NO: 41 (GI:88194870). In the Newman strain it is nwmn_1077 (GI:151221289).

[0150] Useful sta005 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 41 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 41; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 41, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta005 proteins include variants of SEQ ID NO: 41. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 41. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 41 while retaining at least one epitope of SEQ ID NO: 41. The first 18 N-terminal amino acids of SEQ ID NO: 41 can usefully be omitted. Other fragments omit one or more protein domains.

sta006

[0151] The 'sta006' antigen is annotated as 'ferrichrome-binding protein', and has also been referred to as 'FhuD2' in the literature [72]. In the NCTC 8325 strain sta006 is SAOUHSC_02554 and has amino acid sequence SEQ ID NO: 42 (GI:88196199). In the Newman strain it is nwmn_2185 (GI: 151222397).

[0152] Useful sta006 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 42 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 42; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 42, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta006 proteins include variants of SEQ ID NO: 42. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 42. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 42 while retaining at least one epitope of SEQ ID NO: 42. The first 17 N-terminal amino acids of SEQ ID NO: 42 can usefully be omitted (to provide SEQ ID NO: 246). Other fragments omit one or more protein domains. Mutant forms of sta006 are reported

in reference 73. A sta006 antigen may be lipidated e.g. with an acylated N-terminus cysteine. One useful sta006 sequence is SEQ ID NO: 248, which has a Met-Ala-Ser- sequence at the N-terminus.

sta007

[0153] The 'sta007' antigen is annotated as 'secretory antigen precursor'. In the NCTC 8325 strain sta007 is SAOUHSC_02571 and has amino acid sequence SEQ ID NO: 43 (GI:88196215). In the Newman strain it is nwmn_2199 (GI:151222411). Proteomic analysis has revealed that this protein is secreted or surface-exposed.

[0154] Useful sta007 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 43 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 43; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 43, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta007 proteins include variants of SEQ ID NO: 43. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 43. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 43 while retaining at least one epitope of SEQ ID NO: 43. The first 27 N-terminal amino acids of SEQ ID NO: 43 can usefully be omitted. Other fragments omit one or more protein domains.

sta008

[0155] The 'sta008' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta008 is SAOUHSC_02650 and has amino acid sequence SEQ ID NO: 44 (GI:88196290). In the Newman strain it is nwmn_2270 (GI:151222482).

[0156] Useful sta008 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 44 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 44; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 44, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta008 proteins include variants of SEQ ID NO: 44. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 44. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 44 while retaining at least one epitope of SEQ ID NO: 44. The first 17 N-terminal amino acids of SEQ ID NO: 44 can usefully be omitted. Other fragments omit one or more protein domains.

sta009

[0157] The 'sta009' antigen is annotated as 'immunoglobulin G-binding protein Sbi'. In the NCTC 8325 strain sta009 is SAOUHSC_02706 and has amino acid sequence SEQ ID NO: 45 (GI:88196346). In the Newman strain it is nwmn_2317 (GI:151222529).

[0158] Useful sta009 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 45 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 45; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 45, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta009 proteins include variants of SEQ ID NO: 45. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 45. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 45 while retaining at least one epitope of SEQ ID NO: 45. The first 29 N-terminal amino acids of SEQ ID NO: 45 can usefully be omitted. Other fragments omit one or more protein domains.

sta010

[0159] The 'sta010' antigen is annotated as 'immunodominant antigen A'. In the NCTC 8325 strain sta010 is SAOUHSC_02887 and has amino acid sequence SEQ ID NO: 46 (GI:88196515). In the Newman strain it is nwmn_2469 (GI:151222681). Proteomic analysis has revealed that this protein is secreted or surface-exposed.

[0160] Useful sta010 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 46 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 46; and/or (b)

comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 46, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta010 proteins include variants of SEQ ID NO: 46. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 46. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 46 while retaining at least one epitope of SEQ ID NO: 46. The first 29 N-terminal amino acids of SEQ ID NO: 46 can usefully be omitted. Other fragments omit one or more protein domains.

sta011

[0161] The 'sta011' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta011 is SAOUHSC_00052 and has amino acid sequence SEQ ID NO: 47 (GI:88193872).

[0162] Useful sta011 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 47 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 47; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 47, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta011 proteins include variants of SEQ ID NO: 47. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 47. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 47 while retaining at least one epitope of SEQ ID NO: 47. The first 23 N-terminal amino acids of SEQ ID NO: 47 can usefully be omitted (to provide SEQ ID NO: 247). Other fragments omit one or more protein domains. A sta011 antigen may be lipidated e.g. with an acylated N-terminus cysteine. One useful sta011 sequence is SEQ ID NO: 249, which has a N-terminus methionine.

[0163] Variant forms of SEQ ID NO: 47 which may be used as or for preparing sta011 antigens include, but are not limited to, SEQ ID NOs: 213, 214 and 215 with various Ile/Val/Leu substitutions.

[0164] Sta011 can exist as a monomer or an oligomer, with Ca⁺⁺ ions favouring oligomerisation. The invention can use monomers and/or oligomers of Sta011.

sta012

[0165] The 'sta012' antigen is annotated as 'protein with leader'. In the NCTC 8325 strain sta012 is SAOUHSC_00106 and has amino acid sequence SEQ ID NO: 48 (GI:88193919).

[0166] Useful sta012 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 48 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 48; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 48, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta012 proteins include variants of SEQ ID NO: 48. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 48. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 48 while retaining at least one epitope of SEQ ID NO: 48. The first 21 N-terminal amino acids of SEQ ID NO: 48 can usefully be omitted. Other fragments omit one or more protein domains.

sta013

[0167] The 'sta013' antigen is annotated as 'poly-gamma-glutamate capsule biosynthesis protein'. In the NCTC 8325 strain sta013 is SAOUHSC_00107 and has amino acid sequence SEQ ID NO: 49 (GI:88193920).

[0168] Useful sta013 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 49 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 49; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 49, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta013 proteins include variants of SEQ ID NO: 49. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 49. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 49 while retaining at least one epitope of SEQ ID NO: 49. Other fragments omit one or more protein domains.

sta014

[0169] The 'sta014' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta014 is SAOUHSC_00137 and has amino acid sequence SEQ ID NO: 50 (GI:88193950).

[0170] Useful sta014 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 50 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 50; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 50, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta014 proteins include variants of SEQ ID NO: 50. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 50. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 50 while retaining at least one epitope of SEQ ID NO: 50. The first 17 N-terminal amino acids of SEQ ID NO: 50 can usefully be omitted. Other fragments omit one or more protein domains.

sta015

[0171] The 'sta015' antigen is annotated as 'extracellular solute-binding protein; RGD containing lipoprotein'. In the NCTC 8325 strain sta015 is SAOUHSC_00170 and has amino acid sequence SEQ ID NO: 51 (GI:88193980).

[0172] Useful sta015 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 51 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 51; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 51, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta015 proteins include variants of SEQ ID NO: 51. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 51. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 51 while retaining at least one epitope of SEQ ID NO: 51. The first 18 N-terminal amino acids of SEQ ID NO: 51 can usefully be omitted. Other fragments omit one or more protein domains.

sta016

[0173] The 'sta016' antigen is annotated as 'gamma-glutamyltranspeptidase'. In the NCTC 8325 strain sta016 is SAOUHSC_00171 and has amino acid sequence SEQ ID NO: 52 (GI:88193981).

[0174] Useful sta016 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 52 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 52; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 52, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta016 proteins include variants of SEQ ID NO: 52. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 52. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 52 while retaining at least one epitope of SEQ ID NO: 52. Other fragments omit one or more protein domains.

sta017

[0175] The 'sta017' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta017 is SAOUHSC_00186 and has amino acid sequence SEQ ID NO: 53 (GI:88193996).

[0176] Useful sta017 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 53 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 53; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 53, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta017 proteins include variants of SEQ ID NO: 53. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 53. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 53 while retaining at least one epitope of SEQ ID NO: 53. The first 17 N-terminal amino acids of SEQ ID NO: 53 can usefully be omitted. Other fragments omit one or more protein domains.

sta018

[0177] The 'sta018' antigen is annotated as 'extracellular solute-binding protein'. In the NCTC 8325 strain sta018 is SAOUHSC_00201 and has amino acid sequence SEQ ID NO: 54 (GI:88194011).

[0178] Useful sta018 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 54 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 54; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 54, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta018 proteins include variants of SEQ ID NO: 54. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 54. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 54 while retaining at least one epitope of SEQ ID NO: 54. Other fragments omit one or more protein domains.

sta019

[0179] The 'sta019' antigen is annotated as 'peptidoglycan hydrolase'. In the NCTC 8325 strain sta019 is SAOUHSC_00248 and has amino acid sequence SEQ ID NO: 55 (GI:88194055). In the Newman, strain it is nwmn_0210 (GI:151220422).

[0180] Useful sta019 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 55 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 55; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 55, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta019 proteins include variants of SEQ ID NO: 55. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 55. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 55 while retaining at least one epitope of SEQ ID NO: 55. The first 25 N-terminal amino acids of SEQ ID NO: 55 can usefully be omitted. Other fragments omit one or more protein domains. Useful fragments are SEQ ID NOs: 228 and 229.

[0181] Sta019 does not adsorb well to aluminium hydroxide adjuvants, so Sta019 present in a composition may be unadsorbed or may be adsorbed to an alternative adjuvant e.g. to an aluminium phosphate.

sta020

[0182] The 'sta020' antigen is annotated as 'exported protein'. In the NCTC 8325 strain sta020 is SAOUHSC_00253 and has amino acid sequence SEQ ID NO: 56 (GI:88194059).

[0183] Useful sta020 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 56 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 56; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 56, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta020 proteins include variants of SEQ ID NO: 56. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 56. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 56 while retaining at least one epitope of SEQ ID NO: 56. The first 30 N-terminal amino acids of SEQ ID NO: 56 can usefully be omitted. Other fragments omit one or more protein domains.

sta021

[0184] The 'sta021' antigen is annotated as 'secretory antigen SsaA-like protein'. In the NCTC 8325 strain sta021 is SAOUHSC_00256 and has amino acid sequence SEQ ID NO: 57 (GI:88194062).

[0185] Useful sta021 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 57 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 57; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 57, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta021 proteins include variants of SEQ ID NO: 57. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 57. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more

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amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 57 while retaining at least one epitope of SEQ ID NO: 57. The first 24 N-terminal amino acids of SEQ ID NO: 57 can usefully be omitted. Other fragments omit one or more protein domains.

5 *sta022*

[0186] The 'sta022' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta022 is SAOUHSC_00279 and has amino acid sequence SEQ ID NO: 58 (GI:88194083).

10 **[0187]** Useful sta022 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 58 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 58; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 58, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These sta022 proteins include variants of SEQ ID NO: 58. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 58. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 58 while retaining at least one epitope of SEQ ID NO: 58. The first 17 N-terminal amino acids of SEQ ID NO: 58 can usefully be omitted. Other fragments omit one or more protein domains.

20 *sta023*

[0188] The 'sta023' antigen is annotated as '5'-nucleotidase; lipoprotein e(P4) family'. In the NCTC 8325 strain sta023 is SAOUHSC_00284 and has amino acid sequence SEQ ID NO: 59 (GI:88194087).

25 **[0189]** Useful sta023 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 59 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 59; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 59, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta023 proteins include variants of SEQ ID NO: 59. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 59. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 59 while retaining at least one epitope of SEQ ID NO: 59. The first 31 N-terminal amino acids of SEQ ID NO: 59 can usefully be omitted. Other fragments omit one or more protein domains.

35 *sta024*

[0190] The 'sta024' antigen is annotated as 'lipase precursor'. In the NCTC 8325 strain sta024 is SAOUHSC_00300 and has amino acid sequence SEQ ID NO: 60 (GI:88194101).

40 **[0191]** Useful sta024 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 60 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 60; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 60, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta024 proteins include variants of SEQ ID NO: 60. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 60. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 60 while retaining at least one epitope of SEQ ID NO: 60. The first 37 N-terminal amino acids of SEQ ID NO: 60 can usefully be omitted. Other fragments omit one or more protein domains.

50 *sta025*

[0192] The 'sta025' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta025 is SAOUHSC_00362 and has amino acid sequence SEQ ID NO: 61 (GI:88194160).

55 **[0193]** Useful sta025 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 61 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 61; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 61, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta025 proteins include variants of SEQ

ID NO: 61. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 61. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 61 while retaining at least one epitope of SEQ ID NO: 61. The first 19 N-terminal amino acids of SEQ ID NO: 61 can usefully be omitted. Other fragments omit one or more protein domains.

sta026

[0194] The 'sta026' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta026 is SAOUHSC_00404 and has amino acid sequence SEQ ID NO: 62 (GI:88194198).

[0195] Useful sta026 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 62 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 62; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 62, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta026 proteins include variants of SEQ ID NO: 62. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 62. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 62 while retaining at least one epitope of SEQ ID NO: 62. The first 22 N-terminal amino acids of SEQ ID NO: 62 can usefully be omitted. Other fragments omit one or more protein domains.

sta027

[0196] The 'sta027' antigen is annotated as 'probable lipase'. In the NCTC 8325 strain sta027 is SAOUHSC_00661 and has amino acid sequence SEQ ID NO: 63 (GI:88194426).

[0197] Useful sta027 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 63 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 63; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 63, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta027 proteins include variants of SEQ ID NO: 63. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 63. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 63 while retaining at least one epitope of SEQ ID NO: 63. The first 23 N-terminal amino acids of SEQ ID NO: 63 can usefully be omitted. Other fragments omit one or more protein domains.

sta028

[0198] The 'sta028' antigen is annotated as 'secretory antigen SsaA-like protein'. In the NCTC 8325 strain sta028 is SAOUHSC_00671 and has amino acid sequence SEQ ID NO: 64 (GI:88194436). In the Newman strain it is nwmn_0634 (GI:151220846).

[0199] Useful sta028 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 64 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 64; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 64, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta028 proteins include variants of SEQ ID NO: 64. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 64. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 64 while retaining at least one epitope of SEQ ID NO: 64. The first 25 N-terminal amino acids of SEQ ID NO: 64 can usefully be omitted. Other fragments omit one or more protein domains.

sta029

[0200] The 'sta029' antigen is annotated as 'ferrichrome binding protein'. In the NCTC 8325 strain sta029 is SAOUHSC_00754 and has amino acid sequence SEQ ID NO: 65 (GI:88194518).

[0201] Useful sta029 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 65 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%,

80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 65; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 65, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta029 proteins include variants of SEQ ID NO: 65. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 65. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 65 while retaining at least one epitope of SEQ ID NO: 65. The final 25 C-terminal amino acids of SEQ ID NO: 65 can usefully be omitted. The first 19 N-terminal amino acids of SEQ ID NO: 65 can usefully be omitted. Other fragments omit one or more protein domains.

stu030

[0202] The 'sta030' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta030 is SAOUHSC_00808 and has amino acid sequence SEQ ID NO: 66 (GI:88194568).

[0203] Useful sta030 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 66 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 66; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 66, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta030 proteins include variants of SEQ ID NO: 66. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 66. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 66 while retaining at least one epitope of SEQ ID NO: 66. The first 17 N-terminal amino acids of SEQ ID NO: 66 can usefully be omitted. Other fragments omit one or more protein domains.

sta031

[0204] The 'sta031' antigen is annotated as '5-nucleotidase family protein'. In the NCTC 8325 strain sta031 is SAOUHSC_00860 and has amino acid sequence SEQ ID NO: 67 (GI:88194617).

[0205] Useful sta031 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 67 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 67; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 67, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta031 proteins include variants of SEQ ID NO: 67. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 67. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 67 while retaining at least one epitope of SEQ ID NO: 67. Other fragments omit one or more protein domains.

sta032

[0206] The 'sta032' antigen is annotated as 'serine protease HtrA'. In the NCTC 8325 strain sta032 is SAOUHSC_00958 and has amino acid sequence SEQ ID NO: 68 (GI:88194715).

[0207] Useful sta032 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 68 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 68; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 68, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta032 proteins include variants of SEQ ID NO: 68. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 68. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 68 while retaining at least one epitope of SEQ ID NO: 68. Other fragments omit one or more protein domains.

sta033

[0208] The 'sta033' antigen is annotated as 'cysteine protease precursor'. In the NCTC 8325 strain sta033 is SAOUHSC_00987 and has amino acid sequence SEQ ID NO: 69 (GI:88194744).

[0209] Useful sta033 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID

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NO: 69 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 69; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 69, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta033 proteins include variants of SEQ ID NO: 69. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 69. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 69 while retaining at least one epitope of SEQ ID NO: 69. The first 29 N-terminal amino acids of SEQ ID NO: 69 can usefully be omitted. Other fragments omit one or more protein domains.

sta034

[0210] The 'sta034' antigen is annotated as 'glutamyl endopeptidase precursor'. In the NCTC 8325 strain sta034 is SAOUHSC_00988 and has amino acid sequence SEQ ID NO: 70 (GI:88194745).

[0211] Useful sta034 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 70 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 70; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 70, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta034 proteins include variants of SEQ ID NO: 70. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 70. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 70 while retaining at least one epitope of SEQ ID NO: 70. The first 29 N-terminal amino acids of SEQ ID NO: 70 can usefully be omitted. Other fragments omit one or more protein domains.

sta035

[0212] The 'sta035' antigen is annotated as 'fmt protein'. In the NCTC 8325 strain sta035 is SAOUHSC_00998 and has amino acid sequence SEQ ID NO: 71 (GI:88194754).

[0213] Useful sta035 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 71 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 71; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 71, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta035 proteins include variants of SEQ ID NO: 71. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 71. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 71 while retaining at least one epitope of SEQ ID NO: 71. The first 25 N-terminal amino acids of SEQ ID NO: 71 can usefully be omitted. Other fragments omit one or more protein domains.

sta036

[0214] The 'sta036' antigen is annotated as 'iron-regulated protein with leader'. In the NCTC 8325 strain sta036 is SAOUHSC_01084 and has amino acid sequence SEQ ID NO: 72 (GI:88194831).

[0215] Useful sta036 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 72 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 72; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 72, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta036 proteins include variants of SEQ ID NO: 72. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 72. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 72 while retaining at least one epitope of SEQ ID NO: 72. The final 27 C-terminal amino acids of SEQ ID NO: 72 can usefully be omitted. The first 32 N-terminal amino acids of SEQ ID NO: 72 can usefully be omitted. Other fragments omit one or more protein domains.

sta037

[0216] The 'sta037' antigen is annotated as 'iron ABC transporter; iron -binding protein lsdE'. In the NCTC 8325 strain sta037 is SAOUHSC_01085 and has amino acid sequence SEQ ID NO: 73 (GI:88194832).

[0217] Useful sta037 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 73 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 73; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 73, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta037 proteins include variants of SEQ ID NO: 73. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 73. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 73 while retaining at least one epitope of SEQ ID NO: 73. The first 9 N-terminal amino acids of SEQ ID NO: 73 can usefully be omitted. Other fragments omit one or more protein domains.

sta038

[0218] The 'sta038' antigen is annotated as 'NPQTN specific sortase B'. In the NCTC 8325 strain spa038 is SAOUHSC_01088 and has amino acid sequence SEQ ID NO: 74 (GI:88194835).

[0219] Useful sta038 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 74 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 74; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 74, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta038 proteins include variants of SEQ ID NO: 74. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 74. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 74 while retaining at least one epitope of SEQ ID NO: 74. The first 21 N-terminal amino acids of SEQ ID NO: 74 can usefully be omitted. Other fragments omit one or more protein domains.

sta039

[0220] The 'sta039' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta039 is SAOUHSC_01124 and has amino acid sequence SEQ ID NO: 75 (GI:88194868).

[0221] Useful sta039 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 75 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 75; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 75, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta039 proteins include variants of SEQ ID NO: 75. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 75. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 75 while retaining at least one epitope of SEQ ID NO: 75. The first 22 N-terminal amino acids of SEQ ID NO: 75 can usefully be omitted. Other fragments omit one or more protein domains.

sta040

[0222] The 'sta040' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta040 is SAOUHSC_01125 and has amino acid sequence SEQ ID NO: 76 (GI:88194869). In the Newman strain it is nwmn_1076 (GI:151221288).

[0223] Useful sta040 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 76 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 76; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 76, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta040 proteins include variants of SEQ ID NO: 76. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 76. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 76 while retaining at least

one epitope of SEQ ID NO: 76. The first 21 N-terminal amino acids of SEQ ID NO: 76 can usefully be omitted. Other fragments omit one or more protein domains.

sta041

[0224] The 'sta041' antigen is annotated as 'fibronectin-binding protein A-related'. In the NCTC 8325 strain sta041 is SAOUHSC_01175 and has amino acid sequence SEQ ID NO: 77 (GI: 88194914).

[0225] Useful sta041 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 77 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 77; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 77, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta041 proteins include variants of SEQ ID NO: 77. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 77. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 77 while retaining at least one epitope of SEQ ID NO: 77. Other fragments omit one or more protein domains.

sta042

[0226] The 'sta042' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta042 is SAOUHSC_01180 and has amino acid sequence SEQ ID NO: 78 (GI:88194919).

[0227] Useful sta042 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 78 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 78; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 78, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta042 proteins include variants of SEQ ID NO: 78. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 78. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 78 while retaining at least one epitope of SEQ ID NO: 78. The first 18 N-terminal amino acids of SEQ ID NO: 78 can usefully be omitted. Other fragments omit one or more protein domains.

sta043

[0228] The 'sta043' antigen is annotated as 'cell wall hydrolase'. In the NCTC 8325 strain sta043 is SAOUHSC_01219 and has amino acid sequence SEQ ID NO: 79 (GI:88194955).

[0229] Useful sta043 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 79 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 79; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 79, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta043 proteins include variants of SEQ ID NO: 79. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 79. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 79 while retaining at least one epitope of SEQ ID NO: 79. The first 38 N-terminal amino acids of SEQ ID NO: 79 can usefully be omitted. Other fragments omit one or more protein domains.

sta044

[0230] The 'sta044' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta044 is SAOUHSC_01508 and has amino acid sequence SEQ ID NO: 80 (GI:88195223).

[0231] Useful sta044 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 80 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 80; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 80, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta044 proteins include variants of SEQ ID NO: 80. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 80. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more

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amino acids (e.g. 1, 2; 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 80 while retaining at least one epitope of SEQ ID NO: 80. The first 17 N-terminal amino acids of SEQ ID NO: 80 can usefully be omitted. Other fragments omit one or more protein domains.

5 *sta045*

[0232] The 'sta045' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta045 is SAOUHSC_01627 and has amino acid sequence SEQ ID NO: 81 (GI:88195337).

10 **[0233]** Useful sta045 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 81 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 81; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 81, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150 or more). These sta045 proteins include variants of SEQ ID NO: 81. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 81. Other preferred fragments lack one or
15 more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 81 while retaining at least one epitope of SEQ ID NO: 81. The first 16 N-terminal amino acids of SEQ ID NO: 81 can usefully be omitted. Other fragments omit one or more protein domains.

20 *sta046*

[0234] The 'sta046' antigen is annotated as 'Excalibur protein'. In the NCTC 8325 strain sta046 is SAOUHSC_01918 and has amino acid sequence SEQ ID NO: 82 (GI:88195613).

25 **[0235]** Useful sta046 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 82 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 82; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 82, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta046 proteins include variants of SEQ ID NO: 82. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 82. Other preferred fragments lack one or
30 more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 82 while retaining at least one epitope of SEQ ID NO: 82. The first 53 N-terminal amino acids of SEQ ID NO: 82 can usefully be omitted. Other fragments omit one or more protein domains.

35 *sta047*

[0236] The 'sta047' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta047 is SAOUHSC_01920 and has amino acid sequence SEQ ID NO: 83 (GI:88195615).

40 **[0237]** Useful sta047 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 83 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 83; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 83, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta047 proteins include variants of SEQ ID NO: 83. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 83. Other preferred fragments lack
45 one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 83 while retaining at least one epitope of SEQ ID NO: 83. The first 18 N-terminal amino acids of SEQ ID NO: 83 can usefully be omitted. Other fragments omit one or more protein domains.

50 *sta048*

[0238] The 'sta048' antigen is annotated as 'intracellular serine protease'. In the NCTC 8325 strain sta048 is SAOUHSC_01949 and has amino acid sequence SEQ ID NO: 84 (GI:88195642).

55 **[0239]** Useful sta048 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 84 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 84; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 84, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta048 proteins include variants

of SEQ ID NO: 84. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 84. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 84 while retaining at least one epitope of SEQ ID NO: 84. The first 27 N-terminal amino acids of SEQ ID NO: 84 can usefully be omitted. Other fragments omit one or more protein domains.

sta049

[0240] The 'sta049' antigen is annotated as 'protein export protein PrsA'. In the NCTC 8325 strain sta049 is SAOUHSC_01972 and has amino acid sequence SEQ ID NO: 85 (GI:88195663). In the Newman strain it is nwmn_1733 (GI: 151221945).

[0241] Useful sta049 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 85 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 85; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 85, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta049 proteins include variants of SEQ ID NO: 85. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 85. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 85 while retaining at least one epitope of SEQ ID NO: 85. The first 25 N-terminal amino acids of SEQ ID NO: 85 can usefully be omitted. Other fragments omit one or more protein domains.

sta050

[0242] The 'sta050' antigen is annotated as 'staphopain thiol proteinase'. In the NCTC 8325 strain sta050 is SAOUHSC_02127 and has amino acid sequence SEQ ID NO: 86 (GI:88195808).

[0243] Useful sta050 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 86 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 86; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 86, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta050 proteins include variants of SEQ ID NO: 86. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 86. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 86 while retaining at least one epitope of SEQ ID NO: 86. The first 25 N-terminal amino acids of SEQ ID NO: 86 can usefully be omitted. Other fragments omit one or more protein domains.

sta051

[0244] The 'sta051' antigen is annotated as 'protein with leader'. In the NCTC 8325 strain sta051 is SAOUHSC_02147 and has amino acid sequence SEQ ID NO: 87 (GI:88195827).

[0245] Useful sta051 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 87 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 87; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 87, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta051 proteins include variants of SEQ ID NO: 87. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 87. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 87 while retaining at least one epitope of SEQ ID NO: 87. The first 24 N-terminal amino acids of SEQ ID NO: 87 can usefully be omitted. Other fragments omit one or more protein domains.

sta052

[0246] The 'sta052' antigen is annotated as 'ferric hydroxamate receptor 1'. In the NCTC 8325 strain sta052 is SAOUHSC_02246 and has amino acid sequence SEQ ID NO: 88 (GI:88195918).

[0247] Useful sta052 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 88 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%,

80%, 85%, 90%, 91 %, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 88; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 88, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta052 proteins include variants of SEQ ID NO: 88. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 88. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 88 while retaining at least one epitope of SEQ ID NO: 88. The first 17 N-terminal amino acids of SEQ ID NO: 88 can usefully be omitted. Other fragments omit one or more protein domains.

sta053

[0248] The 'sta053' antigen is annotated as 'srdH family protein'. In the NCTC 8325 strain sta053 is SAOUHSC_02257 and has amino acid sequence SEQ ID NO: 89 (GI:88195928).

[0249] Useful sta053 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 89 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 89; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 89, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta053 proteins include variants of SEQ ID NO: 89. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 89. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 89 while retaining at least one epitope of SEQ ID NO: 89. The first 26 N-terminal amino acids of SEQ ID NO: 89 can usefully be omitted. Other fragments omit one or more protein domains.

sta054

[0250] The 'sta054' antigen is annotated as 'Probable transglycosylase isaA precursor'. In the NCTC 8325 strain sta054 is SAOUHSC_02333 and has amino acid sequence SEQ ID NO: 90 (GI:88195999). Useful sta054 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 90 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 90; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 90, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta054 proteins include variants of SEQ ID NO: 90. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 90. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 90 while retaining at least one epitope of SEQ ID NO: 90. The first 27 N-terminal amino acids of SEQ ID NO: 90 can usefully be omitted. Other fragments omit one or more protein domains.

sta055

[0251] The 'sta055' antigen is annotated as 'surface hydrolase'. In the NCTC 8325 strain sta055 is SAOUHSC_02448 and has amino acid sequence SEQ ID NO: 91 (GI:88196100).

[0252] Useful sta055 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 91 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 91; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 91, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta055 proteins include variants of SEQ ID NO: 91. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 91. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 91 while retaining at least one epitope of SEQ ID NO: 91. The first 31 N-terminal amino acids of SEQ ID NO: 91 can usefully be omitted. Other fragments omit one or more protein domains.

sta056

[0253] The 'sta056' antigen is annotated as 'hyaluronate lyase'. In the NCTC 8325 strain sta056 is SAOUHSC_02463 and has amino acid sequence SEQ ID NO: 92 (GI:88196115).

[0254] Useful sta056 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID

NO: 92 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91 %, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 92; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 92, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta056 proteins include variants of SEQ ID NO: 92. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 92. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 92 while retaining at least one epitope of SEQ ID NO: 92. The first 24 N-terminal amino acids of SEQ ID NO: 92 can usefully be omitted. Other fragments omit one or more protein domains.

sta057

[0255] The 'sta057' antigen is annotated as 'secretory antigen precursor SsaA'. In the NCTC 8325 strain sta057 is SAOUHSC_02576 and has amino acid sequence SEQ ID NO: 93 (GI:88196220). In the Newman strain it is nwmn_2203 (GI:151222415).

[0256] Useful sta057 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 93 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 93; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 93, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150 or more). These sta057 proteins include variants of SEQ ID NO: 93. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 93. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 93 while retaining at least one epitope of SEQ ID NO: 93. The first 27 N'-terminal amino acids of SEQ ID NO: 93 can usefully be omitted. Other fragments omit one or more protein domains.

sta058

[0257] The 'sta058' antigen is annotated as 'Zn-binding lipoprotein adcA-like'. In the NCTC 8325 strain sta058 is SAOUHSC_02690 and has amino acid sequence SEQ ID NO: 94 (GI:88196330).

[0258] Useful sta058 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 94 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 94; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 94, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta058 proteins include variants of SEQ ID NO: 94. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 94. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 94 while retaining at least one epitope of SEQ ID NO: 94. The first 20 N-terminal amino acids of SEQ ID NO: 94 can usefully be omitted. Other fragments omit one or more protein domains.

sta059

[0259] The 'sta059' antigen is annotated as 'gamma-hemolysin h-gamma-ii subunit'. In the NCTC 8325 strain sta059 is SAOUHSC_02708 and has amino acid sequence SEQ ID NO: 95 (GI:88196348).

[0260] Useful sta059 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 95 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 95; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 95, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta059 proteins include variants of SEQ ID NO: 95. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 95. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 95 while retaining at least one epitope of SEQ ID NO: 95. The first 20 N-terminal amino acids of SEQ ID NO: 95 can usefully be omitted. Other fragments omit one or more protein domains.

sta060

[0261] The 'sta060' antigen is annotated as 'peptide ABC transporter; peptide-binding protein'. In the NCTC 8325 strain sta060 is SAOUHSC_02767 and has amino acid sequence (SEQ ID NO: 96 (GI:88196403)).

[0262] Useful sta060 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 96 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 96; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 96, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta060 proteins include variants of SEQ ID NO: 96. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 96. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 96 while retaining at least one epitope of SEQ ID NO: 96. The first 20 N-terminal amino acids of SEQ ID NO: 96 can usefully be omitted. Other fragments omit one or more protein domains.

sta061

[0263] The 'sta061' antigen is annotated as 'protein with leader'. In the NCTC 8325 strain sta061 is SAOUHSC_02783 and has amino acid sequence SEQ ID NO: 97 (GI:88196419).

[0264] Useful sta061 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 97 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 97; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 97, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta061 proteins include variants of SEQ ID NO: 97. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 97. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 97 while retaining at least one epitope of SEQ ID NO: 97. The first 21 N-terminal amino acids of SEQ ID NO: 97 can usefully be omitted. Other fragments omit one or more protein domains.

sta062

[0265] The 'sta062' antigen is annotated as 'protein with leader'. In the NCTC 8325 strain sta062 is SAOUHSC_02788 and has amino acid sequence SEQ ID NO: 98 (GI:88196424).

[0266] Useful sta062 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 98 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 98; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 98, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta062 proteins include variants of SEQ ID NO: 98. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 98. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 98 while retaining at least one epitope of SEQ ID NO: 98. The first 22 N-terminal amino acids of SEQ ID NO: 98 can usefully be omitted. Other fragments omit one or more protein domains.

sta063

[0267] The 'sta063' antigen is annotated as 'aureolysin'. In the NCTC 8325 strain sta063 is SAOUHSC_02971 and has amino acid sequence SEQ ID NO: 99 (GI:88196592).

[0268] Useful sta063 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 99 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 99; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 99, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta063 proteins include variants of SEQ ID NO: 99. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 99. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 99 while retaining at least one epitope of SEQ ID NO: 99. The first 16 N-terminal amino acids of SEQ ID NO: 99 can usefully be omitted.

Other fragments omit one or more protein domains.

sta064

- 5 **[0269]** The 'sta064' antigen is annotated as 'lipase'. In the NCTC 8325 strain sta064 is SAOUHSC_03006 and has amino acid sequence SEQ ID NO: 100 (GI:88196625). In the Newman strain it is nwmn_2569 (GI:151222781).
- [0270]** Useful sta064 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 100 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 100; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 100, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta064 proteins include variants of SEQ ID NO: 100. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 100. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 100 while retaining at least one epitope of SEQ ID NO: 100. The first 34 N-terminal amino acids of SEQ ID NO: 100 can usefully be omitted. Other fragments omit one or more protein domains.

sta065

- 20 **[0271]** The 'sta065' antigen is annotated as '1-phosphatidylinositol phosphodiesterase precursor'. In the NCTC 8325 strain sta065 is SAOUHSC_00051 and has amino acid sequence SEQ ID NO: 101 (GI:88193871).
- [0272]** Useful sta065 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 101 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 101; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 101, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta065 proteins include variants of SEQ ID NO: 101. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 101. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 101 while retaining at least one epitope of SEQ ID NO: 101. The first 26 N-terminal amino acids of SEQ ID NO: 101 can usefully be omitted. Other fragments omit one or more protein domains.

sta066

- 35 **[0273]** The 'sta066' antigen is annotated as 'protein'. In the NCTC 8325 strain sta066 is SAOUHSC_00172 and has amino acid sequence SEQ ID NO: 102 (GI:88193982).
- [0274]** Useful sta066 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 102 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 102; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 102, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta066 proteins include variants of SEQ ID NO: 102. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 102. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 102 while retaining at least one epitope of SEQ ID NO: 102. The first 21 N-terminal amino acids of SEQ ID NO: 102 can usefully be omitted. Other fragments omit one or more protein domains.

sta067

- 50 **[0275]** The 'sta067' antigen is annotated as 'bacterial extracellular solute-binding protein'. In the NCTC 8325 strain sta067 is SAOUHSC_00176 and has amino acid sequence SEQ ID NO: 103 (GI:88193986).
- [0276]** Useful sta067 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 103 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 103; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 103, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta067 proteins include variants of SEQ ID NO: 103. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 103. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or

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more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 103 while retaining at least one epitope of SEQ ID NO: 103. The first 20 N-terminal amino acids of SEQ ID NO: 103 can usefully be omitted. Other fragments omit one or more protein domains.

5 *sta068*

[0277] The 'sta068' antigen is annotated as 'iron permease FTR1'. In the NCTC 8325 strain sta068 is SAOUHSC_00327 and has amino acid sequence SEQ ID NO: 104 (GI:88194127).

10 **[0278]** Useful sta068 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 104 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 104; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 104, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta068 proteins include variants of SEQ ID NO: 104. Preferred fragments, of (b) comprise an epitope from SEQ ID NO: 104. Other preferred fragments
15 lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 104 while retaining at least one epitope of SEQ ID NO: 104. The final 20 C-terminal amino acids of SEQ ID NO: 104 can usefully be omitted. The first 14 N-terminal amino acids of SEQ ID NO: 104 can usefully be omitted. Other fragments omit one or more protein domains.

20

sta069

[0279] The 'sta069' antigen is annotated as 'autolysin precursor'. In the NCTC 8325 strain sta069 is SAOUHSC_00427 and has amino acid sequence SEQ ID NO: 105 (GI:88194219).

25 **[0280]** Useful sta069 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 105 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 105; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 105, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta069 proteins include variants of SEQ ID NO: 105. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 105. Other preferred fragments
30 lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 105 while retaining at least one epitope of SEQ ID NO: 105. The first 25 N-terminal amino acids of SEQ ID NO: 105 can usefully be omitted. Other fragments omit one or more protein domains.

35

sta070

[0281] The 'sta070' antigen is annotated as 'immunogenic secreted precursor-like protein (truncated)'. In the NCTC 8325 strain sta070 is SAOUHSC_00773 and has amino acid sequence SEQ ID NO: 106 (GI:88194535).

40 **[0282]** Useful sta070 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 106 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 106; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 106, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta070 proteins include variants of SEQ ID NO: 106. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 106. Other preferred fragments
45 lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 106 while retaining at least one epitope of SEQ ID NO: 106. The first 24 N-terminal amino acids of SEQ ID NO: 106 can usefully be omitted. Other fragments omit one or more protein domains.

50

sta071

[0283] The 'sta071' antigen is annotated as 'hemolysin'. In the NCTC 8325 strain sta071 is SAOUHSC_00854 and has amino acid sequence SEQ ID NO: 107 (GI:88194612).

55 **[0284]** Useful sta071 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 107 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 107; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 107, wherein 'n' is 7 or more (e.g. 8, 10,

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12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta071 proteins include variants of SEQ ID NO: 107. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 107. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 107 while retaining at least one epitope of SEQ ID NO: 107. The first 24 N-terminal amino acids of SEQ ID NO: 107 can usefully be omitted. Other fragments omit one or more protein domains.

sta072

[0285] The 'sta072' antigen is annotated as 'extramembranal protein'. In the NCTC 8325 strain sta072 is SAOUHSC_00872 and has amino acid sequence SEQ ID NO: 108 (GI:88194629).

[0286] Useful sta072 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 108 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 108; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 108, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta072 proteins include variants of SEQ ID NO: 108. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 108. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 108 while retaining at least one epitope of SEQ ID NO: 108. The first 24 N-terminal amino acids of SEQ ID NO: 108 can usefully be omitted. Other fragments omit one or more protein domains.

sta073

[0287] The 'sta073' antigen is annotated as 'bifunctional autolysin precursor'. In the NCTC 8325 strain sta073 is SAOUHSC_00994 and has amino acid sequence SEQ ID NO: 109 (GI:88194750). In the Newman strain it is nwmn_0922 (GI:151221134). Proteomic analysis has revealed that this protein is secreted or surface-exposed.

[0288] Useful sta073 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 109 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 109; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 109, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta073 proteins include variants of SEQ ID NO: 109. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 109. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 109 while retaining at least one epitope of SEQ ID NO: 109. The first 24 N-terminal amino acids of SEQ ID NO: 109 can usefully be omitted. Other fragments omit one or more protein domains.

[0289] A Sta073 antigen can usefully be included in a composition in combination with a Sta112 [74].

[0290] Sta073 does not adsorb well to aluminium hydroxide adjuvants, so Sta073 present in a composition may be unadsorbed or may be adsorbed to an alternative adjuvant e.g. to an aluminium phosphate.

sta074

[0291] The 'sta074' antigen is annotated as 'factor essential for methicillin resistance'. In the NCTC 8325 strain sta074 is SAOUHSC_01220 and has amino acid sequence SEQ ID NO: 110 (GI:88194956).

[0292] Useful sta074 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 110 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 110; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 110, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta074 proteins include variants of SEQ ID NO: 110. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 110. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 110 while retaining at least one epitope of SEQ ID NO: 110. Other fragments omit one or more protein domains.

sta075

[0293] The 'sta075' antigen is annotated as 'insulysin; peptidase family M16'. In the NCTC 8325 strain sta075 is

SAOUHSC_01256 and has amino acid sequence SEQ ID NO: 111 (GI:88194989).

[0294] Useful sta075 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 111 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 111; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 111, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta075 proteins include variants of SEQ ID NO: 111. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 111. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 111 while retaining at least one epitope of SEQ ID NO: 111. Other fragments omit one or more protein domains.

sta076

[0295] The 'sta076' antigen is annotated as 'hydrolase'. In the NCTC 8325 strain sta076 is SAOUHSC_01263 and has amino acid sequence SEQ ID NO: 112 (GI:88194996).

[0296] Useful sta076 antigens can elicit an antibody (e.g. when administered to a human) that recognise SEQ ID NO: 112 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 112; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 112, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta076 proteins include variants of SEQ ID NO: 112. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 112. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 112 while retaining at least one epitope of SEQ ID NO: 112. The first 24 N-terminal amino acids of SEQ ID NO: 112 can usefully be omitted. Other fragments omit one or more protein domains.

sta077

[0297] The 'sta077' antigen is annotated as 'protein'. In the NCTC 8325 strain sta077 is SAOUHSC_01317 and has amino acid sequence SEQ ID NO: 113 (GI:88195047). Proteomic analysis has revealed that this protein is secreted or surface-exposed.

[0298] Useful sta077 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 113 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 113; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 113, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta077 proteins include variants of SEQ ID NO: 113. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 113. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 113 while retaining at least one epitope of SEQ ID NO: 113. The first 20 N-terminal amino acids of SEQ ID NO: 113 can usefully be omitted. Other fragments omit one or more protein domains.

sta078

[0299] The 'sta078' antigen is annotated as 'FtsK/SpoIIIE family protein'. In the NCTC 8325 strain sta078 is SAOUHSC_01857 and has amino acid sequence SEQ ID NO: 114 (GI:88195555).

[0300] Useful sta078 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 114 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 114; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 114, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta078 proteins include variants of SEQ ID NO: 114. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 114. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 114 while retaining at least one epitope of SEQ ID NO: 114. Other fragments omit one or more protein domains.

sta079

[0301] The 'sta079' antigen is annotated as 'serine protease SpIF'. In the NCTC 8325 strain sta079 is SAOUHSC_01935 and has amino acid sequence SEQ ID NO: 115 (GI:88195630).

[0302] Useful sta079 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 115 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 115; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 115, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta079 proteins include variants of SEQ ID NO: 115. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 115. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 115 while retaining at least one epitope of SEQ ID NO: 115. The first 36 N-terminal amino acids of SEQ ID NO: 115 can usefully be omitted. Other fragments omit one or more protein domains.

sta080

[0303] The 'sta080' antigen is annotated as 'serine protease Sp1E'. In the NCTC 8325 strain sta080 is SAOUHSC_01936 and has amino acid sequence SEQ ID NO: 116 (GI:88195631).

[0304] Useful sta080 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 116 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 116; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 116, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta080 proteins include variants of SEQ ID NO: 116. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 116. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 116 while retaining at least one epitope of SEQ ID NO: 116. The first 36 N-terminal amino acids of SEQ ID NO: 116 can usefully be omitted. Other fragments omit one or more protein domains.

sta081

[0305] The 'sta081' antigen is annotated as 'serine protease SpID (EC:3.4.21.19)'. In the NCTC 8325 strain sta081 is SAOUHSC_01938 and has amino acid sequence SEQ ID NO: 170 (GI:88195633).

[0306] Useful sta081 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 170 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 170; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 170, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta081 proteins include variants of SEQ ID NO: 170. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 170. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 170 while retaining at least one epitope of SEQ ID NO: 170. The first 36 N-terminal amino acids of SEQ ID NO: 170 can usefully be omitted. Other fragments omit one or more protein domains.

sta082

[0307] The 'sta082' antigen is annotated as 'serine protease SpIC'. In the NCTC 8325 strain sta082 is SAOUHSC_01939 and has amino acid sequence SEQ ID NO: 117 (GI:88195634).

[0308] Useful sta082 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 117 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 117; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 117, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta082 proteins include variants of SEQ ID NO: 117. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 117. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 117 while retaining at least one epitope of SEQ ID NO: 117. The first 36 N-terminal amino acids of SEQ ID NO: 117 can usefully be omitted.

Other fragments omit one or more protein domains.

sta083

5 **[0309]** The 'sta083' antigen is annotated as 'serine protease SplB'. In the NCTC 8325 strain sta083 is SAOUHSC_01941 and has amino acid sequence SEQ ID NO: 118 (GI:88195635).

[0310] Useful sta083 antigens can elicit an antibody (e.g. when administered to a human) that recognise SEQ ID NO: 118 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 118; and/or (b) comprising
10 a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 118, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta083 proteins include variants of SEQ ID NO: 118. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 118. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3; 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 118 while retaining at least one
15 epitope of SEQ ID NO: 118. The first 36 N-terminal amino acids of SEQ ID NO: 118 can usefully be omitted. Other fragments omit one or more protein domains.

sta084

20 **[0311]** The 'sta084' antigen is annotated as 'serine protease SplA'. In the NCTC 8325 strain sta084 is SAOUHSC_01942 and has amino acid sequence SEQ ID NO: 119 (GI:88195636).

[0312] Useful sta084 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 119 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 119; and/or (b)
25 comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 119, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta084 proteins include variants of SEQ ID NO: 119. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 119. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 119 while retaining
30 at least one epitope of SEQ ID NO: 119. The first 35 N-terminal amino acids of SEQ ID NO: 119 can usefully be omitted. Other fragments omit one or more protein domains.

sta085

35 **[0313]** The 'sta085' antigen is annotated as 'staphylokinase precursor'. In the NCTC 8325' strain sta085' is SAOUHSC_02171 and has amino acid sequence SEQ ID NO: 120 (GI:88195848).

[0314] Useful sta085 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 120 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 120; and/or (b)
40 comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 120, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150 or more). These sta085 proteins include variants of SEQ ID NO: 120. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 120. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 120 while retaining at least
45 one epitope of SEQ ID NO: 120. The first 27 N-terminal amino acids of SEQ ID NO: 120 can usefully be omitted. Other fragments omit one or more protein domains.

sta086

50 **[0315]** The 'sta086' antigen is annotated as 'OxaA-like protein'. In the NCTC 8325 strain sta086 is SAOUHSC_02327 and has amino acid sequence SEQ ID NO: 121 (GI:88195993).

[0316] Useful sta086 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 121 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 121; and/or (b)
55 comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 121, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta086 proteins include variants of SEQ ID NO: 121. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 121. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or

more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 121 while retaining at least one epitope of SEQ ID NO: 121. The first 19 N-terminal amino acids of SEQ ID NO: 121 can usefully be omitted. Other fragments omit one or more protein domains.

5 *sta087*

[0317] The 'sta087' antigen is annotated as 'teicoplanin resistance protein TcaA'. In the NCTC 8325 strain sta087 is SAOUHSC_02635 and has amino acid sequence SEQ ID NO: 122 (GI:88196276).

10 **[0318]** Useful sta087 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 122 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 122; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 122, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta087 proteins include variants of SEQ ID NO: 122. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 122. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 122 while retaining at least one epitope of SEQ ID NO: 122. Other fragments omit one or more protein domains.

20 *sta088*

[0319] The 'sta088' antigen is annotated as 'esterase'. In the NCTC 8325 strain sta088 is SAOUHSC_02844 and has amino acid sequence SEQ ID NO: 123 (GI:88196477).

25 **[0320]** Useful sta088 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 123 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 123; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 123, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta088 proteins include variants of SEQ ID NO: 123. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 123. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 123 while retaining at least one epitope of SEQ ID NO: 123. The first 18 N-terminal amino acids of SEQ ID NO: 123 can usefully be omitted. Other fragments omit one or more protein domains.

35 *sta089*

[0321] The 'sta089' antigen is annotated as 'LysM domain protein'. In the NCTC 8325 strain sta089 is SAOUHSC_02855 and has amino acid sequence SEQ ID NO: 124 (GI:88196486).

40 **[0322]** Useful sta089 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 124 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 124; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 124, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These sta089 proteins include variants of SEQ ID NO: 124. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 124. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 124 while retaining at least one epitope of SEQ ID NO: 124. The first 20 N-terminal amino acids of SEQ ID NO: 124 can usefully be omitted. Other fragments omit one or more protein domains.

50 *sea090*

[0323] The 'sta090' antigen is annotated as 'LysM domain protein'. In the NCTC 8325 strain sta090 is SAOUHSC_02883 and has amino acid sequence SEQ ID NO: 125 (GI:88196512).

55 **[0324]** Useful sta090 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 125 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 125; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 125, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta090 proteins include variants of SEQ ID NO: 125. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 125. Other preferred fragments

lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 125 while retaining at least one epitope of SEQ ID NO: 125. The first 26 N-terminal amino acids of SEQ ID NO: 125 can usefully be omitted. Other fragments omit one or more protein domains.

5 *sta091*

[0325] The 'sta091' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta091 is SAOUHSC_00685 and has amino acid sequence SEQ ID NO: 126 (GI:88194450).

10 **[0326]** Useful sta091 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 126 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 126; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 126, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These sta091 proteins include variants of SEQ ID NO: 126. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 126. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 126 while retaining at least one epitope of SEQ ID NO: 126. The first 15 N-terminal amino acids of SEQ ID NO: 126 can usefully be omitted. Other fragments omit one or more protein domains.

20 *sta092*

[0327] The 'sta092' antigen is annotated as 'M23/M37 peptidase domain protein'. In the NCTC 8325 strain sta092 is SAOUHSC_00174 and has amino acid sequence SEQ ID NO: 127 (GI:88193984).

25 **[0328]** Useful sta092 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 127 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 127; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 127, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150 or more). These sta092 proteins include variants of SEQ ID NO: 127. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 127. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 127 while retaining at least one epitope of SEQ ID NO: 127. The first 25 N-terminal amino acids of SEQ ID NO: 127 can usefully be omitted. Other fragments omit one or more protein domains.

35 *sta093*

[0329] The 'sta093' antigen is annotated as 'protein'. In the NCTC 8325 strain sta093 is SAOUHSC_01854 and has amino acid sequence SEQ ID NO: 128 (GI:88195552).

40 **[0330]** Useful sta093 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 128 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 128; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 128, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta093 proteins include variants of SEQ ID NO: 128. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 128. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 128 while retaining at least one epitope of SEQ ID NO: 128. Other fragments omit one or more protein domains.

50 *sta094*

[0331] The 'sta094' antigen is annotated as 'protein'. In the NCTC 8325 strain sta094 is SAOUHSC_01512 and has amino acid sequence SEQ ID NO: 129 (GI:88195226).

55 **[0332]** Useful sta094 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 129 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 129; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 129, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta094 proteins include variants

of SEQ ID NO: 129. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 129. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 1-29 while retaining at least one epitope of SEQ ID NO: 129. The first 17 N-terminal amino acids of SEQ ID NO: 129 can usefully be omitted. Other fragments omit one or more protein domains.

sta095

[0333] The 'sta095' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta095 is SAOUHSC_00383 and has amino acid sequence SEQ ID NO: 130 (GI:88194180). In the Newman strain it is nwmn_0388 (GI:151220600).

[0334] Useful sta095 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 130 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 130; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 130, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta095 proteins include variants of SEQ ID NO: 130. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 130. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 130 while retaining at least one epitope of SEQ ID NO: 130. The first 32 N-terminal amino acids of SEQ ID NO: 130 can usefully be omitted. Other fragments omit one or more protein domains.

sta096

[0335] The 'sta096' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta096 is SAOUHSC_00384 and has amino acid sequence SEQ ID NO: 131 (GI:88194181).

[0336] Useful sta096 antigens can elicit an antibody (e.g. when administered to a human) that recognises (SEQ ID NO: 131 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 131; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 131, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta096 proteins include variants of SEQ ID NO: 131. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 131. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 131 while retaining at least one epitope of SEQ ID NO: 131. The first 30 N-terminal amino acids of SEQ ID NO: 131 can usefully be omitted. Other fragments omit one or more protein domains.

sta097

[0337] The 'sta097' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta097 is SAOUHSC_00386 and has amino acid sequence SEQ ID NO: 132 (GI:88194182).

[0338] Useful sta097 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 132 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 132; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 132, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta097 proteins include variants of SEQ ID NO: 132. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 132. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 132 while retaining at least one epitope of SEQ ID NO: 132. The first 30 N-terminal amino acids of SEQ ID NO: 132 can usefully be omitted. Other fragments omit one or more protein domains.

sta098

[0339] The 'sta098' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta098 is SAOUHSC_00389 and has amino acid sequence SEQ ID NO: 133 (GI:88194184). In the Newman strain it is nwmn_0391 (GI:151220603).

[0340] Useful sta098 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID

NO: 133 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%; 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 133; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 133, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta098 proteins include variants of SEQ ID NO: 133. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 133. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 133 while retaining at least one epitope of SEQ ID NO: 133. The first 30 N-terminal amino acids of SEQ ID NO: 133 can usefully be omitted. Other fragments omit one or more protein domains.

sta099

[0341] The 'sta099' antigen is annotated as 'superantigen-like protein 5'. In the NCTC 8325 strain sta099 is SAOUHSC_00390 and has amino acid sequence SEQ ID NO: 134 (GI:88194185).

[0342] Useful sta099 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 134 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 134; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 134, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta099 proteins include variants of SEQ ID NO: 134. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 134. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 134 while retaining at least one epitope of SEQ ID NO: 134. The first 30 N-terminal amino acids of SEQ ID NO: 134 can usefully be omitted. Other fragments omit one or more protein domains.

sta100

[0343] The 'sta100' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta100 is SAOUHSC_00391 and has amino acid sequence SEQ ID NO: 135 (GI:88194186).

[0344] Useful sta100 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 135 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 135; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 135, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta100 proteins include variants of SEQ ID NO: 135. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 135. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 135 while retaining at least one epitope of SEQ ID NO: 135. The first 30 N-terminal amino acids of SEQ ID NO: 135 can usefully be omitted. Other fragments omit one or more protein domains.

sta101

[0345] The 'sta101' antigen is annotated as 'superantigen-like protein 7'. In the NCTC 8325 strain sta101 is SAOUHSC_00392 and has amino acid sequence SEQ ID NO: 136 (GI:88194187). In the Newman strain it is nwmn_0394 (GI:151220606).

[0346] Useful sta101 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 136 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 136; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 136, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta101 proteins include variants of SEQ ID NO: 136. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 136. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 136 while retaining at least one epitope of SEQ ID NO: 136. The first 30 N-terminal amino acids of SEQ ID NO: 136 can usefully be omitted. Other fragments omit one or more protein domains.

sta102

[0347] The 'sta102' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta102 is SAOUHSC_00393 and has amino acid sequence SEQ ID NO: 137 (GI:88194188).

[0348] Useful sta102 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 137 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 137; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 137, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta102 proteins include variants of SEQ ID NO: 137. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 137. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 137 while retaining at least one epitope of SEQ ID NO: 137. The first 17 N-terminal amino acids of SEQ ID NO: 137 can usefully be omitted. Other fragments omit one or more protein domains.

sta103

[0349] The 'sta103' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta103 is SAOUHSC_00394 and has amino acid sequence SEQ ID NO: 138 (GI:88194189).

[0350] Useful sta103 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 138 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 138; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 138, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta103 proteins include variants of SEQ ID NO: 138. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 138. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 138 while retaining at least one epitope of SEQ ID NO: 138. The first 23 N-terminal amino acids of SEQ ID NO: 138 can usefully be omitted. Other fragments omit one or more protein domains.

sta104

[0351] The 'sta104' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta104 is SAOUHSC_00395 and has amino acid sequence SEQ ID NO: 139 (GI:88194190).

[0352] Useful sta104 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 139 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 139; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 139, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta104 proteins include variants of SEQ ID NO: 139. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 139. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 139 while retaining at least one epitope of SEQ ID NO: 139. Other fragments omit one or more protein domains.

sta105

[0353] The 'sta105' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta105 is SAOUHSC_00399 and has amino acid sequence SEQ ID NO: 140 (GI:88194194). In the Newman strain it is nwmn_0400 (GI:151220612).

[0354] Useful sta105 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 140 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 140; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 140, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta105 proteins include variants of SEQ ID NO: 140. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 140. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 140 while retaining at least one epitope of SEQ ID NO: 140. The first 30 N-terminal amino acids of SEQ ID NO: 140 can usefully be omitted.

Other fragments omit one or more protein domains.

sta106

5 **[0355]** The 'sta106' antigen is annotated as 'hypothetical protein'. In the NCTC 8325 strain sta106 is SAOUHSC_01115 and has amino acid sequence SEQ ID NO: 141 (GI:88194861).

[0356] Useful sta106 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 141 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 141; and/or (b) 10 comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 141, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These sta106 proteins include variants of SEQ ID NO: 141. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 141. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 141 while retaining at least 15 one epitope of SEQ ID NO: 141. The first 16 N-terminal amino acids of SEQ ID NO: 141 can usefully be omitted. Other fragments omit one or more protein domains.

sta107

20 **[0357]** The 'sta107' antigen is annotated as 'hypothetical protein'. In the NCTC 8325 strain sta107 is SAOUHSC_00354 and has amino acid sequence SEQ ID NO: 177 (GI:88194153).

[0358] Useful sta107 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 177 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 177; and/or (b) 25 comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 177, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta107 proteins include variants of SEQ ID NO: 177. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 177. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 177 while retaining 30 at least one epitope of SEQ ID NO: 177. The first 35 N-terminal amino acids of SEQ ID NO: 177 can usefully be omitted. Other fragments omit one or more protein domains.

sta108

35 **[0359]** The 'sta108' antigen is annotated as 'hypothetical protein'. In the NCTC 8325 strain sta108 is SAOUHSC_00717 and has amino acid sequence SEQ ID NO: 178 (GI:88194482).

[0360] Useful sta108 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 178 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 178; and/or (b) 40 comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 178, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These sta108 proteins include variants of SEQ ID NO: 178. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 178. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 178 while retaining at least 45 one epitope of SEQ ID NO: 178. The first 20 N-terminal amino acids of SEQ ID NO: 178 can usefully be omitted. Other fragments omit one or more protein domains.

sta109

50 **[0361]** The 'sta109' antigen is annotated as 'N-acetylmuramoyl-L-alanine amidase'. In the NCTC 8325 strain sta109 is SAOUHSC_02979 and has amino acid sequence SEQ ID NO: 179 (GI:88196599).

[0362] Useful sta109 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 179 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 179; and/or (b) 55 comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 179, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta109 proteins include variants of SEQ ID NO: 179. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 179. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or

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more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 179 while retaining at least one epitope of SEQ ID NO: 179. The first 27 N-terminal amino acids of SEQ ID NO: 179 can usefully be omitted. Other fragments omit one or more protein domains.

5 *sta110*

[0363] The 'sta110' antigen is annotated as 'hypothetical protein'. In the NCTC 8325 strain sta110 is SAOUHSC_01039 and has amino acid sequence SEQ ID NO: 180 (GI:88194791).

10 **[0364]** Useful sta110 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 180 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 180; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 180, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta110 proteins include variants of SEQ ID NO: 180. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 180. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 180 while retaining at least one epitope of SEQ ID NO: 180. The first 19 N-terminal amino acids of SEQ ID NO: 180 can usefully be omitted. Other fragments omit one or more protein domains.

20 *sta111*

[0365] The 'sta111' antigen is annotated as 'hypothetical protein'. In the NCTC 8325 strain sta111 is SAOUHSC_01005 and has amino acid sequence SEQ ID NO: 181 (GI:88194760).

25 **[0366]** Useful sta111 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 181 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 181; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 181, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These sta111 proteins include variants of SEQ ID NO: 181. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 181. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 181 while retaining at least one epitope of SEQ ID NO: 181. The first 20 N-terminal amino acids of SEQ ID NO: 181 can usefully be omitted. Other fragments omit one or more protein domains.

35 *sta112*

[0367] The 'sta112' antigen is annotated as a putative 'ABC transporter, substrate-binding protein'. In the NCTC 8325 strain sta112 is SAOUHSC_00634 and has amino acid sequence SEQ ID NO: 182 (GI:88194402).

40 **[0368]** Useful sta112 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 182 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 182; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 182, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta112 proteins include variants of SEQ ID NO: 182. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 182. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 182 while retaining at least one epitope of SEQ ID NO: 182. The first 17 N-terminal amino acids of SEQ ID NO: 182 can usefully be omitted. Other fragments omit one or more protein domains.

45 **[0369]** A Sta112 antigen can usefully be included in a composition in combination with a Sta073 [74].

50 *sta113*

[0370] The 'sta113' antigen is annotated as 'hypothetical protein'. In the NCTC 8325 strain sta113 is SAOUHSC_00728 and has amino acid sequence SEQ ID NO: 183 (GI:88194493).

55 **[0371]** Useful sta113 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 183 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 183; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 183, wherein 'n' is 7 or more (e.g. 8, 10,

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12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta113 proteins include variants of SEQ ID NO: 183. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 183. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 183 while retaining at least one epitope of SEQ ID NO: 183. The first 173 N-terminal amino acids of SEQ ID NO: 183 can usefully be omitted. Other fragments omit one or more protein domains.

sta114

[0372] The 'sta114' antigen is annotated as 'hypothetical protein'. In the NCTC 8325 strain sta114 is SAOUHSC_00810 and has amino acid sequence SEQ ID NO: 184 (GI:88194570).

[0373] Useful sta114 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 184 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 184; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 184, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150 or more). These sta114 proteins include variants of SEQ ID NO: 184. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 184. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 184 while retaining at least one epitope of SEQ ID NO: 184. Other fragments omit one or more protein domains.

sta115

[0374] The 'sta115' antigen is annotated as 'hypothetical protein'. In the NCTC 8325 strain sta115 is SAOUHSC_00817 and has amino acid sequence SEQ ID NO: 185 (GI:88194576).

[0375] Useful sta115 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 185 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 185; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 185, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150 or more). These sta115 proteins include variants of SEQ ID NO: 185. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 185. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 185 while retaining at least one epitope of SEQ ID NO: 185. The first 18 N-terminal amino acids of SEQ ID NO: 185 can usefully be omitted. Other fragments omit one or more protein domains.

sta116

[0376] The 'sta116' antigen is annotated as 'formyl peptide receptor-like 1 inhibitory protein'. In the NCTC 8325 strain sta116 is SAOUHSC_01112 and has amino acid sequence SEQ ID NO: 186 (GI:88194858).

[0377] Useful sta116 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 186 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 186; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 186, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These sta116 proteins include variants of SEQ ID NO: 186. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 186. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 186 while retaining at least one epitope of SEQ ID NO: 186. The first 20 N-terminal amino acids of SEQ ID NO: 186 can usefully be omitted. Other fragments omit one or more protein domains.

sta117

[0378] The 'sta117' antigen is annotated as 'truncated beta-hemolysin'. In the NCTC 8325 strain sta117 is SAOUHSC_02240 and has amino acid sequence SEQ ID NO: 187 (GI:88195913).

[0379] Useful sta117 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 187 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 187; and/or (b)

comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 187, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta117 proteins include variants of SEQ ID NO: 187. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 187. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 187 while retaining at least one epitope of SEQ ID NO: 187. Other fragments omit one or more protein domains.

sta118

[0380] The 'sta118' antigen is annotated as 'cell division protein FtsZ'. In the NCTC 8325 strain sta118 is SAOUHSC_01150 and has amino acid sequence SEQ ID NO: 188 (GI:88194892).

[0381] Useful sta118 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 188 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 188; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 188, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta118 proteins include variants of SEQ ID NO: 188. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 188. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 188, while retaining at least one epitope of SEQ ID NO: 188. Other fragments omit one or more protein domains.

sta119

[0382] The 'sta119' antigen is annotated as 'thioredoxin'. In the NCTC 8325 strain sta119 is SAOUHSC_01100 and has amino acid sequence SEQ ID NO: 200 (GI:88194846).

[0383] Useful sta119 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 200 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 200; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 200, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These sta119 proteins include variants of SEQ ID NO: 200. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 200. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 200 while retaining at least one epitope of SEQ ID NO: 200. Other fragments omit one or more protein domains.

sta120

[0384] The 'sta120' antigen is annotated as 'alkyl hydroperoxide reductase subunit C'. In the NCTC 8325 strain sta120 is SAOUHSC_00365 and has amino acid sequence SEQ ID NO: 201 (GI:88194163).

[0385] Useful sta120 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 201 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 201; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 201, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150 or more). These sta120 proteins include variants of SEQ ID NO: 201. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 201. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 201 while retaining at least one epitope of SEQ ID NO: 201. Other fragments omit one or more protein domains.

NW_6

[0386] The 'NW_6' antigen is annotated as 'secreted von Willebrand factor-binding protein precursor'. In the Newman strain NW_6 is NWMN_0757 and has amino acid sequence SEQ ID NO: 142 (GI:151220969).

[0387] Useful NW_6 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 142 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 142; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 142, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These NW_6 proteins include variants of SEQ

ID NO: 142. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 142. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 142 while retaining at least one epitope of SEQ ID NO: 142. The first 13 N-terminal amino acids of SEQ ID NO: 142 can usefully be omitted. Other fragments omit one or more protein domains.

NW_9

[0388] The 'NW_9' antigen is annotated as 'lipoprotein'. In the Newman strain NW_9 is NWMN_0958 and has amino acid sequence SEQ ID NO: 143 (GI:151221170).

[0389] Useful NW_9 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 143 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 143; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 143, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These NW_9 proteins include variants of SEQ ID NO: 143. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 143. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 143 while retaining at least one epitope of SEQ ID NO: 143. The first 19 N-terminal amino acids of SEQ ID NO: 143 can usefully be omitted. Other fragments omit one or more protein domains.

NW_10

[0390] The NW_10' antigen is annotated as 'fibrinogen binding-related protein'. In the Newman strain NW_10 is NWMN_1066 and has amino acid sequence SEQ ID NO: 144 (GI:151221278).

[0391] Useful NW_10 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 144 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 144; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 144, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These NW_10 proteins include variants of SEQ ID NO: 144. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 144. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 144 while retaining at least one epitope of SEQ ID NO: 144. The first 20 N-terminal amino acids of SEQ ID NO: 144 can usefully be omitted. Other fragments omit one or more protein domains.

NW_7

[0392] The 'NW_7' antigen is annotated as 'staphylococcal complement inhibitor SCIN'. In the Newman strain NW_7 is NWMN_1876 and has amino acid sequence SEQ ID NO: 145 (GI:151222088).

[0393] Useful NW_7 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 145 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 145; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 145, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These NW_7 proteins include variants of SEQ ID NO: 145. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 145. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 145 while retaining at least one epitope of SEQ ID NO: 145. The first 17 N-terminal amino acids of SEQ ID NO: 145 can usefully be omitted. Other fragments omit one or more protein domains.

NW_8

[0394] The 'NW_8' antigen is annotated as 'chemotaxis-inhibiting protein CHIPS'. In the Newman strain NW_8 is NWMN_1877 and has amino acid sequence SEQ ID NO: 146 (GI:151222089).

[0395] Useful NW_8 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 146 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 146; and/or (b) comprising

a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 146, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These NW_8 proteins include variants of SEQ ID NO: 146. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 146. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 146 while retaining at least one epitope of SEQ ID NO: 146. The first 19 N-terminal amino acids of SEQ ID NO: 146 can usefully be omitted. Other fragments omit one or more protein domains.

NW_2

[0396] The 'NW_2' antigen is annotated as 'enterotoxin type A precursor'. In the Newman strain NW_2 is NWMN_1883 and has amino acid sequence SEQ ID NO: 147 (GI:151222095).

[0397] Useful NW_2 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 147 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 147; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 147, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These NW_2 proteins include variants of SEQ ID NO: 147. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 147. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 147 while retaining at least one epitope of SEQ ID NO: 147. The first 16 N-terminal amino acids of SEQ ID NO: 147 can usefully be omitted. Other fragments omit one or more protein domains.

NW_1

[0398] The 'NW_1' antigen is annotated as 'lipoprotein'. In the Newman strain NW_1 is NWMN_1924 and has amino acid sequence SEQ ID NO: 148 (GI:151222136).

[0399] Useful NW_1 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 148 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 148; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 148, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150 or more). These NW_1 proteins include variants of SEQ ID NO: 148. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 148. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 148 while retaining at least one epitope of SEQ ID NO: 148. The first 17 N-terminal amino acids of SEQ ID NO: 148 can usefully be omitted. Other fragments omit one or more protein domains.

NW_5

[0400] The 'NW_5' antigen is annotated as 'cell wall surface anchor family protein'. In the Newman strain NW_5 is NWMN_2392 and has amino acid sequence SEQ ID NO: 149 (GI:151222604).

[0401] Useful NW_5 antigens can elicit an antibody (e.g. when administered to a human) that recognises SEQ ID NO: 149 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 149; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 149, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These NW_5 proteins include variants of SEQ ID NO: 149. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 149. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 149 while retaining at least one epitope of SEQ ID NO: 149. The first 52 N-terminal amino acids of SEQ ID NO: 149 can usefully be omitted. Other fragments omit one or more protein domains.

Hybrid polypeptides

[0402] Antigens used in the invention may be present in the composition as individual separate polypeptides. Where more than one antigen is used, however, they do not have to be present as separate polypeptides. Instead, at least two (e.g. 2, 3, 4, 5, or more) antigens can be expressed as a single polypeptide chain (a 'hybrid' polypeptide). Hybrid

polypeptides offer two main advantages: first, a polypeptide that may be unstable or poorly expressed on its own can be assisted by adding a suitable hybrid partner that overcomes the problem; second, commercial manufacture is simplified as only one expression and purification need be employed in order to produce two polypeptides which are both antigenically useful.

[0403] The hybrid polypeptide may comprise two or more polypeptide sequences from the first antigen group. The hybrid polypeptide may comprise one or more polypeptide sequences from the first antigen group and one or more polypeptide sequences from the second antigen group. Moreover, the hybrid polypeptide may comprise two or more polypeptide sequences from each of the antigens listed above, or two or more variants of the same antigen in the cases in which the sequence has partial variability across strains.

[0404] Hybrids consisting of amino acid sequences from two, three, four, five, six, seven, eight, nine, or ten antigens are useful. In particular, hybrids consisting of amino acid sequences from two, three, four, or five antigens are preferred, such as two or three antigens.

[0405] Different hybrid polypeptides may be mixed together in a single formulation. Hybrids may be combined with non-hybrid, antigens selected from the first, second or third antigen groups. Within such combinations, an antigen may be present in more than one hybrid polypeptide and/or as a non-hybrid polypeptide. It is preferred, however, that an antigen is present either as a hybrid or as a non-hybrid, but not as both.

[0406] The hybrid polypeptides can also be combined with conjugates or non-*S.aureus* antigens as described above.

[0407] Hybrid polypeptides can be represented by the formula $\text{NH}_2\text{-A}\{-\text{X-L}\}_n\text{-B-COOH}$, wherein: X is an amino acid sequence of a *S.aureus* antigen, as described above; L is an optional linker amino acid sequence; A is an optional N-terminal amino acid sequence; B is an optional C-terminal amino acid sequence; n is an integer of 2 or more (e.g. 2, 3, 4, 5, 6, etc.). Usually n is 2 or 3.

[0408] If a -X- moiety has a leader peptide sequence in its wild-type form, this may be included or omitted in the hybrid protein. In some embodiments, the leader peptides will be deleted except for that of the -X- moiety located at the N-terminus of the hybrid protein i.e. the leader peptide of X_1 will be retained, but the leader peptides of $X_2 \dots X_n$ will be omitted. This is equivalent to deleting all leader peptides and using the leader peptide of X_1 as moiety -A-.

[0409] For each n instances of $\{-\text{X-L}\}$, linker amino acid sequence -L- may be present or absent. For instance, when $n=2$ the hybrid may be $\text{NH}_2\text{-X}_1\text{-L}_1\text{-X}_2\text{-L}_2\text{-COOH}$, $\text{NH}_2\text{-X}_1\text{-X}_2\text{-COOH}$, $\text{NH}_2\text{-X}_1\text{-L}_1\text{-X}_2\text{-COOH}$, $\text{NH}_2\text{-X}_1\text{-X}_2\text{-L}_2\text{-COOH}$, etc. Linker amino acid sequence(s) -L- will typically be short (e.g. 20 or fewer amino acids i.e. 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1). Examples comprise short peptide sequences which facilitate cloning, poly-glycine linkers (i.e. comprising Gly_n where $n = 2, 3, 4, 5, 6, 7, 8, 9, 10$ or more), and histidine tags (i.e. His_n where $n = 3, 4, 5, 6, 7, 8, 9, 10$ or more). Other suitable linker amino acid sequences will be apparent to those skilled in the art. A useful linker is GSGGGG (SEQ ID NO: 171) or GSGSGGGG (SEQ ID NO: 172), with the Gly-Ser dipeptide being formed from a *Bam*HI restriction site (or two of them, to form the SEQ ID NO: 230 tetrapeptide), thus aiding cloning and manipulation, and the $(\text{Gly})_4$ tetrapeptide (SEQ ID NO: 227) being a typical poly-glycine linker. Other suitable linkers, particularly for use as the final L_n are ASGGGS (SEQ ID NO: 173 e.g. encoded by SEQ ID NO: 174) or a Leu-Glu dipeptide.

-A- is an optional N-terminal amino acid sequence. This will typically be short (e.g. 40 or fewer amino acids i.e. 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1). Examples include leader sequences to direct protein trafficking, or short peptide sequences which facilitate cloning or purification (e.g. histidine tags i.e. His_n where $n = 3, 4, 5, 6, 7, 8, 9, 10$ or more). Other suitable N-terminal amino acid sequences will be apparent to those skilled in the art. If X_1 lacks its own N-terminus methionine, -A- is preferably an oligopeptide (e.g. with 1, 2, 3, 4, 5, 6, 7 or 8 amino acids) which provides a N-terminus methionine e.g. Met-Ala-Ser, or a single Met residue.

-B- is an optional C-terminal amino acid sequence. This will typically be short (e.g. 40 or fewer amino acids i.e. 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1). Examples include sequences to direct protein trafficking, short peptide sequences which facilitate cloning or purification (e.g. comprising histidine tags i.e. His_n where $n = 3, 4, 5, 6, 7, 8, 9, 10$ or more, such as SEQ ID NO: 226), or sequences which enhance protein stability. Other suitable C-terminal amino acid sequences will be apparent to those skilled in the art.

[0410] One hybrid polypeptide of the invention may include both EsxA and EsxB antigens. These may be in either order, N- to C- terminus. SEQ ID NOs: 151 ('EsxAB'; encoded by SEQ ID NO: 169) and 152 ('EsxBA') are examples of such hybrids, both having hexapeptide linkers ASGGGS (SEQ ID NO: 173). Another 'EsxAB' hybrid comprises SEQ ID NO: 241, which may be provided with a N-terminus methionine (e.g. SEQ ID NO: 250).

[0411] Another hybrid polypeptide of the invention may include both SdrD and SdrE antigens. These may be in either order, N- to C- terminus. SEQ ID NO: 168 ('SdrED') is an example of such a hybrid, having a hexapeptide linker ASGGGS (SEQ ID NO: 173).

[0412] Another hybrid polypeptide of the invention may include both ClfB and SdrD antigens. These may be in either

order, N- to C- terminus. SEQ ID NO: 202 ('ClfB-SdrD') is an example of such a hybrid, having a hexapeptide linker ASGGGS (SEQ ID NO: 173). SEQ ID NO: 203 ('SdrD-ClfB') is another example of such a hybrid, having a hexapeptide linker ASGGGS (SEQ ID NO: 173). SEQ ID NO: 211 ('ClfB-N3-sdrD-N3') is another example of such a hybrid, where the N3 fragments of ClfB and SdrD are joined by hexapeptide linker ASGGGS (SEQ ID NO: 173).

[0413] Another hybrid polypeptide of the invention may include both LsdA and EsxA antigens. These may be in either order, N- to C- terminus. SEQ ID NO: 204 ('LsdA-EsxA') is an example of such a hybrid, having a hexapeptide linker ASGGGS (SEQ ID NO: 173). SEQ ID NO: 209 ('lsdA40-184-esxA') is another example of such a hybrid, in which LsdA₄₀₋₁₈₄ is joined to EsxA via linker ASGGGS (SEQ ID NO: 173).

[0414] Another hybrid polypeptide of the invention may include both LsdA and sta006 antigens. These may be in either order, N- to C- terminus. SEQ ID NO: 221 ('lsdA40-184-sta006') is an example of such a hybrid, in which LsdA₄₀₋₁₈₄ is joined to Sta006 via hexapeptide linker ASGGGS (SEQ ID NO: 173).

[0415] Another hybrid polypeptide of the invention may include both Hla and sta006 antigens. These may be in either order, N- to C- terminus. SEQ ID NO: 222 ('HlaH35L-sta006') is an example of such a hybrid, in which a H35L mutant of Hla is joined to Sta006 via hexapeptide linker ASGGGS (SEQ ID NO: 173).

[0416] Another hybrid polypeptide of the invention may include both Hla and Emp antigens. These may be in either order, N- to C- terminus. SEQ ID NO: 205 ('HlaH35L-Emp') is an example of such a hybrid, in which a H35L mutant Hla is joined to Emp via linker ASGGGS (SEQ ID NO: 173). SEQ ID NO: 206 ('Hla27-76-Emp') is another example of such a hybrid, in which a Hla fragment is joined to Emp via linker ASGGGS (SEQ ID NO: 173); SEQ ID NO: 207 is a H35L mutant of SEQ ID NO: 206. SEQ ID NO: 208 ('HlaPSGS-Emp') is another example of such a hybrid, in which a Hla mutant is joined to Emp via linker ASGGGS (SEQ ID NO: 173).

[0417] Another hybrid polypeptide of the invention may include LsdA and EsxA and EsxB antigens. These may be in any order, N- to C- terminus. SEQ ID NO: 210 ('lsdA40-184-esxAB') is an example of such a triple hybrid, in which LsdA₄₀₋₁₈₄ is joined to EsxAB via linker ASGGGS (SEQ ID NO: 173). The EsxAB already includes the same linker, so SEQ ID NO: 210 includes two of these linkers. SEQ ID NO: 212 ('lsdA-esxAB') is another example of such a triple hybrid, in which LsdA is joined to EsxAB via linker ASGGGS (SEQ ID NO: 173).

[0418] Another hybrid polypeptide of the invention may include Hla and EsxA and EsxB antigens. These may be in any order, N- to C- terminus. SEQ ID NO: 220 ('HlaH35L-esxAB') is an example of such a triple hybrid, in which a H35L mutant of Hla is joined to EsxAB via linker ASGGGS (SEQ ID NO: 173). The EsxAB already includes the same linker, so SEQ ID NO: 220 includes two of these linkers. Another example of a hybrid polypeptide including Hla and EsxA and EsxB antigens is SEQ ID NO: 237 ('HlaH35L-esxAB' as used in the examples), in which a H35L mutant of Hla is joined to EsxA via linker APTARG (SEQ ID NO: 239) to replace its N-terminus, then to EsxB via linker ASGGGS (SEQ ID NO: 173) to replace its N-terminus. This hybrid can be provided with a suitable N-terminal sequence such as SEQ ID NO: 240.

[0419] Another hybrid polypeptide of the invention may include sta006 and EsxA and EsxB antigens. These may be in any order, N- to C- terminus. SEQ ID NO: 223 ('sta006-esxAB') is an example of such a triple hybrid, in which sta006 is joined to EsxAB via linker ASGGGS (SEQ ID NO: 173). The EsxAB already includes the same linker, so SEQ ID NO: 223 includes two of these linkers. Another example of a hybrid polypeptide including sta006 and EsxA and EsxB antigens is SEQ ID NO: 238 ('sta006-esxAB' as used in the examples), in which a sta006 is joined to EsxA via linker APTARG (SEQ ID NO: 239) to replace its N-terminus, then to EsxB via linker ASGGGS (SEQ ID NO: 173) to replace its N-terminus. This hybrid can be provided with a suitable N-terminal sequence such as SEQ ID NO: 240.

[0420] Usefully, these hybrid polypeptides can elicit an antibody (e.g. when administered to a human) that recognise each of the wild-type staphylococcal proteins (e.g. as shown in the sequence listing) represented in the hybrid e.g. which recognise both wild-type EsxA and wild-type EsxB, or which recognise both wild-type SdrD and wild-type SdrE, or which recognise both wild-type SdrD and wild-type ClfB, or which recognise both wild-type LsdA and wild-type EsxA, or which recognise both wild-type LsdA and wild-type sta006, or which recognise both wild-type Hla and wild-type sta006, or which recognise both wild-type Hla and wild-type Emp, or which recognise wild-type LsdA and wild-type EsxA and wild-type EsxB, or which recognise wild-type Hla and wild-type EsxA and wild-type EsxB, or which recognise wild-type sta006 and wild-type EsxA and wild-type EsxB.

Polypeptides used with the invention

[0421] Polypeptides used with the invention can take various forms (e.g. native, fusions, glycosylated, non-glycosylated, lipidated, non-lipidated, phosphorylated, non-phosphorylated, myristoylated, non-myristoylated, monomeric, multimeric, particulate, denatured, etc.).

[0422] Polypeptides used with the invention can be prepared by various means (e.g. recombinant expression, purification from cell culture, chemical synthesis, etc.). Recombinantly-expressed proteins are preferred, particularly for hybrid polypeptides.

[0423] Polypeptides used with the invention are preferably provided in purified or substantially purified form i.e. substantially free from other polypeptides (e.g. free from naturally-occurring polypeptides), particularly from other staphy-

lococcal or host cell polypeptides, and are generally at least about 50% pure (by weight), and usually at least about 90% pure *i.e.* less than about 50%, and more preferably less than about 10% (e.g. 5%) of a composition is made up of other expressed polypeptides. Thus the antigens in the compositions are separated from the whole organism with which the molecule is expressed.

[0424] Polypeptides used with the invention are preferably staphylococcal polypeptides.

[0425] The term "polypeptide" refers to amino acid polymers of any length. The polymer may be linear or branched, it may comprise modified amino acids, and it may be interrupted by non-amino acids. The terms also encompass an amino acid polymer that has been modified naturally or by intervention; for example, disulfide bond formation, glycosylation, lipidation, acetylation, phosphorylation, or any other manipulation or modification, such as conjugation with a labeling component. Also included are, for example, polypeptides containing one or more analogs of an amino acid (including, for example, unnatural amino acids, *etc.*), as well as other modifications known in the art. Polypeptides can occur as single chains or associated chains.

[0426] The invention provides polypeptides comprising a sequence -P-Q- or -Q-P-, wherein: -P- is an amino acid sequence as defined above and -Q- is not a sequence as defined above *i.e.* the invention provides fusion proteins. Where the N-terminus codon of -P- is not ATG, but this codon is not present at the N-terminus of a polypeptide, it will be translated as the standard amino acid for that codon rather than as a Met. Where this codon is at the N-terminus of a polypeptide, however, it will be translated as Met. Examples of -Q- moieties include, but are not limited to, histidine tags (*i.e.* His_n where *n* = 3, 4, 5, 6, 7, 8, 9, 10 or more), maltose-binding protein, or glutathione-S-transferase (GST).

[0427] The invention also provides a process for producing a polypeptide of the invention, comprising the step of culturing a host cell transformed with nucleic acid of the invention under conditions which induce polypeptide expression.

[0428] Although expression of the polypeptides of the invention may take place in a *Staphylococcus*, the invention will usually use a heterologous host for expression (recombinant expression). The heterologous host may be prokaryotic (e.g. a bacterium) or eukaryotic. It may be *E.coli*, but other suitable hosts include *Bacillus subtilis*, *Vibrio cholerae*, *Salmonella typhi*, *Salmonella typhimurium*, *Neisseria lactamica*, *Neisseria cinerea*, *Mycobacteria* (e.g. *M.tuberculosis*), yeasts, *etc.* Compared to the wild-type *S.aureus* genes encoding polypeptides of the invention, it is helpful to change codons to optimise expression efficiency in such hosts without affecting the encoded amino acids.

[0429] The invention provides a process for producing a polypeptide of the invention, comprising the step of synthesising at least part of the polypeptide by chemical means.

Nucleic acids

[0430] The invention also provides nucleic acid encoding polypeptides and hybrid polypeptides of the invention. It also provides nucleic acid comprising a nucleotide sequence that encodes one or more polypeptides or hybrid polypeptides of the invention.

[0431] The invention also provides nucleic acid comprising nucleotide sequences having sequence identity to such nucleotide sequences. Identity between sequences is preferably determined by the Smith-Waterman homology search algorithm as described above. Such nucleic acids include those using alternative codons to encode the same amino acid.

[0432] The invention also provides nucleic acid which can hybridize to these nucleic acids. Hybridization reactions can be performed under conditions of different "stringency". Conditions that increase stringency of a hybridization reaction of widely known and published in the art (e.g. page 7.52 of reference 276). Examples of relevant conditions include (in order of increasing stringency): incubation temperatures of 25°C, 37°C, 50°C, 55°C and 68°C; buffer concentrations of 10 x SSC, 6 x SSC, 1 x SSC, 0.1 x SSC (where SSC is 0.15 M NaCl and 15 mM citrate buffer) and their equivalents using other buffer systems; formamide concentrations of 0%, 25%, 50%, and 75%; incubation times from 5 minutes to 24 hours; 1, 2, or more washing steps; wash incubation times of 1, 2, or 15 minutes; and wash solutions of 6 x SSC, 1 x SSC, 0.1 x SSC, or de-ionized water. Hybridization techniques and their optimization are well known in the art (e.g. see refs 75, 76, 276, 278, *etc.*).

[0433] In some embodiments, nucleic acid of the invention hybridizes to a target under low stringency conditions; in other embodiments it hybridizes under intermediate stringency conditions; in preferred embodiments, it hybridizes under high stringency conditions. An exemplary set of low stringency hybridization conditions is 50°C and 10 x SSC. An exemplary set of intermediate stringency hybridization conditions is 55°C and 1 x SSC. An exemplary set of high stringency hybridization conditions is 68°C and 0.1 x SSC.

[0434] The invention includes nucleic acid comprising sequences complementary to these sequences (e.g. for anti-sense or probing, or for use as primers).

[0435] Nucleic acids of the invention can be used in hybridisation reactions (e.g. Northern or Southern blots, or in nucleic acid microarrays or 'gene chips') and amplification reactions (e.g. PCR, SDA, SSSR, LCR, TMA, NASBA, *etc.*) and other nucleic acid techniques.

[0436] Nucleic acid according to the invention can take various forms (e.g. single-stranded, double-stranded, vectors, primers, probes, labelled *etc.*). Nucleic acids of the invention may be circular or branched, but will generally be linear.

Unless otherwise specified or required, any embodiment of the invention that utilizes a nucleic acid may utilize both the double-stranded form and each of two complementary single-stranded forms which make up the double-stranded form. Primers and probes are generally single-stranded, as are antisense nucleic acids.

[0437] Nucleic acids of the invention are preferably provided in purified or substantially purified form *i.e.* substantially free from other nucleic acids (e.g. free from naturally-occurring nucleic acids), particularly from other staphylococcal or host cell nucleic acids, generally being at least about 50% pure (by weight), and usually at least about 90% pure. Nucleic acids of the invention are preferably staphylococcal nucleic acids.

[0438] Nucleic acids of the invention may be prepared in many ways e.g. by chemical synthesis (e.g. phosphoramidite synthesis of DNA) in whole or in part, by digesting longer nucleic acids using nucleases (e.g. restriction enzymes), by joining shorter nucleic acids or nucleotides (e.g. using ligases or polymerases), from genomic or cDNA libraries, etc.

[0439] Nucleic acid of the invention may be attached to a solid support (e.g. a bead, plate, filter, film, slide, microarray support, resin, etc.). Nucleic acid of the invention may be labelled e.g. with a radioactive or fluorescent label, or a biotin label. This is particularly useful where the nucleic acid is to be used in detection techniques e.g. where the nucleic acid is a primer or as a probe.

[0440] The term "nucleic acid" includes in general means a polymeric form of nucleotides of any length, which contain deoxyribonucleotides, ribonucleotides, and/or their analogs. It includes DNA, RNA, DNA/RNA hybrids. It also includes DNA or RNA analogs, such as those containing modified backbones (e.g. peptide nucleic acids (PNAs) or phosphorothioates) or modified bases. Thus the invention includes mRNA, tRNA, rRNA, ribozymes, DNA, cDNA, recombinant nucleic acids, branched nucleic acids, plasmids, vectors, probes, primers, etc. Where nucleic acid of the invention takes the form of RNA, it may or may not have a 5' cap.

[0441] Nucleic acids of the invention may be part of a vector *i.e.* part of a nucleic acid construct designed for transduction/transfection of one or more cell types. Vectors may be, for example, "cloning vectors" which are designed for isolation, propagation and replication of inserted nucleotides, "expression vectors" which are designed for expression of a nucleotide sequence in a host cell, "viral vectors" which is designed to result in the production of a recombinant virus or virus-like particle, or "shuttle vectors", which comprise the attributes of more than one type of vector. Preferred vectors are plasmids. A "host cell" includes an individual cell or cell culture which can be or has been a recipient of exogenous nucleic acid. Host cells include progeny of a single host cell, and the progeny may not necessarily be completely identical (in morphology or in total DNA complement) to the original parent cell due to natural, accidental, or deliberate mutation and/or change. Host cells include cells transfected or infected *in vivo* or *in vitro* with nucleic acid of the invention.

[0442] Where a nucleic acid is DNA, it will be appreciated that "U" in a RNA sequence will be replaced by "T" in the DNA. Similarly, where a nucleic acid is RNA, it will be appreciated that "T" in a DNA sequence will be replaced by "U" in the RNA.

[0443] The term "complement" or "complementary" when used in relation to nucleic acids refers to Watson-Crick base pairing. Thus the complement of C is G, the complement of G is C, the complement of A is T (or U), and the complement of T (or U) is A. It is also possible to use bases such as I (the purine inosine) e.g. to complement pyrimidines (C or T).

[0444] Nucleic acids of the invention can be used, for example: to produce polypeptides; as hybridization probes for the detection of nucleic acid in biological samples; to generate additional copies of the nucleic acids; to generate ribozymes or antisense oligonucleotides; as single-stranded DNA primers or probes; or as triple-strand forming oligonucleotides.

[0445] The invention provides a process for producing nucleic acid of the invention, wherein the nucleic acid is synthesised in part or in whole using chemical means.

[0446] The invention provides vectors comprising nucleotide sequences of the invention (e.g. cloning or expression vectors) and host cells transformed with such vectors.

[0447] Nucleic acid amplification according to the invention may be quantitative and/or real-time.

[0448] For certain embodiments of the invention, nucleic acids are preferably at least 7 nucleotides in length (e.g. 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, 45, 50, 55, 60, 65, 70, 75, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 225, 250, 275, 300 nucleotides or longer).

[0449] For certain embodiments of the invention, nucleic acids are preferably at most 500 nucleotides in length (e.g. 450, 400, 350, 300, 250, 200, 150, 140, 130, 120, 110, 100, 90, 80, 75, 70, 65, 60, 55, 50, 45, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15 nucleotides or shorter).

[0450] Primers and probes of the invention, and other nucleic acids used for hybridization, are preferably between 10 and 30 nucleotides in length (e.g. 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides).

Strains and variants

[0451] Antigens are defined above by reference to existing nomenclature (e.g. "ClfA"), to "sta" numbers or to "NW_"

numbers. Table 1 herein relates these three naming/numbering systems to existing SAOUHSC numbering and/or NWMN numbering. SAOUHSC numbering refers to the genome of *S.aureus* strain NCTC 8325 (sequenced by Oklahoma University Health Sciences Center and disclosed in GenBank as CP000253.1; GI:87201381), and individual SAOUHSC numbers are given as "locus_tag" entries in the genome sequence's "features" section. Similarly, NWMN numbering refers to the genome of *S.aureus* strain Newman (isolated in 1952 from a human infection, and having robust virulence phenotype) disclosed in GenBank as AP009351.1 (GI:150373012) and individual NWMN numbers are given as "locus_tag" entries in the genome sequence's "features" section. Functional annotations for each antigen are also given in the databases.

[0452] Table 1 also includes the GI number for each antigen of the invention. Thus an exemplary amino acid and nucleotide sequence for any of these antigens can easily be found in public sequence databases from the NCTC 8325 and/or Newman strain, but the invention is not limited to sequences from the NCTC 8325 and Newman strains. Genome sequences of several other strains of *S.aureus* are available, including those of MRSA strains N315 and Mu50 [77], MW2, N315, COL, MRSA252, MSSA476, RF122, USA300 (very virulent), JH1 and JH9. Standard search and alignment techniques can be used to identify in any of these (or other) further genome sequences the homolog of any particular sequence from the Newman or NCTC 8325 strain.. Moreover, the available sequences from the Newman and NCTC 8325 strains can be used to design primers for amplification of homologous sequences from other strains. Thus the invention is not limited to these two strains, but rather encompasses such variants and homologs from other strains of *S.aureus*, as well as non-natural variants. In general, suitable variants of a particular SEQ ID NO include its allelic variants, its polymorphic forms, its homologs, its orthologs, its paralogs, its mutants, etc.

[0453] Thus, for instance, polypeptides used with the invention may, compared to the SEQ ID NO herein, include one or more (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, etc.) amino acid substitutions, such as conservative substitutions (i.e. substitutions of one amino acid with another which has a related side chain). Genetically-encoded amino acids are generally divided into four families: (1) acidic i.e. aspartate, glutamate; (2) basic i.e. lysine, arginine, histidine; (3) non-polar i.e. alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan; and (4) uncharged polar i.e. glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine. Phenylalanine, tryptophan, and tyrosine are sometimes classified jointly as aromatic amino acids. In general, substitution of single amino acids within these families does not have a major effect on the biological activity. The polypeptides may also include one or more (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, etc.) single amino acid deletions relative to the SEQ ID NO sequences. The polypeptides may also include one or more (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, etc.) insertions (e.g. each of 1, 2, 3, 4 or 5 amino acids) relative to the SEQ ID NO sequences.

[0454] Similarly, a polypeptide used with the invention may comprise an amino acid sequence that:

is identical (i.e. 100% identical) to a sequence disclosed in the sequence listing;
shares sequence identity (e.g. 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) with a sequence disclosed in the sequence listing;

has 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 (or more) single amino acid alterations (deletions, insertions, substitutions), which may be at separate locations or may be contiguous, as compared to the sequences of (a) or (b); and

when aligned with a particular sequence from the sequence listing using a pairwise alignment algorithm, each moving window of x amino acids from N-terminus to C-terminus (such that for an alignment that extends to p amino acids, where $p > x$, there are $p-x+1$ such windows) has at least $x \cdot y$ identical aligned amino acids, where: x is selected from 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 150, 200; y is selected from 0.50, 0.60, 0.70, 0.75, 0.80, 0.85, 0.90, 0.91, 0.92, 0.93, 0.94, 0.95, 0.96, 0.97, 0.98, 0.99; and if $x \cdot y$ is not an integer then it is rounded up to the nearest integer. The preferred pairwise alignment algorithm is the Needleman-Wunsch global alignment algorithm [78], using default parameters (e.g. with Gap opening penalty = 10.0, and with Gap extension penalty = 0.5, using the EBLOSUM62 scoring matrix). This algorithm is conveniently implemented in the *needle* tool in the EMBOSS package [79].

[0455] Where hybrid polypeptides are used, the individual antigens within the hybrid (i.e. individual -X-moieties) may be from one or more strains. Where $n=2$, for instance, X_2 may be from the same strain as X_1 or from a different strain. Where $n=3$, the strains might be (i) $X_1=X_2=X_3$ (ii) $X_1=X_2X_3$ (iii) $X_1X_2=X_3$ (iv) $X_1X_2X_3$ or (v) $X_1=X_3X_2$, etc.

[0456] Within group (c), deletions or substitutions may be at the N-terminus and/or C-terminus, or may be between the two termini. Thus a truncation is an example of a deletion. Truncations may involve deletion of up to 40 (or more) amino acids at the N-terminus and/or C-terminus. N-terminus truncation can remove leader peptides e.g. to facilitate recombinant expression in a heterologous host. C-terminus truncation can remove anchor sequences e.g. to facilitate recombinant expression in a heterologous host.

[0457] In general, when an antigen comprises a sequence that is not identical to a complete *S.aureus* sequence from the sequence listing (e.g. when it comprises a sequence listing with <100% sequence identity thereto, or when it comprises a fragment thereof) it is preferred in each individual instance that the antigen can elicit an antibody which recognises the respective complete *S.aureus* sequence.

Mutant bacteria

[0458] The invention also provides a *S.aureus* bacterium in which one or more of the antigens from the various antigen groups of the invention has/have been knocked out. Techniques for producing knockout bacteria are well known, and knockout *S.aureus* strains have been reported. A knockout mutation may be situated in the coding region of the gene or may lie within its transcriptional control regions (e.g. within its promoter). A knockout mutation will reduce the level of mRNA encoding the antigen to <1% of that produced by the wild-type bacterium, preferably <0.5%, more preferably <0.1%, and most preferably to 0%.

[0459] The invention also provides a *S.aureus* in which one or more of the antigens from the various antigen groups of the invention has a mutation which inhibits its activity. The gene encoding the antigen will have a mutation that changes the encoded amino acid sequence. Mutation may involve deletion, substitution, and/or insertion, any of which may be involve one or more amino acids.

[0460] The invention also provides a bacterium, such as a *S.aureus* bacterium, which hyper-expresses an antigen of the invention.

[0461] The invention also provides a bacterium, such as a *S.aureus* bacterium, that constitutively expresses an antigen of the invention. The invention also provides a meningococcus comprising a gene encoding an antigen of the invention, wherein the gene is under the control of an inducible promoter.

Immunogenic compositions and medicaments

[0462] Immunogenic compositions of the invention may be useful as vaccines. Vaccines according to the invention may either be prophylactic (i.e. to prevent infection) or therapeutic (i.e. to treat infection), but will typically be prophylactic.

[0463] Compositions may thus be pharmaceutically acceptable. They will usually include components in addition to the antigens e.g. they typically include one or more pharmaceutical carrier(s) and/or excipient(s). A thorough discussion of such components is available in reference 273.

[0464] Compositions will generally be administered to a mammal in aqueous form. Prior to administration, however, the composition may have been in a non-aqueous form. For instance, although some vaccines are manufactured in aqueous form, then filled and distributed and administered also in aqueous form, other vaccines are lyophilised during manufacture and are reconstituted into an aqueous form at the time of use. Thus a composition of the invention may be dried, such as a lyophilised formulation.

[0465] The composition may include preservatives such as thiomersal or 2-phenoxyethanol. It is preferred, however, that the vaccine should be substantially free from (i.e. less than 5µg/ml) mercurial material e.g. thiomersal-free. Vaccines containing no mercury are more preferred. Preservative-free vaccines are particularly preferred.

[0466] To improve thermal stability, a composition may include a temperature protective agent. Further details of such agents are provided below.

[0467] To control tonicity, it is preferred to include a physiological salt, such as a sodium salt. Sodium chloride (NaCl) is preferred, which may be present at between 1 and 20 mg/ml e.g. about 10±2mg/ml NaCl. Other salts that may be present include potassium chloride, potassium dihydrogen phosphate, disodium phosphate dehydrate, magnesium chloride, calcium chloride, etc.

[0468] Compositions will generally have an osmolality of between 200 mOsm/kg and 400 mOsm/kg, preferably between 240-360 mOsm/kg, and will more preferably fall within the range of 290-310 mOsm/kg.

[0469] Compositions may include one or more buffers. Typical buffers include: a phosphate buffer; a Tris buffer; a borate buffer; a succinate buffer; a histidine buffer (particularly with an aluminum hydroxide adjuvant); or a citrate buffer. Buffers will typically be included in the 5-20mM range.

[0470] The pH of a composition will generally be between 5.0 and 8.1, and more typically between 6.0 and 8.0 e.g. 6.5 and 7.5, or between 7.0 and 7.8.

[0471] The composition is preferably sterile. The composition is preferably non-pyrogenic e.g. containing <1 EU (endotoxin unit, a standard measure) per dose, and preferably <0.1 EU per dose. The composition is preferably gluten free.

[0472] The composition may include material for a single immunisation, or may include material for multiple immunisations (i.e. a 'multidose' kit). The inclusion of a preservative is preferred in multidose arrangements. As an alternative (or in addition) to including a preservative in multidose compositions, the compositions may be contained in a container having an aseptic adaptor for removal of material.

[0473] Human vaccines are typically administered in a dosage volume of about 0.5ml, although a half dose (i.e. about 0.25ml) may be administered to children.

[0474] Immunogenic compositions of the invention may also comprise one or more immunoregulatory agents. Preferably, one or more of the immunoregulatory agents include one or more adjuvants. The adjuvants may include a TH1 adjuvant and/or a TH2 adjuvant, further discussed below.

[0475] Thus the invention provides an immunogenic composition comprising a combination of:

- (1) one or more antigen(s) selected from the first, second, third and fourth antigen groups (as defined above); and
 (2) an adjuvant, such as an aluminium hydroxide adjuvant (for example, one or more antigens may be adsorbed to aluminium hydroxide).

[0476] For instance, the invention provides an immunogenic composition comprising a combination of a sta006 antigen and an adjuvant, such as an aluminium hydroxide adjuvant. Similarly, the invention provides an immunogenic composition comprising a combination of a sta011 antigen and an adjuvant, such as an aluminium hydroxide adjuvant. These compositions are ideally buffered e.g. with a histidine buffer.

[0477] Adjuvants which may be used in compositions of the invention include, but are not limited to:

A. Mineral-containing compositions

[0478] Mineral containing compositions suitable for use as adjuvants in the invention include mineral salts, such as aluminium salts and calcium salts (or mixtures thereof). Calcium salts include calcium phosphate (e.g. the "CAP" particles disclosed in ref. 80). Aluminum salts include hydroxides, phosphates, sulfates, etc., with the salts taking any suitable form (e.g. gel, crystalline, amorphous, etc.). Adsorption to these salts is preferred (e.g. all antigens may be adsorbed). The mineral containing compositions may also be formulated as a particle of metal salt [81].

[0479] The adjuvants known as aluminum hydroxide and aluminum phosphate may be used. These names are conventional, but are used for convenience only, as neither is a precise description of the actual chemical compound which is present (e.g. see chapter 9 of reference 82)). The invention can use any of the "hydroxide" or "phosphate" adjuvants that are in general use as adjuvants. The adjuvants known as "aluminium hydroxide" are typically aluminium oxyhydroxide salts, which are usually at least partially crystalline. The adjuvants known as "aluminium phosphate" are typically aluminium hydroxyphosphates, often also containing a small amount of sulfate (i.e. aluminium hydroxyphosphate sulfate). They may be obtained by precipitation, and the reaction conditions and concentrations during precipitation influence the degree of substitution of phosphate for hydroxyl in the salt.

[0480] A fibrous morphology (e.g. as seen in transmission electron micrographs) is typical for aluminium hydroxide adjuvants. The pl of aluminium hydroxide adjuvants is typically about 11 i.e. the adjuvant itself has a positive surface charge at physiological pH. Adsorptive capacities of between 1.8-2.6 mg protein per mg Al⁺⁺⁺ at pH 7.4 have been reported for aluminium hydroxide adjuvants.

[0481] Aluminium phosphate adjuvants generally have a PO₄/Al molar ratio between 0.3 and 1.2, preferably between 0.8 and 1.2, and more preferably 0.95±0.1. The aluminium phosphate will generally be amorphous, particularly for hydroxyphosphate salts. A typical adjuvant is amorphous aluminium hydroxyphosphate with PO₄/Al molar ratio between 0.84 and 0.92, included at 0.6mg Al³⁺/ml. The aluminium phosphate will generally be particulate (e.g. plate-like morphology as seen in transmission electron micrographs). Typical diameters of the particles are in the range 0.5-20µm (e.g. about 5-10µm) after any antigen adsorption. Adsorptive capacities of between 0.7-1.5 mg protein per mg Al⁺⁺⁺ at pH 7.4 have been reported for aluminium phosphate adjuvants.

[0482] The point of zero charge (PZC) of aluminium phosphate is inversely related to the degree of substitution of phosphate for hydroxyl, and this degree of substitution can vary depending on reaction conditions and concentration of reactants used for preparing the salt by precipitation. PZC is also altered by changing the concentration of free phosphate ions in solution (more phosphate = more acidic PZC) or by adding a buffer such as a histidine buffer (makes PZC more basic). Aluminium phosphates used according to the invention will generally have a PZC of between 4.0 and 7.0, more preferably between 5.0 and 6.5 e.g. about 5.7.

[0483] As shown below, adsorption of *S.aureus* protein antigens (except IsdA, Sta019 and Sta073) to an aluminium hydroxide adjuvant is advantageous, particularly in a multi-protein combination (in which all antigens may be adsorbed). A histidine buffer can usefully be included in such adjuvanted compositions.

[0484] Suspensions of aluminium salts used to prepare compositions of the invention may contain a buffer (e.g. a phosphate or a histidine or a Tris buffer), but this is not always necessary. The suspensions are preferably sterile and pyrogen-free. A suspension may include free aqueous phosphate ions e.g. present at a concentration between 1.0 and 20 mM, preferably between 5 and 15 mM, and more preferably about 10 mM. The suspensions may also comprise sodium chloride.

[0485] The invention can use a mixture of both an aluminium hydroxide and an aluminium phosphate. In this case there may be more aluminium phosphate than hydroxide e.g. a weight ratio of at least 2:1 e.g. ≥5:1, ≥6:1, ≥7:1, ≥8:1, ≥9:1, etc.

[0486] The concentration of Al⁺⁺⁺ in a composition for administration to a patient is preferably less than 10mg/ml e.g. ≤5 mg/ml, ≤4 mg/ml, ≤3 mg/ml, ≤2 mg/ml, ≤1 mg/ml, etc. A preferred range is between 0.3 and 1mg/ml. A maximum of 0.85mg/dose is preferred.

B. Oil Emulsions

[0487] Oil emulsion compositions suitable for use as adjuvants in the invention include squalene-water emulsions, such as MF59 [Chapter 10 of ref. 82; see also ref. 83] (5% Squalene, 0.5% Tween 80, and 0.5% Span 85, formulated into submicron particles using a microfluidizer). Complete Freund's adjuvant (CFA) and incomplete Freund's adjuvant (IFA) may also be used.

[0488] Various oil-in-water emulsion adjuvants are known, and they typically include at least one oil and at least one surfactant, with the oil(s) and surfactant(s) being biodegradable (metabolisable) and biocompatible. The oil droplets in the emulsion are generally less than 5 μm in diameter, and ideally have a sub-micron diameter, with these small sizes being achieved with a microfluidiser to provide stable emulsions. Droplets with a size less than 220nm are preferred as they can be subjected to filter sterilization.

[0489] The emulsion can comprise oils such as those from an animal (such as fish) or vegetable source. Sources for vegetable oils include nuts, seeds and grains. Peanut oil, soybean oil, coconut oil, and olive oil, the most commonly available, exemplify the nut oils. Jojoba oil can be used e.g. obtained from the jojoba bean. Seed oils include safflower oil, cottonseed oil, sunflower seed oil, sesame seed oil and the like. In the grain group, corn oil is the most readily available, but the oil of other cereal grains such as wheat, oats, rye, rice, teff, triticale and the like may also be used. 6-10 carbon fatty acid esters of glycerol and 1,2-propanediol, while not occurring naturally in seed oils, may be prepared by hydrolysis, separation and esterification of the appropriate materials starting from the nut and seed oils. Fats and oils from mammalian milk are metabolizable and may therefore be used in the practice of this invention. The procedures for separation, purification, saponification and other means necessary for obtaining pure oils from animal sources are well known in the art. Most fish contain metabolizable oils which may be readily recovered. For example, cod liver oil, shark liver oils, and whale oil such as spermaceti exemplify several of the fish oils which may be used herein. A number of branched chain oils are synthesized biochemically in 5-carbon isoprene units and are generally referred to as terpenoids. Shark liver oil contains a branched, unsaturated terpenoids known as squalene, 2,6,10,15,19,23-hexamethyl-2,6,10,14,18,22-tetracosahexaene, which is particularly preferred herein. Squalane, the saturated analog to squalene, is also a preferred oil. Fish oils, including squalene and squalane, are readily available from commercial sources or may be obtained by methods known in the art. Other preferred oils are the tocopherols (see below). Mixtures of oils can be used.

[0490] Surfactants can be classified by their 'HLB' (hydrophilic/lipophile balance). Preferred surfactants of the invention have a HLB of at least 10, preferably at least 15, and more preferably at least 16. The invention can be used with surfactants including, but not limited to: the polyoxyethylene sorbitan esters surfactants (commonly referred to as the Tweens), especially polysorbate 20 and polysorbate 80; copolymers of ethylene oxide (EO), propylene oxide (PO), and/or butylene oxide (BO), sold under the DOWFAXTM tradename, such as linear EO/PO block copolymers; octoxynols, which can vary in the number of repeating ethoxy (oxy-1,2-ethanediyl) groups, with octoxynol-9 (Triton X-100, or t-octylphenoxypolyethoxyethanol) being of particular interest; (octylphenoxy)polyethoxyethanol (IGEPAL CA-630/NP-40); phospholipids such as phosphatidylcholine (lecithin); nonylphenol ethoxylates, such as the TergitolTM NP series; polyoxyethylene fatty ethers derived from lauryl, cetyl, stearyl and oleyl alcohols (known as Brij surfactants), such as triethyleneglycol monolauryl ether (Brij 30); and sorbitan esters (commonly known as the SPANs), such as sorbitan trioleate (Span 85) and sorbitan monolaurate. Non-ionic surfactants are preferred. Preferred surfactants for including in the emulsion are Tween 80 (polyoxyethylene sorbitan monooleate), Span 85 (sorbitan trioleate), lecithin and Triton X-100.

[0491] Mixtures of surfactants can be used e.g. Tween 80/Span 85 mixtures. A combination of a polyoxyethylene sorbitan ester such as polyoxyethylene sorbitan monooleate (Tween 80) and an octoxynol such as t-octylphenoxypolyethoxyethanol (Triton X-100) is also suitable. Another useful combination comprises laureth 9 plus a polyoxyethylene sorbitan ester and/or an octoxynol.

[0492] Preferred amounts of surfactants (% by weight) are: polyoxyethylene sorbitan esters (such as Tween 80) 0.01 to 1%, in particular about 0.1 %; octyl- or nonylphenoxy polyoxyethanols (such as Triton X-100, or other detergents in the Triton series) 0.001 to 0.1 %, in particular 0.005 to 0.02%; polyoxyethylene ethers (such as laureth 9) 0.1 to 20 %, preferably 0.1 to 10 % and in particular 0.1 to 1 % or about 0.5%.

[0493] Preferred emulsion adjuvants have an average droplets size of <1 μm e.g. <750nm, $\leq 500\text{nm}$, $\leq 400\text{nm}$, $\leq 300\text{nm}$, $\leq 250\text{nm}$, $\leq 220\text{nm}$, $\leq 200\text{nm}$, or smaller. These droplet sizes can conveniently be achieved by techniques such as microfluidisation. -

[0494] Specific oil-in-water emulsion adjuvants useful with the invention include, but are not limited to:

- A submicron emulsion of squalene, Tween 80, and Span 85. The composition of the emulsion by volume can be about 5% squalene, about 0.5% polysorbate 80 and about 0.5% Span 85. In weight terms, these ratios become 4.3% squalene, 0.5% polysorbate 80 and 0.48% Span 85. This adjuvant is known as 'MF59' [84-86], as described in more detail in Chapter 10 of ref. 87 and chapter 12 of ref. 88. The MF59 emulsion advantageously includes citrate ions e.g. 10mM sodium citrate buffer.

- An emulsion of squalene, a tocopherol, and polysorbate 80 (Tween 80). The emulsion may include phosphate buffered saline. It may also include Span 85 (*e.g.* at 1%) and/or lecithin. These emulsions may have from 2 to 10% squalene, from 2 to 10% tocopherol and from 0.3 to 3% Tween 80, and the weight ratio of squalene:tocopherol is preferably ≤ 1 as this provides a more stable emulsion. Squalene and Tween 80 may be present volume ratio of about 5:2 or at a weight ratio of about 11:5. One such emulsion can be made by dissolving Tween 80 in PBS to give a 2% solution, then mixing 90ml of this solution with a mixture of (5g of DL- α -tocopherol and 5ml squalene), then microfluidising the mixture. The resulting emulsion may have submicron oil droplets *e.g.* with an average diameter of between 100 and 250nm, preferably about 180nm. The emulsion may also include a 3-de-O-acylated monophosphoryl lipid A (3d-MPL). Another useful emulsion of this type may comprise, per human dose, 0.5-10 mg squalene, 0.5-11 mg tocopherol, and 0.1-4 mg polysorbate 80 [89].
- An emulsion of squalene, a tocopherol, and a Triton detergent (*e.g.* Triton X-100). The emulsion may also include a 3d-MPL (see below). The emulsion may contain a phosphate buffer.
- An emulsion comprising a polysorbate (*e.g.* polysorbate 80), a Triton detergent (*e.g.* Triton X-100) and a tocopherol (*e.g.* an α -tocopherol succinate). The emulsion may include these three components at a mass ratio of about 75:11:10 (*e.g.* 750 μ g/ml polysorbate 80, 110 μ g/ml Triton X-100 and 100 μ g/ml α -tocopherol succinate), and these concentrations should include any contribution of these components from antigens. The emulsion may also include squalene. The emulsion may also include a 3d-MPL (see below). The aqueous phase may contain a phosphate buffer.
- An emulsion of squalene, polysorbate 80 and poloxamer 401 ("Pluronic™ L121"). The emulsion can be formulated in phosphate buffered saline, pH 7.4. This emulsion is a useful delivery vehicle for muramyl dipeptides, and has been used with threonyl-MDP in the "SAF-1" adjuvant [90] (0.05-1% Thr-MDP, 5% squalene, 2.5% Pluronic L121 and 0.2% polysorbate 80). It can also be used without the Thr-MDP, as in the "AF" adjuvant [91] (5% squalene, 1.25% Pluronic L121 and 0.2% polysorbate 80). Microfluidisation is preferred.
- An emulsion comprising squalene, an aqueous solvent, a polyoxyethylene alkyl ether hydrophilic nonionic surfactant (*e.g.* polyoxyethylene (12) cetostearyl ether) and a hydrophobic nonionic surfactant (*e.g.* a sorbitan ester or mannide ester, such as sorbitan monooleate or 'Span 80'). The emulsion is preferably thermoreversible and/or has at least 90% of the oil droplets (by volume) with a size less than 200 nm [92]. The emulsion may also include one or more of: alditol; a cryoprotective agent (*e.g.* a sugar, such as dodecylmaltoside and/or sucrose); and/or an alkylpolyglycoside. The emulsion may include a TLR4 agonist [93]. Such emulsions may be lyophilized.
- An emulsion of squalene, poloxamer 105 and Abil-Care [94]. The final concentration (weight) of these components in adjuvanted vaccines are 5% squalene, 4% poloxamer 105 (pluronic polyol) and 2% Abil-Care 85 (Bis-PEG/PPG-16/16 PEG/PPG-16/16 dimethicone; caprylic/capric triglyceride).
- An emulsion having from 0.5-50% of an oil, 0.1-10% of a phospholipid, and 0.05-5% of a non-ionic surfactant. As described in reference 95, preferred phospholipid components are phosphatidylcholine, phosphatidylethanolamine, phosphatidylserine, phosphatidylinositol, phosphatidylglycerol, phosphatidic acid, sphingomyelin and cardiolipin. Submicron droplet sizes are advantageous.
- A submicron oil-in-water emulsion of a non-metabolisable oil (such as light mineral oil) and at least one surfactant (such as lecithin, Tween 80 or Span 80). Additives may be included, such as QuilA saponin, cholesterol, a saponin-lipophile conjugate (such as GPI-0100, described in reference 96, produced by addition of aliphatic amine to desacylsaponin via the carboxyl group of glucuronic acid), dimethyldioctadecylammonium bromide and/or N,N-dioctadecyl-N,N-bis (2-hydroxyethyl)propanediamine.
- An emulsion in which a saponin (*e.g.* QuilA or QS21) and a sterol (*e.g.* a cholesterol) are associated as helical micelles [97].
- An emulsion comprising a mineral oil, a non-ionic lipophilic ethoxylated fatty alcohol, and a non-ionic hydrophilic surfactant (*e.g.* an ethoxylated fatty alcohol and/or polyoxyethylene-polyoxypropylene block copolymer) [98].
- An emulsion comprising a mineral oil, a non-ionic hydrophilic ethoxylated fatty alcohol, and a non-ionic lipophilic surfactant (*e.g.* an ethoxylated fatty alcohol and/or polyoxyethylene-polyoxypropylene block copolymer) [98].

[0495] In some embodiments an emulsion may be mixed with antigen extemporaneously, at the time of delivery, and

thus the adjuvant and antigen may be kept separately in a packaged or distributed vaccine, ready for final formulation at the time of use. In other embodiments an emulsion is mixed with antigen during manufacture, and thus the composition is packaged in a liquid adjuvanted form,. The antigen will generally be in an aqueous form, such that the vaccine is finally prepared by mixing two liquids. The volume ratio of the two liquids for mixing can vary (e.g. between 5:1 and 1:5) but is generally about 1:1. Where concentrations of components are given in the above descriptions of specific emulsions, these concentrations are typically for an undiluted composition, and the concentration after mixing with an antigen solution will thus decrease.

[0496] Where a composition includes a tocopherol, any of the α , β , γ , δ , ϵ or ξ tocopherols can be used, but α -tocopherols are preferred. The tocopherol can take several forms e.g. different salts and/or isomers. Salts include organic salts, such as succinate, acetate, nicotinate, etc. D- α -tocopherol and DL- α -tocopherol can both be used. Tocopherols are advantageously included in vaccines for use in elderly patients (e.g. aged 60 years or older) because vitamin E has been reported to have a positive effect on the immune response in this patient group [99]. They also have antioxidant properties that may help to stabilize the emulsions [100]. A preferred α -tocopherol is DL- α -tocopherol, and the preferred salt of this tocopherol is the succinate. The succinate salt has been found to cooperate with TNF-related ligands *in vivo*.

C. Saponin formulations [chapter 22 of ref. 82]

[0497] Saponin formulations may also be used as adjuvants in the invention. Saponins are a heterogeneous group of sterol glycosides and triterpenoid glycosides that are found in the bark, leaves, stems, roots and even flowers of a wide range of plant species. Saponin from the bark of the *Quillaia saponaria* Molina tree have been widely studied as adjuvants. Saponin can also be commercially obtained from *Smilax ornata* (sarsapilla), *Gypsophilla paniculata* (brides veil), and *Saponaria officianalis* (soap root). Saponin adjuvant formulations include purified formulations, such as QS21, as well as lipid formulations, such as ISCOMs. QS21 is marketed as Stimulon™.

[0498] Saponin compositions have been purified using HPLC and RP-HPLC. Specific purified fractions using these techniques have been identified, including QS7, QS17, QS18, QS21, QH-A, QH-B and QH-C. Preferably, the saponin is QS21. A method of production of QS21 is disclosed in ref. 101. Saponin formulations may also comprise a sterol, such as cholesterol [102].

[0499] Combinations of saponins and cholesterol can be used to form unique particles called immunostimulating complexes (ISCOMs) [chapter 23 of ref. 82]. ISCOMs typically also include a phospholipid such as phosphatidylethanolamine or phosphatidylcholine. Any known saponin can be used in ISCOMs. Preferably, the ISCOM includes one or more of QuilA, QHA & QHC. ISCOMs are further described in refs. 102-104. Optionally, the ISCOMS may be devoid of additional detergent [105].

[0500] A review of the development of saponin based adjuvants can be found in refs. 106 & 107.

D. Virosomes and virus-like particles

[0501] Virosomes and virus-like particles (VLPs) can also be used as adjuvants in the invention. These structures generally contain one or more proteins from a virus optionally combined or formulated with a phospholipid. They are generally non-pathogenic, non-replicating and generally do not contain any of the native viral genome. The viral proteins may be recombinantly produced or isolated from whole viruses. These viral proteins suitable for use in virosomes or VLPs include proteins derived from influenza virus (such as HA or NA), Hepatitis B virus (such as core or capsid proteins), Hepatitis E virus, measles virus, Sindbis virus, Rotavirus, Foot-and-Mouth Disease virus, Retrovirus, Norwalk virus, human Papilloma virus, HIV, RNA-phages, Q β -phage (such as coat proteins), GA-phage, fr-phage, AP205 phage, and Ty (such as retrotransposon Ty protein p1). VLPs are discussed further in refs. 108-113. Virosomes are discussed further in, for example, ref. 114

E. Bacterial or microbial derivatives

[0502] Adjuvants suitable for use in the invention include bacterial or microbial derivatives such as non-toxic derivatives of enterobacterial lipopolysaccharide (LPS), Lipid A derivatives, immunostimulatory oligonucleotides and ADP-ribosylating toxins and detoxified derivatives thereof.

[0503] Non-toxic derivatives of LPS include monophosphoryl lipid A (MPL) and 3-O-deacylated MPL (3dMPL). 3dMPL is a mixture of 3 de-O-acylated monophosphoryl lipid A with 4, 5 or 6 acylated chains. A preferred "small particle" form of 3 De-O-acylated monophosphoryl lipid A is disclosed in ref. 115. Such "small particles" of 3dMPL are small enough to be sterile filtered through a 0.22 μ m membrane [115]. Other non-toxic LPS derivatives include monophosphoryl lipid A mimics, such as aminoalkyl glucosaminide phosphate derivatives e.g. RC-529 [116,117].

[0504] Lipid A derivatives include derivatives of lipid A from *Escherichia coli* such as OM-174. OM-174 is described for example in refs. 118 & 119.

[0505] Immunostimulatory oligonucleotides suitable for use as adjuvants in the invention include nucleotide sequences containing a CpG motif (a dinucleotide sequence containing an unmethylated cytosine linked by a phosphate bond to a guanosine). Double-stranded RNAs and oligonucleotides containing palindromic or poly(dG) sequences have also been shown to be immunostimulatory.

[0506] The CpG's can include nucleotide modifications/analogues such as phosphorothioate modifications and can be double-stranded or single-stranded. References 120, 121 and 122 disclose possible analog substitutions e.g. replacement of guanosine with 2'-deoxy-7-deazaguanosine. The adjuvant effect of CpG oligonucleotides is further discussed in refs. 123-128.

[0507] The CpG sequence may be directed to TLR9, such as the motif GTCGTT or TTCGTT [129]. The CpG sequence may be specific for inducing a Th1 immune response, such as a CpG-A ODN, or it may be more specific for inducing a B cell response, such as a CpG-B ODN. CpG-A and CpG-B ODNs are discussed in refs. 130-132. Preferably, the CpG is a CpG-A ODN.

[0508] Preferably, the CpG oligonucleotide is constructed so that the 5' end is accessible for receptor recognition. Optionally, two CpG oligonucleotide sequences may be attached at their 3' ends to form "immunomers". See, for example, refs. 129 & 133-135.

[0509] A useful CpG adjuvant is CpG7909, also known as ProMune™ (Coley Pharmaceutical Group, Inc.). Another is CpG 1826. As an alternative, or in addition, to using CpG sequences, TpG sequences can be used [136], and these oligonucleotides may be free from unmethylated CpG motifs. The immunostimulatory oligonucleotide may be pyrimidine-rich. For example, it may comprise more than one consecutive thymidine nucleotide (e.g. TTTT, as disclosed in ref. 136), and/or it may have a nucleotide composition with >25% thymidine (e.g. >35%, >40%, >50%, >60%, >80%, etc.). For example, it may comprise more than one consecutive cytosine nucleotide (e.g. CCCC, as disclosed in ref. 136), and/or it may have a nucleotide composition with >25% cytosine (e.g. >35%, >40%, >50%, >60%, >80%, etc.). These oligonucleotides may be free from unmethylated CpG motifs. Immunostimulatory oligonucleotides will typically comprise at least 20 nucleotides. They may comprise fewer than 100 nucleotides.

[0510] A particularly useful adjuvant based around immunostimulatory oligonucleotides is known as IC-31™ [137]. Thus an adjuvant used with the invention may comprise a mixture of (i) an oligonucleotide (e.g. between 15-40 nucleotides) including at least one (and preferably multiple) Cpl motifs (i.e. a cytosine linked to an inosine to form a dinucleotide), and (ii) a polycationic polymer, such as an oligopeptide (e.g. between 5-20 amino acids) including at least one (and preferably multiple) Lys-Arg-Lys tripeptide sequence(s). The oligonucleotide may be a deoxynucleotide comprising 26-mer sequence 5'-(IC)₁₃-3' (SEQ ID NO: 175). The polycationic polymer may be a peptide comprising 11-mer amino acid sequence KLKLLLLLKLK (SEQ ID NO: 176). The oligonucleotide and polymer can form complexes e.g. as disclosed in references 138 & 139.

[0511] Bacterial ADP-ribosylating toxins and detoxified derivatives thereof may be used as adjuvants in the invention. Preferably, the protein is derived from *E. coli* (*E. coli* heat labile enterotoxin "LT"), cholera ("CT"), or pertussis ("PT"). The use of detoxified ADP-ribosylating toxins as mucosal adjuvants is described in ref. 140 and as parenteral adjuvants in ref. 141. The toxin or toxoid is preferably in the form of a holotoxin, comprising both A and B subunits. Preferably, the A subunit contains a detoxifying mutation; preferably the B subunit is not mutated. Preferably, the adjuvant is a detoxified LT mutant such as LT-K63, LT-R72, and LT-G192. The use of ADP-ribosylating toxins and detoxified derivatives thereof, particularly LT-K63 and LT-R72, as adjuvants can be found in refs. 142-149. A useful CT mutant is or CT-E29H [150]. Numerical reference for amino acid substitutions is preferably based on the alignments of the A and B subunits of ADP-ribosylating toxins set forth in ref. 151.

F. Human immunomodulators

[0512] Human immunomodulators suitable for use as adjuvants in the invention include cytokines, such as interleukins (e.g. IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12 [152], etc.) [153], interferons (e.g. interferon- γ), macrophage colony stimulating factor, and tumor necrosis factor. A preferred immunomodulator is IL-12.

G. Bioadhesives and Mucoadhesives

[0513] Bioadhesives and mucoadhesives may also be used as adjuvants in the invention. Suitable bioadhesives include esterified hyaluronic acid microspheres [154] or mucoadhesives such as cross-linked derivatives of poly(acrylic acid), polyvinyl alcohol, polyvinyl pyrrolidone, polysaccharides and carboxymethylcellulose. Chitosan and derivatives thereof may also be used as adjuvants in the invention [155].

H. Microparticles

[0514] Microparticles may also be used as adjuvants in the invention. Microparticles (i.e. a particle of ~100nm to

~150 μ m in diameter, more preferably ~200nm to ~30 μ m in diameter, and most preferably ~500nm to ~10 μ m in diameter) formed from materials that are biodegradable and non-toxic (e.g. a poly(α -hydroxy acid), a polyhydroxybutyric acid, a polyorthoester, a polyanhydride, a polycaprolactone, etc.), with poly(lactide-co-glycolide) are preferred, optionally treated to have a negatively-charged surface (e.g. with SDS) or a positively-charged surface (e.g. with a cationic detergent, such as CTAB).

I. Liposomes (Chapters 13 & 14 of ref. 82)

[0515] Examples of liposome formulations suitable for use as adjuvants are described in refs. 156-158.

J. Polyoxyethylene ether and polyoxyethylene ester formulations

[0516] Adjuvants suitable for use in the invention include polyoxyethylene ethers and polyoxyethylene esters [159]. Such formulations further include polyoxyethylene sorbitan ester surfactants in combination with an octoxynol [160] as well as polyoxyethylene alkyl ethers or ester surfactants in combination with at least one additional non-ionic surfactant such as an octoxynol [161]. Preferred polyoxyethylene ethers are selected from the following group: polyoxyethylene-9-lauryl ether (laureth 9), polyoxyethylene-9-stearyl ether, polyoxyethylene-8-stearyl ether, polyoxyethylene-4-lauryl ether, polyoxyethylene-35-lauryl ether, and polyoxyethylene-23-lauryl ether.

K. Phosphazenes

[0517] A phosphazene, such as poly[di(carboxylatophenoxy)phosphazene] ("PCPP") as described, for example, in references 162 and 163, may be used.

L. Muramyl peptides

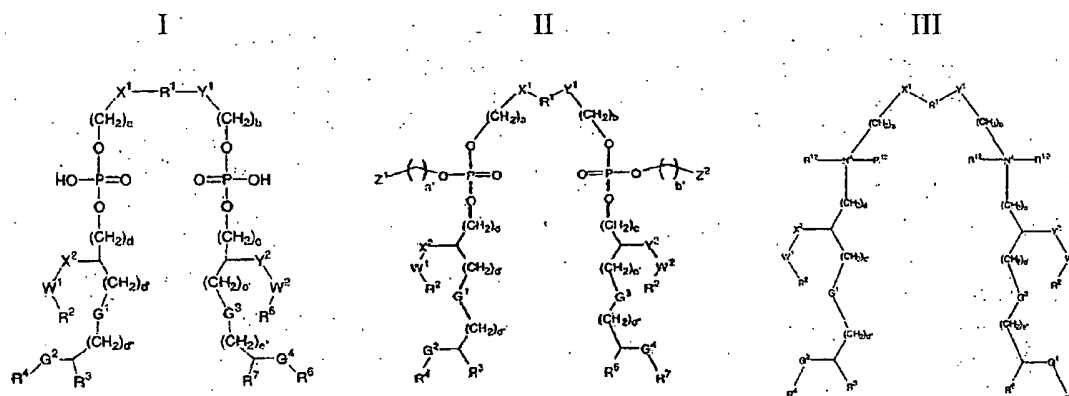
[0518] Examples of muramyl peptides suitable for use as adjuvants in the invention include N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), and N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine MTP-PE).

M. Imidazoquinolone Compounds.

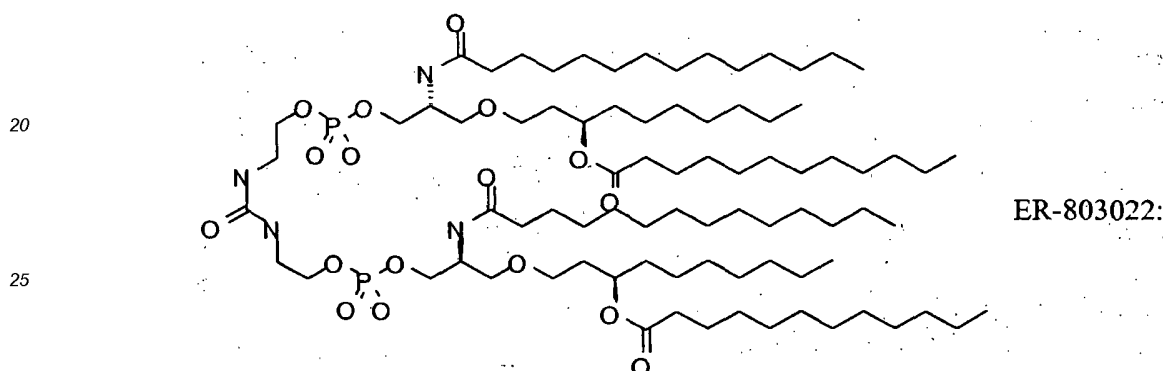
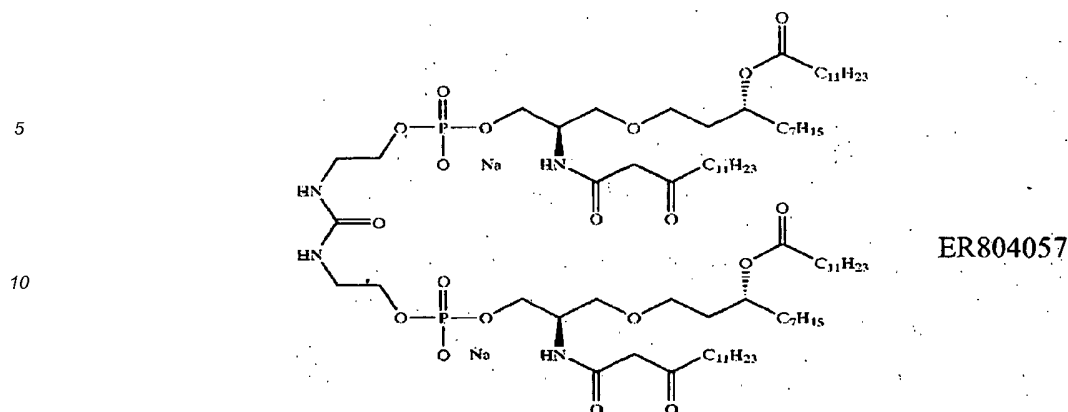
[0519] Examples of imidazoquinolone compounds suitable for use as adjuvants in the invention include Imiquimod ("R-837") [164,165], Resiquimod ("R-848") [166], and their analogs; and salts thereof (e.g. the hydrochloride salts). Further details about immunostimulatory imidazoquinolones can be found in references 167 to 171.

N. Substituted ureas

[0520] Substituted ureas useful as adjuvants include compounds of formula I, II or III, or salts thereof:



as defined in reference 172, such as 'ER 803058', 'ER 803732', 'ER 804053', 'ER 804058', 'ER 804059', 'ER 804442', 'ER 804680', 'ER 804764', 'ER 803022 or 'ER 804057' e.g.:



O. Further adjuvants

[0521] Further adjuvants that may be used with the invention include:

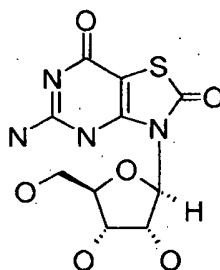
- An aminoalkyl glucosaminide phosphate derivative, such as RC-529 [173,174].

Cyclic diguanylate ('c-di-GMP'), which has been reported as a useful adjuvant for *S.aureus* vaccines [175].

[0522] A thiosemicarbazone compound, such as those disclosed in reference 176. Methods of formulating, manufacturing, and screening for active compounds are also described in reference 176. The thiosemicarbazones are particularly effective in the stimulation of human peripheral blood mononuclear cells for the production of cytokines, such as TNF- α .

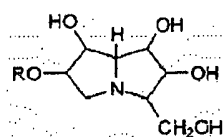
[0523] A tryptanthrin compound, such as those disclosed in reference 177. Methods of formulating, manufacturing, and screening for active compounds are also described in reference 177. The thiosemicarbazones are particularly effective in the stimulation of human peripheral blood mononuclear cells for the production of cytokines, such as TNF- α .

- A nucleoside analog, such as: (a) Isatorabine (ANA-245; 7-thia-8-oxoguanosine):



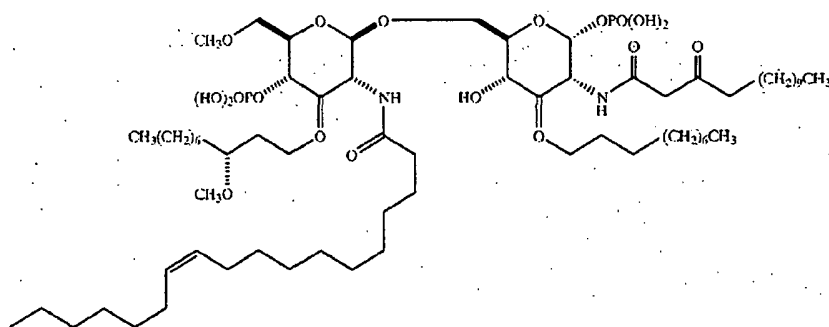
and prodrugs thereof; (b) ANA975; (c) ANA-025-1; (d) ANA380; (e) the compounds disclosed in references 178 to 180 Loxoribine (7-allyl-8-oxoguanosine) [181].

- Compounds disclosed in reference 182, including: Acylpiperazine compounds, Indoleione compounds, Tetrahydroisoquinoline (THIQ) compounds, Benzocycloione compounds, Aminoazavinyl compounds, Aminobenzimidazole quinolinone (ABIQ) compounds [183,184], Hydrapthalamide compounds, Benzophenone compounds, Isoxazole compounds, Sterol compounds, Quinazolinone compounds, Pyrrole compounds [185], Anthraquinone compounds, Quinoxaline compounds, Triazine compounds, Pyrazalopyrimidine compounds, and Benzazole compounds [186].
- Compounds containing lipids linked to a phosphate-containing acyclic backbone, such as the TLR4 antagonist E5564 [187,188]:
- A polyoxidonium polymer [189,190] or other N-oxidized polyethylene-piperazine derivative.
- Methyl inosine 5'-monophosphate ("MIMP") [191].
- A polyhydroxylated pyrrolizidine compound [192], such as one having formula:



where R is selected from the group comprising hydrogen, straight or branched, unsubstituted or substituted, saturated or unsaturated acyl, alkyl (e.g. cycloalkyl), alkenyl, alkynyl and aryl groups, or a pharmaceutically acceptable salt or derivative thereof. Examples include, but are not limited to: casuarine, casuarine-6- α -D-glucopyranose, 3-*epi*-casuarine, 7-*epi*-casuarine, 3,7-diepi-casuarine, etc.

- A CD1d ligand, such as an α -glycosylceramide [193-200] (e.g. α -galactosylceramide), phytosphingosine-containing α -glycosylceramides, OCH, KRN7000 [(2S,3S,4R)-1-O-(α -D-galactopyranosyl)-2-(N-hexacosanoylamino)-1,3,4-octadecanetriol], CRONY-101, 3"-O-sulfo-galactosylceramide, etc.
- A gamma inulin [201] or derivative thereof, such-as-algammulin.



Adjuvant combinations

[0524] The invention may also comprise combinations of one or more of the adjuvants identified above. For example, the following adjuvant compositions may be used in the invention: (1) a saponin and an oil-in-water emulsion [202]; (2) a saponin (e.g. QS21) + a non-toxic LPS derivative (e.g. 3dMPL) [203]; (3) a saponin (e.g. QS21) + a non-toxic LPS derivative (e.g. 3dMPL) + a cholesterol; (4) a saponin (e.g. QS21) + 3dMPL + IL-12 (optionally + a sterol) [204]; (5) combinations of 3dMPL with, for example, QS21 and/or oil-in-water emulsions [205]; (6) SAF, containing 10% squalene, 0.4% Tween 80™, 5% pluronic-block polymer L121, and thr-MDP, either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion. (7) Ribi™ adjuvant system (RAS), (Ribi Immunochem) containing 2% squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (Detox™); and (8) one or more mineral salts (such as an aluminum salt) + a non-toxic derivative of LPS (such as 3dMPL).

[0525] Other substances that act as immunostimulating agents are disclosed in chapter 7 of ref. 82.

[0526] The use of an aluminium hydroxide and/or aluminium phosphate adjuvant is particularly preferred, and antigens

are generally adsorbed to these salts. Calcium phosphate is another preferred adjuvant. Other preferred adjuvant combinations include combinations of Th1 and Th2 adjuvants such as CpG & alum or resiquimod & alum. A combination of aluminium phosphate and 3dMPL may be used.

[0527] The compositions of the invention may elicit both a cell mediated immune response as well as a humoral immune response. This immune response will preferably induce long lasting (e.g. neutralising) antibodies and a cell mediated immunity that can quickly respond upon exposure to pneumococcus.

[0528] Two types of T cells, CD4 and CD8 cells, are generally thought necessary to initiate and/or enhance cell mediated immunity and humoral immunity. CD8 T cells can express a CD8 co-receptor and are commonly referred to as Cytotoxic T lymphocytes (CTLs). CD8 T cells are able to recognize or interact with antigens displayed on MHC Class I molecules.

[0529] CD4 T cells can express a CD4 co-receptor and are commonly referred to as T helper cells. CD4 T cells are able to recognize antigenic peptides bound to MHC class II molecules. Upon interaction with a MHC class II molecule, the CD4 cells can secrete factors such as cytokines. These secreted cytokines can activate B cells, cytotoxic T cells, macrophages, and other cells that participate in an immune response. Helper T cells or CD4+ cells can be further divided into two functionally distinct subsets: TH1 phenotype and TH2 phenotypes which differ in their cytokine and effector function.

[0530] Activated TH1 cells enhance cellular immunity (including an increase in antigen-specific CTL production) and are therefore of particular value in responding to intracellular infections. Activated TH1 cells may secrete one or more of IL-2, IFN- γ , and TNF- β . A TH1 immune response may result in local inflammatory reactions by activating macrophages, NK (natural killer) cells, and CD8 cytotoxic T cells (CTLs). A TH1 immune response may also act to expand the immune response by stimulating growth of B and T cells with IL-12. TH1 stimulated B cells may secrete IgG2a.

[0531] Activated TH2 cells enhance antibody production and are therefore of value in responding to extracellular infections. Activated TH2 cells may secrete one or more of IL-4, IL-5, IL-6, and IL-10. A TH2 immune response may result in the production of IgG1, IgE, IgA and memory B cells for future protection.

[0532] An enhanced immune response may include one or more of an enhanced TH1 immune response and a TH2 immune response.

[0533] A TH1 immune response may include one or more of an increase in CTLs, an increase in one or more of the cytokines associated with a TH1 immune response (such as IL-2, IFN- γ , and TNF- β), an increase in activated macrophages, an increase in NK activity, or an increase in the production of IgG2a. Preferably, the enhanced TH1 immune response will include an increase in IgG2a production.

[0534] A TH1 immune response may be elicited using a TH1 adjuvant. A TH1 adjuvant will generally elicit increased levels of IgG2a production relative to immunization of the antigen without adjuvant. TH1 adjuvants suitable for use in the invention may include for example saponin formulations, virosomes and virus like particles, non-toxic derivatives of enterobacterial lipopolysaccharide (LPS), immunostimulatory oligonucleotides. Immunostimulatory oligonucleotides, such as oligonucleotides containing a CpG motif, are preferred TH1 adjuvants for use in the invention.

[0535] A TH2 immune response may include one or more of an increase in one or more of the cytokines associated with a TH2 immune response (such as IL-4, IL-5, IL-6 and IL-10), or an increase in the production of IgG1, IgE, IgA and memory B cells. Preferably, the enhanced TH2 immune response will include an increase in IgG1 production.

[0536] A TH2 immune response may be elicited using a TH2 adjuvant. A TH2 adjuvant will generally elicit increased levels of IgG1 production relative to immunization of the antigen without adjuvant. TH2 adjuvants suitable for use in the invention include, for example, mineral containing compositions, oil-emulsions, and ADP-ribosylating toxins and detoxified derivatives thereof. Mineral containing compositions, such as aluminium salts are preferred TH2 adjuvants for use in the invention.

[0537] Preferably, the invention includes a composition comprising a combination of a TH1 adjuvant and a TH2 adjuvant. Preferably, such a composition elicits an enhanced TH1 and an enhanced TH2 response, i.e., an increase in the production of both IgG1 and IgG2a production relative to immunization without an adjuvant. Still more preferably, the composition comprising a combination of a TH1 and a TH2 adjuvant elicits an increased TH1 and/or an increased TH2 immune response relative to immunization with a single adjuvant (i.e., relative to immunization with a TH1 adjuvant alone or immunization with a TH2 adjuvant alone).

[0538] The immune response may be one or both of a TH1 immune response and a TH2 response. Preferably, immune response provides for one or both of an enhanced TH1 response and an enhanced TH2 response.

[0539] The enhanced immune response may be one or both of a systemic and a mucosal immune response. Preferably, the immune response provides for one or both of an enhanced systemic and an enhanced mucosal immune response. Preferably the mucosal immune response is a TH2 immune response. Preferably, the mucosal immune response includes an increase in the production of IgA.

[0540] *S.aureus* infections can affect various areas of the body and so the compositions of the invention may be prepared in various forms. For example, the compositions may be prepared as injectables, either as liquid solutions or suspensions. Solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared

(e.g. a lyophilised composition or a spray-freeze dried composition). The composition may be prepared for topical administration e.g. as an ointment, cream or powder. The composition may be prepared for oral administration e.g. as a tablet or capsule, as a spray, or as a syrup (optionally flavoured). The composition may be prepared for pulmonary administration e.g. as an inhaler, using a fine powder or a spray. The composition may be prepared as a suppository or pessary. The composition may be prepared for nasal, aural or ocular administration e.g. as drops. The composition may be in kit form, designed such that a combined composition is reconstituted just prior to administration to a patient. Such kits may comprise one or more antigens in liquid form and one or more lyophilised antigens.

[0541] Where a composition is to be prepared extemporaneously prior to use (e.g. where a component is presented in lyophilised form) and is presented as a kit, the kit may comprise two vials, or it may comprise one ready-filled syringe and one vial, with the contents of the syringe being used to reactivate the contents of the vial prior to injection.

[0542] Immunogenic compositions used as vaccines comprise an immunologically effective amount of antigen(s), as well as any other components, as needed. By 'immunologically effective amount', it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, age, the taxonomic group of individual to be treated (e.g. non-human primate, primate, etc.), the capacity of the individual's immune system to synthesise antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials. Where more than one antigen is included in a composition then two antigens may be present at the same dose as each other or at different doses.

[0543] As mentioned above, a composition may include a temperature protective agent, and this component may be particularly useful in adjuvanted compositions (particularly those containing a mineral adjuvant, such as an aluminium salt). As described in reference 206, a liquid temperature protective agent may be added to an aqueous vaccine composition to lower its freezing point e.g. to reduce the freezing point to below 0°C. Thus the composition can be stored below 0°C, but above its freezing point, to inhibit thermal breakdown. The temperature protective agent also permits freezing of the composition while protecting mineral salt adjuvants against agglomeration or sedimentation after freezing and thawing, and may also protect the composition at elevated temperatures e.g. above 40°C. A starting aqueous vaccine and the liquid temperature protective agent may be mixed such that the liquid temperature protective agent forms from 1-80% by volume of the final mixture. Suitable temperature protective agents should be safe for human administration, readily miscible/soluble in water, and should not damage other components (e.g. antigen and adjuvant) in the composition. Examples include glycerin, propylene glycol, and/or polyethylene glycol (PEG). Suitable PEGs may have an average molecular weight ranging from 200-20,000 Da. In a preferred embodiment, the polyethylene glycol can have an average molecular weight of about 300 Da ('PEG-300').

[0544] The invention provides an immunogenic composition comprising: (i) one or more antigen(s) selected from the first, second, third or fourth antigen groups; and (ii) a temperature protective agent. This composition may be formed by mixing (i) an aqueous composition comprising one or more antigen(s) selected from the first, second, third or fourth antigen groups, with (ii) a temperature protective agent. The mixture may then be stored e.g. below 0°C, from 0-20°C, from 20-35°C, from 35-55°C, or higher. It may be stored in liquid or frozen form. The mixture may be lyophilised. The composition may alternatively be formed by mixing (i) a dried composition comprising one or more antigen(s) selected from the first, second, third or fourth antigen groups, with (ii) a liquid composition comprising the temperature protective agent. Thus component (ii) can be used to reconstitute component (i).

Methods of treatment, and administration of the vaccine

[0545] The invention also provides a method for raising an immune response in a mammal comprising the step of administering an effective amount of a composition of the invention. The immune response, is preferably protective and preferably involves antibodies and/or cell-mediated immunity. The method may raise a booster response.

[0546] The invention also provides at least two antigens of the invention for combined use as a medicament e.g. for use in raising an immune response in a mammal.

[0547] The invention also provides the use of at least two antigens of the invention in the manufacture of a medicament for raising an immune response in a mammal.

[0548] By raising an immune response in the mammal by these uses and methods, the mammal can be protected against *S.aureus* infection, including a nosocomial infection. More particularly, the mammal may be protected against a skin infection, pneumonia, meningitis, osteomyelitis endocarditis, toxic shock syndrome, and/or septicemia.

[0549] The invention also provides a kit comprising a first component and a second component wherein neither the first component nor the second component is a composition of the invention as described above, but wherein the first component and the second component can be combined to provide a composition of the invention as described above. The kit may further include a third component comprising one or more of the following: instructions, syringe or other delivery device, adjuvant, or pharmaceutically acceptable formulating solution.

[0550] The invention also provides a delivery device pre-filled with an immunogenic composition of the invention.

[0551] The mammal is preferably a human. Where the vaccine is for prophylactic use, the human is preferably a child (e.g. a toddler or infant) or a teenager; where the vaccine is for therapeutic use, the human is preferably a teenager or an adult. A vaccine intended for children may also be administered to adults e.g. to assess safety, dosage, immunogenicity, etc. Other mammals which can usefully be immunised according to the invention are cows, dogs, horses, and pigs.

[0552] One way of checking efficacy of therapeutic treatment involves monitoring *S.aureus* infection after administration of the compositions of the invention. One way of checking efficacy of prophylactic treatment involves monitoring immune responses, systemically (such as monitoring the level of IgG1 and IgG2a production) and/or mucosally (such as monitoring the level of IgA production), against the antigens in the compositions of the invention after administration of the composition. Typically, antigen-specific serum antibody responses are determined post-immunisation but pre-challenge whereas antigen-specific mucosal antibody responses are determined post-immunisation and post-challenge.

[0553] Another way of assessing the immunogenicity of the compositions of the present invention is to express the proteins recombinantly for screening patient sera or mucosal secretions by immunoblot and/or microarrays. A positive reaction between the protein and the patient sample indicates that the patient has mounted an immune response to the protein in question. This method may also be used to identify immunodominant antigens and/or epitopes within antigens.

[0554] The efficacy of vaccine compositions can also be determined *in vivo* by challenging animal models of *S.aureus* infection, e.g., guinea pigs or mice, with the vaccine compositions. In particular, there are three useful animal models for the study of *S.aureus* infectious disease, namely: (i) the murine abscess model [207], (ii) the murine lethal infection model [207] and (iii) the murine pneumonia model [208]. The abscess model looks at abscesses in mouse kidneys after intravenous challenge. The lethal infection model looks at the number of mice which survive after being infected by a normally-lethal dose of *S.aureus* by the intravenous or intraperitoneal route. The pneumonia model also looks at the survival rate, but uses intranasal infection. A useful vaccine may be effective in one or more of these models. For instance, for some clinical situations it may be desirable to protect against pneumonia, without needing to prevent hematic spread or to promote opsonisation; in other situations the main desire may be to prevent hematic spread. Different antigens, and different antigen combinations, may contribute to different aspects of an effective vaccine.

[0555] Compositions of the invention will generally be administered directly to a patient. Direct delivery may be accomplished by parenteral injection (e.g. subcutaneously, intraperitoneally, intravenously, intramuscularly, or to the interstitial space of a tissue), or mucosally, such as by rectal, oral (e.g. tablet, spray), vaginal, topical, transdermal or transcutaneous, intranasal, ocular, aural, pulmonary or other mucosal administration.

[0556] The invention may be used to elicit systemic and/or mucosal immunity, preferably to elicit an enhanced systemic and/or mucosal immunity.

[0557] Preferably the enhanced systemic and/or mucosal immunity is reflected in an enhanced TH1 and/or TH2 immune response. Preferably, the enhanced immune response includes an increase in the production of IgG1 and/or IgG2a and/or IgA.

[0558] Dosage can be by a single dose schedule or a multiple dose schedule. Multiple doses may be used in a primary immunisation schedule and/or in a booster immunisation schedule. In a multiple dose schedule the various doses may be given by the same or different routes e.g. a parenteral prime and mucosal boost, a mucosal prime and parenteral boost, etc. Multiple doses will typically be administered at least 1 week apart (e.g. about 2 weeks, about 3 weeks, about 4 weeks, about 6 weeks, about 8 weeks, about 10 weeks, about 12 weeks, about 16 weeks, etc.).

[0559] Vaccines prepared according to the invention may be used to treat both children and adults. Thus a human patient may be less than 1 year old, 1-5 years old, 5-15 years old, 15-55 years old, or at least 55 years old. Preferred patients for receiving the vaccines are the elderly (e.g. ≥ 50 years old, ≥ 60 years old, and preferably ≥ 65 years), the young (e.g. ≤ 5 years old), hospitalised patients, healthcare workers, armed service and military personnel, pregnant women, the chronically ill, or immunodeficient patients. The vaccines are not suitable solely for these groups, however, and may be used more generally in a population.

[0560] Vaccines produced by the invention may be administered to patients at substantially the same time as (e.g. during the same medical consultation or visit to a healthcare professional or vaccination centre) other vaccines e.g. at substantially the same time as an influenza vaccine, a measles vaccine, a mumps vaccine, a rubella vaccine, a MMR vaccine, a varicella vaccine, a MMRV vaccine, a diphtheria vaccine, a tetanus vaccine, a pertussis vaccine, a DTP vaccine, a conjugated *H.influenzae* type b vaccine, an inactivated poliovirus vaccine, a hepatitis B virus vaccine, a meningococcal conjugate vaccine (such as a tetravalent A-C-W135-Y vaccine), a respiratory syncytial virus vaccine, etc. Further non-staphylococcal vaccines suitable for co-administration may include one or more antigens listed on pages 33-46 of reference 51.

Nucleic acid immunisation

[0561] The immunogenic compositions described above include polypeptide antigens from *S.aureus*. In all cases, however, the polypeptide antigens can be replaced by nucleic acids (typically DNA) encoding those polypeptides, to

give compositions, methods and uses based on nucleic acid immunisation. Nucleic acid immunisation is now a developed field (e.g. see references 209 to 216 etc.).

[0562] The nucleic acid encoding the immunogen is expressed *in vivo* after delivery to a patient and the expressed immunogen then stimulates the immune system. The active ingredient will typically take the form of a nucleic acid vector comprising: (i) a promoter; (ii) a sequence encoding the immunogen, operably linked to the promoter; and optionally (iii) a selectable marker. Preferred vectors may further comprise (iv) an origin of replication; and (v) a transcription terminator downstream of and operably linked to (ii). In general, (i) & (v) will be eukaryotic and (iii) & (iv) will be prokaryotic.

[0563] Preferred promoters are viral promoters e.g. from cytomegalovirus (CMV). The vector may also include transcriptional regulatory sequences (e.g. enhancers) in addition to the promoter and which interact functionally with the promoter. Preferred vectors include the immediate-early CMV enhancer/promoter, and more preferred vectors also include CMV intron A. The promoter is operably linked to a downstream sequence encoding an immunogen, such that expression of the immunogen-encoding sequence is under the promoter's control.

[0564] Where a marker is used, it preferably functions in a microbial host (e.g. in a prokaryote, in a bacteria, in a yeast). The marker is preferably a prokaryotic selectable marker (e.g. transcribed under the control of a prokaryotic promoter). For convenience, typical markers are antibiotic resistance genes.

[0565] The vector is preferably an autonomously replicating episomal or extrachromosomal vector, such as a plasmid.

[0566] The vector preferably comprises an origin of replication. It is preferred that the origin of replication is active in prokaryotes but not in eukaryotes.

[0567] Preferred vectors thus include a prokaryotic marker for selection of the vector, a prokaryotic origin of replication, but a eukaryotic promoter for driving transcription of the immunogen-encoding sequence. The vectors will therefore (a) be amplified and selected in prokaryotic hosts without polypeptide expression, but (b) be expressed in eukaryotic hosts without being amplified. This arrangement is ideal for nucleic acid immunization vectors.

[0568] The vector may comprise a eukaryotic transcriptional terminator sequence downstream of the coding sequence. This can enhance transcription levels. Where the coding sequence does not have its own, the vector of the invention preferably comprises a polyadenylation sequence. A preferred polyadenylation sequence is from bovine growth hormone.

[0569] The vector may comprise a multiple cloning site

[0570] In addition to sequences encoding the immunogen and a marker, the vector may comprise a second eukaryotic coding sequence. The vector may also comprise an IRES upstream of said second sequence in order to permit translation of a second eukaryotic polypeptide from the same transcript as the immunogen. Alternatively, the immunogen-coding sequence may be downstream of an IRES.

[0571] The vector may comprise unmethylated CpG motifs e.g. unmethylated DNA sequences which have in common a cytosine preceding a guanosine, flanked by two 5' purines and two 3' pyrimidines. In their unmethylated form these DNA motifs have been demonstrated to be potent stimulators of several types of immune cell.

[0572] Vectors may be delivered in a targeted way. Receptor-mediated DNA delivery techniques are described in, for example, references 217 to 222. Therapeutic compositions containing a nucleic acid are administered in a range of about 100ng to about 200mg of DNA for local administration in a gene therapy protocol. Concentration ranges of about 500 ng to about 50 mg, about 1µg to about 2 mg, about 5µg to about 500µg, and about 20µg to about 100µg of DNA can also be used during a gene therapy protocol. Factors such as method of action (e.g. for enhancing or inhibiting levels of the encoded gene product) and efficacy of transformation and expression are considerations which will affect the dosage required for ultimate efficacy. Where greater expression is desired over a larger area of tissue, larger amounts of vector or the same amounts re-administered in a successive protocol of administrations, or several administrations to different adjacent or close tissue portions may be required to effect a positive therapeutic outcome. In all cases, routine experimentation in clinical trials will determine specific ranges for optimal therapeutic effect.

[0573] Vectors can be delivered using gene delivery vehicles. The gene delivery vehicle can be of viral or non-viral origin (see generally references 223 to 226).

[0574] Viral-based vectors for delivery of a desired nucleic acid and expression in a desired cell are well known in the art. Exemplary viral-based vehicles include, but are not limited to, recombinant retroviruses (e.g. references 227 to 237), alphavirus-based vectors (e.g. Sindbis virus vectors, Semliki forest virus (ATCC VR-67; ATCC VR-1247), Ross River virus (ATCC VR-373; ATCC VR-1246) and Venezuelan equine encephalitis virus (ATCC VR-923; ATCC VR-1250; ATCC VR 1249; ATCC VR-532); hybrids or chimeras of these viruses may also be used), poxvirus vectors (e.g. vaccinia, fowlpox, canarypox, modified vaccinia Ankara, etc.), adenovirus vectors, and adeno-associated virus (AAV) vectors (e.g. see refs. 238 to 243). Administration of DNA linked to killed adenovirus [244] can also be employed.

[0575] Non-viral delivery vehicles and methods can also be employed, including, but not limited to, polycationic condensed DNA linked or unlinked to killed adenovirus alone [e.g. 244], ligand-linked DNA [245], eukaryotic cell delivery vehicles cells [e.g. refs. 246 to 250] and nucleic charge neutralization or fusion with cell membranes. Naked DNA can also be employed. Exemplary naked DNA introduction methods are described in refs. 251 and 252. Liposomes (e.g. immunoliposomes) that can act as gene delivery vehicles are described in refs. 253 to 257. Additional approaches are described in references 258 & 259.

[0576] Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in ref. 259. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials or use of ionizing radiation [e.g. refs. 260 & 261]. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun [262] or use of ionizing radiation for activating transferred genes [260 & 261].

[0577] Delivery DNA using PLG {poly(lactide-co-glycolide)} microparticles is a particularly preferred method e.g. by adsorption to the microparticles, which are optionally treated to have a negatively-charged surface (e.g. treated with SDS) or a positively-charged surface (e.g. treated with a cationic detergent, such as CTAB).

S.epidermidis

[0578] Although the invention focuses on *S.aureus*, the inventors also realise that the sta006 and sta011 antigens have homologs in *S.epidermidis*. For example, SEQ ID NO: 234 is the 'iron (Fe+3) ABC superfamily ATP binding cassette transporter, binding protein' from *S.epidermidis* strain M23864:W1, with 73% identity to SEQ ID NO: 42 (sta006), and SEQ ID NO: 235 is the 'putative lipoprotein' from *S.epidermidis* strain RP62A, with 67% identity to SEQ ID NO: 47 (sta011). *S.epidermidis* is commonly present on human skin and can sometimes cause illness. Infection is usually associated with medical devices, such as catheters, and is a cause of nosocomial infections. The results disclosed herein for sta006 and sta011 against *S.aureus* suggest that the homologous proteins in *S.epidermidis* could be useful for immunising against this pathogen.

[0579] The invention provides an immunogenic composition comprising:

(i) a polypeptide comprising an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91 %, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 234; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 234, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more); and/or

(ii) a polypeptide comprising an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 235; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 235, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more).

[0580] The composition may also include an adjuvant. These compositions are particularly useful for immunising a mammal (including a human) against *S.epidermidis* infection.

[0581] Preferred fragments of (b) comprise an epitope from SEQ ID NO: 234 or 235, respectively. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 234/235 while retaining at least one epitope of SEQ ID NO: 234/235.

[0582] More generally, the invention provides the use of the sta006 and/or sta011 homolog from any *Staphylococcus* species for immunising a mammal against that species.

Antibodies

[0583] Antibodies against *S.aureus* antigens can be used for passive immunisation. Thus the invention describes an antibody which is specific for an antigen in the first, second, third or fourth antigen groups. The invention also describes the use of such antibodies in therapy. The invention also describes the use of such antibodies in the manufacture of a medicament. The invention also describes a method for treating a mammal comprising the step of administering an effective amount of an antibody of the invention. As described above for immunogenic compositions, these methods and uses allow a mammal to be protected against *S.aureus* infection.

[0584] The term "antibody" includes intact immunoglobulin molecules, as well as fragments thereof which are capable of binding an antigen. These include hybrid (chimeric) antibody molecules [263, 264]; F(ab')₂ and F(ab) fragments and Fv molecules; non-covalent heterodimers [265, 266]; single-chain Fv molecules (sFv) [267]; dimeric and trimeric antibody fragment constructs; minibodies [268, 269]; humanized antibody molecules [270-272]; and any functional fragments obtained from such molecules, as well as antibodies obtained through non-conventional processes such as phage display. Preferably, the antibodies are monoclonal antibodies. Methods of obtaining monoclonal antibodies are well known in the art. Humanised or fully-human antibodies are preferred.

General

[0585] The practice of the present invention will employ, unless otherwise indicated, conventional methods of chemistry, biochemistry, molecular biology, immunology and pharmacology, within the skill of the art. Such techniques are explained fully in the literature. See, *e.g.*, references 273-280, *etc.*

[0586] "GI" numbering is used above. A GI number, or "GenInfo Identifier", is a series of digits assigned consecutively to each sequence record processed by NCBI when sequences are added to its databases. The GI number bears no resemblance to the accession number of the sequence record. When a sequence is updated (*e.g.* for correction, or to add more annotation or information) then it receives a new GI number. Thus the sequence associated with a given GI number is never changed.

[0587] Where the invention concerns an "epitope", this epitope may be a B-cell epitope and/or a T-cell epitope. Such epitopes can be identified empirically (*e.g.* using PEPSCAN [281,282] or similar methods), or they can be predicted (*e.g.* using the Jameson-Wolf antigenic index [283], matrix-based approaches [284], MAPITOPE [285], TEPITOPE [286,287], neural networks [288], OptiMer & EpiMer [289, 290], ADEPT [291], Tsites [292], hydrophilicity [293], antigenic index [294] or the methods disclosed in references 295-299, *etc.*). Epitopes are the parts of an antigen that are recognised by and bind to the antigen binding sites of antibodies or T-cell receptors, and they may also be referred to as "antigenic determinants".

[0588] Where an antigen "domain" is omitted, this may involve omission of a signal peptide, of a cytoplasmic domain, of a transmembrane domain, of an extracellular domain, *etc.*

[0589] The term "comprising" encompasses "including" as well as "consisting" *e.g.* a composition "comprising" X may consist exclusively of X or may include something additional *e.g.* X + Y.

[0590] The term "about" in relation to a numerical value *x* is optional and means, for example, $x \pm 10\%$.

[0591] References to a percentage sequence identity between two amino acid sequences means that, when aligned, that percentage of amino acids are the same in comparing the two sequences. This alignment and the percent homology or sequence identity can be determined using software programs known in the art, for example those described in section 7.7.18 of ref. 300. A preferred alignment is determined by the Smith-Waterman homology search algorithm using an affine gap search with a gap open penalty of 12 and a gap extension penalty of 2, BLOSUM matrix of 62. The Smith-Waterman homology search algorithm is disclosed in ref. 301.

BRIEF DESCRIPTION OF DRAWINGS**[0592]**

Figure 1 shows bacterial counts (Log cfu/ml) after challenge of mice previously immunised with the indicated antigens.

Figures 2 to 4 show survival (%) after challenge of mice previously immunised with various mixtures of antigens over 14 days. In Figure 2, the six groups from SA-10-a are, from top to bottom at day 14. groups (i), (iii) & (iv) together, (ii), lsdB, then the negative control. In Figure 3, the six groups from SA-10-a are, from top to bottom at day 14. groups (i), (iii) & (iv) together, (ii), lsdB, then the negative control. In Figure 3, the six groups from SA-10-b are, from top to bottom at day 14. groups (iii), (i), (iv), (ii) and lsdB together, then the negative control. In Figure 4, the six groups from SA-14 are, from top to bottom at day 14. groups (iv), (ii), (i), (iii), negative control, and lsdB.

Figure 5 shows collected data on mouse survival from four different experiments after challenge of mice previously immunised with various compositions (PBS negative control; lsdB antigen; and "Combo-1" and "Combo-2" antigen combinations of the invention). Individual symbols show the survival duration of individual mice; the horizontal bar for each group shows the median survival duration; the percentage figures are survival 14 days after challenge; and the *p* values at the top are t-Test comparisons of median survival durations between groups.

Figure 6 shows the number of colony forming units (cfu) in mouse kidneys after infection with 9×10^6 cfu of Newman strain in the abscess model. Horizontal bars are averages per group, and the figure beneath each group is the log reduction relative to the PBS control group.

Figure 7 shows bacterial count (log CFU/ml) in kidneys of mice in an abscess model experiment. Mice were challenged with the following strains: (A) MW2; (B) LAC; (C) Staph19; or (D) MU50. Each point is an individual animal and the bar shows the median count per group. Mice had been immunised as shown on the x-axis label.

Figure 8 shows the formation of Sta011 oligomers in the presence of increasing concentrations of Ca^{++} ions. Numbers indicate mM concentrations, and a * indicates the presence of 50mM EDTA.

Figure 9 shows IgG titers against (A) EsxAB (B) Sta006 (C) Hla-H35L (D) Sta011. Each graph has three groups, with a pair of bars per group. The right-hand bar in a pair shows pre-immune IgG and the left-hand bar shows post-immune IgG. The three groups are the compositions used for immunising and, from left to right, are: negative control of adjuvant alone; the Combol combination; and the relevant antigen alone.

Figure 10 shows bacterial counts values (log CFU/ml) in mice after challenge with the indicated strains. Each point is an individual animal and the bar shows the median CFU. The P value beneath the lsdB and Combo columns is a comparison against the adjuvant-only control.

Figure 11 shows the area of abscesses (mm²) in mice after challenge with Newman strain.

Figure 12 shows days of survival of mice after challenge with four different strains: Newman (○), ST-80 (□), USA300-FPR3757 (Δ) or USA300-Lac (×) strains. Each point is an individual animal, the bar shows the median survival, and the heading number shows the % of animals surviving after 15 days. Mice received aluminium hydroxide adjuvant alone, lsdB or Combol.

Figure 13 shows the median survival (days) of mice after challenge. The mice had been immunised with the antigens indicated on the X-axis. Each point is an individual animal and the bar shows the median survival. The heading numbers show the % of animals surviving after 15 days.

MODES FOR CARRYING OUT THE INVENTION

Antigen selection

[0593] *S.aureus* proteins have been selected for use as vaccine components based on various criteria.

[0594] lsdA is a surface protein involved in iron uptake. It is detectable with a high molecular weight (>250kDa) in immunoblots of whole cell lysates and cell wall fractions of *S. aureus*. Furthermore, labelled anti-lsdA antibodies revealed extracellular structures. These structures were seen in a variety of growth and infection conditions, including iron positive conditions (in which lsdA expression is reported to be suppressed). The structures have a tail up to 4μm long, with a typical orientation parallel to the mammalian cell surface. Detached lsdA-positive structures were observed to adhere on the surface of epithelial cells, but lose cell junction localization. Epithelia/bacteria interaction may stimulate expression of the structures. In addition, the inventors have found that lsdA is well conserved between different strains (present in 36/36 strains tested; see below), thus offering protection across a broad population of circulating strains. Iron uptake is important for virulence, so the protein is likely to be available for immune attack at pathological stages of the bacterial life cycle. The inventors have found that the protein is not cytotoxic to human cells (see below). The protein can also adsorb reasonably well to aluminium hydroxide (see below), which is useful for stable formulation for delivery to humans. It is useful for providing an immune response to prevent hematic spread of the bacterium.

[0595] EsxA and EsxB are small acidic dimeric secreted proteins. The inventors have found that EsxA is highly conserved between different strains (present in 36/36 strains tested; see below), while EsxB is present in 25/36 strains. The proteins are involved in persisting an infection and so are likely to be available for immune attack at pathological stages of the bacterial life cycle. The inventors have found that a fusion of EsxA and EsxB ('EsxAB') is not cytotoxic to human cells (see below). It can also adsorb well to aluminium hydroxide (see below), which is useful for stable formulation for delivery to humans. Thus the antigens are useful for providing an immune response to prevent hematic spread of the bacterium.

[0596] Hla is a pore-forming secreted toxin. This protein is well conserved between different strains (present in 36/36 strains tested; see below), thus offering protection across a broad population of circulating strains. It is an important virulence factor so is likely to be available for immune attack at pathological stages of the bacterial life cycle. It is not cytotoxic to human cells (see below). The protein can adsorb reasonably well to aluminium hydroxide (see below), which is useful for stable formulation for delivery to humans. It is useful for providing an immune response to prevent pneumonia.

[0597] Spa is a surface protein involved in Fc binding. The inventors have found that this protein is well conserved between different strains (present in 36/36 strains tested), thus offering protection across a broad population of circulating strains. It is important for virulence so is likely to be available for immune attack at pathological stages of the bacterial life cycle. The protein can also adsorb reasonably well to aluminium hydroxide (see below), which is useful for stable formulation for delivery to humans. It is useful for providing an immune response to prevent hematic spread of the bacterium.

[0598] Sta006 (also known as FhuD2) is a surface protein involved in iron uptake. The inventors have found that this protein is well conserved between different strains (present in 36/36 strains tested; see below), thus offering protection across a broad population of circulating strains. The inventors have found that the protein is not cytotoxic to human cells

(see below). The protein can also adsorb well to aluminium hydroxide (see below), which is useful for stable formulation for delivery to humans. It is useful for providing an immune response to prevent hematic spread of the bacterium.

[0599] Sta011 is a surface lipoprotein. The inventors have found that this protein is well conserved between different strains (present in 36/36 strains tested; see below), thus offering protection across a broad population of circulating strains. The inventors have found that the protein is not cytotoxic to human cells (see below). The protein can also adsorb reasonably well to aluminium hydroxide (see below), which is useful for stable formulation for delivery to humans. It is useful for providing an immune response to prevent hematic spread of the bacterium. This protein has been shown to assemble into oligomers in the presence of Ca^{++} ions, but not Mg^{++} ions (see Figure 8). These experiments used 5 μg recombinant tag-free Sta011, incubated at 37°C for 25 minutes with increasing CaCl_2 concentrations from 0.5-50mM, then analysed by gel electrophoresis on a clear native gel. A mobility shift (indicating oligomerisation) was evident from 2mM Ca^{++} , and particularly >5mM. These levels compare to blood Ca^{++} concentrations of about 1.2mM, serum concentrations of about 11mM, and milk concentrations of about 32mM. EDTA reversed the shift.

[0600] Surface digestion [302] and/or analysis of secreted proteins revealed peptide fragments from ClfA, ClfB, coA, eap, ebhA, ebpS, efb, emp, FnBA, FnBB, hla, lsdA, lsdB, lsdH, ukD, lukS, sdrD, sdrE, sasB, sasD, sasF, spa, sta001, sta002, sta003, sta004, sta005, sta006, sta007, sta008, sta009, sta010, sta011, sta019, sta023, sta024, sta028, sta036, sta040, sta049, sta050, sta054, sta057, sta064, sta065, sta073, sta095, sta096, sta098, sta100, sta101, sta102, sta103, sta105, sta107, sta108, sta109, sta111, sta112, sta113, sta115, sta116, sta117, sta118, sta120, NW_06, NW_07, NW_08, NW_09 and NW_10 e.g. SEQ ID NOs: 228 and 229 were identified as fragments of sta019.

[0601] Conjugated capsular saccharides are useful for providing opsonic immunity. Serotypes 5 and 8 cover about 85% of clinical isolates.

Strain coverage

[0602] A panel of 36 clinical isolates was used to represent circulating strains, including strains belonging to the five clonal lineages representing the vast majority of worldwide circulating CA-MRSA (community-associated methicillin-resistant *S. aureus*). HA-MRSA (hospital-associated MRSA) and non-MRSA strains were also included. Overall the panel included 9 HA-MRSA strains, 7 CA-MRSA strains, 2 MRSA strains, and 18 other strains.

[0603] Genes encoding lsdA, Hla, EsxA, Sta006, Sta011, Spa, and ClfB were present in all 36 strains. The gene for EsxB was absent from 11/36 strains, and the gene for SdrD was absent from 6/36 strains.

[0604] The encoded lsdA sequences were 95-100% identical across the panel, and the protein was expressed in iron-limited conditions in the stationary growth phase. The encoded SdrD sequences were 95-100% identical in the 30/36 SdrD⁺ panel members. The encoded EsxA sequences were 100% identical across the panel; the encoded EsxB sequences were 95-100% identical in the 25 EsxB⁺ strains. The encoded ClfB sequences were 93-100% identical across the panel, and this protein was also found to be highly surface-exposed in the early exponential growth phase.

[0605] Conservation in the encoded amino acid sequences were as follows (% identity):

Antigen	lsdA	ClfB	SdrD	Spa	Hla	EsxA	EsxB	Sta006
%	95-100	97-100	88-100	98-100	97-100	100	95-100	99.7-100

[0606] A larger panel of 61 strains was screened for the presence of genes encoding Hla and Sta006, as well as for their expression. This panel covered both MRSA and MSSA strains, a variety of geographical origins, and a variety of ST and clonal complex types. 9/61 strains did not express Hla, whereas all but one strain expressed Sta006 (data for the 61st strain were inconclusive). Thus a vaccine based on Hla alone is unlikely to give adequate coverage for a universal vaccine, but this problem could be overcome by addition of Sta006.

Cytotoxicity and cell binding studies

[0607] The analysis of the potential cellular cytotoxicity by *S. aureus* recombinant antigens Hla, Hla-H35L, lsdA, lsdB, sta006, sta011 and EsxAB was conducted on HBMECs and A549 cells. Annexin V and propidium iodide staining were used to measure the percentage of early and late apoptotic cells by flow cytometry. Endothelial cells were grown in 24 well plates up to fully confluent. Cells were then incubated for 24 hours with three different concentration of recombinant antigens (10 $\mu\text{g}/\text{ml}$, 1 $\mu\text{g}/\text{ml}$, 0.1 $\mu\text{g}/\text{ml}$). The combination of TNF- α and cycloheximide (CHX), which has been reported to induce apoptosis in endothelial cells, was used as a positive control. Incubation with PBS buffer alone was a negative control. Analysis was then performed by FACS.

[0608] None of the antigens induced a cytotoxic effect on HBMECs or A549 cells. Indeed, the percentage of live cell population compared to control cells remained essentially constant up to 24 hours of incubation. In contrast, the com-

bination of TNF- α and CHX induced a 25% increase in the number of apoptotic cells.

[0609] HBMECs were also used as an *in vitro* model for testing the binding of *S.aureus* recombinant antigens to human endothelial cells. HBMECs were grown up to confluence at 37°C in humidified atmosphere in RPMI 1640 medium supplemented with 10% heat-inactivated fetal calf serum, 10% NuSerum, 2mM glutamine, 1 mM pyruvate, 1% non-essential amino acids, 1% MEM vitamins, 100 units/ml penicillin, and 100 μ g/ml streptomycin. Binding of recombinant antigens to the cells was tested by indirect immunofluorescence and analyzed by FACS. The cells positive for binding were measured as net mean intensity of fluorescence respect to negative controls, identified as unspecific antibody recognition. Binding experiments were performed at 4°C. Mouse polyclonal antibodies specific for each of the recombinant antigens were used as primary antibodies and binding was detected by R-Phycoerythrin-conjugated goat anti-mouse IgG secondary antibody. As negative control, HBMECs were incubated with primary polyclonal antibodies detected by fluorescence-labeled secondary antibody or fluorescence-labeled secondary antibody alone. Binding of a known surfaced-exposed GBS antigen was used as positive control.

[0610] Hla and Hla-H35L were the only antigens able to strongly bind to endothelial cells. The haemolytic activity of these two antigens was also tested.

[0611] De-fibrinated sheep and rabbit blood were used to measure their haemolytic activity by spectrophotometric assay. The blood was incubated at 37°C for 30 minutes with serial dilution 1:4 of the two proteins. Incubation with water, to cause osmotic lysis, and incubation with a *S.pyogenes* protein, were positive controls; as negative control, the blood was incubated with PBS+ BSA 0.5%.

[0612] Recombinant native Hla, but not its H35L mutant form, showed haemolytic activity on rabbit erythrocytes. The mutant was at least 150-fold less haemolytic than wild-type. Both proteins had no haemolytic activity on sheep blood.

[0613] Thus the *S.aureus* recombinant vaccine candidates do not show any cytotoxicity both on A549 epithelial cell line and HBMEC endothelial cell line. Importantly, Hla, a secreted toxin known to form pores into the plasma membrane of host cells, could bind A549 cells but did not induce cytotoxicity on them; it was also able to induce haemolysis of rabbit erythrocytes. In contrast, recombinant Hla-H35L, a variant toxin with a single amino acid substitution that cannot form cytolytic pores, did not induce cellular damage in both human cell lines and rabbit erythrocytes. These findings indicate that this mutant form of Hla may be more safely used in a vaccine composition. None of the other antigens showed the capacity to bind to host cells.

Adjuvant formulation

[0614] Selected *S.aureus* protein antigen candidates have been formulated with aluminium hydroxide, either individually or as a combination of proteins, with or without capsular polysaccharide conjugate(s). The formulations have been optimized for pH and osmolality.

[0615] The antigens were EsxA-B, Sta006, Sta011, Hla-H35L, SdrD, IsdA, IsdA₄₀₋₁₈₄, Sta019, Sta021, Sta073, ClfB₄₅₋₅₅₂, SdrD₅₃₋₅₉₂, SasF, and IsdB. These are formulated as monovalent antigens at 100 μ g/ml, or as combinations at 50 μ g/ml each. Capsular saccharide conjugates from type 5 or type 8 strains are added at 5 μ g/ml, 10 μ g/ml or 25 μ g/ml. Aluminium hydroxide was used at 2mg/ml, in a 10mM histidine buffer (pH 6.5) and with 9mg/ml NaCl.

[0616] All monovalent and combination formulations, with or without conjugates, could be adjusted with respect to a desired pH and osmolality. The formulations had pH in the range 6.2-7.3, and osmolality in the range 248-360 mOsm/kg. Glycerol was excluded from formulations as it had a negative impact on osmolality.

[0617] All proteins tested, in various monovalent and combination formulations, adsorbed well to the aluminium hydroxide adjuvant, except for IsdA, IsdA₄₀₋₁₈₄, Sta019, and Sta073.

[0618] The individual Sta006, Sta011, EsxA-B and Hla-H35L proteins were completely adsorbed, and could be desorbed without altering their pre-adsorption electrophoretic profile.

[0619] Each antigen in a combination of Sta006, Sta011, EsxA-B and Hla-H35L was completely adsorbed, with no inter-antigen competition for the adjuvant. The antigens in a combination of Sta006, Sta011, EsxA-B and IsdA₄₀₋₁₈₄ were also completely adsorbed, except for IsdA₄₀₋₁₈₄, which behaved in the same way as the monovalent protein. For both combinations, the antigens could be desorbed without altering their pre-adsorption electrophoretic profile.

[0620] The additional presence of type 5 and/or type 8 conjugates also did not change the adsorption or desorption characteristics of the antigens e.g. in combination with Sta006+Sta011+EsxA-B.

[0621] A short stability study (2 weeks at 4°C) was performed to evaluate the stability of monovalent formulations and to evaluate antigen integrity. All tested formulations were stable for their pH and osmolality. All antigens remained completely adsorbed to the adjuvant. All antigens maintained their desorption characteristics. There was no evidence of increased degradation or aggregation of antigens after desorption.

Efficacy testing

[0622] Individual antigens sta006, sta011, sta012, sta017, sta019, sta021 and sta028 were tested for their ability to

protect against IV challenge by 1.2×10^7 cfu of Newman strain (type 5). Results are shown in Figure 1. All antigens reduced bacterial numbers compared with the control, and the best results were seen with sta006, sta011 and sta019.

[0623] Further individual antigens were tested: (i) NW₁₀; (ii) lsdA₄₀₋₁₈₄; (iii) Sta002; (iv) Sta003; (v) Sta073; (vi) Sta101; (vii) Sta014; (viii) Hla-PSGS; (ix) SdrD_{CnaB}. The increase in survival, compared to the negative control group, 15 days after challenge was: (i) 50%; (ii) 19%; (iii) 37%; (iv) 43%; (v) 25%; (vi) 12%; (vii) 25%; (viii) 56%; (ix) 39%.

[0624] Two hybrid polypeptides were also tested: (i) HlaH35L-EsxAB; (ii) Sta006-EsxAB. The increase in survival after challenge, compared to the negative control group, was: (i) 25%; (ii) 25%.

[0625] Table 2 gives a summary of results obtained with various antigens in the abscess model.

[0626] Experiment SA-10-a tested the efficacy of antigen combinations. Six groups of twelve CD-1 mice received a negative control (PBS), lsdB, or one of the following combinations, adjuvanted with aluminium hydroxide: (i) EsxAB + Hla-H35L; (ii) Sta006 + Sta011 + EsxAB; (iii) Sta006 + Sta011 + EsxAB + Hla-H35L; or (iv) Sta006 + Sta011 + lsdA₄₀₋₁₈₄ + EsxAB. Two administrations were given, at days 0 and 14. At day 24 mice received 3×10^8 cfu of Newman strain staphylococcus and survival in each group was assessed every 24 hours for two weeks. Results are shown in Figure 2. After 14 days, 25% of animals in the positive control group had survived, but 50% of animals in group (ii) had survived, as had 58% of animals in groups (iii) & (iv), and 75% in group (i).

[0627] Experiment SA-10-b used the same methods to test: (i) ClfB₄₅₋₅₅₂ + Hla-H35L + Sta006 + EsxAB; (ii) ClfB₄₅₋₅₅₂ + Sta011 + Sta006 + EsxAB; (iii) ClfB₄₅₋₅₅₂ + lsdA₄₀₋₁₈₄ + Sta006 + EsxAB; or (iv) SdrD₅₃₋₅₉₂ + lsdA₄₀₋₁₈₄ + Sta006 + EsxAB. Results are shown in Figure 3. After 14 days, 25% of animals in the positive control group and in group (ii) had survived, but 33% of animals in group (iv) had survived, 75% of animals in group (i), and 83% of animals in group (iii).

[0628] Further combinations were also used to immunise mice. The combinations were typically adjuvanted with aluminium hydroxide (see above) and were administered on days 0 and 14. The immunisations were in CD1 mice, 12 per group. On day 24 the mice were challenged with a lethal dose of live bacteria and survival was then followed for 14 further days. For comparison, PBS was used as a negative control and lsdB as a positive control [2].

[0629] Experiment SA-11 tested: (i) a type 5 conjugate combined with EsxAB + Sta006 + Sta011; (ii) EsxAB + Sta019 + Sta006 + Sta011; (iii) a type 5 conjugate + Hla-H35L + Sta006 + Sta011; (iv) EsxAB + Hla-H35L + Sta006 + Sta011; or (v) EsxAB + lsdA₄₀₋₁₈₄ + Sta006 + Sta011. 14 days after challenge all of the negative control animals had died, but 42% of positive control animals had survived. Survival results in the test groups were as follows: (i) 67%; (ii) 42%; (iii) 75%; (iv) 33%; and (v) 25%.

[0630] Experiment SA-12 tested: (i) Hla-H35L + lsdA₄₀₋₁₈₄ + Sta006 + Sta011; (ii) Hla-H35L + EsxAB + Sta006 + Sta011; (iii) EsxAB + lsdA₄₀₋₁₈₄ + Sta006 + Sta011; (iv) EsxAB + lsdA + Sta006 + Sta011. 14 days after challenge 8% of the negative control animals and 17% of positive control animals had survived. Survival results in the test groups were as follows: (i) 50%; (ii) 50%; (iii) 25%; (iv) 33%.

[0631] Experiment SA-14 tested: (i) EsxAB + Hla-H35L + Sta006 + Sta011; (ii) EsxAB + lsdA₄₀₋₁₈₄ + Sta006 + Sta011; (iii) Sta006 + Sta011 + Sta019 + EsxAB; (iv) Sta006 + Sta011 + Sta019 + Hla-H35L. 14 days after challenge with 5×10^8 CFU of Newman strain, 18% of the negative control animals and 9% of positive control animals had survived; survival results in the test groups were as follows: (i) 58%; (ii) 67%; (iii) 42%; (iv) 83%. Survival numbers over 14 days are shown in Figure 4, showing that all combinations performed better than the two controls on every post-challenge day.

[0632] Experiment SA-17a tested: (i) EsxAB + Sta006 + Sta011 + serotype 5 conjugate + serotype 8 conjugate; (ii) EsxAB + Sta073 + Sta011 + serotype 5 conjugate + serotype 8 conjugate; (iii) EsxAB + Hla-H35L + Sta011 + Sta073. Compared to the negative control, the increase in survival 15 days after challenge with Newman strain was: (i) 17%; (ii) 42%; (iii) 34%. The median survival in groups (ii) and (iii) was the full 15 days, and was 12 days in group (i).

[0633] Further antigen combination experiments tested: (a) serotype 5 conjugate + serotype 8 conjugate + EsxAB + Sta006 + Sta011; (b) Sta002+Sta003+Sta021+NW-10; (c) EsxAB+ HlaH35L + Sta006 + Sta019; and (d) EsxAB + Sta006+Sta019. Compared to the negative control, the increase in survival after challenge with Newman strain was: (a) 37%; (b) 36%; (c) 13%. ; and (d) 0%.

[0634] Survival data from studies SA-10, SA-11, SA-12 and SA-14 were combined to assess the efficacy of two combinations when compared to PBS or lsdB. "Combo-1" was EsxAB+Hla-H35L+Sta006+Sta011 (with polypeptides comprising SEQ ID NOs: 241, 150, 246 & 247). "Combo-2" was EsxAB+lsdA₄₀₋₁₈₄+Sta006+Sta011. The median survival times for each group of 48 mice after 14 days were compared. Whereas the PBS and lsdB groups had a median survival time of 1 day, mice in the "Combo-1" and "Combo-2" groups had a median survival time of 14 days. The differences in median survival duration were compared by a t-test: survival in the "combo-1" group was statistically superior to both the PBS group ($p < 0.0001$) and the lsdB group ($p < 0.0001$); survival in the "Combo-2" group was statistically superior to both the PBS group ($p < 0.0001$) and the lsdB group ($p = 0.0049$). These data are shown in Figure 5.

[0635] Figure 6 shows data with Combo-1 and Combo-2 in the abscess model. Kidneys of mice are isolated after challenge and are then homogenised and plated. The cfu count indicates the level of abscess formation. Figure 6 shows data from a single experiment. The numbers beneath the data show the log reduction relative to the PBS group. The reduction is bigger in the two combination groups than with lsdB alone, with U-test (one tail) values of 0.0001 for Combo-1 and 0.0005 for Combo-2. The same effect was seen in the two combination groups in a second experiment in which

an lsdB group was not included.

[0636] Further experiments compared protection achieved with Combo-1, lsdB or PBS against challenge with three different strains: Staph-19, FPR3757(USA300) and Lac(USA300). There were 44 mice per group and results were as follows (see also Figure 12), including one-tailed p-values for the survival proportion, where: P1 compares Combo-1 with PBS; P2 compares Combo-1 with lsdB; and P3 compared PBS with lsdB:

	Staph-19		FPR3757		Lac	
Survival	%	Days	%	Days	%	Days
PBS	20	1	45	8	47	7
lsdB	32	1	52	15	61	15
Combo-1	80	15	91	15	89	15
P1	<0.0001	-	<0.0001	-	0.0001	-
P2	<0.0001	-	<0.0004	-	0.0052	-
P3	0.1715	-	0.2137	-	0.1789	-

[0637] Further experiments showed that immunisation with adjuvanted Combo1 reduced CFU counts after challenge with Newman, USA100, CC30 and USA300 strains, when compared to immunisation with adjuvant alone (aluminium hydroxide) or lsdB. Figure 10 shows CFU values (log/ml) for the four challenge strains. The lowest count, with $p < 0.015$ in each case, was achieved with Combo1. The area of abscess was also assessed and was also lower in the Combo1-immunised mice (e.g. Figure 11).

[0638] Further experiments showed that Combo1 is highly protective against clinically relevant strains in the sepsis model, and always achieved a higher survival % than lsdB. Figure 12 shows that the median survival in Combo1-immunised mice (40 per group, 3 experiments) was the full 15 days when challenged with Newman, ST-80, FPR3757 or Lac strains, and that the proportion of mice surviving was $\geq 75\%$. In contrast, the median survival in lsdB-immunised mice was only 1 day with Newman and ST-80 challenge, with $< 65\%$ survival for all four challenge strains.

Comparison of Combo1 to its individual polypeptides

[0639] Various tests were performed to compare Combo1 to its four individual polypeptides (*i.e.* EsxAB, Hla-H35L, Sta006, Sta011), as well as to lsdB or to an antigen-free negative control.

[0640] The opsonophagocytic activity of sera from immunised animals was tested. Sera were obtained using (i) the four individual polypeptides, (ii) all pairs of the polypeptides, (iii) all triplets, or (iv) the full Combo1 combination. For comparison, anti-lsdB serum was used. Pre-immune and negative control sera showed no killing of Newman strain in this assay. In a first experiment: anti-lsdB serum showed 27% killing; sera against each of the four individual polypeptides showed between 26-34% killing; all multi-polypeptide combinations showed at least 34% killing; and sera raised with Combo-1 showed 39% killing. In a second experiment sera with Combo-1 showed 43% killing but anti-lsdB serum performed slightly better; all single or multi-polypeptide sera using the Combo-1 polypeptides showed at least 26% killing.

[0641] Further experiments looked at passive protection achieved by transferring into mice (20 per group, 8 week old CD1 mice) antiserum from immunised rabbits. Four groups received 200 μ l of sera from rabbits immunised with one of EsxAB, Hla-H35L, Sta006, Sta011; a fifth group received 50 μ l of each serum (200 μ l in total). Two other groups received serum from lsdB-immunised rabbits or serum from rabbits immunised with saline+adjuvant. 15 minutes later the mice were challenged intraperitoneally (10^8 CFU of Newman strain) and then mortality was assessed after 14 days. Results were as follows:

	EsxA-B	Sta006	Sta011	HlaH35L	Combo1	lsdB	-ve ctrl
Survival	5%	26%	0%	15%	25%	10%	5%

[0642] In further experiments the level of specific antibodies induced in CD1 mice were examined to assess the immunogenicity of the four polypeptides in Combo 1. Compositions included either 20 μ g of each of the four single polypeptides, or 4x10 μ g in the combination. The compositions included an aluminium hydroxide adjuvant. Serum levels of antigen-specific IgG were determined by Luminex 4Plex assay As shown in Figure 9, all four polypeptides were highly immunogenic in CD1 mice on their own and in combination. In each case the titer against a polypeptide was higher

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when it was administered in the combination than when administered alone (compare middle and right pairs).

[0643] Further experiments compared protection achieved either with Combo-1 or with its four individual polypeptides. IsdB was also included for comparison. The proportions of animals surviving (40 animals per group) 15 days after challenge with Newman strain, and the average (median) survival in days, were as follows, including a one-tailed p-value of the surviving proportion in comparison with a PBS+adjuvant negative control:

	EsxA-B	Sta006	Sta011	HlaH35L	Combo1	IsdB	PBS
Survival	34%	28%	16%	39%	59%	22%	5%
p	0.0017	0.0003	0.0064	<0.0001	<0.0001	0.0006	-
Days	1	2	1	10	15	1	0

[0644] The murine abscess model was used to compare the four individual polypeptides with the Combo1 combination. In some experiments mice were immunised with IsdB for comparison. Antigens were adjuvanted with aluminium hydroxide, and adjuvant alone was used as a negative control. Figure 7 shows the numbers of bacteria in animals' kidneys after challenge with four different strains. The lowest average counts were seen for the Combo1 combination.

[0645] Challenge experiments were performed following immunisation with (i) the four individual polypeptides, (ii) all pairs, (iii) all triplets, or (iv) the full Combo1 combination. IsdB or buffer alone were used for comparison. Survival results from 24 mice per group (3 experiments) after challenge with 5×10^8 CFU of Newman strain are shown in Figure 13. The median survival for IsdB was only 2 days. The median survival for the individual Combo1 polypeptides ranged from 1-6 days. Pairs of the polypeptides gave median survival of 2-11 days. Triplets gave median survival of 8-15 days. The full Combol combination gave a median survival of the full 15 days, with 59% of mice surviving this long (*cf.* only 35% with IsdB).

TABLE 1: NOMENCLATURE CROSS-REFERENCE

SEQ ID NO	Name	NCTC 8325 strain		Newman strain	
		SAOUHSC_#	GI	NWMN_#	GI
1	clfA	SAOUHSC_00812	88194572	NWMN_0756	151220968
2	clfB	SAOUHSC_02963	881965855	NWMN_2529	151222741
3	coA	SAOUHSC_00192	88194002	NWMN_0166	151220378
4	eap	SAOUHSC_02161	88195840	NWMN_1872	151222084
5	ebhA	SAOUHSC_01447	88195168	-	-
6	ebpS	SAOUHSC_01501	88195217	NWMN_1389	151221601
7	efb	SAOUHSC_01114	88194860	NWMN_1069	151221281
8	emp	SAOUHSC_00816	88194575	NWMN_0758	151220970
9	esaC	SAOUHSC_00264	88194069	-	-
10	esxA	SAOUHSC_00257	88194063	-	-
11	esxB	SAOUHSC_00265	88194070	-	-
12	FnBA	SAOUHSC_02803	88196438	NWMN_2399	151222611
13	FnBB	SAOUHSC_02802	88196437	NWMN_2397	151222609
14	hla	SAOUHSC_01121	88194865	NWMN_1073	151221285
15	hlgB	SAOUHSC_02710	88196350	-	-
16	hlgC	SAOUHSC_02709	88196349	-	-
17	isdA	SAOUHSC_01081	88194829	NWMN_1041	151221253
18	isdB	SAOUHSC_01079	88194828	-	-
19	isdC	SAOUHSC_01082	88194830	-	-
20	isdG	SAOUHSC_01089	88194836	-	-

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(continued)

SEQ ID NO	Name	NCTC 8325 strain		Newman strain	
		SAOUHSC_#	GI	NWMN_#	GI
21	isdH	SAOUHSC_01843	88195542	NWMN_1624	151221836
22	isdI	SAOUHSC_00130	88193943	-	-
23	lukD	SAOUHSC_01954	88195647	NWMN_1718	151221930
24	lukE	SAOUHSC_01955	88195648	-	-
25	lukF	SAOUHSC_02241	88195914	-	-
26	lukS	SAOUHSC_02243	88195915	NWMN_1928	151222140
27	nuc	SAOUHSC_01316	88195046	-	-
28	sasA	SAOUHSC_02990	88196609	-	-
29	sasB	SAOUHSC_02404	88196065	-	-
30	sasC	SAOUHSC_01873	88195570	-	-
31	sasD	SAOUHSC_00094	88193909	-	-
32	sasF	SAOUHSC_02982	88196601	-	-
33	sdrC	SAOUHSC_00544	88194324	-	-
34	sdrD	SAOUHSC_00545	88194325	-	-
35	sdrE2	-	-	NWMN_0525	151220737
36	spa	SAOUHSC_00069	88193885	NWMN_0055	151220267
37	sta001	SAOUHSC_00025	88193846	NWMN_0022	151220234
38	sta002	SAOUHSC_00356	88194155	NWMN_0364	151220576
39	sta003	SAOUHSC_00400	88194195	NWMN_0401	151220613
40	sta004	SAOUHSC_00749	88194514	NWMN_0705	151220917
41	sta005	SAOUHSC_01127	88194870	NWMN_1077	151221289
42	sta006	SAOUHSC_02554	88196199	NWMN_2185	151222397
43	sta007	SAOUHSC_02571	88196215	NWMN_2199	151222411
44	sta008	SAOUHSC_02650	88196290	NWMN_2270	151222482
45	sta009	SAOUHSC_02706	88196346	NWMN_2317	151222529
46	sta010	SAOUHSC_02887	88196515	NWMN_2469	151222681
47	sta011	SAOUHSC_00052	88193872	-	-
48	sta012	SAOUHSC_00106	88193919	-	-
49	sta013	SAOUHSC_00107	88193920	-	-
50	sta014	SAOUHSC_00137	88193950	-	-
51	sta015	SAOUHSC_00170	88193980	-	-
52	sta016	SAOUHSC_00171	88193981	-	-
53	sta017	SAOUHSC_00186	88193996	-	-
54	sta018	SAOUHSC_00201	88194011	-	-
55	sta019	SAOUHSC_00248	88194055	NWMN_0210	151220422
56	sta020	SAOUHSC_00253	88194059	-	-
57	sta021	SAOUHSC_00256	88194062	-	-

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(continued)

SEQ ID NO	Name	NCTC 8325 strain		Newman strain	
		SAOUHSC_#	GI	NWMN_#	GI
58	sta022	SAOUHSC_00279	88194083	-	-
59	sta023	SAOUHSC_00284	88194087	-	-
60	sta024	SAOUHSC_00300	88194101	-	-
61	sta025	SAOUHSC_00362	88194160	-	-
62	sta026	SAOUHSC_00404	88194198	-	-
63	sta027	SAOUHSC_00661	88194426	-	-
64	sta028	SAOUHSC_00671	88194436	NWMN_0634	151220846
65	sta029	SAOUHSC_00754	88194518	-	-
66	sta030	SAOUHSC_00808	88194568	-	-
67	sta031	SAOUHSC_00860	88194617	-	-
68	sta032	SAOUHSC_00958	88194715	-	-
69	sta033	SAOUHSC_00987	88194744	-	-
70	sta034	SAOUHSC_00988	88194745	-	-
71	sta035	SAOUHSC_00998	88194754	-	-
72	sta036	SAOUHSC_01084	88194831	-	-
73	sta037	SAOUHSC_01085	88194832	-	-
74	sta038	SAOUHSC_01088	88194835	-	-
75	sta039	SAOUHSC_01124	88194868	-	-
76	sta040	SAOUHSC_01125	88194869	NWMN_1076	151221288
77	sta041	SAOUHSC_01175	88194914	-	-
78	sta042	SAOUHSC_01180	88194919	-	-
79	sta043	SAOUHSC_01219	88194955	-	-
80	sta044	SAOUHSC_01508	88195223	-	-
81	sta045	SAOUHSC_01627	88195337	-	-
82	sta046	SAOUHSC_01918	88195613	-	-
83	sta047	SAOUHSC_01920	88195615	-	-
84	sta048	SAOUHSC_01949	88195642	-	-
85	sta049	SAOUHSC_01972	88195663	NWMN_733	151221945
86	sta050	SAOUHSC_02127	88195808	-	-
87	sta051	SAOUHSC_02147	88195827	-	-
88	sta052	SAOUHSC_02246	88195918	-	-
89	sta053	SAOUHSC_02257	88195928	-	-
90	sta054	SAOUHSC_02333	88195999	-	-
91	sta055	SAOUHSC_02448	88196100	-	-
92	sta056	SAOUHSC_02463	88196115	-	-
93	sta057	SAOUHSC_02576	88196220	NWMN_2203	151222415
94	sta058	SAOUHSC_02690	88196330	-	-

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(continued)

SEQ ID NO	Name	NCTC 8325 strain		Newman strain	
		SAOUHSC_#	GI	NMWN_#	GI
5	95	sta059	SAOUHSC_02708	88196348	-
	96	sta060	SAOUHSC_02767	88196403	-
	97	sta061	SAOUHSC_02783	88196419	-
10	98	sta062	SAOUHSC_02788	88196424	-
	99	sta063	SAOUHSC_02971	88196592	-
	100	sta064	SAOUHSC_03006	88196625	NWMN_2569
15	101	sta065	SAOUHSC_00051	88193871	-
	102	sta066	SAOUHSC_00172	88193982	-
	103	sta067	SAOUHSC_00176	88193986	-
	104	sta068	SAOUHSC_00327	88194127	-
20	105	sta069	SAOUHSC_00427	88194219	-
	106	sta070	SAOUHSC_00773	88194535	-
	107	sta071	SAOUHSC_00854	88194612	-
25	108	sta072	SAOUHSC_00872	88194629	-
	109	sta073	SAOUHSC_00994	88194750	NWMN_0922
	110	sta074	SAOUHSC_01220	88194956	-
	111	sta075	SAOUHSC_01256	88194989	-
30	112	sta076	SAOUHSC_01263	88194996	-
	113	sta077	SAOUHSC_01317	88195047	-
	114	sta078	SAOUHSC_01857	88195555	-
35	115	sta079	SAOUHSC_01935	88195630	-
	116	sta080	SAOUHSC_01936	88195631	-
	170	sta081	SAOUHSC_01938	88195633	
	117	sta082	SAOUHSC_01939	88195634	-
40	118	sta083	SAOUHSC_01941	88195635	-
	119	sta084	SAOUHSC_01942	88195636	-
	120	sta085	SAOUHSC_02171	88195848	-
45	121	sta086	SAOUHSC_02327	88195993	-
	122	sta087	SAOUHSC_02635	88196276	-
	123	sta088	SAOUHSC_02844	88196477	-
	124	sta089	SAOUHSC_02855	88196486	-
50	125	sta090	SAOUHSC_02883	88196512	-
	126	sta091	SAOUHSC_00685	88194450	-
	127	sta092	SAOUHSC_00174	88193984	-
55	128	sta093	SAOUHSC_01854	88195552	-
	129	sta094	SAOUHSC_01512	88195226	-
	130	sta095	SAOUHSC_00383	88194180	NWMN_0388
					151220600

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(continued)

SEQ ID NO	Name	NCTC 8325 strain		Newman strain	
		SAOUHSC_#	GI	NWMN_#	GI
131	sta096	SAOUHSC_00384	88194181	-	-
132	sta097	SAOUHSC_00386	88194182	-	-
133	sta098	SAOUHSC_00389	88194184	NWMN_0391	151220603
134	sta099	SAOUHSC_00390	88194185	-	-
135	sta100	SAOUHSC_00391	88194186	-	-
136	sta101	SAOUHSC_00392	88194187	NWMN_0394	151220606
137	sta102	SAOUHSC_00393	88194188	-	-
138	sta103	SAOUHSC_00394	88194189	-	-
139	sta104	SAOUHSC_00395	88194190	-	-
140	sta105	SAOUHSC_00399	88194194	NWMN_0400	151220612
141	sta106	SAOUHSC_01115	88194861	-	-
177	sta107	SAOUHSC_00354	88194153	NWMN_0362	151220574
178	sta108	SAOUHSC_00717	88194482	NWMN_0677	151220889
179	sta109	SAOUHSC_02979	88196599	NWMN_2543	151222755
180	sta110	SAOUHSC_01039	88194791		
181	sta111	SAOUHSC_01005	88194760	NWMN_0931	151221143
182	sta112	SAOUHSC_00634	88194402	NWMN_0601	151220813
183	sta113	SAOUHSC_00728	88194493	NWMN_0687	151220899
184	sta114	SAOUHSC_00810	88194570		
185	sta115	SAOUHSC_00817	88194576	NWMN_0759	151220971
186	sta116	SAOUHSC_01112	88194858	NWMN_1067	151221279
187	sta117	SAOUHSC_02240	88195913	NWMN_1926	151222138
188	sta118	SAOUHSC_01150	88194892	NWMN_1096	151221308
200	sta119	SAOUHSC_01100	88194846		
201	sta120	SAOUHSC_00365	88194163		
142	NW_6	-	-	NWMN_0757	151220969
143	NW_9	-	-	NWMN_0958	151221170
144	NW_10	-	-	NWMN_1066	151221278
145	NW_7	-	-	NWMN_1876	151222088
146	NW_8	-	-	NWMN_1877	151222089
147	NW_2	-	-	NWMN_1883	151222095
148	NW_1	-	-	NWMN_1924	151222136
149	NW_5	-	-	NWMN_2392	151222604

TABLE 2: ABSCESS MODEL RESULTS SUMMARY

Immunising antigen(s)	Adjuvant	infecting strain & dose		Reduction**
Fnb	alum *	Newman	1.4E+07	2.13
Sta005	alum	Newman	1.4E+07	1.26
LukE	alum	Newman	1.4E+07	1.68
SasD	alum	Newman	1.4E+07	0.10
SpA	alum	Newman	1.4E+07	0.41
SasFHis	alum	Newman	1.4E+07	1.33
CoA	alum	Newman	1.4E+07	1.01
Sta028	alum	Newman	1.2E+07	1.85
Sta017	alum	Newman	1.2E+07	1.23
Sta006	alum	Newman	1.2E+07	2.33
Sta012	alum	Newman	1.2E+07	1.69
Sta011	alum	Newman	1.2E+07	2.66
Sta019	alum	Newman	1.2E+07	2.36
Sta021	alum	Newman	1.2E+07	1.58
IsdA + EsxAB	alum	Newman	1.8E+07	0.11
EsxAB	alum	Newman	1.8E+07	1.31
NW 1	alum	Newman	1.8E+07	1.00
NW 10	alum	Newman	1.8E+07	-0.65
Sta073	alum	Newman	1.8E+07	1.46
Sta002	alum	Newman	1.8E+07	0.17
Sta064	alum	Newman	1.8E+07	1.04
Sta014	alum	Newman	1.8E+07	1.74
Sta002	alum	Newman	1.0E+07	0.52
Sta014	alum	Newman	1.0E+07	1.02
Sta064	alum	Newman	1.0E+07	1.22
Sta006	alum	Newman	1.0E+07	0.80
Sta073	alum	Newman	1.0E+07	0.92
NW 1	alum	Newman	1.0E+07	0.77
NW 10	alum	Newman	1.0E+07	2.25
Sta017	alum	Newman	1.0E+07	2.13
Sta028	alum	Newman	1.0E+07	0.64
Sta021	alum	Newman	1.0E+07	1.03
Sta019	alum	Newman	1.0E+07	1.28
Sta011	alum	Newman	1.0E+07	0.78
IsdB	alum	Newman	1.0E+07	1.22
IsdA ₄₀₋₁₈₄	none	Newman	1.0E+07	0.58
Sta006	none	Newman	1.0E+07	0.30
Sta011	none	Newman	1.0E+07	0.62
EsxAB	none	Newman	1.0E+07	1.09
Sasf	none	Newman	1.0E+07	0.11
IsdB	none	Newman	1.0E+07	0.93
IsdA ₄₀₋₁₈₄	alum	Newman	1.0E+07	1.02
Sta006	alum	Newman	1.0E+07	0.45
Sta011	alum	Newman	1.0E+07	0.80
EsxAB	alum	Newman	1.0E+07	0.47
Sasf	alum	Newman	1.0E+07	-0.78
IsdB	alum	Newman	1.0E+07	1.24
Type 5 conjugate + IsdA ₄₀₋₁₈₄	alum	Newman	1.5E+07	0.34
Type 5 conjugate	alum	Newman	1.5E+07	0.72
IsdA ₄₀₋₁₈₄	alum	Newman	1.5E+07	1.08

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	Type 5 conjugate	MF59	Newman	1.5E+07	0.45
	IsdB	alum	Newman	1.5E+07	1.50
	ClfB ₄₅₋₅₅₂	alum	Newman	1.5E+07	-0.05
5	Sta019	alum	Newman	1.5E+07	0.82
	IsdA ₄₀₋₁₈₄ + ClfB ₄₅₋₅₅₂	alum	Newman	1.5E+07	0.72
	Type 8 conjugate	alum	Becker	4.0E+07	1.51
	Type 8 conjugate	MF59	Becker	4.0E+07	0.35
	EsxAB + Sta019 + Sta006 + Sta011	alum	Newman	1.0E+07	1.54
10	combol	alum	Newman	1.0E+07	2.04
	EsxAB + IsdA ₄₀₋₁₈₄ + Sta006 + Sta011	alum	Newman	1.0E+07	0.84
	SdrD ₅₃₋₅₉₂	alum	Newman	1.0E+07	1.15
	Sta105	alum	Newman	1.0E+07	0.54
15	Sta101	alum	Newman	1.0E+07	1.51
	Sta116	alum	Newman	1.0E+07	1.23
	Sta106	alum	Newman	1.0E+07	1.20
	Sta107	alum	Newman	1.0E+07	1.77
	Sta004	alum	Newman	1.0E+07	0.70
20	Sta003	alum	Newman	1.0E+07	1.32
	EsxAB + Sta019 + Sta006 + Sta011	alum	Newman	9.0E+06	3.04
	combol	alum	Newman	9.0E+06	2.53
	EsxAB + IsdA ₄₀₋₁₈₄ + Sta006 + Sta011	alum	Newman	9.0E+06	1.85
	SdrD ₅₃₋₅₉₂	alum	Newman	9.0E+06	1.80
25	Sta105	alum	Newman	9.0E+06	0.60
	Sta101	alum	Newman	9.0E+06	0.83
	Sta116	alum	Newman	9.0E+06	1.96
	Sta106	alum	Newman	9.0E+06	2.56
	IsdB	alum	Newman	9.0E+06	1.37
30	Sta004	alum	Newman	9.0E+06	1.01
	Sta003	alum	Newman	9.0E+06	2.20
	IsdB	alum	Newman	1.0E+07	0.83
	Sta107	alum	Newman	1.0E+07	0.24
35	SrdC ₅₁₋₅₁₈	alum	Newman	1.0E+07	0.84
	SdrE ₅₃₋₆₃₂	alum	Newman	1.0E+07	1.08
	Hla ₂₇₋₇₆	alum	Newman	1.0E+07	0.18
	EsxAB + HlaH35L + Sta006 + Sta021	alum	Newman	1.0E+07	0.59
	EsxAB + HlaH35L + Sta006 + Sta019	alum	Newman	1.0E+07	0.85
40	EsxAB + HlaH35L + Sta006 + Sta017	alum	Newman	1.0E+07	1.88
	EsxAB + Hla27-76 + Sta006 + Sta021	alum	Newman	1.0E+07	1.49
	Hla ₂₇₋₇₆ + Sta006 + Sta017 + Sta019	alum	Newman	1.0E+07	0.00
	IsdB	alum	Newman	1.2E+07	1.07
	Sta107	alum	Newman	1.2E+07	1.35
45	SrdC ₅₁₋₅₁₈	alum	Newman	1.2E+07	2.17
	SdrE ₅₃₋₆₃₂	alum	Newman	1.2E+07	2.82
	Hla ₂₇₋₇₆	alum	Newman	1.2E+07	0.17
	EsxAB + HlaH35L + Sta006 + Sta021	alum	Newman	1.2E+07	1.70
	EsxAB + HlaH35L + Sta006 + Sta019	alum	Newman	1.2E+07	1.20
50	EsxAB + HlaH35L + Sta006 + Sta017	alum	Newman	1.2E+07	1.52
	EsxAB + Hla ₂₇₋₇₆ + Sta006 + Sta021	alum	Newman	1.2E+07	1.81
	Hla ₂₇₋₇₆ + Sta006 + Sta017 + Sta019	alum	Newman	1.2E+07	0.89
	IsdB	alum	Mu-50	3.8E+07	0.44
	Combol	alum	Mu-50	3.8E+07	1.73
55	IsdB	alum	USA 200	2.0E+07	1.17
	Combol	alum	USA 200	2.0E+07	1.87

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IsdB	alum	USA 300	3.0E+07	0.09
Comb01	alum	USA 300	3.0E+07	2.19
IsdB	alum	Staph19	2.7E+07	0.66
Comb01	alum	Staph19	2.7E+07	0.46
IsdB	alum	Mu-50	4.5E+07	0.98
Comb01	alum	Mu-50	4.5E+07	0.76
IsdB	alum	USA 200	1.6E+07	0.18
Comb01	alum	USA 200	1.6E+07	0.19
IsdB	alum	USA 300	2.2E+07	-0.21
Comb01	alum	USA 300	2.2E+07	-0.29
IsdB	alum	Staph19	2.3E+07	0.57
Comb01	alum	Staph19	2.3E+07	0.80
IsdB	alum	LAC	3.50E+07	2.67
Sta011	alum	LAC	3.50E+07	1.35
EsxAB	alum	LAC	3.50E+07	2.21
HlaH35L	alum	LAC	3.50E+07	0.71
Sta006	alum	LAC	3.50E+07	2.39
Comb01	alum	LAC	3.50E+07	2.66
IsdB	alum	MW2	3.00E+07	1.17
Sta011	alum	MW2	3.00E+07	0.82
EsxAB	alum	MW2	3.00E+07	1.39
HlaH35L	alum	MW2	3.00E+07	0.87
Sta006	alum	MW2	3.00E+07	0.91
Comb01	alum	MW2	3.00E+07	2.69
IsdB	alum	LAC	4.00E+07	1.54
Sta011	alum	LAC	4.00E+07	1.95
EsxAB	alum	LAC	4.00E+07	1.31
HlaH35L	alum	LAC	4.00E+07	0.75
Sta006	alum	LAC	4.00E+07	1.74
Comb01	alum	LAC	4.00E+07	2.21
IsdB	alum	MW2	2.75E+07	1.22
Sta011	alum	MW2	2.75E+07	1.25
EsxAB	alum	MW2	2.75E+07	1.16
HlaH35L	alum	MW2	2.75E+07	1.61
Sta006	alum	MW2	2.75E+07	1.13
Comb01	alum	MW2	2.75E+07	1.97
Sta011	alum	Mu-50	4.00E+07	1.10
EsxAB	alum	Mu-50	4.00E+07	0.86
HlaH35L	alum	Mu-50	4.00E+07	0.71
Sta006	alum	Mu-50	4.00E+07	1.57
Comb01	alum	Mu-50	4.00E+07	1.72
Sta011	alum	Staph19	5.30E+07	1.23
EsxAB	alum	Staph19	5.30E+07	1.19
HlaH35L	alum	Staph19	5.30E+07	0.65
Sta006	alum	Staph19	5.30E+07	2.00
Comb01	alum	Staph19	5.30E+07	2.02
Sta011	alum	Mu-50	4.30E+07	1.33
EsxAB	alum	Mu-50	4.30E+07	0.36
HlaH35L	alum	Mu-50	4.30E+07	0.11
Sta006	alum	Mu-50	4.30E+07	1.05
Comb01	alum	Mu-50	4.30E+07	1.34
Sta011	alum	Staph19	4.40E+07	1.07
EsxAB	alum	Staph19	4.40E+07	0.94

HlaH35L	alum	Staph19	4.40E+07	1.19
Sta006	alum	Staph19	4.40E+07	2.31
Combo1	alum	Staph19	4.40E+07	2.45

* alum = aluminium hydroxide

** Log reduction in kidney CFU

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THE INVENTION describes

[0647]

1. An immunogenic composition comprising a combination of antigens, said combination comprising two or more antigens selected from the group consisting of: (1) a sta006 antigen; (2) a sta011 antigen; (3) a esxA antigen; (4) a esxB antigen; (5) a hla antigen; (6) a ebpS antigen; (7) a efb antigen; (8) a emp antigen; (9) a esaC antigen; (10) a coA antigen; (11) a eap antigen; (12) a FnBA antigen; (13) a FnBB antigen; (14) a ebhA antigen; (15) a hlgB antigen; (16) a hlgC antigen; (17) a isdA antigen; (18) a isdB antigen; (19) a isdC antigen; (20) a isdG antigen; (21) a isdH antigen; (22) a isdI antigen; (23) a lukD antigen; (24) a lukE antigen; (25) a lukF antigen; (26) a lukS antigen; (27) a nuc antigen; (28) a sasA antigen; (29) a sasB antigen; (30) a sasC antigen; (31) a sasD antigen; (32) a sasF antigen; (33) a sdrC antigen; (34) a sdrD antigen; (35) a sdrE2 antigen; (36) a spa antigen; (37) a clfA antigen; (38) a clfB antigen; (39) a sta001 antigen; (40) a sta002 antigen; (41) a sta003 antigen; (42) a sta004 antigen; (43) a sta005 antigen; (44) a sta007 antigen; (45) a sta008 antigen; (46) a sta009 antigen; (47) a sta010 antigen; (48) a sta012 antigen; (49) a sta013 antigen; (50) a sta014 antigen; (51) a sta015 antigen; (52) a sta016 antigen; (53) a sta017 antigen; (54) a sta018 antigen; (55) a sta019 antigen; (56) a sta020 antigen; (57) a sta021 antigen; (58) a sta022 antigen; (59) a sta023 antigen; (60) a sta024 antigen; (61) a sta025 antigen; (62) a sta026 antigen; (63) a sta027 antigen; (64) a sta028 antigen; (65) a sta029 antigen; (66) a sta030 antigen; (67) a sta031 antigen; (68) a sta032 antigen; (69) a sta033 antigen; (70) a sta034 antigen; (71) a sta035 antigen; (72) a sta036 antigen; (73) a sta037 antigen; (74) a sta038 antigen; (75) a sta039 antigen; (76) a sta040 antigen; (77) a sta041 antigen; (78) a sta042 antigen; (79) a sta043 antigen; (80) a sta044 antigen; (81) a sta045 antigen; (82) a sta046 antigen; (83) a sta047 antigen; (84) a sta048 antigen; (85) a sta049 antigen; (86) a sta050 antigen; (87) a sta051 antigen; (88) a sta052 antigen; (89) a sta053 antigen; (90) a sta054 antigen; (91) a sta055 antigen; (92) a sta056 antigen; (93) a sta057 antigen; (94) a sta058 antigen; (95) a sta059 antigen; (96) a sta060 antigen; (97) a sta061 antigen; (98) a sta062 antigen; (99) a sta063 antigen; (100) a sta064 antigen; (101) a sta065 antigen; (102) a sta066 antigen; (103)

a sta067 antigen; (104) a sta068 antigen; (105) a sta069 antigen; (106) a sta070 antigen; (107) a sta071 antigen; (108) a sta072 antigen; (109) a sta073 antigen; (110) a sta074 antigen; (111) a sta075 antigen; (112) a sta076 antigen; (113) a sta077 antigen; (114) a sta078 antigen; (115) a sta079 antigen; (116) a sta080 antigen; (117) a sta082 antigen; (118) a sta083 antigen; (119) a sta084 antigen; (120) a sta085 antigen; (121) a sta086 antigen; (122) a sta087 antigen; (123) a sta088 antigen; (124) a sta089 antigen; (125) a sta090 antigen; (126) a sta091 antigen; (127) a sta092 antigen; (128) a sta093 antigen; (129) a sta094 antigen; (130) a sta095 antigen; (131) a sta096 antigen; (132) a sta097 antigen; (133) a sta098 antigen; (134) a sta099 antigen; (135) a sta100 antigen; (136) a sta101 antigen; (137) a sta102 antigen; (138) a sta103 antigen; (139) a sta104 antigen; (140) a sta105 antigen; (141) a sta106 antigen; (142) a sta107 antigen; (143) a sta108 antigen; (144) a sta109 antigen; (145) a sta110 antigen; (146) a sta111 antigen; (147) a sta112 antigen; (148) a sta113 antigen; (149) a sta114 antigen; (150) a sta115 antigen; (151) a sta116 antigen; (152) a sta117 antigen; (153) a sta118 antigen; (154) a sta119 antigen; (155) a sta120 antigen; (156) a NW_6 antigen; (157) a NW_9 antigen; (158) a NW_10 antigen; (159) a NW_7 antigen; (160) a NW_8 antigen; (161) a NW_2 antigen; (162) a NW_1 antigen; (163) a sta081 antigen; and (164) a NW_5 antigen.

2. The composition of embodiment 1, comprising at least one antigen selected from numbers (3) to (38) and at least one antigen selected from numbers (1), (2) and (37) to (149).

3. The composition of embodiment 2, comprising:

at least one antigen selected from numbers (37), (38), (8), (9), (3), (4), (5), (17), (18), (19), (31), (32), (33), (34), (35) and (36);
and at least one antigen selected from (40), (1), (43), (2), (64), (96), (133) and (147).

4. The composition of embodiment 1, comprising two or more antigens selected from the group consisting of: (1) a clfA antigen; (2) a clfB antigen; (3) a sdrE2 antigen; (4) a sdrC antigen; (5) a SasF antigen; (6) a emp antigen; (7) a sdrD antigen; (8) a spa antigen; (9) a esaC antigen; (10) a esxA antigen; (11) a esxB antigen; (12) a sta006 antigen; (13) a isdC antigen; (14) a hla antigen; (15) a sta011 antigen; (16) isdA antigen; (17) a isdB antigen; (18) a sasF antigen.

5. The composition of embodiment 1, two or more antigens selected from the group consisting of: (1) a esxA antigen; (2) a esxB antigen; (3) a sta006 antigen; (4) a hla antigen; (5) a sta011 antigen.

6. The composition of any preceding embodiment, wherein one or more of said antigens is adsorbed to an aluminium hydroxide adjuvant, and optionally wherein the composition includes a histidine buffer.

7. The composition of any preceding embodiment, further comprising: one or more conjugates of (i) a *S.aureus* exopolysaccharide and (ii) a carrier protein.

8. The composition of any preceding embodiment, further comprising: one or more conjugates of (i) a *S.aureus* capsular polysaccharide and (ii) a carrier protein.

9. A polypeptide of formula $\text{NH}_2\text{-A-}\{-\text{X-L-}\}_n\text{-B-COOH}$, wherein:

X is an amino acid sequence of a staphylococcal antigen, selected from the group consisting of *S.aureus* antigens sta006, sta011, esxA, esxB, hla, clfA, clfB, coA, eap, ebhA, ebpS, efb, emp, esaC, FnBA, FnBB, hlgB, hlgC, isdA, isdB, isdC, isdG, isdH, isdI, lukD, lukE, lukF, lukS, nuc, sasA, sasB, sasC, sasD, sasF, sdrC, sdrD, sdrE2, spa, sta001, sta002, sta003, sta004, sta005, sta007, sta008, sta009, sta010, sta012, sta013, sta014, sta015, sta016, sta017, sta018, sta019, sta020, sta021, sta022, sta023, sta024, sta025, sta026, sta027, sta028, sta029, sta030, sta031, sta032, sta033, sta034, sta035, sta036, sta037, sta038, sta039, sta040, sta041, sta042, sta043, sta044, sta045, sta046, sta047, sta048, sta049, sta050, sta051, sta052, sta053, sta054, sta055, sta056, sta057, sta058, sta059, sta060, sta061, sta062, sta063, sta064, sta065, sta066, sta067, sta068, sta069, sta070, sta071, sta072, sta073, sta074, sta075, sta076, sta077, sta078, sta079, sta080, sta081, sta082, sta083, sta084, sta085, sta086, sta087, sta088, sta089, sta090, sta091, sta092, sta093, sta094, sta095, sta096, sta097, sta098, sta099, sta100, sta101, sta102, sta103, sta104, sta105, sta106, sta107, sta108, sta109, sta110, sta111, sta112, sta113, sta114, sta115, sta116, sta117, sta118, NW_6, NW_9, NW_10, NW_7, NW_8, NW_2, NW_1, and NW_5;

L is an optional linker amino acid sequence;

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A is an optional N-terminal amino acid sequence;
B is an optional C-terminal amino acid sequence; and
n is an integer of 2 or more.

- 5 10. An immunogenic composition comprising the polypeptide of embodiment 9 and further comprising: (A) one or more conjugates of (i) a *S.aureus* exopolysaccharide and (ii) a carrier protein; and/or (B) one or more conjugates of (i) a *S.aureus* capsular polysaccharide and (ii) a carrier protein.
- 10 11. The composition or polypeptide of any preceding embodiment, wherein the clfA antigen can elicit an antibody which recognises SEQ ID NO: 1 and comprises an amino acid sequence (a) having 80% or more identity to SEQ ID NO: 1; and/or (b) comprising a fragment of at least 7 consecutive amino acids of SEQ ID NO: 1, wherein the fragment comprises an epitope from SEQ ID NO: 1.
- 15 12. A polypeptide comprising amino acid sequence (a) having 80% or more identity to SEQ ID NO: 151; and/or (b) comprising a fragment of at least 7 consecutive amino acids from amino acids 1-97 of SEQ ID NO: 151 and at least 7 consecutive amino acids from amino acids 104-207 of SEQ ID NO: 151, wherein the polypeptide can elicit antibodies which recognise both the wild-type staphylococcal protein comprising SEQ ID NO: 10 and the wild-type staphylococcal protein comprising SEQ ID NO: 11.
- 20 13. An immunogenic composition comprising the polypeptide of embodiment 12 and one or more of (i) a sta006 antigen; (ii) a hla antigen; and/or (iii) a sta011 antigen.
14. The composition of embodiment 13, including an adjuvant.
- 25 15. A polypeptide comprising amino acid sequence having 80% or more identity to an amino acid sequence selected from SEQ ID NOs: 151, 152, 168, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 220, 221, 222, 223, 224, 237, 238, 241.
- 30 16. A polypeptide comprising an amino acid sequence selected from SEQ ID NOs: 151, 152, 168, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 220, 221, 222, 223, 224, 237, 238, 241, 242, 243, 244, 245.
17. A polypeptide comprising: (a) a first sequence having 90% or more identity to SEQ ID NO: 218; and (b) a second sequence having 90% or more identity to SEQ ID NO: 219, wherein the first and second sequences are either directly joined or are joined by an intervening amino acid sequence having fewer than 10 amino acids.
- 35 18. A pharmaceutical composition comprising the polypeptide of any one of embodiments 12, 15, 16 or 17.
19. A method for raising an immune response in a mammal comprising the step of administering to the mammal an effective amount of the polypeptide or composition of any preceding embodiment.
- 40 20. Nucleic acid encoding the polypeptide of embodiment 9, 12, 15, 16 or 17.

SEQUENCE LISTING

45 [0648]

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	Glu	Thr	Lys	Lys	Ala	Val	Lys	Glu	Ala	Asp	Asp	Ser	Trp	Lys	Lys	Lys
		290					295					300				
15	Thr	Val	Lys	Lys	Tyr	Gly	Glu	Thr	Glu	Thr	Lys	Ser	Pro	Val	Val	Lys
	305					310					315					320
	Glu	Glu	Lys	Lys	Val	Glu	Glu	Pro	Gln	Ala	Pro	Lys	Val	Asp	Asn	Gln
					325					330					335	
20	Gln	Glu	Val	Lys	Thr	Thr	Ala	Gly	Lys	Ala	Glu	Glu	Thr	Thr	Gln	Pro
				340					345					350		
	Val	Ala	Gln	Pro	Leu	Val	Lys	Ile	Pro	Gln	Gly	Thr	Ile	Thr	Gly	Glu
			355					360					365			
25	Ile	Val	Lys	Gly	Pro	Glu	Tyr	Pro	Thr	Met	Glu	Asn	Lys	Thr	Val	Gln
		370					375					380				
	Gly	Glu	Ile	Val	Gln	Gly	Pro	Asp	Phe	Leu	Thr	Met	Glu	Gln	Ser	Gly
	385					390					395					400
30	Pro	Ser	Leu	Ser	Asn	Asn	Tyr	Thr	Asn	Pro	Pro	Leu	Thr	Asn	Pro	Ile
					405					410					415	
	Leu	Glu	Gly	Leu	Glu	Gly	Ser	Ser	Ser	Lys	Leu	Glu	Ile	Lys	Pro	Gln
				420						425				430		
35	Gly	Thr	Glu	Ser	Thr	Leu	Lys	Gly	Thr	Gln	Gly	Glu	Ser	Ser	Asp	Ile
			435					440					445			
	Glu	Val	Lys	Pro	Gln	Ala	Thr	Glu	Thr	Thr	Glu	Ala	Ser	Gln	Tyr	Gly
		450					455					460				
40	Pro	Arg	Pro	Gln	Phe	Asn	Lys	Thr	Pro	Lys	Tyr	Val	Lys	Tyr	Arg	Asp
	465					470					475					480
	Ala	Gly	Thr	Gly	Ile	Arg	Glu	Tyr	Asn	Asp	Gly	Thr	Phe	Gly	Tyr	Glu
					485					490					495	
45	Ala	Arg	Pro	Arg	Phe	Asn	Lys	Pro	Ser	Glu	Thr	Asn	Ala	Tyr	Asn	Val
				500					505					510		
	Thr	Thr	His	Ala	Asn	Gly	Gln	Val	Ser	Tyr	Gly	Ala	Arg	Pro	Thr	Tyr
			515					520					525			
50	Lys	Lys	Pro	Ser	Glu	Thr	Asn	Ala	Tyr	Asn	Val	Thr	Thr	His	Ala	Asn
		530					535					540				
	Gly	Gln	Val	Ser	Tyr	Gly	Ala	Arg	Pro	Thr	Gln	Asn	Lys	Pro	Ser	Lys
	545					550					555					560
55	Thr	Asn	Ala	Tyr	Asn	Val	Thr	Thr	His	Gly	Asn	Gly	Gln	Val	Ser	Tyr
					565					570					575	
	Gly	Ala	Arg	Pro	Thr	Gln	Asn	Lys	Pro	Ser	Lys	Thr	Asn	Ala	Tyr	Asn
				580					585					590		
	Val	Thr	Thr	His	Ala	Asn	Gly	Gln	Val	Ser	Tyr	Gly	Ala	Arg	Pro	Thr

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595 600 605

Tyr Lys Lys Pro Ser Lys Thr Asn Ala Tyr Asn Val Thr Thr His Ala
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Asp Gly Thr Ala Thr Tyr Gly Pro Arg Val Thr Lys
625 630 635

<210> 4

<211> 584

<212> PRT

<213> Staphylococcus aureus

<400> 4

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 Ala Ser Thr Gly Ala Asn Phe Asn Asn Asn Glu Ala Ser Ala Ala Ala
 20 25 30
 Lys Pro Leu Asp Lys Ser Ser Ser Leu His His Gly Tyr Ser Lys
 35 40 45
 Val His Val Pro Tyr Ala Ile Thr Val Asn Gly Thr Ser Gln Asn Ile
 50 55 60
 Leu Ser Ser Leu Thr Phe Asn Lys Asn Gln Asn Ile Ser Tyr Lys Asp
 65 70 75 80
 Leu Glu Asp Arg Val Lys Ser Val Leu Lys Ser Asp Arg Gly Ile Ser
 85 90 95
 Asp Ile Asp Leu Arg Leu Ser Lys Gln Ala Lys Tyr Thr Val Tyr Phe
 100 105 110
 Lys Asn Gly Thr Lys Lys Val Ile Asp Leu Lys Ala Gly Ile Tyr Thr
 115 120 125
 Ala Asp Leu Ile Asn Thr Ser Glu Ile Lys Ala Ile Asn Ile Asn Val
 130 135 140
 Asp Thr Lys Lys Gln Val Glu Asp Lys Lys Lys Asp Lys Ala Asn Tyr
 145 150 155 160
 Gln Val Pro Tyr Thr Ile Thr Val Asn Gly Thr Ser Gln Asn Ile Leu
 165 170 175
 Ser Asn Leu Thr Phe Asn Lys Asn Gln Asn Ile Ser Tyr Lys Asp Leu
 180 185 190
 Glu Asp Lys Val Lys Ser Val Leu Glu Ser Asn Arg Gly Ile Thr Asp
 195 200 205
 Val Asp Leu Arg Leu Ser Lys Gln Ala Lys Tyr Thr Val Asn Phe Lys
 210 215 220
 Asn Gly Thr Lys Lys Val Ile Asp Leu Lys Ser Gly Ile Tyr Thr Ala
 225 230 235 240
 Asn Leu Ile Asn Ser Ser Asp Ile Lys Ser Ile Asn Ile Asn Val Asp
 245 250 255
 Thr Lys Lys His Ile Glu Asn Lys Ala Lys Arg Asn Tyr Gln Val Pro
 260 265 270
 Tyr Ser Ile Asn Leu Asn Gly Thr Ser Thr Asn Ile Leu Ser Asn Leu
 275 280 285
 Ser Phe Ser Asn Lys Pro Trp Thr Asn Tyr Lys Asn Leu Thr Ser Gln
 290 295 300

5 Ile Lys Ser Val Leu Lys His Asp Arg Gly Ile Ser Glu Gln Asp Leu
 305 310 315 320
 Lys Tyr Ala Lys Lys Ala Tyr Tyr Thr Val Tyr Phe Lys Asn Gly Gly
 325 330 335
 Lys Arg Ile Leu Gln Leu Asn Ser Lys Asn Tyr Thr Ala Asn Leu Val
 340 345 350
 10 His Ala Lys Asp Val Lys Arg Ile Glu Ile Thr Val Lys Thr Gly Thr
 355 360 365
 Lys Ala Lys Ala Asp Arg Tyr Val Pro Tyr Thr Ile Ala Val Asn Gly
 370 375 380
 15 Thr Ser Thr Pro Ile Leu Ser Asp Leu Lys Phe Thr Gly Asp Pro Arg
 385 390 395 400
 Val Gly Tyr Lys Asp Ile Ser Lys Lys Val Lys Ser Val Leu Lys His
 405 410 415
 20 Asp Arg Gly Ile Gly Glu Arg Glu Leu Lys Tyr Ala Lys Lys Ala Thr
 420 425 430
 Tyr Thr Val His Phe Lys Asn Gly Thr Lys Lys Val Ile Asn Ile Asn
 435 440 445
 25 Ser Asn Ile Ser Gln Leu Asn Leu Leu Tyr Val Gln Asp Ile Lys Lys
 450 455 460
 Ile Asp Ile Asp Val Lys Thr Gly Thr Lys Ala Lys Ala Asp Ser Tyr
 465 470 475 480
 30 Val Pro Tyr Thr Ile Ala Val Asn Gly Thr Ser Thr Pro Ile Leu Ser
 485 490 495
 Lys Leu Lys Ile Ser Asn Lys Gln Leu Ile Ser Tyr Lys Tyr Leu Asn
 500 505 510
 35 Asp Lys Val Lys Ser Val Leu Lys Ser Glu Arg Gly Ile Ser Asp Leu
 515 520 525
 Asp Leu Lys Phe Ala Lys Gln Ala Lys Tyr Thr Val Tyr Phe Lys Asn
 530 535 540
 40 Gly Lys Lys Gln Val Val Asn Leu Lys Ser Asp Ile Phe Thr Pro Asn
 545 550 555 560
 Leu Phe Ser Ala Lys Asp Ile Lys Lys Ile Asp Ile Asp Val Lys Gln
 565 570 575
 45 Tyr Thr Lys Ser Lys Lys Asn Lys
 580

<210> 5

<211> 9535

50 <212> PRT

<213> Staphylococcus aureus

<400> 5

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Met	Asn	Tyr	Arg	Asp	Lys	Ile	Gln	Lys	Phe	Ser	Ile	Arg	Lys	Tyr	Thr
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Val	Gly	Thr	Phe	Ser	Thr	Val	Ile	Ala	Thr	Leu	Val	Phe	Leu	Gly	Phe
			20					25					30		
Asn	Thr	Ser	Gln	Ala	His	Ala	Ala	Glu	Thr	Asn	Gln	Pro	Ala	Ser	Val
		35					40					45			

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Val Lys Gln Lys Gln Gln Ser Asn Asn Glu Gln Thr Glu Asn Arg Glu
50 55 60

5 Ser Gln Val Gln Asn Ser Gln Asn Ser Gln Asn Gly Gln Ser Leu Ser
65 70 75 80

Ala Thr His Glu Asn Glu Gln Pro Asn Ile Ser Gln Ala Asn Leu Val
85 90 95

10 Asp Gln Lys Val Ala Gln Ser Ser Thr Thr Asn Asp Glu Gln Pro Ala
100 105 110

Ser Gln Asn Val Asn Thr Lys Lys Asp Ser Ala Thr Ala Ala Thr Thr
115 120 125

15 Gln Pro Asp Lys Glu Gln Ser Lys His Lys Gln Asn Glu Ser Gln Ser
130 135 140

Ala Asn Lys Asn Gly Asn Asp Asn Arg Ala Ala His Val Glu Asn His
145 150 155 160

20 Glu Ala Asn Val Val Thr Ala Ser Asp Ser Ser Asp Asn Gly Asn Val
165 170 175

Gln His Asp Arg Asn Glu Leu Gln Ala Phe Phe Asp Ala Asn Tyr His
180 185 190

25 Asp Tyr Arg Phe Ile Asp Arg Glu Asn Ala Asp Ser Gly Thr Phe Asn
195 200 205

Tyr Val Lys Gly Ile Phe Asp Lys Ile Asn Thr Leu Leu Gly Ser Asn
210 215 220

30 Asp Pro Ile Asn Asn Lys Asp Leu Gln Leu Ala Tyr Lys Glu Leu Glu
225 230 235 240

Gln Ala Val Ala Leu Ile Arg Thr Met Pro Gln Arg Gln Gln Thr Ser
245 250 255

35 Arg Arg Ser Asn Arg Ile Gln Thr Arg Ser Val Glu Ser Arg Ala Ala
260 265 270

Glu Pro Arg Ser Val Ser Asp Tyr Gln Asn Ala Asn Ser Ser Tyr Tyr
275 280 285

40 Val Glu Asn Ala Asn Asp Gly Ser Gly Tyr Pro Val Gly Thr Tyr Ile
290 295 300

Asn Ala Ser Ser Lys Gly Ala Pro Tyr Asn Leu Pro Thr Thr Pro Trp
305 310 315 320

45 Asn Thr Leu Lys Ala Ser Asp Ser Lys Glu Ile Ala Leu Met Thr Ala
325 330 335

Lys Gln Thr Gly Asp Gly Tyr Gln Trp Val Ile Lys Phe Asn Lys Gly
340 345 350

His Ala Pro His Gln Asn Met Ile Phe Trp Phe Ala Leu Pro Ala Asp
355 360 365

50 Gln Val Pro Val Gly Arg Thr Asp Phe Val Thr Val Asn Ser Asp Gly
370 375 380

Thr Asn Val Gln Trp Ser His Gly Ala Gly Ala Gly Ala Asn Lys Pro
385 390 395 400

55 Leu Gln Gln Met Trp Glu Tyr Gly Val Asn Asp Pro His Arg Ser His
405 410 415

Asp Phe Lys Ile Arg Asn Arg Ser Gly Gln Val Ile Tyr Asp Trp Pro

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	420					425					430					
	Thr	Val	His	Ile	Tyr	Ser	Leu	Glu	Asp	Leu	Ser	Arg	Ala	Ser	Asp	Tyr
			435					440					445			
5	Phe	Ser	Glu	Ala	Gly	Ala	Thr	Pro	Ala	Thr	Lys	Ala	Phe	Gly	Arg	Gln
	450					455					460					
	Asn	Phe	Glu	Tyr	Ile	Asn	Gly	Gln	Lys	Pro	Ala	Glu	Ser	Pro	Gly	Val
	465					470					475					480
10	Pro	Lys	Val	Tyr	Thr	Phe	Ile	Gly	Gln	Gly	Asp	Ala	Ser	Tyr	Thr	Ile
					485					490					495	
	Ser	Phe	Lys	Thr	Gln	Gly	Pro	Thr	Val	Asn	Lys	Leu	Tyr	Tyr	Ala	Ala
				500					505					510		
15	Gly	Gly	Arg	Ala	Leu	Glu	Tyr	Asn	Gln	Leu	Phe	Met	Tyr	Ser	Gln	Leu
			515					520					525			
	Tyr	Val	Glu	Ser	Thr	Gln	Asp	His	Gln	Gln	Arg	Leu	Asn	Gly	Leu	Arg
	530					535					540					
20	Gln	Val	Val	Asn	Arg	Thr	Tyr	Arg	Ile	Gly	Thr	Thr	Lys	Arg	Val	Glu
	545					550					555					560
	Val	Ser	Gln	Gly	Asn	Val	Gln	Thr	Lys	Lys	Val	Leu	Glu	Ser	Thr	Asn
				565						570					575	
25	Leu	Asn	Ile	Asp	Asp	Phe	Val	Asp	Asp	Pro	Leu	Ser	Tyr	Val	Lys	Thr
				580					585					590		
	Pro	Ser	Asn	Lys	Val	Leu	Gly	Phe	Tyr	Ser	Asn	Asn	Ala	Asn	Thr	Asn
			595					600					605			
30	Ala	Phe	Arg	Pro	Gly	Gly	Ala	Gln	Gln	Leu	Asn	Glu	Tyr	Gln	Leu	Ser
	610					615						620				
	Gln	Leu	Phe	Thr	Asp	Gln	Lys	Leu	Gln	Glu	Ala	Ala	Arg	Thr	Arg	Asn
	625				630					635						640
35	Pro	Ile	Arg	Leu	Met	Ile	Gly	Phe	Asp	Tyr	Pro	Asp	Ala	Tyr	Gly	Asn
				645						650					655	
	Ser	Glu	Thr	Leu	Val	Pro	Val	Asn	Leu	Thr	Val	Leu	Pro	Glu	Ile	Gln
				660					665					670		
40	His	Asn	Ile	Lys	Phe	Phe	Lys	Asn	Asp	Asp	Thr	Gln	Asn	Ile	Ala	Glu
			675					680					685			
	Lys	Pro	Phe	Ser	Lys	Gln	Ala	Gly	His	Pro	Val	Phe	Tyr	Val	Tyr	Ala
	690					695					700					
45	Gly	Asn	Gln	Gly	Asn	Ala	Ser	Val	Asn	Leu	Gly	Gly	Ser	Val	Thr	Ser
	705				710						715					720
	Ile	Gln	Pro	Leu	Arg	Ile	Asn	Leu	Thr	Ser	Asn	Glu	Asn	Phe	Thr	Asp
				725						730					735	
	Lys	Asp	Trp	Gln	Ile	Thr	Gly	Ile	Pro	Arg	Thr	Leu	His	Ile	Glu	Asn
				740				745						750		
50	Ser	Thr	Asn	Arg	Pro	Asn	Asn	Ala	Arg	Glu	Arg	Asn	Ile	Glu	Leu	Val
			755					760					765			
	Gly	Asn	Leu	Leu	Pro	Gly	Asp	Tyr	Phe	Gly	Thr	Ile	Arg	Phe	Gly	Arg
	770					775						780				
55	Lys	Glu	Gln	Leu	Phe	Glu	Ile	Arg	Val	Lys	Pro	His	Thr	Pro	Thr	Ile
	785					790					795					800

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Thr Thr Thr Ala Glu Gln Leu Arg Gly Thr Ala Leu Gln Lys Val Pro
805 810 815

5 Val Asn Ile Ser Gly Ile Pro Leu Asp Pro Ser Ala Leu Val Tyr Leu
820 825 830

Val Ala Pro Thr Asn Gln Thr Thr Asn Gly Gly Ser Glu Ala Asp Gln
835 840 845

10 Ile Pro Ser Gly Tyr Thr Ile Leu Ala Thr Gly Thr Pro Asp Gly Val
850 855 860

His Asn Thr Ile Thr Ile Arg Pro Gln Asp Tyr Val Val Phe Ile Pro
865 870 875 880

15 Pro Val Gly Lys Gln Ile Arg Ala Val Val Tyr Tyr Asn Lys Val Val
885 890 895

Ala Ser Asn Met Ser Asn Ala Val Thr Ile Leu Pro Asp Asp Ile Pro
900 905 910

20 Pro Thr Ile Asn Asn Pro Val Gly Ile Asn Ala Lys Tyr Tyr Arg Gly
915 920 925

Asp Glu Val Asn Phe Thr Met Gly Val Ser Asp Arg His Ser Gly Ile
930 935 940

25 Lys Asn Thr Thr Ile Thr Thr Leu Pro Asn Gly Trp Thr Ser Asn Leu
945 950 955 960

Thr Lys Ala Asp Lys Asn Asn Gly Ser Leu Ser Ile Thr Gly Arg Val
965 970 975

30 Ser Met Asn Gln Ala Phe Asn Ser Asp Ile Thr Phe Lys Val Ser Ala
980 985 990

Thr Asp Asn Val Asn Asn Thr Thr Asn Asp Ser Gln Ser Lys His Val
995 1000 1005

35 Ser Ile His Val Gly Lys Ile Ser Glu Asp Ala His Pro Ile Val Leu
1010 1015 1020

Gly Asn Thr Glu Lys Val Val Val Val Asn Pro Thr Ala Val Ser Asn
1025 1030 1035 1040

40 Asp Glu Lys Gln Ser Ile Ile Thr Ala Phe Met Asn Lys Asn Gln Asn
1045 1050 1055

Ile Arg Gly Tyr Leu Ala Ser Thr Asp Pro Val Thr Val Asp Asn Asn
1060 1065 1070

45 Gly Asn Val Thr Leu His Tyr Arg Asp Gly Ser Ser Thr Thr Leu Asp
1075 1080 1085

Ala Thr Asn Val Met Thr Tyr Glu Pro Val Val Lys Pro Glu Tyr Gln
1090 1095 1100

50 Thr Val Asn Ala Ala Lys Thr Ala Thr Val Thr Ile Ala Lys Gly Gln
1105 1110 1115 1120

Ser Phe Ser Ile Gly Asp Ile Lys Gln Tyr Phe Thr Leu Ser Asn Gly
1125 1130 1135

Gln Pro Ile Pro Ser Gly Thr Phe Thr Asn Ile Thr Ser Asp Arg Thr
1140 1145 1150

55 Ile Pro Thr Ala Gln Glu Val Ser Gln Met Asn Ala Gly Thr Gln Leu
1155 1160 1165

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Tyr His Ile Thr Ala Thr Asn Ala Tyr His Lys Asp Ser Glu Asp Phe
 1170 1175 1180
 Tyr Ile Ser Leu Lys Ile Ile Asp Val Lys Gln Pro Glu Gly Asp Gln
 1185 1190 1195 1200
 Arg Val Tyr Arg Thr Ser Thr Tyr Asp Leu Thr Thr Asp Glu Ile Ser
 1205 1210 1215
 Lys Val Lys Gln Ala Phe Ile Asn Ala Asn Arg Asp Val Ile Thr Leu
 1220 1225 1230
 Ala Glu Gly Asp Ile Ser Val Thr Asn Thr Pro Asn Gly Ala Asn Val
 1235 1240 1245
 Ser Thr Ile Thr Val Asn Ile Asn Lys Gly Arg Leu Thr Lys Ser Phe
 1250 1255 1260
 Ala Ser Asn Leu Ala Asn Met Asn Phe Leu Arg Trp Val Asn Phe Pro
 1265 1270 1275 1280
 Gln Asp Tyr Thr Val Thr Trp Thr Asn Ala Lys Ile Ala Asn Arg Pro
 1285 1290 1295
 Thr Asp Gly Gly Leu Ser Trp Ser Asp Asp His Lys Ser Leu Ile Tyr
 1300 1305 1310
 Arg Tyr Asp Ala Thr Leu Gly Thr Gln Ile Thr Thr Asn Asp Ile Leu
 1315 1320 1325
 Thr Met Leu Lys Ala Thr Thr Thr Val Pro Gly Leu Arg Asn Asn Ile
 1330 1335 1340
 Thr Gly Asn Glu Lys Ser Gln Ala Glu Ala Gly Gly Arg Pro Asn Phe
 1345 1350 1355 1360
 Arg Thr Thr Gly Tyr Ser Gln Ser Asn Ala Thr Thr Asp Gly Gln Arg
 1365 1370 1375
 Gln Phe Thr Leu Asn Gly Gln Val Ile Gln Val Leu Asp Ile Ile Asn
 1380 1385 1390
 Pro Ser Asn Gly Tyr Gly Gly Gln Pro Val Thr Asn Ser Asn Thr Arg
 1395 1400 1405
 Ala Asn His Ser Asn Ser Thr Val Val Asn Val Asn Glu Pro Ala Ala
 1410 1415 1420
 Asn Gly Ala Gly Ala Phe Thr Ile Asp His Val Val Lys Ser Asn Ser
 1425 1430 1435 1440
 Thr His Asn Ala Ser Asp Ala Val Tyr Lys Ala Gln Leu Tyr Leu Thr
 1445 1450 1455
 Pro Tyr Gly Pro Lys Gln Tyr Val Glu His Leu Asn Gln Asn Thr Gly
 1460 1465 1470
 Asn Thr Thr Asp Ala Ile Asn Ile Tyr Phe Val Pro Ser Asp Leu Val
 1475 1480 1485
 Asn Pro Thr Ile Ser Val Gly Asn Tyr Thr Asn His Gln Val Phe Ser
 1490 1495 1500
 Gly Glu Thr Phe Thr Asn Thr Ile Thr Ala Asn Asp Asn Phe Gly Val
 1505 1510 1515 1520
 Gln Ser Val Thr Val Pro Asn Thr Ser Gln Ile Thr Gly Thr Val Asp
 1525 1530 1535
 Asn Asn His Gln His Val Ser Ala Thr Ala Pro Asn Val Thr Ser Ala

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	1540	1545	1550
	Thr Asn Lys Thr Ile Asn Leu	Leu Ala Thr Asp Thr	Ser Gly Asn Thr
	1555	1560	1565
5	Ala Thr Thr Ser Phe Asn Val Thr Val Lys Pro Leu Arg Asp Lys Tyr		
	1570	1575	1580
	Arg Val Gly Thr Ser Ser Thr Ala Ala Asn Pro Val Arg Ile Ala Asn		
	1585	1590	1595
10	Ile Ser Asn Asn Ala Thr Val Ser Gln Ala Asp Gln Thr Thr Ile Ile		
	1605	1610	1615
	Asn Ser Leu Thr Phe Thr Glu Thr Val Pro Asn Arg Ser Tyr Ala Arg		
	1620	1625	1630
15	Ala Ser Ala Asn Glu Ile Thr Ser Lys Thr Val Ser Asn Val Ser Arg		
	1635	1640	1645
	Thr Gly Asn Asn Ala Asn Val Thr Val Thr Val Thr Tyr Gln Asp Gly		
	1650	1655	1660
20	Thr Thr Ser Thr Val Thr Val Pro Val Lys His Val Ile Pro Glu Ile		
	1665	1670	1675
	Val Ala His Ser His Tyr Thr Val Gln Gly Gln Asp Phe Pro Ala Gly		
	1685	1690	1695
25	Asn Gly Ser Ser Ala Ser Asp Tyr Phe Lys Leu Ser Asn Gly Ser Asp		
	1700	1705	1710
	Ile Ala Asp Ala Thr Ile Thr Trp Val Ser Gly Gln Ala Pro Asn Lys		
	1715	1720	1725
30	Asp Asn Thr Arg Ile Gly Glu Asp Ile Thr Val Thr Ala His Ile Leu		
	1730	1735	1740
	Ile Asp Gly Glu Thr Thr Pro Ile Thr Lys Thr Ala Thr Tyr Lys Val		
	1745	1750	1755
35	Val Arg Thr Val Pro Lys His Val Phe Glu Thr Ala Arg Gly Val Leu		
	1765	1770	1775
	Tyr Pro Gly Val Ser Asp Met Tyr Asp Ala Lys Gln Tyr Val Lys Pro		
	1780	1785	1790
40	Val Asn Asn Ser Trp Ser Thr Asn Ala Gln His Met Asn Phe Gln Phe		
	1795	1800	1805
	Val Gly Thr Tyr Gly Pro Asn Lys Asp Val Val Gly Ile Ser Thr Arg		
	1810	1815	1820
45	Leu Ile Arg Val Thr Tyr Asp Asn Arg Gln Thr Glu Asp Leu Thr Ile		
	1825	1830	1835
	Leu Ser Lys Val Lys Pro Asp Pro Pro Arg Ile Asp Ala Asn Ser Val		
	1845	1850	1855
50	Thr Tyr Lys Ala Gly Leu Thr Asn Gln Glu Ile Lys Val Asn Asn Val		
	1860	1865	1870
	Leu Asn Asn Ser Ser Val Lys Leu Phe Lys Ala Asp Asn Thr Pro Leu		
	1875	1880	1885
55	Asn Val Thr Asn Ile Thr His Gly Ser Gly Phe Ser Ser Val Val Thr		
	1890	1895	1900
	Val Ser Asp Ala Leu Pro Asn Gly Gly Ile Lys Ala Lys Ser Ser Ile		
	1905	1910	1915
			1920

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Ser Met Asn Asn Val Thr Tyr Thr Thr Gln Asp Glu His Gly Gln Val
 1925 1930 1935
 Val Thr Val Thr Arg Asn Glu Ser Val Asp Ser Asn Asp Ser Ala Thr
 5 1940 1945 1950
 Val Thr Val Thr Pro Gln Leu Gln Ala Thr Thr Glu Gly Ala Val Phe
 1955 1960 1965
 Ile Lys Gly Gly Asp Gly Phe Asp Phe Gly His Val Glu Arg Phe Ile
 10 1970 1975 1980
 Gln Asn Pro Pro His Gly Ala Thr Val Ala Trp His Asp Ser Pro Asp
 1985 1990 1995 2000
 Thr Trp Lys Asn Thr Val Gly Asn Thr His Lys Thr Ala Val Val Thr
 15 2005 2010 2015
 Leu Pro Asn Gly Gln Gly Thr Arg Asn Val Glu Val Pro Val Lys Val
 2020 2025 2030
 Tyr Pro Val Ala Asn Ala Lys Ala Pro Ser Arg Asp Val Lys Gly Gln
 20 2035 2040 2045
 Asn Leu Thr Asn Gly Thr Asp Ala Met Asn Tyr Ile Thr Phe Asp Pro
 2050 2055 2060
 Asn Thr Asn Thr Asn Gly Ile Thr Ala Ala Trp Ala Asn Arg Gln Gln
 25 2065 2070 2075 2080
 Pro Asn Asn Gln Gln Ala Gly Val Gln His Leu Asn Val Asp Val Thr
 2085 2090 2095
 Tyr Pro Gly Ile Ser Ala Ala Lys Arg Val Pro Val Thr Val Asn Val
 30 2100 2105 2110
 Tyr Gln Phe Glu Phe Pro Gln Thr Thr Tyr Thr Thr Thr Val Gly Gly
 2115 2120 2125
 Thr Leu Ala Ser Gly Thr Gln Ala Ser Gly Tyr Ala His Met Gln Asn
 35 2130 2135 2140
 Ala Thr Gly Leu Pro Thr Asp Gly Phe Thr Tyr Lys Trp Asn Arg Asp
 2145 2150 2155 2160
 Thr Thr Gly Thr Asn Asp Ala Asn Trp Ser Ala Met Asn Lys Pro Asn
 40 2165 2170 2175
 Val Ala Lys Val Val Asn Ala Lys Tyr Asp Val Ile Tyr Asn Gly His
 2180 2185 2190
 Thr Phe Ala Thr Ser Leu Pro Ala Lys Phe Val Val Lys Asp Val Gln
 2195 2200 2205
 Pro Ala Lys Pro Thr Val Thr Glu Thr Ala Ala Gly Ala Ile Thr Ile
 45 2210 2215 2220
 Ala Pro Gly Ala Asn Gln Thr Val Asn Thr His Ala Gly Asn Val Thr
 2225 2230 2235 2240
 Thr Tyr Ala Asp Lys Leu Val Ile Lys Arg Asn Gly Asn Val Val Thr
 50 2245 2250 2255
 Thr Phe Thr Arg Arg Asn Asn Thr Ser Pro Trp Val Lys Glu Ala Ser
 2260 2265 2270
 Ala Ala Thr Val Ala Gly Ile Ala Gly Thr Asn Asn Gly Ile Thr Val
 55 2275 2280 2285

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Ala Ala Gly Thr Phe Asn Pro Ala Asp Thr Ile Gln Val Val Ala Thr
2290 2295 2300

5 Gln Gly Ser Gly Glu Thr Val Ser Asp Glu Gln Arg Ser Asp Asp Phe
2305 2310 2315 2320

Thr Val Val Ala Pro Gln Pro Asn Gln Ala Thr Thr Lys Ile Trp Gln
2325 2330 2335

10 Asn Gly His Ile Asp Ile Thr Pro Asn Asn Pro Ser Gly His Leu Ile
2340 2345 2350

Asn Pro Thr Gln Ala Met Asp Ile Ala Tyr Thr Glu Lys Val Gly Asn
2355 2360 2365

15 Gly Ala Glu His Ser Lys Thr Ile Asn Val Val Arg Gly Gln Asn Asn
2370 2375 2380

Gln Trp Thr Ile Ala Asn Lys Pro Asp Tyr Val Thr Leu Asp Ala Gln
2385 2390 2395 2400

20 Thr Gly Lys Val Thr Phe Asn Ala Asn Thr Ile Lys Pro Asn Ser Ser
2405 2410 2415

Ile Thr Ile Thr Pro Lys Ala Gly Thr Gly His Ser Val Ser Ser Asn
2420 2425 2430

25 Pro Ser Thr Leu Thr Ala Pro Ala Ala His Thr Val Asn Thr Thr Glu
2435 2440 2445

Ile Val Lys Asp Tyr Gly Ser Asn Val Thr Ala Ala Glu Ile Asn Asn
2450 2455 2460

30 Ala Val Gln Val Ala Asn Lys Arg Thr Ala Thr Ile Lys Asn Gly Thr
2465 2470 2475 2480

Ala Met Pro Thr Asn Leu Ala Gly Gly Ser Thr Thr Thr Ile Pro Val
2485 2490 2495

Thr Val Thr Tyr Asn Asp Gly Ser Thr Glu Glu Val Gln Glu Ser Ile
2500 2505 2510

35 Phe Thr Lys Ala Asp Lys Arg Glu Leu Ile Thr Ala Lys Asn His Leu
2515 2520 2525

Asp Asp Pro Val Ser Thr Glu Gly Lys Lys Pro Gly Thr Ile Thr Gln
2530 2535 2540

40 Tyr Asn Asn Ala Met His Asn Ala Gln Gln Gln Ile Asn Thr Ala Lys
2545 2550 2555 2560

Thr Glu Ala Gln Gln Val Ile Asn Asn Glu Arg Ala Thr Pro Gln Gln
2565 2570 2575

45 Val Ser Asp Ala Leu Thr Lys Val Arg Ala Ala Gln Thr Lys Ile Asp
2580 2585 2590

Gln Ala Lys Ala Leu Leu Gln Asn Lys Glu Asp Asn Ser Gln Leu Val
2595 2600 2605

50 Thr Ser Lys Asn Asn Leu Gln Ser Ser Val Asn Gln Val Pro Ser Thr
2610 2615 2620

Ala Gly Met Thr Gln Gln Ser Ile Asp Asn Tyr Asn Ala Lys Lys Arg
2625 2630 2635 2640

55 Glu Ala Glu Thr Glu Ile Thr Ala Ala Gln Arg Val Ile Asp Asn Gly
2645 2650 2655

Asp Ala Thr Ala Gln Gln Ile Ser Asp Glu Lys His Arg Val Asp Asn

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	2660	2665	2670
	Ala Leu Thr Ala Leu Asn Gln	Ala Lys His Asp Leu Thr	Ala Asp Thr
	2675	2680	2685
5	His Ala Leu Glu Gln Ala Val Gln Gln Leu Asn Arg Thr Gly Thr Thr		
	2690	2695	2700
	Thr Gly Lys Lys Pro Ala Ser Ile Thr Ala Tyr Asn Asn Ser Ile Arg		
	2705	2710	2715 2720
10	Ala Leu Gln Ser Asp Leu Thr Ser Ala Lys Asn Ser Ala Asn Ala Ile		
	2725	2730	2735
	Ile Gln Lys Pro Ile Arg Thr Val Gln Glu Val Gln Ser Ala Leu Thr		
	2740	2745	2750
15	Asn Val Asn Arg Val Asn Glu Arg Leu Thr Gln Ala Ile Asn Gln Leu		
	2755	2760	2765
	Val Pro Leu Ala Asp Asn Ser Ala Leu Lys Thr Ala Lys Thr Lys Leu		
	2770	2775	2780
20	Asp Glu Glu Ile Asn Lys Ser Val Thr Thr Asp Gly Met Thr Gln Ser		
	2785	2790	2795 2800
	Ser Ile Gln Ala Tyr Glu Asn Ala Lys Arg Ala Gly Gln Thr Glu Ser		
	2805	2810	2815
25	Thr Asn Ala Gln Asn Val Ile Asn Asn Gly Asp Ala Thr Asp Gln Gln		
	2820	2825	2830
	Ile Ala Ala Glu Lys Thr Lys Val Glu Glu Lys Tyr Asn Ser Leu Lys		
	2835	2840	2845
30	Gln Ala Ile Ala Gly Leu Thr Pro Asp Leu Ala Pro Leu Gln Thr Ala		
	2850	2855	2860
	Lys Thr Gln Leu Gln Asn Asp Ile Asp Gln Pro Thr Ser Thr Thr Gly		
	2865	2870	2875 2880
35	Met Thr Ser Ala Ser Ile Ala Ala Phe Asn Glu Lys Leu Ser Ala Ala		
	2885	2890	2895
	Arg Thr Lys Ile Gln Glu Ile Asp Arg Val Leu Ala Ser His Pro Asp		
	2900	2905	2910
40	Val Ala Thr Ile Arg Gln Asn Val Thr Ala Ala Asn Ala Ala Lys Ser		
	2915	2920	2925
	Ala Leu Asp Gln Ala Arg Asn Gly Leu Thr Val Asp Lys Ala Pro Leu		
	2930	2935	2940
45	Glu Asn Ala Lys Asn Gln Leu Gln His Ser Ile Asp Thr Gln Thr Ser		
	2945	2950	2955 2960
	Thr Thr Gly Met Thr Gln Asp Ser Ile Asn Ala Tyr Asn Ala Lys Leu		
	2965	2970	2975
	Thr Ala Ala Arg Asn Lys Ile Gln Gln Ile Asn Gln Val Leu Ala Gly		
	2980	2985	2990
50	Ser Pro Thr Val Glu Gln Ile Asn Thr Asn Thr Ser Thr Ala Asn Gln		
	2995	3000	3005
	Ala Lys Ser Asp Leu Asp His Ala Arg Gln Ala Leu Thr Pro Asp Lys		
	3010	3015	3020
55	Ala Pro Leu Gln Thr Ala Lys Thr Gln Leu Glu Gln Ser Ile Asn Gln		
	3025	3030	3035 3040

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Pro Thr Asp Thr Thr Gly Met Thr Thr Ala Ser Leu Asn Ala Tyr Asn
3045 3050 3055

5 Gln Lys Leu Gln Ala Ala Arg Gln Lys Leu Thr Glu Ile Asn Gln Val
3060 3065 3070

Leu Asn Gly Asn Pro Thr Val Gln Asn Ile Asn Asp Lys Val Thr Glu
3075 3080 3085

10 Ala Asn Gln Ala Lys Asp Gln Leu Asn Thr Ala Arg Gln Gly Leu Thr
3090 3095 3100

Leu Asp Arg Gln Pro Ala Leu Thr Thr Leu His Gly Ala Ser Asn Leu
3105 3110 3115 3120

15 Asn Gln Ala Gln Gln Asn Asn Phe Thr Gln Gln Ile Asn Ala Ala Gln
3125 3130 3135

Asn His Ala Ala Leu Glu Thr Ile Lys Ser Asn Ile Thr Ala Leu Asn
3140 3145 3150

20 Thr Ala Met Thr Lys Leu Lys Asp Ser Val Ala Asp Asn Asn Thr Ile
3155 3160 3165

Lys Ser Asp Gln Asn Tyr Thr Asp Ala Thr Pro Ala Asn Lys Gln Ala
3170 3175 3180

25 Tyr Asp Asn Ala Val Asn Ala Ala Lys Gly Val Ile Gly Glu Thr Thr
3185 3190 3195 3200

Asn Pro Thr Met Asp Val Asn Thr Val Asn Gln Lys Ala Ala Ser Val
3205 3210 3215

30 Lys Ser Thr Lys Asp Ala Leu Asp Gly Gln Gln Asn Leu Gln Arg Ala
3220 3225 3230

Lys Thr Glu Ala Thr Asn Ala Ile Thr His Ala Ser Asp Leu Asn Gln
3235 3240 3245

35 Ala Gln Lys Asn Ala Leu Thr Gln Gln Val Asn Ser Ala Gln Asn Val
3250 3255 3260

Gln Ala Val Asn Asp Ile Lys Gln Thr Thr Gln Ser Leu Asn Thr Ala
3265 3270 3275 3280

40 Met Thr Gly Leu Lys Arg Gly Val Ala Asn His Asn Gln Val Val Gln
3285 3290 3295

Ser Asp Asn Tyr Val Asn Ala Asp Thr Asn Lys Lys Asn Asp Tyr Asn
3300 3305 3310

45 Asn Ala Tyr Asn His Ala Asn Asp Ile Ile Asn Gly Asn Ala Gln His
3315 3320 3325

Pro Val Ile Thr Pro Ser Asp Val Asn Asn Ala Leu Ser Asn Val Thr
3330 3335 3340

50 Ser Lys Glu His Ala Leu Asn Gly Glu Ala Lys Leu Asn Ala Ala Lys
3345 3350 3355 3360

Gln Glu Ala Asn Thr Ala Leu Gly His Leu Asn Asn Leu Asn Asn Ala
3365 3370 3375

Gln Arg Gln Asn Leu Gln Ser Gln Ile Asn Gly Ala His Gln Ile Asp
3380 3385 3390

55 Ala Val Asn Thr Ile Lys Gln Asn Ala Thr Asn Leu Asn Ser Ala Met
3395 3400 3405

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Gly Asn Leu Arg Gln Ala Val Ala Asp Lys Asp Gln Val Lys Arg Thr
 3410 3415 3420
 5 Glu Asp Tyr Ala Asp Ala Asp Thr Ala Lys Gln Asn Ala Tyr Asn Ser
 3425 3430 3435 3440
 Ala Val Ser Ser Ala Glu Thr Ile Ile Asn Gln Thr Thr Asn Pro Thr
 3445 3450 3455
 10 Met Ser Val Asp Asp Val Asn Arg Ala Thr Ser Ala Val Thr Ser Asn
 3460 3465 3470
 Lys Asn Ala Leu Asn Gly Tyr Glu Lys Leu Ala Gln Ser Lys Thr Asp
 3475 3480 3485
 15 Ala Ala Arg Ala Ile Asp Ala Leu Pro His Leu Asn Asn Ala Gln Lys
 3490 3495 3500
 Ala Asp Val Lys Ser Lys Ile Asn Ala Ala Ser Asn Ile Ala Gly Val
 3505 3510 3515 3520
 20 Asn Thr Val Lys Gln Gln Gly Thr Asp Leu Asn Thr Ala Met Gly Asn
 3525 3530 3535
 Leu Gln Gly Ala Ile Asn Asp Glu Gln Thr Thr Leu Asn Ser Gln Asn
 3540 3545 3550
 25 Tyr Gln Asp Ala Thr Pro Ser Lys Lys Thr Ala Tyr Thr Asn Ala Val
 3555 3560 3565
 Gln Ala Ala Lys Asp Ile Leu Asn Lys Ser Asn Gly Gln Asn Lys Thr
 3570 3575 3580
 30 Lys Asp Gln Val Thr Glu Ala Met Asn Gln Val Asn Ser Ala Lys Asn
 3585 3590 3595 3600
 Asn Leu Asp Gly Thr Arg Leu Leu Asp Gln Ala Lys Gln Thr Ala Lys
 3605 3610 3615
 Gln Gln Leu Asn Asn Met Thr His Leu Thr Thr Ala Gln Lys Thr Asn
 3620 3625 3630
 35 Leu Thr Asn Gln Ile Asn Ser Gly Thr Thr Val Ala Gly Val Gln Thr
 3635 3640 3645
 Val Gln Ser Asn Ala Asn Thr Leu Asp Gln Ala Met Asn Thr Leu Arg
 3650 3655 3660
 40 Gln Ser Ile Ala Asn Lys Asp Ala Thr Lys Ala Ser Glu Asp Tyr Val
 3665 3670 3675 3680
 Asp Ala Asn Asn Asp Lys Gln Thr Ala Tyr Asn Asn Ala Val Ala Ala
 3685 3690 3695
 45 Ala Glu Thr Ile Ile Asn Ala Asn Ser Asn Pro Glu Met Asn Pro Ser
 3700 3705 3710
 Thr Ile Thr Gln Lys Ala Glu Gln Val Asn Ser Ser Lys Thr Ala Leu
 3715 3720 3725
 50 Asn Gly Asp Glu Asn Leu Ala Ala Ala Lys Gln Asn Ala Lys Thr Tyr
 3730 3735 3740
 Leu Asn Thr Leu Thr Ser Ile Thr Asp Ala Gln Lys Asn Asn Leu Ile
 3745 3750 3755 3760
 55 Ser Gln Ile Thr Ser Ala Thr Arg Val Ser Gly Val Asp Thr Val Lys
 3765 3770 3775
 Gln Asn Ala Gln His Leu Asp Gln Ala Met Ala Ser Leu Gln Asn Gly

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	3780	3785	3790
	Ile Asn Asn Glu Ser Gln Val	Lys Ser Ser Glu Lys Tyr Arg Asp Ala	
	3795	3800	3805
5	Asp Thr Asn Lys Gln Gln Glu Tyr Asp Asn Ala Ile Thr Ala Ala Lys		
	3810	3815	3820
	Ala Ile Leu Asn Lys Ser Thr Gly Pro Asn Thr Ala Gln Asn Ala Val		
	3825	3830	3835
10	Glu Ala Ala Leu Gln Arg Val Asn Asn Ala Lys Asp Ala Leu Asn Gly		
	3845	3850	3855
	Asp Ala Lys Leu Ile Ala Ala Gln Asn Ala Ala Lys Gln His Leu Gly		
	3860	3865	3870
15	Thr Leu Thr His Ile Thr Thr Ala Gln Arg Asn Asp Leu Thr Asn Gln		
	3875	3880	3885
	Ile Ser Gln Ala Thr Asn Leu Ala Gly Val Glu Ser Val Lys Gln Asn		
	3890	3895	3900
20	Ala Asn Ser Leu Asp Gly Ala Met Gly Asn Leu Gln Thr Ala Ile Asn		
	3905	3910	3915
	Asp Lys Ser Gly Thr Leu Ala Ser Gln Asn Phe Leu Asp Ala Asp Glu		
	3925	3930	3935
25	Gln Lys Arg Asn Ala Tyr Asn Gln Ala Val Ser Ala Ala Glu Thr Ile		
	3940	3945	3950
	Leu Asn Lys Gln Thr Gly Pro Asn Thr Ala Lys Thr Ala Val Glu Gln		
	3955	3960	3965
30	Ala Leu Asn Asn Val Asn Asn Ala Lys His Ala Leu Asn Gly Thr Gln		
	3970	3975	3980
	Asn Leu Asn Asn Ala Lys Gln Ala Ala Ile Thr Ala Ile Asn Gly Ala		
	3985	3990	3995
35	Ser Asp Leu Asn Gln Lys Gln Lys Asp Ala Leu Lys Ala Gln Ala Asn		
	4005	4010	4015
	Gly Ala Gln Arg Val Ser Asn Ala Gln Asp Val Gln His Asn Ala Thr		
	4020	4025	4030
40	Glu Leu Asn Thr Ala Met Gly Thr Leu Lys His Ala Ile Ala Asp Lys		
	4035	4040	4045
	Thr Asn Thr Leu Ala Ser Ser Lys Tyr Val Asn Ala Asp Ser Thr Lys		
	4050	4055	4060
45	Gln Asn Ala Tyr Thr Thr Lys Val Thr Asn Ala Glu His Ile Ile Ser		
	4065	4070	4075
	Gly Thr Pro Thr Val Val Thr Thr Pro Ser Glu Val Thr Ala Ala Ala		
	4085	4090	4095
50	Asn Gln Val Asn Ser Ala Lys Gln Glu Leu Asn Gly Asp Glu Arg Leu		
	4100	4105	4110
	Arg Glu Ala Lys Gln Asn Ala Asn Thr Ala Ile Asp Ala Leu Thr Gln		
	4115	4120	4125
	Leu Asn Thr Pro Gln Lys Ala Lys Leu Lys Glu Gln Val Gly Gln Ala		
	4130	4135	4140
55	Asn Arg Leu Glu Asp Val Gln Thr Val Gln Thr Asn Gly Gln Ala Leu		
	4145	4150	4155
			4160

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Asn Asn Ala Met Lys Gly Leu Arg Asp Ser Ile Ala Asn Glu Thr Thr
 4165 4170 4175
 5 Val Lys Thr Ser Gln Asn Tyr Thr Asp Ala Ser Pro Asn Asn Gln Ser
 4180 4185 4190
 Thr Tyr Asn Ser Ala Val Ser Asn Ala Lys Gly Ile Ile Asn Gln Thr
 4195 4200 4205
 10 Asn Asn Pro Thr Met Asp Thr Ser Ala Ile Thr Gln Ala Thr Thr Gln
 4210 4215 4220
 Val Asn Asn Ala Lys Asn Gly Leu Asn Gly Ala Glu Asn Leu Arg Asn
 4225 4230 4235 4240
 15 Ala Gln Asn Thr Ala Lys Gln Asn Leu Asn Thr Leu Ser His Leu Thr
 4245 4250 4255
 Asn Asn Gln Lys Ser Ala Ile Ser Ser Gln Ile Asp Arg Ala Gly His
 4260 4265 4270
 20 Val Ser Glu Val Thr Ala Thr Lys Asn Ala Ala Thr Glu Leu Asn Thr
 4275 4280 4285
 Gln Met Gly Asn Leu Glu Gln Ala Ile His Asp Gln Asn Thr Val Lys
 4290 4295 4300
 25 Gln Ser Val Lys Phe Thr Asp Ala Asp Lys Ala Lys Arg Asp Ala Tyr
 4305 4310 4315 4320
 Thr Asn Ala Val Ser Arg Ala Glu Ala Ile Leu Asn Lys Thr Gln Gly
 4325 4330 4335
 30 Ala Asn Thr Ser Lys Gln Asp Val Glu Ala Ala Ile Gln Asn Val Ser
 4340 4345 4350
 Ser Ala Lys Asn Ala Leu Asn Gly Asp Gln Asn Val Thr Asn Ala Lys
 4355 4360 4365
 35 Asn Ala Ala Lys Asn Ala Leu Asn Asn Leu Thr Ser Ile Asn Asn Ala
 4370 4375 4380
 Gln Lys Arg Asp Leu Thr Thr Lys Ile Asp Gln Ala Thr Thr Val Ala
 4385 4390 4395 4400
 40 Gly Val Glu Ala Val Ser Asn Thr Ser Thr Gln Leu Asn Thr Ala Met
 4405 4410 4415
 Ala Asn Leu Gln Asn Gly Ile Asn Asp Lys Thr Asn Thr Leu Ala Ser
 4420 4425 4430
 45 Glu Asn Tyr His Asp Ala Asp Ser Asp Lys Lys Thr Ala Tyr Thr Gln
 4435 4440 4445
 Ala Val Thr Asn Ala Glu Asn Ile Leu Asn Lys Asn Ser Gly Ser Asn
 4450 4455 4460
 50 Leu Asp Lys Thr Ala Val Glu Asn Ala Leu Ser Gln Val Ala Asn Ala
 4465 4470 4475 4480
 Lys Gly Ala Leu Asn Gly Asn His Asn Leu Glu Gln Ala Lys Ser Asn
 4485 4490 4495
 55 Ala Asn Thr Thr Ile Asn Gly Leu Gln His Leu Thr Thr Ala Gln Lys
 4500 4505 4510
 Asp Lys Leu Lys Gln Gln Val Gln Gln Ala Gln Asn Val Ala Gly Val
 4515 4520 4525

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Asp Thr Val Lys Ser Ser Ala Asn Thr Leu Asn Gly Ala Met Gly Thr
 4530 4535 4540
 5 Leu Arg Asn Ser Ile Gln Asp Asn Thr Ala Thr Lys Asn Gly Gln Asn
 4545 4550 4555 4560
 Tyr Leu Asp Ala Thr Glu Arg Asn Lys Thr Asn Tyr Asn Asn Ala Val
 4565 4570 4575
 10 Asp Ser Ala Asn Gly Val Ile Asn Ala Thr Ser Asn Pro Asn Met Asp
 4580 4585 4590
 Ala Asn Ala Ile Asn Gln Ile Ala Thr Gln Val Thr Ser Thr Lys Asn
 4595 4600 4605
 15 Ala Leu Asp Gly Thr His Asn Leu Thr Gln Ala Lys Gln Thr Ala Thr
 4610 4615 4620
 Asn Ala Ile Asp Gly Ala Thr Asn Leu Asn Lys Ala Gln Lys Asp Ala
 4625 4630 4635 4640
 20 Leu Lys Ala Gln Val Thr Ser Ala Gln Arg Val Ala Asn Val Thr Ser
 4645 4650 4655
 Ile Gln Gln Thr Ala Asn Glu Leu Asn Thr Ala Met Gly Gln Leu Gln
 4660 4665 4670
 His Gly Ile Asp Asp Glu Asn Ala Thr Lys Gln Thr Gln Lys Tyr Arg
 4675 4680 4685
 25 Asp Ala Glu Gln Ser Lys Lys Thr Ala Tyr Asp Gln Ala Val Ala Ala
 4690 4695 4700
 Ala Lys Ala Ile Leu Asn Lys Gln Thr Gly Ser Asn Ser Asp Lys Ala
 4705 4710 4715 4720
 30 Ala Val Asp Arg Ala Leu Gln Gln Val Thr Ser Thr Lys Asp Ala Leu
 4725 4730 4735
 Asn Gly Asp Ala Lys Leu Ala Glu Ala Lys Ala Ala Ala Lys Gln Asn
 4740 4745 4750
 35 Leu Gly Thr Leu Asn His Ile Thr Asn Ala Gln Arg Thr Asp Leu Glu
 4755 4760 4765
 Gly Gln Ile Asn Gln Ala Thr Thr Val Asp Gly Val Asn Thr Val Lys
 4770 4775 4780
 40 Thr Asn Ala Asn Thr Leu Asp Gly Ala Met Asn Ser Leu Gln Gly Ser
 4785 4790 4795 4800
 Ile Asn Asp Lys Asp Ala Thr Leu Arg Asn Gln Asn Tyr Leu Asp Ala
 4805 4810 4815
 45 Asp Glu Ser Lys Arg Asn Ala Tyr Thr Gln Ala Val Thr Ala Ala Glu
 4820 4825 4830
 Gly Ile Leu Asn Lys Gln Thr Gly Gly Asn Thr Ser Lys Ala Asp Val
 4835 4840 4845
 50 Asp Asn Ala Leu Asn Ala Val Thr Arg Ala Lys Ala Ala Leu Asn Gly
 4850 4855 4860
 Ala Asp Asn Leu Arg Asn Ala Lys Thr Ser Ala Thr Asn Thr Ile Asp
 4865 4870 4875 4880
 55 Gly Leu Pro Asn Leu Thr Gln Leu Gln Lys Asp Asn Leu Lys His Gln
 4885 4890 4895
 Val Glu Gln Ala Gln Asn Val Ala Gly Val Asn Gly Val Lys Asp Lys

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	4900	4905	4910
	Gly Asn Thr Leu Asn Thr Ala Met Gly Ala Leu Arg Thr Ser Ile Gln		
	4915	4920	4925
5	Asn Asp Asn Thr Thr Lys Thr Ser Gln Asn Tyr Leu Asp Ala Ser Asp		
	4930	4935	4940
	Ser Asn Lys Asn Asn Tyr Asn Thr Ala Val Asn Asn Ala Asn Gly Val		
	4945	4950	4955 4960
10	Ile Asn Ala Thr Asn Asn Pro Asn Met Asp Ala Asn Ala Ile Asn Gly		
	4965	4970	4975
	Met Ala Asn Gln Val Asn Thr Thr Lys Ala Ala Leu Asn Gly Ala Gln		
	4980	4985	4990
15	Asn Leu Ala Gln Ala Lys Thr Asn Ala Thr Asn Thr Ile Asn Asn Ala		
	4995	5000	5005
	His Asp Leu Asn Gln Lys Gln Lys Asp Ala Leu Lys Thr Gln Val Asn		
	5010	5015	5020
20	Asn Ala Gln Arg Val Ser Asp Ala Asn Asn Val Gln His Thr Ala Thr		
	5025	5030	5035 5040
	Glu Leu Asn Ser Ala Met Thr Ala Leu Lys Ala Ala Ile Ala Asp Lys		
	5045	5050	5055
25	Glu Arg Thr Lys Ala Ser Gly Asn Tyr Val Asn Ala Asp Gln Glu Lys		
	5060	5065	5070
	Arg Gln Ala Tyr Asp Ser Lys Val Thr Asn Ala Glu Asn Ile Ile Ser		
	5075	5080	5085
30	Gly Thr Pro Asn Ala Thr Leu Thr Val Asn Asp Val Asn Ser Ala Ala		
	5090	5095	5100
	Ser Gln Val Asn Ala Ala Lys Thr Ala Leu Asn Gly Asp Asn Asn Leu		
	5105	5110	5115 5120
35	Arg Val Ala Lys Glu His Ala Asn Asn Thr Ile Asp Gly Leu Ala Gln		
	5125	5130	5135
	Leu Asn Asn Ala Gln Lys Ala Lys Leu Lys Glu Gln Val Gln Ser Ala		
	5140	5145	5150
40	Thr Thr Leu Asp Gly Val Gln Thr Val Lys Asn Ser Ser Gln Thr Leu		
	5155	5160	5165
	Asn Thr Ala Met Lys Gly Leu Arg Asp Ser Ile Ala Asn Glu Ala Thr		
	5170	5175	5180
45	Ile Lys Ala Gly Gln Asn Tyr Thr Asp Ala Ser Pro Asn Asn Arg Asn		
	5185	5190	5195 5200
	Glu Tyr Asp Ser Ala Val Thr Ala Ala Lys Ala Ile Ile Asn Gln Thr		
	5205	5210	5215
50	Ser Asn Pro Thr Met Glu Pro Asn Thr Ile Thr Gln Val Thr Ser Gln		
	5220	5225	5230
	Val Thr Thr Lys Glu Gln Ala Leu Asn Gly Ala Arg Asn Leu Ala Gln		
	5235	5240	5245
	Ala Lys Thr Thr Ala Lys Asn Asn Leu Asn Asn Leu Thr Ser Ile Asn		
	5250	5255	5260
55	Asn Ala Gln Lys Asp Ala Leu Thr Arg Ser Ile Asp Gly Ala Thr Thr		
	5265	5270	5275 5280

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Val Ala Gly Val Asn Gln Glu Thr Ala Lys Ala Thr Glu Leu Asn Asn
5285 5290 5295

Ala Met His Ser Leu Gln Asn Gly Ile Asn Asp Glu Thr Gln Thr Lys
5300 5305 5310

Gln Thr Gln Lys Tyr Leu Asp Ala Glu Pro Ser Lys Lys Ser Ala Tyr
5315 5320 5325

Asp Gln Ala Val Asn Ala Ala Lys Ala Ile Leu Thr Lys Ala Ser Gly
5330 5335 5340

Gln Asn Val Asp Lys Ala Ala Val Glu Gln Ala Leu Gln Asn Val Asn
5345 5350 5355 5360

Ser Thr Lys Thr Ala Leu Asn Gly Asp Ala Lys Leu Asn Glu Ala Lys
5365 5370 5375

Ala Ala Ala Lys Gln Thr Leu Gly Thr Leu Thr His Ile Asn Asn Ala
5380 5385 5390

Gln Arg Thr Ala Leu Asp Asn Glu Ile Thr Gln Ala Thr Asn Val Glu
5395 5400 5405

Gly Val Asn Thr Val Lys Ala Lys Ala Gln Gln Leu Asp Gly Ala Met
5410 5415 5420

Gly Gln Leu Glu Thr Ser Ile Arg Asp Lys Asp Thr Thr Leu Gln Ser
5425 5430 5435 5440

Gln Asn Tyr Gln Asp Ala Asp Asp Ala Lys Arg Thr Ala Tyr Ser Gln
5445 5450 5455

Ala Val Asn Ala Ala Ala Thr Ile Leu Asn Lys Thr Ala Gly Gly Asn
5460 5465 5470

Thr Pro Lys Ala Asp Val Glu Arg Ala Met Gln Ala Val Thr Gln Ala
5475 5480 5485

Asn Thr Ala Leu Asn Gly Ile Gln Asn Leu Asp Arg Ala Lys Gln Ala
5490 5495 5500

Ala Asn Thr Ala Ile Thr Asn Ala Ser Asp Leu Asn Thr Lys Gln Lys
5505 5510 5515 5520

Glu Ala Leu Lys Ala Gln Val Thr Ser Ala Gly Arg Val Ser Ala Ala
5525 5530 5535

Asn Gly Val Glu His Thr Ala Thr Glu Leu Asn Thr Ala Met Thr Ala
5540 5545 5550

Leu Lys Arg Ala Ile Ala Asp Lys Ala Glu Thr Lys Ala Ser Gly Asn
5555 5560 5565

Tyr Val Asn Ala Asp Ala Asn Lys Arg Gln Ala Tyr Asp Glu Lys Val
5570 5575 5580

Thr Ala Ala Glu Asn Ile Val Ser Gly Thr Pro Thr Pro Thr Leu Thr
5585 5590 5595 5600

Pro Ala Asp Val Thr Asn Ala Ala Thr Gln Val Thr Asn Ala Lys Thr
5605 5610 5615

Gln Leu Asn Gly Asn His Asn Leu Glu Val Ala Lys Gln Asn Ala Asn
5620 5625 5630

Thr Ala Ile Asp Gly Leu Thr Ser Leu Asn Gly Pro Gln Lys Ala Lys
5635 5640 5645

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Leu Lys Glu Gln Val Gly Gln Ala Thr Thr Leu Pro Asn Val Gln Thr
 5650 5655 5660
 Val Arg Asp Asn Ala Gln Thr Leu Asn Thr Ala Met Lys Gly Leu Arg
 5665 5670 5675 5680
 Asp Ser Ile Ala Asn Glu Ala Thr Ile Lys Ala Gly Gln Asn Tyr Thr
 5685 5690 5695
 Asp Ala Ser Gln Asn Lys Gln Thr Asp Tyr Asn Ser Ala Val Thr Ala
 5700 5705 5710
 Ala Lys Ala Ile Ile Gly Gln Thr Thr Ser Pro Ser Met Asn Ala Gln
 5715 5720 5725
 Glu Ile Asn Gln Ala Lys Asp Gln Val Thr Ala Lys Gln Gln Ala Leu
 5730 5735 5740
 Asn Gly Gln Glu Asn Leu Arg Thr Ala Gln Thr Asn Ala Lys Gln His
 5745 5750 5755 5760
 Leu Asn Gly Leu Ser Asp Leu Thr Asp Ala Gln Lys Asp Ala Val Lys
 5765 5770 5775
 Arg Gln Ile Glu Gly Ala Thr His Val Asn Glu Val Thr Gln Ala Gln
 5780 5785 5790
 Asn Asn Ala Asp Ala Leu Asn Thr Ala Met Thr Asn Leu Lys Asn Gly
 5795 5800 5805
 Ile Gln Asp Gln Asn Thr Ile Lys Gln Gly Val Asn Phe Thr Asp Ala
 5810 5815 5820
 Asp Glu Ala Lys Arg Asn Ala Tyr Thr Asn Ala Val Thr Gln Ala Glu
 5825 5830 5835 5840
 Gln Ile Leu Asn Lys Ala Gln Gly Pro Asn Thr Ser Lys Asp Gly Val
 5845 5850 5855
 Glu Thr Ala Leu Glu Asn Val Gln Arg Ala Lys Asn Glu Leu Asn Gly
 5860 5865 5870
 Asn Gln Asn Val Ala Asn Ala Lys Thr Thr Ala Lys Asn Ala Leu Asn
 5875 5880 5885
 Asn Leu Thr Ser Ile Asn Asn Ala Gln Lys Glu Ala Leu Lys Ser Gln
 5890 5895 5900
 Ile Glu Gly Ala Thr Thr Val Ala Gly Val Asn Gln Val Ser Thr Thr
 5905 5910 5915 5920
 Ala Ser Glu Leu Asn Thr Ala Met Ser Asn Leu Gln Asn Gly Ile Asn
 5925 5930 5935
 Asp Glu Ala Ala Thr Lys Ala Ala Leu Asn Gly Thr Gln Asn Leu Glu
 5940 5945 5950
 Lys Ala Lys Gln His Ala Asn Thr Ala Ile Asp Gly Leu Ser His Leu
 5955 5960 5965
 Thr Asn Ala Gln Lys Glu Ala Leu Lys Gln Leu Val Gln Gln Ser Thr
 5970 5975 5980
 Thr Val Ala Glu Ala Gln Gly Asn Glu Gln Lys Ala Asn Asn Val Asp
 5985 5990 5995 6000
 Ala Ala Met Asp Lys Leu Arg Gln Ser Ile Ala Asp Asn Ala Thr Thr
 6005 6010 6015
 Lys Gln Asn Gln Asn Tyr Thr Asp Ala Ser Gln Asn Lys Lys Asp Ala

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	6020	6025	6030
	Tyr Asn Asn Ala Val Thr Thr	Ala Gln Gly Ile Ile	Asp Gln Thr Thr
5	6035	6040	6045
	Ser Pro Thr Leu Asp Pro Thr Val Ile Asn Gln Ala Ala Gly Gln Val		
	6050	6055	6060
	Ser Thr Thr Lys Asn Ala Leu Asn Gly Asn Glu Asn Leu Glu Ala Ala		
	6065	6070	6075 6080
10	Lys Gln Gln Ala Ser Gln Ser Leu Gly Ser Leu Asp Asn Leu Asn Asn		
	6085	6090	6095
	Ala Gln Lys Gln Thr Val Thr Asp Gln Ile Asn Gly Ala His Thr Val		
	6100	6105	6110
15	Asp Glu Ala Asn Gln Ile Lys Gln Asn Ala Gln Asn Leu Asn Thr Ala		
	6115	6120	6125
	Met Gly Asn Leu Lys Gln Ala Ile Ala Asp Lys Asp Ala Thr Lys Ala		
	6130	6135	6140
20	Thr Val Asn Phe Thr Asp Ala Asp Gln Ala Lys Gln Gln Ala Tyr Asn		
	6145	6150	6155 6160
	Thr Ala Val Thr Asn Ala Glu Asn Ile Ile Ser Lys Ala Asn Gly Gly		
	6165	6170	6175
25	Asn Ala Thr Gln Ala Glu Val Glu Gln Ala Ile Lys Gln Val Asn Ala		
	6180	6185	6190
	Ala Lys Gln Ala Leu Asn Gly Asn Ala Asn Val Gln His Ala Lys Asp		
	6195	6200	6205
30	Glu Ala Thr Ala Leu Ile Asn Ser Ser Asn Asp Leu Asn Gln Ala Gln		
	6210	6215	6220
	Lys Asp Ala Leu Lys Gln Gln Val Gln Asn Ala Thr Thr Val Ala Gly		
	6225	6230	6235 6240
35	Val Asn Asn Val Lys Gln Thr Ala Gln Glu Leu Asn Asn Ala Met Thr		
	6245	6250	6255
	Gln Leu Lys Gln Gly Ile Ala Asp Lys Glu Gln Thr Lys Ala Asp Gly		
	6260	6265	6270
40	Asn Phe Val Asn Ala Asp Pro Asp Lys Gln Asn Ala Tyr Asn Gln Ala		
	6275	6280	6285
	Val Ala Lys Ala Glu Ala Leu Ile Ser Ala Thr Pro Asp Val Val Val		
	6290	6295	6300
45	Thr Pro Ser Glu Ile Thr Ala Ala Leu Asn Lys Val Thr Gln Ala Lys		
	6305	6310	6315 6320
	Asn Asp Leu Asn Gly Asn Thr Asn Leu Ala Thr Ala Lys Gln Asn Val		
	6325	6330	6335
50	Gln His Ala Ile Asp Gln Leu Pro Asn Leu Asn Gln Ala Gln Arg Asp		
	6340	6345	6350
	Glu Tyr Ser Lys Gln Ile Thr Gln Ala Thr Leu Val Pro Asn Val Asn		
	6355	6360	6365
55	Ala Ile Gln Gln Ala Ala Thr Thr Leu Asn Asp Ala Met Thr Gln Leu		
	6370	6375	6380
	Lys Gln Gly Ile Ala Asn Lys Ala Gln Ile Lys Gly Ser Glu Asn Tyr		
	6385	6390	6395 6400

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His Asp Ala Asp Thr Asp Lys Gln Thr Ala Tyr Asp Asn Ala Val Thr
 6405 6410 6415
 5 Lys Ala Glu Glu Leu Leu Lys Gln Thr Thr Asn Pro Thr Met Asp Pro
 6420 6425 6430
 Asn Thr Ile Gln Gln Ala Leu Thr Lys Val Asn Asp Thr Asn Gln Ala
 6435 6440 6445
 10 Leu Asn Gly Asn Gln Lys Leu Ala Asp Ala Lys Gln Asp Ala Lys Thr
 6450 6455 6460
 Thr Leu Gly Thr Leu Asp His Leu Asn Asp Ala Gln Lys Gln Ala Leu
 6465 6470 6475 6480
 15 Thr Thr Gln Val Glu Gln Ala Pro Asp Ile Ala Thr Val Asn Asn Val
 6485 6490 6495
 Lys Gln Asn Ala Gln Asn Leu Asn Asn Ala Met Thr Asn Leu Asn Asn
 6500 6505 6510
 20 Ala Leu Gln Asp Lys Thr Glu Thr Leu Asn Ser Ile Asn Phe Thr Asp
 6515 6520 6525
 Ala Asp Gln Ala Lys Lys Asp Ala Tyr Thr Asn Ala Val Ser His Ala
 6530 6535 6540
 25 Glu Gly Ile Leu Ser Lys Ala Asn Gly Ser Asn Ala Ser Gln Thr Glu
 6545 6550 6555 6560
 Val Glu Gln Ala Met Gln Arg Val Asn Glu Ala Lys Gln Ala Leu Asn
 6565 6570 6575
 30 Gly Asn Asp Asn Val Gln Arg Ala Lys Asp Ala Ala Lys Gln Val Ile
 6580 6585 6590
 Thr Asn Ala Asn Asp Leu Asn Gln Ala Met Thr Gln Leu Lys Gln Gly
 6595 6600 6605
 35 Ile Ala Asp Lys Asp Gln Thr Lys Ala Asn Gly Asn Phe Val Asn Ala
 6610 6615 6620
 Asp Thr Asp Lys Gln Asn Ala Tyr Asn Asn Ala Val Ala His Ala Glu
 6625 6630 6635 6640
 40 Gln Ile Ile Ser Gly Thr Pro Asn Ala Asn Val Asp Pro Gln Gln Val
 6645 6650 6655
 Ala Gln Ala Leu Gln Gln Val Asn Gln Ala Lys Gly Asp Leu Asn Gly
 6660 6665 6670
 Asn His Asn Leu Gln Val Ala Lys Asp Asn Ala Asn Thr Ala Ile Asp
 6675 6680 6685
 45 Gln Leu Pro Asn Leu Asn Gln Pro Gln Lys Thr Ala Leu Lys Asp Gln
 6690 6695 6700
 Val Ser His Ala Glu Leu Val Thr Gly Val Asn Ala Ile Lys Gln Asn
 6705 6710 6715 6720
 50 Ala Asp Ala Leu Asn Asn Ala Met Gly Thr Leu Lys Gln Gln Ile Gln
 6725 6730 6735
 Ala Asn Ser Gln Val Pro Gln Ser Val Asp Phe Thr Gln Ala Asp Gln
 6740 6745 6750
 55 Asp Lys Gln Gln Ala Tyr Asn Asn Ala Ala Asn Gln Ala Gln Gln Ile
 6755 6760 6765

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Ala Asn Gly Ile Pro Thr Pro Val Leu Thr Pro Asp Thr Val Thr Gln
6770 6775 6780

Ala Val Thr Thr Met Asn Gln Ala Lys Asp Ala Leu Asn Gly Asp Glu
5 6785 6790 6795 6800

Lys Leu Ala Gln Ala Lys Gln Glu Ala Leu Ala Asn Leu Asp Thr Leu
6805 6810 6815

Arg Asp Leu Asn Gln Pro Gln Arg Asp Ala Leu Arg Asn Gln Ile Asn
10 6820 6825 6830

Gln Ala Gln Ala Leu Ala Thr Val Glu Gln Thr Lys Gln Asn Ala Gln
6835 6840 6845

Asn Val Asn Thr Ala Met Ser Asn Leu Lys Gln Gly Ile Ala Asn Lys
15 6850 6855 6860

Asp Thr Val Lys Ala Ser Glu Asn Tyr His Asp Ala Asp Ala Asp Lys
6865 6870 6875 6880

Gln Thr Ala Tyr Thr Asn Ala Val Ser Gln Ala Glu Gly Ile Ile Asn
20 6885 6890 6895

Gln Thr Thr Asn Pro Thr Leu Asn Pro Asp Glu Ile Thr Arg Ala Leu
6900 6905 6910

Thr Gln Val Thr Asp Ala Lys Asn Gly Leu Asn Gly Glu Ala Lys Leu
25 6915 6920 6925

Ala Thr Glu Lys Gln Asn Ala Lys Asp Ala Val Ser Gly Met Thr His
6930 6935 6940

Leu Asn Asp Ala Gln Lys Gln Ala Leu Lys Gly Gln Ile Asp Gln Ser
30 6945 6950 6955 6960

Pro Glu Ile Ala Thr Val Asn Gln Val Lys Gln Thr Ala Thr Ser Leu
6965 6970 6975

Asp Gln Ala Met Asp Gln Leu Ser Gln Ala Ile Asn Asp Lys Ala Gln
6980 6985 6990

Thr Leu Ala Asp Gly Asn Tyr Leu Asn Ala Asp Pro Asp Lys Gln Asn
35 6995 7000 7005

Ala Tyr Lys Gln Ala Val Ala Lys Ala Glu Ala Leu Leu Asn Lys Gln
7010 7015 7020

Ser Gly Thr Asn Glu Val Gln Ala Gln Val Glu Ser Ile Thr Asn Glu
40 7025 7030 7035 7040

Val Asn Ala Ala Lys Gln Ala Leu Asn Gly Asn Asp Asn Leu Ala Asn
7045 7050 7055

Ala Lys Gln Gln Ala Lys Gln Gln Leu Ala Asn Leu Thr His Leu Asn
45 7060 7065 7070

Asp Ala Gln Lys Gln Ser Phe Glu Ser Gln Ile Thr Gln Ala Pro Leu
7075 7080 7085

Val Thr Asp Val Thr Thr Ile Asn Gln Lys Ala Gln Thr Leu Asp His
50 7090 7095 7100

Ala Met Glu Leu Leu Arg Asn Ser Val Ala Asp Asn Gln Thr Thr Leu
7105 7110 7115 7120

Ala Ser Glu Asp Tyr His Asp Ala Thr Ala Gln Arg Gln Asn Asp Tyr
55 7125 7130 7135

Asn Gln Ala Val Thr Ala Ala Asn Asn Ile Ile Asn Gln Thr Thr Ser

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	7140	7145	7150
	Pro Thr Met Asn Pro Asp Asp Val Asn Gly Ala Thr Thr Gln Val Asn		
	7155	7160	7165
5	Asn Thr Lys Val Ala Leu Asp Gly Asp Glu Asn Leu Ala Ala Ala Lys		
	7170	7175	7180
	Gln Gln Ala Asn Asn Arg Leu Asp Gln Leu Asp His Leu Asn Asn Ala		
	7185	7190	7195
10	Gln Lys Gln Gln Leu Gln Ser Gln Ile Thr Gln Ser Ser Asp Ile Ala		
	7205	7210	7215
	Ala Val Asn Gly His Lys Gln Thr Ala Glu Ser Leu Asn Thr Ala Met		
	7220	7225	7230
15	Gly Asn Leu Ile Asn Ala Ile Ala Asp His Gln Ala Val Glu Gln Arg		
	7235	7240	7245
	Gly Asn Phe Ile Asn Ala Asp Thr Asp Lys Gln Thr Ala Tyr Asn Thr		
	7250	7255	7260
20	Ala Val Asn Glu Ala Ala Ala Met Ile Asn Lys Gln Thr Gly Gln Asn		
	7265	7270	7275
	Ala Asn Gln Thr Glu Val Glu Gln Ala Ile Thr Lys Val Gln Thr Thr		
	7285	7290	7295
25	Leu Gln Ala Leu Asn Gly Asp His Asn Leu Gln Val Ala Lys Thr Asn		
	7300	7305	7310
	Ala Thr Gln Ala Ile Asp Ala Leu Thr Ser Leu Asn Asp Pro Gln Lys		
	7315	7320	7325
30	Thr Ala Leu Lys Asp Gln Val Thr Ala Ala Thr Leu Val Thr Ala Val		
	7330	7335	7340
	His Gln Ile Glu Gln Asn Ala Asn Thr Leu Asn Gln Ala Met His Gly		
	7345	7350	7355
35	Leu Arg Gln Ser Ile Gln Asp Asn Ala Ala Thr Lys Ala Asn Ser Lys		
	7365	7370	7375
	Tyr Ile Asn Glu Asp Gln Pro Glu Gln Gln Asn Tyr Asp Gln Ala Val		
	7380	7385	7390
40	Gln Ala Ala Asn Asn Ile Ile Asn Glu Gln Thr Ala Thr Leu Asp Asn		
	7395	7400	7405
	Asn Ala Ile Asn Gln Ala Ala Thr Thr Val Asn Thr Thr Lys Ala Ala		
	7410	7415	7420
45	Leu His Gly Asp Val Lys Leu Gln Asn Asp Lys Asp His Ala Lys Gln		
	7425	7430	7435
	Thr Val Ser Gln Leu Ala His Leu Asn Asn Ala Gln Lys His Met Glu		
	7445	7450	7455
50	Asp Thr Leu Ile Asp Ser Glu Thr Thr Arg Thr Ala Val Lys Gln Asp		
	7460	7465	7470
	Leu Thr Glu Ala Gln Ala Leu Asp Gln Leu Met Asp Ala Leu Gln Gln		
	7475	7480	7485
55	Ser Ile Ala Asp Lys Asp Ala Thr Arg Ala Ser Ser Ala Tyr Val Asn		
	7490	7495	7500
	Ala Glu Pro Asn Lys Lys Gln Ser Tyr Asp Glu Ala Val Gln Asn Ala		
	7505	7510	7515
			7520

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Glu Ser Ile Ile Ala Gly Leu Asn Asn Pro Thr Ile Asn Lys Gly Asn
 7525 7530 7535
 5 Val Ser Ser Ala Thr Gln Ala Val Ile Ser Ser Lys Asn Ala Leu Asp
 7540 7545 7550
 Gly Val Glu Arg Leu Ala Gln Asp Lys Gln Thr Ala Gly Asn Ser Leu
 7555 7560 7565
 10 Asn His Leu Asp Gln Leu Thr Pro Ala Gln Gln Gln Ala Leu Glu Asn
 7570 7575 7580
 Gln Ile Asn Asn Ala Thr Thr Arg Asp Lys Val Ala Glu Ile Ile Ala
 7585 7590 7595 7600
 15 Gln Ala Gln Ala Leu Asn Glu Ala Met Lys Ala Leu Lys Glu Ser Ile
 7605 7610 7615
 Lys Asp Gln Pro Gln Thr Glu Ala Ser Ser Lys Phe Ile Asn Glu Asp
 7620 7625 7630
 20 Gln Ala Gln Lys Asp Ala Tyr Thr Gln Ala Val Gln His Ala Lys Asp
 7635 7640 7645
 Leu Ile Asn Lys Thr Thr Asp Pro Thr Leu Ala Lys Ser Ile Ile Asp
 7650 7655 7660
 25 Gln Ala Thr Gln Ala Val Thr Asp Ala Lys Asn Asn Leu His Gly Asp
 7665 7670 7675 7680
 Gln Lys Leu Ala Gln Asp Lys Gln Arg Ala Thr Glu Thr Leu Asn Asn
 7685 7690 7695
 30 Leu Ser Asn Leu Asn Thr Pro Gln Arg Gln Ala Leu Glu Asn Gln Ile
 7700 7705 7710
 Asn Asn Ala Ala Thr Arg Gly Glu Val Ala Gln Lys Leu Thr Glu Ala
 7715 7720 7725
 35 Gln Ala Leu Asn Gln Ala Met Glu Ala Leu Arg Asn Ser Ile Gln Asp
 7730 7735 7740
 Gln Gln Gln Thr Glu Ala Gly Ser Lys Phe Ile Asn Glu Asp Lys Pro
 7745 7750 7755 7760
 40 Gln Lys Asp Ala Tyr Gln Ala Ala Val Gln Asn Ala Lys Asp Leu Ile
 7765 7770 7775
 Asn Gln Thr Asn Asn Pro Thr Leu Asp Lys Ala Gln Val Glu Gln Leu
 7780 7785 7790
 45 Thr Gln Ala Val Asn Gln Ala Lys Asp Asn Leu His Gly Asp Gln Lys
 7795 7800 7805
 Leu Ala Asp Asp Lys Gln His Ala Val Thr Asp Leu Asn Gln Leu Asn
 7810 7815 7820
 50 Gly Leu Asn Asn Pro Gln Arg Gln Ala Leu Glu Ser Gln Ile Asn Asn
 7825 7830 7835 7840
 Ala Ala Thr Arg Gly Glu Val Ala Gln Lys Leu Ala Glu Ala Lys Ala
 7845 7850 7855
 55 Leu Asp Gln Ala Met Gln Ala Leu Arg Asn Ser Ile Gln Asp Gln Gln
 7860 7865 7870
 Gln Thr Glu Ser Gly Ser Lys Phe Ile Asn Glu Asp Lys Pro Gln Lys
 7875 7880 7885

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Asp Ala Tyr Gln Ala Ala Val Gln Asn Ala Lys Asp Leu Ile Asn Gln
 7890 7895 7900
 5 Thr Gly Asn Pro Thr Leu Asp Lys Ser Gln Val Glu Gln Leu Thr Gln
 7905 7910 7915 7920
 Ala Val Thr Thr Ala Lys Asp Asn Leu His Gly Asp Gln Lys Leu Ala
 7925 7930 7935
 10 Arg Asp Gln Gln Gln Ala Val Thr Thr Val Asn Ala Leu Pro Asn Leu
 7940 7945 7950
 Asn His Ala Gln Gln Gln Ala Leu Thr Asp Ala Ile Asn Ala Ala Pro
 7955 7960 7965
 15 Thr Arg Thr Glu Val Ala Gln His Val Gln Thr Ala Thr Glu Leu Asp
 7970 7975 7980
 His Ala Met Glu Thr Leu Lys Asn Lys Val Asp Gln Val Asn Thr Asp
 7985 7990 7995 8000
 20 Lys Ala Gln Pro Asn Tyr Thr Glu Ala Ser Thr Asp Lys Lys Glu Ala
 8005 8010 8015
 Val Asp Gln Ala Leu Gln Ala Ala Glu Ser Ile Thr Asp Pro Thr Asn
 8020 8025 8030
 25 Gly Ser Asn Ala Asn Lys Asp Ala Val Asp Gln Val Leu Thr Lys Leu
 8035 8040 8045
 Gln Glu Lys Glu Asn Glu Leu Asn Gly Asn Glu Arg Val Ala Glu Ala
 8050 8055 8060
 30 Lys Thr Gln Ala Lys Gln Thr Ile Asp Gln Leu Thr His Leu Asn Ala
 8065 8070 8075 8080
 Asp Gln Ile Ala Thr Ala Lys Gln Asn Ile Asp Gln Ala Thr Lys Leu
 8085 8090 8095
 Gln Pro Ile Ala Glu Leu Val Asp Gln Ala Thr Gln Leu Asn Gln Ser
 8100 8105 8110
 35 Met Asp Gln Leu Gln Gln Ala Val Asn Glu His Ala Asn Val Glu Gln
 8115 8120 8125
 Thr Val Asp Tyr Thr Gln Ala Asp Ser Asp Lys Gln Asn Ala Tyr Lys
 8130 8135 8140
 40 Gln Ala Ile Ala Asp Ala Glu Asn Val Leu Lys Gln Asn Ala Asn Lys
 8145 8150 8155 8160
 Gln Gln Val Asp Gln Ala Leu Gln Asn Ile Leu Asn Ala Lys Gln Ala
 8165 8170 8175
 45 Leu Asn Gly Asp Glu Arg Val Ala Leu Ala Lys Thr Asn Gly Lys His
 8180 8185 8190
 Asp Ile Asp Gln Leu Asn Ala Leu Asn Asn Ala Gln Gln Asp Gly Phe
 8195 8200 8205
 50 Lys Gly Arg Ile Asp Gln Ser Asn Asp Leu Asn Gln Ile Gln Gln Ile
 8210 8215 8220
 Val Asp Glu Ala Lys Ala Leu Asn Arg Ala Met Asp Gln Leu Ser Gln
 8225 8230 8235 8240
 55 Glu Ile Thr Asp Asn Glu Gly Arg Thr Lys Gly Ser Thr Asn Tyr Val
 8245 8250 8255
 Asn Ala Asp Thr Gln Val Lys Gln Val Tyr Asp Glu Thr Val Asp Lys

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	8260	8265	8270
	Ala Lys Gln Ala Leu Asp Lys Ser Thr Gly Gln Asn Leu Thr Ala Lys		
	8275	8280	8285
5	Gln Val Ile Lys Leu Asn Asp Ala Val Thr Ala Ala Lys Lys Ala Leu		
	8290	8295	8300
	Asn Gly Glu Glu Arg Leu Asn Asn Arg Lys Ala Glu Ala Leu Gln Arg		
	8305	8310	8315 8320
10	Leu Asp Gln Leu Thr His Leu Asn Asn Ala Gln Arg Gln Leu Ala Ile		
	8325	8330	8335
	Gln Gln Ile Asn Asn Ala Glu Thr Leu Asn Lys Ala Ser Arg Ala Ile		
	8340	8345	8350
15	Asn Arg Ala Thr Lys Leu Asp Asn Ala Met Gly Ser Val Gln Gln Tyr		
	8355	8360	8365
	Ile Asp Glu Gln His Leu Gly Val Ile Ser Ser Thr Asn Tyr Ile Asn		
	8370	8375	8380
20	Ala Asp Asp Asn Leu Lys Ala Asn Tyr Asp Asn Ala Ile Ala Asn Ala		
	8385	8390	8395 8400
	Ala His Glu Leu Asp Lys Val Gln Gly Asn Ala Ile Ala Lys Ala Glu		
	8405	8410	8415
25	Ala Glu Gln Leu Lys Gln Asn Ile Ile Asp Ala Gln Asn Ala Leu Asn		
	8420	8425	8430
	Gly Asp Gln Asn Leu Ala Asn Ala Lys Asp Lys Ala Asn Ala Phe Val		
	8435	8440	8445
30	Asn Ser Leu Asn Gly Leu Asn Gln Gln Gln Gln Asp Leu Ala His Lys		
	8450	8455	8460
	Ala Ile Asn Asn Ala Asp Thr Val Ser Asp Val Thr Asp Ile Val Asn		
	8465	8470	8475 8480
35	Asn Gln Ile Asp Leu Asn Asp Ala Met Glu Thr Leu Lys His Leu Val		
	8485	8490	8495
	Asp Asn Glu Ile Pro Asn Ala Glu Gln Thr Val Asn Tyr Gln Asn Ala		
	8500	8505	8510
40	Asp Asp Asn Ala Lys Thr Asn Phe Asp Asp Ala Lys Arg Leu Ala Asn		
	8515	8520	8525
	Thr Leu Leu Asn Ser Asp Asn Thr Asn Val Asn Asp Ile Asn Gly Ala		
	8530	8535	8540
45	Ile Gln Ala Val Asn Asp Ala Ile His Asn Leu Asn Gly Asp Gln Arg		
	8545	8550	8555 8560
	Leu Gln Asp Ala Lys Asp Lys Ala Ile Gln Ser Ile Asn Gln Ala Leu		
	8565	8570	8575
50	Ala Asn Lys Leu Lys Glu Ile Glu Ala Ser Asn Ala Thr Asp Gln Asp		
	8580	8585	8590
	Lys Leu Ile Ala Lys Asn Lys Ala Glu Glu Leu Ala Asn Ser Ile Ile		
	8595	8600	8605
55	Asn Asn Ile Asn Lys Ala Thr Ser Asn Gln Ala Val Ser Gln Val Gln		
	8610	8615	8620
	Thr Ala Gly Asn His Ala Ile Glu Gln Val His Ala Asn Glu Ile Pro		
	8625	8630	8635 8640

Lys Ala Lys Ile Asp Ala Asn Lys Asp Val Asp Lys Gln Val Gln Ala
 8645 8650 8655
 5 Leu Ile Asp Glu Ile Asp Arg Asn Pro Asn Leu Thr Asp Lys Glu Lys
 8660 8665 8670
 Gln Ala Leu Lys Asp Arg Ile Asn Gln Ile Leu Gln Gln Gly His Asn
 8675 8680 8685
 10 Gly Ile Asn Asn Ala Met Thr Lys Glu Glu Ile Glu Gln Ala Lys Ala
 8690 8695 8700
 Gln Leu Ala Gln Ala Leu Gln Asp Ile Lys Asp Leu Val Lys Ala Lys
 8705 8710 8715 8720
 15 Glu Asp Ala Lys Gln Asp Val Asp Lys Gln Val Gln Ala Leu Ile Asp
 8725 8730 8735
 Glu Ile Asp Gln Asn Pro Asn Leu Thr Asp Lys Glu Lys Gln Ala Leu
 8740 8745 8750
 20 Lys Asp Arg Ile Asn Gln Ile Leu Gln Gln Gly His Asn Asp Ile Asn
 8755 8760 8765
 Asn Ala Met Thr Lys Glu Ala Ile Glu Gln Ala Lys Glu Arg Leu Ala
 8770 8775 8780
 25 Gln Ala Leu Gln Asp Ile Lys Asp Leu Val Lys Ala Lys Glu Asp Ala
 8785 8790 8795 8800
 Lys Asn Asp Ile Asp Lys Arg Val Gln Ala Leu Ile Asp Glu Ile Asp
 8805 8810 8815
 30 Gln Asn Pro Asn Leu Thr Asp Lys Glu Lys Gln Ala Leu Lys Asp Arg
 8820 8825 8830
 Ile Asn Gln Ile Leu Gln Gln Gly His Asn Asp Ile Asn Asn Ala Leu
 8835 8840 8845
 35 Thr Lys Glu Glu Ile Glu Gln Ala Lys Ala Gln Leu Ala Gln Ala Leu
 8850 8855 8860
 Gln Asp Ile Lys Asp Leu Val Lys Ala Lys Glu Asp Ala Lys Asn Ala
 8865 8870 8875 8880
 40 Ile Lys Ala Leu Ala Asn Ala Lys Arg Asp Gln Ile Asn Ser Asn Pro
 8885 8890 8895
 Asp Leu Thr Pro Glu Gln Lys Ala Lys Ala Leu Lys Glu Ile Asp Glu
 8900 8905 8910
 45 Ala Glu Lys Arg Ala Leu Gln Asn Val Glu Asn Ala Gln Thr Ile Asp
 8915 8920 8925
 Gln Leu Asn Arg Gly Leu Asn Leu Gly Leu Asp Asp Ile Arg Asn Thr
 8930 8935 8940
 50 His Val Trp Glu Val Asp Glu Gln Pro Ala Val Asn Glu Ile Phe Glu
 8945 8950 8955 8960
 Ala Thr Pro Glu Gln Ile Leu Val Asn Gly Glu Leu Ile Val His Arg
 8965 8970 8975
 Asp Asp Ile Ile Thr Glu Gln Asp Ile Leu Ala His Ile Asn Leu Ile
 8980 8985 8990
 55 Asp Gln Leu Ser Ala Glu Val Ile Asp Thr Pro Ser Thr Ala Thr Ile
 8995 9000 9005

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Ser Asp Ser Leu Thr Ala Lys Val Glu Val Thr Leu Leu Asp Gly Ser
 9010 9015 9020
 5 Lys Val Ile Val Asn Val Pro Val Lys Val Val Glu Lys Glu Leu Ser
 9025 9030 9035 9040
 Val Val Lys Gln Gln Ala Ile Glu Ser Ile Glu Asn Ala Ala Gln Gln
 9045 9050 9055
 10 Lys Ile Asn Glu Ile Asn Asn Ser Val Thr Leu Thr Leu Glu Gln Lys
 9060 9065 9070
 Glu Ala Ala Ile Ala Glu Val Asn Lys Leu Lys Gln Gln Ala Ile Asp
 9075 9080 9085
 15 His Val Asn Asn Ala Pro Asp Val His Ser Val Glu Glu Ile Gln Gln
 9090 9095 9100
 Gln Glu Gln Ala His Ile Glu Gln Phe Asn Pro Glu Gln Phe Thr Ile
 9105 9110 9115 9120
 20 Glu Gln Ala Lys Ser Asn Ala Ile Lys Ser Ile Glu Asp Ala Ile Gln
 9125 9130 9135
 His Met Ile Asp Glu Ile Lys Ala Arg Thr Asp Leu Thr Asp Lys Glu
 9140 9145 9150
 25 Lys Gln Glu Ala Ile Ala Lys Leu Asn Gln Leu Lys Glu Gln Ala Ile
 9155 9160 9165
 Gln Ala Ile Gln Arg Ala Gln Ser Ile Asp Glu Ile Ser Glu Gln Leu
 9170 9175 9180
 30 Glu Gln Phe Lys Ala Gln Met Lys Ala Ala Asn Pro Thr Ala Lys Glu
 9185 9190 9195 9200
 Leu Ala Lys Arg Lys Gln Glu Ala Ile Ser Arg Ile Lys Asp Phe Ser
 9205 9210 9215
 35 Asn Glu Lys Ile Asn Ser Ile Arg Asn Ser Glu Ile Gly Thr Ala Asp
 9220 9225 9230
 Glu Lys Gln Ala Ala Met Asn Gln Ile Asn Glu Ile Val Leu Glu Thr
 9235 9240 9245
 40 Ile Arg Asp Ile Asn Asn Ala His Thr Leu Gln Gln Val Glu Ala Ala
 9250 9255 9260
 Leu Asn Asn Gly Ile Ala Arg Ile Ser Ala Val Gln Ile Val Thr Ser
 9265 9270 9275 9280
 Asp Arg Ala Lys Gln Ser Ser Ser Thr Gly Asn Glu Ser Asn Ser His
 9285 9290 9295
 45 Leu Thr Ile Gly Tyr Gly Thr Ala Asn His Pro Phe Asn Ser Ser Thr
 9300 9305 9310
 Ile Gly His Lys Lys Lys Leu Asp Glu Asp Asp Asp Ile Asp Pro Leu
 9315 9320 9325
 50 His Met Arg His Phe Ser Asn Asn Phe Gly Asn Val Ile Lys Asn Ala
 9330 9335 9340
 Ile Gly Val Val Gly Ile Ser Gly Leu Leu Ala Ser Phe Trp Phe Phe
 9345 9350 9355 9360
 55 Ile Ala Lys Arg Arg Arg Lys Glu Asp Glu Glu Glu Glu Leu Glu Ile
 9365 9370 9375
 Arg Asp Asn Asn Lys Asp Ser Ile Lys Glu Thr Leu Asp Asp Thr Lys

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9380 9385 9390

His Leu Pro Leu Leu Phe Ala Lys Arg Arg Arg Lys Glu Asp Glu Glu
9395 9400 9405

Asp Val Thr Val Glu Glu Lys Asp Ser Leu Asn Asn Gly Glu Ser Leu
9410 9415 9420

Asp Lys Val Lys His Thr Pro Phe Phe Leu Pro Lys Arg Arg Arg Lys
9425 9430 9435 9440

Glu Asp Glu Glu Asp Val Glu Val Thr Asn Glu Asn Thr Asp Glu Lys
9445 9450 9455

Val Leu Lys Asp Asn Glu His Ser Pro Leu Leu Phe Ala Lys Arg Arg
9460 9465 9470

Lys Asp Lys Glu Glu Asp Val Glu Thr Thr Thr Ser Ile Glu Ser Lys
9475 9480 9485

Asp Glu Asp Val Pro Leu Leu Leu Ala Lys Lys Lys Asn Gln Lys Asp
9490 9495 9500

Asn Gln Ser Lys Asp Lys Lys Ser Ala Ser Lys Asn Thr Ser Lys Lys
9505 9510 9515 9520

Val Ala Ala Lys Lys Lys Lys Lys Lys Ala Lys Lys Asn Lys Lys
9525 9530 9535

<210> 6
<211> 486
<212> PRT
<213> Staphylococcus aureus

<400> 6

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Met Ser Asn Asn Phe Lys Asp Asp Phe Glu Lys Asn Arg Gln Ser Ile
 1 5 10 15
 Asp Thr Asn Ser His Gln Asp His Thr Glu Asp Val Glu Lys Asp Gln
 5 20 25 30
 Ser Glu Leu Glu His Gln Asp Thr Ile Glu Asn Thr Glu Gln Gln Phe
 35 40 45
 Pro Pro Arg Asn Ala Gln Arg Arg Lys Arg Arg Arg Asp Leu Ala Thr
 10 50 55 60
 Asn His Asn Lys Gln Val His Asn Glu Ser Gln Thr Ser Glu Asp Asn
 65 70 75 80
 Val Gln Asn Glu Ala Gly Thr Ile Asp Asp Arg Gln Val Glu Ser Ser
 15 85 90 95
 His Ser Thr Glu Ser Gln Glu Pro Ser His Gln Asp Ser Thr Pro Gln
 100 105 110
 His Glu Glu Glu Tyr Tyr Asn Lys Asn Ala Phe Ala Met Asp Lys Ser
 115 120 125
 20 His Pro Glu Pro Ile Glu Asp Asn Asp Lys His Asp Thr Ile Lys Asn
 130 135 140
 Ala Glu Asn Asn Thr Glu His Ser Thr Val Ser Asp Lys Ser Glu Ala
 145 150 155 160
 25 Glu Gln Ser Gln Gln Pro Lys Pro Tyr Phe Thr Thr Gly Ala Asn Gln
 165 170 175
 Ser Glu Thr Ser Lys Asn Glu His Asp Asn Asp Ser Val Lys Gln Asp
 180 185 190
 30
 35
 40
 45
 50
 55

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5 Gln Asp Glu Pro Lys Glu His His Asn Gly Lys Lys Ala Ala Ala Ile
 195 200 205
 Gly Ala Gly Thr Ala Gly Val Ala Gly Ala Ala Gly Ala Met Ala Ala
 210 215 220
 Ser Lys Ala Lys Lys His Ser Asn Asp Ala Gln Asn Lys Ser Asn Ser
 225 230 235 240
 10 Gly Lys Ala Asn Asn Ser Thr Glu Asp Lys Ala Ser Gln Asp Lys Ser
 245 250 255
 Lys Asp His His Asn Gly Lys Lys Gly Ala Ala Ile Gly Ala Gly Thr
 260 265 270
 15 Ala Gly Leu Ala Gly Gly Ala Ala Ser Lys Ser Ala Ser Ala Ala Ser
 275 280 285
 Lys Pro His Ala Ser Asn Asn Ala Ser Gln Asn His Asp Glu His Asp
 290 295 300
 20 Asn His Asp Arg Asp Lys Glu Arg Lys Lys Gly Gly Met Ala Lys Val
 305 310 315 320
 Leu Leu Pro Leu Ile Ala Ala Val Leu Ile Ile Gly Ala Leu Ala Ile
 325 330 335
 25 Phe Gly Gly Met Ala Leu Asn Asn His Asn Asn Gly Thr Lys Glu Asn
 340 345 350
 Lys Ile Ala Asn Thr Asn Lys Asn Asn Ala Asp Glu Ser Lys Asp Lys
 355 360 365
 30 Asp Thr Ser Lys Asp Ala Ser Lys Asp Lys Ser Lys Ser Thr Asp Ser
 370 375 380
 Asp Lys Ser Lys Glu Asp Gln Asp Lys Ala Thr Lys Asp Glu Ser Asp
 385 390 395 400
 35 Asn Asp Gln Asn Asn Ala Asn Gln Ala Asn Asn Gln Ala Gln Asn Asn
 405 410 415
 Gln Asn Gln Gln Gln Ala Asn Gln Asn Gln Gln Gln Gln Gln Arg
 420 425 430
 40 Gln Gly Gly Gly Gln Arg His Thr Val Asn Gly Gln Glu Asn Leu Tyr
 435 440 445
 Arg Ile Ala Ile Gln Tyr Tyr Gly Ser Gly Ser Pro Glu Asn Val Glu
 450 455 460
 45 Lys Ile Arg Arg Ala Asn Gly Leu Ser Gly Asn Asn Ile Arg Asn Gly
 465 470 475 480
 Gln Gln Ile Val Ile Pro
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<210> 7

<211> 165

<212> PRT

<213> Staphylococcus aureus

<400> 7

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Met Lys Asn Lys Leu Ile Ala Lys Ser Leu Leu Thr Leu Ala Ala Ile
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Gly Ile Thr Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly
5 20 25 30
Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val
35 40 45
Glu Tyr Asn Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn
10 50 55 60
Ser Thr Pro Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu
65 70 75 80
Phe Asn Asp Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys
15 85 90 95
Pro Ala Ala Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile
100 105 110
Gln Ala Gln Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser
20 115 120 125
Ala His Arg Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr
130 135 140
Lys Val Lys Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu Lys
25 145 150 155 160
Gln Gly Leu Val Lys
165

30 <210> 8
<211> 340
<212> PRT
<213> staphylococcus aureus

35 <400> 8

40

45

50

55

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Met Lys Lys Lys Leu Leu Val Leu Thr Met Ser Thr Leu Phe Ala Thr
 1 5 10 15
 Gln Ile Met Asn Ser Asn His Ala Lys Ala Ser Val Thr Glu Ser Val
 5 20 25 30
 Asp Lys Lys Phe Val Val Pro Glu Ser Gly Ile Asn Lys Ile Ile Pro
 35 40 45
 Ala Tyr Asp Glu Phe Lys Asn Ser Pro Lys Val Asn Val Ser Asn Leu
 10 50 55 60
 Thr Asp Asn Lys Asn Phe Val Ala Ser Glu Asp Lys Leu Asn Lys Ile
 65 70 75 80
 Ala Asp Ser Ser Ala Ala Ser Lys Ile Val Asp Lys Asn Phe Val Val
 15 85 90 95
 Pro Glu Ser Lys Leu Gly Asn Ile Val Pro Glu Tyr Lys Glu Ile Asn
 100 105 110
 Asn Arg Val Asn Val Ala Thr Asn Asn Pro Ala Ser Gln Gln Val Asp
 20 115 120 125
 Lys His Phe Val Ala Lys Gly Pro Glu Val Asn Arg Phe Ile Thr Gln
 130 135 140
 Asn Lys Val Asn His His Phe Ile Thr Thr Gln Thr His Tyr Lys Lys
 25 145 150 155 160
 Val Ile Thr Ser Tyr Lys Ser Thr His Val His Lys His Val Asn His
 165 170 175
 Ala Lys Asp Ser Ile Asn Lys His Phe Ile Val Lys Pro Ser Glu Ser
 30 180 185 190
 Pro Arg Tyr Thr His Pro Ser Gln Ser Leu Ile Ile Lys His His Phe
 195 200 205
 Ala Val Pro Gly Tyr His Ala His Lys Phe Val Thr Pro Gly His Ala
 35 210 215 220
 Ser Ile Lys Ile Asn His Phe Cys Val Val Pro Gln Ile Asn Ser Phe
 225 230 235 240
 Lys Val Ile Pro Pro Tyr Gly His Asn Ser His Arg Met His Val Pro
 40 245 250 255
 Ser Phe Gln Asn Asn Thr Thr Ala Thr His Gln Asn Ala Lys Val Asn
 260 265 270
 Lys Ala Tyr Asp Tyr Lys Tyr Phe Tyr Ser Tyr Lys Val Val Lys Gly
 45 275 280 285
 Val Lys Lys Tyr Phe Ser Phe Ser Gln Ser Asn Gly Tyr Lys Ile Gly
 290 295 300
 Lys Pro Ser Leu Asn Ile Lys Asn Val Asn Tyr Gln Tyr Ala Val Pro
 50 305 310 315 320
 Ser Tyr Ser Pro Thr His Tyr Val Pro Glu Phe Lys Gly Ser Leu Pro
 325 330 335
 Ala Pro Arg Val
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<210> 9

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<211> 130
<212> PRT
<213> Staphylococcus aureus

5 <400> 9

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10 Ile Lys Lys His Ala Glu Glu Ile Ala His Glu Ile Glu Val Arg Ser
20 25 30
Gly Tyr Leu Arg Lys Ala Glu Gln Tyr Lys Arg Leu Glu Phe Asn Leu
35 40 45
15 Ser Phe Ala Leu Asp Asp Ile Glu Ser Thr Ala Lys Asp Val Gln Thr
50 55 60
Ala Lys Ser Ser Ala Asn Lys Asp Ser Val Thr Val Lys Gly Lys Ala
65 70 75 80
20 Pro Asn Thr Leu Tyr Ile Glu Lys Arg Asn Leu Met Lys Gln Lys Leu
85 90 95
Glu Met Leu Gly Glu Asp Ile Asp Lys Asn Lys Glu Ser Leu Gln Lys
100 105 110
25 Ala Lys Glu Ile Ala Gly Glu Lys Ala Ser Glu Tyr Phe Asn Lys Ala
115 120 125
Met Asn
130

30 <210> 10
<211> 97
<212> PRT
<213> Staphylococcus aureus

35 <400> 10

Met Ala Met Ile Lys Met Ser Pro Glu Glu Ile Arg Ala Lys Ser Gln
1 5 10 15
40 Ser Tyr Gly Gln Gly Ser Asp Gln Ile Arg Gln Ile Leu Ser Asp Leu
20 25 30
45 Thr Arg Ala Gln Gly Glu Ile Ala Ala Asn Trp Glu Gly Gln Ala Phe
35 40 45
Ser Arg Phe Glu Glu Gln Phe Gln Gln Leu Ser Pro Lys Val Glu Lys
50 55 60
50 Phe Ala Gln Leu Leu Glu Glu Ile Lys Gln Gln Leu Asn Ser Thr Ala
65 70 75 80
Asp Ala Val Gln Glu Gln Asp Gln Gln Leu Ser Asn Asn Phe Gly Leu
85 90 95
55 Gln

<210> 11
<211> 104

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<212> PRT

<213> Staphylococcus aureus

<400> 11

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Met Gly Gly Tyr Lys Gly Ile Lys Ala Asp Gly Gly Lys Val Asp Gln
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Ala Lys Gln Leu Ala Ala Lys Thr Ala Lys Asp Ile Glu Ala Cys Gln
10      20      25      30
Lys Gln Thr Gln Gln Leu Ala Glu Tyr Ile Glu Gly Ser Asp Trp Glu
      35      40      45
Gly Gln Phe Ala Asn Lys Val Lys Asp Val Leu Leu Ile Met Ala Lys
15      50      55      60
Phe Gln Glu Glu Leu Val Gln Pro Met Ala Asp His Gln Lys Ala Ile
65      70      75      80
Asp Asn Leu Ser Gln Asn Leu Ala Lys Tyr Asp Thr Leu Ser Ile Lys
20      85      90      95
Gln Gly Leu Asp Arg Val Asn Pro
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<210> 12

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<211> 990

<212> PRT

<213> Staphylococcus aureus

<400> 12

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Met Gly Gln Asp Lys Glu Ala Ala Ala Ser Glu Gln Lys Thr Thr Thr
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Val Glu Glu Asn Gly Asn Ser Ala Thr Asp Asn Lys Thr Ser Glu Thr
35      20      25      30
Gln Thr Thr Ala Thr Asn Val Asn His Ile Glu Glu Thr Gln Ser Tyr
      35      40      45
Asn Ala Thr Val Thr Glu Gln Pro Ser Asn Ala Thr Gln Val Thr Thr
40      50      55      60
Glu Glu Ala Pro Lys Ala Val Gln Ala Pro Gln Thr Ala Gln Pro Ala
65      70      75      80
Asn Ile Glu Thr Val Lys Glu Glu Val Val Lys Glu Glu Ala Lys Pro
45      85      90      95

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Gln Val Lys Glu Thr Thr Gln Ser Gln Asp Asn Ser Gly Asp Gln Arg
 100 105 110
 5 Gln Val Asp Leu Thr Pro Lys Lys Ala Thr Gln Asn Gln Val Ala Glu
 115 120 125
 Thr Gln Val Glu Val Ala Gln Pro Arg Thr Ala Ser Glu Ser Lys Pro
 130 135 140
 10 Arg Val Thr Arg Ser Ala Asp Val Ala Glu Ala Lys Glu Ala Ser Asn
 145 150 155 160
 Ala Lys Val Glu Thr Gly Thr Asp Val Thr Ser Lys Val Thr Val Glu
 165 170 175
 15 Ile Gly Ser Ile Glu Gly His Asn Asn Thr Asn Lys Val Glu Pro His
 180 185 190
 Ala Gly Gln Arg Ala Val Leu Lys Tyr Lys Leu Lys Phe Glu Asn Gly
 195 200 205
 20 Leu His Gln Gly Asp Tyr Phe Asp Phe Thr Leu Ser Asn Asn Val Asn
 210 215 220
 Thr His Gly Val Ser Thr Ala Arg Lys Val Pro Glu Ile Lys Asn Gly
 225 230 235 240
 25 Ser Val Val Met Ala Thr Gly Glu Val Leu Glu Gly Gly Lys Ile Arg
 245 250 255
 Tyr Thr Phe Thr Asn Asp Ile Glu Asp Lys Val Asp Val Thr Ala Glu
 260 265 270
 30 Leu Glu Ile Asn Leu Phe Ile Asp Pro Lys Thr Val Gln Thr Asn Gly
 275 280 285
 Asn Gln Thr Ile Thr Ser Thr Leu Asn Glu Glu Gln Thr Ser Lys Glu
 290 295 300
 35 Leu Asp Val Lys Tyr Lys Asp Gly Ile Gly Asn Tyr Tyr Ala Asn Leu
 305 310 315 320
 Asn Gly Ser Ile Glu Thr Phe Asn Lys Ala Asn Asn Arg Phe Ser His
 325 330 335
 Val Ala Phe Ile Lys Pro Asn Asn Gly Lys Thr Thr Ser Val Thr Val
 340 345 350
 40 Thr Gly Thr Leu Met Lys Gly Ser Asn Gln Asn Gly Asn Gln Pro Lys
 355 360 365
 Val Arg Ile Phe Glu Tyr Leu Gly Asn Asn Glu Asp Ile Ala Lys Ser
 370 375 380
 45 Val Tyr Ala Asn Thr Thr Asp Thr Ser Lys Phe Lys Glu Val Thr Ser
 385 390 395 400
 Asn Met Ser Gly Asn Leu Asn Leu Gln Asn Asn Gly Ser Tyr Ser Leu
 405 410 415
 50 Asn Ile Glu Asn Leu Asp Lys Thr Tyr Val Val His Tyr Asp Gly Glu
 420 425 430
 Tyr Leu Asn Gly Thr Asp Glu Val Asp Phe Arg Thr Gln Met Val Gly
 435 440 445
 55 His Pro Glu Gln Leu Tyr Lys Tyr Tyr Tyr Asp Arg Gly Tyr Thr Leu
 450 455 460
 Thr Trp Asp Asn Gly Leu Val Leu Tyr Ser Asn Lys Ala Asn Gly Asn

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	465	470					475					480				
	Glu	Lys	Asn	Gly	Pro	Ile	Ile	Gln	Asn	Asn	Lys	Phe	Glu	Tyr	Lys	Glu
					485					490					495	
5	Asp	Thr	Ile	Lys	Glu	Thr	Leu	Thr	Gly	Gln	Tyr	Asp	Lys	Asn	Leu	Val
				500					505					510		
	Thr	Thr	Val	Glu	Glu	Glu	Tyr	Asp	Ser	Ser	Thr	Leu	Asp	Ile	Asp	Tyr
			515					520					525			
10	His	Thr	Ala	Ile	Asp	Gly	Gly	Gly	Gly	Tyr	Val	Asp	Gly	Tyr	Ile	Glu
		530				535						540				
	Thr	Ile	Glu	Glu	Thr	Asp	Ser	Ser	Ala	Ile	Asp	Ile	Asp	Tyr	His	Thr
	545					550					555					560
15	Ala	Val	Asp	Ser	Glu	Ala	Gly	His	Val	Gly	Gly	Tyr	Thr	Glu	Ser	Ser
					565					570					575	
	Glu	Glu	Ser	Asn	Pro	Ile	Asp	Phe	Glu	Glu	Ser	Thr	His	Glu	Asn	Ser
				580					585					590		
20	Lys	His	His	Ala	Asp	Val	Val	Glu	Tyr	Glu	Glu	Asp	Thr	Asn	Pro	Gly
			595					600					605			
	Gly	Gly	Gln	Val	Thr	Thr	Glu	Ser	Asn	Leu	Val	Glu	Phe	Asp	Glu	Glu
		610					615					620				
25	Ser	Thr	Lys	Gly	Ile	Val	Thr	Gly	Ala	Val	Ser	Asp	His	Thr	Thr	Val
	625					630					635					640
	Glu	Asp	Thr	Lys	Glu	Tyr	Thr	Thr	Glu	Ser	Asn	Leu	Ile	Glu	Leu	Val
					645					650					655	
30	Asp	Glu	Leu	Pro	Glu	Glu	His	Gly	Gln	Ala	Gln	Gly	Pro	Val	Glu	Glu
				660					665					670		
	Ile	Thr	Lys	Asn	Asn	His	His	Ile	Ser	His	Ser	Gly	Leu	Gly	Thr	Glu
			675					680					685			
35	Asn	Gly	His	Gly	Asn	Tyr	Asp	Val	Ile	Glu	Glu	Ile	Glu	Glu	Asn	Ser
		690					695					700				
	His	Val	Asp	Ile	Lys	Ser	Glu	Leu	Gly	Tyr	Glu	Gly	Gly	Gln	Asn	Ser
	705					710					715					720
40	Gly	Asn	Gln	Ser	Phe	Glu	Glu	Asp	Thr	Glu	Glu	Asp	Lys	Pro	Lys	Tyr
					725					730					735	
	Glu	Gln	Gly	Gly	Asn	Ile	Val	Asp	Ile	Asp	Phe	Asp	Ser	Val	Pro	Gln
				740					745					750		
45	Ile	His	Gly	Gln	Asn	Lys	Gly	Asn	Gln	Ser	Phe	Glu	Glu	Asp	Thr	Glu
			755					760					765			
	Lys	Asp	Lys	Pro	Lys	Tyr	Glu	His	Gly	Gly	Asn	Ile	Ile	Asp	Ile	Asp
		770					775					780				
50	Phe	Asp	Ser	Val	Pro	His	Ile	His	Gly	Phe	Asn	Lys	His	Thr	Glu	Ile
	785					790					795					800
	Ile	Glu	Glu	Asp	Thr	Asn	Lys	Asp	Lys	Pro	Ser	Tyr	Gln	Phe	Gly	Gly
					805					810					815	
	His	Asn	Ser	Val	Asp	Phe	Glu	Glu	Asp	Thr	Leu	Pro	Lys	Val	Ser	Gly
				820					825					830		
55	Gln	Asn	Glu	Gly	Gln	Gln	Thr	Ile	Glu	Glu	Asp	Thr	Thr	Pro	Pro	Ile
			835					840					845			

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	Val	Pro	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ser	Glu	Pro	Glu	Thr
	850						855					860				
5	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ser	Glu	Pro	Glu	Thr	Pro	Thr
	865					870					875					880
	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ser	Glu	Pro	Glu	Thr	Pro	Thr	Pro	Pro
					885					890					895	
10	Thr	Pro	Glu	Val	Pro	Ala	Glu	Pro	Gly	Lys	Pro	Val	Pro	Pro	Ala	Lys
				900					905					910		
	Glu	Glu	Pro	Lys	Lys	Pro	Ser	Lys	Pro	Val	Glu	Gln	Gly	Lys	Val	Val
			915					920					925			
15	Thr	Pro	Val	Ile	Glu	Ile	Asn	Glu	Lys	Val	Lys	Ala	Val	Ala	Pro	Thr
		930					935					940				
	Lys	Lys	Pro	Gln	Ser	Lys	Lys	Ser	Glu	Leu	Pro	Glu	Thr	Gly	Gly	Glu
	945					950					955					960
20	Glu	Ser	Thr	Asn	Lys	Gly	Met	Leu	Phe	Gly	Gly	Leu	Phe	Ser	Ile	Leu
				965						970					975	
	Gly	Leu	Ala	Leu	Leu	Arg	Arg	Asn	Lys	Lys	Asn	His	Lys	Ala		
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<210> 13

25 <211> 917

<212> PRT

<213> Staphylococcus aureus

<400> 13

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Met Ile Val Val Gly Met Gly Gln Glu Lys Glu Ala Ala Ala Ser Glu
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 Gln Asn Asn Thr Thr Val Glu Glu Ser Gly Ser Ser Ala Thr Glu Ser
 5 20 25 30
 Lys Ala Ser Glu Thr Gln Thr Thr Thr Asn Asn Val Asn Thr Ile Asp
 35 40 45
 Glu Thr Gln Ser Tyr Ser Ala Thr Ser Thr Glu Gln Pro Ser Gln Ser
 10 50 55 60
 Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Thr Val Gln Ala Pro Lys
 65 70 75 80
 Val Glu Thr Ser Arg Val Asp Leu Pro Ser Glu Lys Val Ala Asp Lys
 15 85 90 95
 Glu Thr Thr Gly Thr Gln Val Asp Ile Ala Gln Pro Ser Asn Val Ser
 100 105 110
 Glu Ile Lys Pro Arg Met Lys Arg Ser Thr Asp Val Thr Ala Val Ala
 115 120 125
 Glu Lys Glu Val Val Glu Glu Thr Lys Ala Thr Gly Thr Asp Val Thr
 130 135 140
 Asn Lys Val Glu Val Glu Glu Gly Ser Glu Ile Val Gly His Lys Gln
 145 150 155 160
 Asp Thr Asn Val Val Asn Pro His Asn Ala Glu Arg Val Thr Leu Lys
 165 170 175
 Tyr Lys Trp Lys Phe Gly Glu Gly Ile Lys Ala Gly Asp Tyr Phe Asp
 180 185 190

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	Phe	Thr	Leu	Ser	Asp	Asn	Val	Glu	Thr	His	Gly	Ile	Ser	Thr	Leu	Arg
			195					200					205			
5	Lys	Val	Pro	Glu	Ile	Lys	Ser	Thr	Asp	Gly	Gln	Val	Met	Ala	Thr	Gly
		210					215					220				
	Glu	Ile	Ile	Gly	Glu	Arg	Lys	Val	Arg	Tyr	Thr	Phe	Lys	Glu	Tyr	Val
	225					230					235					240
10	Gln	Glu	Lys	Lys	Asp	Leu	Thr	Ala	Glu	Leu	Ser	Leu	Asn	Leu	Phe	Ile
					245					250					255	
	Asp	Pro	Thr	Thr	Val	Thr	Gln	Lys	Gly	Asn	Gln	Asn	Val	Glu	Val	Lys
				260					265					270		
15	Leu	Gly	Glu	Thr	Thr	Val	Ser	Lys	Ile	Phe	Asn	Ile	Gln	Tyr	Leu	Gly
			275					280					285			
	Gly	Val	Arg	Asp	Asn	Trp	Gly	Val	Thr	Ala	Asn	Gly	Arg	Ile	Asp	Thr
		290					295					300				
20	Leu	Asn	Lys	Val	Asp	Gly	Lys	Phe	Ser	His	Phe	Ala	Tyr	Met	Lys	Pro
	305					310					315					320
	Asn	Asn	Gln	Ser	Leu	Ser	Ser	Val	Thr	Val	Thr	Gly	Gln	Val	Thr	Lys
					325					330					335	
25	Gly	Asn	Lys	Pro	Gly	Val	Asn	Asn	Pro	Thr	Val	Lys	Val	Tyr	Lys	His
				340					345					350		
	Ile	Gly	Ser	Asp	Asp	Leu	Ala	Glu	Ser	Val	Tyr	Ala	Lys	Leu	Asp	Asp
			355					360					365			
30	Val	Ser	Lys	Phe	Glu	Asp	Val	Thr	Asp	Asn	Met	Ser	Leu	Asp	Phe	Asp
		370					375					380				
	Thr	Asn	Gly	Gly	Tyr	Ser	Leu	Asn	Phe	Asn	Asn	Leu	Asp	Gln	Ser	Lys
	385					390					395					400
35	Asn	Tyr	Val	Ile	Lys	Tyr	Glu	Gly	Tyr	Tyr	Asp	Ser	Asn	Ala	Ser	Asn
					405					410					415	
	Leu	Glu	Phe	Gln	Thr	His	Leu	Phe	Gly	Tyr	Tyr	Asn	Tyr	Tyr	Tyr	Thr
				420					425					430		
40	Ser	Asn	Leu	Thr	Trp	Lys	Asn	Gly	Val	Ala	Phe	Tyr	Ser	Asn	Asn	Ala
			435					440					445			
	Gln	Gly	Asp	Gly	Lys	Asp	Lys	Leu	Lys	Glu	Pro	Ile	Ile	Glu	His	Ser
		450					455					460				
45	Thr	Pro	Ile	Glu	Leu	Glu	Phe	Lys	Ser	Glu	Pro	Pro	Val	Glu	Lys	His
	465					470					475					480
	Glu	Leu	Thr	Gly	Thr	Ile	Glu	Glu	Ser	Asn	Asp	Ser	Lys	Pro	Ile	Asp
					485					490					495	
50	Phe	Glu	Tyr	His	Thr	Ala	Val	Glu	Gly	Ala	Glu	Gly	His	Ala	Glu	Gly
				500					505					510		
	Thr	Ile	Glu	Thr	Glu	Glu	Asp	Ser	Ile	His	Val	Asp	Phe	Glu	Glu	Ser
			515					520					525			
55	Thr	His	Glu	Asn	Ser	Lys	His	His	Ala	Asp	Val	Val	Glu	Tyr	Glu	Glu
		530					535					540				
	Asp	Thr	Asn	Pro	Gly	Gly	Gly	Gln	Val	Thr	Thr	Glu	Ser	Asn	Leu	Val
	545					550					555					560
	Glu	Phe	Asp	Glu	Asp	Ser	Thr	Lys	Gly	Ile	Val	Thr	Gly	Ala	Val	Ser

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	565										570										575									
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5				580					585					590																
	Leu	Ile	Glu	Leu	Val	Asp	Glu	Leu	Pro	Glu	Glu	His	Gly	Gln	Ala	Gln														
			595					600					605																	
	Gly	Pro	Ile	Glu	Glu	Ile	Thr	Glu	Asn	Asn	His	His	Ile	Ser	His	Ser														
		610					615					620																		
10	Gly	Leu	Gly	Thr	Glu	Asn	Gly	His	Gly	Asn	Tyr	Gly	Val	Ile	Glu	Glu														
		625				630					635																			
	Ile	Glu	Glu	Asn	Ser	His	Val	Asp	Ile	Lys	Ser	Glu	Leu	Gly	Tyr	Glu														
				645						650					655															
15	Gly	Gly	Gln	Asn	Ser	Gly	Asn	Gln	Ser	Phe	Glu	Glu	Asp	Thr	Glu	Glu														
				660					665					670																
	Asp	Lys	Pro	Lys	Tyr	Glu	Gln	Gly	Gly	Asn	Ile	Val	Asp	Ile	Asp	Phe														
			675					680					685																	
20	Asp	Ser	Val	Pro	Gln	Ile	His	Gly	Gln	Asn	Asn	Gly	Asn	Gln	Ser	Phe														
		690					695					700																		
	Glu	Glu	Asp	Thr	Glu	Lys	Asp	Lys	Pro	Lys	Tyr	Glu	Gln	Gly	Gly	Asn														
		705				710					715					720														
25	Ile	Ile	Asp	Ile	Asp	Phe	Asp	Ser	Val	Pro	His	Ile	His	Gly	Phe	Asn														
				725						730					735															
	Lys	His	Thr	Glu	Ile	Ile	Glu	Glu	Asp	Thr	Asn	Lys	Asp	Lys	Pro	Asn														
				740					745					750																
30	Tyr	Gln	Phe	Gly	Gly	His	Asn	Ser	Val	Asp	Phe	Glu	Glu	Asp	Thr	Leu														
			755					760					765																	
	Pro	Gln	Val	Ser	Gly	His	Asn	Glu	Gly	Gln	Gln	Thr	Ile	Glu	Glu	Asp														
		770					775					780																		
35	Thr	Thr	Pro	Pro	Ile	Val	Pro	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro														
		785				790					795					800														
	Ser	Glu	Pro	Glu	Thr	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ser	Glu														
					805					810					815															
40	Pro	Glu	Thr	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Thr	Glu	Pro	Gly														
				820					825					830																
	Lys	Pro	Ile	Pro	Pro	Ala	Lys	Glu	Glu	Pro	Lys	Lys	Pro	Ser	Lys	Pro														
			835					840					845																	
45	Val	Glu	Gln	Gly	Lys	Val	Val	Thr	Pro	Val	Ile	Glu	Ile	Asn	Glu	Lys														
		850					855					860																		
	Val	Lys	Ala	Val	Val	Pro	Thr	Lys	Lys	Ala	Gln	Ser	Lys	Lys	Ser	Glu														
		865				870					875					880														
50	Leu	Pro	Glu	Thr	Gly	Gly	Glu	Glu	Ser	Thr	Asn	Asn	Gly	Met	Leu	Phe														
				885						890					895															
	Gly	Gly	Leu	Phe	Ser	Ile	Leu	Gly	Leu	Ala	Leu	Leu	Arg	Arg	Asn	Lys														
				900					905					910																
55	Lys	Asn	His	Lys	Ala																									
				915																										

<210> 14

<211> 319

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<212> PRT

<213> Staphylococcus aureus

<400> 14

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Met Lys Thr Arg Ile Val Ser Ser Val Thr Thr Thr Leu Leu Leu Gly
1      5      10      15
Ser Ile Leu Met Asn Pro Val Ala Asn Ala Ala Asp Ser Asp Ile Asn
20      25      30
Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser Asn Thr Thr Val Lys Thr
35      40      45
Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn Gly Met His Lys Lys Val
50      55      60
Phe Tyr Ser Phe Ile Asp Asp Lys Asn His Asn Lys Lys Leu Leu Val
65      70      75      80
Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln Tyr Arg Val Tyr Ser Glu
85      90      95
Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp Pro Ser Ala Phe Lys Val
100     105
Gln Leu Gln Leu Pro Asp Asn Glu Val Ala Gln Ile Ser Asp Tyr Tyr
115     120     125
Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr Met Ser Thr Leu Thr Tyr
130     135     140
Gly Phe Asn Gly Asn Val Thr Gly Asp Asp Thr Gly Lys Ile Gly Gly
145     150     155     160
Leu Ile Gly Ala Asn Val Ser Ile Gly His Thr Leu Lys Tyr Val Gln
165     170     175
Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro Thr Asp Lys Lys Val Gly
180     185     190
Trp Lys Val Ile Phe Asn Asn Met Val Asn Gln Asn Trp Gly Pro Tyr
195     200     205
Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly Asn Gln Leu Phe Met Lys
210     215     220
Thr Arg Asn Gly Ser Met Lys Ala Ala Asp Asn Phe Leu Asp Pro Asn
225     230     235     240
Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe Ser Pro Asp Phe Ala Thr
245     250     255
Val Ile Thr Met Asp Arg Lys Ala Ser Lys Gln Gln Thr Asn Ile Asp
260     265     270
Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr Gln Leu His Trp Thr Ser
275     280     285
Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp Lys Trp Ile Asp Arg Ser
290     295     300
Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys Glu Glu Met Thr Asn
305     310     315

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<210> 15

<211> 325

<212> PRT

EP 2 510 947 B1

<213> Staphylococcus aureus

<400> 15

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10 Val Ser Val Lys Lys Val Asp Asp Lys Val Thr Leu Tyr Lys Thr Thr
35 40 45
Ala Thr Ala Asp Ser Asp Lys Phe Lys Ile Ser Gln Ile Leu Thr Phe
50 55 60
15 Asn Phe Ile Lys Asp Lys Ser Tyr Asp Lys Asp Thr Leu Val Leu Lys
65 70 75 80
Ala Thr Gly Asn Ile Asn Ser Gly Phe Val Lys Pro Asn Pro Asn Asp
85 90 95
20 Tyr Asp Phe Ser Lys Leu Tyr Trp Gly Ala Lys Tyr Asn Val Ser Ile
100 105 110
Ser Ser Gln Ser Asn Asp Ser Val Asn Val Val Asp Tyr Ala Pro Lys
115 120 125
25 Asn Gln Asn Glu Glu Phe Gln Val Gln Asn Thr Leu Gly Tyr Thr Phe
130 135 140
Gly Gly Asp Ile Ser Ile Ser Asn Gly Leu Ser Gly Gly Leu Asn Gly
145 150 155 160
30 Asn Thr Ala Phe Ser Glu Thr Ile Asn Tyr Lys Gln Glu Ser Tyr Arg
165 170 175
Thr Thr Leu Ser Arg Asn Thr Asn Tyr Lys Asn Val Gly Trp Gly Val
180 185 190
35 Glu Ala His Lys Ile Met Asn Asn Gly Trp Gly Pro Tyr Gly Arg Asp
195 200 205
Ser Phe His Pro Thr Tyr Gly Asn Glu Leu Phe Leu Ala Gly Arg Gln
210 215 220
40 Ser Ser Ala Tyr Ala Gly Gln Asn Phe Ile Ala Gln His Gln Met Pro
225 230 235 240
Leu Leu Ser Arg Ser Asn Phe Asn Pro Glu Phe Leu Ser Val Leu Ser
245 250 255
45 His Arg Gln Asp Gly Ala Lys Lys Ser Lys Ile Thr Val Thr Tyr Gln
260 265 270
Arg Glu Met Asp Leu Tyr Gln Ile Arg Trp Asn Gly Phe Tyr Trp Ala
275 280 285
50 Gly Ala Asn Tyr Lys Asn Phe Lys Thr Arg Thr Phe Lys Ser Thr Tyr
290 295 300
Glu Ile Asp Trp Glu Asn His Lys Val Lys Leu Leu Asp Thr Lys Glu
305 310 315 320
55 Thr Glu Asn Asn Lys
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<210> 16

<211> 315

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<212> PRT

<213> Staphylococcus aureus

<400> 16

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Met Leu Lys Asn Lys Ile Leu Thr Thr Thr Leu Ser Val Ser Leu Leu

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1 5 10 15
Ala Pro Leu Ala Asn Pro Leu Leu Glu Asn Ala Lys Ala Ala Asn Asp
20 25 30

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Thr Glu Asp Ile Gly Lys Gly Ser Asp Ile Glu Ile Ile Lys Arg Thr
35 40 45
Glu Asp Lys Thr Ser Asn Lys Trp Gly Val Thr Gln Asn Ile Gln Phe
50 55 60

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Asp Phe Val Lys Asp Lys Lys Tyr Asn Lys Asp Ala Leu Ile Leu Lys
65 70 75 80
Met Gln Gly Phe Ile Ser Ser Arg Thr Thr Tyr Tyr Asn Tyr Lys Lys
85 90 95

25

Thr Asn His Val Lys Ala Met Arg Trp Pro Phe Gln Tyr Asn Ile Gly
100 105 110
Leu Lys Thr Asn Asp Lys Tyr Val Ser Leu Ile Asn Tyr Leu Pro Lys
115 120 125

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Asn Lys Ile Glu Ser Thr Asn Val Ser Gln Thr Leu Gly Tyr Asn Ile
130 135 140
Gly Gly Asn Phe Gln Ser Ala Pro Ser Leu Gly Gly Asn Gly Ser Phe
145 150 155 160

35

Asn Tyr Ser Lys Ser Ile Ser Tyr Thr Gln Gln Asn Tyr Val Ser Glu
165 170 175
Val Glu Gln Gln Asn Ser Lys Ser Val Leu Trp Gly Val Lys Ala Asn
180 185 190

40

Ser Phe Ala Thr Glu Ser Gly Gln Lys Ser Ala Phe Asp Ser Asp Leu
195 200 205
Phe Val Gly Tyr Lys Pro His Ser Lys Asp Pro Arg Asp Tyr Phe Val
210 215 220

45

Pro Asp Ser Glu Leu Pro Pro Leu Val Gln Ser Gly Phe Asn Pro Ser
225 230 235 240
Phe Ile Ala Thr Val Ser His Glu Lys Gly Ser Ser Asp Thr Ser Glu
245 250 255

50

Phe Glu Ile Thr Tyr Gly Arg Asn Met Asp Val Thr His Ala Ile Lys
260 265 270
Arg Ser Thr His Tyr Gly Asn Ser Tyr Leu Asp Gly His Arg Val His
275 280 285

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Asn Ala Phe Val Asn Arg Asn Tyr Thr Val Lys Tyr Glu Val Asn Trp
290 295 300
Lys Thr His Glu Ile Lys Val Lys Gly Gln Asn
305 310 315

<210> 17

EP 2 510 947 B1

<211> 350
 <212> PRT
 <213> Staphylococcus aureus

5 <400> 17

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10	Ser	Ala	Met	Lys	Lys	Ile	Thr	Met	Gly	Thr	Ala	Ser	Ile	Ile	Leu	Gly
				20					25					30		

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Ser Leu Val Tyr Ile Gly Ala Asp Ser Gln Gln Val Asn Ala Ala Thr
 35 40 45
 5 Glu Ala Thr Asn Ala Thr Asn Asn Gln Ser Thr Gln Val Ser Gln Ala
 50 55 60
 Thr Ser Gln Pro Ile Asn Phe Gln Val Gln Lys Asp Gly Ser Ser Glu
 65 70 75 80
 10 Lys Ser His Met Asp Asp Tyr Met Gln His Pro Gly Lys Val Ile Lys
 85 90 95
 Gln Asn Asn Lys Tyr Tyr Phe Gln Thr Val Leu Asn Asn Ala Ser Phe
 100 105 110
 15 Trp Lys Glu Tyr Lys Phe Tyr Asn Ala Asn Asn Gln Glu Leu Ala Thr
 115 120 125
 Thr Val Val Asn Asp Asn Lys Lys Ala Asp Thr Arg Thr Ile Asn Val
 130 135 140
 20 Ala Val Glu Pro Gly Tyr Lys Ser Leu Thr Thr Lys Val His Ile Val
 145 150 155 160
 Val Pro Gln Ile Asn Tyr Asn His Arg Tyr Thr Thr His Leu Glu Phe
 165 170 175
 25 Glu Lys Ala Ile Pro Thr Leu Ala Asp Ala Ala Lys Pro Asn Asn Val
 180 185 190
 Lys Pro Val Gln Pro Lys Pro Ala Gln Pro Lys Thr Pro Thr Glu Gln
 195 200 205
 30 Thr Lys Pro Val Gln Pro Lys Val Glu Lys Val Lys Pro Thr Val Thr
 210 215 220
 Thr Thr Ser Lys Val Glu Asp Asn His Ser Thr Lys Val Val Ser Thr
 225 230 235 240
 35 Asp Thr Thr Lys Asp Gln Thr Lys Thr Gln Thr Ala His Thr Val Lys
 245 250 255
 Thr Ala Gln Thr Ala Gln Glu Gln Asn Lys Val Gln Thr Pro Val Lys
 260 265 270
 40 Asp Val Ala Thr Ala Lys Ser Glu Ser Asn Asn Gln Ala Val Ser Asp
 275 280 285
 Asn Lys Ser Gln Gln Thr Asn Lys Val Thr Lys His Asn Glu Thr Pro
 290 295 300
 45 Lys Gln Ala Ser Lys Ala Lys Glu Leu Pro Lys Thr Gly Leu Thr Ser
 305 310 315 320
 Val Asp Asn Phe Ile Ser Thr Val Ala Phe Ala Thr Leu Ala Leu Leu
 325 330 335
 50 Gly Ser Leu Ser Leu Leu Leu Phe Lys Arg Lys Glu Ser Lys
 340 345 350

<210> 18

<211> 645

<212> PRT

<213> Staphylococcus aureus

<400> 18

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Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
1 5 10 15

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Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
 20 25 30
 Met Ser Asn Gly Glu Ala Gln Ala Ala Glu Glu Thr Gly Gly Thr
 35 40 45
 Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
 50 55 60
 Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
 65 70 75 80
 Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
 85 90 95
 Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
 100 105 110
 Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
 115 120 125
 Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
 130 135 140
 Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
 145 150 155 160
 Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val
 165 170 175
 Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
 180 185 190
 Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
 195 200 205
 Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
 210 215 220
 Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr
 225 230 235 240
 His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
 245 250 255
 Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
 260 265 270
 Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
 275 280 285
 Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu
 290 295 300
 Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
 305 310 315 320
 Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
 325 330 335
 Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
 340 345 350
 Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
 355 360 365
 His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
 370 375 380
 Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln

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	385		390		395		400									
	Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile
					405					410					415	
5	Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys
				420					425					430		
	Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile
			435					440					445			
10	Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys
		450					455					460				
	Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr
	465				470						475					480
15	Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln
					485					490					495	
	Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu
				500					505					510		
20	Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Thr	Pro	Ala	Thr	Lys
			515					520					525			
	Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val
		530					535						540			
25	Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys
	545					550				555						560
	Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys
					565					570					575	
30	Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly
				580					585					590		
	His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys
			595					600					605			
35	Ser	Leu	Pro	Gln	Thr	Gly	Glu	Glu	Ser	Asn	Lys	Asp	Met	Thr	Leu	Pro
		610					615					620				
	Leu	Met	Ala	Leu	Leu	Ala	Leu	Ser	Ser	Ile	Val	Ala	Phe	Val	Leu	Pro
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40	Arg	Lys	Arg	Lys	Asn											
					645											

<210> 19

<211> 227

45 <212> PRT

<213> Staphylococcus aureus

<400> 19

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EP 2 510 947 B1

Met Lys Asn Ile Leu Lys Val Phe Asn Thr Thr Ile Leu Ala Leu Ile
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Ile Ile Ile Ala Thr Phe Ser Asn Ser Ala Asn Ala Ala Asp Ser Gly
5 20 25 30
Thr Leu Asn Tyr Glu Val Tyr Lys Tyr Asn Thr Asn Asp Thr Ser Ile
35 40 45
Ala Asn Asp Tyr Phe Asn Lys Pro Ala Lys Tyr Ile Lys Lys Asn Gly
10 50 55 60
Lys Leu Tyr Val Gln Ile Thr Val Asn His Ser His Trp Ile Thr Gly
65 70 75 80
Met Ser Ile Glu Gly His Lys Glu Asn Ile Ile Ser Lys Asn Thr Ala
15 85 90 95
Lys Asp Glu Arg Thr Ser Glu Phe Glu Val Ser Lys Leu Asn Gly Lys
100 105 110
Ile Asp Gly Lys Ile Asp Val Tyr Ile Asp Glu Lys Val Asn Gly Lys
20 115 120 125
Pro Phe Lys Tyr Asp His His Tyr Asn Ile Thr Tyr Lys Phe Asn Gly
130 135 140
Pro Thr Asp Val Ala Gly Ala Asn Ala Pro Gly Lys Asp Asp Lys Asn
25 145 150 155 160
Ser Ala Ser Gly Ser Asp Lys Gly Ser Asp Gly Thr Thr Thr Gly Gln
165 170 175
Ser Glu Ser Asn Ser Ser Asn Lys Asp Lys Val Glu Asn Pro Gln Thr
30 180 185 190
Asn Ala Gly Thr Pro Ala Tyr Ile Tyr Ala Ile Pro Val Ala Ser Leu
195 200 205
Ala Leu Leu Ile Ala Ile Thr Leu Phe Val Arg Lys Lys Ser Lys Gly
35 210 215 220
Asn Val Glu
225

40 <210> 20
<211> 107
<212> PRT
<213> Staphylococcus aureus

45 <400> 20

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EP 2 510 947 B1

Met Lys Phe Met Ala Glu Asn Arg Leu Thr Leu Thr Lys Gly Thr Ala
 1 5 10 15
 Lys Asp Ile Ile Glu Arg Phe Tyr Thr Arg His Gly Ile Glu Thr Leu
 5 20 25 30
 Glu Gly Phe Asp Gly Met Phe Val Thr Gln Thr Leu Glu Gln Glu Asp
 35 40 45
 Phe Asp Glu Val Lys Ile Leu Thr Val Trp Lys Ser Lys Gln Ala Phe
 10 50 55 60
 Thr Asp Trp Leu Lys Ser Asp Val Phe Lys Ala Ala His Lys His Val
 65 70 75 80
 Arg Ser Lys Asn Glu Asp Glu Ser Ser Pro Ile Ile Asn Asn Lys Val
 15 85 90 95
 Ile Thr Tyr Asp Ile Gly Tyr Ser Tyr Met Lys
 100 105

<210> 21

<211> 895

<212> PRT

<213> Staphylococcus aureus

<400> 21

Met Asn Lys His His Pro Lys Leu Arg Ser Phe Tyr Ser Ile Arg Lys
 1 5 10 15
 Ser Thr Leu Gly Val Ala Ser Val Ile Val Ser Thr Leu Phe Leu Ile
 20 25 30

EP 2 510 947 B1

Thr Ser Gln His Gln Ala Gln Ala Ala Glu Asn Thr Asn Thr Ser Asp
 35 40 45
 5 Lys Ile Ser Glu Asn Gln Asn Asn Ala Thr Thr Thr Gln Pro Pro
 50 55 60
 Lys Asp Thr Asn Gln Thr Gln Pro Ala Thr Gln Pro Ala Asn Thr Ala
 65 70 75 80
 10 Lys Asn Tyr Pro Ala Ala Asp Glu Ser Leu Lys Asp Ala Ile Lys Asp
 85 90 95
 Pro Ala Leu Glu Asn Lys Glu His Asp Ile Gly Pro Arg Glu Gln Val
 100 105 110
 15 Asn Phe Gln Leu Leu Asp Lys Asn Asn Glu Thr Gln Tyr Tyr His Phe
 115 120 125
 Phe Ser Ile Lys Asp Pro Ala Asp Val Tyr Tyr Thr Lys Lys Lys Ala
 130 135 140
 20 Glu Val Glu Leu Asp Ile Asn Thr Ala Ser Thr Trp Lys Lys Phe Glu
 145 150 155 160
 Val Tyr Glu Asn Asn Gln Lys Leu Pro Val Arg Leu Val Ser Tyr Ser
 165 170 175
 25 Pro Val Pro Glu Asp His Ala Tyr Ile Arg Phe Pro Val Ser Asp Gly
 180 185 190
 Thr Gln Glu Leu Lys Ile Val Ser Ser Thr Gln Ile Asp Asp Gly Glu
 195 200 205
 30 Glu Thr Asn Tyr Asp Tyr Thr Lys Leu Val Phe Ala Lys Pro Ile Tyr
 210 215 220
 Asn Asp Pro Ser Leu Val Lys Ser Asp Thr Asn Asp Ala Val Val Thr
 225 230 235 240
 35 Asn Asp Gln Ser Ser Ser Val Ala Ser Asn Gln Thr Asn Thr Asn Thr
 245 250 255
 Ser Asn Gln Asn Ile Ser Thr Ile Asn Asn Ala Asn Asn Gln Pro Gln
 260 265 270
 40 Ala Thr Thr Asn Met Ser Gln Pro Ala Gln Pro Lys Ser Ser Thr Asn
 275 280 285
 Ala Asp Gln Ala Ser Ser Gln Pro Ala His Glu Thr Asn Ser Asn Gly
 290 295 300
 45 Asn Thr Asn Asp Lys Thr Asn Glu Ser Ser Asn Gln Ser Asp Val Asn
 305 310 315 320
 Gln Gln Tyr Pro Pro Ala Asp Glu Ser Leu Gln Asp Ala Ile Lys Asn
 325 330 335
 50 Pro Ala Ile Ile Asp Lys Glu His Thr Ala Asp Asn Trp Arg Pro Ile
 340 345 350
 Asp Phe Gln Met Lys Asn Asp Lys Gly Glu Arg Gln Phe Tyr His Tyr
 355 360 365
 55 Ala Ser Thr Val Glu Pro Ala Thr Val Ile Phe Thr Lys Thr Gly Pro
 370 375 380
 Ile Ile Glu Leu Gly Leu Lys Thr Ala Ser Thr Trp Lys Lys Phe Glu
 385 390 395 400
 Val Tyr Glu Gly Asp Lys Lys Leu Pro Val Glu Leu Val Ser Tyr Asp

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	405										410										415											
	Ser	Asp	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Pro	Val	Ser	Asn	Gly	Thr																
5				420					425					430			Arg	Glu	Val	Lys	Ile	Val	Ser	Ser	Ile	Glu	Tyr	Gly	Glu	Asn	Ile	His
				435					440					445			Glu	Asp	Tyr	Asp	Tyr	Thr	Leu	Met	Val	Phe	Ala	Gln	Pro	Ile	Thr	Asn
				450					455					460			Asn	Pro	Asp	Asp	Tyr	Val	Asp	Glu	Glu	Thr	Tyr	Asn	Leu	Gln	Lys	Leu
10				465					470					475			Leu	Ala	Pro	Tyr	His	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu
									485					490																		
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																	Thr	Asp	Leu	Gln	Glu	Ala	His	Phe	Val	Val	Phe	Glu	Ser	Glu	Glu	Asn
25																	Ser	Glu	Ser	Val	Met	Asp	Gly	Phe	Val	Glu	His	Pro	Phe	Tyr	Thr	Ala
																	Thr	Leu	Asn	Gly	Gln	Lys	Tyr	Val	Val	Met	Lys	Thr	Lys	Asp	Asp	Ser
30																	Tyr	Trp	Lys	Asp	Leu	Ile	Val	Glu	Gly	Lys	Arg	Val	Thr	Thr	Val	Ser
																	Lys	Asp	Pro	Lys	Asn	Asn	Ser	Arg	Thr	Leu	Ile	Phe	Pro	Tyr	Ile	Pro
35																	Asp	Lys	Ala	Val	Tyr	Asn	Ala	Ile	Val	Lys	Val	Val	Val	Ala	Asn	Ile
																	Gly	Tyr	Glu	Gly	Gln	Tyr	His	Val	Arg	Ile	Ile	Asn	Gln	Asp	Ile	Asn
40																	Thr	Lys	Asp	Asp	Asp	Thr	Ser	Gln	Asn	Asn	Thr	Ser	Glu	Pro	Leu	Asn
																	Val	Gln	Thr	Gly	Gln	Glu	Gly	Lys	Val	Ala	Asp	Thr	Asp	Val	Ala	Glu
45																	Asn	Ser	Ser	Thr	Ala	Thr	Asn	Pro	Lys	Asp	Ala	Ser	Asp	Lys	Ala	Asp
																	Val	Ile	Glu	Pro	Glu	Ser	Asp	Val	Val	Lys	Asp	Ala	Asp	Asn	Asn	Ile
50																	Asp	Lys	Asp	Val	Gln	His	Asp	Val	Asp	His	Leu	Ser	Asp	Met	Ser	Asp
																	Asn	Asn	His	Phe	Asp	Lys	Tyr	Asp	Leu	Lys	Glu	Met	Asp	Thr	Gln	Ile
55																	Ala	Lys	Asp	Thr	Asp	Arg	Asn	Val	Asp	Lys	Asp	Ala	Asp	Asn	Ser	Val
																	Gly	Met	Ser	Ser	Asn	Val	Asp	Thr	Asp	Lys	Asp	Ser	Asn	Lys	Asn	Lys

5 Asp Lys Val Ile Gln Leu Asn His Ile Ala Asp Lys Asn Asn His Thr
 785 790 795 800
 Gly Lys Ala Ala Lys Leu Asp Val Val Lys Gln Asn Tyr Asn Asn Thr
 805 810 815
 10 Asp Lys Val Thr Asp Lys Lys Thr Thr Glu His Leu Pro Ser Asp Ile
 820 825 830
 His Lys Thr Val Asp Lys Thr Val Lys Thr Lys Glu Lys Ala Gly Thr
 835 840 845
 Pro Ser Lys Glu Asn Lys Leu Ser Gln Ser Lys Met Leu Pro Lys Thr
 850 855 860
 15 Gly Glu Thr Thr Ser Ser Gln Ser Trp Trp Gly Leu Tyr Ala Leu Leu
 865 870 875 880
 Gly Met Leu Ala Leu Phe Ile Pro Lys Phe Arg Lys Glu Ser Lys
 885 890 895

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 <210> 22
 <211> 108
 <212> PRT
 <213> Staphylococcus aureus
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 <400> 22

30 Met Phe Met Ala Glu Asn Arg Leu Gln Leu Gln Lys Gly Ser Ala Glu
 1 5 10 15
 Glu Thr Ile Glu Arg Phe Tyr Asn Arg Gln Gly Ile Glu Thr Ile Glu
 20 25 30
 Gly Phe Gln Gln Met Phe Val Thr Lys Thr Leu Asn Thr Glu Asp Thr
 35 35 40 45
 Asp Glu Val Lys Ile Leu Thr Ile Trp Glu Ser Glu Asp Ser Phe Asn
 50 55 60
 40 Asn Trp Leu Asn Ser Asp Val Phe Lys Glu Ala His Lys Asn Val Arg
 65 70 75 80
 Leu Lys Ser Asp Asp Asp Gly Gln Gln Ser Pro Ile Leu Ser Asn Lys
 85 90 95
 Val Phe Lys Tyr Asp Ile Gly Tyr His Tyr Gln Lys
 100 105

45
 <210> 23
 <211> 327
 <212> PRT
 <213> Staphylococcus aureus
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 <400> 23

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EP 2 510 947 B1

Met Lys Met Lys Lys Leu Val Lys Ser Ser Val Ala Ser Ser Ile Ala
1 5 10 15
Leu Leu Leu Leu Ser Asn Thr Val Asp Ala Ala Gln His Ile Thr Pro
20 25 30
Val Ser Glu Lys Lys Val Asp Asp Lys Ile Thr Leu Tyr Lys Thr Thr
35 40 45
Ala Thr Ser Asp Asn Asp Lys Leu Asn Ile Ser Gln Ile Leu Thr Phe
50 55 60
Asn Phe Ile Lys Asp Lys Ser Tyr Asp Lys Asp Thr Leu Val Leu Lys
65 70 75 80
Ala Ala Gly Asn Ile Asn Ser Gly Tyr Lys Lys Pro Asn Pro Lys Asp
85 90 95
Tyr Asn Tyr Ser Gln Phe Tyr Trp Gly Gly Lys Tyr Asn Val Ser Val
100 105 110
Ser Ser Glu Ser Asn Asp Ala Val Asn Val Val Asp Tyr Ala Pro Lys
115 120 125
Asn Gln Asn Glu Glu Phe Gln Val Gln Gln Thr Leu Gly Tyr Ser Tyr
130 135 140
Gly Gly Asp Ile Asn Ile Ser Asn Gly Leu Ser Gly Gly Leu Asn Gly
145 150 155 160
Ser Lys Ser Phe Ser Glu Thr Ile Asn Tyr Lys Gln Glu Ser Tyr Arg
165 170 175
Thr Thr Ile Asp Arg Lys Thr Asn His Lys Ser Ile Gly Trp Gly Val
180 185 190
Glu Ala His Lys Ile Met Asn Asn Gly Trp Gly Pro Tyr Gly Arg Asp
195 200 205
Ser Tyr Asp Pro Thr Tyr Gly Asn Glu Leu Phe Leu Gly Gly Arg Gln
210 215 220
Ser Ser Ser Asn Ala Gly Gln Asn Phe Leu Pro Thr His Gln Met Pro
225 230 235 240
Leu Leu Ala Arg Gly Asn Phe Asn Pro Glu Phe Ile Ser Val Leu Ser
245 250 255
His Lys Gln Asn Asp Thr Lys Lys Ser Lys Ile Lys Val Thr Tyr Gln
260 265 270
Arg Glu Met Asp Arg Tyr Thr Asn Gln Trp Asn Arg Leu His Trp Val
275 280 285
Gly Asn Asn Tyr Lys Asn Gln Asn Thr Val Thr Phe Thr Ser Thr Tyr
290 295 300
Glu Val Asp Trp Gln Asn His Thr Val Lys Leu Ile Gly Thr Asp Ser
305 310 315 320
Lys Glu Thr Asn Pro Gly Val
325

<210> 24

<211> 301

<212> PRT

<213> Staphylococcus aureus

<400> 24

5 Met Ser Val Gly Leu Ile Ala Pro Leu Ala Ser Pro Ile Gln Glu Ser
 1 5 10 15
 Arg Ala Asn Thr Asn Ile Glu Asn Ile Gly Asp Gly Ala Glu Val Ile
 20 25 30
 10 Lys Arg Thr Glu Asp Val Ser Ser Lys Lys Trp Gly Val Thr Gln Asn
 35 40 45
 Val Gln Phe Asp Phe Val Lys Asp Lys Lys Tyr Asn Lys Asp Ala Leu
 50 55 60
 15 Ile Val Lys Met Gln Gly Phe Ile Asn Ser Arg Thr Ser Phe Ser Asp
 65 70 75 80
 Val Lys Gly Ser Gly Tyr Glu Leu Thr Lys Arg Met Ile Trp Pro Phe
 85 90 95
 20 Gln Tyr Asn Ile Gly Leu Thr Thr Lys Asp Pro Asn Val Ser Leu Ile
 100 105 110
 Asn Tyr Leu Pro Lys Asn Lys Ile Glu Thr Thr Asp Val Gly Gln Thr
 115 120 125
 25 Leu Gly Tyr Asn Ile Gly Gly Asn Phe Gln Ser Ala Pro Ser Ile Gly
 130 135 140
 Gly Asn Gly Ser Phe Asn Tyr Ser Lys Thr Ile Ser Tyr Thr Gln Lys
 145 150 155 160
 30 Ser Tyr Val Ser Glu Val Asp Lys Gln Asn Ser Lys Ser Val Lys Trp
 165 170 175
 Gly Val Lys Ala Asn Glu Phe Val Thr Pro Asp Gly Lys Lys Ser Ala
 180 185 190
 35 His Asp Arg Tyr Leu Phe Val Gln Ser Pro Asn Gly Pro Thr Gly Ser
 195 200 205
 Ala Arg Glu Tyr Phe Ala Pro Asp Asn Gln Leu Pro Pro Leu Val Gln
 210 215 220
 40 Ser Gly Phe Asn Pro Ser Phe Ile Thr Thr Leu Ser His Glu Lys Gly
 225 230 235 240
 Ser Ser Asp Thr Ser Glu Phe Glu Ile Ser Tyr Gly Arg Asn Leu Asp
 245 250 255
 45 Ile Thr Tyr Ala Thr Leu Phe Pro Arg Thr Gly Ile Tyr Ala Glu Arg
 260 265 270
 Lys His Asn Ala Phe Val Asn Arg Asn Phe Val Val Arg Tyr Glu Val
 275 280 285
 50 Asn Trp Lys Thr His Glu Ile Lys Val Lys Gly His Asn
 290 295 300

<210> 25

<211> 338

55 <212> PRT

<213> Staphylococcus aureus

<400> 25

EP 2 510 947 B1

1 Met Ile Lys Gln Leu Cys Lys Asn Ile Thr Ile Cys Thr Leu Ala Leu
 5 Ser Thr Thr Phe Thr Val Leu Pro Ala Thr Ser Phe Ala Lys Ile Asn
 Ser Glu Ile Lys Gln Val Ser Glu Lys Asn Leu Asp Gly Asp Thr Lys
 10 Met Tyr Thr Arg Thr Ala Thr Thr Ser Asp Ser Gln Lys Asn Ile Thr
 Gln Ser Leu Gln Phe Asn Phe Leu Thr Glu Pro Asn Tyr Asp Lys Glu
 15 Thr Val Phe Ile Lys Ala Lys Gly Thr Ile Gly Ser Gly Leu Arg Ile
 Leu Asp Pro Asn Gly Tyr Trp Asn Ser Thr Leu Arg Trp Pro Gly Ser
 20 Tyr Ser Val Ser Ile Gln Asn Val Asp Asp Asn Asn Asn Thr Asn Val
 Thr Asp Phe Ala Pro Lys Asn Gln Asp Glu Ser Arg Glu Val Lys Tyr
 25 Thr Tyr Gly Tyr Lys Thr Gly Gly Asp Phe Ser Ile Asn Arg Gly Gly
 Leu Thr Gly Asn Ile Thr Lys Glu Ser Asn Tyr Ser Glu Thr Ile Ser
 30 Tyr Gln Gln Pro Ser Tyr Arg Thr Leu Leu Asp Gln Ser Thr Ser His
 Lys Gly Val Gly Trp Lys Val Glu Ala His Leu Ile Asn Asn Met Gly
 35 His Asp His Thr Arg Gln Leu Thr Asn Asp Ser Asp Asn Arg Thr Lys
 Ser Glu Ile Phe Ser Leu Thr Arg Asn Gly Asn Leu Trp Ala Lys Asp
 40 Asn Phe Thr Pro Lys Asp Lys Met Pro Val Thr Val Ser Glu Gly Phe
 Asn Pro Glu Phe Leu Ala Val Met Ser His Asp Lys Lys Asp Lys Gly
 45 Lys Ser Gln Phe Val Val His Tyr Lys Arg Ser Met Asp Glu Phe Lys
 Ile Asp Trp Asn Arg His Gly Phe Trp Gly Tyr Trp Ser Gly Glu Asn
 50 His Val Asp Lys Lys Glu Glu Lys Leu Ser Ala Leu Tyr Glu Val Asp
 Trp Lys Thr His Asn Val Lys Phe Val Lys Val Leu Asn Asp Asn Glu
 55 Lys Lys

<210> 26

<211> 351

EP 2 510 947 B1

<212> PRT

<213> Staphylococcus aureus

<400> 26

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Met Lys Asn Lys Lys Arg Val Leu Ile Ala Ser Ser Leu Ser Cys Ala
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10

Ile Leu Leu Leu Ser Ala Ala Thr Thr Gln Ala Asn Ser Ala His Lys
20 25 30

Asp Ser Gln Asp Gln Asn Lys Lys Glu His Val Asp Lys Ser Gln Gln
35 40 45

15

Lys Asp Lys Arg Asn Val Thr Asn Lys Asp Lys Asn Ser Thr Ala Pro
50 55 60

Asp Asp Ile Gly Lys Asn Gly Lys Ile Thr Lys Arg Thr Glu Thr Val
65 70 75 80

20

Tyr Asp Glu Lys Thr Asn Ile Leu Gln Asn Leu Gln Phe Asp Phe Ile
85 90 95

Asp Asp Pro Thr Tyr Asp Lys Asn Val Leu Leu Val Lys Lys Gln Gly
100 105 110

25

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EP 2 510 947 B1

Ser Ile His Ser Asn Leu Lys Phe Glu Ser His Lys Glu Glu Lys Asn
 115 120 125
 5 Ser Asn Trp Leu Lys Tyr Pro Ser Glu Tyr His Val Asp Phe Gln Val
 130 135 140
 Lys Arg Asn Arg Lys Thr Glu Ile Leu Asp Gln Leu Pro Lys Asn Lys
 145 150 155 160
 10 Ile Ser Thr Ala Lys Val Asp Ser Thr Phe Ser Tyr Ser Ser Gly Gly
 165 170 175
 Lys Phe Asp Ser Thr Lys Gly Ile Gly Arg Thr Ser Ser Asn Ser Tyr
 180 185 190
 15 Ser Lys Thr Ile Ser Tyr Asn Gln Gln Asn Tyr Asp Thr Ile Ala Ser
 195 200 205
 Gly Lys Asn Asn Asn Trp His Val His Trp Ser Val Ile Ala Asn Asp
 210 215 220
 20 Leu Lys Tyr Gly Gly Glu Val Lys Asn Arg Asn Asp Glu Leu Leu Phe
 225 230 235 240
 Tyr Arg Asn Thr Arg Ile Ala Thr Val Glu Asn Pro Glu Leu Ser Phe
 245 250 255
 25 Ala Ser Lys Tyr Arg Tyr Pro Ala Leu Val Arg Ser Gly Phe Asn Pro
 260 265 270
 Glu Phe Leu Thr Tyr Leu Ser Asn Glu Lys Ser Asn Glu Lys Thr Gln
 275 280 285
 30 Phe Glu Val Thr Tyr Thr Arg Asn Gln Asp Ile Leu Lys Asn Arg Pro
 290 295 300
 Gly Ile His Tyr Ala Pro Pro Ile Leu Glu Lys Asn Lys Asp Gly Gln
 305 310 315 320
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<211> 177

<212> PRT

<213> Staphylococcus aureus

<400> 27

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20 25 30
Lys Gly Thr Asn His Glu Thr Val Gln Asp Leu Asn Gly Lys Asp Lys
35 40 45
Val His Val Gln Arg Val Val Asp Gly Asp Thr Phe Ile Ala Asn Gln
50 55 60
Asn Gly Lys Glu Ile Lys Val Arg Leu Ile Gly Val Asp Thr Pro Glu
65 70 75 80
Thr Val Lys Pro Asn Thr Pro Val Gln Pro Phe Gly Lys Glu Ala Ser
85 90 95
Asn Tyr Ser Lys Lys Thr Leu Thr Asn Gln Asp Val Tyr Leu Glu Tyr
100 105 110
Asp Lys Glu Lys Gln Asp Arg Tyr Gly Arg Thr Leu Ala Tyr Val Trp
115 120 125
Ile Ser Lys Asp Arg Met Tyr Asn Lys Glu Leu Val Glu Lys Gly Leu
130 135 140
Ala Arg Glu Lys Tyr Phe Ser Pro Asn Gly Lys Tyr Arg Asn Val Phe
145 150 155 160
Ile Glu Ala Gln Asn Lys Ala Lys Gln Gln Lys Leu Asn Ile Trp Ser
165 170 175
Lys

<210> 28

<211> 2271

<212> PRT

<213> Staphylococcus aureus

<400> 28

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5	Thr	Arg	Val	Arg	Leu	Tyr	Lys	Ser	Gly	Lys	Asn	Trp	Val	Lys	Ser	Gly
				20					25					30		
	Ile	Lys	Glu	Ile	Glu	Met	Phe	Lys	Ile	Met	Gly	Leu	Pro	Phe	Ile	Ser
			35					40					45			
10	His	Ser	Leu	Val	Ser	Gln	Asp	Asn	Gln	Ser	Ile	Ser	Lys	Lys	Met	Thr
		50					55					60				
	Gly	Tyr	Gly	Leu	Lys	Thr	Thr	Ala	Val	Ile	Gly	Gly	Ala	Phe	Thr	Val
	65					70					75					80
15	Asn	Met	Leu	His	Asp	Gln	Gln	Ala	Phe	Ala	Ala	Ser	Asp	Ala	Pro	Leu
					85					90					95	
	Thr	Ser	Glu	Leu	Asn	Thr	Gln	Ser	Glu	Thr	Val	Gly	Asn	Gln	Asn	Ser
				100					105					110		
20	Thr	Thr	Ile	Glu	Ala	Ser	Thr	Ser	Thr	Ala	Asp	Ser	Thr	Ser	Val	Thr
			115					120					125			
	Lys	Asn	Ser	Ser	Ser	Val	Gln	Thr	Ser	Asn	Ser	Asp	Thr	Val	Ser	Ser
		130					135					140				
25	Glu	Lys	Ser	Glu	Lys	Val	Thr	Ser	Thr	Thr	Asn	Ser	Thr	Ser	Asn	Gln
	145					150					155					160
	Gln	Glu	Lys	Leu	Thr	Ser	Thr	Ser	Glu	Ser	Thr	Ser	Ser	Lys	Asn	Thr
					165					170					175	
30	Thr	Ser	Ser	Ser	Asp	Thr	Lys	Ser	Val	Ala	Ser	Thr	Ser	Ser	Thr	Glu
				180					185					190		
	Gln	Pro	Ile	Asn	Thr	Ser	Thr	Asn	Gln	Ser	Thr	Ala	Ser	Asn	Asn	Thr
			195					200					205			
35	Ser	Gln	Ser	Thr	Thr	Pro	Ser	Ser	Val	Asn	Leu	Asn	Lys	Thr	Ser	Thr
		210					215					220				
	Thr	Ser	Thr	Ser	Thr	Ala	Pro	Val	Lys	Leu	Arg	Thr	Phe	Ser	Arg	Leu
	225					230					235					240
40	Ala	Met	Ser	Thr	Phe	Ala	Ser	Ala	Ala	Thr	Thr	Thr	Ala	Val	Thr	Ala
					245					250					255	

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Asn Thr Ile Thr Val Asn Lys Asp Asn Leu Lys Gln Tyr Met Thr Thr
 260 265 270
 Ser Gly Asn Ala Thr Tyr Asp Gln Ser Thr Gly Ile Val Thr Leu Thr
 275 280 285
 Gln Asp Ala Tyr Ser Gln Lys Gly Ala Ile Thr Leu Gly Thr Arg Ile
 290 295 300
 Asp Ser Asn Lys Ser Phe His Phe Ser Gly Lys Val Asn Leu Gly Asn
 305 310 315 320
 Lys Tyr Glu Gly His Gly Asn Gly Gly Asp Gly Ile Gly Phe Ala Phe
 325 330 335
 Ser Pro Gly Val Leu Gly Glu Thr Gly Leu Asn Gly Ala Ala Val Gly
 340 345 350
 Ile Gly Gly Leu Ser Asn Ala Phe Gly Phe Lys Leu Asp Thr Tyr His
 355 360 365
 Asn Thr Ser Lys Pro Asn Ser Ala Ala Lys Ala Asn Ala Asp Pro Ser
 370 375 380
 Asn Val Ala Gly Gly Gly Ala Phe Gly Ala Phe Val Thr Thr Asp Ser
 385 390 395 400
 Tyr Gly Val Ala Thr Thr Tyr Thr Ser Ser Ser Thr Ala Asp Asn Ala
 405 410 415
 Ala Lys Leu Asn Val Gln Pro Thr Asn Asn Thr Phe Gln Asp Phe Asp
 420 425 430
 Ile Asn Tyr Asn Gly Asp Thr Lys Val Met Thr Val Lys Tyr Ala Gly
 435 440 445
 Gln Thr Trp Thr Arg Asn Ile Ser Asp Trp Ile Ala Lys Ser Gly Thr
 450 455 460
 Thr Asn Phe Ser Leu Ser Met Thr Ala Ser Thr Gly Gly Ala Thr Asn
 465 470 475 480
 Leu Gln Gln Val Gln Phe Gly Thr Phe Glu Tyr Thr Glu Ser Ala Val
 485 490 495
 Thr Gln Val Arg Tyr Val Asp Val Thr Thr Gly Lys Asp Ile Ile Pro
 500 505 510
 Pro Lys Thr Tyr Ser Gly Asn Val Asp Gln Val Val Thr Ile Asp Asn
 515 520 525
 Gln Gln Ser Ala Leu Thr Ala Lys Gly Tyr Asn Tyr Thr Ser Val Asp
 530 535 540
 Ser Ser Tyr Ala Ser Thr Tyr Asn Asp Thr Asn Lys Thr Val Lys Met
 545 550 555 560
 Thr Asn Ala Gly Gln Ser Val Thr Tyr Tyr Phe Thr Asp Val Lys Ala
 565 570 575
 Pro Thr Val Thr Val Gly Asn Gln Thr Ile Glu Val Gly Lys Thr Met
 580 585 590
 Asn Pro Ile Val Leu Thr Thr Thr Asp Asn Gly Thr Gly Thr Val Thr
 595 600 605
 Asn Thr Val Thr Gly Leu Pro Ser Gly Leu Ser Tyr Asp Ser Ala Thr
 610 615 620

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	Asn	Ser	Ile	Ile	Gly	Thr	Pro	Thr	Lys	Ile	Gly	Gln	Ser	Thr	Val	Thr
	625					630					635					640
5	Val	Val	Ser	Thr	Asp	Gln	Ala	Asn	Asn	Lys	Ser	Thr	Thr	Thr	Phe	Thr
					645					650					655	
	Ile	Asn	Val	Val	Asp	Thr	Thr	Ala	Pro	Thr	Val	Thr	Pro	Ile	Gly	Asp
				660					665					670		
10	Gln	Ser	Ser	Glu	Val	Tyr	Ser	Pro	Ile	Ser	Pro	Ile	Lys	Ile	Ala	Thr
			675					680					685			
	Gln	Asp	Asn	Ser	Gly	Asn	Ala	Val	Thr	Asn	Thr	Val	Thr	Gly	Leu	Pro
		690					695					700				
15	Ser	Gly	Leu	Thr	Phe	Asp	Ser	Thr	Asn	Asn	Thr	Ile	Ser	Gly	Thr	Pro
	705				710						715					720
	Thr	Asn	Ile	Gly	Thr	Ser	Thr	Ile	Ser	Ile	Val	Ser	Thr	Asp	Ala	Ser
				725						730					735	
	Gly	Asn	Lys	Thr	Thr	Thr	Thr	Phe	Lys	Tyr	Glu	Val	Thr	Arg	Asn	Ser
				740					745					750		
20	Met	Ser	Asp	Ser	Val	Ser	Thr	Ser	Gly	Ser	Thr	Gln	Gln	Ser	Gln	Ser
			755					760					765			
	Val	Ser	Thr	Ser	Lys	Ala	Asp	Ser	Gln	Ser	Ala	Ser	Thr	Ser	Thr	Ser
		770					775					780				
25	Gly	Ser	Ile	Val	Val	Ser	Thr	Ser	Ala	Ser	Thr	Ser	Lys	Ser	Thr	Ser
	785					790					795					800
	Val	Ser	Leu	Ser	Asp	Ser	Val	Ser	Ala	Ser	Lys	Ser	Leu	Ser	Thr	Ser
				805					810						815	
30	Glu	Ser	Asn	Ser	Val	Ser	Ser	Ser	Thr	Ser	Thr	Ser	Leu	Val	Asn	Ser
				820					825					830		
	Gln	Ser	Val	Ser	Ser	Ser	Met	Ser	Asp	Ser	Ala	Ser	Lys	Ser	Thr	Ser
			835					840					845			
35	Leu	Ser	Asp	Ser	Ile	Ser	Asn	Ser	Ser	Ser	Thr	Glu	Lys	Ser	Glu	Ser
		850					855					860				
	Leu	Ser	Thr	Ser	Thr	Ser	Asp	Ser	Leu	Arg	Thr	Ser	Thr	Ser	Leu	Ser
	865					870					875					880
40	Asp	Ser	Leu	Ser	Met	Ser	Thr	Ser	Gly	Ser	Leu	Ser	Lys	Ser	Gln	Ser
					885					890					895	
	Leu	Ser	Thr	Ser	Ile	Ser	Gly	Ser	Ser	Ser	Thr	Ser	Ala	Ser	Leu	Ser
				900					905					910		
45	Asp	Ser	Thr	Ser	Asn	Ala	Ile	Ser	Thr	Ser	Thr	Ser	Leu	Ser	Glu	Ser
			915				920						925			
	Ala	Ser	Thr	Ser	Asp	Ser	Ile	Ser	Ile	Ser	Asn	Ser	Ile	Ala	Asn	Ser
		930					935					940				
50	Gln	Ser	Ala	Ser	Thr	Ser	Lys	Ser	Asp	Ser	Gln	Ser	Thr	Ser	Ile	Ser
	945					950					955					960
	Leu	Ser	Thr	Ser	Asp	Ser	Lys	Ser	Met	Ser	Thr	Ser	Glu	Ser	Leu	Ser
				965					970						975	
55	Asp	Ser	Thr	Ser	Thr	Ser	Gly	Ser	Val	Ser	Gly	Ser	Leu	Ser	Ile	Ala
				980					985					990		
	Ala	Ser	Gln	Ser	Val	Ser	Thr	Ser	Thr	Ser	Asp	Ser	Met	Ser	Thr	Ser

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	995	1000	1005
	Glu Ile Val Ser Asp Ser	Ile Ser Thr Ser Gly Ser	Leu Ser Ala Ser
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5	Asp Ser Lys Ser Met Ser Val Ser Ser Ser Met Ser Thr Ser Gln Ser		1040
	1025	1030	1035
	Gly Ser Thr Ser Glu Ser Leu Ser Asp Ser Gln Ser Thr Ser Asp Ser		1055
		1045	1050
10	Asp Ser Lys Ser Leu Ser Gln Ser Thr Ser Gln Ser Gly Ser Thr Ser		1070
		1060	1065
	Thr Ser Thr Ser Thr Ser Ala Ser Val Arg Thr Ser Glu Ser Gln Ser		1085
		1075	1080
15	Thr Ser Gly Ser Met Ser Ala Ser Gln Ser Asp Ser Met Ser Ile Ser		1100
		1090	1095
	Thr Ser Phe Ser Asp Ser Thr Ser Asp Ser Lys Ser Ala Ser Thr Ala		1120
		1105	1110
20	Ser Ser Glu Ser Ile Ser Gln Ser Ala Ser Thr Ser Thr Ser Gly Ser		1135
		1115	1120
	Val Ser Thr Ser Thr Ser Leu Ser Thr Ser Asn Ser Glu Arg Thr Ser		1150
		1140	1145
25	Thr Ser Met Ser Asp Ser Thr Ser Leu Ser Thr Ser Glu Ser Asp Ser		1165
		1155	1160
	Ile Ser Glu Ser Thr Ser Thr Ser Asp Ser Ile Ser Glu Ala Ile Ser		1180
		1170	1175
30	Ala Ser Glu Ser Thr Phe Ile Ser Leu Ser Glu Ser Asn Ser Thr Ser		1200
		1185	1190
	Asp Ser Glu Ser Gln Ser Ala Ser Ala Phe Leu Ser Glu Ser Leu Ser		1215
		1205	1210
35	Glu Ser Thr Ser Glu Ser Thr Ser Glu Ser Val Ser Ser Ser Thr Ser		1230
		1220	1225
	Glu Ser Thr Ser Leu Ser Asp Ser Thr Ser Glu Ser Gly Ser Thr Ser		1245
		1235	1240
40	Thr Ser Leu Ser Asn Ser Thr Ser Gly Ser Thr Ser Ile Ser Thr Ser		1260
		1250	1255
	Thr Ser Ile Ser Glu Ser Thr Ser Thr Phe Lys Ser Glu Ser Val Ser		1280
		1265	1270
45	Thr Ser Leu Ser Met Ser Thr Ser Thr Ser Leu Ser Asp Ser Thr Ser		1295
		1285	1290
	Leu Ser Thr Ser Leu Ser Asp Ser Thr Ser Asp Ser Lys Ser Asp Ser		1310
		1300	1305
50	Leu Ser Thr Ser Met Ser Thr Ser Asp Ser Ile Ser Thr Ser Lys Ser		1325
		1315	1320
	Asp Ser Ile Ser Thr Ser Thr Ser Leu Ser Gly Ser Thr Ser Glu Ser		1340
		1330	1335
	Glu Ser Asp Ser Thr Ser Ser Ser Glu Ser Lys Ser Asp Ser Thr Ser		1360
		1345	1350
55	Met Ser Ile Ser Met Ser Gln Ser Thr Ser Gly Ser Thr Ser Thr Ser		1375
		1365	1370

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Thr Ser Thr Ser Leu Ser Asp Ser Thr Ser Thr Ser Leu Ser Leu Ser
1380 1385 1390

5 Ala Ser Met Asn Gln Ser Gly Val Asp Ser Asn Ser Ala Ser Gln Ser
1395 1400 1405

Ala Ser Asn Ser Thr Ser Thr Ser Thr Ser Glu Ser Asp Ser Gln Ser
1410 1415 1420

10 Thr Ser Ser Tyr Thr Ser Gln Ser Thr Ser Gln Ser Glu Ser Thr Ser
1425 1430 1435 1440

Thr Ser Thr Ser Leu Ser Asp Ser Thr Ser Ile Ser Lys Ser Thr Ser
1445 1450 1455

15 Gln Ser Gly Ser Val Ser Thr Ser Ala Ser Leu Ser Gly Ser Glu Ser
1460 1465 1470

Glu Ser Asp Ser Gln Ser Ile Ser Thr Ser Ala Ser Glu Ser Thr Ser
1475 1480 1485

20 Glu Ser Ala Ser Thr Ser Leu Ser Asp Ser Thr Ser Thr Ser Asn Ser
1490 1495 1500

Gly Ser Ala Ser Thr Ser Thr Ser Leu Asn Asn Ser Ala Ser Ala Ser
1505 1510 1515 1520

25 Glu Ser Asp Leu Ser Ser Thr Ser Leu Ser Asp Ser Thr Ser Ala Ser
1525 1530 1535

Met Gln Ser Ser Glu Ser Asp Ser Gln Ser Thr Ser Ala Ser Leu Ser
1540 1545 1550

30 Asp Ser Leu Ser Thr Ser Thr Ser Asn Arg Met Ser Thr Ile Ala Ser
1555 1560 1565

Leu Ser Thr Ser Val Ser Thr Ser Glu Ser Gly Ser Thr Ser Glu Ser
1570 1575 1580

35 Thr Ser Glu Ser Asp Ser Thr Ser Thr Ser Leu Ser Asp Ser Gln Ser
1585 1590 1595 1600

Thr Ser Arg Ser Thr Ser Ala Ser Gly Ser Ala Ser Thr Ser Thr Ser
1605 1610 1615

40 Thr Ser Asp Ser Arg Ser Thr Ser Ala Ser Thr Ser Thr Ser Met Arg
1620 1625 1630

Thr Ser Thr Ser Asp Ser Gln Ser Met Ser Leu Ser Thr Ser Thr Ser
1635 1640 1645

45 Thr Ser Met Ser Asp Ser Thr Ser Leu Ser Asp Ser Val Ser Asp Ser
1650 1655 1660

Thr Ser Asp Ser Thr Ser Ala Ser Thr Ser Gly Ser Met Ser Val Ser
1665 1670 1675 1680

Ile Ser Leu Ser Asp Ser Thr Ser Thr Ser Thr Ser Ala Ser Glu Val
1685 1690 1695

50 Met Ser Ala Ser Ile Ser Asp Ser Gln Ser Met Ser Glu Ser Val Asn
1700 1705 1710

Asp Ser Glu Ser Val Ser Glu Ser Asn Ser Glu Ser Asp Ser Lys Ser
1715 1720 1725

55 Met Ser Gly Ser Thr Ser Val Ser Asp Ser Gly Ser Leu Ser Val Ser
1730 1735 1740

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Thr Ser Leu Arg Lys Ser Glu Ser Val Ser Glu Ser Ser Ser Leu Ser
 1745 1750 1755 1760
 Cys Ser Gln Ser Met Ser Asp Ser Val Ser Thr Ser Asp Ser Ser Ser
 1765 1770 1775
 Leu Ser Val Ser Thr Ser Leu Arg Ser Ser Glu Ser Val Ser Glu Ser
 1780 1785 1790
 Asp Ser Leu Ser Asp Ser Lys Ser Thr Ser Gly Ser Thr Ser Thr Ser
 1795 1800 1805
 Thr Ser Gly Ser Leu Ser Thr Ser Thr Ser Leu Ser Gly Ser Glu Ser
 1810 1815 1820
 Val Ser Glu Ser Thr Ser Leu Ser Asp Ser Ile Ser Met Ser Asp Ser
 1825 1830 1835 1840
 Thr Ser Thr Ser Asp Ser Asp Ser Leu Ser Gly Ser Ile Ser Leu Ser
 1845 1850 1855
 Gly Ser Thr Ser Leu Ser Thr Ser Asp Ser Leu Ser Asp Ser Lys Ser
 1860 1865 1870
 Leu Ser Ser Ser Gln Ser Met Ser Gly Ser Glu Ser Thr Ser Thr Ser
 1875 1880 1885
 Val Ser Asp Ser Gln Ser Ser Ser Thr Ser Asn Ser Gln Phe Asp Ser
 1890 1895 1900
 Met Ser Ile Ser Ala Ser Glu Ser Asp Ser Met Ser Thr Ser Asp Ser
 1905 1910 1915 1920
 Ser Ser Ile Ser Gly Ser Asn Ser Thr Ser Thr Ser Leu Ser Thr Ser
 1925 1930 1935
 Asp Ser Met Ser Gly Ser Val Ser Val Ser Thr Ser Thr Ser Leu Ser
 1940 1945 1950
 Asp Ser Ile Ser Gly Ser Thr Ser Val Ser Asp Ser Ser Ser Thr Ser
 1955 1960 1965
 Thr Ser Thr Ser Leu Ser Asp Ser Met Ser Gln Ser Gln Ser Thr Ser
 1970 1975 1980
 Thr Ser Ala Ser Gly Ser Leu Ser Thr Ser Ile Ser Thr Ser Met Ser
 1985 1990 1995 2000
 Met Ser Ala Ser Thr Ser Ser Ser Gln Ser Thr Ser Val Ser Thr Ser
 2005 2010 2015
 Leu Ser Thr Ser Asp Ser Ile Ser Asp Ser Thr Ser Ile Ser Ile Ser
 2020 2025 2030
 Gly Ser Gln Ser Thr Val Glu Ser Glu Ser Thr Ser Asp Ser Thr Ser
 2035 2040 2045
 Ile Ser Asp Ser Glu Ser Leu Ser Thr Ser Asp Ser Asp Ser Thr Ser
 2050 2055 2060
 Thr Ser Thr Ser Asp Ser Thr Ser Gly Ser Thr Ser Thr Ser Ile Ser
 2065 2070 2075 2080
 Glu Ser Leu Ser Thr Ser Gly Ser Gly Ser Thr Ser Val Ser Asp Ser
 2085 2090 2095
 Thr Ser Met Ser Glu Ser Asn Ser Ser Ser Val Ser Met Ser Gln Asp
 2100 2105 2110
 Lys Ser Asp Ser Thr Ser Ile Ser Asp Ser Glu Ser Val Ser Thr Ser

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	Thr Ser Thr Ser Leu Ser	Thr Ser Asp Ser Thr	Ser Thr Ser Glu Ser
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	Leu Ser Thr Ser Met Ser Gly Ser Gln Ser Ile Ser Asp Ser Thr Ser		
	2145	2150	2155
	Thr Ser Met Ser Gly Ser Thr Ser Thr Ser Glu Ser Asn Ser Met His		
		2165	2170
10			2175
	Pro Ser Asp Ser Met Ser Met His His Thr His Ser Thr Ser Thr Ser		
		2180	2185
	Arg Leu Ser Ser Glu Ala Thr Thr Ser Thr Ser Glu Ser Gln Ser Thr		
		2195	2200
15			2205
	Leu Ser Ala Thr Ser Glu Val Thr Lys His Asn Gly Thr Pro Ala Gln		
		2210	2215
	Ser Glu Lys Arg Leu Pro Asp Thr Gly Asp Ser Ile Lys Gln Asn Gly		
		2225	2230
20			2235
	Leu Leu Gly Gly Val Met Thr Leu Leu Val Gly Leu Gly Leu Met Lys		
		2245	2250
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	Arg Lys Lys Lys Lys Asp Glu Asn Asp Gln Asp Asp Ser Gln Ala		
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25			2270

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 5 20 25 30
 Pro Thr Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln
 35 40 45
 Pro Ala Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly
 10 50 55 60
 Ala Gln Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly
 65 70 75 80
 Gln Pro Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala
 15 85 90 95
 Gly Gly Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln
 100 105 110
 Ala Asp Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr
 115 120 125
 Pro Ala Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn
 130 135 140
 Asn Ala Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala
 145 150 155 160
 Ala Gln Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro
 165 170 175
 Asn Ala Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe
 180 185 190

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	Asp	Asp	Pro	Ala	Ile	Ser	Thr	Asp	Glu	Asn	Arg	Gln	Asp	Pro	Thr	Val
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5	Thr	Val	Thr	Asp	Lys	Val	Asn	Gly	Tyr	Ser	Leu	Ile	Asn	Asn	Gly	Lys
		210					215					220				
	Ile	Gly	Phe	Val	Asn	Ser	Glu	Leu	Arg	Arg	Ser	Asp	Met	Phe	Asp	Lys
	225					230					235					240
10	Asn	Asn	Pro	Gln	Asn	Tyr	Gln	Ala	Lys	Gly	Asn	Val	Ala	Ala	Leu	Gly
					245					250					255	
	Arg	Val	Asn	Ala	Asn	Asp	Ser	Thr	Asp	His	Gly	Asn	Phe	Asn	Gly	Ile
				260					265					270		
15	Ser	Lys	Thr	Val	Asn	Val	Lys	Pro	Asp	Ser	Glu	Leu	Ile	Ile	Asn	Phe
			275					280					285			
	Thr	Thr	Met	Gln	Thr	Asn	Ser	Lys	Gln	Gly	Ala	Thr	Asn	Leu	Val	Ile
		290					295					300				
20	Lys	Asp	Ala	Lys	Lys	Asn	Thr	Glu	Leu	Ala	Thr	Val	Asn	Val	Ala	Lys
	305					310					315					320
	Thr	Gly	Thr	Ala	His	Leu	Phe	Lys	Val	Pro	Thr	Asp	Ala	Asp	Arg	Leu
					325					330					335	
25	Asp	Leu	Gln	Phe	Ile	Pro	Asp	Asn	Thr	Ala	Val	Ala	Asp	Ala	Ser	Arg
				340					345					350		
	Ile	Thr	Thr	Asn	Lys	Asp	Gly	Tyr	Lys	Tyr	Tyr	Ser	Phe	Ile	Asp	Asn
			355					360					365			
30	Val	Gly	Leu	Phe	Ser	Gly	Ser	His	Leu	Tyr	Val	Lys	Asn	Arg	Asp	Leu
		370					375					380				
	Ala	Pro	Lys	Ala	Thr	Asn	Asn	Lys	Glu	Tyr	Thr	Ile	Asn	Thr	Glu	Ile
	385					390					395					400
35	Gly	Asn	Asn	Gly	Asn	Phe	Gly	Ala	Ser	Leu	Lys	Ala	Asp	Gln	Phe	Lys
					405					410					415	
	Tyr	Glu	Val	Thr	Leu	Pro	Gln	Gly	Val	Thr	Tyr	Val	Asn	Asn	Ser	Leu
				420					425					430		
40	Thr	Thr	Thr	Phe	Pro	Asn	Gly	Asn	Glu	Asp	Ser	Thr	Val	Leu	Lys	Asn
			435					440					445			
	Met	Thr	Val	Asn	Tyr	Asp	Gln	Asn	Ala	Asn	Lys	Val	Thr	Phe	Thr	Ser
		450					455					460				
45	Gln	Gly	Val	Thr	Thr	Ala	Arg	Gly	Thr	His	Thr	Lys	Glu	Val	Leu	Phe
	465					470					475					480
	Pro	Asp	Lys	Ser	Leu	Lys	Leu	Ser	Tyr	Lys	Val	Asn	Val	Ala	Asn	Ile
					485					490					495	
50	Asp	Thr	Pro	Lys	Asn	Ile	Asp	Phe	Asn	Glu	Lys	Leu	Thr	Tyr	Arg	Thr
				500					505					510		
	Ala	Ser	Asp	Val	Val	Ile	Asn	Asn	Ala	Gln	Pro	Glu	Val	Thr	Leu	Thr
			515					520					525			
	Ala	Asp	Pro	Phe	Ser	Val	Ala	Val	Glu	Met	Asn	Lys	Asp	Ala	Leu	Gln
		530					535					540				
55	Gln	Gln	Val	Asn	Ser	Gln	Val	Asp	Asn	Ser	His	Tyr	Thr	Thr	Ala	Ser
	545					550					555					560

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Ile Ala Glu Tyr Asn Lys Leu Lys Gln Gln Ala Asp Thr Ile Leu Asn
 565 570 575
 Glu Asp Ala Asn His Val Lys Thr Ala Asn Arg Ala Ser Gln Ala Asp
 580 585 590
 Ile Asp Gly Leu Val Thr Lys Leu Gln Ala Ala Leu Ile Asp Asn Gln
 595 600 605
 Ala Ala Ile Ala Glu Leu Asp Thr Lys Ala Gln Glu Lys Val Thr Ala
 610 615 620
 Ala Gln Gln Ser Lys Lys Val Thr Gln Asp Glu Val Ala Ala Leu Val
 625 630 635 640
 Thr Lys Ile Asn Asn Asp Lys Asn Asn Ala Ile Ala Glu Ile Asn Lys
 645 650 655
 Gln Thr Thr Ala Gln Gly Val Thr Thr Glu Lys Asp Asn Gly Ile Ala
 660 665 670
 Val Leu Glu Gln Asp Val Ile Thr Pro Thr Val Lys Pro Gln Ala Lys
 675 680 685
 Gln Asp Ile Ile Gln Ala Val Thr Thr Arg Lys Gln Gln Ile Lys Lys
 690 695 700
 Ser Asn Ala Ser Leu Gln Asp Glu Lys Asp Val Ala Asn Asp Lys Ile
 705 710 715 720
 Gly Lys Ile Glu Thr Lys Ala Ile Lys Asp Ile Asp Ala Ala Thr Thr
 725 730 735
 Asn Ala Gln Val Glu Ala Ile Lys Thr Lys Ala Ile Asn Asp Ile Asn
 740 745 750
 Gln Thr Thr Pro Ala Thr Thr Ala Lys Ala Ala Ala Leu Glu Glu Phe
 755 760 765
 Asp Glu Val Val Gln Ala Gln Ile Asp Gln Ala Pro Leu Asn Pro Asp
 770 775 780
 Thr Thr Asn Glu Glu Val Ala Glu Ala Ile Glu Arg Ile Asn Ala Ala
 785 790 795 800
 Lys Val Ser Gly Val Lys Ala Ile Glu Ala Thr Thr Thr Ala Gln Asp
 805 810 815
 Leu Glu Arg Val Lys Asn Glu Glu Ile Ser Lys Ile Glu Asn Ile Thr
 820 825 830
 Asp Ser Thr Gln Thr Lys Met Asp Ala Tyr Asn Glu Val Lys Gln Ala
 835 840 845
 Ala Thr Ala Arg Lys Ala Gln Asn Ala Thr Val Ser Asn Ala Thr Asn
 850 855 860
 Glu Glu Val Ala Glu Ala Asp Ala Ala Val Asp Ala Ala Gln Lys Gln
 865 870 875 880
 Gly Leu His Asp Ile Gln Val Val Lys Ser Lys Gln Glu Val Ala Asp
 885 890 895
 Thr Lys Ser Lys Val Leu Asp Lys Ile Asn Ala Ile Gln Thr Gln Ala
 900 905 910
 Lys Val Lys Pro Ala Ala Asp Thr Glu Val Glu Asn Ala Tyr Asn Thr
 915 920 925
 Arg Lys Gln Glu Ile Gln Asn Ser Asn Ala Ser Thr Thr Glu Glu Lys

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	930		935		940
	Gln 945	Ala Ala Tyr Thr	Glu 950	Leu Asp Thr Lys	Lys 955 Gln Glu Ala Arg Thr 960
5	Asn	Leu Asp Ala 965	Asn Thr	Asn Ser Asp 970	Val Thr Thr Ala Lys 975 Asp
	Asn Ser Ile 980	Ala Ala Ile	Asn Gln	Val 985	Gln Ala Ala Thr Thr 990 Lys Lys
10	Ser Asp Ala 995	Lys Ala Glu	Ile Ala 1000	Gln Lys Ala	Ser Glu Arg Lys Thr 1005
	Ala Ile Glu 1010	Ala Met	Asn Asp 1015	Ser Thr Thr	Glu Glu Gln Gln Ala Ala 1020
15	Lys Asp Lys Val Asp 1025	Gln Ala Val Val	Thr Ala 1030	Asn Ala Asp Ile 1035	Asp 1040
	Asn Ala Ala Ala 1045	Asn Asp Val	Asp Asn 1050	Ala Lys Thr Thr	Asn Glu 1055
20	Ala Thr Ile 1060	Ala Ala Ile	Thr Pro 1065	Asp Ala Asn Val	Lys Pro Ala Ala 1070
	Lys Gln Ala Ile Ala Asp 1075	Lys Val	Gln Ala Gln Glu Thr 1080	Ala Ile Asp	1085
25	Gly Asn Asn Gly Ser Thr 1090	Thr Glu Glu Lys Ala 1095	Ala Ala Lys Gln Gln		
	Val Gln Thr Glu Lys Thr Thr 1105	Ala Asp Ala 1110	Ala Ile Asp Ala Ala His 1115		1120
30	Thr Asn Ala Glu Val Glu Ala Ala Lys 1125	Lys Ala Ala Ile Ala Lys Ile 1130			1135
	Glu Ala Ile Gln Pro Ala Thr Thr Thr 1140	Lys Asp Asn Ala Lys Glu Ala 1145			1150
35	Ile Ala Thr Lys Ala Asn Glu Arg Lys Thr Ala Ile Ala Gln Thr Gln 1155				1165
	Asp Ile Thr Ala Glu Glu Ile Ala Ala Ala Asn Ala Asp Val Asp Asn 1170				1180
40	Ala Val Thr Gln Ala Asn Ser Asn Ile Glu Ala Ala Asn Ser Gln Asn 1185				1200
	Asp Val Asp Gln Ala Lys Thr Thr Gly Glu Asn Ser Ile Asp Gln Val 1205				1215
45	Thr Pro Thr Val Asn Lys Lys Ala Thr Ala Arg Asn Glu Ile Thr Ala 1220				1230
	Ile Leu Asn Asn Lys Leu Gln Glu Ile Gln Ala Thr Pro Asp Ala Thr 1235				1245
50	Asp Glu Glu Lys Gln Ala Ala Asp Ala Glu Ala Asn Thr Glu Asn Gly 1250				1260
	Lys Ala Asn Gln Ala Ile Ser Ala Ala Thr Thr Asn Ala Gln Val Asp 1265				1280
55	Glu Ala Lys Ala Asn Ala Glu Ala Ala Ile Asn Ala Val Thr Pro Lys 1285				1295
	Val Val Lys Lys Gln Ala Ala Lys Asp Glu Ile Asp Gln Leu Gln Ala 1300				1310

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Thr Gln Thr Asn Val Ile Asn Asn Asp Gln Asn Ala Thr Thr Glu Glu
 1315 1320 1325
 Lys Glu Ala Ala Ile Gln Gln Leu Ala Thr Ala Val Thr Asp Ala Lys
 1330 1335 1340
 Asn Asn Ile Thr Ala Ala Thr Asp Asp Asn Gly Val Asp Gln Ala Lys
 1345 1350 1355 1360
 Asp Ala Gly Lys Asn Ser Ile Gln Ser Thr Gln Pro Ala Thr Ala Val
 1365 1370 1375
 Lys Ser Asn Ala Lys Asn Asp Val Asp Gln Ala Val Thr Thr Gln Asn
 1380 1385 1390
 Gln Ala Ile Asp Asn Thr Thr Gly Ala Thr Thr Glu Glu Lys Asn Ala
 1395 1400 1405
 Ala Lys Asp Leu Val Leu Lys Ala Lys Glu Lys Ala Tyr Gln Asp Ile
 1410 1415 1420
 Leu Asn Ala Gln Thr Thr Asn Asp Val Thr Gln Ile Lys Asp Gln Ala
 1425 1430 1435 1440
 Val Ala Asp Ile Gln Gly Ile Thr Ala Asp Thr Thr Ile Lys Asp Val
 1445 1450 1455
 Ala Lys Asp Glu Leu Ala Thr Lys Ala Asn Glu Gln Lys Ala Leu Ile
 1460 1465 1470
 Ala Gln Thr Ala Asp Ala Thr Thr Glu Glu Lys Glu Gln Ala Asn Gln
 1475 1480 1485
 Gln Val Asp Ala Gln Leu Thr Gln Gly Asn Gln Asn Ile Glu Asn Ala
 1490 1495 1500
 Gln Ser Ile Asp Asp Val Asn Thr Ala Lys Asp Asn Ala Ile Gln Ala
 1505 1510 1515 1520
 Ile Asp Pro Ile Gln Ala Ser Thr Asp Val Lys Thr Asn Ala Arg Ala
 1525 1530 1535
 Glu Leu Leu Thr Glu Met Gln Asn Lys Ile Thr Glu Ile Leu Asn Asn
 1540 1545 1550
 Asn Glu Thr Thr Asn Glu Glu Lys Gly Asn Asp Ile Gly Pro Val Arg
 1555 1560 1565
 Ala Ala Tyr Glu Glu Gly Leu Asn Asn Ile Asn Ala Ala Thr Thr Thr
 1570 1575 1580
 Gly Asp Val Thr Thr Ala Lys Asp Thr Ala Val Gln Lys Val Gln Gln
 1585 1590 1595 1600
 Leu His Ala Asn Pro Val Lys Lys Pro Ala Gly Lys Lys Glu Leu Asp
 1605 1610 1615
 Gln Ala Ala Ala Asp Lys Lys Thr Gln Ile Glu Gln Thr Pro Asn Ala
 1620 1625 1630
 Ser Gln Gln Glu Ile Asn Asp Ala Lys Gln Glu Val Asp Thr Glu Leu
 1635 1640 1645
 Asn Gln Ala Lys Thr Asn Val Asp Gln Ser Ser Thr Asn Glu Tyr Val
 1650 1655 1660
 Asp Asn Ala Val Lys Glu Gly Lys Ala Lys Ile Asn Ala Val Lys Thr
 1665 1670 1675 1680

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Phe Ser Glu Tyr Lys Lys Asp Ala Leu Ala Lys Ile Glu Asp Ala Tyr
 1685 1690 1695
 5 Asn Ala Lys Val Asn Glu Ala Asp Asn Ser Asn Ala Ser Thr Ser Ser
 1700 1705 1710
 Glu Ile Ala Glu Ala Lys Gln Lys Leu Ala Glu Leu Lys Gln Thr Ala
 1715 1720 1725
 10 Asp Gln Asn Val Asn Gln Ala Thr Ser Lys Asp Asp Ile Glu Val Gln
 1730 1735 1740
 Ile His Asn Asp Leu Asp Asn Ile Asn Asp Tyr Thr Ile Pro Thr Gly
 1745 1750 1755 1760
 15 Lys Lys Glu Ser Ala Thr Thr Asp Leu Tyr Ala Tyr Ala Asp Gln Lys
 1765 1770 1775
 Lys Asn Asn Ile Ser Ala Asp Thr Asn Ala Thr Gln Asp Glu Lys Gln
 1780 1785 1790
 20 Gln Ala Ile Lys Gln Val Asp Gln Asn Val Gln Thr Ala Leu Glu Ser
 1795 1800 1805
 Ile Asn Asn Gly Val Asp Asn Gly Asp Val Asp Asp Ala Leu Thr Gln
 1810 1815 1820
 25 Gly Lys Ala Ala Ile Asp Ala Ile Gln Val Asp Ala Thr Val Lys Pro
 1825 1830 1835 1840
 Lys Ala Asn Gln Ala Ile Glu Val Lys Ala Glu Asp Thr Lys Glu Ser
 1845 1850 1855
 30 Ile Asp Gln Ser Asp Gln Leu Thr Ala Glu Glu Lys Thr Glu Ala Leu
 1860 1865 1870
 Ala Met Ile Lys Gln Ile Thr Asp Gln Ala Lys Gln Gly Ile Thr Asp
 1875 1880 1885
 35 Ala Thr Thr Thr Ala Glu Val Glu Lys Ala Lys Ala Gln Gly Leu Glu
 1890 1895 1900
 Ala Phe Asp Asn Ile Gln Ile Asp Ser Thr Glu Lys Gln Lys Ala Ile
 1905 1910 1915 1920
 Glu Glu Leu Glu Thr Ala Leu Asp Gln Ile Glu Ala Gly Val Asn Val
 1925 1930 1935
 40 Asn Ala Asp Ala Thr Thr Glu Glu Lys Glu Ala Phe Thr Asn Ala Leu
 1940 1945 1950
 Glu Asp Ile Leu Ser Lys Ala Thr Glu Asp Ile Ser Asp Gln Thr Thr
 1955 1960 1965
 45 Asn Ala Glu Ile Ala Thr Val Lys Asn Ser Ala Leu Glu Gln Leu Lys
 1970 1975 1980
 Ala Gln Arg Ile Asn Pro Glu Val Lys Lys Asn Ala Leu Glu Ala Ile
 1985 1990 1995 2000
 50 Arg Glu Val Val Asn Lys Gln Ile Glu Ile Ile Lys Asn Ala Asp Ala
 2005 2010 2015
 Asp Ala Ser Ala Lys Glu Ile Ala Arg Thr Asp Leu Gly Arg Tyr Phe
 2020 2025 2030
 55 Asp Arg Phe Ala Asp Lys Leu Asp Lys Thr Gln Thr Asn Ala Glu Val
 2035 2040 2045
 Ala Glu Leu Gln Asn Val Thr Ile Pro Ala Ile Glu Ala Ile Val Pro

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	2050	2055	2060
	Gln Asn Asp Pro Asp Ala Asn Asp Thr Asn Asn Gly Ile Asp Asn Asn	2065	2070 2075 2080
5	Asp Ala Thr Ala Asn Ser Asn Ala Asn Ala Thr Pro Glu Asn Thr Gly	2085	2090 2095
	Gln Pro Asn Val Ser Glu Thr Thr Ala Asn Gly Lys Ala Asp Ala Ser	2100	2105 2110
10	Pro Thr Thr Pro Asn Asn Ser Asp Ala Ala Thr Gly Glu Thr Thr Ala	2115	2120 2125
	Thr Ser Ala Thr Asp Asp Ala Asn Asp Lys Pro Gln Ala Asn Asn Asn	2130	2135 2140
15	Ser Ser Val Asp Ala Ser Thr Asn Ser Pro Thr Met Asp Asn Asp Val	2145	2150 2155 2160
	Thr Ser Lys Pro Glu Val Glu Ser Thr Asn Asn Gly Thr Thr Asp Lys	2165	2170 2175
20	Pro Val Thr Glu Thr Asp Asn Ala Thr Pro Ala Glu Ser Thr Thr Asn	2180	2185 2190
	Asn Asn Ser Thr Thr Thr Ala Thr Asn Glu Asn Ala Pro Thr Gly Ser	2195	2200 2205
25	Thr Ala Thr Ala Pro Thr Thr Ala Ser Thr Glu Ala Ala Ser Ser Ala	2210	2215 2220
	Asp Ser Lys Asp Asn Ala Ser Val Asn Asp Ser Lys Gln Asn Ala Glu	2225	2230 2235 2240
30	Val Asn Asn Ser Ala Glu Ser Gln Ser Thr Asn Asp Lys Val Ala Gln	2245	2250 2255
	Pro Lys Ser Glu Asn Lys Ala Lys Ala Glu Lys Asp Gly Ser Asp Ser	2260	2265 2270
35	Thr Asn Gln Ser Met Val Glu Ser Thr Thr Glu Thr Leu Pro Ser Ala	2275	2280 2285
	Asp Ile Thr Glu Pro Asn Val Pro Ser Asn Thr Ser Lys Asp Lys Glu	2290	2295 2300
40	Glu Ser Thr Thr Asn Gln Thr Asp Ala Gly Gln Leu Lys Ser Glu Thr	2305	2310 2315 2320
	Asn Val Ala Ser Asn Glu Ala Asp Lys Ser Pro Ser Lys Ala Asp Thr	2325	2330 2335
45	Glu Val Ser Asn Lys Pro Ser Thr Ser Ala Ser Ser Glu Ala Lys Glu	2340	2345 2350
	Lys Met Thr Ser Thr Asn Val Ser Gln Lys Asp Asp Thr Ala Thr Ala	2355	2360 2365
50	Asp Thr Asn Asp Thr Gln Lys Ser Val Gly Ser Ala Ala Asn Asn Lys	2370	2375 2380
	Ala Thr Gln Asn Asp Gly Ala Asn Ala Ser Pro Ala Thr Val Ser Asn	2385	2390 2395 2400
55	Gly Ser Asn Ser Ala Asn Gln Asp Met Leu Asn Val Thr Asn Thr Asp	2405	2410 2415
	Asp His Gln Ala Lys Thr Lys Ser Ala Gln Gln Gly Lys Val Asn Lys	2420	2425 2430

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Ala Lys Gln Gln Ala Lys Thr Leu Pro Asp Thr Gly Met Ser His Asn
2435 2440 2445
Asp Asp Leu Pro Tyr Ala Glu Leu Ala Leu Gly Ala Gly Met Ala Phe
2450 2455 2460
Leu Ile Arg Arg Phe Thr Lys Lys Asp Gln Gln Thr Glu Glu
2465 2470 2475

<210> 30
<211> 2186
<212> PRT
<213> Staphylococcus aureus

<400> 30

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Met Asn Leu Leu Lys Lys Asn Lys Tyr Ser Ile Arg Lys Tyr Lys Val
1 5 10 15
Gly Ile Phe Ser Thr Leu Ile Gly Thr Val Leu Leu Leu Ser Asn Pro
5 20 25 30
Asn Gly Ala Gln Ala Leu Thr Thr Asp Asn Asn Val Gln Ser Asp Thr
35 40 45
Asn Gln Ala Thr Pro Val Asn Ser Gln Asp Lys Asp Val Ala Asn Asn
10 50 55 60
Arg Gly Leu Ala Asn Ser Ala Gln Asn Thr Pro Asn Gln Ser Ala Thr
65 70 75 80
Thr Asn Gln Ala Thr Asn Gln Ala Leu Val Asn His Asn Asn Gly Ser
15 85 90 95
Ile Val Asn Gln Ala Thr Pro Thr Ser Val Gln Ser Ser Thr Pro Ser
100 105 110
Ala Gln Asn Asn Asn His Thr Asp Gly Asn Thr Thr Ala Thr Glu Thr
20 115 120 125
Val Ser Asn Ala Asn Asn Asn Asp Val Val Ser Asn Asn Thr Ala Leu
130 135 140
Asn Val Pro Thr Lys Thr Asn Glu Asn Gly Ser Gly Gly His Leu Thr
25 145 150 155 160
Leu Lys Glu Ile Gln Glu Asp Val Arg His Ser Ser Asn Lys Pro Glu
165 170 175
Leu Val Ala Ile Ala Glu Pro Ala Ser Asn Arg Pro Lys Lys Arg Ser
30 180 185 190
Arg Arg Ala Ala Pro Ala Asp Pro Asn Ala Thr Pro Ala Asp Pro Ala
195 200 205
Ala Ala Ala Val Gly Asn Gly Gly Ala Pro Val Ala Ile Thr Ala Pro
35 210 215 220
Tyr Thr Pro Thr Thr Asp Pro Asn Ala Asn Asn Ala Gly Gln Asn Ala
225 230 235 240
Pro Asn Glu Val Leu Ser Phe Asp Asp Asn Gly Ile Arg Pro Ser Thr
40 245 250 255
Asn Arg Ser Val Pro Thr Val Asn Val Val Asn Asn Leu Pro Gly Phe
260 265 270
Thr Leu Ile Asn Gly Gly Lys Val Gly Val Phe Ser His Ala Met Val
45 275 280 285

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	Arg	Thr	Ser	Met	Phe	Asp	Ser	Gly	Asp	Asn	Lys	Asn	Tyr	Gln	Ala	Gln
	290						295					300				
5	Gly	Asn	Val	Ile	Ala	Leu	Gly	Arg	Ile	His	Gly	Thr	Asp	Thr	Asn	Asp
	305					310					315					320
	His	Gly	Asp	Phe	Asn	Gly	Ile	Glu	Lys	Ala	Leu	Thr	Val	Asn	Pro	Asn
					325					330					335	
10	Ser	Glu	Leu	Ile	Phe	Glu	Phe	Asn	Thr	Met	Thr	Thr	Lys	Asn	Gly	Gln
				340					345					350		
	Gly	Ala	Thr	Asn	Val	Ile	Ile	Lys	Asn	Ala	Asp	Thr	Asn	Asp	Thr	Ile
			355					360					365			
15	Ala	Glu	Lys	Thr	Val	Glu	Gly	Gly	Pro	Thr	Leu	Arg	Leu	Phe	Lys	Val
		370					375					380				
	Pro	Asp	Asn	Val	Arg	Asn	Leu	Lys	Ile	Gln	Phe	Val	Pro	Lys	Asn	Asp
	385					390					395					400
20	Ala	Ile	Thr	Asp	Ala	Arg	Gly	Ile	Tyr	Gln	Leu	Lys	Asp	Gly	Tyr	Lys
					405					410					415	
	Tyr	Tyr	Ser	Phe	Val	Asp	Ser	Ile	Gly	Leu	His	Ser	Gly	Ser	His	Val
				420					425					430		
25	Phe	Val	Glu	Arg	Arg	Thr	Met	Asp	Pro	Thr	Ala	Thr	Asn	Asn	Lys	Glu
			435					440					445			
	Phe	Thr	Val	Thr	Thr	Ser	Leu	Lys	Asn	Asn	Gly	Asn	Ser	Gly	Ala	Ser
		450					455					460				
30	Leu	Asp	Thr	Asn	Asp	Phe	Val	Tyr	Gln	Val	Gln	Leu	Pro	Glu	Gly	Val
	465					470				475						480
	Glu	Tyr	Val	Asn	Asn	Ser	Leu	Thr	Lys	Asp	Phe	Pro	Ser	Asn	Asn	Ser
					485					490					495	
35	Gly	Val	Asp	Val	Asn	Asp	Met	Asn	Val	Thr	Tyr	Asp	Ala	Ala	Asn	Arg
				500					505					510		
	Val	Ile	Thr	Ile	Lys	Ser	Thr	Gly	Gly	Gly	Thr	Ala	Asn	Ser	Pro	Ala
		515						520					525			
40	Arg	Leu	Met	Pro	Asp	Lys	Ile	Leu	Asp	Leu	Arg	Tyr	Lys	Leu	Arg	Val
		530					535					540				
	Asn	Asn	Val	Pro	Thr	Pro	Arg	Thr	Val	Thr	Phe	Asn	Glu	Thr	Leu	Thr
	545					550					555					560
	Tyr	Lys	Thr	Tyr	Thr	Gln	Asp	Phe	Ile	Asn	Ser	Ala	Ala	Glu	Ser	His
					565					570					575	
45	Thr	Val	Ser	Thr	Asn	Pro	Tyr	Thr	Ile	Asp	Ile	Ile	Met	Asn	Lys	Asp
				580					585					590		
	Ala	Leu	Gln	Ala	Glu	Val	Asp	Arg	Arg	Ile	Gln	Gln	Ala	Asp	Tyr	Thr
			595					600					605			
50	Phe	Ala	Ser	Leu	Asp	Ile	Phe	Asn	Gly	Leu	Lys	Arg	Arg	Ala	Gln	Thr
		610					615					620				
	Ile	Leu	Asp	Glu	Asn	Arg	Asn	Asn	Val	Pro	Leu	Asn	Lys	Arg	Val	Ser
	625					630					635					640
55	Gln	Ala	Tyr	Ile	Asp	Ser	Leu	Thr	Asn	Gln	Met	Gln	His	Thr	Leu	Ile
					645					650					655	
	Arg	Ser	Val	Asp	Ala	Glu	Asn	Ala	Val	Asn	Lys	Lys	Val	Asp	Gln	Met

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	660							665							670						
	Glu	Asp	Leu	Val	Asn	Gln	Asn	Asp	Glu	Leu	Thr	Asp	Glu	Glu	Lys	Gln					
			675					680					685								
5	Ala	Ala	Ile	Gln	Val	Ile	Glu	Glu	His	Lys	Asn	Glu	Ile	Ile	Gly	Asn					
		690					695					700									
	Ile	Gly	Asp	Gln	Thr	Thr	Asp	Asp	Gly	Val	Thr	Arg	Ile	Lys	Asp	Gln					
	705					710					715					720					
10	Gly	Ile	Gln	Thr	Leu	Ser	Gly	Asp	Thr	Ala	Thr	Pro	Val	Val	Lys	Pro					
					725					730					735						
	Asn	Ala	Lys	Lys	Ala	Ile	Arg	Asp	Lys	Ala	Thr	Lys	Gln	Arg	Glu	Ile					
				740					745					750							
15	Ile	Asn	Ala	Thr	Pro	Asp	Ala	Thr	Glu	Asp	Glu	Ile	Gln	Asp	Ala	Leu					
			755					760					765								
	Asn	Gln	Leu	Ala	Thr	Asp	Glu	Thr	Asp	Ala	Ile	Asp	Asn	Val	Thr	Asn					
		770					775					780									
20	Ala	Thr	Thr	Asn	Ala	Asp	Val	Glu	Thr	Ala	Lys	Asn	Asn	Gly	Ile	Asn					
	785					790					795					800					
	Thr	Ile	Gly	Ala	Val	Val	Pro	Gln	Val	Thr	His	Lys	Lys	Ala	Ala	Arg					
					805					810					815						
25	Asp	Ala	Ile	Asn	Gln	Ala	Thr	Ala	Thr	Lys	Arg	Gln	Gln	Ile	Asn	Ser					
				820					825					830							
	Asn	Arg	Glu	Ala	Thr	Gln	Glu	Glu	Lys	Asn	Ala	Ala	Leu	Asn	Glu	Leu					
			835					840					845								
30	Thr	Gln	Ala	Thr	Asn	His	Ala	Leu	Glu	Gln	Ile	Asn	Gln	Ala	Thr	Thr					
		850					855					860									
	Asn	Ala	Asn	Val	Asp	Asn	Ala	Lys	Gly	Asp	Gly	Leu	Asn	Ala	Ile	Asn					
	865					870					875					880					
35	Pro	Ile	Ala	Pro	Val	Thr	Val	Val	Lys	Gln	Ala	Ala	Arg	Asp	Ala	Val					
					885					890					895						
	Ser	His	Asp	Ala	Gln	Gln	His	Ile	Ala	Glu	Ile	Asn	Ala	Asn	Pro	Asp					
				900					905					910							
40	Ala	Thr	Gln	Glu	Glu	Arg	Gln	Ala	Ala	Ile	Asp	Lys	Val	Asn	Ala	Ala					
			915					920					925								
	Val	Thr	Ala	Ala	Asn	Thr	Asn	Ile	Leu	Asn	Ala	Asn	Thr	Asn	Ala	Asp					
		930					935					940									
45	Val	Glu	Gln	Val	Lys	Thr	Asn	Ala	Ile	Gln	Gly	Ile	Gln	Ala	Ile	Thr					
	945					950					955					960					
	Pro	Ala	Thr	Lys	Val	Lys	Thr	Asp	Ala	Lys	Asn	Ala	Ile	Asp	Lys	Ser					
					965					970					975						
50	Ala	Glu	Thr	Gln	His	Asn	Thr	Ile	Phe	Asn	Asn	Asn	Asp	Ala	Thr	Leu					
				980					985					990							
	Glu	Glu	Gln	Gln	Ala	Ala	Gln	Gln	Leu	Leu	Asp	Gln	Ala	Val	Ala	Thr					
			995					1000					1005								
55	Ala	Lys	Gln	Asn	Ile	Asn	Ala	Ala	Asp	Thr	Asn	Gln	Glu	Val	Ala	Gln					
		1010					1015					1020									
	Ala	Lys	Asp	Gln	Gly	Thr	Gln	Asn	Ile	Val	Val	Ile	Gln	Pro	Ala	Thr					
	1025					1030					1035					1040					

Gln Val Lys Thr Asp Thr Arg Asn Val Val Asn Asp Lys Ala Arg Glu
 1045 1050 1055
 5 Ala Ile Thr Asn Ile Asn Ala Thr Thr Gly Ala Thr Arg Glu Glu Lys
 1060 1065 1070
 Gln Glu Ala Ile Asn Arg Val Asn Thr Leu Lys Asn Arg Ala Leu Thr
 1075 1080 1085
 10 Asp Ile Gly Val Thr Ser Thr Thr Ala Met Val Asn Ser Ile Arg Asp
 1090 1095 1100
 Asp Ala Val Asn Gln Ile Gly Ala Val Gln Pro His Val Thr Lys Lys
 1105 1110 1115 1120
 15 Gln Thr Ala Thr Gly Val Leu Asn Asp Leu Ala Thr Ala Lys Lys Gln
 1125 1130 1135
 Glu Ile Asn Gln Asn Thr Asn Ala Thr Thr Glu Glu Lys Gln Val Ala
 1140 1145 1150
 20 Leu Asn Gln Val Asp Gln Glu Leu Ala Thr Ala Ile Asn Asn Ile Asn
 1155 1160 1165
 Gln Ala Asp Thr Asn Ala Glu Val Asp Gln Ala Gln Gln Leu Gly Thr
 1170 1175 1180
 25 Lys Ala Ile Asn Ala Ile Gln Pro Asn Ile Val Lys Lys Pro Ala Ala
 1185 1190 1195 1200
 Leu Ala Gln Ile Asn Gln His Tyr Asn Ala Lys Leu Ala Glu Ile Asn
 1205 1210 1215
 30 Ala Thr Pro Asp Ala Thr Asn Asp Glu Lys Asn Ala Ala Ile Asn Thr
 1220 1225 1230
 Leu Asn Gln Asp Arg Gln Gln Ala Ile Glu Ser Ile Lys Gln Ala Asn
 1235 1240 1245
 35 Thr Asn Ala Glu Val Asp Gln Ala Ala Thr Val Ala Glu Asn Asn Ile
 1250 1255 1260
 Asp Ala Val Gln Val Asp Val Val Lys Lys Gln Ala Ala Arg Asp Lys
 1265 1270 1275 1280
 40 Ile Thr Ala Glu Val Ala Lys Arg Ile Glu Ala Val Lys Gln Thr Pro
 1285 1290 1295
 Asn Ala Thr Asp Glu Glu Lys Gln Ala Ala Val Asn Gln Ile Asn Gln
 1300 1305 1310
 45 Leu Lys Asp Gln Ala Ile Asn Gln Ile Asn Gln Asn Gln Thr Asn Asp
 1315 1320 1325
 Gln Val Asp Thr Thr Thr Asn Gln Ala Val Asn Ala Ile Asp Asn Val
 1330 1335 1340
 50 Glu Ala Glu Val Val Ile Lys Thr Lys Ala Ile Ala Asp Ile Glu Lys
 1345 1350 1355 1360
 Ala Val Lys Glu Lys Gln Gln Gln Ile Asp Asn Ser Leu Asp Ser Thr
 1365 1370 1375
 55 Asp Asn Glu Lys Glu Val Ala Ser Gln Ala Leu Ala Lys Glu Lys Glu
 1380 1385 1390
 Lys Ala Leu Ala Ala Ile Asp Gln Ala Gln Thr Asn Ser Gln Val Asn
 1395 1400 1405

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Gln Ala Ala Thr Asn Gly Val Ser Ala Ile Lys Ile Ile Gln Pro Glu
 1410 1415 1420
 Thr Lys Val Lys Pro Ala Ala Arg Glu Lys Ile Asn Gln Lys Ala Asn
 5 1425 1430 1435 1440
 Glu Leu Arg Ala Lys Ile Asn Gln Asp Lys Glu Ala Thr Ala Glu Glu
 1445 1450 1455
 Arg Gln Val Ala Leu Asp Lys Ile Asn Glu Phe Val Asn Gln Ala Met
 10 1460 1465 1470
 Thr Asp Ile Thr Asn Asn Arg Thr Asn Gln Gln Val Asp Asp Thr Thr
 1475 1480 1485
 Ser Gln Ala Leu Asp Ser Ile Ala Leu Val Thr Pro Asp His Ile Val
 15 1490 1495 1500
 Arg Ala Ala Ala Arg Asp Ala Val Lys Gln Gln Tyr Glu Ala Lys Lys
 1505 1510 1515 1520
 Arg Glu Ile Glu Gln Ala Glu His Ala Thr Asp Glu Glu Lys Gln Val
 20 1525 1530 1535
 Ala Leu Asn Gln Leu Ala Asn Asn Glu Lys Arg Ala Leu Gln Asn Ile
 1540 1545 1550
 Asp Gln Ala Ile Ala Asn Asn Asp Val Lys Arg Val Glu Thr Asn Gly
 25 1555 1560 1565
 Ile Ala Thr Leu Lys Gly Val Gln Pro His Ile Val Ile Lys Pro Glu
 1570 1575 1580
 Ala Gln Gln Ala Ile Lys Ala Ser Ala Glu Asn Gln Val Glu Ser Ile
 1585 1590 1595 1600
 Lys Asp Thr Pro His Ala Thr Val Asp Glu Leu Asp Glu Ala Asn Gln
 30 1605 1610 1615
 Leu Ile Ser Asp Thr Leu Lys Gln Ala Gln Gln Glu Ile Glu Asn Thr
 1620 1625 1630
 Asn Gln Asp Ala Ala Val Thr Asp Val Arg Asn Gln Thr Ile Lys Ala
 35 1635 1640 1645
 Ile Glu Gln Ile Lys Pro Lys Val Arg Arg Lys Arg Ala Ala Leu Asp
 1650 1655 1660
 Ser Ile Glu Glu Asn Asn Lys Asn Gln Leu Asp Ala Ile Arg Asn Thr
 40 1665 1670 1675 1680
 Leu Asp Thr Thr Gln Asp Glu Arg Asp Val Ala Ile Asp Thr Leu Asn
 1685 1690 1695
 Lys Ile Val Asn Thr Ile Lys Asn Asp Ile Ala Gln Asn Lys Thr Asn
 45 1700 1705 1710
 Ala Glu Val Asp Arg Thr Glu Thr Asp Gly Asn Asp Asn Ile Lys Val
 1715 1720 1725
 Ile Leu Pro Lys Val Gln Val Lys Pro Ala Ala Arg Gln Ser Val Gly
 50 1730 1735 1740
 Val Lys Ala Glu Ala Gln Asn Ala Leu Ile Asp Gln Ser Asp Leu Ser
 1745 1750 1755 1760
 Thr Glu Glu Glu Arg Leu Ala Ala Lys His Leu Val Glu Gln Ala Leu
 55 1765 1770 1775
 Asn Gln Ala Ile Asp Gln Ile Asn His Ala Asp Lys Thr Ala Gln Val

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	1780	1785	1790
	Asn Gln Asp Ser Ile Asn Ala Gln Asn Ile Ile Ser Lys Ile Lys Pro 1795 1800 1805		
5	Ala Thr Thr Val Lys Ala Thr Ala Leu Gln Gln Ile Gln Asn Ile Ala 1810 1815 1820		
	Thr Asn Lys Ile Asn Leu Ile Lys Ala Asn Asn Glu Ala Thr Asp Glu 1825 1830 1835 1840		
10	Glu Gln Asn Ile Ala Ile Ala Gln Val Glu Lys Glu Leu Ile Lys Ala 1845 1850 1855		
	Lys Gln Gln Ile Ala Ser Ala Val Thr Asn Ala Asp Val Ala Tyr Leu 1860 1865 1870		
15	Leu His Asp Glu Lys Asn Glu Ile Arg Glu Ile Glu Pro Val Ile Asn 1875 1880 1885		
	Arg Lys Ala Ser Ala Arg Glu Gln Leu Thr Thr Leu Phe Asn Asp Lys 1890 1895 1900		
20	Lys Gln Ala Ile Glu Ala Asn Ile Gln Ala Thr Val Glu Glu Arg Asn 1905 1910 1915 1920		
	Ser Ile Leu Ala Gln Leu Gln Asn Ile Tyr Asp Thr Ala Ile Gly Gln 1925 1930 1935		
25	Ile Asp Gln Asp Arg Ser Asn Ala Gln Val Asp Lys Thr Ala Ser Leu 1940 1945 1950		
	Asn Leu Gln Thr Ile His Asp Leu Asp Val His Pro Ile Lys Lys Pro 1955 1960 1965		
30	Asp Ala Glu Lys Thr Ile Asn Asp Asp Leu Ala Arg Val Thr Ala Leu 1970 1975 1980		
	Val Gln Asn Tyr Arg Lys Val Ser Asn Arg Asn Lys Ala Asp Ala Leu 1985 1990 1995 2000		
35	Lys Ala Ile Thr Ala Leu Lys Leu Gln Met Asp Glu Glu Leu Lys Thr 2005 2010 2015		
	Ala Arg Thr Asn Ala Asp Val Asp Ala Val Leu Lys Arg Phe Asn Val 2020 2025 2030		
40	Ala Leu Ser Asp Ile Glu Ala Val Ile Thr Glu Lys Glu Asn Ser Leu 2035 2040 2045		
	Leu Arg Ile Asp Asn Ile Ala Gln Gln Thr Tyr Ala Lys Phe Lys Ala 2050 2055 2060		
45	Ile Ala Thr Pro Glu Gln Leu Ala Lys Val Lys Val Leu Ile Asp Gln 2065 2070 2075 2080		
	Tyr Val Ala Asp Gly Asn Arg Met Ile Asp Glu Asp Ala Thr Leu Asn 2085 2090 2095		
50	Asp Ile Lys Gln His Thr Gln Phe Ile Val Asp Glu Ile Leu Ala Ile 2100 2105 2110		
	Lys Leu Pro Ala Glu Ala Thr Lys Val Ser Pro Lys Glu Ile Gln Pro 2115 2120 2125		
55	Ala Pro Lys Val Cys Thr Pro Ile Lys Lys Glu Glu Thr His Glu Ser 2130 2135 2140		
	Arg Lys Val Glu Lys Glu Leu Pro Asn Thr Gly Ser Glu Gly Met Asp 2145 2150 2155 2160		

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Leu Pro Leu Lys Glu Phe Ala Leu Ile Thr Gly Ala Ala Leu Leu Ala
2165 2170 2175

Arg Arg Arg Thr Lys Asn Glu Lys Glu Ser
2180 2185

<210> 31

<211> 199

<212> PRT

<213> Staphylococcus aureus

<400> 31

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

Val Phe Ser Ser Met Pro Phe Gln Asn Ala His Ala Asp Thr Thr Ser
20 25 30

Met Asn Val Ser Asn Lys Gln Ser Gln Asn Val Gln Asn His Arg Pro
35 40 45

Tyr Gly Gly Val Val Pro Gln Gly Met Thr Gln Ala Gln Tyr Thr Glu
50 55 60

Leu Glu Lys Ala Leu Pro Gln Leu Ser Ala Gly Ser Asn Met Gln Asp
65 70 75 80

Tyr Asn Met Lys Leu Tyr Asp Ala Thr Gln Asn Ile Ala Asp Lys Tyr
85 90 95

Asn Val Ile Ile Thr Thr Asn Val Gly Val Phe Lys Pro His Ala Val
100 105 110

Arg Asp Met Asn Gly His Ala Leu Pro Leu Thr Lys Asp Gly Asn Phe
115 120 125

Tyr Gln Thr Asn Val Asp Ala Asn Gly Val Asn His Gly Gly Ser Glu
130 135 140

Met Val Gln Asn Lys Thr Gly His Met Ser Gln Gln Gly His Met Asn
145 150 155 160

Gln Asn Thr His Glu Pro Thr Ala Thr His Ala Thr Arg Ser Tyr Ala
165 170 175

Ile Ile Lys Pro Ser Asn Asp Glu Ser Lys Ser Lys Tyr Ala Phe Ile
180 185 190

Lys Ser Ser Asn Glu Pro Lys
195

<210> 32

<211> 635

<212> PRT

<213> Staphylococcus aureus

<400> 32

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	Met	Ala	Lys	Tyr	Arg	Gly	Lys	Pro	Phe	Gln	Leu	Tyr	Val	Lys	Leu	Ser
	1				5					10					15	
5	Cys	Ser	Thr	Met	Met	Ala	Thr	Ser	Ile	Ile	Leu	Thr	Asn	Ile	Leu	Pro
				20					25					30		
	Tyr	Asp	Ala	Gln	Ala	Ala	Ser	Glu	Lys	Asp	Thr	Glu	Ile	Thr	Lys	Glu
			35					40					45			
10	Ile	Leu	Ser	Lys	Gln	Asp	Leu	Leu	Asp	Lys	Val	Asp	Lys	Ala	Ile	Arg
		50					55					60				
15																
20																
25																
30																
35																
40																
45																
50																
55																

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 45
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Gln Ile Glu Gln Leu Lys 70 Gln Leu Ser Ala 75 Ser Ser Lys Glu His Tyr 80
 Lys Ala Gln Leu Asn 85 Glu Ala Lys Thr Ala 90 Ser Gln Ile Asp Glu Ile 95
 Ile Lys Arg Ala 100 Asn Glu Leu Asp Ser 105 Lys Asp Asn Lys Ser 110 Ser His
 Thr Glu Met 115 Asn Gly Gln Ser Asp 120 Ile Asp Ser Lys Leu 125 Asp Gln Leu
 Leu Lys 130 Asp Leu Asn Glu Val 135 Ser Ser Asn Val Asp 140 Arg Gly Gln Gln
 Ser Gly Glu Asp Asp Leu 150 Asn Ala Met Lys Asn 155 Asp Met Ser Gln Thr 160
 Ala Thr Thr Lys His 165 Gly Glu Lys Asp Asp 170 Lys Asn Asp Glu Ala Met 175
 Val Asn Lys Ala 180 Leu Glu Asp Leu Asp 185 His Leu Asn Gln Gln Ile His 190
 Lys Ser Lys 195 Asp Ala Ser Lys Asp 200 Thr Ser Glu Asp Pro 205 Ala Val Ser
 Thr Thr 210 Asp Asn Asn His Glu Val 215 Ala Lys Thr Pro 220 Asn Asn Asp Gly
 Ser Gly His Val Val 230 Asn Lys Phe Leu Ser 235 Asn Glu Glu Asn Gln 240
 Ser His Ser Asn Arg 245 Leu Thr Asp Lys Leu 250 Gln Gly Ser Asp Lys Ile 255
 Asn His Ala Met 260 Ile Glu Lys Leu Ala 265 Lys Ser Asn Ala Ser Thr Gln 270
 His Tyr Thr 275 Tyr His Lys Leu Asn Thr Leu Gln Ser Leu 285 Asp Gln Arg
 Ile Ala 290 Asn Thr Gln Leu Pro 295 Lys Asn Gln Lys Ser 300 Asp Leu Met Ser
 Glu Val Asn Lys Thr Lys 310 Glu Arg Ile Lys Ser 315 Gln Arg Asn Ile Ile 320
 Leu Glu Glu Leu Ala 325 Arg Thr Asp Asp Lys 330 Lys Tyr Ala Thr Gln Ser 335
 Ile Leu Glu Ser 340 Ile Phe Asn Lys Asp 345 Glu Ala Val Lys Ile 350 Leu Lys
 Asp Ile Arg 355 Val Asp Gly Lys Thr Asp 360 Gln Gln Ile Ala 365 Asp Gln Ile
 Thr Arg 370 His Ile Asp Gln Leu Ser Leu Thr Thr Ser 380 Asp Asp Leu Leu
 Thr Ser Leu Ile Asp Gln 390 Ser Gln Asp Lys Ser 395 Leu Leu Ile Ser Gln 400
 Ile Leu Gln Thr Lys 405 Leu Gly Lys Ala Glu 410 Ala Asp Lys Leu Ala Lys 415
 Asp Trp Thr Asn 420 Lys Gly Leu Ser Asn Arg 425 Gln Ile Val Asp Gln Leu 430
 Lys Lys His Phe Ala Ser Thr Gly Asp Thr Ser Ser Asp Asp Ile Leu

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	435		440		445												
	Lys	Ala	Ile	Leu	Asn	Asn	Ala	Lys	Asp	Lys	Lys	Gln	Ala	Ile	Glu	Thr	
	450						455					460					
5	Ile	Leu	Ala	Thr	Arg	Ile	Glu	Arg	Gln	Lys	Ala	Lys	Leu	Leu	Ala	Asp	
	465					470					475					480	
	Leu	Ile	Thr	Lys	Ile	Glu	Thr	Asp	Gln	Asn	Lys	Ile	Phe	Asn	Leu	Val	
					485					490					495		
10	Lys	Ser	Ala	Leu	Asn	Gly	Lys	Ala	Asp	Asp	Leu	Leu	Asn	Leu	Gln	Lys	
				500					505					510			
	Arg	Leu	Asn	Gln	Thr	Lys	Lys	Asp	Ile	Asp	Tyr	Ile	Leu	Ser	Pro	Ile	
			515					520					525				
15	Val	Asn	Arg	Pro	Ser	Leu	Leu	Asp	Arg	Leu	Asn	Lys	Asn	Gly	Lys	Thr	
	530						535					540					
	Thr	Asp	Leu	Asn	Lys	Leu	Ala	Asn	Leu	Met	Asn	Gln	Gly	Ser	Asp	Leu	
	545					550					555					560	
20	Leu	Asp	Ser	Ile	Pro	Asp	Ile	Pro	Thr	Pro	Lys	Pro	Glu	Lys	Thr	Leu	
					565					570					575		
	Thr	Leu	Gly	Lys	Gly	Asn	Gly	Leu	Leu	Ser	Gly	Leu	Leu	Asn	Ala	Asp	
				580					585					590			
25	Gly	Asn	Val	Ser	Leu	Pro	Lys	Ala	Gly	Glu	Thr	Ile	Lys	Glu	His	Trp	
			595					600					605				
	Leu	Pro	Ile	Ser	Val	Ile	Val	Gly	Ala	Met	Gly	Val	Leu	Met	Ile	Trp	
	610						615					620					
30	Leu	Ser	Arg	Arg	Asn	Lys	Leu	Lys	Asn	Lys	Ala						
	625					630					635						

<210> 33

<211> 995

35 <212> PRT

<213> Staphylococcus aureus

<400> 33

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Met Asn Asn Lys Lys Thr Ala Thr Asn Arg Lys Gly Met Ile Pro Asn
1 5 10
Arg Leu Asn Lys Phe Ser Ile Arg Lys Tyr Ser Val Gly Thr Ala Ser
5 20 25 30
Ile Leu Val Gly Thr Thr Leu Ile Phe Gly Leu Ser Gly His Glu Ala
35 40 45
Lys Ala Ala Glu His Thr Asn Gly Glu Leu Asn Gln Ser Lys Asn Glu
10 50 55 60
Thr Thr Ala Pro Ser Glu Asn Lys Thr Thr Lys Lys Val Asp Ser Arg
65 70 75 80
Gln Leu Lys Asp Asn Thr Gln Thr Ala Thr Ala Asp Gln Pro Lys Val
15 85 90 95
Thr Met Ser Asp Ser Ala Thr Val Lys Glu Thr Ser Ser Asn Met Gln
100 105 110
Ser Pro Gln Asn Ala Thr Ala Asn Gln Ser Thr Thr Lys Thr Ser Asn
20 115 120 125
Val Thr Thr Asn Asp Lys Ser Ser Thr Thr Tyr Ser Asn Glu Thr Asp
130 135 140

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	Lys	Ser	Asn	Leu	Thr	Gln	Ala	Lys	Asp	Val	Ser	Thr	Thr	Pro	Lys	Thr
	145					150					155					160
5	Thr	Thr	Ile	Lys	Pro	Arg	Thr	Leu	Asn	Arg	Met	Ala	Val	Asn	Thr	Val
					165					170				175		
	Ala	Ala	Pro	Gln	Gln	Gly	Thr	Asn	Val	Asn	Asp	Lys	Val	His	Phe	Ser
				180					185					190		
10	Asn	Ile	Asp	Ile	Ala	Ile	Asp	Lys	Gly	His	Val	Asn	Gln	Thr	Thr	Gly
			195					200					205			
	Lys	Thr	Glu	Phe	Trp	Ala	Thr	Ser	Ser	Asp	Val	Leu	Lys	Leu	Lys	Ala
		210					215					220				
15	Asn	Tyr	Thr	Ile	Asp	Asp	Ser	Val	Lys	Glu	Gly	Asp	Thr	Phe	Thr	Phe
	225					230					235					240
	Lys	Tyr	Gly	Gln	Tyr	Phe	Arg	Pro	Gly	Ser	Val	Arg	Leu	Pro	Ser	Gln
					245					250					255	
20	Thr	Gln	Asn	Leu	Tyr	Asn	Ala	Gln	Gly	Asn	Ile	Ile	Ala	Lys	Gly	Ile
				260					265					270		
	Tyr	Asp	Ser	Thr	Thr	Asn	Thr	Thr	Thr	Tyr	Thr	Phe	Thr	Asn	Tyr	Val
			275					280					285			
25	Asp	Gln	Tyr	Thr	Asn	Val	Arg	Gly	Ser	Phe	Glu	Gln	Val	Ala	Phe	Ala
		290					295					300				
	Lys	Arg	Lys	Asn	Ala	Thr	Thr	Asp	Lys	Thr	Ala	Tyr	Lys	Met	Glu	Val
	305					310					315					320
30	Thr	Leu	Gly	Asn	Asp	Thr	Tyr	Ser	Glu	Glu	Ile	Ile	Val	Asp	Tyr	Gly
					325					330					335	
	Asn	Lys	Lys	Ala	Gln	Pro	Leu	Ile	Ser	Ser	Thr	Asn	Tyr	Ile	Asn	Asn
				340					345					350		
35	Glu	Asp	Leu	Ser	Arg	Asn	Met	Thr	Ala	Tyr	Val	Asn	Gln	Pro	Lys	Asn
		355						360					365			
	Thr	Tyr	Thr	Lys	Gln	Thr	Phe	Val	Thr	Asn	Leu	Thr	Gly	Tyr	Lys	Phe
		370					375					380				
40	Asn	Pro	Asn	Ala	Lys	Asn	Phe	Lys	Ile	Tyr	Glu	Val	Thr	Asp	Gln	Asn
	385					390					395					400
	Gln	Phe	Val	Asp	Ser	Phe	Thr	Pro	Asp	Thr	Ser	Lys	Leu	Lys	Asp	Val
					405					410					415	
45	Thr	Asp	Gln	Phe	Asp	Val	Ile	Tyr	Ser	Asn	Asp	Asn	Lys	Thr	Ala	Thr
				420					425					430		
	Val	Asp	Leu	Met	Lys	Gly	Gln	Thr	Ser	Ser	Asn	Lys	Gln	Tyr	Ile	Ile
			435					440					445			
50	Gln	Gln	Val	Ala	Tyr	Pro	Asp	Asn	Ser	Ser	Thr	Asp	Asn	Gly	Lys	Ile
		450					455					460				
	Asp	Tyr	Thr	Leu	Asp	Thr	Asp	Lys	Thr	Lys	Tyr	Ser	Trp	Ser	Asn	Ser
	465					470					475					480
	Tyr	Ser	Asn	Val	Asn	Gly	Ser	Ser	Thr	Ala	Asn	Gly	Asp	Gln	Lys	Lys
					485					490					495	
55	Tyr	Asn	Leu	Gly	Asp	Tyr	Val	Trp	Glu	Asp	Thr	Asn	Lys	Asp	Gly	Lys
				500					505					510		

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	Gln	Asp	Ala	Asn	Glu	Lys	Gly	Ile	Lys	Gly	Val	Tyr	Val	Ile	Leu	Lys
			515					520					525			
5	Asp	Ser	Asn	Gly	Lys	Glu	Leu	Asp	Arg	Thr	Thr	Thr	Asp	Glu	Asn	Gly
		530					535					540				
	Lys	Tyr	Gln	Phe	Thr	Gly	Leu	Ser	Asn	Gly	Thr	Tyr	Ser	Val	Glu	Phe
	545					550					555				560	
10	Ser	Thr	Pro	Ala	Gly	Tyr	Thr	Pro	Thr	Thr	Ala	Asn	Val	Gly	Thr	Asp
					565					570					575	
	Asp	Ala	Val	Asp	Ser	Asp	Gly	Leu	Thr	Thr	Thr	Gly	Val	Ile	Lys	Asp
				580					585					590		
15	Ala	Asp	Asn	Met	Thr	Leu	Asp	Ser	Gly	Phe	Tyr	Lys	Thr	Pro	Lys	Tyr
			595					600					605			
	Ser	Leu	Gly	Asp	Tyr	Val	Trp	Tyr	Asp	Ser	Asn	Lys	Asp	Gly	Lys	Gln
		610					615					620				
20	Asp	Ser	Thr	Glu	Lys	Gly	Ile	Lys	Gly	Val	Lys	Val	Thr	Leu	Gln	Asn
	625					630					635					640
	Glu	Lys	Gly	Glu	Val	Ile	Gly	Thr	Thr	Glu	Thr	Asp	Glu	Asn	Gly	Lys
					645					650					655	
25	Tyr	Arg	Phe	Asp	Asn	Leu	Asp	Ser	Gly	Lys	Tyr	Lys	Val	Ile	Phe	Glu
				660					665					670		
	Lys	Pro	Ala	Gly	Leu	Thr	Gln	Thr	Gly	Thr	Asn	Thr	Thr	Glu	Asp	Asp
			675					680					685			
30	Lys	Asp	Ala	Asp	Gly	Gly	Glu	Val	Asp	Val	Thr	Ile	Thr	Asp	His	Asp
		690					695					700				
	Asp	Phe	Thr	Leu	Asp	Asn	Gly	Tyr	Tyr	Glu	Glu	Glu	Thr	Ser	Asp	Ser
	705					710					715					720
35	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					725					730					735	
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					740				745					750		
40	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					755				760					765		
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					770				775					780		
45	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					785				790					795		800
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					805				810					815		
50	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					820				825					830		
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					835				840					845		
55	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Ser	Asp	Ser
					850				855					860		
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					865				870					875		880
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser

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[illegible]

<210> 34
<211> 1349
<212> PRT
<213> Staphylococcus aureus

<400> 34

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Met Leu Asn Arg Glu Asn Lys Thr Ala Ile Thr Arg Lys Gly Met Val
1 5 10 15
Ser Asn Arg Leu Asn Lys Phe Ser Ile Arg Lys Tyr Thr Val Gly Thr
5 20 25 30
Ala Ser Ile Leu Val Gly Thr Thr Leu Ile Phe Gly Leu Gly Asn Gln
35 40 45
Glu Ala Lys Ala Ala Glu Ser Thr Asn Lys Glu Leu Asn Glu Ala Thr
10 50 55 60
Thr Ser Ala Ser Asp Asn Gln Ser Ser Asp Lys Val Asp Met Gln Gln
65 70 75 80
Leu Asn Gln Glu Asp Asn Thr Lys Asn Asp Asn Gln Lys Glu Met Val
15 85 90 95
Ser Ser Gln Gly Asn Glu Thr Thr Ser Asn Gly Asn Lys Leu Ile Glu
100 105 110
Lys Glu Ser Val Gln Ser Thr Thr Gly Asn Lys Val Glu Val Ser Thr
20 115 120 125
Ala Lys Ser Asp Glu Gln Ala Ser Pro Lys Ser Thr Asn Glu Asp Leu
130 135 140
Asn Thr Lys Gln Thr Ile Ser Asn Gln Glu Ala Leu Gln Pro Asp Leu
25 145 150 155 160
Gln Glu Asn Lys Ser Val Val Asn Val Gln Pro Thr Asn Glu Glu Asn
165 170 175
Lys Lys Val Asp Ala Lys Thr Glu Ser Thr Thr Leu Asn Val Lys Ser
30 180 185 190
Asp Ala Ile Lys Ser Asn Asp Glu Thr Leu Val Asp Asn Asn Ser Asn
195 200 205
Ser Asn Asn Glu Asn Asn Ala Asp Ile Ile Leu Pro Lys Ser Thr Ala
210 215 220

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	Pro	Lys	Arg	Leu	Asn	Thr	Arg	Met	Arg	Ile	Ala	Ala	Val	Gln	Pro	Ser
	225					230					235					240
5	Ser	Thr	Glu	Ala	Lys	Asn	Val	Asn	Asp	Leu	Ile	Thr	Ser	Asn	Thr	Thr
					245					250					255	
	Leu	Thr	Val	Val	Asp	Ala	Asp	Lys	Asn	Asn	Lys	Ile	Val	Pro	Ala	Gln
				260					265					270		
10	Asp	Tyr	Leu	Ser	Leu	Lys	Ser	Gln	Ile	Thr	Val	Asp	Asp	Lys	Val	Lys
			275					280					285			
	Ser	Gly	Asp	Tyr	Phe	Thr	Ile	Lys	Tyr	Ser	Asp	Thr	Val	Gln	Val	Tyr
		290					295					300				
15	Gly	Leu	Asn	Pro	Glu	Asp	Ile	Lys	Asn	Ile	Gly	Asp	Ile	Lys	Asp	Pro
	305					310					315					320
	Asn	Asn	Gly	Glu	Thr	Ile	Ala	Thr	Ala	Lys	His	Asp	Thr	Ala	Asn	Asn
					325					330					335	
20	Leu	Ile	Thr	Tyr	Thr	Phe	Thr	Asp	Tyr	Val	Asp	Arg	Phe	Asn	Ser	Val
				340					345					350		
	Gln	Met	Gly	Ile	Asn	Tyr	Ser	Ile	Tyr	Met	Asp	Ala	Asp	Thr	Ile	Pro
			355					360					365			
25	Val	Ser	Lys	Asn	Asp	Val	Glu	Phe	Asn	Val	Thr	Ile	Gly	Asn	Thr	Thr
		370					375					380				
	Thr	Lys	Thr	Thr	Ala	Asn	Ile	Gln	Tyr	Pro	Asp	Tyr	Val	Val	Asn	Glu
	385					390					395					400
30	Lys	Asn	Ser	Ile	Gly	Ser	Ala	Phe	Thr	Glu	Thr	Val	Ser	His	Val	Gly
					405					410					415	
	Asn	Lys	Glu	Asn	Pro	Gly	Tyr	Tyr	Lys	Gln	Thr	Ile	Tyr	Val	Asn	Pro
				420					425					430		
35	Ser	Glu	Asn	Ser	Leu	Thr	Asn	Ala	Lys	Leu	Lys	Val	Gln	Ala	Tyr	His
			435					440					445			
	Ser	Ser	Tyr	Pro	Asn	Asn	Ile	Gly	Gln	Ile	Asn	Lys	Asp	Val	Thr	Asp
		450					455					460				
40	Ile	Lys	Ile	Tyr	Gln	Val	Pro	Lys	Gly	Tyr	Thr	Leu	Asn	Lys	Gly	Tyr
	465					470					475					480
	Asp	Val	Asn	Thr	Lys	Glu	Leu	Thr	Asp	Val	Thr	Asn	Gln	Tyr	Leu	Gln
					485					490					495	
45	Lys	Ile	Thr	Tyr	Gly	Asp	Asn	Asn	Ser	Ala	Val	Ile	Asp	Phe	Gly	Asn
				500					505					510		
	Ala	Asp	Ser	Ala	Tyr	Val	Val	Met	Val	Asn	Thr	Lys	Phe	Gln	Tyr	Thr
			515					520					525			
50	Asn	Ser	Glu	Ser	Pro	Thr	Leu	Val	Gln	Met	Ala	Thr	Leu	Ser	Ser	Thr
		530					535					540				
	Gly	Asn	Lys	Ser	Val	Ser	Thr	Gly	Asn	Ala	Leu	Gly	Phe	Thr	Asn	Asn
	545					550					555					560
55	Gln	Ser	Gly	Gly	Ala	Gly	Gln	Glu	Val	Tyr	Lys	Ile	Gly	Asn	Tyr	Val
					565					570					575	
	Trp	Glu	Asp	Thr	Asn	Lys	Asn	Gly	Val	Gln	Glu	Leu	Gly	Glu	Lys	Gly
				580					585					590		

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	Val	Gly	Asn	Val	Thr	Val	Thr	Val	Phe	Asp	Asn	Asn	Thr	Asn	Thr	Lys
			595					600					605			
5	Val	Gly	Glu	Ala	Val	Thr	Lys	Glu	Asp	Gly	Ser	Tyr	Leu	Ile	Pro	Asn
		610					615					620				
	Leu	Pro	Asn	Gly	Asp	Tyr	Arg	Val	Glu	Phe	Ser	Asn	Leu	Pro	Lys	Gly
	625					630					635					640
10	Tyr	Glu	Val	Thr	Pro	Ser	Lys	Gln	Gly	Asn	Asn	Glu	Glu	Leu	Asp	Ser
					645					650					655	
	Asn	Gly	Leu	Ser	Ser	Val	Ile	Thr	Val	Asn	Gly	Lys	Asp	Asn	Leu	Ser
				660					665					670		
15	Ala	Asp	Leu	Gly	Ile	Tyr	Lys	Pro	Lys	Tyr	Asn	Leu	Gly	Asp	Tyr	Val
			675					680					685			
	Trp	Glu	Asp	Thr	Asn	Lys	Asn	Gly	Ile	Gln	Asp	Gln	Asp	Glu	Lys	Gly
		690					695					700				
20	Ile	Ser	Gly	Val	Thr	Val	Thr	Leu	Lys	Asp	Glu	Asn	Gly	Asn	Val	Leu
	705					710					715					720
	Lys	Thr	Val	Thr	Thr	Asp	Ala	Asp	Gly	Lys	Tyr	Lys	Phe	Thr	Asp	Leu
					725					730					735	
25	Asp	Asn	Gly	Asn	Tyr	Lys	Val	Glu	Phe	Thr	Thr	Pro	Glu	Gly	Tyr	Thr
				740					745					750		
	Pro	Thr	Thr	Val	Thr	Ser	Gly	Ser	Asp	Ile	Glu	Lys	Asp	Ser	Asn	Gly
			755					760					765			
30	Leu	Thr	Thr	Thr	Gly	Val	Ile	Asn	Gly	Ala	Asp	Asn	Met	Thr	Leu	Asp
		770					775					780				
	Ser	Gly	Phe	Tyr	Lys	Thr	Pro	Lys	Tyr	Asn	Leu	Gly	Asn	Tyr	Val	Trp
	785					790					795					800
	Glu	Asp	Thr	Asn	Lys	Asp	Gly	Lys	Gln	Asp	Ser	Thr	Glu	Lys	Gly	Ile
					805					810					815	
35	Ser	Gly	Val	Thr	Val	Thr	Leu	Lys	Asn	Glu	Asn	Gly	Glu	Val	Leu	Gln
				820					825					830		
	Thr	Thr	Lys	Thr	Asp	Lys	Asp	Gly	Lys	Tyr	Gln	Phe	Thr	Gly	Leu	Glu
			835					840					845			
40	Asn	Gly	Thr	Tyr	Lys	Val	Glu	Phe	Glu	Thr	Pro	Ser	Gly	Tyr	Thr	Pro
		850					855					860				
	Thr	Gln	Val	Gly	Ser	Gly	Thr	Asp	Glu	Gly	Ile	Asp	Ser	Asn	Gly	Thr
	865					870					875					880
45	Ser	Thr	Thr	Gly	Val	Ile	Lys	Asp	Lys	Asp	Asn	Asp	Thr	Ile	Asp	Ser
					885					890					895	
	Gly	Phe	Tyr	Lys	Pro	Thr	Tyr	Asn	Leu	Gly	Asp	Tyr	Val	Trp	Glu	Asp
				900					905					910		
50	Thr	Asn	Lys	Asn	Gly	Val	Gln	Asp	Lys	Asp	Glu	Lys	Gly	Ile	Ser	Gly
			915					920					925			
	Val	Thr	Val	Thr	Leu	Lys	Asp	Glu	Asn	Asp	Lys	Val	Leu	Lys	Thr	Val
							935					940				
55	Thr	Thr	Asp	Glu	Asn	Gly	Lys	Tyr	Gln	Phe	Thr	Asp	Leu	Asn	Asn	Gly
	945					950					955					960
	Thr	Tyr	Lys	Val	Glu	Phe	Glu	Thr	Pro	Ser	Gly	Tyr	Thr	Pro	Thr	Ser

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	965	970	975
	Val Thr Ser Gly Asn Asp Thr Glu Lys Asp Ser Asn Gly Leu Thr Thr		
	980	985	990
5	Thr Gly Val Ile Lys Asp Ala Asp Asn Met Thr Leu Asp Ser Gly Phe		
	995	1000	1005
	Tyr Lys Thr Pro Lys Tyr Ser Leu Gly Asp Tyr Val Trp Tyr Asp Ser		
	1010	1015	1020
10	Asn Lys Asp Gly Lys Gln Asp Ser Thr Glu Lys Gly Ile Lys Asp Val		
	1025	1030	1035
	Lys Val Thr Leu Leu Asn Glu Lys Gly Glu Val Ile Gly Thr Thr Lys		
	1045	1050	1055
15	Thr Asp Glu Asn Gly Lys Tyr Cys Phe Asp Asn Leu Asp Ser Gly Lys		
	1060	1065	1070
	Tyr Lys Val Ile Phe Glu Lys Pro Ala Gly Leu Thr Gln Thr Val Thr		
	1075	1080	1085
20	Asn Thr Thr Glu Asp Asp Lys Asp Ala Asp Gly Gly Glu Val Asp Val		
	1090	1095	1100
	Thr Ile Thr Asp His Asp Asp Phe Thr Leu Asp Asn Gly Tyr Phe Glu		
	1105	1110	1115
25	Glu Asp Thr Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser		
	1125	1130	1135
	Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser		
	1140	1145	1150
30	Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser		
	1155	1160	1165
	Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser		
	1170	1175	1180
35	Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser		
	1185	1190	1195
	Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser		
	1205	1210	1215
40	Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser		
	1220	1225	1230
	Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser		
	1235	1240	1245
45	Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser		
	1250	1255	1260
	Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser		
	1265	1270	1275
	Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser		
	1285	1290	1295
50	Lys Pro Met Ser Thr Thr Lys Asp His His Asn Lys Ala Lys Ala Leu		
	1300	1305	1310
	Pro Glu Thr Gly Ser Glu Asn Asn Gly Ser Asn Asn Ala Thr Leu Phe		
	1315	1320	1325
55	Gly Gly Leu Phe Ala Ala Leu Gly Ser Leu Leu Leu Phe Gly Arg Arg		
	1330	1335	1340

Lys Lys Gln Asn Lys
1345

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<210> 35

<211> 1166

<212> PRT

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<213> Staphylococcus aureus

<400> 35

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	Met	Ile	Asn	Arg	Asp	Asn	Lys	Lys	Ala	Ile	Thr	Lys	Lys	Gly	Met	Ile
	1				5					10					15	
5	Ser	Asn	Arg	Leu	Asn	Lys	Phe	Ser	Ile	Arg	Lys	Tyr	Thr	Val	Gly	Thr
				20					25					30		
	Ala	Ser	Ile	Leu	Val	Gly	Thr	Thr	Leu	Ile	Phe	Gly	Leu	Gly	Asn	Gln
			35					40					45			
10	Glu	Ala	Lys	Ala	Ala	Glu	Asn	Thr	Ser	Thr	Glu	Asn	Ala	Lys	Gln	Asp
		50					55					60				
	Asp	Ala	Thr	Thr	Ser	Asp	Asn	Lys	Glu	Val	Val	Ser	Glu	Thr	Glu	Asn
	65					70					75					80
15	Asn	Ser	Thr	Thr	Glu	Asn	Asn	Ser	Thr	Asn	Pro	Ile	Lys	Lys	Glu	Thr
					85					90					95	
	Asn	Thr	Asp	Ser	Gln	Pro	Glu	Ala	Lys	Lys	Glu	Ser	Thr	Ser	Ser	Ser
				100					105					110		
20	Thr	Gln	Lys	Gln	Gln	Asn	Asn	Val	Thr	Ala	Thr	Thr	Glu	Thr	Lys	Pro
			115					120					125			
	Gln	Asn	Ile	Glu	Lys	Glu	Asn	Val	Lys	Pro	Ser	Thr	Asp	Lys	Thr	Ala
		130					135					140				
25	Thr	Glu	Asp	Thr	Ser	Val	Ile	Leu	Glu	Glu	Lys	Lys	Ala	Pro	Asn	Asn
	145					150					155					160
	Thr	Asn	Asn	Asp	Val	Thr	Thr	Lys	Pro	Ser	Thr	Ser	Glu	Pro	Ser	Thr
					165					170					175	
30	Ser	Glu	Ile	Gln	Thr	Lys	Pro	Thr	Thr	Pro	Gln	Glu	Ser	Thr	Asn	Ile
				180					185					190		
	Glu	Asn	Ser	Gln	Pro	Gln	Pro	Thr	Pro	Ser	Lys	Val	Asp	Asn	Gln	Val
			195					200					205			
35	Thr	Asp	Ala	Thr	Asn	Pro	Lys	Glu	Pro	Val	Asn	Val	Ser	Lys	Glu	Glu
		210					215					220				
	Leu	Lys	Asn	Asn	Pro	Glu	Lys	Leu	Lys	Glu	Leu	Val	Arg	Asn	Asp	Ser
	225					230					235					240
40	Asn	Thr	Asp	His	Ser	Thr	Lys	Pro	Val	Ala	Thr	Ala	Pro	Thr	Ser	Val
					245					250					255	
	Ala	Pro	Lys	Arg	Val	Asn	Ala	Lys	Met	Arg	Phe	Ala	Val	Ala	Gln	Pro
				260					265					270		
45	Ala	Ala	Val	Ala	Ser	Asn	Asn	Val	Asn	Asp	Leu	Ile	Lys	Val	Thr	Lys
			275					280					285			
	Gln	Thr	Ile	Lys	Val	Gly	Asp	Gly	Lys	Asp	Asn	Val	Ala	Ala	Ala	His
		290					295					300				
50	Asp	Gly	Lys	Asp	Ile	Glu	Tyr	Asp	Thr	Glu	Phe	Thr	Ile	Asp	Asn	Lys
	305					310					315					320

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Val Lys Lys Gly Asp Thr Met Thr Ile Asn Tyr Asp Lys Asn Val Ile
325 330 335

Pro Ser Asp Leu Thr Asp Lys Asn Asp Pro Ile Asp Ile Thr Asp Pro
340 345 350

Ser Gly Glu Val Ile Ala Lys Gly Thr Phe Asp Lys Ala Thr Lys Gln
355 360 365

Ile Thr Tyr Thr Phe Thr Asp Tyr Val Asp Lys Tyr Glu Asp Ile Lys
370 375 380

Ser Arg Leu Thr Leu Tyr Ser Tyr Ile Asp Lys Lys Thr Val Pro Asn
385 390 395 400

Glu Thr Ser Leu Asn Leu Thr Phe Ala Thr Ala Gly Lys Glu Thr Ser
405 410 415

Gln Asn Val Thr Val Asp Tyr Gln Asp Pro Met Val His Gly Asp Ser
420 425 430

Asn Ile Gln Ser Ile Phe Thr Lys Leu Asp Glu Asp Lys Gln Thr Ile
435 440 445

Glu Gln Gln Ile Tyr Val Asn Pro Leu Lys Lys Ser Ala Thr Asn Thr
450 455 460

Lys Val Asp Ile Ala Gly Ser Gln Val Asp Asp Tyr Gly Asn Ile Lys
465 470 475 480

Leu Gly Asn Gly Ser Thr Ile Ile Asp Gln Asn Thr Glu Ile Lys Val
485 490 495

Tyr Lys Val Asn Ser Asp Gln Gln Leu Pro Gln Ser Asn Arg Ile Tyr
500 505 510

Asp Phe Ser Gln Tyr Glu Asp Val Thr Ser Gln Phe Asp Asn Lys Lys
515 520 525

Ser Phe Ser Asn Asn Val Ala Thr Leu Asp Phe Gly Asp Ile Asn Ser
530 535 540

Ala Tyr Ile Ile Lys Val Val Ser Lys Tyr Thr Pro Thr Ser Asp Gly
545 550 555 560

Glu Leu Asp Ile Ala Gln Gly Thr Ser Met Arg Thr Thr Asp Lys Tyr
565 570 575

Gly Tyr Tyr Asn Tyr Ala Gly Tyr Ser Asn Phe Ile Val Thr Ser Asn
580 585 590

Asp Thr Gly Gly Gly Asp Gly Thr Val Lys Pro Glu Glu Lys Leu Tyr
595 600 605

Lys Ile Gly Asp Tyr Val Trp Glu Asp Val Asp Lys Asp Gly Val Gln
610 615 620

Gly Thr Asp Ser Lys Glu Lys Pro Met Ala Asn Val Leu Val Thr Leu
625 630 635 640

Thr Tyr Pro Asp Gly Thr Thr Lys Ser Val Arg Thr Asp Ala Asn Gly
645 650 655

His Tyr Glu Phe Gly Gly Leu Lys Asp Gly Glu Thr Tyr Thr Val Lys
660 665 670

Phe Glu Thr Pro Thr Gly Tyr Leu Pro Thr Lys Val Asn Gly Thr Thr
675 680 685

Asp Gly Glu Lys Asp Ser Asn Gly Ser Ser Val Thr Val Lys Ile Asn

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	690					695						700					
	Gly 705	Lys	Asp	Asp	Met	Ser 710	Leu	Asp	Thr	Gly	Phe 715	Tyr	Lys	Glu	Pro	Lys 720	
5	Tyr	Asn	Leu	Gly	Asp 725	Tyr	Val	Trp	Glu	Asp 730	Thr	Asn	Lys	Asp	Gly 735	Ile	
	Gln	Asp	Ala	Asn 740	Glu	Pro	Gly	Ile	Lys 745	Asp	Val	Lys	Val	Thr 750	Leu	Lys	
10	Asp	Ser	Thr 755	Gly	Lys	Val	Ile	Gly 760	Thr	Thr	Thr	Thr	Asp 765	Ala	Ser	Gly	
	Lys	Tyr 770	Lys	Phe	Thr	Asp	Leu 775	Asp	Asn	Gly	Asn	Tyr 780	Thr	Val	Glu	Phe	
15	Glu 785	Thr	Pro	Ala	Gly	Tyr 790	Thr	Pro	Thr	Val	Lys 795	Asn	Thr	Thr	Ala	Asp 800	
	Asp	Lys	Asp	Ser	Asn 805	Gly	Leu	Thr	Thr	Thr 810	Gly	Val	Ile	Lys	Asp 815	Ala	
20	Asp	Asn	Met	Thr 820	Leu	Asp	Arg	Gly	Phe 825	Tyr	Lys	Thr	Pro	Lys 830	Tyr	Ser	
	Leu	Gly 835	Asp	Tyr	Val	Trp	Tyr	Asp 840	Ser	Asn	Lys	Asp	Gly 845	Lys	Gln	Asp	
25	Ser	Thr 850	Glu	Lys	Gly	Ile	Lys 855	Asp	Val	Thr	Val	Thr 860	Leu	Gln	Asn	Glu	
	Lys 865	Gly	Glu	Val	Ile	Gly 870	Thr	Thr	Lys	Thr	Asp 875	Glu	Asn	Gly	Lys	Tyr 880	
30	Arg	Phe	Asp	Asn 885	Leu	Asp	Ser	Gly	Lys	Tyr 890	Lys	Val	Ile	Phe	Glu 895	Lys	
	Pro	Ala	Gly	Leu 900	Thr	Gln	Thr	Val	Thr 905	Asn	Thr	Thr	Glu	Asp 910	Asp	Lys	
35	Asp	Ala	Asp 915	Gly	Gly	Glu	Val	Asp 920	Val	Thr	Ile	Thr	Asp 925	His	Asp	Asp	
	Phe	Thr 930	Leu	Asp	Asn	Gly	Tyr 935	Phe	Glu	Glu	Asp	Thr 940	Ser	Asp	Ser	Asp	
40	Ser 945	Asp	Ser	Asp	Ser	Asp 950	Ser	Asp	Ser	Asp	Ser 955	Asp	Ser	Asp	Ser	Asp 960	
	Ser	Asp	Ser	Asp	Ser 965	Asp	Ser	Asp	Ser	Asp 970	Ser	Asp	Ser	Asp	Ser	Asp 975	
45	Ser	Asp	Ser	Asp 980	Ser	Asp	Ser	Asp	Ser 985	Asp	Ser	Asp	Ser	Asp 990	Ser	Asp	
	Ser	Asp	Ser 995	Asp	Ser	Asp	Ser	Asp 1000	Ser	Asp	Ser	Asp	Ser 1005	Asp	Ser	Asp	
50	Ser	Asp 1010	Ser	Asp	Ser	Asp	Ser 1015	Asp	Ser	Asp	Ser	Asp 1020	Ser	Asp	Ser	Asp	
	Ser 1025	Asp	Ser	Asp	Ser	Asp 1030	Ser	Asp	Ser	Asp	Ser 1035	Asp	Ser	Asp	Ser	Asp 1040	
55	Ser	Asp	Ser	Asp 1045	Ser	Asp	Ser	Asp	Ser	Asp 1050	Ser	Asp	Ser	Asp	Ser	Asp 1055	
	Ser	Asp	Ser	Asp 1060	Ser	Asp	Ser	Asp	Ser 1065	Asp	Ser	Asp	Ser	Asp 1070	Ser	Asp	

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Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 1075 1080 1085
 5 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 1090 1095 1100
 Ser Asp Ala Gly Lys His Thr Pro Val Lys Pro Met Ser Thr Thr Lys
 1105 1110 1115 1120
 10 Asp His His Asn Lys Ala Lys Ala Leu Pro Glu Thr Gly Ser Glu Asn
 1125 1130 1135
 Asn Gly Ser Asn Asn Ala Thr Leu Phe Gly Gly Leu Phe Ala Ala Leu
 1140 1145 1150
 15 Gly Ser Leu Leu Leu Phe Gly Arg Arg Lys Lys Gln Asn Lys
 1155 1160 1165

<210> 36

<211> 516

<212> PRT

<213> Staphylococcus aureus

<400> 36

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	Met	Lys	Lys	Lys	Asn	Ile	Tyr	Ser	Ile	Arg	Lys	Leu	Gly	Val	Gly	Ile
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5	Ala	Ser	Val	Thr	Leu	Gly	Thr	Leu	Leu	Ile	Ser	Gly	Gly	Val	Thr	Pro
				20					25					30		
	Ala	Ala	Asn	Ala	Ala	Gln	His	Asp	Glu	Ala	Gln	Gln	Asn	Ala	Phe	Tyr
			35					40					45			
10	Gln	Val	Leu	Asn	Met	Pro	Asn	Leu	Asn	Ala	Asp	Gln	Arg	Asn	Gly	Phe
		50					55					60				
	Ile	Gln	Ser	Leu	Lys	Asp	Asp	Pro	Ser	Gln	Ser	Ala	Asn	Val	Leu	Gly
	65					70					75					80
15	Glu	Ala	Gln	Lys	Leu	Asn	Asp	Ser	Gln	Ala	Pro	Lys	Ala	Asp	Ala	Gln
					85					90					95	
	Gln	Asn	Asn	Phe	Asn	Lys	Asp	Gln	Gln	Ser	Ala	Phe	Tyr	Glu	Ile	Leu
				100					105					110		
20	Asn	Met	Pro	Asn	Leu	Asn	Glu	Ala	Gln	Arg	Asn	Gly	Phe	Ile	Gln	Ser
			115					120					125			
	Leu	Lys	Asp	Asp	Pro	Ser	Gln	Ser	Thr	Asn	Val	Leu	Gly	Glu	Ala	Lys
		130					135					140				
25	Lys	Leu	Asn	Glu	Ser	Gln	Ala	Pro	Lys	Ala	Asp	Asn	Asn	Phe	Asn	Lys
	145					150					155					160
	Glu	Gln	Gln	Asn	Ala	Phe	Tyr	Glu	Ile	Leu	Asn	Met	Pro	Asn	Leu	Asn
					165					170					175	
30	Glu	Glu	Gln	Arg	Asn	Gly	Phe	Ile	Gln	Ser	Leu	Lys	Asp	Asp	Pro	Ser
				180					185					190		
	Gln	Ser	Ala	Asn	Leu	Leu	Ser	Glu	Ala	Lys	Lys	Leu	Asn	Glu	Ser	Gln
			195					200					205			
35	Ala	Pro	Lys	Ala	Asp	Asn	Lys	Phe	Asn	Lys	Glu	Gln	Gln	Asn	Ala	Phe
		210					215					220				
	Tyr	Glu	Ile	Leu	His	Leu	Pro	Asn	Leu	Asn	Glu	Glu	Gln	Arg	Asn	Gly
	225					230					235					240

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Phe Ile Gln Ser Leu₂₄₅ Lys Asp Asp Pro Ser₂₅₀ Gln Ser Ala Asn Leu₂₅₅ Leu
 Ala Glu Ala Lys₂₆₀ Lys Leu Asn Asp Ala₂₆₅ Gln Ala Pro Lys Ala₂₇₀ Asp Asn
 Lys Phe Asn₂₇₅ Lys Glu Gln Gln Asn₂₈₀ Ala Phe Tyr Glu₂₈₅ Ile Leu His Leu
 Pro Asn₂₉₀ Leu Thr Glu Glu Gln₂₉₅ Arg Asn Gly Phe Ile₃₀₀ Gln Ser Leu Lys
 Asp₃₀₅ Asp Pro Ser Val₃₁₀ Ser Lys Glu Ile Leu Ala₃₁₅ Glu Ala Lys Lys Leu₃₂₀
 Asn Asp Ala Gln₃₂₅ Ala Pro Lys Glu Glu Asp₃₃₀ Asn Asn Lys Pro Gly₃₃₅ Lys
 Glu Asp Asn Asn₃₄₀ Lys Pro Gly Lys Glu₃₄₅ Asp Asn Asn Lys Pro Gly Lys
 Glu Asp Asn₃₅₅ Asn Lys Pro Gly Lys Glu Asp Asn Asn Lys₃₆₅ Pro Gly Lys
 Glu Asp₃₇₀ Gly Asn Lys Pro Gly₃₇₅ Lys Glu Asp Asn Lys₃₈₀ Lys Pro Gly Lys
 Glu Asp₃₈₅ Gly Asn Lys Pro Gly Lys Glu Asp Asn Lys₃₉₅ Lys Lys Pro Gly Lys₄₀₀
 Glu Asp Gly Asn₄₀₅ Lys Pro Gly Lys Glu Asp₄₁₀ Gly Asn Lys Pro Gly Lys
 Glu Asp Gly Asn₄₂₀ Gly Val His Val₄₂₅ Val Lys Pro Gly Asp Thr₄₃₀ Val Asn
 Asp Ile Ala₄₃₅ Lys Ala Asn Gly Thr Thr Ala Asp Lys Ile₄₄₅ Ala Ala Asp
 Asn Lys₄₅₀ Leu Ala Asp Lys Asn₄₅₅ Met Ile Lys Pro Gly₄₆₀ Gln Glu Leu Val
 Val₄₆₅ Asp Lys Lys Gln Pro Ala Asn His Ala Asp₄₇₅ Ala Asn Lys Ala Gln₄₈₀
 Ala Leu Pro Glu Thr₄₈₅ Gly Glu Glu Asn Pro Phe Ile Gly Thr Thr Val₄₉₅
 Phe Gly Gly Leu₅₀₀ Ser Leu Ala Leu Gly₅₀₅ Ala Ala Leu Leu Ala₅₁₀ Gly Arg
 Arg Arg Glu₅₁₅ Leu

<210> 37
 <211> 772
 <212> PRT
 <213> Staphylococcus aureus

<400> 37

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Met Lys Ala Leu Leu Leu Lys Thr Ser Val Trp Leu Val Leu Leu Phe
1 5 10 15
Ser Val Met Gly Leu Trp Gln Val Ser Asn Ala Ala Glu Gln His Thr
20 25 30
Pro Met Lys Ala His Ala Val Thr Thr Ile Asp Lys Ala Thr Thr Asp
35 40 45
Lys Gln Gln Val Pro Pro Thr Lys Glu Ala Ala His His Ser Gly Lys

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	50					55					60					
	Glu 65	Ala	Ala	Thr	Asn 70	Val	Ser	Ala	Ser	Ala	Gln 75	Gly	Thr	Ala	Asp 80	Asp
5	Thr	Asn	Ser	Lys	Val 85	Thr	Ser	Asn	Ala	Pro 90	Ser	Asn	Lys	Pro	Ser 95	Thr
	Val	Val	Ser	Thr 100	Lys	Val	Asn	Glu	Thr 105	Arg	Asp	Val	Asp	Thr 110	Gln	Gln
10	Ala	Ser	Thr 115	Gln	Lys	Pro	Thr	His 120	Thr	Ala	Thr	Phe	Lys 125	Leu	Ser	Asn
	Ala	Lys 130	Thr	Ala	Ser	Leu	Ser 135	Pro	Arg	Met	Phe	Ala 140	Ala	Asn	Ala	Pro
15	Gln 145	Thr	Thr	Thr	His	Lys 150	Ile	Leu	His	Thr	Asn 155	Asp	Ile	His	Gly	Arg 160
	Leu	Ala	Glu	Glu	Lys 165	Gly	Arg	Val	Ile	Gly 170	Met	Ala	Lys	Leu	Lys 175	Thr
20	Val	Lys	Glu	Gln 180	Glu	Lys	Pro	Asp	Leu 185	Met	Leu	Asp	Ala	Gly 190	Asp	Ala
	Phe	Gln	Gly 195	Leu	Pro	Leu	Ser	Asn 200	Gln	Ser	Lys	Gly	Glu 205	Glu	Met	Ala
25	Lys	Ala 210	Met	Asn	Ala	Val	Gly 215	Tyr	Asp	Ala	Met	Ala 220	Val	Gly	Asn	His
	Glu 225	Phe	Asp	Phe	Gly	Tyr 230	Asp	Gln	Leu	Lys	Lys 235	Leu	Glu	Gly	Met	Leu 240
30	Asp	Phe	Pro	Met	Leu 245	Ser	Thr	Asn	Val	Tyr 250	Lys	Asp	Gly	Lys	Arg 255	Ala
	Phe	Lys	Pro	Ser 260	Thr	Ile	Val	Thr	Lys 265	Asn	Gly	Ile	Arg	Tyr 270	Gly	Ile
35	Ile	Gly	Val 275	Thr	Thr	Pro	Glu	Thr 280	Lys	Thr	Lys	Thr	Arg 285	Pro	Glu	Gly
	Ile	Lys 290	Gly	Val	Glu	Phe	Arg 295	Asp	Pro	Leu	Gln	Ser 300	Val	Thr	Ala	Glu
40	Met 305	Met	Arg	Ile	Tyr	Lys 310	Asp	Val	Asp	Thr	Phe 315	Val	Val	Ile	Ser	His 320
	Leu	Gly	Ile	Asp	Pro 325	Ser	Thr	Gln	Glu	Thr 330	Trp	Arg	Gly	Asp	Tyr 335	Leu
45	Val	Lys	Gln	Leu 340	Ser	Gln	Asn	Pro	Gln 345	Leu	Lys	Lys	Arg	Ile 350	Thr	Val
	Ile	Asp	Gly 355	His	Ser	His	Thr	Val 360	Leu	Gln	Asn	Gly	Gln 365	Ile	Tyr	Asn
50	Asn 370	Asp	Ala	Leu	Ala	Gln	Thr 375	Gly	Thr	Ala	Leu	Ala 380	Asn	Ile	Gly	Lys
	Ile 385	Thr	Phe	Asn	Tyr	Arg 390	Asn	Gly	Glu	Val	Ser 395	Asn	Ile	Lys	Pro	Ser 400
55	Leu	Ile	Asn	Val	Lys 405	Asp	Val	Glu	Asn	Val 410	Thr	Pro	Asn	Lys	Ala 415	Leu
	Ala	Glu	Gln	Ile 420	Asn	Gln	Ala	Asp	Gln 425	Thr	Phe	Arg	Ala	Gln 430	Thr	Ala

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	Glu	Val	Ile	Ile	Pro	Asn	Asn	Thr	Ile	Asp	Phe	Lys	Gly	Glu	Arg	Asp
			435					440					445			
5	Asp	Val	Arg	Thr	Arg	Glu	Thr	Asn	Leu	Gly	Asn	Ala	Ile	Ala	Asp	Ala
		450					455					460				
	Met	Glu	Ala	Tyr	Gly	Val	Lys	Asn	Phe	Ser	Lys	Lys	Thr	Asp	Phe	Ala
	465					470					475					480
10	Val	Thr	Asn	Gly	Gly	Gly	Ile	Arg	Ala	Ser	Ile	Ala	Lys	Gly	Lys	Val
					485					490					495	
	Thr	Arg	Tyr	Asp	Leu	Ile	Ser	Val	Leu	Pro	Phe	Gly	Asn	Thr	Ile	Ala
				500					505					510		
15	Gln	Ile	Asp	Val	Lys	Gly	Ser	Asp	Val	Trp	Thr	Ala	Phe	Glu	His	Ser
			515					520					525			
	Leu	Gly	Ala	Pro	Thr	Thr	Gln	Lys	Asp	Gly	Lys	Thr	Val	Leu	Thr	Ala
		530					535					540				
20	Asn	Gly	Gly	Leu	Leu	His	Ile	Ser	Asp	Ser	Ile	Arg	Val	Tyr	Tyr	Asp
	545					550					555					560
	Ile	Asn	Lys	Pro	Ser	Gly	Lys	Arg	Ile	Asn	Ala	Ile	Gln	Ile	Leu	Asn
					565					570					575	
25	Lys	Glu	Thr	Gly	Lys	Phe	Glu	Asn	Ile	Asp	Leu	Lys	Arg	Val	Tyr	His
				580					585					590		
	Val	Thr	Met	Asn	Asp	Phe	Thr	Ala	Ser	Gly	Gly	Asp	Gly	Tyr	Ser	Met
			595					600					605			
30	Phe	Gly	Gly	Pro	Arg	Glu	Glu	Gly	Ile	Ser	Leu	Asp	Gln	Val	Leu	Ala
		610					615					620				
	Ser	Tyr	Leu	Lys	Thr	Ala	Asn	Leu	Ala	Lys	Tyr	Asp	Thr	Thr	Glu	Pro
	625					630					635					640
35	Gln	Arg	Met	Leu	Leu	Gly	Lys	Pro	Ala	Val	Ser	Glu	Gln	Pro	Ala	Lys
				645						650					655	
	Gly	Gln	Gln	Gly	Ser	Lys	Gly	Ser	Lys	Ser	Gly	Lys	Asp	Thr	Gln	Pro
				660					665					670		
40	Ile	Gly	Asp	Asp	Lys	Val	Met	Asp	Pro	Ala	Lys	Lys	Pro	Ala	Pro	Gly
			675					680					685			
	Lys	Val	Val	Leu	Leu	Leu	Ala	His	Arg	Gly	Thr	Val	Ser	Ser	Gly	Thr
		690					695					700				
45	Glu	Gly	Ser	Gly	Arg	Thr	Ile	Glu	Gly	Ala	Thr	Val	Ser	Ser	Lys	Ser
	705					710					715					720
	Gly	Lys	Gln	Leu	Ala	Arg	Met	Ser	Val	Pro	Lys	Gly	Ser	Ala	His	Glu
					725					730					735	
50	Lys	Gln	Leu	Pro	Lys	Thr	Gly	Thr	Asn	Gln	Ser	Ser	Ser	Pro	Glu	Ala
				740					745					750		
	Met	Phe	Val	Leu	Leu	Ala	Gly	Ile	Gly	Leu	Ile	Ala	Thr	Val	Arg	Arg
			755					760					765			
55	Arg	Lys	Ala	Ser												
		770														

<210> 38
 <211> 190
 <212> PRT

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<213> Staphylococcus aureus

<400> 38

5 Met Lys Leu Lys Ser Leu Ala Val Leu Ser Met Ser Ala Val Val Leu
1 5 10
Thr Ala Cys Gly Asn Asp Thr Pro Lys Asp Glu Thr Lys Ser Thr Glu
20 25 30
10 Ser Asn Thr Asn Gln Asp Thr Asn Thr Thr Lys Asp Val Ile Ala Leu
35 40 45
Lys Asp Val Lys Thr Ser Pro Glu Asp Ala Val Lys Lys Ala Glu Glu
50 55 60
15 Thr Tyr Lys Gly Gln Lys Leu Lys Gly Ile Ser Phe Glu Asn Ser Asn
65 70 75 80
Gly Glu Trp Ala Tyr Lys Val Thr Gln Gln Lys Ser Gly Glu Glu Ser
85 90 95
20 Glu Val Leu Val Ala Asp Lys Asn Lys Lys Val Ile Asn Lys Lys Thr
100 105 110
Glu Lys Glu Asp Thr Met Asn Glu Asn Asp Asn Phe Lys Tyr Ser Asp
115 120 125
25 Ala Ile Asp Tyr Lys Lys Ala Ile Lys Glu Gly Gln Lys Glu Phe Asp
130 135 140
Gly Asp Ile Lys Glu Trp Ser Leu Glu Lys Asp Asp Gly Lys Leu Val
145 150 155 160
30 Tyr Asn Ile Asp Leu Lys Lys Gly Asn Lys Lys Gln Glu Val Thr Val
165 170 175
Asp Ala Lys Asn Gly Lys Val Leu Lys Ser Glu Gln Asp His
180 185 190

35 <210> 39
<211> 502
<212> PRT
<213> Staphylococcus aureus

40 <400> 39

45

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Met Arg Glu Asn Phe Lys Leu Arg Lys Met Lys Val Gly Leu Val Ser
 1 5 10 15
 Val Ala Ile Thr Met Leu Tyr Ile Met Thr Asn Gly Gln Ala Glu Ala
 5 20 25 30
 Ser Glu Asn Gln Asn Ala Leu Ile Ser Asn Ile Asn Val Asp Asn Gln
 35 40 45
 Glu Lys Gln Asn Asn Val Asn Gln Ala Val Gln Pro Gln Asn Asn Thr
 10 50 55 60
 Asn Glu Thr Ser Lys Val Pro Ala Asn Phe Val Lys Leu Asn Asp Ile
 65 70 75 80
 Lys Pro Gly Asp Thr Ser Ile Gln Gly Thr Thr Leu Pro Asn Gln Phe
 15 85 90 95
 Ile Leu Leu Thr Ile Asp Lys Lys Asp Val Ser Ser Val Glu Asp Ser
 100 105 110
 Asp Ser Ser Phe Val Met Ser Asp Lys Asp Gly Asn Phe Lys Tyr Asp
 115 120 125
 Leu Asn Gly Arg Lys Ile Val His Asn Gln Glu Ile Glu Val Ser Ser

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[illegible]

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<210> 40
 <211> 342
 <212> PRT
 <213> Staphylococcus aureus

5

<400> 40

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Met Lys Lys Thr Val Leu Tyr Leu Val Leu Ala Val Met Phe Leu Leu
 1      5      10      15
Ala Ala Cys Gly Asn Asn Ser Asp Lys Glu Gln Ser Lys Ser Glu Thr
 20      25
Lys Gly Ser Lys Asp Thr Val Lys Ile Glu Asn Asn Tyr Lys Met Arg
 35      40      45
Gly Glu Lys Lys Asp Gly Ser Asp Ala Lys Lys Val Lys Glu Thr Val
 50      55      60
Glu Val Pro Lys Asn Pro Lys Asn Ala Val Val Leu Asp Tyr Gly Ala
 65      70      75      80
Leu Asp Val Met Lys Glu Met Gly Leu Ser Asp Lys Val Lys Ala Leu
 85      90      95
Pro Lys Gly Glu Gly Gly Lys Ser Leu Pro Asn Phe Leu Glu Ser Phe
 100      105      110
Lys Asp Asp Lys Tyr Thr Asn Val Gly Asn Leu Lys Glu Val Asn Phe
 115      120      125
Asp Lys Ile Ala Ala Thr Lys Pro Glu Val Ile Phe Ile Ser Gly Arg
 130      135      140
Thr Ala Asn Gln Lys Asn Leu Asp Glu Phe Lys Lys Ala Ala Pro Lys
 145      150      155      160
Ala Lys Ile Val Tyr Val Gly Ala Asp Glu Lys Asn Leu Ile Gly Ser
 165      170      175
Met Lys Gln Asn Thr Glu Asn Ile Gly Lys Ile Tyr Asp Lys Glu Asp
 180      185      190
Lys Ala Lys Glu Leu Asn Lys Asp Leu Asp Asn Lys Ile Ala Ser Met
 195      200      205
Lys Asp Lys Thr Lys Asn Phe Asn Lys Thr Val Met Tyr Leu Leu Val
 210      215      220
Asn Glu Gly Glu Leu Ser Thr Phe Gly Pro Lys Gly Arg Phe Gly Gly
 225      230      235      240
Leu Val Tyr Asp Thr Leu Gly Phe Asn Ala Val Asp Lys Lys Val Ser
 245      250      255
Asn Ser Asn His Gly Gln Asn Val Ser Asn Glu Tyr Val Asn Lys Glu
 260      265      270
Asn Pro Asp Val Ile Leu Ala Met Asp Arg Gly Gln Ala Ile Ser Gly
 275      280      285
Lys Ser Thr Ala Lys Gln Ala Leu Asn Asn Pro Val Leu Lys Asn Val
 290      295      300
Lys Ala Ile Lys Glu Asp Lys Val Tyr Asn Leu Asp Pro Lys Leu Trp
 305      310      315      320
Tyr Phe Ala Ala Gly Ser Thr Thr Thr Thr Ile Lys Gln Ile Glu Glu
 325      330      335

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Leu Asp Lys Val Val Lys
340

5 <210> 41
<211> 241
<212> PRT
<213> Staphylococcus aureus

10 <400> 41

Met Lys Lys Asn Ile Met Asn Lys Leu Val Leu Ser Thr Ala Leu Leu
1 5 10 15
Leu Leu Glu Thr Thr Ser Thr Gln Leu Pro Lys Thr Pro Ile Ser Phe
20 25 30
Ser Ser Glu Ala Lys Ala Tyr Asn Ile Ser Glu Asn Glu Thr Asn Ile
35 40 45
Asn Glu Leu Ile Lys Tyr Tyr Thr Gln Pro His Phe Ser Leu Ser Gly
50 55 60
Lys Trp Leu Trp Gln Lys Pro Asn Gly Ser Ile His Ala Thr Leu Gln
65 70 75 80
Thr Trp Val Trp Tyr Ser His Ile Gln Val Phe Gly Ser Glu Ser Trp
85 90 95
Gly Asn Ile Asn Gln Leu Arg Asn Lys Tyr Val Asp Ile Phe Gly Thr
100 105 110
Lys Asp Glu Asp Thr Val Glu Gly Tyr Trp Thr Tyr Asp Glu Thr Phe
115 120 125
Thr Gly Gly Val Thr Pro Ala Ala Thr Ser Ser Asp Lys Pro Tyr Arg
130 135 140
Leu Phe Leu Lys Tyr Ser Asp Lys Gln Gln Thr Ile Ile Gly Gly His
145 150 155 160
Glu Phe Tyr Lys Gly Asn Lys Pro Val Leu Thr Leu Lys Glu Leu Asp
165 170 175
Phe Arg Ile Arg Gln Thr Leu Ile Lys Asn Lys Lys Leu Tyr Asn Gly
180 185 190
Glu Phe Asn Lys Gly Gln Ile Lys Ile Thr Ala Asp Gly Asn Asn Tyr
195 200 205
Thr Ile Asp Leu Ser Lys Lys Leu Lys Leu Thr Asp Thr Asn Arg Tyr
210 215 220
Val Lys Asn Pro Arg Asn Ala Glu Ile Glu Val Ile Leu Glu Lys Ser
225 230 235 240
Asn

50 <210> 42
<211> 302
<212> PRT
<213> Staphylococcus aureus
55 <400> 42

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Met Lys Lys Leu Leu Leu Pro Leu Ile Ile Met Leu Leu Val Leu Ala
1 5 10 15
Ala Cys Gly Asn Gln Gly Glu Lys Asn Asn Lys Ala Glu Thr Lys Ser
5 20 25 30
Tyr Lys Met Asp Asp Gly Lys Thr Val Asp Ile Pro Lys Asp Pro Lys
10
35 40 45
Arg Ile Ala Val Val Ala Pro Thr Tyr Ala Gly Gly Leu Lys Lys Leu
50 55 60
Gly Ala Asn Ile Val Ala Val Asn Gln Gln Val Asp Gln Ser Lys Val
15 65 70 75 80
Leu Lys Asp Lys Phe Lys Gly Val Thr Lys Ile Gly Asp Gly Asp Val
85 90 95
Glu Lys Val Ala Lys Glu Lys Pro Asp Leu Ile Ile Val Tyr Ser Thr
20 100 105 110
Asp Lys Asp Ile Lys Lys Tyr Gln Lys Val Ala Pro Thr Val Val Val
115 120 125
Asp Tyr Asn Lys His Lys Tyr Leu Glu Gln Gln Glu Met Leu Gly Lys
25 130 135 140
Ile Val Gly Lys Glu Asp Lys Val Lys Ala Trp Lys Lys Asp Trp Glu
145 150 155 160
Glu Thr Thr Ala Lys Asp Gly Lys Glu Ile Lys Lys Ala Ile Gly Gln
30 165 170 175
Asp Ala Thr Val Ser Leu Phe Asp Glu Phe Asp Lys Lys Leu Tyr Thr
180 185 190
Tyr Gly Asp Asn Trp Gly Arg Gly Glu Val Leu Tyr Gln Ala Phe
35 195 200 205
Gly Leu Lys Met Gln Pro Glu Gln Gln Lys Leu Thr Ala Lys Ala Gly
210 215 220
Trp Ala Glu Val Lys Gln Glu Glu Ile Glu Lys Tyr Ala Gly Asp Tyr
40 225 230 235 240
Ile Val Ser Thr Ser Glu Gly Lys Pro Thr Pro Gly Tyr Glu Ser Thr
245 250 255
Asn Met Trp Lys Asn Leu Lys Ala Thr Lys Glu Gly His Ile Val Lys
45 260 265 270
Val Asp Ala Gly Thr Tyr Trp Tyr Asn Asp Pro Tyr Thr Leu Asp Phe
275 280 285
Met Arg Lys Asp Leu Lys Glu Lys Leu Ile Lys Ala Ala Lys
50 290 295 300

<210> 43

<211> 267

<212> PRT

55 <213> Staphylococcus aureus

<400> 43

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1 Met Lys Lys Ile Ala Thr Ala Thr Ile Ala Thr Ala Gly Phe Ala Thr
 5 Ile Ala Ile Ala Ser Gly Asn Gln Ala His Ala Ser Glu Gln Asp Asn
 Tyr Gly Tyr Asn Pro Asn Asp Pro Thr Ser Tyr Ser Tyr Thr Tyr Thr
 10 Ile Asp Ala Gln Gly Asn Tyr His Tyr Thr Trp Lys Gly Asn Trp His
 Pro Ser Gln Leu Asn Gln Asp Asn Gly Tyr Tyr Ser Tyr Tyr Tyr Tyr
 15 Asn Gly Tyr Asn Asn Tyr Asn Asn Tyr Asn Asn Gly Tyr Ser Tyr Asn
 Asn Tyr Ser Arg Tyr Asn Asn Tyr Ser Asn Asn Asn Gln Ser Tyr Asn
 20 Tyr Asn Asn Tyr Asn Ser Tyr Asn Thr Asn Ser Tyr Arg Thr Gly Gly
 Leu Gly Ala Ser Tyr Ser Thr Ser Ser Asn Asn Val Gln Val Thr Thr
 25 Thr Met Ala Pro Ser Ser Asn Gly Arg Ser Ile Ser Ser Gly Tyr Thr
 Ser Gly Arg Asn Leu Tyr Thr Ser Gly Gln Cys Thr Tyr Tyr Val Phe
 30 Asp Arg Val Gly Gly Lys Ile Gly Ser Thr Trp Gly Asn Ala Ser Asn
 Trp Ala Asn Ala Ala Ala Arg Ala Gly Tyr Thr Val Asn Asn Thr Pro
 35 Lys Ala Gly Ala Ile Met Gln Thr Thr Gln Gly Ala Tyr Gly His Val
 Ala Tyr Val Glu Ser Val Asn Ser Asn Gly Ser Val Arg Val Ser Glu
 40 Met Asn Tyr Gly Tyr Gly Pro Gly Val Val Thr Ser Arg Thr Ile Ser
 Ala Ser Gln Ala Ala Gly Tyr Asn Phe Ile His
 260 265

<210> 44

<211> 209

<212> PRT

<213> Staphylococcus aureus

<400> 44

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Met Lys Arg Leu Val Thr Gly Leu Leu Ala Leu Ser Leu Phe Leu Ala
1 5 10 15
Ala Cys Gly Gln Asp Ser Asp Gln Gln Lys Asp Gly Asn Lys Glu Lys
5 20 25 30
Asp Asp Lys Ala Lys Thr Glu Gln Gln Asp Lys Lys Thr Asn Asp Ser
35 40 45
Ser Lys Asp Lys Lys Asp Asn Lys Asp Asp Ser Lys Asp Val Asn Lys
10 50 55 60
Asp Asn Lys Asp Asn Ser Ala Asn Asp Asn Gln Gln Gln Ser Asn Ser
65 70 75 80
Asn Ala Thr Asn Asn Asp Gln Asn Gln Thr Asn Asn Asn Gln Ser Ser
15 85 90 95
Asn Asn Gln Ala Asn Asn Asn Gln Lys Ser Ser Tyr Val Ala Pro Tyr
100 105 110
Tyr Gly Gln Asn Ala Ala Pro Val Ala Arg Gln Ile Tyr Pro Phe Asn
20 115 120 125
Gly Asn Lys Asn Gln Ala Leu Gln Gln Leu Pro Asn Phe Gln Thr Ala
130 135 140
Leu Asn Ala Ala Asn Asn Glu Ala Asn Lys Phe Gly Ser Asn Asn Lys
25 145 150 155 160
Val Tyr Asn Asp Tyr Ser Ile Glu Glu His Asn Gly Asn Tyr Lys Tyr
165 170 175
Val Phe Ser Phe Lys Asp Pro Asn Ala Asn Gly Lys Tyr Ser Ile Val
30 180 185 190
Thr Val Asp Tyr Thr Gly Gln Ala Met Val Thr Asp Pro Asn Tyr Gln
195 200 205
Gln

<210> 45

<211> 436

<212> PRT

<213> Staphylococcus aureus

<400> 45

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	Met	Lys	Asn	Lys	Tyr	Ile	Ser	Lys	Leu	Leu	Val	Gly	Ala	Ala	Thr	Ile
	1				5					10					15	
5	Thr	Leu	Ala	Thr	Met	Ile	Ser	Asn	Gly	Glu	Ala	Lys	Ala	Ser	Glu	Asn
				20					25					30		
	Thr	Gln	Gln	Thr	Ser	Thr	Lys	His	Gln	Thr	Thr	Gln	Asn	Asn	Tyr	Val
			35					40					45			
10	Thr	Asp	Gln	Gln	Lys	Ala	Phe	Tyr	Gln	Val	Leu	His	Leu	Lys	Gly	Ile
		50					55					60				
	Thr	Glu	Glu	Gln	Arg	Asn	Gln	Tyr	Ile	Lys	Thr	Leu	Arg	Glu	His	Pro
	65					70					75					80
15	Glu	Arg	Ala	Gln	Glu	Val	Phe	Ser	Glu	Ser	Leu	Lys	Asp	Ser	Lys	Asn
					85					90					95	
	Pro	Asp	Arg	Arg	Val	Ala	Gln	Gln	Asn	Ala	Phe	Tyr	Asn	Val	Leu	Lys
				100					105					110		
20	Asn	Asp	Asn	Leu	Thr	Glu	Gln	Glu	Lys	Asn	Asn	Tyr	Ile	Ala	Gln	Ile
			115					120					125			
	Lys	Glu	Asn	Pro	Asp	Arg	Ser	Gln	Gln	Val	Trp	Val	Glu	Ser	Val	Gln
		130					135					140				
25	Ser	Ser	Lys	Ala	Lys	Glu	Arg	Gln	Asn	Ile	Glu	Asn	Ala	Asp	Lys	Ala
	145					150					155					160
	Ile	Lys	Asp	Phe	Gln	Asp	Asn	Lys	Ala	Pro	His	Asp	Lys	Ser	Ala	Ala
				165						170					175	
30	Tyr	Glu	Ala	Asn	Ser	Lys	Leu	Pro	Lys	Asp	Leu	Arg	Asp	Lys	Asn	Asn
				180					185					190		
	Arg	Phe	Val	Glu	Lys	Val	Ser	Ile	Glu	Lys	Ala	Ile	Val	Arg	His	Asp
		195						200					205			
35	Glu	Arg	Val	Lys	Ser	Ala	Asn	Asp	Ala	Ile	Ser	Lys	Leu	Asn	Glu	Lys
		210					215					220				
	Asp	Ser	Ile	Glu	Asn	Arg	Arg	Leu	Ala	Gln	Arg	Glu	Val	Asn	Lys	Ala
	225					230					235					240
40	Pro	Met	Asp	Val	Lys	Glu	His	Leu	Gln	Lys	Gln	Leu	Asp	Ala	Leu	Val
					245					250					255	
	Ala	Gln	Lys	Asp	Ala	Glu	Lys	Lys	Val	Ala	Pro	Lys	Val	Glu	Ala	Pro

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	260	265	270
	Gln Ile Gln Ser Pro Gln Ile	Glu Lys Pro Lys Val	Glu Ser Pro Lys
	275	280	285
5	Val Glu Val Pro Gln Ile Gln Ser Pro Lys Val	Glu Val Pro Gln Ser	
	290	295	300
	Lys Leu Leu Gly Tyr Tyr Gln Ser Leu Lys Asp Ser Phe Asn Tyr Gly		
	305	310	315
10	Tyr Lys Tyr Leu Thr Asp Thr Tyr Lys Ser Tyr Lys Glu Lys Tyr Asp		
	325	330	335
	Thr Ala Lys Tyr Tyr Tyr Asn Thr Tyr Tyr Lys Tyr Lys Gly Ala Ile		
	340	345	350
15	Asp Gln Thr Val Leu Thr Val Leu Gly Ser Gly Ser Lys Ser Tyr Ile		
	355	360	365
	Gln Pro Leu Lys Val Asp Asp Lys Asn Gly Tyr Leu Ala Lys Ser Tyr		
	370	375	380
20	Ala Gln Val Arg Asn Tyr Val Thr Glu Ser Ile Asn Thr Gly Lys Val		
	385	390	395
	Leu Tyr Thr Phe Tyr Gln Asn Pro Thr Leu Val Lys Thr Ala Ile Lys		
	405	410	415
25	Ala Gln Glu Thr Ala Ser Ser Ile Lys Asn Thr Leu Ser Asn Leu Leu		
	420	425	430
	Ser Phe Trp Lys		
	435		

30 <210> 46
 <211> 233
 <212> PRT
 <213> Staphylococcus aureus

35 <400> 46

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Met Lys Lys Thr Ile Met Ala Ser Ser Leu Ala Val Ala Leu Gly Val
1 5 10 15
Thr Gly Tyr Ala Ala Gly Thr Gly His Gln Ala His Ala Ala Glu Val
5 20 25 30
Asn Val Asp Gln Ala His Leu Val Asp Leu Ala His Asn His Gln Asp
35 40 45
Gln Leu Asn Ala Ala Pro Ile Lys Asp Gly Ala Tyr Asp Ile His Phe
10 50 55 60
Val Lys Asp Gly Phe Gln Tyr Asn Phe Thr Ser Asn Gly Thr Thr Trp
65 70 75 80
Ser Trp Ser Tyr Glu Ala Ala Asn Gly Gln Thr Ala Gly Phe Ser Asn
15 85 90 95
Val Ala Gly Ala Asp Tyr Thr Thr Ser Tyr Asn Gln Gly Ser Asn Val
100 105 110
Gln Ser Val Ser Tyr Asn Ala Gln Ser Ser Asn Ser Asn Val Glu Ala
20 115 120 125
Val Ser Ala Pro Thr Tyr His Asn Tyr Ser Thr Ser Thr Thr Ser Ser
130 135 140
Ser Val Arg Leu Ser Asn Gly Asn Thr Ala Gly Ala Thr Gly Ser Ser
25 145 150 155 160
Ala Ala Gln Ile Met Ala Gln Arg Thr Gly Val Ser Ala Ser Thr Trp
165 170 175
Ala Ala Ile Ile Ala Arg Glu Ser Asn Gly Gln Val Asn Ala Tyr Asn
30 180 185 190
Pro Ser Gly Ala Ser Gly Leu Phe Gln Thr Met Pro Gly Trp Gly Pro
195 200 205
Thr Asn Thr Val Asp Gln Gln Ile Asn Ala Ala Val Lys Ala Tyr Lys
35 210 215 220
Ala Gln Gly Leu Gly Ala Trp Gly Phe
225 230

<210> 47
<211> 256
<212> PRT
<213> Staphylococcus aureus

<400> 47

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1 Met Met Lys Arg Leu Asn Lys Leu Val Leu Gly Ile Ile Phe Leu Phe
 5 Leu Val Ile Ser Ile Thr Ala Gly Cys Gly Ile Gly Lys Glu Ala Glu
 10 Val Lys Lys Ser Phe Glu Lys Thr Leu Ser Met Tyr Pro Ile Lys Asn
 15 Leu Glu Asp Leu Tyr Asp Lys Glu Gly Tyr Arg Asp Asp Gln Phe Asp
 20 Lys Asn Asp Lys Gly Thr Trp Ile Ile Asn Ser Glu Met Val Ile Gln
 25 Pro Asn Asn Glu Asp Met Val Ala Lys Gly Met Val Leu Tyr Met Asn
 30 Arg Asn Thr Lys Thr Thr Asn Gly Tyr Tyr Tyr Val Asp Val Thr Lys
 35 Asp Glu Asp Glu Gly Lys Pro His Asp Asn Glu Lys Arg Tyr Pro Val
 40 Lys Met Val Asp Asn Lys Ile Ile Pro Thr Lys Glu Ile Lys Asp Glu
 45 Lys Ile Lys Lys Glu Ile Glu Asn Phe Lys Phe Phe Val Gln Tyr Gly
 50 Asp Phe Lys Asn Leu Lys Asn Tyr Lys Asp Gly Asp Ile Ser Tyr Asn
 55 Pro Glu Val Pro Ser Tyr Ser Ala Lys Tyr Gln Leu Thr Asn Asp Asp
 60 Tyr Asn Val Lys Gln Leu Arg Lys Arg Tyr Asp Ile Pro Thr Ser Lys
 65 Ala Pro Lys Leu Leu Leu Lys Gly Ser Gly Asn Leu Lys Gly Ser Ser
 70 Val Gly Tyr Lys Asp Ile Glu Phe Thr Phe Val Glu Lys Lys Glu Glu
 75 Asn Ile Tyr Phe Ser Asp Ser Leu Asp Tyr Lys Lys Ser Gly Asp Val
 80
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 115
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<210> 48

<211> 514

<212> PRT

<213> Staphylococcus aureus

<400> 48

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Met Lys Lys Ile Tyr Lys Ser Leu Thr Val Ser Ala Ile Val Ala Thr
1 5 10 15
Val Ser Leu Ser Ala Leu Pro Gln Ser Leu Ala Ile Thr His Glu Ser
5 20 25 30
Gln Pro Thr Lys Gln Gln Arg Thr Val Leu Phe Asp Arg Ser His Gly
35 40 45
Gln Thr Ala Gly Ala Ala Asp Trp Val Ser Asp Gly Ala Phe Ser Asp
10 50 55 60
Tyr Ala Asp Ser Ile Gln Lys Gln Gly Tyr Asp Val Lys Ala Ile Asp
65 70 75 80
Gly His Ser Asn Ile Thr Glu Ala Ser Leu Lys Ser Ser Lys Ile Phe
15 85 90 95
Val Ile Pro Glu Ala Asn Ile Pro Phe Lys Glu Ser Glu Gln Ala Ala
100 105 110
Ile Val Lys Tyr Val Lys Gln Gly Gly Asn Val Val Phe Ile Ser Asp
20 115 120 125
His Tyr Asn Ala Asp Arg Asn Leu Asn Arg Ile Asp Ser Ser Glu Ala
130 135 140
Met Asn Gly Tyr Arg Arg Gly Ala Tyr Glu Asp Met Ser Lys Gly Met
25 145 150 155 160
Asn Ala Glu Glu Lys Ser Ser Thr Ala Met Gln Gly Val Lys Ser Ser
165 170 175
Asp Trp Leu Ser Thr Asn Phe Gly Val Arg Phe Arg Tyr Asn Ala Leu
30 180 185 190
Gly Asp Leu Asn Thr Ser Asn Ile Val Ser Ser Lys Glu Ser Phe Gly
195 200 205
Ile Thr Glu Gly Val Lys Ser Val Ser Met His Ala Gly Ser Thr Leu
35 210 215 220
Ala Ile Thr Asn Pro Glu Lys Ala Lys Gly Ile Val Tyr Thr Pro Glu
225 230 235 240
Gln Leu Pro Ala Lys Ser Lys Trp Ser His Ala Val Asp Gln Gly Ile
40 245 250 255
Tyr Asn Gly Gly Gly Lys Ala Glu Gly Pro Tyr Val Ala Ile Ser Lys
260 265 270
Val Gly Lys Gly Lys Ala Ala Phe Ile Gly Asp Ser Ser Leu Val Glu
275 280 285
45 Asp Ser Ser Pro Lys Tyr Val Arg Glu Asp Asn Gly Glu Lys Lys Lys
290 295 300
Thr Tyr Asp Gly Phe Lys Glu Gln Asp Asn Gly Lys Leu Leu Asn Asn
305 310 315 320
50 Ile Thr Ala Trp Met Ser Lys Asp Asn Asp Gly Lys Ser Leu Lys Ala
325 330 335
Ser Ser Leu Thr Leu Asp Thr Lys Thr Lys Leu Leu Asp Phe Glu Arg

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				340					345					350			
5	Pro	Glu	Arg	Ser	Thr	Glu	Pro	Glu	Lys	Glu	Pro	Trp	Ser	Gln	Pro	Pro	
			355					360					365				
	Ser	Gly	Tyr	Lys	Trp	Tyr	Asp	Pro	Thr	Thr	Phe	Lys	Ala	Gly	Ser	Tyr	
		370					375					380					
10	Gly	Ser	Glu	Lys	Gly	Ala	Asp	Pro	Gln	Pro	Asn	Thr	Pro	Asp	Asp	His	
	385					390					395					400	
	Thr	Pro	Pro	Asn	Gln	Asn	Glu	Lys	Val	Thr	Phe	Asp	Ile	Pro	Gln	Asn	
					405					410					415		
15	Val	Ser	Val	Asn	Glu	Pro	Phe	Glu	Met	Thr	Ile	His	Leu	Lys	Gly	Phe	
				420					425					430			
	Glu	Ala	Asn	Gln	Thr	Leu	Glu	Asn	Leu	Arg	Val	Gly	Ile	Tyr	Lys	Glu	
			435					440					445				
20	Gly	Gly	Arg	Gln	Ile	Gly	Gln	Phe	Ser	Ser	Lys	Asp	Asn	Asp	Tyr	Asn	
		450					455					460					
	Pro	Pro	Gly	Tyr	Ser	Thr	Leu	Pro	Thr	Val	Lys	Ala	Asp	Glu	Asn	Gly	
	465					470					475					480	
25	Asn	Val	Thr	Ile	Lys	Val	Asn	Ala	Lys	Val	Leu	Glu	Ser	Met	Glu	Gly	
					485					490					495		
	Ser	Lys	Ile	Arg	Leu	Lys	Leu	Gly	Asp	Lys	Thr	Leu	Ile	Thr	Thr	Asp	
				500					505					510			
	Phe	Lys															

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<210> 49

<211> 511

<212> PRT

<213> Staphylococcus aureus

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<400> 49

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1 Met Ser Asn Ile Ala Phe Tyr Val Val Ser Asp Val His Gly Tyr Ile
 5 Phe Pro Thr Asp Phe Thr Ser Arg Asn Gln Tyr Gln Pro Met Gly Leu
 10 Leu Leu Ala Asn His Val Ile Glu Gln Asp Arg Arg Gln Tyr Asp Gln
 15 Ser Phe Lys Ile Asp Asn Gly Asp Phe Leu Gln Gly Ser Pro Phe Cys
 20 Asn Tyr Leu Ile Ala His Ser Gly Ser Ser Gln Pro Leu Val Asp Phe
 25 Tyr Asn Arg Met Ala Phe Asp Phe Gly Thr Leu Gly Asn His Glu Phe
 30 Asn Tyr Gly Leu Pro Tyr Leu Lys Asp Thr Leu Arg Arg Leu Asn Tyr
 35 Pro Val Leu Cys Ala Asn Ile Tyr Glu Asn Asp Ser Thr Leu Thr Asp
 40 Asn Gly Val Lys Tyr Phe Gln Val Gly Asp Gln Thr Val Gly Val Ile
 45 Gly Leu Thr Thr Gln Phe Ile Pro His Trp Glu Gln Pro Glu His Ile
 50 145 150 155 160

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5 Gln Ser Leu Thr Phe₁₆₅ His Ser Ala Phe₁₇₀ Glu Ile Leu Gln Gln Tyr₁₇₅ Leu
 Pro Glu Met Lys₁₈₀ Arg His Ala Asp Ile₁₈₅ Ile Val Val Cys Tyr₁₉₀ His Gly
 Gly Phe Glu₁₉₅ Lys Asp Leu Glu Ser₂₀₀ Gly Thr Pro Thr Glu₂₀₅ Val Leu Thr
 10 Gly Glu₂₁₀ Asn Glu Gly Tyr Ala₂₁₅ Met Leu Glu Ala Phe₂₂₀ Ser Lys Asp Ile
 Asp Ile Phe Ile Thr Gly₂₃₀ His Gln His Arg Gln₂₃₅ Ile Ala Glu Arg Phe₂₄₀
 15 Lys Gln Thr Ala Val₂₄₅ Ile Gln Pro Gly Thr₂₅₀ Arg Gly Thr Thr Val₂₅₅ Gly
 Arg Val Val Leu₂₆₀ Ser Thr Asp Glu Tyr₂₆₅ Glu Asn Leu Ser Val₂₇₀ Glu Ser
 20 Cys Glu Leu₂₇₅ Leu Pro Val Ile Asp₂₈₀ Asp Ser Thr Phe Thr₂₈₅ Ile Asp Glu
 Asp Asp₂₉₀ Gln His Leu Arg Lys₂₉₅ Gln Leu Glu Asp Trp₃₀₀ Leu Asp Tyr Glu
 25 Ile Thr Thr Leu Pro Tyr₃₁₀ Asp Met Thr Ile Asn His Ala Phe Glu Ala₃₂₀
 Arg Val Ala Pro His₃₂₅ Pro Phe Thr Asn Phe₃₃₀ Met Asn Tyr Ala Leu₃₃₅ Leu
 30 Glu Lys Ser Asp₃₄₀ Ala Asp Val Ala Cys₃₄₅ Thr Ala Leu Phe Asp₃₅₀ Ser Ala
 Ser Gly Phe₃₅₅ Lys Gln Val Val Thr₃₆₀ Met Arg Asp Val Ile₃₆₅ Asn Asn Tyr
 35 Pro Phe₃₇₀ Pro Asn Thr Phe Lys₃₇₅ Val Leu Ala Val Ser₃₈₀ Gly Ala Lys Leu
 Lys Glu Ala Ile Glu Arg₃₉₀ Ser Ala Glu Tyr Phe₃₉₅ Asp Val Lys Asn Asp₄₀₀
 40 Glu Val Ser Val Ser₄₀₅ Ala Asp Phe Leu Glu₄₁₀ Pro Lys Pro Gln His Phe₄₁₅
 Asn Tyr Asp Ile₄₂₀ Tyr Gly Gly Val Ser₄₂₅ Tyr Thr Ile His Val₄₃₀ Gly Arg
 45 Pro Lys Gly₄₃₅ Gln Arg Val Ser Asn₄₄₀ Met Met Ile Gln Gly₄₄₅ His Ala Val
 Asp Leu₄₅₀ Lys Gln Thr Tyr Thr₄₅₅ Ile Cys Val Asn Asn Tyr Arg Ala Val
 50 Gly Glu Gly Gln Tyr Asp₄₇₀ Met Tyr Ile Asp Ala₄₇₅ Pro Val Val Lys Asp₄₈₀
 Ile Gln Val Glu Gly₄₈₅ Ala Gln Leu Leu Ile₄₉₀ Asp Phe Leu Ser Asn Asn₄₉₅
 55 Asn Leu Met Arg₅₀₀ Ile Pro Gln Val Val₅₀₅ Asp Phe Lys Val Glu₅₁₀ Lys

<210> 50
 <211> 324
 <212> PRT

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<213> Staphylococcus aureus

<400> 50

5 Met Lys Arg Leu Ser Ile Ile Val Ile Ile Gly Ile Phe Ile Ile Thr
1 5 10 15
Gly Cys Asp Trp Gln Arg Thr Ser Lys Glu Arg Ser Lys Asn Ala Gln
20 25 30
10 Asn Gln Gln Val Ile Lys Ile Gly Tyr Leu Pro Ile Thr His Ser Ala
35 40 45
Asn Leu Met Met Thr Lys Lys Leu Leu Ser Gln Tyr Asn His Pro Lys
50 55 60
15 Tyr Lys Leu Glu Leu Val Lys Phe Asn Asn Trp Pro Asp Leu Met Asp
65 70 75 80
Ala Leu Asn Ser Gly Arg Ile Asp Gly Ala Ser Thr Leu Ile Glu Leu
85 90 95
20 Ala Met Lys Ser Lys Gln Lys Gly Ser Asn Ile Lys Ala Val Ala Leu
100 105 110
Gly His His Glu Gly Asn Val Ile Met Gly Gln Lys Gly Met His Leu
115 120 125
25 Asn Glu Phe Asn Asn Asn Gly Asp Asp Tyr His Phe Gly Ile Pro His
130 135 140
Arg Tyr Ser Thr His Tyr Leu Leu Leu Glu Glu Leu Arg Lys Gln Leu
145 150 155 160
30 Lys Ile Lys Pro Gly His Phe Ser Tyr His Glu Met Ser Pro Ala Glu
165 170 175
Met Pro Ala Ala Leu Ser Glu His Arg Ile Thr Gly Tyr Ser Val Ala
180 185 190
35 Glu Pro Phe Gly Ala Leu Gly Glu Lys Leu Gly Lys Gly Lys Thr Leu
195 200 205
Lys His Gly Asp Asp Val Ile Pro Asp Ala Tyr Cys Cys Val Leu Val
210 215 220
40 Leu Arg Gly Glu Leu Leu Asp Gln His Lys Asp Val Ala Gln Ala Phe
225 230 235 240
Val Gln Asp Tyr Lys Lys Ser Gly Phe Lys Met Asn Asp Arg Lys Gln
245 250 255
45 Ser Val Asp Ile Met Thr His His Phe Lys Gln Ser Arg Asp Val Leu
260 265 270
Thr Gln Ser Ala Ala Trp Thr Ser Tyr Gly Asp Leu Thr Ile Lys Pro
275 280 285
50 Ser Gly Tyr Gln Glu Ile Thr Thr Leu Val Lys Gln His His Leu Phe
290 295 300
Asn Pro Pro Ala Tyr Asp Asp Phe Val Glu Pro Ser Leu Tyr Lys Glu
305 310 315 320
55 Ala Ser Arg Ser

<210> 51

<211> 591

<212> PRT

<213> Staphylococcus aureus

<400> 51

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Met Lys Lys Ile Ile Ser Ile Ala Ile Ile Val Leu Ala Leu Val Leu
 1 5 10 15
 ser Gly cys Gly Val Pro Thr Lys Ser Glu Val Ala Gln Lys Ser Ser
 5 20 25 30
 Lys Val Glu Val Lys Gly Glu Arg Pro Thr Ile His Phe Leu Gly Gln
 35 40 45
 Ala Ser Tyr Glu Asn Asp Met Asn Ile Val Lys Asp Gln Leu Glu Asn
 10 50 55 60
 Ala Gly Phe Asn Val Lys Met Asn Ile Gln Pro Asp Tyr Gly Ser Tyr
 65 70 75 80
 Arg Thr Gln Arg Gln Ala Gly Asn Tyr Asp Ile Gln Ile Asp Asp Trp
 15 85 90 95
 Met Thr Val Phe Gly Asp Pro Asn Tyr Ala Met Thr Ala Leu Phe Ser
 100 105 110
 Ser Thr Gly Ser Asn Ser Leu Leu Lys Asp Lys His Val Asp Gln Leu
 20 115 120 125
 Leu Asn Lys Ala Ser Thr Gln Asn Glu Ala Asp Val Lys Gln Thr Tyr
 130 135 140
 Lys Gln Ile Glu Asp Glu Val Val Phe Asp Lys Gly Tyr Met Ala Pro
 25 145 150 155 160
 Leu Tyr Gly Ser Lys Lys Asn Leu Val Tyr Asp Asn Lys Val Leu Asp
 165 170 175
 Lys Asn Ser Val Gly Leu Pro Asn Ser Arg Ala Leu Ile Trp Gln Gln
 180 185 190
 Phe Asp Tyr Asn Asn Ser Arg Glu Arg Asp Thr Arg Pro Leu Val Met
 195 200 205
 Thr Gln Gln Asp Gly Glu Ile Pro Thr Leu Asp Pro Ile Arg Ser Ile
 210 215 220
 Ala Pro Ser Val Tyr Ser Ile Asn Met Asn Met Tyr Thr Arg Leu Leu
 225 230 235 240
 Leu Leu Asp Glu Asn Asp His Leu Thr Thr Lys Gly Ser Leu Ser His
 245 250 255
 Asp Tyr Ala Val Asn Lys Asp Asn Lys Ala Phe Tyr Phe Leu Leu Arg
 260 265 270
 Asp Asp Asp Tyr Phe Ala Lys Val Val Asn Gly Gln Ala Arg Asn Thr
 275 280 285
 Gly Glu Arg Val Ser Ala Glu Asp Val Lys Phe Ser Leu Asp Arg Ala
 290 295 300
 Arg Asp Lys Lys Ser Val Pro Asn Asn Asn Thr Tyr Asn Met His Lys
 305 310 315 320
 His Ile Asn Asp Ile Lys Ile Leu Lys Asp Glu Asp Ile Asp Gln Leu
 325 330 335
 Arg Lys Glu Lys Asp Lys Asp Asp Lys Ser Ile Tyr Asp Lys Leu Ile
 340 345 350
 Lys Ala Tyr Asn Val Lys Ser Leu Thr Thr Asp Gly Gln Lys Val Asn
 355 360 365

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Asn Lys Asp Gly Ile Tyr Gln Ile Val Lys Ile Thr Thr Asp Gln Ser
 370 375 380
 Met Pro Arg Glu Val Asn Tyr Leu Thr His Ser Ser Ala Gly Ile Leu
 385 390 395 400
 Ser Lys Lys Phe Val Asn Gln Val Asn Gln Glu Tyr Pro Lys Gly Tyr
 405 410 415
 Gly Asp Ser Ser Thr Ile Pro Ala Asn Ser Asp Gly Lys Asn Ala Leu
 420 425 430
 Tyr Ala Ser Gly Ala Tyr Ile Met Thr Gln Lys Asn Ala Tyr Gln Ala
 435 440 445
 Thr Phe Gln Arg Asn Pro Gly Phe Asn Glu Thr Glu Lys Gly Ser Tyr
 450 455 460
 Gly Pro Ala Lys Ile Lys Asn Ile Thr Leu Lys Phe Asn Gly Asp Pro
 465 470 475 480
 Asn Asn Ala Leu Ser Glu Leu Arg Asn His Ser Ile Asp Met Leu Ala
 485 490 495
 Asp Val Asn Gln Lys His Phe Asp Leu Ile Lys Ser Asp Lys Asn Leu
 500 505 510
 Ser Ile Ile Arg Lys Asn Gly Arg Lys Ser Val Phe Leu Met Leu Asn
 515 520 525
 Ile Lys Lys Gly Ile Phe Lys Thr His Pro Asn Leu Arg Gln Ala Val
 530 535 540
 Val Asn Ala Ile Asp Gln Asp Gln Phe Ile Lys Phe Tyr Arg Gly Asp
 545 550 555 560
 Lys Phe Lys Ile Ala Ser Pro Ile Thr Pro Leu Val Asp Thr Gly Asn
 565 570 575
 Glu Gln Arg Gln Asp Leu Glu Lys Val Glu Lys Ala Ile Asn Gln
 580 585 590

<210> 52

<211> 668

<212> PRT

<213> Staphylococcus aureus

<400> 52

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	Met	Val	Ile	Asn	Leu	Asn	Asp	Lys	Gln	Thr	Lys	Thr	Ser	Lys	Glu	Gly
	1				5					10					15	
5	Leu	Ile	Ser	Val	Ser	His	Pro	Leu	Ala	Ala	Lys	Ile	Gly	Lys	Asp	Val
				20					25					30		
	Leu	Asp	Gln	Gly	Gly	Asn	Ala	Met	Asp	Ala	Val	Ile	Ala	Ile	Gln	Leu
			35					40					45			
10	Ala	Leu	Asn	Val	Val	Glu	Pro	Phe	Ala	Ser	Gly	Ile	Gly	Gly	Gly	Gly
		50					55					60				
	Tyr	Leu	Leu	Tyr	Tyr	Glu	Gln	Ser	Thr	Gly	Ser	Ile	Thr	Ala	Phe	Asp
	65					70					75					80
15	Ala	Arg	Glu	Thr	Ala	Pro	Glu	His	Val	Asp	Lys	Gln	Phe	Tyr	Leu	Asp
					85					90					95	
	Asp	Ser	Gly	Glu	Tyr	Lys	Ser	Phe	Phe	Asp	Met	Thr	Thr	His	Gly	Lys
				100					105					110		

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Thr Val Ala Val Pro Ala Ile Pro Lys Leu Phe Asp Tyr Ile His Lys
 115 120
 Arg Tyr Ala Lys Leu Ser Leu Glu Asp Leu Ile Asn Pro Ala Ile Glu
 130 135 140
 5 Leu Ala Ile Glu Gly His Ala Ala Asn Trp Ala Thr Glu Lys Tyr Ser
 145 150 155 160
 Arg Gln Gln His Ala Arg Leu Thr Lys Tyr His Glu Thr Ala Gln Val
 165 170 175
 10 Phe Thr His Glu Asn Gln Tyr Trp Arg Glu Gly Asp Trp Ile Val Gln
 180 185 190
 Pro Glu Leu Gly Lys Thr Phe Gln Ile Leu Arg Glu Gln Gly Phe Asn
 195 200 205
 15 Ala Phe Tyr Lys Gly Asp Ile Ala Lys Gln Leu Val Asn Val Val Lys
 210 215 220
 Ala Cys Gly Gly Thr Ile Thr Leu Glu Asp Leu Ala Lys Tyr Asp Ile
 225 230 235 240
 20 Gln Ile Lys Ala Pro Ile Ser Ala Thr Phe Lys Asp Tyr Asp Ile Tyr
 245 250 255
 Ser Met Gly Pro Ser Ser Ser Gly Gly Ile Thr Val Ile Gln Ile Leu
 260 265 270
 25 Lys Leu Leu Glu His Val Asp Leu Pro Ser Met Gly Pro Arg Ser Val
 275 280 285
 Asp Tyr Leu His His Leu Ile Gln Ala Met His Leu Ala Tyr Ser Asp
 290 295 300
 30 Arg Ala Gln Tyr Leu Ala Asp Asp Asn Phe His Glu Val Pro Val Gln
 305 310 315 320
 Ser Leu Ile Asp Asp Asp Tyr Leu Lys Ala Arg Ser Thr Leu Ile Asp
 325 330 335
 35 Ser Asn Lys Ala Asn Ile Asp Ile Glu His Gly Val Val Ser Asp Cys
 340 345 350
 Ile Ser His Thr Asp Val Glu Glu Asn His Thr Glu Thr Thr His Phe
 355 360 365
 40 Cys Val Ile Asp Lys Glu Gly Asn Ile Ala Ser Phe Thr Thr Ser Ile
 370 375 380
 Gly Met Ile Tyr Gly Ser Gly Ile Thr Ile Pro Gly Tyr Gly Val Leu
 385 390 395 400
 45 Leu Asn Thr Thr Met Asp Gly Phe Asp Val Val Asp Gly Gly Ile Asn
 405 410 415
 Glu Ile Ala Pro Tyr Lys Arg Pro Leu Ser Asn Met Ala Pro Thr Ile
 420 425 430
 50 Val Met Tyr His Gly Lys Pro Ile Leu Thr Val Gly Ala Pro Gly Ala
 435 440 445
 Ile Ser Ile Ile Ala Ser Val Ala Gln Thr Leu Ile Asn Val Leu Val
 450 455 460
 55 Phe Gly Met Asp Ile Gln Gln Ala Ile Asp Glu Pro Arg Ile Tyr Ser
 465 470 475 480
 Ser His Pro Asn Arg Ile Glu Trp Glu Pro Gln Phe Ser Gln Ser Thr

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					485					490					495
	Ile	Leu	Ala	Leu	Ile	Ala	His	Gly	His	Ala	Met	Glu	His	Lys	Pro Asp
				500					505					510	
5	Ala	Tyr	Ile	Gly	Asp	Val	His	Gly	Leu	Gln	Val	Asp	Pro	Thr	Thr Tyr
			515					520					525		
	Glu	Ala	Ser	Gly	Gly	Ser	Asp	Asp	Thr	Arg	Glu	Gly	Thr	Val	Met Gly
		530					535					540			
10	Gly	Glu	Val	Leu	Val	Ile	Arg	Lys	Gln	Pro	Leu	Pro	Tyr	Arg	Gln Met
	545					550					555				560
	Tyr	Asp	Ser	Asp	Gly	Phe	Arg	Leu	Tyr	Phe	Asn	Asp	Val	Gln	Leu Pro
					565					570					575
15	Leu	Leu	Ala	Asp	Gln	Val	Arg	Trp	Met	His	Asp	Lys	Tyr	Trp	Val Asp
				580					585					590	
	Glu	Ser	Val	Val	Arg	Ile	Ile	Phe	Pro	Glu	Val	Ser	Ala	His	Ile Glu
			595					600					605		
20	Asp	Leu	Arg	Ser	Tyr	Glu	Asn	Ala	Gly	Glu	Asn	Tyr	Ile	Asp	Ile Ala
		610					615					620			
	Trp	Leu	Ala	Arg	Lys	Tyr	Ala	Tyr	Gln	Val	Thr	Leu	Lys	Asp	Asp Gly
	625					630					635				640
25	Leu	Tyr	Leu	Thr	Asp	Asp	Thr	Tyr	Thr	Ser	Val	Lys	Arg	Asn	Thr Asn
					645					650					655
	Ala	Tyr	Tyr	Arg	Tyr	Asp	Arg	Asp	Ser	Ile	Thr	Arg			
				660					665						

<210> 53
 <211> 322
 <212> PRT
 <213> Staphylococcus aureus

<400> 53

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1 Met Lys Ser Lys 5 Ile Tyr Ile Leu Leu 10 Leu Phe Leu Ile Phe Leu Ser 15
 5 Ala Cys Ala Asn 20 Thr Arg His Ser Glu 25 Ser Asp Lys Asn Val 30 Leu Thr
 Val Tyr Ser 35 Pro Tyr Gln Ser Asn 40 Leu Ile Arg Pro Ile 45 Leu Asn Glu
 10 Phe Glu 50 Lys Gln Glu His Val 55 Lys Ile Glu Ile Lys 60 His Gly Ser Thr
 Gln Val 65 Leu Leu Ser Asn 70 Leu His Asn Glu 75 Asp Phe Ser Glu Arg Gly 80
 15 Asp Val Phe Met 85 Gly Gly Val Leu Ser Glu 90 Thr Ile Asp His Pro Glu 95
 Asp Phe Val 100 Pro Tyr Gln Asp Thr Ser 105 Val Thr Gln Gln Leu 110 Glu Asp
 20 Tyr Arg Ser 115 Asn Asn Lys Tyr Val 120 Thr Ser Phe Leu Leu Met Pro Thr
 Val Ile Val 130 Val Asn Ser Asp 135 Leu Gln Gly Asp Ile 140 Lys Ile Arg Gly
 25 Tyr Gln Asp Leu Leu 150 Gln Pro Ile Leu Lys Gly 155 Lys Ile Ala Tyr Ser 160
 Asn Pro Asn Thr 165 Thr Thr Gly Tyr Gln 170 His Met Arg Ala Ile Tyr 175
 30 Ser Met His 180 His Arg Val Ser Asp Val 185 His Gln Phe Gln Asn His Ala 190
 Met Gln 195 Leu Ser Lys Thr Ser Lys 200 Val Ile Glu Asp Val 205 Ala Lys Gly
 35 Lys Tyr 210 Tyr Ala Gly Leu Ser 215 Tyr Glu Gln Asp Ala 220 Arg Thr Trp Lys
 Asn Lys Gly Tyr Pro Val 230 Ser Ile Val Tyr Pro 235 Ile Glu Gly Thr Met 240
 40 Leu Asn Val Asp 245 Gly Ile Ala Leu Val Lys 250 Asn Ala His Pro His Pro 255
 Lys Arg Lys 260 Lys Leu Val Gln Tyr Leu 265 Thr Ser Arg Ser Val 270 Gln Gln
 45 Arg Leu Val 275 Ala Glu Phe Asp Ala 280 Lys Ser Ile Arg Lys 285 Asp Val Ser
 Glu Gln 290 Ser Asp Gln Ser Ile 295 Glu Asn Leu Lys Asn 300 Ile Pro Leu Ile
 50 Pro Lys Ser Lys Leu Pro 310 Asp Ile Pro His His 315 Lys Phe Leu Glu Met 320
 Ile Gln

<210> 54

<211> 470

<212> PRT

<213> Staphylococcus aureus

<400> 54

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1 Met His Ser Ser Gly Lys Asp Leu Asn Ile Ser Leu Pro Leu Lys Thr
 5 Lys Ser Ile Ala Pro Tyr Glu Thr Asp Val Pro Val Lys Ile Gly Ala
 10 Ala Glu Ser Leu Phe Lys Thr Asn Asp Gln Gly Lys Ile Glu Lys Ala
 15 Lys Val Lys Ser Tyr His Gln Pro Asn Asp Thr Thr Leu Asp Ile Glu
 20 Leu Lys Asp Asn Ile Lys Phe Gln Asn Gly Gln Lys Leu Thr Ala Glu
 25 Lys Val Lys Ser Ser Leu Glu Asn Ser Met Lys Lys Ser Asp Leu Val
 30 Lys Tyr Ser Leu Pro Ile Ser Ser Ile Thr Ala Lys Gly Gln Lys Leu
 35 Thr Ile Lys Thr Asn Ser Ala Tyr Pro Glu Leu Val Ser Glu Leu Ala
 40 Asn Pro Phe Met Ala Ile Tyr Asp Thr Asp Ala Lys Ser Asp Val Asn
 45 Gln Thr Pro Val Gly Thr Gly Pro Tyr Gln Ile Lys Asp Tyr Lys Gln
 50 145 150 155 160

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Ser Arg Lys Ile Ser Leu Ser Asn Phe Lys Asp Tyr Trp Gln Gly Lys
 165 170 175
 Pro Lys Leu Asp His Ile Thr Val Thr Tyr Gln Glu Asp Gly Asn Asn
 180 185 190
 Arg Val Arg Asn Leu Glu Ser Gln Lys Asp Asp Leu Ile Thr Asp Val
 195 200 205
 Pro Val Asn Lys Val Gln Asp Ile Glu Asn Asn Gln Asn Leu Lys Val
 210 215 220
 Ser Lys Glu Ser Gly Phe Arg Thr Ser Leu Leu Met Tyr Asn His Thr
 225 230 235 240
 Asn Lys Lys Met Thr Lys Ser Val Arg Glu Ala Leu Asp His Ile Ile
 245 250 255
 Asp Arg Gln Gly Ile Ala Asp His Ile Tyr Gln Gly Tyr Ala Lys Pro
 260 265 270
 Ala Thr Ser Pro Phe Asn Asp Lys Ile Pro Tyr Ile Lys Glu Pro Lys
 275 280 285
 Leu Thr Lys Gln Asn Ile Glu Gln Ala Lys Met Leu Leu Ala Lys Asp
 290 295 300
 Gly Tyr Thr Lys Glu His Pro Leu Lys Ile Lys Leu Ile Thr Tyr Asp
 305 310 315 320
 Gly Arg Pro Glu Leu Ser Lys Ile Ala Gln Val Leu Gln Ser Asp Ala
 325 330 335
 Lys Lys Ala Asn Ile Glu Ile Asp Ile Lys Ser Val Asp Asp Ile Glu
 340 345 350
 Gly Tyr Leu Lys Asp Arg Ser Ala Trp Asp Ala Thr Met Tyr Ser Phe
 355 360 365
 Gly Thr Ile Pro Arg Gly Asp Thr Gly Tyr Phe Phe Asn Gln Ala Tyr
 370 375 380
 Lys Lys Asp Gly Ala Ile Asn Lys Gly Asp Tyr Asn Asn Ser Asn Val
 385 390 395 400
 Asp Asp Leu Ile Asn Gln Leu Asn His Thr Val Asp Val Lys Glu Arg
 405 410 415
 His Asn Ile Ser Asn Asp Ile Ile Lys Leu Ser Ser Arg Asp Val Pro
 420 425 430
 Asn Ser Tyr Ile Ala Tyr Asn Asp Gln Ile Val Ala Ala Asn Ser Lys
 435 440 445
 Val Lys Asn Tyr Lys Val Thr Pro Glu Gly Ile Tyr Leu Ile Asp Tyr
 450 455 460
 Arg Thr Thr Ile Glu Arg
 465 470

<210> 55

<211> 316

<212> PRT

<213> Staphylococcus aureus

<400> 55

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Met Lys Lys Leu Thr Ala Ala Ala Ile Ala Thr Met Gly Phe Ala Thr
1 5 10 15
Phe Thr Met Ala His Gln Ala Asp Ala Ala Glu Thr Thr Asn Thr Gln
5
20 25 30
Gln Ala His Thr Gln Met Ser Thr Gln Ser Gln Asp Val Ser Tyr Gly
35 40 45
10 Thr Tyr Tyr Thr Ile Asp Ser Asn Gly Asp Tyr His His Thr Pro Asp
50 55 60
Gly Asn Trp Asn Gln Ala Met Phe Asp Asn Lys Glu Tyr Ser Tyr Thr
65 70 75 80
15 Phe Val Asp Ala Gln Gly His Thr His Tyr Phe Tyr Asn Cys Tyr Pro
85 90 95
Lys Asn Ala Asn Ala Asn Gly Ser Gly Gln Thr Tyr Val Asn Pro Ala
100 105 110
20 Thr Ala Gly Asp Asn Asn Asp Tyr Thr Ala Ser Gln Ser Gln Gln His
115 120 125
Ile Asn Gln Tyr Gly Tyr Gln Ser Asn Val Gly Pro Asp Ala Ser Tyr
130 135 140
25 Tyr Ser His Ser Asn Asn Asn Gln Ala Tyr Asn Ser His Asp Gly Asn
145 150 155 160
Gly Lys Val Asn Tyr Pro Asn Gly Thr Ser Asn Gln Asn Gly Gly Ser
165 170 175
30 Ala Ser Lys Ala Thr Ala Ser Gly His Ala Lys Asp Ala Ser Trp Leu
180 185 190
Thr Ser Arg Lys Gln Leu Gln Pro Tyr Gly Gln Tyr His Gly Gly Gly
195 200 205
35 Ala His Tyr Gly Val Asp Tyr Ala Met Pro Glu Asn Ser Pro Val Tyr
210 215 220
Ser Leu Thr Asp Gly Thr Val Val Gln Ala Gly Trp Ser Asn Tyr Gly
225 230 235 240
40 Gly Gly Asn Gln Val Thr Ile Lys Glu Ala Asn Ser Asn Asn Tyr Gln
245 250 255
Trp Tyr Met His Asn Asn Arg Leu Thr Val Ser Ala Gly Asp Lys Val
260 265 270
45 Lys Ala Gly Asp Gln Ile Ala Tyr Ser Gly Ser Thr Gly Asn Ser Thr
275 280 285
Ala Pro His Val His Phe Gln Arg Met Ser Gly Gly Ile Gly Asn Gln
290 295 300
50 Tyr Ala Val Asp Pro Thr Ser Tyr Leu Gln Ser Arg
305 310 315

<210> 56

<211> 507

55 <212> PRT

<213> staphylococcus aureus

<400> 56

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Met	Ser	Lys	Lys	Leu	Lys	Ile	Ile	Ile	Pro	Ile	Ile	Ile	Val	Leu	Leu
1				5					10					15	
Leu	Ile	Gly	Gly	Ile	Ala	Trp	Gly	Val	Tyr	Ala	Phe	Phe	Ala	Asn	Thr
			20					25					30		
Pro	Lys	Asn	Thr	Tyr	Leu	Lys	Ser	Glu	Gln	Gln	Thr	Ala	Lys	Met	Tyr
		35					40					45			

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	Lys	Asp	Tyr	Phe	Asn	Asp	Arg	Phe	Glu	Asn	Glu	Val	Lys	Phe	Gln	Glu
	50						55					60				
5	Lys	Met	Lys	Asp	Asn	Ser	Phe	Leu	Ser	Ser	Leu	Glu	Leu	Ser	Ala	Asp
	65					70					75					80
	Ala	Ser	Asp	Glu	Ile	Val	Lys	Gly	Leu	Gly	Ile	Pro	Lys	Ser	Val	Val
					85					90					95	
10	Asn	Ala	Ser	Lys	Ile	Lys	Met	Ser	Tyr	Gly	His	Asp	Pro	Lys	Lys	Glu
				100					105					110		
	Lys	Ser	Met	Ile	Asn	Leu	Glu	Pro	Thr	Ile	Ala	Asp	Ser	Ala	Leu	Gly
			115					120					125			
15	Lys	Phe	Gln	Leu	Ala	Ala	Asp	Lys	Asp	Lys	His	Tyr	Phe	Glu	Ser	Pro
	130						135					140				
	Leu	Phe	Lys	Gly	Lys	Tyr	Ser	Val	Asn	Asn	Ser	Asp	Leu	Leu	Ser	Thr
	145					150					155					160
20	Tyr	Ser	Lys	Leu	Thr	Gly	Glu	Asp	Glu	Glu	Thr	Ala	Lys	Glu	Asn	Gly
					165					170					175	
	Ile	Thr	Asn	Gln	Gln	Leu	Asn	Leu	Asn	Thr	Leu	Phe	Asn	Asn	Ala	Gln
				180					185					190		
25	Ala	Gln	Gln	Ser	Asp	Tyr	Ser	Lys	Ile	Ala	Glu	Lys	Tyr	Ser	Glu	Leu
			195					200					205			
	Ile	Val	Asp	Lys	Leu	Asp	Asp	Asp	Asn	Phe	Asp	Lys	Gly	Lys	Lys	Glu
		210					215					220				
30	Glu	Ile	Lys	Val	Asn	Gly	Glu	Lys	Tyr	Lys	Val	Arg	Pro	Val	Thr	Leu
	225					230					235					240
	Thr	Leu	Ser	Arg	Ala	Asp	Thr	Lys	Lys	Ile	Thr	Leu	Ala	Val	Leu	Glu
					245					250					255	
35	Glu	Ala	Lys	Lys	Asp	Lys	Asp	Leu	Lys	Lys	Leu	Met	Glu	Glu	Gln	Gly
				260					265					270		
	Ala	Thr	Lys	Asp	Phe	Glu	Lys	Asp	Ile	Lys	Lys	Ala	Ile	Asp	Asp	Val
			275					280					285			
40	Lys	Glu	Thr	Lys	Lys	Asp	Glu	Phe	Ala	Lys	Ile	Gln	Ser	Lys	Ile	Tyr
		290					295					300				
	Thr	Glu	Lys	His	Thr	Ile	Val	Lys	Arg	Glu	Ile	Thr	Ile	Thr	Asp	Lys
	305					310					315					320
	Glu	Asn	Asn	Lys	Thr	Lys	Ile	Lys	Gly	Thr	Asn	Thr	Leu	Glu	Asp	Asp
					325					330					335	
45	Lys	Leu	Lys	Leu	Asp	Tyr	Ala	Leu	Asp	Phe	Asp	Gln	Asp	Lys	Tyr	Thr
				340					345					350		
	Tyr	Ala	Glu	Ala	Lys	Tyr	Thr	Ile	Lys	Gly	Val	Ser	Ser	Lys	Glu	Lys
			355					360					365			
50	Asp	Asn	Lys	Tyr	Asn	Asp	Lys	Tyr	Glu	Phe	Gly	Lys	Lys	Thr	Glu	Tyr
		370					375					380				
	Asp	Glu	Ser	Lys	Ile	Lys	Leu	Asp	Asn	Gln	Glu	Lys	Val	Asp	Gly	Thr
	385					390					395					400
55	Lys	Arg	Gln	Asp	Lys	Gly	Lys	Ile	Thr	Val	Ala	Leu	Asp	Lys	Tyr	Ser
					405					410					415	

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	Asp	Glu	Asn	Glu	Phe	Thr	Phe	Glu	Asn	Asn	Ile	Asp	Ser	Asp	Val	Lys
				420					425					430		
5	Asn	Asn	Thr	Gln	Lys	Ser	Thr	Leu	Asn	Ile	Gly	Ile	Lys	Tyr	Ala	Glu
			435					440					445			
	Glu	Pro	Ile	Asn	Phe	Ile	Leu	Lys	Ser	Ser	Thr	Lys	Leu	Lys	Ala	Asp
		450					455					460				
10	Ile	Asp	Phe	Asp	Asp	Ser	Gly	Ala	Lys	Asp	Phe	Asn	Ser	Leu	Ser	Ser
	465					470					475					480
	Lys	Asp	Arg	Glu	Lys	Leu	Glu	Lys	Glu	Ile	Glu	Lys	Asn	Gly	Gly	Lys
					485					490					495	
15	Met	Phe	Glu	Ser	Ile	Leu	Lys	Lys	Ala	Ser	Lys					
				500					505							

<210> 57

<211> 297

<212> PRT

20 <213> Staphylococcus aureus

<400> 57

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1 Met Lys Lys Thr Ile Leu Leu Thr Met Thr Thr Leu Thr Leu Phe Ser
 5 Met Ser Pro Asn Ser Ala Gln Ala Tyr Thr Asn Asp Ser Lys Thr Leu
 10 Glu Glu Ala Lys Lys Ala His Pro Asn Ala Gln Phe Lys Val Asn Lys
 15 Asn Asp Thr Gly Ala Tyr Thr Tyr Thr Tyr Asp Lys Asn Thr Pro Asn
 20 Asn Asn His Gln Asn Gln Ser Arg Thr Asn Asp Asn His Gln His Ala
 25 Asn Gln Arg Asp Leu Asn Asn Asn Gln Tyr His Ser Ser Leu Ser Gly
 30 Gln Tyr Thr His Ile Asn Asp Ala Ile Asp Ser His Thr Pro Pro Gln
 35 Thr Ser Pro Ser Asn Pro Leu Thr Pro Ala Ile Pro Asn Val Glu Asp
 40 Asn Asp Asp Glu Leu Asn Asn Ala Phe Ser Lys Asp Asn Lys Gly Leu
 45 Ile Thr Gly Ile Asp Leu Asp Glu Leu Tyr Asp Glu Leu Gln Ile Ala
 50 Glu Phe Asn Asp Lys Ala Lys Thr Ala Asp Gly Lys Pro Leu Ala Leu
 55 Gly Asn Gly Lys Ile Ile Asp Gln Pro Leu Ile Thr Ser Lys Asn Asn
 60 Leu Tyr Thr Ala Gly Gln Cys Thr Trp Tyr Val Phe Asp Lys Arg Ala
 65 Lys Asp Gly His Thr Ile Ser Thr Phe Trp Gly Asp Ala Lys Asn Trp
 70 Ala Gly Gln Ala Ser Ser Asn Gly Phe Lys Val Asp Arg His Pro Thr
 75 Arg Gly Ser Ile Leu Gln Thr Val Asn Gly Pro Phe Gly His Val Ala
 80
 85 245 250 255
 90 Tyr Val Glu Lys Val Asn Ile Asp Gly Ser Ile Leu Ile Ser Glu Met
 95 Asn Trp Ile Gly Glu Tyr Ile Val Ser Ser Arg Thr Ile Ser Ala Ser
 100 Glu Val Ser Ser Tyr Asn Tyr Ile His
 105
 110 <210> 58
 115 <211> 124
 120 <212> PRT
 125 <213> Staphylococcus aureus
 130
 135 <400> 58

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Met Lys Arg Ile Leu Val Val Phe Leu Met Leu Ala Ile Ile Leu Ala
1 5 10 15
Gly Cys Ser Asn Lys Gly Glu Lys Tyr Gln Lys Asp Ile Asp Lys Val
5 20 25 30
Tyr Lys Glu Gln Asn Gln Met Asn Lys Ile Ala Ser Lys Val Gln Asn
35 40 45
Thr Ile Lys Thr Asp Ile Lys Gln Glu Asp Ser Asn Thr His Val Tyr
10 50 55 60
Lys Asp Gly Lys Val Ile Val Ile Gly Ile Gln Leu Tyr Lys Asp Arg
65 70 75 80
Glu Lys Met Tyr Tyr Phe Ala Tyr Glu Ile Lys Asp Gly Lys Ala Glu
15 85 90 95
Ile Asn Arg Glu Ile Asp Pro Ile Lys Tyr Met Lys Asp His Lys Ala
100 105 110
Asp Tyr Glu Asp Glu Asn Val Glu Val Glu Lys Asp
20 115 120

<210> 59

<211> 296

<212> PRT

25 <213> Staphylococcus aureus

<400> 59

Met Asn Lys Ile Ser Lys Tyr Ile Ala Ile Ala Ser Leu Ser Val Ala
30 1 5 10 15
Val Thr Val Ser Ala Pro Gln Thr Thr Asn Ser Thr Ala Phe Ala Lys
20 25 30
Ser Ser Ala Glu Val Gln Gln Thr Gln Gln Ala Ser Ile Pro Ala Ser
35 35 40 45
Gln Lys Ala Asn Leu Gly Asn Gln Asn Ile Met Ala Val Ala Trp Tyr
50 55 60
Gln Asn Ser Ala Glu Ala Lys Ala Leu Tyr Leu Gln Gly Tyr Asn Ser
40 65 70 75 80
Ala Lys Thr Gln Leu Asp Lys Glu Ile Lys Lys Asn Lys Gly Lys His
85 90 95
Lys Leu Ala Ile Ala Leu Asp Leu Asp Glu Thr Val Leu Asp Asn Ser
45 100 105 110
Pro Tyr Gln Gly Tyr Ala Ser Ile His Asn Lys Pro Phe Pro Glu Gly
115 120 125

50

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Trp His Glu Trp Val Gln Ala Ala Lys Ala Lys Pro Val Tyr Gly Ala
 130 135 140
 5 Lys Glu Phe Leu Lys Tyr Ala Asp Lys Lys Gly Val Asp Ile Tyr Tyr
 145 150 155 160
 Ile Ser Asp Arg Asp Lys Glu Lys Asp Leu Lys Ala Thr Gln Lys Asn
 165 170 175
 10 Leu Lys Gln Gln Gly Ile Pro Gln Ala Lys Lys Ser His Ile Leu Leu
 180 185 190
 Lys Gly Lys Asp Asp Lys Ser Lys Glu Ser Arg Arg Gln Met Val Gln
 195 200 205
 15 Lys Asp His Lys Leu Val Met Leu Phe Gly Asp Asn Leu Leu Asp Phe
 210 215 220
 Thr Asp Pro Lys Glu Ala Thr Ala Glu Ser Arg Glu Ala Leu Ile Glu
 225 230 235 240
 20 Lys His Lys Asp Asp Phe Gly Lys Lys Tyr Ile Ile Phe Pro Asn Pro
 245 250 255
 Met Tyr Gly Ser Trp Glu Ala Thr Ile Tyr Asn Asn Asn Tyr Lys Ala
 260 265 270
 25 Ser Asp Lys Ala Lys Asp Lys Leu Arg Lys Asn Ala Ile Lys Gln Phe
 275 280 285
 Asp Pro Lys Thr Gly Glu Val Lys
 290 295

30 <210> 60
 <211> 690
 <212> PRT
 <213> Staphylococcus aureus

35 <400> 60

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	Met	Leu	Arg	Gly	Gln	Glu	Glu	Arg	Lys	Tyr	Ser	Ile	Arg	Lys	Tyr	Ser
	1				5					10					15	
5	Ile	Gly	Val	Val	Ser	Val	Leu	Ala	Ala	Thr	Met	Phe	Val	Val	Ser	Ser
				20					25					30		
	His	Glu	Ala	Gln	Ala	Ser	Glu	Lys	Thr	Ser	Thr	Asn	Ala	Ala	Ala	Gln
			35					40					45			
10	Lys	Glu	Thr	Leu	Asn	Gln	Pro	Gly	Glu	Gln	Gly	Asn	Ala	Ile	Thr	Ser
		50					55					60				
	His	Gln	Met	Gln	Ser	Gly	Lys	Gln	Leu	Asp	Asp	Met	His	Lys	Glu	Asn
	65					70					75					80
15	Gly	Lys	Ser	Gly	Thr	Val	Thr	Glu	Gly	Lys	Asp	Thr	Leu	Gln	Ser	Ser
					85					90					95	
	Lys	His	Gln	Ser	Thr	Gln	Asn	Ser	Lys	Thr	Ile	Arg	Thr	Gln	Asn	Asp
				100					105					110		
20	Asn	Gln	Val	Lys	Gln	Asp	Ser	Glu	Arg	Gln	Gly	Ser	Lys	Gln	Ser	His
			115					120					125			
	Gln	Asn	Asn	Ala	Thr	Asn	Asn	Thr	Glu	Arg	Gln	Asn	Asp	Gln	Val	Gln
		130					135					140				
25	Asn	Thr	His	His	Ala	Glu	Arg	Asn	Gly	Ser	Gln	Ser	Thr	Thr	Ser	Gln
	145					150					155					160

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Ser Asn Asp Val Asp Lys Ser Gln Pro Ser Ile Pro Ala Gln Lys Val
 165 170 175
 5 Ile Pro Asn His Asp Lys Ala Ala Pro Thr Ser Thr Thr Pro Pro Ser
 180 185 190
 Asn Asp Lys Thr Ala Pro Lys Ser Thr Lys Ala Gln Asp Ala Thr Thr
 195 200 205
 10 Asp Lys His Pro Asn Gln Gln Asp Thr His Gln Pro Ala His Gln Ile
 210 215 220
 Ile Asp Ala Lys Gln Asp Asp Thr Val Arg Gln Ser Glu Gln Lys Pro
 225 230 235 240
 Gln Val Gly Asp Leu Ser Lys His Ile Asp Gly Gln Asn Ser Pro Glu
 245 250 255
 15 Lys Pro Thr Asp Lys Asn Thr Asp Asn Lys Gln Leu Ile Lys Asp Ala
 260 265 270
 Leu Gln Ala Pro Lys Thr Arg Ser Thr Thr Asn Ala Ala Ala Asp Ala
 275 280 285
 20 Lys Lys Val Arg Pro Leu Lys Ala Asn Gln Val Gln Pro Leu Asn Lys
 290 295 300
 Tyr Pro Val Val Phe Val His Gly Phe Leu Gly Leu Val Gly Asp Asn
 305 310 315 320
 25 Ala Pro Ala Leu Tyr Pro Asn Tyr Trp Gly Gly Asn Lys Phe Lys Val
 325 330 335
 Ile Glu Glu Leu Arg Lys Gln Gly Tyr Asn Val His Gln Ala Ser Val
 340 345 350
 30 Ser Ala Phe Gly Ser Asn Tyr Asp Arg Ala Val Glu Leu Tyr Tyr Tyr
 355 360 365
 Ile Lys Gly Gly Arg Val Asp Tyr Gly Ala Ala His Ala Ala Lys Tyr
 370 375 380
 35 Gly His Glu Arg Tyr Gly Lys Thr Tyr Lys Gly Ile Met Pro Asn Trp
 385 390 395 400
 Glu Pro Gly Lys Lys Val His Leu Val Gly His Ser Met Gly Gly Gln
 405 410 415
 40 Thr Ile Arg Leu Met Glu Glu Phe Leu Arg Asn Gly Asn Lys Glu Glu
 420 425 430
 Ile Ala Tyr His Lys Ala His Gly Gly Glu Ile Ser Pro Leu Phe Thr
 435 440 445
 45 Gly Gly His Asn Asn Met Val Ala Ser Ile Thr Thr Leu Ala Thr Pro
 450 455 460
 His Asn Gly Ser Gln Ala Ala Asp Lys Phe Gly Asn Thr Glu Ala Val
 465 470 475 480
 50 Arg Lys Ile Met Phe Ala Leu Asn Arg Phe Met Gly Asn Lys Tyr Ser
 485 490 495
 Asn Ile Asp Leu Gly Leu Thr Gln Trp Gly Phe Lys Gln Leu Pro Asn
 500 505 510
 55 Glu Ser Tyr Ile Asp Tyr Ile Lys Arg Val Ser Lys Ser Lys Ile Trp
 515 520 525
 Thr Ser Asp Asp Asn Ala Ala Tyr Asp Leu Thr Leu Asp Gly Ser Ala

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	530		535		540											
	Lys	Leu	Asn	Asn	Met	Thr	Ser	Met	Asn	Pro	Asn	Ile	Thr	Tyr	Thr	Thr
	545					550					555					560
5	Tyr	Thr	Gly	Val	Ser	Ser	His	Thr	Gly	Pro	Leu	Gly	Tyr	Glu	Asn	Pro
					565					570					575	
	Asp	Leu	Gly	Thr	Phe	Phe	Leu	Met	Ala	Thr	Thr	Ser	Arg	Ile	Ile	Gly
				580					585					590		
10	His	Asp	Ala	Arg	Glu	Glu	Trp	Arg	Lys	Asn	Asp	Gly	Val	Val	Pro	Val
			595					600					605			
	Ile	Ser	Ser	Leu	His	Pro	Ser	Asn	Gln	Pro	Phe	Val	Asn	Val	Thr	Asn
	610						615					620				
15	Asp	Glu	Pro	Ala	Thr	Arg	Arg	Gly	Ile	Trp	Gln	Val	Lys	Pro	Ile	Ile
	625					630					635					640
	Gln	Gly	Trp	Asp	His	Val	Asp	Phe	Ile	Gly	Val	Asp	Phe	Leu	Asp	Phe
					645					650					655	
20	Lys	Arg	Lys	Gly	Ala	Glu	Leu	Ala	Asn	Phe	Tyr	Thr	Gly	Ile	Ile	Asn
				660					665					670		
	Asp	Leu	Leu	Arg	Val	Glu	Ala	Thr	Glu	Ser	Lys	Gly	Thr	Gln	Leu	Lys
			675					680					685			
25	Ala	Ser														
		690														

<210> 61

<211> 208

30 <212> PRT

<213> Staphylococcus aureus

<400> 61

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1 Met Lys Lys Arg Leu Leu Leu Ser Thr Phe Leu Ala Ser Thr Leu Ile
 5 Leu Thr Gly Cys Ala Ser Asp Gln Ser Asp Asn Glu Asp His His Thr
 Ser Thr Gly Ile His Ala Pro Lys Ser Ala Lys Lys Leu Glu Thr Lys
 10 Asp Ile Phe Asn Ser Asp Lys Lys Asn Ser Asp Ile Ser Asp Ala Glu
 Met Lys Gln Ala Ile Glu Lys Tyr Leu Ser Val Asn Ser Asp Ile Leu
 15 Asp Asn Lys Tyr Ile Met Gln His Lys Leu Asp Lys Gln Ile Asp Ser
 Gln Thr Lys Val Thr Glu Lys Gln Ala Glu Thr Leu Ser His Leu Ser
 20 Asn Leu Ala Val Lys Asn Asp Leu His Phe Lys Lys Phe Val Thr Glu
 Asn Asn Ile Pro Lys Glu Tyr Lys Lys Pro Val Glu Leu Met Met Asn
 25 Tyr Phe Lys Ala Leu Asn Ser Thr Ile Ala Asn Val Asp Glu Asp Ile
 Glu Lys Leu Ser Tyr Gln Pro Gln Asn Lys Ile Asn Val Val Asp Val
 30 Pro Thr Lys Tyr Ala Gly Asp Val Asn Lys Lys Gln Gln Asp Lys Ile
 Lys Asp Phe Leu Lys Ser Lys Gly Ile Lys Ser Asp Val Ile Asp Lys
 35 <210> 62
 <211> 261
 <212> PRT
 <213> Staphylococcus aureus
 40 <400> 62
 45
 50
 55

Met Lys Ser Ile Lys Arg Ile Gly Leu Cys Ile Ser Leu Leu Ile Leu
 1 5 10 15
 Ile Ile Phe Val Thr Ser Cys Asp Gly Asp Asn Lys Ile Ile Gly Asp
 5 20 25 30
 Ser Lys Glu Glu Gln Ile Lys Lys Ser Phe Ala Lys Thr Leu Asp Ile
 35 40 45
 Tyr Pro Ile Lys Asn Leu Glu Asp Leu Tyr Asp Lys Glu Gly Tyr Arg
 10 50 55 60
 Asp Gly Glu Phe Lys Lys Asp Asp Lys Gly Thr Trp Leu Ile Arg Ser
 65 70 75 80
 Glu Met Lys Ile Gln Leu Lys Gly Glu Asn Leu Glu Ser Arg Gly Ala
 15 85 90 95
 Val Leu Glu Ile Asn Arg Asn Thr Arg Thr Ala Lys Gly His Tyr Ile
 100 105 110
 Val Arg Glu Val Val Glu Asp Ser Asp Gly Met Thr His Asn His Thr
 20 115 120 125
 Lys Arg Tyr Pro Val Lys Met Glu Asn Asn Lys Met Ile Pro Leu Lys
 130 135 140
 Pro Ile Asp Asp Glu Lys Val Lys Lys Glu Ile Glu Glu Phe Asn Phe
 25 145 150 155 160
 Phe Val Gln Tyr Gly Asn Phe Lys Glu Leu Glu Asn Tyr Lys Glu Asp
 165 170 175
 Glu Val Ser Tyr Asn Pro Glu Val Pro Ile Tyr Ser Ala Lys Tyr Gln
 30 180 185 190
 Leu Lys Asn Ser Asp Tyr Asn Val Glu Gln Leu Arg Lys Arg Tyr Asn
 195 200 205
 Ile Pro Thr Gln Lys Ala Pro Lys Leu Leu Leu Lys Gly Ser Gly Asn
 35 210 215 220
 Leu Lys Gly Ser Ser Val Gly Tyr Lys Asn Ile Glu Phe Thr Phe Ile
 225 230 235 240
 Glu Asn Lys Glu Glu Asn Ile Tyr Phe Thr Asp Ser Ile Tyr Phe Asn
 40 245 250 255
 Pro Ser Glu Asp Lys
 260

<210> 63

<211> 347

<212> PRT

<213> Staphylococcus aureus

<400> 63

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Met Asn Lys Asp Asn Lys Trp Thr Met Ile Thr Ala Leu Phe Ile Thr
1 5 10 15
Val Ile Ser Val Leu Leu Ala Phe His Leu Lys Gln His Tyr Asp Gln
5 20 25 30
Ile Thr Asn Glu Asn His Ala Asn Lys Asp Lys Ile Asn Ile Lys Asn
35 40 45
Lys Asn Val Arg Ile Tyr Gln Asn Leu Thr Tyr Asn Arg Val Phe Pro
10 50 55 60
Asn Ser Lys Leu Asp Ile Ile Thr Pro Val Asp Met Ser Ser Asn Ala
65 70 75 80
Lys Leu Pro Val Ile Phe Trp Met His Gly Gly Gly Tyr Ile Ala Gly
15 85 90 95
Asp Lys Gln Tyr Lys Asn Pro Leu Leu Ala Lys Ile Ala Glu Gln Gly
100 105 110
Tyr Ile Val Val Asn Val Asn Tyr Ala Leu Ala Pro Gln Tyr Lys Tyr
20 115 120 125
Pro Thr Pro Leu Ile Gln Met Asn Gln Ala Thr Gln Phe Ile Lys Glu
130 135 140
Asn Lys Met Asn Leu Pro Ile Asp Phe Asn Gln Val Ile Ile Gly Gly
25 145 150 155 160
Asp Ser Ala Gly Ala Gln Leu Ala Ser Gln Phe Thr Ala Ile Gln Thr
165 170 175
Asn Asp Arg Leu Arg Glu Ala Met Lys Phe Asp Gln Ser Phe Lys Pro
30 180 185 190
Ser Gln Ile Lys Gly Ala Ile Leu Phe Gly Gly Phe Tyr Asn Met Gln
195 200 205
Thr Val Arg Glu Thr Glu Phe Pro Arg Ile Gln Leu Phe Met Lys Ser
35 210 215 220
Tyr Thr Gly Glu Glu Asp Trp Glu Lys Ser Phe Lys Asn Ile Ser Gln
225 230 235 240
Met Ser Thr Val Lys Gln Ser Thr Lys Asn Tyr Pro Pro Thr Phe Leu
40 245 250 255
Ser Val Gly Asp Ser Asp Pro Phe Glu Ser Gln Asn Ile Glu Phe Ser
260 265 270
Lys Lys Leu Gln Glu Leu Asn Val Pro Val Asp Thr Leu Phe Tyr Asp
45 275 280 285
Gly Thr His His Leu His His Gln Tyr Gln Phe His Leu Asn Lys Pro
290 295 300
Glu Ser Ile Asp Asn Ile Lys Lys Val Leu Leu Phe Leu Ser Arg Asn
50 305 310 315 320
Thr Ser Ser Ser Gly Ile Gln Thr Glu Glu Lys Pro Gln Ile Glu Asn
325 330 335
Pro Ser Asn Glu Leu Pro Leu Asn Pro Leu Asn
340 345

<210> 64
<211> 265
<212> PRT

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<213> Staphylococcus aureus

<400> 64

5 Met Lys Lys Leu Ala Phe Ala Ile Thr Ala Thr Ser Gly Ala Ala Ala
1 5 10 15
Phe Leu Thr His His Asp Ala Gln Ala Ser Thr Gln His Thr Val Gln
20 25 30
10 Ser Gly Glu Ser Leu Trp Ser Ile Ala Gln Lys Tyr Asn Thr Ser Val
35 40 45
Glu Ser Ile Lys Gln Asn Asn Gln Leu Asp Asn Asn Leu Val Phe Pro
50 55 60
15 Gly Gln Val Ile Ser Val Gly Gly Ser Asp Ala Gln Asn Thr Ser Asn
65 70 75 80
Thr Ser Pro Gln Ala Gly Ser Ala Ser Ser His Thr Val Gln Ala Gly
85 90 95
20 Glu Ser Leu Asn Ile Ile Ala Ser Arg Tyr Gly Val Ser Val Asp Gln
100 105 110
Leu Met Ala Ala Asn Asn Leu Arg Gly Tyr Leu Ile Met Pro Asn Gln
115 120 125
25 Thr Leu Gln Ile Pro Asn Gly Gly Ser Gly Gly Thr Thr Pro Thr Ala
130 135 140
Thr Thr Gly Ser Asn Gly Asn Ala Ser Ser Phe Asn His Gln Asn Leu
145 150 155 160
30 Tyr Thr Ala Gly Gln Cys Thr Trp Tyr Val Phe Asp Arg Arg Ala Gln
165 170 175
Ala Gly Ser Pro Ile Ser Thr Tyr Trp Ser Asp Ala Lys Tyr Trp Ala
180 185 190
35 Gly Asn Ala Ala Asn Asp Gly Tyr Gln Val Asn Asn Thr Pro Ser Val
195 200 205
Gly Ser Ile Met Gln Ser Thr Pro Gly Pro Tyr Gly His Val Ala Tyr
210 215 220
40 Val Glu Arg Val Asn Gly Asp Gly Ser Ile Leu Ile Ser Glu Met Asn
225 230 235 240
Tyr Thr Tyr Gly Pro Tyr Asn Met Asn Tyr Arg Thr Ile Pro Ala Ser
245 250 255
45 Glu Val Ser Ser Tyr Ala Phe Ile His
260 265

<210> 65

<211> 292

<212> PRT

<213> Staphylococcus aureus

<400> 65

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Met Lys Lys Ile Val Ile Ile Ala Val Leu Ala Ile Leu Phe Val Val
 1 5 10 15
 Ile Ser Ala Cys Gly Asn Lys Glu Lys Glu Ala Gln His Gln Phe Thr
 5 20 25 30
 Lys Gln Phe Lys Asp Val Glu Gln Lys Gln Lys Glu Leu Gln His Val
 35 40 45
 Met Asp Asn Ile His Leu Lys Glu Ile Asp His Leu Ser Lys Thr Asp
 10 50 55 60
 Thr Thr Asp Lys Asn Ser Lys Glu Phe Lys Ala Leu Gln Glu Asp Val
 65 70 75 80
 Lys Asn His Leu Ile Pro Lys Phe Glu Ala Tyr Tyr Lys Ser Ala Lys
 15 85 90 95
 Asn Leu Pro Asp Asp Thr Met Lys Val Lys Lys Leu Lys Lys Glu Tyr
 100 105 110
 Met Thr Leu Ala Asn Glu Lys Lys Asp Ala Ile Tyr Gln Leu Lys Lys
 20 115 120 125
 Phe Ile Gly Leu Cys Asn Gln Ser Ile Lys Tyr Asn Glu Asp Ile Leu
 130 135 140
 Asp Tyr Thr Lys Gln Phe Glu Lys Asn Arg Tyr Lys Val Glu Ser Glu
 25 145 150 155 160
 Ile Lys Leu Ala Asp Asn Lys Ser Glu Ala Thr Asn Leu Thr Thr Lys
 165 170 175
 Leu Glu His Asn Asn Lys Ala Leu Arg Asp Thr Ala Lys Lys Asn Leu
 30 180 185 190
 Asp Asp Ser Lys Glu Asn Glu Val Lys Gly Ala Ile Lys Asn His Ile
 195 200 205
 Met Pro Met Ile Glu Lys Gln Ile Thr Asp Ile Asn Gln Thr Asn Ile
 35 210 215 220
 Ser Asp Lys His Val Asn Asn Ala Arg Lys Asn Ala Ile Glu Met Tyr
 225 230 235 240
 Tyr Ser Leu Gln Asn Tyr Tyr Asn Thr Arg Ile Glu Thr Ile Lys Val
 40 245 250 255
 Ser Glu Lys Leu Ser Lys Val Asp Val Asp Lys Leu Pro Lys Lys Gly
 260 265 270
 Ile Asp Ile Thr His Gly Asp Lys Ala Phe Glu Lys Lys Leu Glu Lys
 45 275 280 285
 Leu Glu Glu Lys
 290

<210> 66

<211> 242

<212> PRT

<213> Staphylococcus aureus

<400> 66

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Met Lys Lys Val Met Gly Ile Leu Leu Ala Ser Thr Leu Ile Leu Gly
1 5 10 15
Ala Cys Gly His His Gln Asp Ser Ala Lys Lys Glu Ser Thr Ser His
5 20 25 30
Lys Lys Lys Glu Asn Asp Asn Glu Glu Leu Asn Glu Glu Leu Lys Glu
35 40 45
Phe Lys Ser Lys Lys Asn Met Asp Ile Lys Ile Lys Gly Asp Thr Ile
10 50 55 60
Val Ser Asp Lys Phe Glu Ala Lys Ile Lys Glu Pro Phe Ile Ile Asn
65 70 75 80
Glu Lys Asp Glu Lys Lys Lys Tyr Ile Ala Phe Lys Met Glu Ile Thr
15 85 90 95
Ala Lys Lys Asp Asp Lys Asp Leu Asn Pro Ser Ser Ile Ser His Asp
20 100 105 110
Tyr Ile Asn Ile Thr Gln Asp Asp Lys Asn Thr Val Asn Lys Leu Arg
115 120 125
Asp Gly Tyr Leu Leu Ser Asp Lys Lys Tyr Lys Asp Trp Thr Glu His
130 135 140
25 Asn Gln Asp Gln Ile Lys Lys Gly Lys Thr Ala Gln Ala Met Phe Ile
145 150 155 160
Tyr Glu Leu Arg Gly Asp Gly Asn Ile Asn Leu Asn Val His Lys Tyr
165 170 175
30 Ser Glu Asp Lys Thr Val Asp Ser Lys Ser Phe Lys Phe Ser Lys Leu
180 185 190
Lys Thr Glu Asp Phe Ser His Arg Ala Glu Thr Arg Glu Glu Val Glu
195 200 205
35 Lys Lys Glu Lys Glu Phe Glu Glu Glu Tyr Lys Lys Glu Gln Glu Arg
210 215 220
Glu Lys Glu Lys Glu Lys Gln Lys Asp Asp Asp His Ser Gly Leu Asp
225 230 235 240
40 Glu Val

<210> 67

<211> 439

<212> PRT

45 <213> Staphylococcus aureus

<400> 67

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Met Arg Leu Thr Ile Tyr His Thr Asn Asp Ile His Ser His Leu His
1 5 10 15
Glu Tyr Glu Arg Ile Lys Ala Tyr Met Ala Glu His Arg Pro Arg Leu
5 20 25 30
Asn His Pro Ser Leu Tyr Val Asp Leu Gly Asp His Val Asp Leu Ser
35 40 45
Ala Pro Ile Thr Glu Ala Thr Leu Gly Lys Lys Asn Val Ala Leu Leu
10 50 55 60
Asn Glu Ala Lys Cys Asp Val Ala Thr Ile Gly Asn Asn Glu Gly Met
65 70 75 80
Thr Ile Ser Tyr Glu Ala Leu Asn His Leu Tyr Asp Glu Ala Lys Phe
15 85 90 95
Ile Val Thr Cys Ser Asn Val Ile Asp Glu Ser Gly His Leu Pro Asn
100 105 110
Asn Ile Val Ser Ser Tyr Ile Lys Asp Ile Asp Gly Val Lys Ile Leu
115 120 125
20 Phe Val Ala Ala Thr Ala Pro Phe Thr Pro Phe Tyr Arg Ala Leu Asn
130 135 140
Trp Ile Val Thr Asp Pro Leu Glu Ser Ile Lys Glu Glu Ile Glu Leu
145 150 155 160
25 Gln Arg Gly Lys Phe Asp Val Leu Ile Val Leu Ser His Cys Gly Ile
165 170 175
Phe Phe Asp Glu Thr Leu Cys Gln Glu Leu Pro Glu Ile Asp Val Ile

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				180					185					190			
	Phe	Gly	Ser	His	Thr	His	His	Tyr	Phe	Glu	His	Gly	Glu	Ile	Asn	Asn	
			195					200					205				
5	Gly	Val	Leu	Met	Ala	Ala	Ala	Gly	Lys	Tyr	Gly	Asn	Tyr	Leu	Gly	Glu	
		210					215					220					
	Val	Asn	Leu	Thr	Phe	Glu	Ala	His	Lys	Val	Val	His	Lys	Thr	Ala	Lys	
	225					230					235					240	
10	Ile	Ile	Pro	Leu	Glu	Thr	Leu	Pro	Glu	Val	Glu	Thr	Ser	Phe	Glu	Glu	
					245					250					255		
	Glu	Gly	Lys	Thr	Leu	Met	Ser	Asn	Ser	Val	Ile	Gln	His	Pro	Val	Val	
				260					265					270			
15	Leu	Lys	Arg	Ser	Met	Asn	His	Ile	Thr	Glu	Ala	Ala	Tyr	Leu	Leu	Ala	
			275					280					285				
	Gln	Ser	Val	Cys	Glu	Tyr	Thr	His	Ala	Gln	Cys	Ala	Ile	Ile	Asn	Ala	
		290					295					300					
20	Gly	Leu	Leu	Val	Lys	Asp	Ile	Val	Lys	Asp	Glu	Val	Thr	Glu	Tyr	Asp	
	305					310					315					320	
	Ile	His	Gln	Met	Leu	Pro	His	Pro	Ile	Asn	Met	Val	Arg	Val	Arg	Leu	
					325					330					335		
25	Phe	Gly	Val	Lys	Leu	Lys	Glu	Ile	Ile	Ala	Lys	Ser	Asn	Lys	Gln	Glu	
				340					345					350			
	Tyr	Met	Tyr	Glu	His	Ala	Gln	Gly	Leu	Gly	Phe	Arg	Gly	Asn	Ile	Phe	
			355					360					365				
30	Gly	Gly	Tyr	Ile	Leu	Tyr	Asn	Leu	Gly	Tyr	Ile	His	Ser	Thr	Gly	Arg	
		370					375					380					
	Tyr	Tyr	Leu	Asn	Gly	Glu	Glu	Ile	Glu	Asp	Asp	Lys	Glu	Tyr	Val	Leu	
	385					390				395						400	
35	Gly	Thr	Ile	Asp	Met	Tyr	Thr	Phe	Gly	Arg	Tyr	Phe	Pro	Thr	Leu	Lys	
				405						410					415		
	Glu	Leu	Pro	Lys	Glu	Tyr	Leu	Met	Pro	Glu	Phe	Leu	Arg	Asp	Ile	Phe	
				420					425					430			
40	Lys	Glu	Lys	Leu	Leu	Glu	Tyr										
			435														

<210> 68

<211> 774

45 <212> PRT

<213> Staphylococcus aureus

<400> 68

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Met	Glu	Trp	Thr	Leu	Val	Asp	Ile	Gly	Lys	Lys	His	Val	Ile	Pro	Lys
1				5					10					15	
Ser	Gln	Tyr	Arg	Arg	Lys	Arg	Arg	Glu	Phe	Phe	His	Asn	Glu	Asp	Arg
			20					25					30		
Glu	Glu	Asn	Leu	Asn	Gln	His	Gln	Asp	Lys	Gln	Asn	Ile	Asp	Asn	Thr
		35					40					45			
Thr	Ser	Lys	Lys	Ala	Asp	Lys	Gln	Ile	His	Lys	Asp	Ser	Ile	Asp	Lys
	50					55					60				
His	Glu	Arg	Phe	Lys	Asn	Ser	Leu	Ser	Ser	His	Leu	Glu	Gln	Arg	Asn
65					70					75					80

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EP 2 510 947 B1

	Arg	Asp	Val	Asn	Glu	Asn	Lys	Ala	Glu	Glu	Ser	Lys	Ser	Asn	Gln	Asp	
					85					90					95		
5	Ser	Lys	Ser	Ala	Tyr	Asn	Arg	Asp	His	Tyr	Leu	Thr	Asp	Asp	Val	Ser	
				100					105					110			
	Lys	Lys	Gln	Asn	Ser	Leu	Asp	Ser	Val	Asp	Gln	Asp	Thr	Glu	Lys	Ser	
			115					120					125				
10	Lys	Tyr	Tyr	Glu	Gln	Asn	Ser	Glu	Ala	Thr	Leu	Ser	Thr	Lys	Ser	Thr	
		130					135					140					
	Asp	Lys	Val	Glu	Ser	Thr	Glu	Met	Arg	Lys	Leu	Ser	Ser	Asp	Lys	Asn	
	145					150					155					160	
15	Lys	Val	Gly	His	Glu	Glu	Gln	His	Val	Leu	Ser	Lys	Pro	Ser	Glu	His	
				165						170					175		
	Asp	Lys	Glu	Thr	Arg	Ile	Asp	Ser	Glu	Ser	Ser	Arg	Thr	Asp	Ser	Asp	
			180						185					190			
20	Ser	Ser	Met	Gln	Thr	Glu	Lys	Ile	Lys	Lys	Asp	Ser	Ser	Asp	Gly	Asn	
			195					200					205				
	Lys	Ser	Ser	Asn	Leu	Lys	Ser	Glu	Val	Ile	Ser	Asp	Lys	Ser	Asn	Thr	
		210					215					220					
25	Val	Pro	Lys	Leu	Ser	Glu	Ser	Asp	Asp	Glu	Val	Asn	Asn	Gln	Lys	Pro	
	225					230					235					240	
	Leu	Thr	Leu	Pro	Glu	Glu	Gln	Lys	Leu	Lys	Arg	Gln	Gln	Ser	Gln	Asn	
				245						250					255		
30	Glu	Gln	Thr	Lys	Thr	Tyr	Thr	Tyr	Gly	Asp	Ser	Glu	Gln	Asn	Asp	Lys	
				260					265					270			
	Ser	Asn	His	Glu	Asn	Asp	Leu	Ser	His	His	Ile	Pro	Ser	Ile	Ser	Asp	
			275					280					285				
35	Asp	Lys	Asp	Asn	Val	Met	Arg	Glu	Asn	His	Ile	Val	Asp	Asp	Asn	Pro	
		290					295					300					
	Asp	Asn	Asp	Ile	Asn	Thr	Pro	Ser	Leu	Ser	Lys	Thr	Asp	Asp	Asp	Arg	
	305					310					315					320	
40	Lys	Leu	Asp	Glu	Lys	Ile	His	Val	Glu	Asp	Lys	His	Lys	Gln	Asn	Ala	
				325						330					335		
	Asp	Ser	Ser	Glu	Thr	Val	Gly	Tyr	Gln	Ser	Gln	Ser	Thr	Ala	Ser	His	
				340				345						350			
45	Arg	Ser	Thr	Glu	Lys	Arg	Asn	Ile	Ser	Ile	Asn	Asp	His	Asp	Lys	Leu	
			355					360					365				
	Asn	Gly	Gln	Lys	Thr	Asn	Thr	Lys	Thr	Ser	Ala	Asn	Asn	Asn	Gln	Lys	
		370					375					380					
50	Lys	Ala	Thr	Ser	Lys	Leu	Asn	Lys	Gly	Arg	Ala	Thr	Asn	Asn	Asn	Tyr	
	385					390					395					400	
	Ser	Asp	Ile	Leu	Lys	Lys	Phe	Trp	Met	Met	Tyr	Trp	Pro	Lys	Leu	Val	
				405						410					415		
55	Ile	Leu	Met	Gly	Ile	Ile	Ile	Leu	Ile	Val	Ile	Leu	Asn	Ala	Ile	Phe	
			420						425					430			
	Asn	Asn	Val	Asn	Lys	Asn	Asp	Arg	Met	Asn	Asp	Asn	Asn	Asp	Ala	Asp	
			435					440					445				

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Ala Gln Lys Tyr Thr Thr Thr Met Lys Asn Ala Asn Asn Thr Val Lys
450 455 460

5 Ser Val Val Thr Val Glu Asn Glu Thr Ser Lys Asp Ser Ser Leu Pro
465 470 475 480

Lys Asp Lys Ala Ser Gln Asp Glu Val Gly Ser Gly Val Val Tyr Lys
485 490 495

10 Lys Ser Gly Asp Thr Leu Tyr Ile Val Thr Asn Ala His Val Val Gly
500 505 510

Asp Lys Glu Asn Gln Lys Ile Thr Phe Ser Asn Asn Lys Ser Val Val
515 520 525

15 Gly Lys Val Leu Gly Lys Asp Lys Trp Ser Asp Leu Ala Val Val Lys
530 535 540

Ala Thr Ser Ser Asp Ser Ser Val Lys Glu Ile Ala Ile Gly Asp Ser
545 550 555 560

20 Asn Asn Leu Val Leu Gly Glu Pro Ile Leu Val Val Gly Asn Pro Leu
565 570 575

Gly Val Asp Phe Lys Gly Thr Val Thr Glu Gly Ile Ile Ser Gly Leu
580 585 590

25 Asn Arg Asn Val Pro Ile Asp Phe Asp Lys Asp Asn Lys Tyr Asp Met
595 600 605

Leu Met Lys Ala Phe Gln Ile Asp Ala Ser Val Asn Pro Gly Asn Ser
610 615 620

30 Gly Gly Ala Val Val Asn Arg Glu Gly Lys Leu Ile Gly Val Val Ala
625 630 635 640

Ala Lys Ile Ser Met Pro Asn Val Glu Asn Met Ser Phe Ala Ile Pro
645 650 655

35 Val Asn Glu Val Gln Lys Ile Val Lys Asp Leu Glu Thr Lys Gly Lys
660 665 670

Ile Asp Tyr Pro Asp Val Gly Val Lys Met Lys Asn Ile Val Ser Leu
675 680 685

40 Asn Ser Phe Glu Arg Gln Ala Val Lys Leu Pro Gly Lys Val Lys Asn
690 695 700

Gly Val Val Val Asp Gln Val Asp Asn Asn Gly Leu Ala Asp Gln Ser
705 710 715 720

Gly Leu Lys Lys Gly Asp Val Ile Thr Glu Leu Asp Gly Lys Leu Leu
725 730 735

45 Glu Asp Asp Leu Arg Phe Arg Gln Ile Ile Phe Ser His Lys Asp Asp
740 745 750

Leu Lys Ser Ile Thr Ala Lys Ile Tyr Arg Asp Gly Lys Glu Lys Glu
755 760 765

50 Ile Asn Ile Lys Leu Lys
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<210> 69

<211> 393

<212> PRT

<213> Staphylococcus aureus

<400> 69

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Met Asn Ser Ser Cys Lys Ser Arg Val Phe Asn Ile Ile Ser Ile Ile

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	1		5		10		15									
	Met	Val	Ser	Met	Leu	Ile	Leu	Ser	Leu	Gly	Ala	Phe	Ala	Asn	Asn	Asn
				20					25					30		
5	Lys	Ala	Lys	Ala	Asp	Ser	His	Ser	Lys	Gln	Leu	Glu	Ile	Asn	Val	Lys
			35					40					45			
	Ser	Asp	Lys	Val	Pro	Gln	Lys	Val	Lys	Asp	Leu	Ala	Gln	Gln	Gln	Phe
		50					55					60				
10	Ala	Gly	Tyr	Ala	Lys	Ala	Leu	Asp	Lys	Gln	Ser	Asn	Ala	Lys	Thr	Gly
	65					70					75					80
	Lys	Tyr	Glu	Leu	Gly	Glu	Ala	Phe	Lys	Ile	Tyr	Lys	Phe	Asn	Gly	Glu
				85						90					95	
15	Glu	Asp	Asn	Ser	Tyr	Tyr	Tyr	Pro	Val	Ile	Lys	Asp	Gly	Lys	Ile	Val
				100					105					110		
	Tyr	Thr	Leu	Thr	Leu	Ser	Pro	Lys	Asn	Lys	Asp	Asp	Leu	Asn	Lys	Ser
			115					120					125			
20	Lys	Glu	Asp	Met	Asn	Tyr	Ser	Val	Lys	Ile	Ser	Asn	Phe	Ile	Ala	Lys
		130					135					140				
	Asp	Leu	Asp	Gln	Ile	Lys	Asp	Lys	Asn	Ser	Asn	Ile	Thr	Val	Leu	Thr
	145					150				155						160
25	Asp	Glu	Lys	Gly	Phe	Tyr	Phe	Glu	Glu	Asp	Gly	Lys	Val	Arg	Leu	Val
				165						170					175	
	Lys	Ala	Thr	Pro	Leu	Pro	Gly	Asn	Val	Lys	Glu	Lys	Glu	Ser	Ala	Lys
				180					185					190		
30	Thr	Val	Ser	Ala	Lys	Leu	Lys	Gln	Glu	Leu	Lys	Asn	Thr	Val	Thr	Pro
			195					200					205			
	Thr	Lys	Val	Glu	Glu	Asn	Glu	Ala	Ile	Gln	Glu	Asp	Gln	Val	Gln	Tyr
		210					215					220				
35	Glu	Asn	Thr	Leu	Lys	Asn	Phe	Lys	Ile	Arg	Glu	Gln	Gln	Phe	Asp	Asn
	225					230					235					240
	Ser	Trp	Cys	Ala	Gly	Phe	Ser	Met	Ala	Ala	Leu	Leu	Asn	Ala	Thr	Lys
				245						250					255	
40	Asn	Thr	Asp	Thr	Tyr	Asn	Ala	His	Asp	Ile	Met	Arg	Thr	Leu	Tyr	Pro
				260					265					270		
	Glu	Val	Ser	Glu	Gln	Asp	Leu	Pro	Asn	Cys	Ala	Thr	Phe	Pro	Asn	Gln
			275					280					285			
45	Met	Ile	Glu	Tyr	Gly	Lys	Ser	Gln	Gly	Arg	Asp	Ile	His	Tyr	Gln	Glu
		290					295					300				
	Gly	Val	Pro	Ser	Tyr	Glu	Gln	Val	Asp	Gln	Leu	Thr	Lys	Asp	Asn	Val
	305					310					315					320
50	Gly	Ile	Met	Ile	Leu	Ala	Gln	Ser	Val	Ser	Gln	Asn	Pro	Asn	Asp	Pro
					325					330				335		
	His	Leu	Gly	His	Ala	Leu	Ala	Val	Val	Gly	Asn	Ala	Lys	Ile	Asn	Asp
				340					345					350		
	Gln	Glu	Lys	Leu	Ile	Tyr	Trp	Asn	Pro	Trp	Asp	Thr	Glu	Leu	Ser	Ile
			355					360					365			
55	Gln	Asp	Ala	Asp	Ser	Ser	Leu	Leu	His	Leu	Ser	Phe	Asn	Arg	Asp	Tyr
		370					375					380				

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Asn Trp Tyr Gly Ser Met Ile Gly Tyr
385 390

5 <210> 70
<211> 336
<212> PRT
<213> Staphylococcus aureus

10 <400> 70

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Met Lys Gly Lys Phe Leu Lys Val Ser Ser Leu Phe Val Ala Thr Leu
1 5 10
Thr Thr Ala Thr Leu Val Ser Ser Pro Ala Ala Asn Ala Leu Ser Ser
5 20 25 30
Lys Ala Met Asp Asn His Pro Gln Gln Thr Gln Ser Ser Lys Gln Gln
35 40 45
Thr Pro Lys Ile Gln Lys Gly Gly Asn Leu Lys Pro Leu Glu Gln Arg
10 50 55 60
Glu His Ala Asn Val Ile Leu Pro Asn Asn Asp Arg His Gln Ile Thr
65 70 75
Asp Thr Thr Asn Gly His Tyr Ala Pro Val Thr Tyr Ile Gln Val Glu
15 85 90 95
Ala Pro Thr Gly Thr Phe Ile Ala Ser Gly Val Val Val Gly Lys Asp
100 105 110
Thr Leu Leu Thr Asn Lys His Val Val Asp Ala Thr His Gly Asp Pro
20 115 120 125
His Ala Leu Lys Ala Phe Pro Ser Ala Ile Asn Gln Asp Asn Tyr Pro
130 135 140
Asn Gly Gly Phe Thr Ala Glu Gln Ile Thr Lys Tyr Ser Gly Glu Gly
25 145 150 155 160
Asp Leu Ala Ile Val Lys Phe Ser Pro Asn Glu Gln Asn Lys His Ile
165 170 175
Gly Glu Val Val Lys Pro Ala Thr Met Ser Asn Asn Ala Glu Thr Gln
30 180 185 190
Val Asn Gln Asn Ile Thr Val Thr Gly Tyr Pro Gly Asp Lys Pro Val
195 200 205
Ala Thr Met Trp Glu Ser Lys Gly Lys Ile Thr Tyr Leu Lys Gly Glu
35 210 215 220
Ala Met Gln Tyr Asp Leu Ser Thr Thr Gly Gly Asn Ser Gly Ser Pro
225 230 235 240
Val Phe Asn Glu Lys Asn Glu Val Ile Gly Ile His Trp Gly Gly Val
40 245 250 255
Pro Asn Glu Phe Asn Gly Ala Val Phe Ile Asn Glu Asn Val Arg Asn
260 265 270
Phe Leu Lys Gln Asn Ile Glu Asp Ile His Phe Ala Asn Asp Asp Gln
45 275 280 285
Pro Asn Asn Pro Asp Asn Pro Asp Asn Pro Asn Asn Pro Asp Ash Pro
290 295 300
Asn Asn Pro Asp Glu Pro Asn Asn Pro Asp Asn Pro Asn Asn Pro Asp
50 305 310 315 320
Asn Pro Asp Asn Gly Asp Asn Asn Asn Ser Asp Asn Pro Asp Ala Ala
325 330 335

55 <210> 71
<211> 397
<212> PRT
<213> Staphylococcus aureus

<400> 71

5 Met Lys Phe Asn Lys Val Lys Leu Val Ile His Ala Cys Val Leu Leu
 1 5 10 15
 Phe Ile Ile Ile Ser Ile Ala Leu Ile Phe His Arg Leu Gln Thr Lys
 20 25 30
 Thr His Ser Ile Asp Pro Ile His Lys Glu Thr Lys Leu Ser Asp Asn
 35 40 45
 10 Glu Lys Tyr Leu Val Asp Arg Asn Lys Glu Lys Val Ala Pro Ser Lys
 50 55 60
 Leu Lys Glu Val Tyr Asn Ser Lys Asp Pro Lys Tyr Lys Lys Ile Asp
 65 70 75 80
 15 Lys Tyr Leu Gln Ser Ser Leu Phe Asn Gly Ser Val Ala Ile Tyr Glu
 85 90 95
 Asn Gly Lys Leu Lys Met Ser Lys Gly Tyr Gly Tyr Gln Asp Phe Glu
 100 105 110
 20 Lys Gly Ile Lys Asn Thr Pro Asn Thr Met Phe Leu Ile Gly Ser Ala
 115 120 125
 Gln Lys Phe Ser Thr Gly Leu Leu Leu Lys Gln Leu Glu Glu Glu His
 130 135 140
 25 Lys Ile Asn Ile Asn Asp Pro Val Ser Lys Tyr Leu Pro Trp Phe Lys
 145 150 155 160
 Thr Ser Lys Pro Ile Pro Leu Lys Asp Leu Met Leu His Gln Ser Gly
 165 170 175
 30 Leu Tyr Lys Tyr Lys Ser Ser Lys Asp Tyr Lys Asn Leu Asp Gln Ala
 180 185 190
 Val Lys Ala Ile Gln Lys Arg Gly Ile Asp Pro Lys Lys Tyr Lys Lys
 195 200 205
 35 His Met Tyr Asn Asp Gly Asn Tyr Leu Val Leu Ala Lys Val Ile Glu
 210 215 220
 Glu Val Thr Gly Lys Ser Tyr Ala Glu Asn Tyr Tyr Thr Lys Ile Gly
 225 230 235 240
 40 Asp Pro Leu Lys Leu Gln His Thr Ala Phe Tyr Asp Glu Gln Pro Phe
 245 250 255
 Lys Lys Tyr Leu Ala Lys Gly Tyr Ala Tyr Asn Ser Thr Gly Leu Ser
 260 265 270
 45 Phe Leu Arg Pro Asn Ile Leu Asp Gln Tyr Tyr Gly Ala Gly Asn Leu
 275 280 285
 Tyr Met Thr Pro Thr Asp Met Gly Lys Leu Ile Thr Gln Ile Gln Gln
 290 295 300
 50 Tyr Lys Leu Phe Ser Pro Lys Ile Thr Asn Pro Leu Leu His Glu Phe
 305 310 315 320
 Gly Thr Lys Lys Tyr Pro Asp Glu Tyr Arg Tyr Gly Phe Tyr Ala Lys

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				325					330					335			
	Pro	Thr	Leu	Asn	Arg	Leu	Asn	Gly	Gly	Phe	Phe	Gly	Gln	Val	Phe	Thr	
				340					345					350			
5	Val	Tyr	Tyr	Asn	Asp	Lys	Tyr	Val	Val	Val	Leu	Ala	Leu	Asn	Val	Lys	
			355					360					365				
	Gly	Asn	Asn	Glu	Val	Arg	Ile	Lys	His	Ile	Tyr	Asn	Asp	Ile	Leu	Lys	
		370					375					380					
10	Gln	Asn	Lys	Pro	Tyr	Asn	Thr	Lys	Gly	Val	Ile	Val	Gln				
	385					390					395						

<210> 72

<211> 358

15 <212> PRT

<213> Staphylococcus aureus

<400> 72

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1 Met Arg Asn Val Lys Gln Ile Ala Thr Lys Ser Ile Ile Ala Ile Ile
 5 Ser Leu Gly Ile Leu Thr Tyr Thr Thr Met Ile Gly Ser Val Leu Ala
 10 Asp Glu Ile Lys Tyr Pro Ser Ala Lys Phe Asn Gln Pro Glu Ala Lys
 15 Thr Glu Glu Gln Gln Leu Val Asp Glu Lys Ala Gln Leu Ile Ser Asp
 20 Lys Glu Gln Leu Val Phe Gln Asn Asp Lys Asn Glu Glu Phe Pro Phe
 25 Val Ile Lys Asp Glu Lys Asp Asp Thr Ile Val Arg Ile Leu Ile Glu
 30 Asn Gln Glu Asn Asn Gln Asp Gln Leu Lys Lys Asp Ile Asp Asp Lys
 35 Thr Glu Lys Gly Leu Asn Asp Ile Pro Val Gln Lys Asp Lys Val Gln
 40 Gln Asp Ser Asn Lys Lys Ile Glu Asn Glu Arg Pro Lys Ala Ser Gly
 45 Thr Leu Lys Val Glu Asn Ser Pro Pro Thr Ile Lys Lys Val Glu Asn
 50 Asn His Lys Glu Gln Pro Lys His Lys Asp Glu Lys Ser Lys Lys Glu
 55 Lys Lys Lys Val Val Glu Lys Glu Lys Ala Leu Pro Ala Phe Asn Arg
 60 Asp Asp Asp Ser Lys Asn Ser Ser Gln Leu Ser Ser Asp Ile Lys Glu
 65 Leu Asp Glu Pro Asn His Lys Lys Gln Tyr Met Leu Phe Ala Ala Gly
 70 Ile Val Leu Ala Thr Ile Leu Leu Ile Ser Ala His Leu Tyr Ser Arg
 75 Lys Arg Gly Asn Gln Val
 80 355

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<210> 73
 <211> 282
 <212> PRT
 <213> Staphylococcus aureus

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<400> 73

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Met Ile Ser Val Val Ile Leu Thr Ser Cys Gln Ser Ser Ser Ser Gln
 1      5      10      15
Glu Ser Thr Lys Ser Gly Glu Phe Arg Ile Val Pro Thr Thr Val Ala
 20      25      30
Leu Thr Met Thr Leu Asp Lys Leu Asp Leu Pro Ile Val Gly Lys Pro
 35      40      45
Thr Ser Tyr Lys Thr Leu Pro Asn Arg Tyr Lys Asp Val Pro Glu Ile
 50      55      60
Gly Gln Pro Met Glu Pro Asn Val Glu Ala Val Lys Lys Leu Lys Pro
 65      70      75      80
Thr His Val Leu Ser Val Ser Thr Ile Lys Asp Glu Met Gln Pro Phe
 85      90      95
Tyr Lys Gln Leu Asn Met Lys Gly Tyr Phe Tyr Asp Phe Asp Ser Leu
100      105      110
Lys Gly Met Gln Lys Ser Ile Thr Gln Leu Gly Asp Gln Phe Asn Arg
115      120      125
Lys Ala Gln Ala Lys Glu Leu Asn Asp His Leu Asn Ser Val Lys Gln
130      135      140
Lys Ile Glu Asn Lys Ala Ala Lys Gln Lys Lys His Pro Lys Val Leu
145      150      155      160
Ile Leu Met Gly Val Pro Gly Ser Tyr Leu Val Ala Thr Asp Lys Ser
165      170      175
Tyr Ile Gly Asp Leu Val Lys Ile Ala Gly Gly Glu Asn Val Ile Lys
180      185      190
Val Lys Asp Arg Gln Tyr Ile Ser Ser Asn Thr Glu Asn Leu Leu Asn
195      200      205
Ile Asn Pro Asp Ile Ile Leu Arg Leu Pro His Gly Met Pro Glu Glu
210      215      220
Val Lys Lys Met Phe Gln Lys Glu Phe Lys Gln Asn Asp Ile Trp Lys
225      230      235      240
His Phe Lys Ala Val Lys Asn Asn His Val Tyr Asp Leu Glu Glu Val
245      250      255
Pro Phe Gly Ile Thr Ala Asn Val Asp Ala Asp Lys Ala Met Thr Gln
260      265      270
Leu Tyr Asp Leu Phe Tyr Lys Asp Lys Lys
275      280
    
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<210> 74
 <211> 244
 <212> PRT
 <213> Staphylococcus aureus

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<400> 74

5 Met Arg Met Lys Arg Phe Leu Thr Ile Val Gln Ile Leu Leu Val Val
 1 5 10 15
 Ile Ile Ile Ile Phe Gly Tyr Lys Ile Val Gln Thr Tyr Ile Glu Asp
 20 25 30
 Lys Gln Glu Arg Ala Asn Tyr Glu Lys Leu Gln Gln Lys Phe Gln Met
 35 40 45
 10 Leu Met Ser Lys His Gln Glu His Val Arg Pro Gln Phe Glu Ser Leu
 50 55 60
 Glu Lys Ile Asn Lys Asp Ile Val Gly Trp Ile Lys Leu Ser Gly Thr
 65 70 75 80
 15 Ser Leu Asn Tyr Pro Val Leu Gln Gly Lys Thr Asn His Asp Tyr Leu
 85 90 95
 Asn Leu Asp Phe Glu Arg Glu His Arg Arg Lys Gly Ser Ile Phe Met
 100 105 110
 20 Asp Phe Arg Asn Glu Leu Lys Asn Leu Asn His Asn Thr Ile Leu Tyr
 115 120 125
 Gly His His Val Gly Asp Asn Thr Met Phe Asp Val Leu Glu Asp Tyr
 130 135 140
 25 Leu Lys Gln Ser Phe Tyr Glu Lys His Lys Ile Ile Glu Phe Asp Asn
 145 150 155 160
 Lys Tyr Gly Lys Tyr Gln Leu Gln Val Phe Ser Ala Tyr Lys Thr Thr
 165 170 175
 30 Thr Lys Asp Asn Tyr Ile Arg Thr Asp Phe Glu Asn Asp Gln Asp Tyr
 180 185 190
 Gln Gln Phe Leu Asp Glu Thr Lys Arg Lys Ser Val Ile Asn Ser Asp
 195 200 205
 35 Val Asn Val Thr Val Lys Asp Arg Ile Met Thr Leu Ser Thr Cys Glu
 210 215 220
 Asp Ala Tyr Ser Glu Thr Thr Lys Arg Ile Val Val Val Ala Lys Ile
 225 230 235 240
 40 Ile Lys Val Ser

<210> 75

<211> 238

<212> PRT

45 <213> Staphylococcus aureus

<400> 75

50 Met Ser Lys Asn Ile Thr Lys Asn Ile Ile Leu Thr Thr Thr Leu Leu

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1 5 10 15
 Leu Leu Gly Thr Val Leu Pro Gln Asn Gln Lys Pro Val Phe Ser Phe
 20 25 30
 5 Tyr Ser Glu Ala Lys Ala Tyr Ser Ile Gly Gln Asp Glu Thr Asn Ile
 35 40 45
 Asn Glu Leu Ile Lys Tyr Tyr Thr Gln Pro His Phe Ser Phe Ser Asn
 50 55 60
 10 Lys Trp Leu Tyr Gln Tyr Asp Asn Gly Asn Ile Tyr Val Glu Leu Lys
 65 70 75 80
 Arg Tyr Ser Trp Ser Ala His Ile Ser Leu Trp Gly Ala Glu Ser Trp
 85 90 95
 15 Gly Asn Ile Asn Gln Leu Lys Asp Arg Tyr Val Asp Val Phe Gly Leu
 100 105 110
 Lys Asp Lys Asp Thr Asp Gln Leu Trp Trp Ser Tyr Arg Glu Thr Phe
 115 120 125
 20 Thr Gly Gly Val Thr Pro Ala Ala Lys Pro Ser Asp Lys Thr Tyr Asn
 130 135 140
 Leu Phe Val Gln Tyr Lys Asp Lys Leu Gln Thr Ile Ile Gly Ala His
 145 150 155 160
 25 Lys Ile Tyr Gln Gly Asn Lys Pro Val Leu Thr Leu Lys Glu Ile Asp
 165 170 175
 Phe Arg Ala Arg Glu Ala Leu Ile Lys Asn Lys Ile Leu Tyr Asn Glu
 180 185 190
 30 Asn Arg Asn Lys Gly Lys Leu Lys Ile Thr Gly Gly Gly Asn Asn Tyr
 195 200 205
 Thr Ile Asp Leu Ser Lys Arg Leu His Ser Asp Leu Ala Asn Val Tyr
 210 215 220
 35 Val Lys Asn Pro Asn Lys Ile Thr Val Asp Val Leu Phe Asp
 225 230 235

<210> 76

<211> 241

40 <212> PRT

<213> Staphylococcus aureus

<400> 76

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1 Met Asn Asn Asn Ile Thr Lys Lys Ile Ile Leu Ser Thr Thr Leu Leu
 5 1 5 10
 20 Leu Leu Gly Thr Ala Ser Thr Gln Phe Pro Asn Thr Pro Ile Asn Ser
 25 30
 35 Ser Ser Glu Ala Lys Ala Tyr Tyr Ile Asn Gln Asn Glu Thr Asn Val
 40 45
 50 Asn Glu Leu Thr Lys Tyr Tyr Ser Gln Lys Tyr Leu Thr Phe Ser Asn
 55 60
 65 Ser Thr Leu Trp Gln Lys Asp Asn Gly Thr Ile His Ala Thr Leu Leu
 70 75 80
 85 Gln Phe Ser Trp Tyr Ser His Ile Gln Val Tyr Gly Pro Glu Ser Trp
 90 95
 100 Gly Asn Ile Asn Gln Leu Arg Asn Lys Ser Val Asp Ile Phe Gly Ile
 105 110
 115
 120 Lys Asp Gln Glu Thr Ile Asp Ser Phe Ala Leu Ser Gln Glu Thr Phe
 125
 130 Thr Gly Gly Val Thr Pro Ala Ala Thr Ser Asn Asp Lys His Tyr Lys
 135 140
 145 Leu Asn Val Thr Tyr Lys Asp Lys Ala Glu Thr Phe Thr Gly Gly Phe
 150 155 160
 165 Pro Val Tyr Glu Gly Asn Lys Pro Val Leu Thr Leu Lys Glu Leu Asp
 170 175
 180 Phe Arg Ile Arg Gln Thr Leu Ile Lys Ser Lys Lys Leu Tyr Asn Asn
 185 190
 195 Ser Tyr Asn Lys Gly Gln Ile Lys Ile Thr Gly Ala Asp Asn Asn Tyr
 200 205
 210 Thr Ile Asp Leu Ser Lys Arg Leu Pro Ser Thr Asp Ala Asn Arg Tyr
 215 220
 225 Val Lys Lys Pro Gln Asn Ala Lys Ile Glu Val Ile Leu Glu Lys Ser
 230 235 240
 40 Asn

<210> 77

<211> 565

<212> PRT

<213> Staphylococcus aureus

<400> 77

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Met Ala Tyr Asp Gly Leu Phe Thr Lys Lys Met Val Glu Ser Leu Gln
 1 5 10 15
 Phe Leu Thr Thr Gly Arg Val His Lys Ile Asn Gln Pro Asp Asn Asp
 5 20 25 30
 Thr Ile Leu Met Val Val Arg Gln Asn Arg Gln Asn His Gln Leu Leu
 35 40 45
 Leu Ser Ile His Pro Asn Phe Ser Arg Leu Gln Leu Thr Thr Lys Lys
 10 50 55 60
 Tyr Asp Asn Pro Phe Asn Pro Pro Met Phe Ala Arg Val Phe Arg Lys
 65 70 75 80
 His Leu Glu Gly Gly Ile Ile Glu Ser Ile Lys Gln Ile Gly Asn Asp
 15 85 90 95
 Arg Arg Ile Glu Ile Asp Ile Lys Ser Lys Asp Glu Ile Gly Asp Thr
 100 105 110
 Ile Tyr Arg Thr Val Ile Leu Glu Ile Met Gly Lys His Ser Asn Leu
 115 120 125
 Ile Leu Val Asp Glu Asn Arg Lys Ile Ile Glu Gly Phe Lys His Leu
 130 135 140
 Thr Pro Asn Thr Asn His Tyr Arg Thr Val Met Pro Gly Phe Asn Tyr
 145 150 155 160
 Glu Ala Pro Pro Thr Gln His Lys Ile Asn Pro Tyr Asp Ile Thr Gly
 165 170 175
 Ala Glu Val Leu Lys Tyr Ile Asp Phe Asn Ala Gly Asn Ile Ala Lys
 180 185 190

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Gln Leu Leu Asn Gln Phe Glu Gly Phe Ser Pro Leu Ile Thr Asn Glu
 195 200 205
 Ile Val Ser Arg Arg Gln Phe Met Thr Ser Ser Thr Leu Pro Glu Ala
 210 215 220
 Phe Asp Glu Val Met Ala Glu Thr Lys Leu Pro Pro Thr Pro Ile Phe
 225 230 235 240
 His Lys Asn His Glu Thr Gly Lys Glu Asp Phe Tyr Phe Ile Lys Leu
 245 250 255
 Asn Gln Phe Asn Asp Asp Thr Val Thr Tyr Asp Ser Leu Asn Asp Leu
 260 265 270
 Leu Asp Arg Phe Tyr Asp Ala Arg Gly Glu Arg Glu Arg Val Lys Gln
 275 280 285
 Arg Ala Asn Asp Leu Val Arg Phe Val Gln Gln Gln Leu His Lys Tyr
 290 295 300
 Gln Asn Lys Leu Ala Lys Leu Ile Glu Glu Tyr Glu Gln Ser Lys Asn
 305 310 315 320
 Lys Asp Thr Glu Gln Leu Tyr Gly Glu Leu Ile Thr Ala Asn Ile Tyr
 325 330 335
 Arg Ile Lys Gln Gly Asp Lys Glu Val Thr Ala Leu Asn Tyr Tyr Thr
 340 345 350
 Asn Glu Glu Val Val Ile Pro Leu Asn Pro Thr Lys Ser Pro Ser Ala
 355 360 365
 Asn Ala Gln Tyr Tyr Tyr Lys Gln Tyr Asn Arg Met Lys Thr Arg Glu
 370 375 380
 Arg Glu Leu Gln His Gln Ile Gln Leu Thr Lys Asp Asn Ile Asp Tyr
 385 390 395 400
 Phe Ser Thr Ile Glu Gln Gln Leu His His Ile Ser Val His Asp Ile
 405 410 415
 Asp Glu Ile Arg Asp Glu Leu Ala Glu Gln Gly Phe Met Lys Gln Arg
 420 425 430
 Lys Asn Gln Thr Lys Lys Lys Lys Ala Gln Ile Gln Leu Gln His Tyr
 435 440 445
 Val Ser Thr Asp Gly Asp Asp Ile Tyr Val Gly Lys Asn Asn Lys Gln
 450 455 460
 Asn Asp Tyr Leu Thr Asn Lys Lys Ala Lys Lys Thr His Thr Trp Leu
 465 470 475 480
 His Thr Lys Asp Ile Pro Gly Ser His Val Val Ile Phe Asn Asp Ala
 485 490 495
 Pro Ser Asp Thr Thr Ile Lys Glu Ala Ala Met Leu Ala Gly Tyr Phe
 500 505 510
 Ser Lys Ala Gly Asn Ser Gly Gln Ile Pro Val Asp Tyr Thr Leu Ile
 515 520 525
 Lys Asn Val His Lys Pro Ser Gly Ala Lys Pro Gly Phe Val Thr Tyr
 530 535 540
 Asp Asn Gln Lys Thr Leu Tyr Ala Thr Pro Asp Tyr Glu Leu Ile Gln
 545 550 555 560
 Lys Met Lys Gln Ser

565

5 <210> 78
 <211> 317
 <212> PRT
 <213> Staphylococcus aureus

10 <400> 78

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Met Lys Lys Thr Leu Gly Cys Leu Leu Leu Ile Met Leu Leu Val Val
1 5 10 15
Ala Gly Cys Ser Phe Gly Gly Asn His Lys Leu Ser Ser Lys Lys Ser
5 20 25 30
Glu Glu Ser Lys Gln Glu Thr Val Lys Lys Glu Ser Glu Glu Lys
35 40 45
Asp Pro Asp Leu Glu Lys Tyr Glu Glu Ile Glu Lys Lys Met Lys Gly
10 50 55 60
Ile Lys Asp Ala Pro Ser Leu Asp Lys Leu Asp Pro Leu Met Thr Glu
65 70 75 80
Lys Ser Phe Thr Asn Ser Lys Gly Ile Gln Gly Trp Lys Asp Tyr Lys
15 85 90 95
Glu Leu Met Gly Lys Val Glu Leu Ala Asp Tyr Arg Phe Thr Lys Asp
100 105 110
Ser Lys Gly Ser Ser Ile Lys Asp Val Asp Ala Phe Phe Lys Gly Lys
20 115 120 125
Lys Gly Ile Lys Arg Lys Val Ile Glu Thr His Asp Asp Val Lys Gln
130 135 140
Val Asp Tyr Trp Tyr Val Asp Pro Asp Gly Lys Lys Ile Gly Asn Ser
25 145 150 155 160
Asn Thr Pro Val Phe Tyr Ala Glu Ile Met Thr Lys Tyr Lys Asp Gly
165 170 175
Lys Leu Val Tyr Ala Ser Val Glu Pro Gly Ser Tyr Val Ile His Lys
30 180 185 190
Asp Asp Ala Ile Lys Tyr Asp Asp Tyr Ser Lys Leu Lys Lys Leu Ser
195 200 205
Gln Leu Thr Lys Leu Asp His Pro Lys Pro Val Pro Tyr Ser Val Ala
35 210 215 220
Gln Ile Lys Ser Phe Gly Val Pro Leu Thr Ser Val Ser Phe Met Thr
225 230 235 240
His Gly Ser Lys Asp Thr Lys Asp Glu Val Leu Pro Ala Leu Ala Tyr
40 245 250 255
Phe Thr Phe Ser Pro Lys Asn Tyr Glu Asp Lys Ser Asn Pro Asp Pro
260 265 270
Lys Val Leu Asn Leu Val His Met Asp Phe Leu Asn Ala Ser Ser Asp
45 275 280 285
Phe Gly Asn Ala His Phe Val Val Leu Ser Lys Tyr Ile Lys Glu Tyr
290 295 300
Glu Ser Asn Tyr Glu Thr Ala Ser Asp Asp Ser Leu Lys
50 305 310 315

<210> 79

<211> 372

<212> PRT

<213> Staphylococcus aureus

<400> 79

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Met Asn Lys Gln Gln Ser Lys Val Arg Tyr Ser Ile Arg Lys Val Ser
 1 5 10 15
 Ile Gly Ile Leu Ser Ile Ser Ile Gly Met Phe Leu Ala Leu Gly Met
 5 20 25 30
 Ser Asn Lys Ala Tyr Ala Asp Glu Ile Asp Lys Ser Lys Asp Phe Thr
 35 40 45
 Arg Gly Tyr Glu Gln Asn Val Phe Ala Lys Ser Glu Leu Asn Ala Asn
 10 50 55 60
 Lys Asn Thr Thr Lys Asp Lys Ile Lys Asn Glu Gly Ala Val Lys Thr
 65 70 75 80
 Ser Asp Thr Ser Leu Lys Leu Asp Asn Lys Ser Ala Ile Ser Asn Gly
 15 85 90 95
 Asn Glu Ile Asn Gln Asp Ile Lys Ile Ser Asn Thr Pro Lys Asn Ser
 100 105 110
 Ser Gln Gly Asn Asn Leu Val Ile Asn Asn Asn Glu Leu Thr Lys Glu
 20 115 120 125
 Ile Lys Ile Ala Asn Leu Glu Ala Gln Asn Ser Asn Gln Lys Lys Thr
 130 135 140
 Asn Lys Val Thr Asn Asn Tyr Phe Gly Tyr Tyr Ser Phe Arg Glu Ala
 25 145 150 155 160
 Pro Lys Thr Gln Ile Tyr Thr Val Lys Lys Gly Asp Thr Leu Ser Ala
 165 170 175
 Ile Ala Leu Lys Tyr Lys Thr Thr Val Ser Asn Ile Gln Asn Thr Asn
 30 180 185 190
 Asn Ile Ala Asn Pro Asn Leu Ile Phe Ile Gly Gln Lys Leu Lys Val
 195 200 205
 Pro Met Thr Pro Leu Val Glu Pro Lys Pro Lys Thr Val Ser Ser Asn
 35 210 215 220
 Asn Lys Ser Asn Ser Asn Ser Ser Thr Leu Asn Tyr Leu Lys Thr Leu
 225 230 235 240
 Glu Asn Arg Gly Trp Asp Phe Asp Gly Ser Tyr Gly Trp Gln Cys Phe
 40 245 250 255
 Asp Leu Val Asn Val Tyr Trp Asn His Leu Tyr Gly His Gly Leu Lys
 260 265 270
 Gly Tyr Gly Ala Lys Asp Ile Pro Tyr Ala Asn Asn Phe Asn Ser Glu
 275 280 285
 Ala Lys Ile Tyr His Asn Thr Pro Thr Phe Lys Ala Glu Pro Gly Asp
 45 290 295 300
 Leu Val Val Phe Ser Gly Arg Phe Gly Gly Gly Tyr Gly His Thr Ala
 305 310 315 320
 Ile Val Leu Asn Gly Asp Tyr Asp Gly Lys Leu Met Lys Phe Gln Ser
 50 325 330 335
 Leu Asp Gln Asn Trp Asn Asn Gly Gly Trp Arg Lys Ala Glu Val Ala
 340 345 350

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His Lys Val Val His Asn Tyr Glu Asn Asp Met Ile Phe Ile Arg Pro
 355 360 365

Phe Lys Lys Ala
 370

5

<210> 80

<211> 304

<212> PRT

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<213> Staphylococcus aureus

<400> 80

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1 Met Leu Lys Lys Ala Lys Phe Ile Leu Met Ala Thr Ile Leu Leu Ser
 5 Gly Cys Ser Thr Thr Asn Asn Glu Ser Asn Lys Glu Thr Lys Ser Val
 10 Pro Glu Glu Met Asp Ala Ser Lys Tyr Val Gly Gln Gly Phe Gln Pro
 15 Val Lys Ala Thr Asn Val Ile Gly Ser Gly Asp Gly Val Glu Val Phe
 20 Asp Lys Ser Ile Ile Asp Ser Asp Ser Ser Leu Arg Ser Lys Asp Lys
 25 Tyr Arg Ala Gln Lys Glu Lys Tyr Asp Lys Leu Tyr Lys Phe Phe Lys
 30 Asn Lys Thr Gln Asn Ser Gly Tyr Glu Asn Glu Tyr Phe Tyr Ile Ser
 35 Lys Gln Leu Lys Asp Lys Ser Lys Val Ser Val Thr Thr Thr Leu Phe
 40 Lys Met Ala Glu Glu Ile Lys Lys Asp Lys Glu Ile Pro Asn Gly Ile
 45 Glu Leu Ser Ile Lys Phe Ser Asp Asn Lys Ile Asn Thr Val Lys Pro
 50 Asn Phe Asn Gly Glu Ser Thr Ser Glu Tyr Gly Val Phe Asp Gln Glu

<210> 81

<211> 193

<212> PRT

<213> Staphylococcus aureus

<400> 81

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Met Lys Lys Leu Val Ser Ile Val Gly Ala Thr Leu Leu Leu Ala Gly
1 5 10 15
Cys Gly Ser Gln Asn Leu Ala Pro Leu Glu Glu Lys Thr Thr Asp Leu
5 20 25 30
Arg Glu Asp Asn His Gln Leu Lys Leu Asp Ile Gln Glu Leu Asn Gln
35 40 45
Gln Ile Ser Asp Ser Lys Ser Lys Ile Lys Gly Leu Glu Lys Asp Lys
10 50 55 60
Glu Asn Ser Lys Lys Thr Ala Ser Asn Asn Thr Lys Ile Lys Leu Met
65 70 75 80
Asn Val Thr Ser Thr Tyr Tyr Asp Lys Val Ala Lys Ala Leu Lys Ser
15 85 90 95
Tyr Asn Asp Ile Glu Lys Asp Val Ser Lys Asn Lys Gly Asp Lys Asn
100 105 110
Val Gln Ser Lys Leu Asn Gln Ile Ser Asn Asp Ile Gln Ser Ala His
20 115 120 125
Thr Ser Tyr Lys Asp Ala Ile Asp Gly Leu Ser Leu Ser Asp Asp Asp
130 135 140
Lys Lys Thr Ser Lys Asn Ile Asp Lys Leu Asn Ser Asp Leu Asn His
25 145 150 155 160
Ala Phe Asp Asp Ile Lys Asn Gly Tyr Gln Asn Lys Asp Lys Lys Gln
165 170 175
Leu Thr Lys Gly Gln Gln Ala Leu Ser Lys Leu Asn Leu Asn Ala Lys
30 180 185 190
Ser

<210> 82

<211> 216

35 <212> PRT

<213> Staphylococcus aureus

<400> 82

40 Met Lys Ile Thr Tyr Lys Tyr Arg Gly Asp Leu Pro Leu Asn Thr Glu
1 5 10 15
Asn Asn Lys Asn Gln Asn Gln Ser Val Lys Asn Ser Glu Arg Arg Gly
20 25 30
45 Met Leu Lys Gly Cys Gly Gly Cys Leu Ile Ser Phe Ile Leu Leu Ile
35 40 45
Ile Leu Leu Ser Ala Cys Ser Met Met Phe Ser Asn Asn Asp Asn Ser
50 55 60
Thr Asn Asn Gln Ser Ser Lys Thr Gln Leu Thr Gln Lys Asp Glu Asn
65 70 75 80
Lys Asn Glu Asp Lys Pro Glu Glu Lys Ser Glu Thr Ala Thr Asp Glu
85 90 95
55 Asp Leu Gln Ser Thr Glu Glu Val Pro Ala Asn Glu Asn Thr Glu Asn
100 105 110

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Asn Gln His Glu Ile Asp Glu Ile Thr Thr Lys Asp Gln Ser Asp Asp
 115 120 125
 Asp Ile Asn Thr Pro Asn Val Ala Glu Asp Lys Ser Gln Asp Asp Leu
 130 135 140
 Lys Asp Asp Leu Lys Glu Lys Gln Gln Ser Ser Asn His His Gln Ser
 145 150 155 160
 Thr Gln Pro Lys Thr Ser Pro Ser Thr Glu Thr Asn Thr Gln Gln Ser
 165 170 175
 Phe Ala Asn Cys Lys Gln Leu Arg Gln Val Tyr Pro Asn Gly Val Thr
 180 185 190
 Ala Asp His Pro Ala Tyr Arg Pro His Leu Asp Arg Asp Lys Asp Lys
 195 200 205
 Arg Ala Cys Glu Pro Asp Lys Tyr
 210 215

<210> 83

<211> 208

<212> PRT

<213> Staphylococcus aureus

<400> 83

Met Lys Phe Lys Ala Ile Val Ala Ile Thr Leu Ser Leu Ser Leu Leu
 1 5 10 15
 Thr Ala Cys Gly Ala Asn Gln His Lys Glu Asn Ser Ser Lys Ser Asn
 20 25 30
 Asp Thr Asn Lys Lys Thr Gln Gln Thr Asp Asn Thr Thr Gln Ser Asn
 35 40 45
 Thr Glu Lys Gln Met Thr Pro Gln Glu Ala Glu Asp Ile Val Arg Asn
 50 55 60
 Asp Tyr Lys Ala Arg Gly Val Asn Glu Tyr Gln Thr Leu Asn Tyr Lys
 65 70 75 80
 Thr Asn Leu Glu Arg Ser Asn Glu His Glu Tyr Tyr Val Glu His Leu
 85 90 95
 Val Arg Asp Ala Val Gly Thr Pro Leu Lys Arg Cys Ala Ile Val Asn
 100 105 110
 Arg His Asn Gly Thr Ile Ile Asn Ile Phe Asp Asp Met Ser Glu Lys
 115 120 125
 Asp Lys Glu Glu Phe Glu Ala Phe Lys Lys Arg Ser Pro Lys Tyr Asn
 130 135 140
 Pro Gly Met Asn Asn His Asp Glu Thr Asp Gly Glu Ser Glu Asp Ile
 145 150 155 160
 Gln His His Asp Ile Asp Asn Asn Lys Ala Ile Gln Asn Asp Ile Pro
 165 170 175
 Asp Gln Lys Val Asp Asp Lys Asn Asp Lys Asn Ala Val Asn Lys Glu
 180 185 190
 Glu Lys His Asp Asn Gly Ala Asn Asn Ser Glu Glu Thr Lys Val Lys
 195 200 205

<210> 84
<211> 457
<212> PRT
<213> Staphylococcus aureus

5

<400> 84

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Met Lys Ile Ile Lys Arg Ala Ile Ile Ser Leu Ile Ile Leu Ser Leu
 1 5 10 15
 Leu Ile Ser Ile Thr Met Ser Asn Ala Ser Ala Ser Glu Glu Leu Tyr
 5 20 25 30
 Tyr Ser Val Glu Tyr Lys Asn Thr Ala Thr Phe Asn Lys Leu Val Lys
 35 40 45
 Lys Lys Ser Leu Asn Val Val Tyr Asn Ile Pro Glu Leu His Val Ala
 10 50 55 60
 Gln Ile Lys Met Thr Lys Met His Ala Asn Ala Leu Ala Asn Tyr Lys
 65 70 75 80
 Asn Asp Ile Lys Tyr Ile Asn Ala Thr Cys Ser Thr Cys Ile Thr Ser
 15 85 90 95
 Glu Lys Thr Ile Asp Arg Thr Ser Asn Glu Ser Leu Phe Ser Arg Gln
 100 105 110
 Trp Asp Met Asn Lys Ile Thr Asn Asn Gly Ala Ser Tyr Asp Asp Leu
 115 120 125
 Pro Lys His Ala Asn Thr Lys Ile Ala Ile Ile Asp Thr Gly Val Met
 130 135 140
 Lys Asn His Asp Asp Leu Lys Asn Asn Phe Ser Thr Asp Ser Lys Asn
 145 150 155 160
 Leu Val Pro Leu Asn Gly Phe Arg Gly Thr Glu Pro Glu Glu Thr Gly
 165 170 175
 Asp Val His Asp Val Asn Asp Arg Lys Gly His Gly Thr Met Val Ser
 180 185 190
 Gly Gln Thr Ser Ala Asn Gly Lys Leu Ile Gly Val Ala Pro Asn Asn
 195 200 205
 Lys Phe Thr Met Tyr Arg Val Phe Gly Ser Lys Lys Thr Glu Leu Leu
 210 215 220
 Trp Val Ser Lys Ala Ile Val Gln Ala Ala Asn Asp Gly Asn Gln Val
 225 230 235 240
 Ile Asn Ile Ser Val Gly Ser Tyr Ile Ile Leu Asp Lys Asn Asp His
 245 250 255
 Gln Thr Phe Arg Lys Asp Glu Lys Val Glu Tyr Asp Ala Leu Gln Lys
 260 265 270
 Ala Ile Asn Tyr Ala Lys Lys Lys Lys Ser Ile Val Val Ala Ala Ala
 275 280 285
 Gly Asn Asp Gly Ile Asp Val Asn Asp Lys Gln Lys Leu Lys Leu Gln
 290 295 300
 Arg Glu Tyr Gln Gly Asn Gly Glu Val Lys Asp Val Pro Ala Ser Met
 305 310 315 320
 Asp Asn Val Val Thr Val Gly Ser Thr Asp Gln Lys Ser Asn Leu Ser
 325 330 335
 Glu Phe Ser Asn Phe Gly Met Asn Tyr Thr Asp Ile Ala Ala Pro Gly
 340 345 350
 Gly Ser Phe Ala Tyr Leu Asn Gln Phe Gly Val Asp Lys Trp Met Asn

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355 360 365
 Glu Gly Tyr Met His Lys Glu Asn Ile Leu Thr Thr Ala Asn Asn Gly
 370 375 380
 5 Arg Tyr Ile Tyr Gln Ala Gly Thr Ser Leu Ala Thr Pro Lys Val Ser
 385 390 395 400
 Gly Ala Leu Ala Leu Ile Ile Asp Lys Tyr His Leu Glu Lys His Pro
 405 410 415
 10 Asp Lys Ala Ile Glu Leu Leu Tyr Gln His Gly Thr Ser Lys Asn Asn
 420 425 430
 Lys Pro Phe Ser Arg Tyr Gly His Gly Glu Leu Asp Val Tyr Lys Ala
 435 440 445
 15 Leu Asn Val Ala Asn Gln Lys Ala Ser
 450 455

<210> 85

<211> 320

<212> PRT

<213> Staphylococcus aureus

<400> 85

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Met Lys Met Ile Asn Lys Leu Ile Val Pro Val Thr Ala Ser Ala Leu
 1 5 10 15
 5 Leu Leu Gly Ala Cys Gly Ala Ser Ala Thr Asp Ser Lys Glu Asn Thr
 20 25 30
 Leu Ile Ser Ser Lys Ala Gly Asp Val Thr Val Ala Asp Thr Met Lys
 35 40 45
 10 Lys Ile Gly Lys Asp Gln Ile Ala Asn Ala Ser Phe Thr Glu Met Leu
 50 55 60
 Asn Lys Ile Leu Ala Asp Lys Tyr Lys Asn Lys Val Asn Asp Lys Lys
 65 70 75 80
 15 Ile Asp Glu Gln Ile Glu Lys Met Gln Lys Gln Tyr Gly Gly Lys Asp
 85 90 95
 Lys Phe Glu Lys Ala Leu Gln Gln Gln Gly Leu Thr Ala Asp Lys Tyr
 100 105 110
 20 Lys Glu Asn Leu Arg Thr Ala Ala Tyr His Lys Glu Leu Leu Ser Asp
 115 120 125
 Lys Ile Lys Ile Ser Asp Ser Glu Ile Lys Glu Asp Ser Lys Lys Ala
 130 135 140
 25 Ser His Ile Leu Ile Lys Val Lys Ser Lys Lys Ser Asp Lys Glu Gly
 145 150 155 160
 Leu Asp Asp Lys Glu Ala Lys Gln Lys Ala Glu Glu Ile Gln Lys Glu
 165 170 175
 30 Val Ser Lys Asp Pro Ser Lys Phe Gly Glu Ile Ala Lys Lys Glu Ser
 180 185 190
 Met Asp Thr Gly Ser Ala Lys Lys Asp Gly Glu Leu Gly Tyr Val Leu
 195 200 205
 35 Lys Gly Gln Thr Asp Lys Asp Phe Glu Lys Ala Leu Phe Lys Leu Lys
 210 215 220
 Asp Gly Glu Val Ser Glu Val Val Lys Ser Ser Phe Gly Tyr His Ile
 225 230 235 240
 40 Ile Lys Ala Asp Lys Pro Thr Asp Phe Asn Ser Glu Lys Gln Ser Leu
 245 250 255
 Lys Glu Lys Leu Val Asp Gln Lys Val Gln Lys Asn Pro Lys Leu Leu
 260 265 270
 45 Thr Asp Ala Tyr Lys Asp Leu Leu Lys Glu Tyr Asp Val Asp Phe Lys
 275 280 285
 Asp Arg Asp Ile Lys Ser Val Val Glu Asp Lys Ile Leu Asn Pro Glu
 290 295 300
 50 Lys Leu Lys Gln Gly Gly Ala Gln Gly Gly Gln Ser Gly Met Ser Gln
 305 310 315 320

<210> 86

<211> 388

<212> PRT

55 <213> Staphylococcus aureus

<400> 86

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	Met	Lys	Arg	Asn	Phe	Pro	Lys	Leu	Ile	Ala	Leu	Ser	Leu	Ile	Phe	Ser
	1				5					10					15	
5	Leu	Ser	Val	Thr	Pro	Ile	Ala	Asn	Ala	Glu	Ser	Asn	Ser	Asn	Ile	Lys
				20					25					30		
	Ala	Lys	Asp	Lys	Lys	His	Val	Gln	Val	Asn	Val	Glu	Asp	Lys	Ser	Val
			35					40					45			
10	Pro	Thr	Asp	Val	Arg	Asn	Leu	Ala	Gln	Lys	Asp	Tyr	Leu	Ser	Tyr	Val
		50					55					60				
	Thr	Ser	Leu	Asp	Lys	Ile	Tyr	Asn	Lys	Glu	Lys	Ala	Ser	Tyr	Thr	Leu
	65					70					75					80
15	Gly	Glu	Pro	Phe	Lys	Ile	Tyr	Lys	Phe	Asn	Lys	Lys	Ser	Asp	Gly	Asn
					85					90					95	
	Tyr	Tyr	Phe	Pro	Val	Leu	Asn	Thr	Glu	Gly	Asn	Ile	Asp	Tyr	Ile	Val
				100					105					110		
20	Thr	Ile	Ser	Pro	Lys	Ile	Thr	Lys	Tyr	Ser	Ser	Ser	Ser	Ser	Lys	Tyr
			115					120					125			
	Thr	Ile	Asn	Val	Ser	Pro	Phe	Leu	Ser	Lys	Val	Leu	Asn	Gln	Tyr	Lys
			130				135					140				
25	Asp	Gln	Gln	Ile	Thr	Ile	Leu	Thr	Asn	Ser	Lys	Gly	Tyr	Tyr	Val	Val
	145					150					155					160
	Thr	Gln	Asn	His	Lys	Ala	Lys	Leu	Val	Leu	Lys	Thr	Pro	Arg	Leu	Glu
					165					170					175	
30	Asp	Lys	Lys	Leu	Lys	Lys	Thr	Glu	Ser	Ile	Pro	Thr	Gly	Asn	Asn	Val
				180					185					190		
	Thr	Gln	Leu	Lys	Gln	Lys	Ala	Ser	Val	Thr	Met	Pro	Thr	Ser	Gln	Phe
			195					200					205			
35	Lys	Ser	Asn	Asn	Tyr	Thr	Tyr	Asn	Glu	Gln	Tyr	Ile	Asn	Lys	Leu	Glu
		210					215					220				
	Asn	Phe	Lys	Ile	Arg	Glu	Thr	Gln	Gly	Asn	Asn	Gly	Trp	Cys	Ala	Gly
	225					230					235					240
40	Tyr	Thr	Met	Ser	Glu	Leu	Leu	Asn	Ala	Thr	Tyr	Asn	Thr	Asn	Lys	Tyr
					245					250					255	

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His Ala Glu Ala Val Met Arg Phe Leu His Pro Asn Leu Gln Gly Gln
 260 265 270
 Arg Phe Gln Phe Thr Gly Leu Thr Pro Arg Glu Met Ile Tyr Phe Gly
 275 280 285
 Gln Thr Gln Gly Arg Ser Pro Gln Leu Leu Asn Arg Met Thr Thr Tyr
 290 295 300
 Asn Glu Val Asp Asn Leu Thr Lys Asn Asn Lys Gly Ile Ala Val Leu
 305 310 315 320
 Gly Ser Arg Val Glu Ser Arg Asn Gly Met His Ala Gly His Ala Met
 325 330 335
 Ala Val Val Gly Asn Ala Lys Leu Asp Asn Gly Gln Glu Val Ile Ile
 340 345 350
 Ile Trp Asn Pro Trp Asp Asn Gly Phe Met Thr Gln Asp Ala Lys Asn
 355 360 365
 Asn Val Ile Pro Val Ser Asn Gly Asp His Tyr Arg Trp Tyr Ser Ser
 370 375 380
 Ile Tyr Gly Tyr
 385

<210> 87

<211> 280

<212> PRT

<213> Staphylococcus aureus

<400> 87

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Met Lys Lys Phe Phe Phe Ile Gly Leu Leu Val Phe Val Val Phe Phe
1 5 10
Thr Ala Ala Thr Ile Ile Trp Phe Ser Tyr Asp Lys Asn Lys Tyr Gly
5 20 25 30
Thr Lys Gln Tyr Asp Lys Thr Phe Lys Asp Asp Ala Phe Asp Asn Val
35 40 45
Ser Ile Asn Leu Asp Ser Thr Glu Leu Arg Ile Lys Arg Gly Asn Gln
10 50 55 60
Phe Arg Val Lys Tyr Asp Gly Asp Asn Asp Ile Leu Ile Asn Ile Val
65 70 75 80
Asp Lys Thr Leu Lys Ile Ser Asp Lys Arg Ser Lys Thr Arg Gly Tyr
15 85 90 95
Ala Ile Asp Met Asn Pro Phe His Glu Asn Lys Lys Thr Leu Thr Ile
100 105 110
Glu Met Pro Asp Lys Met Ile Lys Arg Leu Asn Leu Ser Ser Gly Ala
20 115 120 125
Gly Ser Val Arg Ile Ser Asp Val Asp Leu Glu Asn Thr Ser Ile Gln
130 135 140
Ser Ile Asn Gly Glu Val Val Ile Lys Asn Ser Asn Leu Asp Ala Leu
25 145 150 155 160
Asp Ser Lys Thr Asn Asn Ser Ser Thr Tyr Ile Ser Lys Ser Asn Ile
165 170 175
Lys Asn Ser Asn Ile Lys Val Val Ile Gly Thr Leu Gln Ile Asp Lys
30 180 185 190
Ser Gln Ile Lys Gln Ser Ile Phe Leu Asn Asp His Gly Asp Ile Glu
195 200 205
Phe Lys Asn Met Pro Ser Lys Val Asp Ala Lys Ala Ser Thr Lys Gln
35 210 215 220
Gly Asp Ile Arg Phe Lys Tyr Asp Ser Lys Pro Glu Asp Thr Ile Leu
225 230 235 240
Lys Leu Asn Pro Gly Thr Gly Asp Ser Val Val Lys Asn Lys Thr Phe
40 245 250 255
Thr Asn Gly Lys Val Gly Lys Ser Asp Asn Val Leu Glu Phe Tyr Thr
260 265 270
Ile Asp Gly Asn Ile Lys Val Glu
45 275 280

<210> 88

<211> 303

50 <212> PRT

<213> Staphylococcus aureus

<400> 88

55

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Met Lys Arg Leu Ile Gly Ile Leu Leu Cys Asn Leu Phe Ile Leu Thr
1 5 10 15
Ala Cys Ser Ala Ser Val Asp Lys Thr Ser Asn Ser Thr Lys Thr Thr
20 25 30
Asp Tyr Lys Ile Glu Asn Gly Glu Thr Leu Lys Val Pro Glu Lys Pro
35 40 45
Lys Arg Val Ala Val Leu Thr Gly Phe Tyr Val Gly Asp Phe Ile Lys
50 55 60
Leu Gly Ile Lys Pro Ile Ala Val Ser Asp Ile Thr Lys Asp Ser Ser
65 70 75 80
Ile Leu Lys Pro Tyr Leu Lys Gly Val Asp Tyr Ile Gly Glu Asn Asp
85 90 95
Val Glu Arg Val Ala Lys Ala Lys Pro Asp Leu Ile Val Val Asp Ala
100 105 110
Met Asp Lys Asn Ile Lys Lys Tyr Gln Lys Ile Ala Pro Thr Ile Pro
115 120 125
Tyr Thr Tyr Asn Lys Tyr Asn His Lys Glu Ile Leu Lys Glu Ile Gly
130 135 140
Lys Leu Thr Asn Asn Glu Asp Lys Ala Lys Lys Trp Ile Glu Glu Trp
145 150 155 160
Asp Asp Lys Thr Arg Lys Asp Lys Lys Glu Ile Gln Ser Lys Ile Gly
165 170 175
Gln Ala Thr Ala Ser Val Phe Glu Pro Asp Glu Lys Gln Ile Tyr Ile
180 185 190
Tyr Asn Ser Thr Trp Gly Arg Gly Leu Asp Ile Val His Asp Ala Phe
195 200 205
Gly Met Pro Met Thr Lys Gln Tyr Lys Asp Lys Leu Gln Glu Asp Lys
210 215 220
Lys Gly Tyr Ala Ser Ile Ser Lys Glu Asn Ile Ser Lys Tyr Ala Gly
225 230 235 240
Asp Tyr Ile Phe Leu Ser Lys Pro Ser Tyr Gly Lys Phe Asp Phe Glu
245 250 255
Lys Thr His Thr Trp Gln Asn Ile Glu Ala Val Lys Lys Gly His Val
260 265 270
Ile Ser Tyr Lys Ala Glu Asp Tyr Trp Phe Thr Asp Pro Ile Thr Leu
275 280 285
Glu His Leu Arg Ser Lys Leu Lys Lys Glu Ile Leu Asn Lys Lys
290 295 300

<210> 89

<211> 419

<212> PRT

<213> Staphylococcus aureus

<400> 89

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	Met	Ser	Tyr	His	Trp	Phe	Lys	Lys	Met	Leu	Leu	Ser	Thr	Ser	Ile	Leu
	1				5					10					15	
5	Ile	Leu	Ser	Ser	Ser	Ser	Leu	Gly	Leu	Ala	Thr	His	Thr	Val	Glu	Ala
				20					25					30		
	Lys	Asp	Asn	Leu	Asn	Gly	Glu	Lys	Pro	Thr	Thr	Asn	Leu	Asn	His	Asn
			35					40					45			
10	Ile	Thr	Ser	Pro	Ser	Val	Asn	Ser	Glu	Met	Asn	Asn	Asn	Glu	Thr	Gly
		50					55					60				
	Thr	Pro	His	Glu	Ser	Asn	Gln	Thr	Gly	Asn	Glu	Gly	Thr	Gly	Ser	Asn
	65					70					75					80
15	Ser	Arg	Asp	Ala	Asn	Pro	Asp	Ser	Asn	Asn	Val	Lys	Pro	Asp	Ser	Asn
					85					90					95	
	Asn	Gln	Asn	Pro	Ser	Thr	Asp	Ser	Lys	Pro	Asp	Pro	Asn	Asn	Gln	Asn
				100					105					110		
20	Ser	Ser	Pro	Asn	Pro	Lys	Pro	Asp	Pro	Asp	Asn	Pro	Lys	Pro	Lys	Pro
			115					120					125			
	Asp	Pro	Lys	Pro	Asp	Pro	Asp	Lys	Pro	Lys	Pro	Asn	Pro	Asp	Pro	Lys
		130					135					140				
25	Pro	Asp	Pro	Asp	Asn	Pro	Lys	Pro	Asn	Pro	Asp	Pro	Lys	Pro	Asp	Pro
	145					150				155						160
	Asp	Lys	Pro	Lys	Pro	Asn	Pro	Asp	Pro	Lys	Pro	Asp	Pro	Asp	Lys	Pro
					165					170					175	
30	Lys	Pro	Asn	Pro	Asn	Pro	Lys	Pro	Asp	Pro	Asn	Lys	Pro	Asn	Pro	Asn
				180					185					190		
	Pro	Ser	Pro	Asp	Pro	Asp	Gln	Pro	Gly	Asp	Ser	Asn	His	Ser	Gly	Gly
			195					200					205			
35	Ser	Lys	Asn	Gly	Gly	Thr	Trp	Asn	Pro	Asn	Ala	Ser	Asp	Gly	Ser	Asn
		210					215					220				
	Gln	Gly	Gln	Trp	Gln	Pro	Asn	Gly	Asn	Gln	Gly	Asn	Ser	Gln	Asn	Pro
	225					230					235					240
40	Thr	Gly	Asn	Asp	Phe	Val	Ser	Gln	Arg	Phe	Leu	Ala	Leu	Ala	Asn	Gly
					245					250					255	
	Ala	Tyr	Lys	Tyr	Asn	Pro	Tyr	Ile	Leu	Asn	Gln	Ile	Asn	Lys	Leu	Gly
				260					265					270		
45	Lys	Asp	Tyr	Gly	Glu	Val	Thr	Asp	Glu	Asp	Ile	Tyr	Asn	Ile	Ile	Arg
			275					280					285			

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Lys Gln Asn Phe Ser Gly Asn Ala Tyr Leu Asn Gly Leu Gln Gln Gln
 290 295 300
 5 Ser Asn Tyr Phe Arg Phe Gln Tyr Phe Asn Pro Leu Lys Ser Glu Arg
 305 310 315 320
 Tyr Tyr Arg Asn Leu Asp Glu Gln Val Leu Ala Leu Ile Thr Gly Glu
 325 330 335
 10 Ile Gly Ser Met Pro Asp Leu Lys Lys Pro Glu Asp Lys Pro Asp Ser
 340 345 350
 Lys Gln Arg Ser Phe Glu Pro His Glu Lys Asp Asp Phe Thr Val Val
 355 360 365
 15 Lys Lys Gln Glu Asp Asn Lys Lys Ser Ala Ser Thr Ala Tyr Ser Lys
 370 375 380
 Ser Trp Leu Ala Ile Val Cys Ser Met Met Val Val Phe Ser Ile Met
 385 390 395 400
 20 Leu Phe Leu Phe Val Lys Arg Asn Lys Lys Lys Asn Lys Asn Glu Ser
 405 410 415
 Gln Arg Arg

<210> 90

<211> 231

<212> PRT

<213> Staphylococcus aureus

<400> 90

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Met Lys Lys Thr Leu Leu Ala Ser Ser Leu Ala Val Gly Leu Gly Ile
1 5 10 15
Val Ala Gly Asn Ala Gly His Glu Ala His Ala Ser Glu Ala Asp Leu
5 20 25 30
Asn Lys Ala Ser Leu Ala Gln Met Ala Gln Ser Asn Asp Gln Thr Leu
35 40 45
Asn Gln Lys Pro Ile Glu Ala Gly Ala Tyr Asn Tyr Thr Phe Asp Tyr
10 50 55 60
Glu Gly Phe Thr Tyr His Phe Glu Ser Asp Gly Thr His Phe Ala Trp
65 70 75 80
Asn Tyr His Ala Thr Gly Thr Asn Gly Ala Asp Met Ser Ala Gln Ala
15 85 90 95
Pro Ala Thr Asn Asn Val Ala Pro Ser Ala Val Gln Ala Asn Gln Val
100 105 110
Gln Ser Gln Glu Val Glu Ala Pro Gln Asn Ala Gln Thr Gln Gln Pro
20 115 120 125
Gln Ala Ser Thr Ser Asn Asn Ser Gln Val Thr Ala Thr Pro Thr Glu
130 135 140
Ser Lys Ser Ser Glu Gly Ser Ser Val Asn Val Asn Ala His Leu Lys
25 145 150 155 160
Gln Ile Ala Gln Arg Glu Ser Gly Gly Asn Ile His Ala Val Asn Pro
165 170 175
Thr Ser Gly Ala Ala Gly Lys Tyr Gln Phe Leu Gln Ser Thr Trp Asp
30 180 185 190
Ser Val Ala Pro Ala Lys Tyr Lys Gly Val Ser Pro Ala Asn Ala Pro
195 200 205
35 Glu Ser Val Gln Asp Ala Ala Ala Val Lys Leu Tyr Asn Thr Gly Gly
210 215 220
Ala Gly His Trp Val Thr Ala
40 225 230

<210> 91
<211> 294
<212> PRT
<213> staphylococcus aureus

<400> 91

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1 Met Gly Val Lys Ser Val Lys Lys Ile Phe Val Ile Ile Thr Thr Leu
 5 Leu Ala Val Ala Ile Ile Ile Gly Ser Ile Ile Met Val Val Phe Ser
 10 Gln Arg Gln Ala Gln Thr Phe Lys Ile Gln Gln Gln Gln Phe Val Lys
 15 Lys Pro Ile Pro Thr Leu Phe Leu His Gly Phe Gly Gly Ser Ala Asn
 20 Ser Glu Lys Phe Met Val Lys Gln Ala Glu Lys Arg Gly Val Thr Lys
 25 Asp Ile Ile Thr Ala Tyr Val Ser Lys Asp Gly Ala Val Thr Phe Lys
 30 Gly Lys Leu Arg Lys Asp Ala Val Asn Pro Ile Val Lys Ile Glu Leu
 35 Glu Asn Asn Arg Gln Gly Tyr Leu Asp Lys Asn Ala Ala Trp Phe Lys
 40 Asn Val Leu Thr Lys Leu Gln Ser Glu Tyr Asn Phe Asp Lys Phe Asn
 45 Phe Val Gly His Ser Met Gly Asn Leu Thr Phe Ala Gln Tyr Met Met
 50 Thr Tyr Gly Asn Asp Lys Ser Leu Pro Gln Leu Asn Lys Gln Val Asn
 55 Ile Ala Gly Thr Phe Asn Gly Val Leu Asn Met Asn Glu Asp Val Asn
 60 Glu Ile Thr Val Asp Lys Asp Gly Lys Pro Ser Arg Met Asn Gln Pro
 65 Tyr Gln Gln Leu Arg Val Leu Lys Asp Ile Tyr Lys Gly Lys Gly Ile
 70 Glu Val Leu Asn Ile Tyr Gly Asp Leu Lys Asp Gly Thr His Ser Asp
 75 Gly Arg Val Ser Asn Ser Ser Ser Lys Ser Leu Lys Tyr Leu Leu Gly
 80 Asn Ser Pro Lys Ser Tyr Arg Glu Ser Lys Tyr Glu Gly Glu Pro Ala
 85 Gln His Ser Gln Leu His Glu Asn Glu Asn Val Ala Asn Glu Leu Ile
 90 Asp Phe Leu Trp Lys Lys
 95

<210> 92

<211> 807

<212> PRT

<213> Staphylococcus aureus

<400> 92

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Met Thr Tyr Arg Ile Lys Lys Trp Gln Lys Leu Ser Thr Ile Thr Leu
1 5 10 15
Leu Met Ala Gly Val Ile Thr Leu Asn Gly Gly Glu Phe Arg Ser Val
20 25 30
Asp Lys His Gln Ile Ala Val Ala Asp Thr Asn Val Gln Thr Pro Asp
35 40 45
Tyr Glu Lys Leu Arg Asn Thr Trp Leu Asp Val Asn Tyr Gly Tyr Asp
50 55 60
Lys Tyr Asp Glu Asn Asn Pro Asp Met Lys Lys Lys Phe Asp Ala Thr
65 70 75 80
Glu Lys Glu Ala Thr Asn Leu Leu Lys Glu Met Lys Thr Glu Ser Gly
85 90 95
Arg Lys Tyr Leu Trp Ser Gly Ala Glu Thr Leu Glu Thr Asn Ser Ser
100 105 110
His Met Thr Arg Thr Tyr Arg Asn Ile Glu Lys Ile Ala Glu Ala Met
115 120 125
Arg Asn Pro Lys Thr Thr Leu Asn Thr Asp Glu Asn Lys Lys Lys Val
130 135 140
Lys Asp Ala Leu Glu Trp Leu His Lys Asn Ala Tyr Gly Lys Glu Pro
145 150 155 160
Asp Lys Lys Val Lys Glu Leu Ser Glu Asn Phe Thr Lys Thr Thr Gly
165 170 175
Lys Asn Thr Asn Leu Asn Trp Trp Asp Tyr Glu Ile Gly Thr Pro Lys
180 185 190
Ser Leu Thr Asn Thr Leu Ile Leu Leu Asn Asp Gln Phe Ser Asn Glu
195 200 205
Glu Lys Lys Lys Phe Thr Ala Pro Ile Lys Thr Phe Ala Pro Asp Ser
210 215 220
Asp Lys Ile Leu Ser Ser Val Gly Lys Ala Glu Leu Ala Lys Gly Gly
225 230 235 240
Asn Leu Val Asp Ile Ser Lys Val Lys Leu Leu Glu Cys Ile Ile Glu
245 250 255
Glu Asp Lys Asp Met Met Lys Lys Ser Ile Asp Ser Phe Asn Lys Val
260 265 270
Phe Thr Tyr Val Gln Asp Ser Ala Thr Gly Lys Glu Arg Asn Gly Phe
275 280 285
Tyr Lys Asp Gly Ser Tyr Ile Asp His Gln Asp Val Pro Tyr Thr Gly
290 295 300
Ala Tyr Gly Val Val Leu Leu Glu Gly Ile Ser Gln Met Met Pro Met
305 310 315 320
Ile Lys Glu Thr Pro Phe Asn Asp Lys Thr Gln Asn Asp Thr Thr Leu
325 330 335

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Lys Ser Trp Ile Asp Asp Gly Phe Met Pro Leu Ile Tyr Lys Gly Glu
 340 345 350
 Met Met Asp Leu Ser Arg Gly Arg Ala Ile Ser Arg Glu Asn Glu Thr
 355 360 365
 Ser His Ser Ala Ser Ala Thr Val Met Lys Ser Leu Leu Arg Leu Ser
 370 375 380
 Asp Ala Met Asp Asp Ser Thr Lys Ala Lys Tyr Lys Lys Ile Val Lys
 385 390 395 400
 Ser Ser Val Glu Ser Asp Ser Ser Tyr Lys Gln Asn Asp Tyr Leu Asn
 405 410 415
 Ser Tyr Ser Asp Ile Asp Lys Met Lys Ser Leu Met Thr Asp Asn Ser
 420 425 430
 Ile Ser Lys Asn Gly Leu Thr Gln Gln Leu Lys Ile Tyr Asn Asp Met
 435 440 445
 Asp Arg Val Thr Tyr His Asn Lys Asp Leu Asp Phe Ala Phe Gly Leu
 450 455 460
 Ser Met Thr Ser Lys Asn Val Ala Arg Tyr Glu Ser Ile Asn Gly Glu
 465 470 475 480
 Asn Leu Lys Gly Trp His Thr Gly Ala Gly Met Ser Tyr Leu Tyr Asn
 485 490 495
 Ser Asp Val Lys His Tyr His Asp Asn Phe Trp Val Thr Ala Asp Met
 500 505 510
 Lys Arg Leu Ser Gly Thr Thr Thr Leu Asp Asn Glu Ile Leu Lys Asp
 515 520 525
 Thr Asp Asp Lys Lys Ser Ser Lys Thr Phe Val Gly Gly Thr Lys Val
 530 535 540
 Asp Asp Gln His Ala Ser Ile Gly Met Asp Phe Glu Asn Gln Asp Lys
 545 550 555 560
 Thr Leu Thr Ala Lys Lys Ser Tyr Phe Ile Leu Asn Asp Lys Ile Val
 565 570 575
 Phe Leu Gly Thr Gly Ile Lys Ser Thr Asp Ser Ser Lys Asn Pro Val
 580 585 590
 Thr Thr Ile Glu Asn Arg Lys Ala Asn Gly Tyr Thr Leu Tyr Thr Asp
 595 600 605
 Asp Lys Gln Thr Thr Asn Ser Asp Asn Gln Glu Asn Asn Ser Val Phe
 610 615 620
 Leu Glu Ser Thr Asp Thr Lys Lys Asn Ile Gly Tyr His Phe Leu Asn
 625 630 635 640
 Lys Pro Lys Ile Thr Val Lys Lys Glu Ser His Thr Gly Lys Trp Lys
 645 650 655
 Glu Ile Asn Lys Ser Gln Lys Asp Thr Gln Lys Thr Asp Glu Tyr Tyr
 660 665 670
 Glu Val Thr Gln Lys His Ser Asn Ser Asp Asn Lys Tyr Gly Tyr Val
 675 680 685
 Leu Tyr Pro Gly Leu Ser Lys Asp Val Phe Lys Thr Lys Lys Asp Glu
 690 695 700
 Val Thr Val Val Lys Gln Glu Asp Asp Phe His Val Val Lys Asp Asn

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	705		710		715		720									
	Glu	Ser	Val	Trp	Ala	Gly	Val	Asn	Tyr	Ser	Asn	Ser	Thr	Gln	Thr	Phe
					725					730					735	
5	Asp	Ile	Asn	Asn	Thr	Lys	Val	Glu	Val	Lys	Ala	Lys	Gly	Met	Phe	Ile
				740					745					750		
	Leu	Lys	Lys	Lys	Asp	Asp	Asn	Thr	Tyr	Glu	Cys	Ser	Phe	Tyr	Asn	Pro
			755					760					765			
10	Glu	Ser	Thr	Asn	Ser	Ala	Ser	Asp	Ile	Glu	Ser	Lys	Ile	Ser	Met	Thr
		770					775					780				
	Gly	Tyr	Ser	Ile	Thr	Asn	Lys	Asn	Thr	Ser	Thr	Ser	Asn	Glu	Ser	Gly
	785					790					795					800
15	Val	His	Phe	Glu	Leu	Thr	Lys									
					805											

<210> 93

<211> 166

20 <212> PRT

<213> Staphylococcus aureus

<400> 93

25	Met	Lys	Lys	Leu	Val	Thr	Ala	Thr	Thr	Leu	Thr	Ala	Gly	Ile	Gly	Thr
	1				5					10					15	
	Ala	Leu	Val	Gly	Gln	Ala	His	His	Ala	Asp	Ala	Ala	Glu	Asn	Tyr	Thr
				20					25					30		
30	Asn	Tyr	Asn	Asn	Tyr	Asn	Tyr	Asn	Thr	Thr	Gln	Thr	Thr	Thr	Thr	Thr
			35					40					45			
	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Ser	Ile	Ser	His	Ser	Gly	Asn	Leu	Tyr
		50					55					60				
35	Thr	Ala	Gly	Gln	Cys	Thr	Trp	Tyr	Val	Tyr	Asp	Lys	Val	Gly	Gly	Glu
	65					70					75					80
	Ile	Gly	Ser	Thr	Trp	Gly	Asn	Ala	Asn	Asn	Trp	Ala	Ala	Ala	Ala	Gln
					85					90					95	
40	Gly	Ala	Gly	Phe	Thr	Val	Asn	His	Thr	Pro	Ser	Lys	Gly	Ala	Ile	Leu
				100					105					110		
	Gln	Ser	Ser	Glu	Gly	Pro	Phe	Gly	His	Val	Ala	Tyr	Val	Glu	Ser	Val
			115					120					125			
45	Asn	Ser	Asp	Gly	Ser	Val	Thr	Ile	Ser	Glu	Met	Asn	Tyr	Ser	Gly	Gly
		130					135					140				
	Pro	Phe	Ser	Val	Ser	Ser	Arg	Thr	Ile	Ser	Ala	Ser	Glu	Ala	Gly	Asn
	145					150					155					160
50	Tyr	Asn	Tyr	Ile	His	Ile										
					165											

<210> 94

<211> 516

55 <212> PRT

<213> Staphylococcus aureus

<400> 94

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Met	Lys	Lys	Lys	Leu	Gly	Met	Leu	Leu	Leu	Val	Pro	Ala	Val	Thr	Leu
1				5					10					15	
Ser	Leu	Ala	Ala	Cys	Gly	Asn	Asp	Asp	Gly	Lys	Asp	Lys	Asp	Gly	Lys
			20					25					30		

5

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15

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25

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55

Val Thr Ile Lys Thr Thr Val Tyr Pro Leu Gln Ser Phe Ala Glu Gln
 35 40 45
 5 Ile Gly Gly Lys His Val Lys Val Ser Ser Ile Tyr Pro Ala Gly Thr
 50 55 60
 Asp Leu His Ser Tyr Glu Pro Thr Gln Lys Asp Ile Leu Ser Ala Ser
 65 70 75 80
 10 Lys Ser Asp Leu Phe Met Tyr Thr Gly Asp Asn Leu Asp Pro Val Ala
 85 90 95
 Lys Lys Val Ala Ser Thr Ile Lys Asp Lys Asp Lys Lys Leu Ser Leu
 100 105 110
 15 Glu Asp Lys Leu Asp Lys Ala Lys Leu Leu Thr Asp Gln His Glu His
 115 120 125
 Gly Glu Glu His Glu His Glu Gly His Asp His Glu Lys Glu Glu His
 130 135 140
 20 His His His His Gly Gly Tyr Asp Pro His Val Trp Leu Asp Pro Lys
 145 150 155 160
 Ile Asn Gln Thr Phe Ala Lys Glu Ile Lys Asp Glu Leu Val Lys Lys
 165 170 175
 25 Asp Pro Lys His Lys Asp Asp Tyr Glu Lys Asn Tyr Lys Lys Leu Asn
 180 185 190
 Asp Asp Leu Lys Lys Ile Asp Asn Asp Met Lys Gln Val Thr Lys Asp
 195 200 205
 30 Lys Gln Gly Asn Ala Val Phe Ile Ser His Glu Ser Ile Gly Tyr Leu
 210 215 220
 Ala Asp Cys Tyr Gly Phe Val Gln Lys Gly Ile Gln Asn Met Asn Ala
 225 230 235 240
 35 Glu Asp Pro Ser Gln Lys Glu Leu Thr Lys Ile Val Lys Glu Ile Arg
 245 250 255
 Asp Ser Asn Ala Lys Tyr Ile Leu Tyr Glu Asp Asn Val Ala Asn Lys
 260 265 270
 40 Val Thr Glu Thr Ile Arg Lys Glu Thr Asp Ala Lys Pro Leu Lys Phe
 275 280 285
 Tyr Asn Met Glu Ser Leu Asn Lys Glu Gln Gln Lys Lys Asp Asn Ile
 290 295 300
 45 Thr Tyr Gln Ser Leu Met Lys Ser Asn Ile Glu Asn Ile Gly Lys Ala
 305 310 315 320
 Leu Asp Ser Gly Val Lys Val Lys Asp Asp Lys Ala Glu Ser Lys His
 325 330 335
 Asp Lys Ala Ile Ser Asp Gly Tyr Phe Lys Asp Glu Gln Val Lys Asp
 340 345 350
 50 Arg Glu Leu Ser Asp Tyr Ala Gly Glu Trp Gln Ser Val Tyr Pro Tyr
 355 360 365
 Leu Lys Asp Gly Thr Leu Asp Glu Val Met Glu His Lys Ala Glu Asn
 370 375 380
 55 Asp Pro Lys Lys Ser Ala Lys Asp Leu Lys Ala Tyr Tyr Asp Lys Gly
 385 390 395 400

EP 2 510 947 B1

Tyr Lys Thr Asp Ile Thr Asn Ile Asp Ile Lys Gly Asn Glu Ile Thr
 405 410 415
 5 Phe Thr Lys Asp Gly Lys Lys His Thr Gly Lys Tyr Glu Tyr Asn Gly
 420 425 430
 Lys Lys Thr Leu Lys Tyr Pro Lys Gly Asn Arg Gly Val Arg Phe Met
 435 440 445
 10 Phe Lys Leu Val Asp Gly Asn Asp Lys Asp Leu Pro Lys Phe Ile Gln
 450 455 460
 Phe Ser Asp His Asn Ile Ala Pro Lys Lys Ala Glu His Phe His Ile
 465 470 475 480
 15 Phe Met Gly Asn Asp Asn Asp Ala Leu Leu Lys Glu Met Asp Asn Trp
 485 490 495
 Pro Thr Tyr Tyr Pro Ser Lys Leu Asn Lys Asp Gln Ile Lys Glu Glu
 500 505 510
 20 Met Leu Ala His
 515

<210> 95

<211> 309

<212> PRT

<213> Staphylococcus aureus

<400> 95

EP 2 510 947 B1

Met Ile Lys Asn Lys Ile Leu Thr Ala Thr Leu Ala Val Gly Leu Ile
 1 5 10 15
 Ala Pro Leu Ala Asn Pro Phe Ile Glu Ile Ser Lys Ala Glu Asn Lys
 5 20 25 30
 Ile Glu Asp Ile Gly Gln Gly Ala Glu Ile Ile Lys Arg Thr Gln Asp
 35 40 45
 Ile Thr Ser Lys Arg Leu Ala Ile Thr Gln Asn Ile Gln Phe Asp Phe
 10 50 55 60
 Val Lys Asp Lys Lys Tyr Asn Lys Asp Ala Leu Val Val Lys Met Gln
 65 70 75 80
 Gly Phe Ile Ser Ser Arg Thr Thr Tyr Ser Asp Leu Lys Lys Tyr Pro
 15 85 90 95
 Tyr Ile Lys Arg Met Ile Trp Pro Phe Gln Tyr Asn Ile Ser Leu Lys
 100 105 110
 Thr Lys Asp Ser Asn Val Asp Leu Ile Asn Tyr Leu Pro Lys Asn Lys
 20 115 120 125
 Ile Asp Ser Ala Asp Val Ser Gln Lys Leu Gly Tyr Asn Ile Gly Gly
 130 135 140
 Asn Phe Gln Ser Ala Pro Ser Ile Gly Gly Ser Gly Ser Phe Asn Tyr
 25 145 150 155 160
 Ser Lys Thr Ile Ser Tyr Asn Gln Lys Asn Tyr Val Thr Glu Val Glu
 165 170 175
 Ser Gln Asn Ser Lys Gly Val Lys Trp Gly Val Lys Ala Asn Ser Phe
 30 180 185 190
 Val Thr Pro Asn Gly Gln Val Ser Ala Tyr Asp Gln Tyr Leu Phe Ala
 195 200 205
 Gln Asp Pro Thr Gly Pro Ala Ala Arg Asp Tyr Phe Val Pro Asp Asn
 35
 210 215 220
 Gln Leu Pro Pro Leu Ile Gln Ser Gly Phe Asn Pro Ser Phe Ile Thr
 225 230 235 240
 Thr Leu Ser His Glu Arg Gly Lys Gly Asp Lys Ser Glu Phe Glu Ile
 245 250 255
 Thr Tyr Gly Arg Asn Met Asp Ala Thr Tyr Ala Tyr Val Thr Arg His
 260 265 270
 Arg Leu Ala Val Asp Arg Lys His Asp Ala Phe Lys Asn Arg Asn Val
 275 280 285
 Thr Val Lys Tyr Glu Val Asn Trp Lys Thr His Glu Val Lys Ile Lys
 290 295 300
 Ser Ile Thr Pro Lys
 305

<210> 96

<211> 532

<212> PRT

<213> Staphylococcus aureus

<400> 96

EP 2 510 947 B1

Met Arg Lys Leu Thr Lys Met Ser Ala Met Leu Leu Ala Ser Gly Leu
1 5 10 15
Ile Leu Thr Gly Cys Gly Gly Asn Lys Gly Leu Glu Glu Lys Lys Glu
5 20 25 30
Asn Lys Gln Leu Thr Tyr Thr Thr Val Lys Asp Ile Gly Asp Met Asn
35 40 45
Pro His Val Tyr Gly Gly Ser Met Ser Ala Glu Ser Met Ile Tyr Glu
10 50 55 60
Pro Leu Val Arg Asn Thr Lys Asp Gly Ile Lys Pro Leu Leu Ala Lys
65 70 75 80
Lys Trp Asp Val Ser Glu Asp Gly Lys Thr Tyr Thr Phe His Leu Arg
15 85 90 95
Asp Asp Val Lys Phe His Asp Gly Thr Pro Phe Asp Ala Asp Ala Val
100 105 110
Lys Lys Asn Ile Asp Ala Val Gln Glu Asn Lys Lys Leu His Ser Trp
20 115 120 125
Leu Lys Ile Ser Thr Leu Ile Asp Asn Val Lys Val Lys Asp Lys Tyr
130 135 140
Thr Val Glu Leu Asn Leu Lys Glu Ala Tyr Gln Pro Ala Leu Ala Glu
25 145 150 155 160
Leu Ala Met Pro Arg Pro Tyr Val Phe Val Ser Pro Lys Asp Phe Lys
165 170 175
Asn Gly Thr Thr Lys Asp Gly Val Lys Lys Phe Asp Gly Thr Gly Pro
30 180 185 190
Phe Lys Leu Gly Glu His Lys Lys Asp Glu Ser Ala Asp Phe Asn Lys
195 200 205
Asn Asp Gln Tyr Trp Gly Glu Lys Ser Lys Leu Asn Lys Val Gln Ala
35 210 215 220
Lys Val Met Pro Ala Gly Glu Thr Ala Phe Leu Ser Met Lys Lys Gly
225 230 235 240

EP 2 510 947 B1

Glu Thr Asn Phe Ala Phe Thr Asp Asp Arg Gly Thr Asp Ser Leu Asp
 245 250 255
 Lys Asp Ser Leu Lys Gln Leu Lys Asp Thr Gly Asp Tyr Gln Val Lys
 260 265 270
 Arg Ser Gln Pro Met Asn Thr Lys Met Leu Val Val Asn Ser Gly Lys
 275 280 285
 Lys Asp Asn Ala Val Ser Asp Lys Thr Val Arg Gln Ala Ile Gly His
 290 295 300
 Met Val Asn Arg Asp Lys Ile Ala Lys Glu Ile Leu Asp Gly Gln Glu
 305 310 315 320
 Lys Pro Ala Thr Gln Leu Phe Ala Lys Asn Val Thr Asp Ile Asn Phe
 325 330 335
 Asp Met Pro Thr Arg Lys Tyr Asp Leu Lys Lys Ala Glu Ser Leu Leu
 340 345 350
 Asp Glu Ala Gly Trp Lys Lys Gly Lys Asp Ser Asp Val Arg Gln Lys
 355 360 365
 Asp Gly Lys Asn Leu Glu Met Ala Met Tyr Tyr Asp Lys Gly Ser Ser
 370 375 380
 Ser Gln Lys Glu Gln Ala Glu Tyr Leu Gln Ala Glu Phe Lys Lys Met
 385 390 395 400
 Gly Ile Lys Leu Asn Ile Asn Gly Glu Thr Ser Asp Lys Ile Ala Glu
 405 410 415
 Arg Arg Thr Ser Gly Asp Tyr Asp Leu Met Phe Asn Gln Thr Trp Gly
 420 425 430
 Leu Leu Tyr Asp Pro Gln Ser Thr Ile Ala Ala Phe Lys Glu Lys Asn
 435 440 445
 Gly Tyr Glu Ser Ala Thr Ser Gly Ile Glu Asn Lys Asp Lys Ile Tyr
 450 455 460
 Asn Ser Ile Asp Asp Ala Phe Lys Ile Gln Asn Gly Lys Glu Arg Ser
 465 470 475 480
 Asp Ala Tyr Lys Asn Ile Leu Lys Gln Ile Asp Asp Glu Gly Ile Phe
 485 490 495
 Ile Pro Ile Ser His Gly Ser Met Thr Val Val Ala Pro Lys Asp Leu
 500 505 510
 Glu Lys Val Ser Phe Thr Gln Ser Gln Tyr Glu Leu Pro Phe Asn Glu
 515 520 525
 Met Gln Tyr Lys
 530

<210> 97

<211> 264

<212> PRT

<213> Staphylococcus aureus

<400> 97

EP 2 510 947 B1

Met Ile His Ser Lys Lys Leu Thr Leu Gly Ile Cys Leu Val Leu Leu
1 5 10 15
Ile Ile Leu Ile Val Gly Tyr Val Ile Met Thr Lys Thr Asn Gly Arg
5 20 25 30
Asn Ala Gln Ile Lys Asp Thr Phe Asn Gln Thr Leu Lys Leu Tyr Pro
35 40 45
Thr Lys Asn Leu Asp Asp Phe Tyr Asp Lys Glu Gly Phe Arg Asp Gln
10 50 55 60
Glu Phe Lys Lys Gly Asp Lys Gly Thr Trp Ile Val Asn Ser Glu Met
65 70 75 80
Val Ile Glu Pro Lys Gly Lys Asp Met Glu Thr Arg Gly Met Val Leu
15 85 90 95
Tyr Ile Asn Arg Asn Thr Arg Thr Thr Lys Gly Tyr Tyr Phe Ile Ser
100 105 110
Glu Met Thr Asp Asp Ser Asn Gly Arg Pro Lys Asp Asp Glu Lys Arg
20 115 120 125
Tyr Pro Val Lys Met Glu His Asn Lys Ile Ile Pro Thr Lys Pro Leu
130 135 140
Pro Asn Asp Lys Leu Lys Lys Glu Ile Glu Asn Phe Lys Phe Phe Val
25 145 150 155 160
Gln Tyr Gly Asn Phe Lys Asp Ile Asn Asp Tyr Lys Asp Gly Asp Ile
165 170 175
Ser Tyr Asn Pro Asn Val Pro Ser Tyr Ser Ala Lys Tyr Gln Leu Asn
30 180 185 190
Asn Asp Asp Tyr Asn Val Gln Gln Leu Arg Lys Arg Tyr Asp Ile Pro
195 200 205
Thr Lys Gln Ala Pro Lys Leu Leu Leu Lys Gly Asp Gly Asp Leu Lys
35 210 215 220
Gly Ser Ser Val Gly Ser Arg Ser Leu Glu Phe Thr Phe Val Glu Asn
225 230 235 240
Lys Glu Glu Asn Ile Tyr Phe Thr Asp Ser Val Gln Tyr Thr Pro Ser
40 245 250 255
Glu Asp Thr Arg Tyr Glu Ser Asn
260

<210> 98
<211> 261
<212> PRT
<213> Staphylococcus aureus

<400> 98

EP 2 510 947 B1

Met Ile His Ser Lys Lys Leu Thr Leu Gly Ile Cys Leu Val Leu Leu
 1 5 10 15
 Ile Ile Leu Ile Gly Gly Cys Val Ile Met Thr Lys Thr Asn Gly Arg
 5 20 25 30
 Asn Ala Gln Ile Lys Glu Asn Phe Asn Lys Thr Leu Ser Val Tyr Leu
 35 40 45
 Thr Lys Asn Leu Asp Asp Phe Tyr Asp Lys Glu Gly Phe Arg Asp Gln
 10 50 55 60
 Glu Phe Asp Lys Arg Asp Lys Gly Thr Trp Ile Ile Tyr Ser Glu Met
 65 70 75 80
 Val Ile Glu Pro Lys Gly Lys Asn Met Glu Ser Arg Gly Met Val Leu
 15 85 90 95
 Tyr Ile Asn Arg Asn Thr Arg Thr Thr Lys Gly Asn Phe Ile Val Thr
 100 105 110
 Glu Ile Thr Glu Asp Ser Lys Gly Tyr Ser Arg Ser Lys Glu Lys Lys
 20 115 120 125
 Tyr Pro Val Lys Met Glu Asn Asn Arg Ile Ile Pro Thr Lys Pro Ile
 130 135 140
 Pro Asp Asp Lys Leu Lys Lys Glu Ile Glu Asn Phe Lys Phe Phe Val
 25 145 150 155 160
 Gln Tyr Gly Asn Phe Lys Asp Phe Lys Asp Tyr Lys Asn Gly Asp Ile
 165 170 175
 Ser Tyr Asn Pro Asn Val Pro Ser Tyr Ser Ala Lys Tyr Gln Leu Asn
 30 180 185 190
 Asn Asp Asp Tyr Asn Val Gln Gln Leu Arg Lys Arg Tyr His Ile Pro
 195 200 205
 Thr Lys Gln Ala Pro Glu Leu Lys Leu Lys Gly Ser Gly Asn Leu Lys
 35 210 215 220
 Gly Ser Ser Val Gly Ser Lys Asp Leu Glu Phe Thr Phe Val Glu Asn
 225 230 235 240
 Gln Glu Glu Asn Ile Tyr Phe Ser Asp Ser Val Glu Phe Thr Pro Ser
 40 245 250 255
 Glu Asp Asp Lys Ser
 260

<210> 99
 <211> 498
 <212> PRT
 <213> Staphylococcus aureus

<400> 99

EP 2 510 947 B1

Met Ala Ala Leu Thr Leu Leu Ser Thr Leu Ser Pro Ala Ala Leu Ala
 1 5 10 15
 Ile Asp Ser Lys Asn Lys Pro Ala Asn Ser Asp Ile Lys Phe Glu Val
 5 20 25 30
 Thr Gln Lys Ser Asp Ala Val Lys Ala Leu Lys Glu Leu Pro Lys Ser
 35 40 45
 Glu Asn Val Lys Asn Ile Tyr Gln Asp Tyr Ala Val Thr Asp Val Lys
 10 50 55 60
 Thr Asp Lys Lys Gly Phe Thr His Tyr Thr Leu Gln Pro Ser Val Asp
 65 70 75 80
 Gly Val His Ala Pro Asp Lys Glu Val Lys Val His Ala Asp Lys Ser
 15 85 90 95
 Gly Lys Val Val Leu Ile Asn Gly Asp Thr Asp Ala Lys Lys Val Lys
 100 105 110
 Pro Thr Asn Lys Val Thr Leu Ser Lys Asp Asp Ala Ala Asp Lys Ala
 20 115 120 125
 Phe Lys Ala Val Lys Ile Asp Lys Asn Lys Ala Lys Asn Leu Lys Asp
 130 135 140
 Lys Val Ile Lys Glu Asn Lys Val Glu Ile Asp Gly Asp Ser Asn Lys
 25 145 150 155 160
 Tyr Val Tyr Asn Val Glu Leu Ile Thr Val Thr Pro Glu Ile Ser His
 165 170 175

EP 2 510 947 B1

Trp Lys Val Lys Ile Asp Ala Gln Thr Gly Glu Ile Leu Glu Lys Met
 180 185 190
 Asn Leu Val Lys Glu Ala Ala Glu Thr Gly Lys Gly Lys Gly Val Leu
 195 200 205
 Gly Asp Thr Lys Asp Ile Asn Ile Asn Ser Ile Asp Gly Gly Phe Ser
 210 215 220
 Leu Glu Asp Leu Thr His Gln Gly Lys Leu Ser Ala Phe Ser Phe Asn
 225 230 235 240
 Asp Gln Thr Gly Gln Ala Thr Leu Ile Thr Asn Glu Asp Glu Asn Phe
 245 250 255
 Val Lys Asp Glu Gln Arg Ala Gly Val Asp Ala Asn Tyr Tyr Ala Lys
 260 265 270
 Gln Thr Tyr Asp Tyr Tyr Lys Asp Thr Phe Gly Arg Glu Ser Tyr Asp
 275 280 285
 Asn Gln Gly Ser Pro Ile Val Ser Leu Thr His Val Asn Asn Tyr Gly
 290 295 300
 Gly Gln Asp Asn Arg Asn Asn Ala Ala Trp Ile Gly Asp Lys Met Ile
 305 310 315 320
 Tyr Gly Asp Gly Asp Gly Arg Thr Phe Thr Ser Leu Ser Gly Ala Asn
 325 330 335
 Asp Val Val Ala His Glu Leu Thr His Gly Val Thr Gln Glu Thr Ala
 340 345 350
 Asn Leu Glu Tyr Lys Asp Gln Ser Gly Ala Leu Asn Glu Ser Phe Ser
 355 360 365
 Asp Val Phe Gly Tyr Phe Val Asp Asp Glu Asp Phe Leu Met Gly Glu
 370 375 380
 Asp Val Tyr Thr Pro Gly Lys Glu Gly Asp Ala Leu Arg Ser Met Ser
 385 390 395 400
 Asn Pro Glu Gln Phe Gly Gln Pro Ala His Met Lys Asp Tyr Val Phe
 405 410 415
 Thr Glu Lys Asp Asn Gly Gly Val His Thr Asn Ser Gly Ile Pro Asn
 420 425 430
 Lys Ala Ala Tyr Asn Val Ile Gln Ala Ile Gly Lys Ser Lys Ser Glu
 435 440 445
 Gln Ile Tyr Tyr Arg Ala Leu Thr Glu Tyr Leu Thr Ser Asn Ser Asn
 450 455 460
 Phe Lys Asp Cys Lys Asp Ala Leu Tyr Gln Ala Ala Lys Asp Leu Tyr
 465 470 475 480
 Asp Glu Gln Thr Ala Glu Gln Val Tyr Glu Ala Trp Asn Glu Val Gly
 485 490 495
 Val Glu

<210> 100

<211> 680

<212> PRT

<213> Staphylococcus aureus

<400> 100

EP 2 510 947 B1

1 Met Lys Ser Gln Asn Lys Tyr Ser Ile Arg Lys Phe Ser Val Gly Ala
 5 Ser Ser Ile Leu Ile Ala Thr Leu Leu Phe Leu Ser Gly Gly Gln Ala
 10 Gln Ala Ala Glu Lys Gln Val Asn Met Gly Asn Ser Gln Glu Asp Thr
 15 Val Thr Ala Gln Ser Ile Gly Asp Gln Gln Thr Arg Glu Asn Ala Asn
 20 Tyr Gln Arg Glu Asn Gly Val Asp Glu Gln Gln His Thr Glu Asn Leu
 25 Thr Lys Asn Leu His Asn Asp Lys Thr Ile Ser Glu Glu Asn His Arg
 30 Lys Thr Asp Asp Leu Asn Lys Asp Gln Leu Lys Asp Asp Lys Lys Ser
 35 Ser Leu Asn Asn Lys Asn Ile Gln Arg Asp Thr Thr Lys Asn Asn Asn
 40 Ala Asn Pro Ser Asp Val Asn Gln Gly Leu Glu Gln Ala Ile Asn Asp
 45 Gly Lys Gln Ser Lys Val Ala Ser Gln Gln Gln Ser Lys Glu Ala Asp
 50 Asn Ser Gln Asp Ser Asn Ala Asn Asn Asn Leu Pro Ser Gln Ser Arg
 55 Ile Lys Glu Ala Pro Ser Leu Asn Lys Leu Asp Gln Thr Ser Gln Arg
 60 Glu Ile Val Asn Glu Thr Glu Ile Glu Lys Val Gln Pro Gln Gln Asn
 65 Asn Gln Ala Asn Asp Lys Ile Thr Asn Tyr Asn Phe Asn Asn Glu Gln
 70 Glu Val Lys Pro Gln Lys Asp Glu Lys Thr Leu Ser Val Ser Asp Leu
 75 Lys Asn Asn Gln Lys Ser Pro Val Glu Pro Thr Lys Asp Asn Asp Lys
 80 Lys Asn Gly Leu Asn Leu Leu Lys Ser Ser Ala Val Ala Thr Leu Pro
 85 Asn Lys Gly Thr Lys Glu Leu Thr Ala Lys Ala Lys Asp Asp Gln Thr
 90 Asn Lys Val Ala Lys Gln Gly Gln Tyr Lys Asn Gln Asp Pro Ile Val
 95 Leu Val His Gly Phe Asn Gly Phe Thr Asp Asp Ile Asn Pro Ser Val
 100 Leu Ala His Tyr Trp Gly Gly Asn Lys Met Asn Ile Arg Gln Asp Leu
 105 Glu Glu Asn Gly Tyr Lys Ala Tyr Glu Ala Ser Ile Ser Ala Phe Gly
 110 Ser Asn Tyr Asp Arg Ala Val Glu Leu Tyr Tyr Tyr Ile Lys Gly Gly
 115 Arg Val Asp Tyr Gly Ala Ala His Ala Ala Lys Tyr Gly His Glu Arg

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	370					375						380					
	Tyr	Gly	Lys	Thr	Tyr	Glu	Gly	Ile	Tyr	Lys	Asp	Trp	Lys	Pro	Gly	Gln	
	385					390					395					400	
5	Lys	Val	His	Leu	Val	Gly	His	Ser	Met	Gly	Gly	Gln	Thr	Ile	Arg	Gln	
					405					410					415		
	Leu	Glu	Glu	Leu	Leu	Arg	Asn	Gly	Asn	Arg	Glu	Glu	Ile	Glu	Tyr	Gln	
				420					425					430			
10	Lys	Lys	His	Gly	Gly	Glu	Ile	Ser	Pro	Leu	Phe	Lys	Gly	Asn	His	Asp	
			435					440					445				
	Asn	Met	Ile	Ser	Ser	Ile	Thr	Thr	Leu	Gly	Thr	Pro	His	Asn	Gly	Thr	
	450						455					460					
15	His	Ala	Ser	Asp	Leu	Ala	Gly	Asn	Glu	Ala	Leu	Val	Arg	Gln	Ile	Val	
	465					470					475					480	
	Phe	Asp	Ile	Gly	Lys	Met	Phe	Gly	Asn	Lys	Asn	Ser	Arg	Val	Asp	Phe	
					485					490					495		
20	Gly	Leu	Ala	Gln	Trp	Gly	Leu	Lys	Gln	Lys	Pro	Asn	Glu	Ser	Tyr	Ile	
				500					505					510			
	Asp	Tyr	Val	Lys	Arg	Val	Lys	Gln	Ser	Asn	Leu	Trp	Lys	Ser	Lys	Asp	
			515					520					525				
25	Asn	Gly	Phe	Tyr	Asp	Leu	Thr	Arg	Glu	Gly	Ala	Thr	Asp	Leu	Asn	Arg	
	530						535					540					
	Lys	Thr	Ser	Leu	Asn	Pro	Asn	Ile	Val	Tyr	Lys	Thr	Tyr	Thr	Gly	Glu	
	545				550						555					560	
30	Ala	Thr	His	Lys	Ala	Leu	Asn	Ser	Asp	Arg	Gln	Lys	Ala	Asp	Leu	Asn	
					565					570					575		
	Met	Phe	Phe	Pro	Phe	Val	Ile	Thr	Gly	Asn	Leu	Ile	Gly	Lys	Ala	Thr	
				580					585					590			
35	Glu	Lys	Glu	Trp	Arg	Glu	Asn	Asp	Gly	Leu	Val	Ser	Val	Ile	Ser	Ser	
			595					600					605				
	Gln	His	Pro	Phe	Asn	Gln	Ala	Tyr	Thr	Lys	Ala	Thr	Asp	Lys	Ile	Gln	
		610					615					620					
40	Lys	Gly	Ile	Trp	Gln	Val	Thr	Pro	Thr	Lys	His	Asp	Trp	Asp	His	Val	
	625				630						635					640	
	Asp	Phe	Val	Gly	Gln	Asp	Ser	Ser	Asp	Thr	Val	Arg	Thr	Arg	Glu	Glu	
					645					650					655		
45	Leu	Gln	Asp	Phe	Trp	His	His	Leu	Ala	Asp	Asp	Leu	Val	Lys	Thr	Glu	
				660					665					670			
	Lys	Leu	Thr	Asp	Thr	Lys	Gln	Ala									
				675				680									

50 <210> 101
 <211> 328
 <212> PRT
 <213> Staphylococcus aureus
 55 <400> 101

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Met Lys Lys Cys Ile Lys Thr Leu Phe Leu Ser Ile Ile Leu Val Val
1 5 10 15
Met Ser Gly Trp Tyr His Ser Ala His Ala Ser Asp Ser Leu Ser Lys
5 20 25 30
Ser Pro Glu Asn Trp Met Ser Lys Leu Asp Asp Gly Lys His Leu Thr
35 40 45
Glu Ile Asn Ile Pro Gly Ser His Asp Ser Gly Ser Phe Thr Leu Lys
10 50 55 60
Asp Pro Val Lys Ser Val Trp Ala Lys Thr Gln Asp Lys Asp Tyr Leu
65 70 75 80
Thr Gln Met Lys Ser Gly Val Arg Phe Phe Asp Ile Arg Gly Arg Ala
15 85 90 95
Ser Ala Asp Asn Met Ile Ser Val His His Gly Met Val Tyr Leu His
100 105 110
His Glu Leu Gly Lys Phe Leu Asp Asp Ala Lys Tyr Tyr Leu Ser Ala
20 115 120 125
Tyr Pro Asn Glu Thr Ile Val Met Ser Met Lys Lys Asp Tyr Asp Ser
130 135 140
Asp Ser Lys Val Thr Lys Thr Phe Glu Glu Ile Phe Arg Glu Tyr Tyr
25 145 150 155 160
Tyr Asn Asn Pro Gln Tyr Gln Asn Leu Phe Tyr Thr Gly Ser Asn Ala
165 170 175
Asn Pro Thr Leu Lys Glu Thr Lys Gly Lys Ile Val Leu Phe Asn Arg
30 180 185 190
Met Gly Gly Thr Tyr Ile Lys Ser Gly Tyr Gly Ala Asp Thr Ser Gly
195 200 205
Ile Gln Trp Ala Asp Asn Ala Thr Phe Glu Thr Lys Ile Asn Asn Gly
35 210 215 220
Ser Leu Asn Leu Lys Val Gln Asp Glu Tyr Lys Asp Tyr Tyr Asp Lys
225 230 235 240
Lys Val Glu Ala Val Lys Asn Leu Leu Ala Lys Ala Lys Thr Asp Ser
40 245 250 255
Asn Lys Asp Asn Val Tyr Val Asn Phe Leu Ser Val Ala Ser Gly Gly
260 265 270
Ser Ala Phe Asn Ser Thr Tyr Asn Tyr Ala Ser His Ile Asn Pro Glu
45 275 280 285
Ile Ala Lys Thr Ile Lys Ala Asn Gly Lys Ala Arg Thr Gly Trp Leu
290 295 300
Ile Val Asp Tyr Ala Gly Tyr Thr Trp Pro Gly Tyr Asp Asp Ile Val
50 305 310 315 320
Ser Glu Ile Ile Asp Ser Asn Lys
325

<210> 102

55 <211> 257

<212> PRT

<213> Staphylococcus aureus

<400> 102

5 Met Lys Ala His Lys Ile Phe Trp Leu Asn Leu Ala Ala Ile Ile Ile
 1 5 10 15
 Ile Ser Ile Val Val Ser Gly Asp Met Phe Leu Ala Met Lys Trp Glu
 20 25 30
 10 Gln Ile His Leu Lys Asp Gly Leu Lys Lys Val Leu Ser Thr Tyr Pro
 35 40 45
 Ile Lys Asn Leu Glu Thr Leu Tyr Glu Ile Asp Gly His Asp Asn Pro
 50 55 60
 15 His Tyr Glu Asn Asn Asp Gln Asp Thr Trp Tyr Ile Glu Ser Ser Tyr
 65 70 75 80
 Ser Val Val Gly Ser Asp Glu Leu Leu Lys Glu Asp Arg Met Leu Leu
 85 90 95
 20 Lys Val Asp Lys Asn Thr His Lys Ile Thr Gly Glu Tyr Asp Thr Thr
 100 105 110
 Thr Asn Asp Arg Lys Asn Ala Thr Asp Ser Thr Tyr Lys Ser Tyr Pro
 115 120 125
 25 Val Lys Val Val Asn Asn Lys Ile Val Phe Thr Lys Asp Val Lys Asp
 130 135 140
 Pro Ala Leu Lys Gln Lys Ile Glu Asn Asn Gln Phe Leu Ile Gln Ser
 145 150 155 160
 30 Gly Asp Leu Thr Ser Ile Leu Asn Ser Asn Asp Leu Lys Val Thr His
 165 170 175
 Asp Pro Thr Thr Asp Tyr Tyr Asn Leu Ser Gly Lys Leu Ser Asn Asp
 180 185 190
 35 Asn Pro Asn Val Lys Gln Leu Lys Arg Arg Tyr Asn Ile Pro Lys Asn
 195 200 205
 Ala Ser Thr Lys Val Glu Leu Lys Gly Met Ser Asp Leu Lys Gly Asn
 210 215 220
 40 Asn His Gln Asp Gln Lys Leu Tyr Phe Tyr Phe Ser Ser Pro Gly Lys
 225 230 235 240
 Asp Gln Ile Ile Tyr Lys Glu Ser Leu Thr Tyr Asn Lys Ile Ser Glu
 245 250 255

His

<210> 103

<211> 423

<212> PRT

<213> Staphylococcus aureus

<400> 103

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	Met	Ser	Lys	Ile	Leu	Lys	Cys	Ile	Thr	Leu	Ala	Val	Val	Met	Leu	Leu
	1				5					10					15	
	Ile	Val	Thr	Ala	Cys	Gly	Pro	Asn	Arg	Ser	Lys	Glu	Asp	Ile	Asp	Lys
5				20					25					30		
	Ala	Leu	Asn	Lys	Asp	Asn	Ser	Lys	Asp	Lys	Pro	Asn	Gln	Leu	Thr	Met
			35					40					45			
	Trp	Val	Asp	Gly	Asp	Lys	Gln	Met	Ala	Phe	Tyr	Lys	Lys	Ile	Thr	Asp
10		50					55					60				
	Gln	Tyr	Thr	Lys	Lys	Thr	Gly	Ile	Lys	Val	Lys	Leu	Val	Asn	Ile	Gly
	65					70					75					80
	Gln	Asn	Asp	Gln	Leu	Glu	Asn	Ile	Ser	Leu	Asp	Ala	Pro	Ala	Gly	Lys
15					85					90					95	
	Gly	Pro	Asp	Ile	Phe	Phe	Leu	Ala	His	Asp	Asn	Thr	Gly	Ser	Ala	Tyr

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	100		105		110
	Leu Gln Gly 115	Leu Ala Ala Glu Ile 120	Lys Leu Ser Lys Asp 125	Glu Leu Lys	
5	Gly Phe Asn 130	Lys Gln Ala Leu 135	Ala Met Asn Tyr 140	Asp Asn Lys Gln	
	Leu Ala Leu Pro Ala Ile 150	Val Glu Thr Thr Ala 155	Leu Phe Tyr Asn Lys 160		
10	Lys Leu Val Lys 165	Asn Ala Pro Gln Thr Leu 170	Glu Glu Val Glu Ala Asn 175		
	Ala Ala Lys Leu 180	Thr Asp Ser Lys Lys 185	Gln Tyr Gly Met Leu Phe 190		
15	Asp Ala Lys 195	Asn Phe Tyr Phe Asn 200	Tyr Pro Phe Leu Phe Gly Asn Asp 205		
	Asp Tyr Ile Phe Lys Lys Asn 215	Gly Ser Glu Tyr Asp Ile His Gln Leu 220			
20	Gly Leu Asn Ser Lys His 230	Val Val Lys Asn Ala Glu Arg Leu Gln Lys 240			
	Trp Tyr Asp Lys Gly Tyr Leu Pro Lys Ala Ala Thr His Asp Val Met 255				
25	Ile Gly Leu Phe Lys Glu Gly Lys Val 265	Gly Gln Phe Val Thr Gly Pro 270			
	Trp Asn Ile Asn Glu Tyr Gln Glu Thr Phe Gly Lys Asp Leu Gly Val 285				
30	Thr Thr Leu Pro Thr Asp Gly Gly Lys Pro Met Lys Pro Phe Leu Gly 300				
	Val Arg Gly Trp Tyr Leu Ser Glu Tyr Ser Lys His Lys Tyr Trp Ala 320				
35	Lys Asp Leu Met Leu Tyr Ile Thr Ser Lys Asp Thr Leu Gln Lys Tyr 335				
	Thr Asp Glu Met Ser Glu Ile Thr Gly Arg Val Asp Val Lys Ser Ser 350				
40	Asn Pro Asn Leu Lys Val Phe Glu Lys Gln Ala Arg His Ala Glu Pro 365				
	Met Pro Asn Ile Pro Glu Met Arg Gln Val Trp Glu Pro Met Gly Asn 380				
45	Ala Ser Ile Phe Ile Ser Asn Gly Lys Asn Pro Lys Gln Ala Leu Asp 400				
	Glu Ala Thr Asn Asp Ile Thr Gln Asn Ile Lys Ile Leu His Pro Ser 415				
50	Gln Asn Asp Lys Lys Gly Asp 420				

<210> 104

<211> 560

<212> PRT

55 <213> Staphylococcus aureus

<400> 104

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

5

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Gln Ala Ala Glu Gln Gln Ser Ile Ser Asp Val Tyr Ser Val Ile Thr
 20 25 30
 Asp Ala Lys Ser Ala Leu Ser Asn Asn Ser Ile Ser Asn Asp Asn Lys
 5 35 40 45
 Gln Lys Ala Ile Glu Gln Val Val Ser Ala Val Lys Lys Leu Ser Leu
 50 55 60
 Glu Asp Asn Ser Glu Ser Asn Ala Val Lys Ser Asp Val Arg Lys Leu
 10 65 70 75 80
 Glu Asp Ala Lys Ala Asn Asp Asn Gln Lys Asp Thr Leu Ser Gln Leu
 85 90 95
 Thr Lys Ser Leu Ile Ala Tyr Glu Glu Lys Leu Ala Ser Lys Asp Ala
 15 100 105 110
 Gly Ser Lys Ile Lys Leu Leu Gln Gln Gln Val Asp Ala Lys Asp Ala
 115 120 125
 Ala Met Thr Lys Ala Ile Lys Asp Lys Asn Lys Ala Glu Leu Glu Ser
 20 130 135 140
 Leu Asn Asn Ser Leu Asn Gln Ile Trp Thr Ser Asn Glu Thr Val Ile
 145 150 155 160
 Arg Asn Tyr Asp Ala Asn Gln Tyr Gly Gln Ile Glu Val Ala Leu Leu
 25 165 170 175
 Gln Leu Arg Ile Ala Ile His Lys Ser Pro Leu Asp Thr Ala Lys Val
 180 185 190
 Ser His Ala Trp Thr Thr Phe Lys Ser Asn Ile Asp His Val Asp Lys
 30 195 200 205
 Lys Ser Asn Thr Ser Ala Asn Asp Gln Tyr His Val Ser Gln Leu Asn
 210 215 220
 Asp Ala Leu Glu Lys Ala Ile Lys Ala Ile Asp Asp Asn Gln Leu Ser
 35 225 230 235 240
 Asp Ala Asp Ala Ala Leu Thr His Phe Ile Glu Thr Trp Pro Tyr Val
 245 250 255
 Glu Gly Gln Ile Gln Thr Lys Asp Gly Ala Leu Tyr Thr Lys Ile Glu
 40 260 265 270
 Asp Lys Ile Pro Tyr Tyr Gln Ser Val Leu Asp Glu His Asn Lys Ala
 275 280 285
 His Val Lys Asp Gly Leu Val Asp Leu Asn Asn Gln Ile Lys Glu Val
 290 295 300
 Val Gly His Ser Tyr Ser Phe Val Asp Val Met Ile Ile Phe Leu Arg
 45 305 310 315 320
 Glu Gly Leu Glu Val Leu Leu Ile Val Met Thr Leu Thr Thr Met Thr
 325 330 335
 Arg Asn Val Lys Asp Lys Lys Gly Thr Ala Ser Val Ile Gly Gly Ala
 50 340 345 350
 Ile Ala Gly Leu Val Leu Ser Ile Ile Leu Ala Ile Thr Phe Val Glu
 355 360 365
 Thr Leu Gly Asn Ser Gly Ile Leu Arg Glu Ser Met Glu Ala Gly Leu
 55 370 375 380

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Gly Ile Val Ala Val Ile Leu Met Phe Ile Val Gly Val Trp Met His
 385 390 395 400
 Lys Arg Ser Asn Ala Lys Arg Trp Asn Asp Met Ile Lys Asn Met Tyr
 405 410 415
 Ala Asn Ala Ile Ser Asn Gly Asn Leu Val Leu Leu Ala Thr Ile Gly
 420 425 430
 Leu Ile Ser Val Leu Arg Glu Gly Val Glu Val Ile Ile Phe Tyr Met
 435 440 445
 Gly Met Ile Gly Glu Leu Ala Thr Lys Asp Phe Ile Ile Gly Ile Ala
 450 455 460
 Leu Ala Ile Val Ile Leu Ile Ile Phe Ala Leu Leu Phe Arg Phe Ile
 465 470 475 480
 Val Lys Leu Ile Pro Ile Phe Tyr Ile Phe Arg Val Leu Ser Ile Phe
 485 490 495
 Ile Phe Ile Met Gly Phe Lys Met Leu Gly Val Ser Ile Gln Lys Leu
 500 505 510
 Gln Leu Leu Gly Ala Met Pro Arg His Val Ile Glu Gly Phe Pro Thr
 515 520 525
 Ile Asn Trp Leu Gly Phe Tyr Pro Ser Tyr Glu Pro Leu Ile Ala Gln
 530 535 540
 Gly Ala Tyr Ile Met Val Val Ala Ile Leu Ile Phe Lys Phe Lys Lys
 545 550 555 560

<210> 105

<211> 334

<212> PRT

<213> Staphylococcus aureus

<400> 105

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Met Gln Lys Lys Val Ile Ala Ala Ile Ile Gly Thr Ser Ala Ile Ser
 1 5 10 15
 Ala Val Ala Ala Thr Gln Ala Asn Ala Ala Thr Thr His Thr Val Lys
 5 20 25 30
 Pro Gly Glu Ser Val Trp Ala Ile Ser Asn Lys Tyr Gly Ile Ser Ile
 35 40 45
 Ala Lys Leu Lys Ser Leu Asn Asn Leu Thr Ser Asn Leu Ile Phe Pro
 10 50 55 60
 Asn Gln Val Leu Lys Val Ser Gly Ser Ser Asn Ser Thr Ser Asn Ser
 65 70 75 80
 Ser Arg Pro Ser Thr Asn Ser Gly Gly Gly Ser Tyr Tyr Thr Val Gln
 15 85 90 95
 Ala Gly Asp Ser Leu Ser Leu Ile Ala Ser Lys Tyr Gly Thr Thr Tyr
 100 105 110
 Gln Asn Ile Met Arg Leu Asn Gly Leu Asn Asn Phe Phe Ile Tyr Pro
 115 120 125
 Gly Gln Lys Leu Lys Val Ser Gly Thr Ala Ser Ser Asn Ala Ala
 130 135 140
 Ser Asn Ser Ser Arg Pro Ser Thr Asn Ser Gly Gly Gly Ser Tyr Tyr
 145 150 155 160
 Thr Val Gln Ala Gly Asp Ser Leu Ser Leu Ile Ala Ser Lys Tyr Gly
 165 170 175
 Thr Thr Tyr Gln Lys Ile Met Ser Leu Asn Gly Leu Asn Asn Phe Phe
 180 185 190
 Ile Tyr Pro Gly Gln Lys Leu Lys Val Thr Gly Asn Ala Ser Thr Asn
 195 200 205
 Ser Gly Ser Ala Thr Thr Thr Asn Arg Gly Tyr Asn Thr Pro Val Phe
 210 215 220
 Ser His Gln Asn Leu Tyr Thr Trp Gly Gln Cys Thr Tyr His Val Phe
 225 230 235 240
 Asn Arg Arg Ala Glu Ile Gly Lys Gly Ile Ser Thr Tyr Trp Trp Asn
 245 250 255
 Ala Asn Asn Trp Asp Asn Ala Ala Ala Ala Asp Gly Tyr Thr Ile Asp
 260 265 270
 Asn Arg Pro Thr Val Gly Ser Ile Ala Gln Thr Asp Val Gly Tyr Tyr
 275 280 285
 Gly His Val Met Phe Val Glu Arg Val Asn Asn Asp Gly Ser Ile Leu
 290 295 300
 Val Ser Glu Met Asn Tyr Ser Ala Ala Pro Gly Ile Leu Thr Tyr Arg
 305 310 315 320
 Thr Val Pro Ala Tyr Gln Val Asn Asn Tyr Arg Tyr Ile His
 325 330

<210> 106

<211> 279

<212> PRT

<213> Staphylococcus aureus

<400> 106

5 Met Lys Lys Ser Leu Thr Val Thr Val Ser Ser Val Leu Ala Phe Leu
 1 5 10
 Ala Leu Asn Asn Ala Ala His Ala Gln Gln His Gly Thr Gln Val Lys
 20 25 30
 10 Thr Pro Val Gln His Asn Tyr Val Ser Asn Val Gln Ala Gln Thr Gln
 35 40 45
 Ser Pro Thr Thr Tyr Thr Val Val Ala Gly Asp Ser Leu Tyr Lys Ile
 50 55 60
 15 Ala Leu Glu His His Leu Thr Leu Asn Gln Leu Tyr Ser Tyr Asn Pro
 65 70 75 80
 Gly Val Thr Pro Leu Ile Phe Pro Gly Asp Val Ile Ser Leu Val Pro
 85 90 95
 20 Gln Asn Lys Val Lys Gln Thr Lys Ala Val Lys Ser Pro Val Arg Lys
 100 105 110
 Ala Ser Gln Ala Lys Lys Val Val Lys Gln Pro Val Gln Gln Ala Ser
 115 120 125
 25 Lys Lys Val Val Val Lys Gln Ala Pro Lys Gln Ala Val Thr Lys Thr
 130 135 140
 Val Asn Val Ala Tyr Lys Pro Ala Gln Val Gln Lys Ser Val Pro Thr
 145 150 155 160
 30 Val Pro Val Ala His Asn Tyr Asn Lys Ser Val Ala Asn Arg Gly Asn
 165 170 175
 Leu Tyr Ala Tyr Gly Asn Cys Thr Tyr Tyr Ala Phe Asp Arg Arg Ala
 180 185 190
 35 Gln Leu Gly Arg Ser Ile Gly Ser Leu Trp Gly Asn Ala Asn Asn Trp
 195 200 205
 Asn Tyr Ala Ala Lys Val Ala Gly Phe Lys Val Asp Lys Thr Pro Glu
 210 215 220
 40 Val Gly Ala Ile Phe Gln Thr Ala Ala Gly Pro Tyr Gly His Val Gly
 225 230 235 240
 Val Val Glu Ser Val Asn Pro Asn Gly Thr Ile Thr Val Ser Glu Met
 245 250 255
 45 Asn Tyr Ala Gly Phe Asn Val Lys Ser Ser Arg Thr Ile Leu Asn Pro
 260 265 270
 Gly Lys Tyr Asn Tyr Ile His
 275

<210> 107

50 <211> 346

<212> PRT

<213> Staphylococcus aureus

<400> 107

55

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1 Met Ile Ile Ala 5 Ile Ile Ile Leu Ile Phe 10 Ile Ser Phe Phe Phe Ser
 5 Gly Ser Glu Thr 20 Ala Leu Thr Ala 25 Asn Lys Thr Lys 30 Phe Lys Thr
 Glu Ala 35 Asp Lys Gly Asp Lys 40 Lys Ala Lys Gly Ile 45 Val Lys Leu Leu
 10 Glu Lys 50 Pro Ser Glu Phe 55 Ile Thr Thr Ile Leu 60 Gly Asn Asn Val
 Ala Asn Ile Leu Leu 70 Pro Thr Leu Val Thr 75 Ile Met Ala Leu Arg Trp 80
 15 Gly Ile Ser Val 85 Gly Ile Ala Ser Ala 90 Val Leu Thr Val Val 95 Ile Ile
 Leu Ile Ser 100 Glu Val Ile Pro Lys 105 Val Ala Ala Thr Phe 110 Pro Asp
 20 Lys Ile Thr 115 Arg Leu Val Tyr Pro 120 Ile Ile Asn Ile Cys 125 Val Ile Val
 Phe Arg 130 Pro Ile Thr Leu 135 Leu Asn Lys Leu Thr 140 Asp Ser Ile Asn
 25 Arg Ser Leu Ser Lys 150 Gly Gln Pro Gln Glu 155 His Gln Phe Ser Lys Glu 160
 Glu Phe Lys Thr 165 Met Leu Ala Ile Ala 170 Gly His Glu Gly Ala 175 Leu Asn
 30 Glu Ile Glu Thr 180 Ser Arg Leu Glu 185 Gly Val Ile Asn Phe 190 Glu Asn Leu
 Lys Val Lys 195 Asp Val Asp Thr Thr 200 Pro Arg Ile Asn Val 205 Thr Ala Phe
 35 Ala Ser 210 Asn Ala Thr Tyr Glu 215 Glu Val Tyr Glu Thr 220 Val Met Asn Lys
 Pro Tyr Thr Arg Tyr 230 Val Tyr Glu Gly 235 Asp Ile Asp Asn Ile Ile 240
 40 Gly Val Phe His Ser 245 Lys Tyr Leu Leu 250 Ala Trp Ser Asn Lys Lys Glu 255
 Asn Gln Ile Thr 260 Asn Tyr Ser Ala 265 Lys Pro Leu Phe Val 270 Asn Glu His
 45 Asn Lys Ala 275 Glu Trp Val Leu Arg 280 Lys Met Thr Ile Ser 285 Arg Lys His
 Leu Ala 290 Ile Val Leu Asp Glu 295 Phe Gly Gly Thr Glu 300 Ala Ile Val Ser
 50 His Glu Asp Leu Ile 310 Glu Glu Leu Leu Gly 315 Met Glu Ile Glu Asp Glu 320
 Met Asp Lys Lys 325 Glu Lys Glu Lys Leu Ser 330 Gln Gln Gln Ile Gln 335 Phe
 55 Gln Gln Arg Lys 340 Asn Arg Asn Val Ser 345 Ile

<210> 108

<211> 391

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<212> PRT

<213> Staphylococcus aureus

<400> 108

5

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

10

Ile Val Phe Leu Leu Leu Pro Ala Ser Trp Phe Thr Gly Leu Val Asn
20 25 30

Glu Lys Thr Val Glu Asp Asn Arg Thr Ser Leu Thr Asp Gln Val Leu
35 40 45

15

Lys Gly Thr Leu Ile Gln Asp Lys Leu Tyr Glu Ser Asn Lys Tyr Tyr
50 55 60

Pro Ile Tyr Gly Ser Ser Glu Leu Gly Lys Asp Pro Phe Asn Pro
65 70 75 80

20

Ala Ile Ala Leu Asn Lys His Asn Ala Asn Lys Lys Ala Phe Leu Leu
85 90 95

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

25

Gln Tyr Asp Lys Leu Lys Gly Lys Lys Leu Thr Phe Ile Ile Ser Pro
115 120 125

Gln Trp Phe Thr Asn His Gly Leu Thr Asn Gln Asn Phe Asp Ala Arg
130 135 140

30

Met Ser Gln Thr Gln Ile Asn Gln Met Phe Gln Gln Lys Asn Met Ser
145 150 155 160

Thr Glu Leu Lys Arg Arg Tyr Ala Gln Arg Leu Leu Gln Phe Pro His
165 170 175

Val His Asn Lys Glu Tyr Leu Lys Ser Tyr Ala Lys Asn Pro Lys Glu
180 185 190

35

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

Ile Glu Ala Ile Lys Ser Leu Phe Ala Met Asp Lys Ser Pro Leu Glu

40

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	210		215		220											
	His	Val	Lys	Pro	Ala	Thr	Lys	Pro	Asp	Ala	Ser	Trp	Asp	Glu	Met	Lys
5	225					230					235					240
	Gln	Lys	Ala	Val	Glu	Ile	Gly	Lys	Ala	Asp	Thr	Thr	Ser	Asn	Lys	Phe
					245					250					255	
	Gly	Ile	Arg	Asp	Gln	Tyr	Trp	Lys	Leu	Ile	Gln	Glu	Ser	Lys	Arg	Lys
				260					265					270		
10	Val	Arg	Arg	Asp	Tyr	Glu	Phe	Asn	Val	Asn	Ser	Pro	Glu	Phe	Gln	Asp
			275					280					285			
	Leu	Glu	Leu	Leu	Val	Lys	Thr	Met	Arg	Ala	Ala	Gly	Ala	Asp	Val	Gln
	290						295					300				
15	Tyr	Val	Ser	Ile	Pro	Ser	Asn	Gly	Val	Trp	Tyr	Asp	His	Ile	Gly	Ile
	305					310					315					320
	Asp	Lys	Glu	Arg	Arg	Gln	Ala	Val	Tyr	Lys	Lys	Ile	His	Ser	Thr	Val
					325					330					335	
20	Val	Asp	Asn	Gly	Gly	Lys	Ile	Tyr	Asp	Met	Thr	Asp	Lys	Asp	Tyr	Glu
				340					345					350		
	Lys	Tyr	Val	Ile	Ser	Asp	Ala	Val	His	Ile	Gly	Trp	Lys	Gly	Trp	Val
			355					360					365			
25	Tyr	Met	Asp	Glu	Gln	Ile	Ala	Lys	His	Met	Lys	Gly	Glu	Pro	Gln	Pro
	370						375					380				
	Glu	Val	Asp	Lys	Pro	Lys	Asn									
	385					390										

<210> 109
 <211> 1256
 <212> PRT
 <213> Staphylococcus aureus

<400> 109

EP 2 510 947 B1

1 Met Ala Lys Lys Phe Asn Tyr Lys Leu Pro Ser Met Val Ala Leu Thr
 5 5 10 15
 Leu Val Gly Ser Ala Val Thr Ala His Gln Val Gln Ala Ala Glu Thr
 20 25 30
 Thr Gln Asp Gln Thr Thr Asn Lys Asn Val Leu Asp Ser Asn Lys Val
 35 40 45
 Lys Ala Thr Thr Glu Gln Ala Lys Ala Glu Val Lys Asn Pro Thr Gln
 50 55 60
 10 Asn Ile Ser Gly Thr Gln Val Tyr Gln Asp Pro Ala Ile Val Gln Pro
 65 70 75 80
 Lys Thr Ala Asn Asn Lys Thr Gly Asn Ala Gln Val Ser Gln Lys Val
 85 90 95
 15 Asp Thr Ala Gln Val Asn Gly Asp Thr Arg Ala Asn Gln Ser Ala Thr
 100 105 110
 Thr Asn Asn Thr Gln Pro Val Ala Lys Ser Thr Ser Thr Thr Ala Pro
 115 120 125
 20 Lys Thr Asn Thr Asn Val Thr Asn Ala Gly Tyr Ser Leu Val Asp Asp
 130 135 140
 25 Glu Asp Asp Asn Ser Glu Asn Gln Ile Asn Pro Glu Leu Ile Lys Ser
 145 150 155 160

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	Ala	Ala	Lys	Pro	Ala 165	Ala	Leu	Glu	Thr	Gln 170	Tyr	Lys	Thr	Ala	Ala 175	Pro
5	Lys	Ala	Ala	Thr 180	Thr	Ser	Ala	Pro	Lys 185	Ala	Lys	Thr	Glu	Ala 190	Thr	Pro
	Lys	Val	Thr 195	Thr	Phe	Ser	Ala	Ser 200	Ala	Gln	Pro	Arg	Ser 205	Val	Ala	Ala
10	Thr	Pro 210	Lys	Thr	Ser	Leu	Pro 215	Lys	Tyr	Lys	Pro	Gln 220	Val	Asn	Ser	Ser
	Ile 225	Asn	Asp	Tyr	Ile	Cys 230	Lys	Asn	Asn	Leu	Lys 235	Ala	Pro	Lys	Ile	Glu 240
15	Glu	Asp	Tyr	Thr	Ser 245	Tyr	Phe	Pro	Lys	Tyr 250	Ala	Tyr	Arg	Asn	Gly 255	Val
	Gly	Arg	Pro	Glu 260	Gly	Ile	Val	Val	His 265	Asp	Thr	Ala	Asn	Asp 270	Arg	Ser
20	Thr	Ile	Asn 275	Gly	Glu	Ile	Ser	Tyr 280	Met	Lys	Asn	Asn	Tyr 285	Gln	Asn	Ala
	Phe	Val 290	His	Ala	Phe	Val	Asp 295	Gly	Asp	Arg	Ile	Ile 300	Glu	Thr	Ala	Pro
25	Thr 305	Asp	Tyr	Leu	Ser	Trp 310	Gly	Val	Gly	Ala	Val 315	Gly	Asn	Pro	Arg	Phe 320
	Ile	Asn	Val	Glu	Ile 325	Val	His	Thr	His	Asp 330	Tyr	Ala	Ser	Phe	Ala 335	Arg
30	Ser	Met	Asn	Asn 340	Tyr	Ala	Asp	Tyr	Ala 345	Ala	Thr	Gln	Leu	Gln 350	Tyr	Tyr
	Gly	Leu	Lys 355	Pro	Asp	Ser	Ala	Glu 360	Tyr	Asp	Gly	Asn	Gly 365	Thr	Val	Trp
35	Thr	His 370	Tyr	Ala	Val	Ser	Lys 375	Tyr	Leu	Gly	Gly	Thr 380	Asp	His	Ala	Asp
	Pro 385	His	Gly	Tyr	Leu	Arg 390	Ser	His	Asn	Tyr	Ser 395	Tyr	Asp	Gln	Leu	Tyr 400
40	Asp	Leu	Ile	Asn 405	Glu	Lys	Tyr	Leu	Ile 410	Lys	Met	Gly	Lys	Val	Ala 415	Pro
	Trp	Gly	Thr	Gln 420	Ser	Thr	Thr	Thr	Pro 425	Thr	Thr	Pro	Ser	Lys 430	Pro	Thr
45	Thr	Pro	Ser 435	Lys	Pro	Ser	Thr	Gly 440	Lys	Leu	Thr	Val	Ala 445	Ala	Asn	Asn
	Gly	Val 450	Ala	Gln	Ile	Lys	Pro 455	Thr	Asn	Ser	Gly	Leu 460	Tyr	Thr	Thr	Val
50	Tyr 465	Asp	Lys	Thr	Gly	Lys 470	Ala	Thr	Asn	Glu	Val 475	Gln	Lys	Thr	Phe	Ala 480
	Val	Ser	Lys	Thr	Ala 485	Thr	Leu	Gly	Asn	Gln 490	Lys	Phe	Tyr	Leu	Val 495	Gln
55	Asp	Tyr	Asn	Ser 500	Gly	Asn	Lys	Phe	Gly 505	Trp	Val	Lys	Glu	Gly 510	Asp	Val
	Val	Tyr	Asn 515	Thr	Ala	Lys	Ser	Pro 520	Val	Asn	Val	Asn	Gln 525	Ser	Tyr	Ser

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Ile Lys Pro Gly Thr Lys Leu Tyr Thr Val Pro Trp Gly Thr Ser Lys
 530 535 540
 5 Gln Val Ala Gly Ser Val Ser Gly Ser Gly Asn Gln Thr Phe Lys Ala
 545 550 555
 Ser Lys Gln Gln Gln Ile Asp Lys Ser Ile Tyr Leu Tyr Gly Ser Val
 565 570 575
 10 Asn Gly Lys Ser Gly Trp Val Ser Lys Ala Tyr Leu Val Asp Thr Ala
 580 585 590
 Lys Pro Thr Pro Thr Pro Thr Pro Lys Pro Ser Thr Pro Thr Thr Asn
 595 600 605
 15 Asn Lys Leu Thr Val Ser Ser Leu Asn Gly Val Ala Gln Ile Asn Ala
 610 615 620
 Lys Asn Asn Gly Leu Phe Thr Thr Val Tyr Asp Lys Thr Gly Lys Pro
 625 630 635 640
 20 Thr Lys Glu Val Gln Lys Thr Phe Ala Val Thr Lys Glu Ala Ser Leu
 645 650 655
 Gly Gly Asn Lys Phe Tyr Leu Val Lys Asp Tyr Asn Ser Pro Thr Leu
 660 665 670
 25 Ile Gly Trp Val Lys Gln Gly Asp Val Ile Tyr Asn Asn Ala Lys Ser
 675 680 685
 Pro Val Asn Val Met Gln Thr Tyr Thr Val Lys Pro Gly Thr Lys Leu
 690 695 700
 30 Tyr Ser Val Pro Trp Gly Thr Tyr Lys Gln Glu Ala Gly Ala Val Ser
 705 710 715 720
 Gly Thr Gly Asn Gln Thr Phe Lys Ala Thr Lys Gln Gln Gln Ile Asp
 725 730 735
 35 Lys Ser Ile Tyr Leu Phe Gly Thr Val Asn Gly Lys Ser Gly Trp Val
 740 745 750
 Ser Lys Ala Tyr Leu Ala Val Pro Ala Ala Pro Lys Lys Ala Val Ala
 755 760 765
 40 Gln Pro Lys Thr Ala Val Lys Ala Tyr Thr Val Thr Lys Pro Gln Thr
 770 775 780
 Thr Gln Thr Val Ser Lys Ile Ala Gln Val Lys Pro Asn Asn Thr Gly
 785 790 795 800
 45 Ile Arg Ala Ser Val Tyr Glu Lys Thr Ala Lys Asn Gly Ala Lys Tyr
 805 810 815
 Ala Asp Arg Thr Phe Tyr Val Thr Lys Glu Arg Ala His Gly Asn Glu
 820 825 830
 50 Thr Tyr Val Leu Leu Asn Asn Thr Ser His Asn Ile Pro Leu Gly Trp
 835 840 845
 Phe Asn Val Lys Asp Leu Asn Val Gln Asn Leu Gly Lys Glu Val Lys
 850 855 860
 55 Thr Thr Gln Lys Tyr Thr Val Asn Lys Ser Asn Asn Gly Leu Ser Met
 865 870 875 880
 Val Pro Trp Gly Thr Lys Asn Gln Val Ile Leu Thr Gly Asn Asn Ile
 885 890 895
 Ala Gln Gly Thr Phe Asn Ala Thr Lys Gln Val Ser Val Gly Lys Asp

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	900	905	910
	Val Tyr Leu Tyr Gly Thr Ile	Asn Asn Arg Thr Gly Trp	Val Asn Ala
	915	920	925
5	Lys Asp Leu Thr Ala Pro Thr	Ala Val Lys Pro Thr	Thr Ser Ala Ala
	930	935	940
	Lys Asp Tyr Asn Tyr Thr Tyr Val Ile Lys	Asn Gly Asn Gly Tyr Tyr	
	945	950	955
10	Tyr Val Thr Pro Asn Ser Asp Thr Ala	Lys Tyr Ser Leu Lys Ala Phe	
	965	970	975
	Asn Glu Gln Pro Phe Ala Val Val	Lys Glu Gln Val Ile Asn Gly Gln	
	980	985	990
15	Thr Trp Tyr Tyr Gly Lys Leu Ser Asn Gly Lys Leu Ala Trp Ile Lys		
	995	1000	1005
	Ser Thr Asp Leu Ala Lys Glu Leu Ile Lys Tyr Asn Gln Thr Gly Met		
	1010	1015	1020
20	Thr Leu Asn Gln Val Ala Gln Ile Gln Ala Gly Leu Gln Tyr Lys Pro		
	1025	1030	1035
	Gln Val Gln Arg Val Pro Gly Lys Trp Thr Asp Ala Lys Phe Asn Asp		
	1045	1050	1055
25	Val Lys His Ala Met Asp Thr Lys Arg Leu Ala Gln Asp Pro Ala Leu		
	1060	1065	1070
	Lys Tyr Gln Phe Leu Arg Leu Asp Gln Pro Gln Asn Ile Ser Ile Asp		
	1075	1080	1085
30	Lys Ile Asn Gln Phe Leu Lys Gly Lys Gly Val Leu Glu Asn Gln Gly		
	1090	1095	1100
	Ala Ala Phe Asn Lys Ala Ala Gln Met Tyr Gly Ile Asn Glu Val Tyr		
	1105	1110	1115
35	Leu Ile Ser His Ala Leu Leu Glu Thr Gly Asn Gly Thr Ser Gln Leu		
	1125	1130	1135
	Ala Lys Gly Ala Asp Val Val Asn Asn Lys Val Val Thr Asn Ser Asn		
	1140	1145	1150
40	Thr Lys Tyr His Asn Val Phe Gly Ile Ala Ala Tyr Asp Asn Asp Pro		
	1155	1160	1165
	Leu Arg Glu Gly Ile Lys Tyr Ala Lys Gln Ala Gly Trp Asp Thr Val		
	1170	1175	1180
45	Ser Lys Ala Ile Val Gly Gly Ala Lys Phe Ile Gly Asn Ser Tyr Val		
	1185	1190	1195
	Lys Ala Gly Gln Asn Thr Leu Tyr Lys Met Arg Trp Asn Pro Ala His		
	1205	1210	1215
50	Pro Gly Thr His Gln Tyr Ala Thr Asp Val Asp Trp Ala Asn Ile Asn		
	1220	1225	1230
	Ala Lys Ile Ile Lys Gly Tyr Tyr Asp Lys Ile Gly Glu Val Gly Lys		
	1235	1240	1245
55	Tyr Phe Asp Ile Pro Gln Tyr Lys		
	1250	1255	

<210> 110

<211> 414

<212> PRT

<213> Staphylococcus aureus

<400> 110

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	Met	Lys	Phe	Ser	Thr	Leu	Ser	Glu	Glu	Glu	Phe	Thr	Asn	Tyr	Thr	Lys
	1				5					10					15	
5	Lys	His	Phe	Lys	His	Tyr	Thr	Gln	Ser	Ile	Glu	Leu	Tyr	Asn	Tyr	Arg
				20					25					30		
	Asn	Lys	Ile	Asn	His	Glu	Ala	His	Ile	Val	Gly	Val	Lys	Asn	Asp	Lys
			35					40					45			
10	Asn	Glu	Val	Ile	Ala	Ala	Cys	Leu	Leu	Thr	Glu	Ala	Arg	Ile	Phe	Lys
		50					55					60				
	Phe	Tyr	Lys	Tyr	Phe	Tyr	Ser	His	Arg	Gly	Pro	Leu	Leu	Asp	Tyr	Phe
	65					70					75					80
15	Asp	Ala	Lys	Leu	Val	Cys	Tyr	Phe	Phe	Lys	Glu	Leu	Ser	Lys	Phe	Ile
					85					90					95	
	Tyr	Lys	Asn	Arg	Gly	Val	Phe	Ile	Leu	Val	Asp	Pro	Tyr	Leu	Ile	Glu
				100					105					110		
20	Asn	Leu	Arg	Asp	Ala	Asn	Gly	Arg	Ile	Ile	Lys	Asn	Tyr	Asn	Asn	Ser
			115					120					125			
	Val	Ile	Val	Lys	Met	Leu	Gly	Lys	Ile	Gly	Tyr	Leu	His	Gln	Gly	Tyr
		130					135					140				
25	Thr	Thr	Gly	Tyr	Ser	Asn	Lys	Ser	Gln	Ile	Arg	Trp	Ile	Ser	Val	Leu
	145					150					155					160
	Asp	Leu	Lys	Asp	Lys	Asp	Glu	Asn	Gln	Leu	Leu	Lys	Glu	Met	Glu	Tyr
					165					170					175	
30	Gln	Thr	Arg	Arg	Asn	Ile	Lys	Lys	Thr	Ile	Glu	Ile	Gly	Val	Lys	Val
				180					185					190		
	Glu	Asp	Leu	Ser	Ile	Glu	Glu	Thr	Asn	Arg	Phe	Tyr	Lys	Leu	Phe	Gln
			195					200					205			
35	Met	Ala	Glu	Glu	Lys	His	Gly	Phe	His	Phe	Met	Asn	Glu	Asp	Tyr	Phe
		210					215					220				
	Lys	Arg	Met	Gln	Glu	Ile	Tyr	Lys	Asp	Lys	Ala	Met	Leu	Lys	Ile	Ala
		225				230					235					240
40	Cys	Ile	Asn	Leu	Asn	Glu	Tyr	Gln	Asp	Lys	Leu	Lys	Ile	Gln	Leu	Leu
					245					250					255	
	Lys	Ile	Glu	Asn	Glu	Met	Met	Thr	Val	Asn	Arg	Ala	Leu	Asn	Glu	Asn
				260					265					270		
45	Pro	Asn	Ser	Lys	Lys	Asn	Lys	Ser	Lys	Leu	Asn	Gln	Leu	Asn	Met	Gln
			275					280					285			
	Leu	Ser	Ser	Ile	Asn	Asn	Arg	Ile	Ser	Lys	Thr	Glu	Glu	Leu	Ile	Phe
		290					295					300				
50	Glu	Asp	Gly	Pro	Val	Leu	Asp	Leu	Ala	Ala	Ala	Leu	Phe	Ile	Cys	Thr
		305				310				315					320	
	Asp	Asp	Glu	Val	Tyr	Tyr	Leu	Ser	Ser	Gly	Ser	Asn	Pro	Lys	Tyr	Asn
					325					330					335	
55	Gln	Tyr	Met	Gly	Ala	Tyr	His	Leu	Gln	Trp	His	Met	Ile	Lys	Tyr	Ala
				340					345					350		

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Lys Ser His Asn Ile Asn Arg Tyr Asn Phe Tyr Gly Ile Thr Gly Val
 355 360 365
 5 Phe Ser Asn Glu Ala Asp Asp Phe Gly Val Gln Gln Phe Lys Lys Gly
 370 375 380
 Phe Asn Ala His Val Glu Glu Leu Ile Gly Asp Phe Ile Lys Pro Val
 385 390 395 400
 10 Arg Pro Ile Leu Tyr Lys Phe Ala Lys Leu Ile Tyr Lys Val
 405 410

<210> 111

<211> 428

<212> PRT

15 <213> Staphylococcus aureus

<400> 111

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Met Lys Glu Arg Tyr Tyr Glu Leu Ile Asp Glu Arg Val Phe Glu Gln
 1 5 10 15
 Glu Leu Glu Asn Gly Leu Arg Leu Phe Ile Ile Pro Lys Pro Gly Phe
 5 20 25 30
 Gln Lys Thr Phe Val Thr Tyr Thr Thr Gln Phe Gly Ser Leu Asp Asn
 35 40 45
 Gln Phe Lys Pro Leu Gly Gln Asp Gln Phe Val Thr Val Pro Asp Gly
 10 50 55 60
 Val Ala His Phe Leu Glu His Lys Leu Phe Glu Lys Glu Glu Glu Asp
 65 70 75 80
 Leu Phe Thr Ala Phe Ala Glu Asp Asn Ala Gln Ala Asn Ala Phe Thr
 15 85 90 95
 Ser Phe Asp Arg Thr Ser Tyr Leu Phe Ser Ala Thr Asp Asn Ile Glu
 100 105 110
 Asn Asn Ile Lys Arg Leu Leu Thr Met Val Glu Thr Pro Tyr Phe Thr
 20 115 120 125
 Lys Glu Thr Val Asp Lys Glu Lys Gly Ile Ile Ala Glu Glu Ile Lys
 130 135 140
 Met Tyr Gln Glu Gln Pro Gly Tyr Lys Leu Met Phe Asn Thr Leu Arg
 25 145 150 155 160
 Ala Met Tyr Gln Gln His Pro Ile Arg Val Asp Ile Ala Gly Ser Val
 165 170 175
 Glu Ser Ile Tyr Asp Ile Thr Lys Asp Asp Leu Tyr Leu Cys Tyr Glu
 30 180 185 190
 Thr Phe Tyr His Pro Ser Asn Met Val Leu Phe Val Val Gly Asp Val
 195 200 205
 Asp Pro Glu Ala Ile Cys Arg Ile Val Lys Gln His Glu Asp Ala Arg
 210 215 220
 Asn Lys Val Asn Gln Pro Lys Ile Glu Arg Gly Leu Val Asp Glu Pro
 35 225 230 235 240
 Glu Asp Val Lys Glu Ala Phe Val Thr Glu Ser Met Lys Ile Gln Ser
 245 250 255
 Pro Arg Leu Met Leu Gly Phe Lys Asn Lys Pro Leu Gln Glu Ala Pro
 40 260 265 270
 Gln Lys Tyr Val Gln Arg Asp Leu Glu Met Ser Leu Phe Phe Glu Leu
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	275		280		285											
	Ile	Phe	Gly	Glu	Glu	Thr	Asp	Phe	Tyr	Gln	Asn	Leu	Leu	Asn	Glu	Gly
	290						295					300				
5	Leu	Ile	Asp	Asp	Thr	Phe	Gly	Tyr	Gln	Phe	Val	Leu	Glu	Pro	Thr	Tyr
	305					310					315					320
	Ser	Phe	Ser	Ile	Val	Thr	Ser	Ala	Thr	Glu	Glu	Pro	Asp	Lys	Leu	Lys
					325					330					335	
10	Lys	Leu	Leu	Leu	Asp	Glu	Leu	Arg	Asp	Lys	Lys	Gly	Asn	Phe	Gln	Asp
				340					345					350		
	Ala	Glu	Ala	Phe	Glu	Leu	Leu	Lys	Lys	Gln	Phe	Ile	Gly	Glu	Phe	Ile
			355					360					365			
15	Ser	Ser	Leu	Asn	Ser	Pro	Glu	Tyr	Ile	Ala	Asn	Gln	Tyr	Thr	Lys	Leu
	370						375					380				
	Tyr	Phe	Glu	Gly	Val	Ser	Val	Phe	Asp	Met	Leu	Asp	Ile	Val	Glu	Asn
	385					390					395					400
20	Ile	Thr	Leu	Asp	Ser	Ile	Asn	Glu	Thr	Ser	Ser	Leu	Tyr	Leu	Asn	Leu
					405					410					415	
	Asp	Gln	Gln	Val	Asp	Ser	Arg	Leu	Glu	Ile	Lys	Lys				
				420					425							

<210> 112
 <211> 519
 <212> PRT
 <213> Staphylococcus aureus
 <400> 112

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Met Asn Leu Leu Ser Leu Leu Leu Ile Leu Leu Gly Ile Ile Leu Gly
 1 5 10 15
 Val Val Gly Gly Tyr Val Val Ala Arg Asn Leu Leu Leu Gln Lys Gln
 5 20 25 30
 Ser Gln Ala Arg Gln Thr Ala Glu Asp Ile Val Asn Gln Ala His Lys
 35 40 45
 Glu Ala Asp Asn Ile Lys Lys Glu Lys Leu Leu Glu Ala Lys Glu Glu
 10 50 55 60
 Asn Gln Ile Leu Arg Glu Gln Thr Glu Ala Glu Leu Arg Glu Arg Arg
 65 70 75 80
 Ser Glu Leu Gln Arg Gln Glu Thr Arg Leu Leu Gln Lys Glu Glu Asn
 15 85 90 95
 Leu Glu Arg Lys Ser Asp Leu Leu Asp Lys Lys Asp Glu Ile Leu Glu
 100 105 110
 Gln Lys Glu Ser Lys Ile Glu Glu Lys Gln Gln Gln Val Asp Ala Lys
 115 120 125
 Glu Ser Ser Val Gln Thr Leu Ile Met Lys His Glu Gln Glu Leu Glu
 130 135 140
 Arg Ile Ser Gly Leu Thr Gln Glu Glu Ala Ile Asn Glu Gln Leu Gln
 145 150 155 160
 Arg Val Glu Glu Glu Leu Ser Gln Asp Ile Ala Val Leu Val Lys Glu
 165 170 175
 Lys Glu Lys Glu Ala Lys Glu Lys Val Asp Lys Thr Ala Lys Glu Leu
 180 185 190

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5 Leu Ala Thr Ala Val Gln Arg Leu Ala Ala Asp His Thr Ser Glu Ser
 195 200 205
 Thr Val Ser Val Val Asn Leu Pro Asn Asp Glu Met Lys Gly Arg Ile
 210 215 220
 10 Ile Gly Arg Glu Gly Arg Asn Ile Arg Thr Leu Glu Thr Leu Thr Gly
 225 230 235 240
 Ile Asp Leu Ile Ile Asp Asp Thr Pro Glu Ala Val Ile Leu Ser Gly
 245 250 255
 Phe Asp Pro Ile Arg Arg Glu Ile Ala Arg Thr Ala Leu Val Asn Leu
 260 265 270
 15 Val Ser Asp Gly Arg Ile His Pro Gly Arg Ile Glu Asp Met Val Glu
 275 280 285
 Lys Ala Arg Lys Glu Val Asp Asp Ile Ile Arg Glu Ala Gly Glu Gln
 290 295 300
 20 Ala Thr Phe Glu Val Asn Ala His Asn Met His Pro Asp Leu Val Lys
 305 310 315 320
 Ile Val Gly Arg Leu Asn Tyr Arg Thr Ser Tyr Gly Gln Asn Val Leu
 325 330 335
 25 Lys His Ser Ile Glu Val Ala His Leu Ala Ser Met Leu Ala Ala Glu
 340 345 350
 Leu Gly Glu Asp Glu Thr Leu Ala Lys Arg Ala Gly Leu Leu His Asp
 355 360 365
 30 Val Gly Lys Ala Ile Asp His Glu Val Glu Gly Ser His Val Glu Ile
 370 375 380
 Gly Val Glu Leu Ala Lys Lys Tyr Gly Glu Asn Glu Thr Val Ile Asn
 385 390 395 400
 35 Ala Ile His Ser His His Gly Asp Val Glu Pro Thr Ser Ile Ile Ser
 405 410 415
 Ile Leu Val Ala Ala Ala Asp Ala Leu Ser Ala Ala Arg Pro Gly Ala
 420 425 430
 40 Arg Lys Glu Thr Leu Glu Asn Tyr Ile Arg Arg Leu Glu Arg Leu Glu
 435 440 445
 Thr Leu Ser Glu Ser Tyr Asp Gly Val Glu Lys Ala Phe Ala Ile Gln
 450 455 460
 45 Ala Gly Arg Glu Ile Arg Val Ile Val Ser Pro Glu Glu Ile Asp Asp
 465 470 475 480
 Leu Lys Ser Tyr Arg Leu Ala Arg Asp Ile Lys Asn Gln Ile Glu Asp
 485 490 495
 50 Glu Leu Gln Tyr Pro Gly His Ile Lys Val Thr Val Val Arg Glu Thr
 500 505 510
 Arg Ala Val Glu Tyr Ala Lys
 515

<210> 113

55 <211> 284

<212> PRT

<213> Staphylococcus aureus

<400> 113

5 Met Ser Phe Tyr Val Val Leu Ile Ile Ile Ile Val Ala Leu Ile Gly
 1 5 10 15
 Ile Leu Val Leu Asn Gln Arg Tyr Ser Asn Ser Lys Ile Asp Thr Glu
 20 25 30
 Val Tyr Ala Arg Lys Gln Leu Ile Lys Lys Asn Lys Ala Leu Ser Ala
 35 40 45
 10 Glu Asn Ala Glu Leu Arg Ser Gln Met Leu Ser Ser Asn Asn Asp Val
 50 55 60
 Gly His His Ala Tyr Lys Asn Ala Lys Arg Glu Leu Arg Lys Ile Leu
 65 70 75 80
 15 Asp Ser Tyr Leu Glu Asn Gly Lys Leu Lys Tyr Tyr Asp Ile Ile Val
 85 90 95
 Thr Ser Asn Leu Ala Thr Lys His Pro Phe Phe Glu Tyr Ala Arg Ser
 100 105 110
 20 Phe Asp Phe Ile Ile Val Ser Asp Ile Gly Leu Ile Asn Val Asp Val
 115 120 125
 Lys Ser Trp Gly Glu Lys Thr Phe Tyr His Phe Asp Val Pro Asp Glu
 130 135 140
 25 His Asp Thr Glu Ile Ser Asn Ser Asn Ile Glu Lys Val Val Gly His
 145 150 155 160
 Tyr Ile Ser Gln Gln Tyr His Asp Gln Phe Asn Ser Ser Arg Lys Ser
 165 170 175
 30 Ile Tyr Thr Phe Thr Glu Thr Val Gln Pro Asn Arg Val Ile Tyr Asp
 180 185 190
 Phe Tyr Asp Tyr Asp Pro Tyr Gln Leu Ala Ala Asn Asn Ala Lys Ala
 195 200 205
 35 Leu Lys Asp His Ile Glu Gln Asn Phe Asn Phe Lys Val Gln Ser Thr
 210 215 220
 Gly Val Ile Tyr Phe Ser Asp Gly Thr Val Asn Ile Ile Gln Gly Ser
 225 230 235 240
 40 Glu Glu Arg Asp Lys Tyr Val Asp Thr Val Ser Thr Lys Ser Ser Leu
 245 250 255
 Arg Arg Ile Ile Ser Glu Ala Ile Glu Leu Ser Lys His Pro Leu Asn
 260 265 270
 45 Lys Glu Gln Val Asp Gln Ile Thr Ala Ile Phe Lys
 275 280

<210> 114

<211> 1274

50 <212> PRT

<213> Staphylococcus aureus

<400> 114

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Met Ser Trp Phe Asp Lys Leu Phe Gly Glu Asp Asn Asp Ser Asn Asp
 1 5 10 15
 Asp Leu Ile His Arg Lys Lys Lys Arg Arg Gln Glu Ser Gln Asn Ile
 5 20 25 30
 Asp Asn Asp His Asp Ser Leu Leu Pro Gln Asn Asn Asp Ile Tyr Ser
 35 40 45
 Arg Pro Arg Gly Lys Phe Arg Phe Pro Met Ser Val Ala Tyr Glu Asn
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	50		55		60													
	Glu	Asn	Val	Glu	Gln	Ser	Ala	Asp	Thr	Ile	Ser	Asp	Glu	Lys	Glu	Gln		
5	65					70					75					80		
	Tyr	His	Arg	Asp	Tyr	Arg	Lys	Gln	Ser	His	Asp	Ser	Arg	Ser	Gln	Lys		
					85					90					95			
	Arg	His	Arg	Arg	Arg	Arg	Asn	Gln	Thr	Thr	Glu	Glu	Gln	Asn	Tyr	Ser		
				100					105					110				
10	Glu	Gln	Arg	Gly	Asn	Ser	Lys	Ile	Ser	Gln	Gln	Ser	Ile	Lys	Tyr	Lys		
			115					120					125					
	Asp	His	Ser	His	Tyr	His	Thr	Asn	Lys	Pro	Gly	Thr	Tyr	Val	Ser	Ala		
		130					135					140						
15	Ile	Asn	Gly	Ile	Glu	Lys	Glu	Thr	His	Lys	Pro	Lys	Thr	His	Asn	Met		
	145					150					155					160		
	Tyr	Ser	Asn	Asn	Thr	Asn	His	Arg	Ala	Lys	Asp	Ser	Thr	Pro	Asp	Tyr		
					165					170					175			
20	His	Lys	Glu	Ser	Phe	Lys	Thr	Ser	Glu	Val	Pro	Ser	Ala	Ile	Phe	Gly		
				180					185					190				
	Thr	Met	Lys	Pro	Lys	Lys	Leu	Glu	Asn	Gly	Arg	Ile	Pro	Val	Ser	Lys		
			195					200					205					
25	Pro	Ser	Glu	Lys	Val	Glu	Ser	Asp	Lys	Gln	Lys	Tyr	Asp	Lys	Tyr	Val		
		210					215					220						
	Ala	Lys	Thr	Gln	Thr	Ser	Gln	Asn	Lys	Gln	Leu	Glu	Gln	Glu	Lys	Gln		
	225					230					235					240		
30	Asn	Asp	Ser	Val	Val	Lys	Gln	Gly	Thr	Ala	Ser	Lys	Ser	Ser	Asp	Glu		
					245					250					255			
	Asn	Val	Ser	Ser	Thr	Thr	Lys	Ser	Met	Pro	Asn	Tyr	Ser	Lys	Val	Asp		
				260					265					270				
35	Asn	Thr	Ile	Lys	Ile	Glu	Asn	Ile	Tyr	Ala	Ser	Gln	Ile	Val	Glu	Glu		
			275					280					285					
	Ile	Arg	Arg	Glu	Arg	Glu	Arg	Lys	Val	Leu	Gln	Lys	Arg	Arg	Phe	Lys		
		290					295					300						
40	Lys	Ala	Leu	Gln	Gln	Lys	Arg	Glu	Glu	His	Lys	Asn	Glu	Glu	Gln	Asp		
	305					310					315					320		
	Ala	Ile	Gln	Arg	Ala	Ile	Asp	Glu	Met	Tyr	Ala	Lys	Gln	Ala	Glu	Arg		
					325					330					335			
45	Tyr	Val	Gly	Asp	Ser	Ser	Leu	Asn	Asp	Asp	Ser	Asp	Leu	Thr	Asp	Asn		
				340					345					350				
	Ser	Thr	Asp	Ala	Ser	Gln	Leu	His	Thr	Asn	Gly	Ile	Glu	Asn	Glu	Thr		
			355					360					365					
50	Val	Ser	Asn	Asp	Glu	Asn	Lys	Gln	Ala	Ser	Ile	Gln	Asn	Glu	Asp	Thr		
		370					375					380						
	Asn	Asp	Thr	His	Val	Asp	Glu	Ser	Pro	Tyr	Asn	Tyr	Glu	Glu	Val	Ser		
	385					390					395					400		
	Leu	Asn	Gln	Val	Ser	Thr	Thr	Lys	Gln	Leu	Ser	Asp	Asp	Glu	Val	Thr		
					405					410					415			
55	Val	Ser	Asn	Val	Thr	Ser	Gln	His	Gln	Ser	Ala	Leu	Gln	His	Asn	Val		
				420					425					430				

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	Glu	Val	Asn	Asp	Lys	Asp	Glu	Lys	Asn	Gln	Ser	Arg	Leu	Ile	Ala
			435				440					445			
5	Asp	Ser	Glu	Glu	Asp	Gly	Ala	Thr	Asn	Lys	Glu	Glu	Tyr	Ser	Gly
	450						455					460			
	Gln	Ile	Asp	Asp	Ala	Glu	Phe	Tyr	Glu	Leu	Asn	Asp	Thr	Glu	Val
	465					470					475				480
10	Glu	Asp	Thr	Thr	Ser	Asn	Ile	Glu	Asp	Asn	Thr	Asn	Arg	Asn	Ala
					485					490					495
	Glu	Met	His	Val	Asp	Ala	Pro	Lys	Thr	Gln	Glu	Tyr	Ala	Val	Thr
				500					505					510	
15	Ser	Gln	Val	Asn	Asn	Ile	Asp	Lys	Thr	Val	Asp	Asn	Glu	Ile	Glu
			515					520					525		Leu
	Ala	Pro	Arg	His	Lys	Lys	Asp	Asp	Gln	Thr	Asn	Leu	Ser	Val	Asn
	530						535					540			Ser
20	Leu	Lys	Thr	Asn	Asp	Val	Asn	Asp	Asn	His	Val	Val	Glu	Asp	Ser
	545					550					555				560
	Met	Asn	Glu	Ile	Glu	Lys	Asn	Asn	Ala	Glu	Ile	Thr	Glu	Asn	Val
					565					570					575
25	Asn	Glu	Ala	Ala	Glu	Ser	Glu	Gln	Asn	Val	Glu	Glu	Lys	Thr	Ile
				580					585					590	
	Asn	Val	Asn	Pro	Lys	Lys	Gln	Thr	Glu	Lys	Val	Ser	Thr	Leu	Ser
			595					600					605		Lys
30	Arg	Pro	Phe	Asn	Val	Val	Met	Thr	Pro	Ser	Asp	Lys	Lys	Arg	Met
	610						615					620			Met
	Asp	Arg	Lys	Lys	His	Ser	Lys	Val	Asn	Val	Pro	Glu	Leu	Lys	Pro
	625					630					635				Val
35	Gln	Ser	Lys	Gln	Ala	Val	Ser	Glu	Arg	Met	Pro	Ala	Ser	Gln	Ala
					645					650					655
	Pro	Ser	Ser	Arg	Ser	Asp	Ser	Gln	Glu	Ser	Asn	Thr	Asn	Ala	Tyr
				660					665					670	Lys
40	Thr	Asn	Asn	Met	Thr	Ser	Asn	Asn	Val	Glu	Asn	Asn	Gln	Leu	Ile
			675					680					685		Gly
	His	Ala	Glu	Thr	Glu	Asn	Asp	Tyr	Gln	Asn	Ala	Gln	Gln	Tyr	Ser
		690					695					700			Glu
45	Gln	Lys	Pro	Ser	Val	Asp	Ser	Thr	Gln	Thr	Glu	Ile	Phe	Glu	Glu
	705					710					715				Ser
	Gln	Asp	Asp	Asn	Gln	Leu	Glu	Asn	Glu	Gln	Val	Asp	Gln	Ser	Thr
					725					730					735
	Ser	Ser	Val	Ser	Glu	Val	Ser	Asp	Ile	Thr	Glu	Glu	Ser	Glu	Glu
				740					745					750	Thr
50	Thr	His	Pro	Asn	Asn	Thr	Ser	Gly	Gln	Gln	Asp	Asn	Asp	Asp	Gln
			755					760					765		Gln
	Lys	Asp	Leu	Gln											

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Val Gln Thr Ser Lys₈₀₅ Pro Met Ile Arg Lys₈₁₀ Gly Pro Asn Ile Lys₈₁₅ Leu
 5 Pro Ser Val Ser₈₂₀ Leu Leu Glu Glu Pro₈₂₅ Gln Val Ile Glu Ser₈₃₀ Asp Glu
 Asp Trp Ile₈₃₅ Thr Asp Lys Lys₈₄₀ Glu Leu Asn Asp Ala₈₄₅ Leu Phe Tyr
 10 Phe Asn Val Pro Ala Glu Val₈₅₅ Gln Asp Val Thr Glu₈₆₀ Gly Pro Ser Val
 Thr Arg Phe Glu Leu Ser₈₇₀ Val Glu Lys Gly Val₈₇₅ Lys Val Ser Arg Ile₈₈₀
 15 Thr Ala Leu Gln Asp₈₈₅ Asp Ile Lys Met Ala₈₉₀ Leu Ala Ala Lys Asp₈₉₅ Ile
 Arg Ile Glu Ala₉₀₀ Pro Ile Pro Gly Thr₉₀₅ Ser Arg Val Gly Ile₉₁₀ Glu Val
 20 Pro Asn Gln₉₁₅ Asn Pro Thr Thr Val₉₂₀ Asn Leu Arg Ser Ile₉₂₅ Ile Glu Ser
 Pro Ser Phe Lys Asn Ala Glu₉₃₅ Ser Lys Leu Thr Val₉₄₀ Ala Met Gly Tyr
 25 Arg Ile Asn Asn Glu Pro₉₅₀ Leu Leu Met Asp Ile₉₅₅ Ala Lys Thr Pro His₉₆₀
 Ala Leu Ile Ala Gly₉₆₅ Ala Thr Gly Ser Gly₉₇₀ Lys Ser Val Cys Ile₉₇₅ Asn
 Ser Ile Leu Met₉₈₀ Ser Leu Leu Tyr Lys₉₈₅ Asn His Pro Glu Glu₉₉₀ Leu Arg
 30 Leu Leu Leu Ile Asp Pro Lys Met Val Glu Leu Ala Pro Tyr Asn Gly
 995 1000 1005
 Leu Pro His Leu Val Ala Pro Val Ile Thr Asp Val Lys Ala Ala Thr
 1010 1015 1020
 35 Gln Ser Leu Lys Trp Ala Val Glu Glu Met Glu Arg Arg Tyr Lys Leu
 1025 1030 1035 1040
 Phe Ala His Tyr His Val Arg Asn Ile Thr Ala Phe Asn Lys Lys Ala
 1045 1050 1055
 40 Pro Tyr Asp Glu Arg Met Pro Lys Ile Val Ile Val Ile Asp Glu Leu
 1060 1065 1070
 Ala Asp Leu Met Met Met Ala Pro Gln Glu Val Glu Gln Ser Ile Ala
 1075 1080 1085
 45 Arg Ile Ala Gln Lys Ala Arg Ala Cys Gly Ile His Met Leu Val Ala
 1090 1095 1100
 Thr Gln Arg Pro Ser Val Asn Val Ile Thr Gly Leu Ile Lys Ala Asn
 1105 1110 1115 1120
 Ile Pro Thr Arg Ile Ala Phe Met Val Ser Ser Ser Val Asp Ser Arg
 1125 1130 1135
 50 Thr Ile Leu Asp Ser Gly Gly Ala Glu Arg Leu Leu Gly Tyr Gly Asp
 1140 1145 1150
 Met Leu Tyr Leu Gly Ser Gly Met Asn Lys Pro Ile Arg Val Gln Gly
 1155 1160 1165
 55 Thr Phe Val Ser Asp Asp Glu Ile Asp Asp Val Val Asp Phe Ile Lys

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	1170		1175		1180
	Gln Gln Arg Glu Pro Asp Tyr Leu Phe Glu Glu Lys Glu Leu Leu Lys				
	1185		1190		1195
5	Lys Thr Gln Thr Gln Ser Gln Asp Glu Leu Phe Asp Asp Val Cys Ala				
		1205		1210	1215
	Phe Met Val Asn Glu Gly His Ile Ser Thr Ser Leu Ile Gln Arg His				
		1220		1225	1230
10	Phe Gln Ile Gly Tyr Asn Arg Ala Ala Arg Ile Ile Asp Gln Leu Glu				
		1235		1240	1245
	Gln Leu Gly Tyr Val Ser Ser Ala Asn Gly Ser Lys Pro Arg Asp Val				
		1250		1255	1260
15	Tyr Val Thr Glu Ala Asp Leu Asn Lys Glu				
	1265		1270		

<210> 115

<211> 239

20 <212> PRT

<213> Staphylococcus aureus

<400> 115

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EP 2 510 947 B1

Met Asn Lys Asn Ile Ile Ile Lys Ser Ile Ala Ala Leu Thr Ile Leu
1 5 10 15
Thr ser Ile Thr Gly Val Gly Thr Thr Met Val Glu Gly Ile Gln Gln
5 20 25 30
Thr Ala Lys Ala Glu Asn Thr Val Lys Gln Ile Thr Asn Thr Asn Val
35 40 45
Ala Pro Tyr Ser Gly Val Thr Trp Met Gly Ala Gly Thr Gly Phe Val
10 50 55 60
Val Gly Asn His Thr Ile Ile Thr Asn Lys His Val Thr Tyr His Met
65 70 75 80
Lys Val Gly Asp Glu Ile Lys Ala His Pro Asn Gly Phe Tyr Asn Asn
15 85 90 95
Gly Gly Gly Leu Tyr Lys Val Thr Lys Ile Val Asp Tyr Pro Gly Lys
100 105 110
Glu Asp Ile Ala Val Val Gln Val Glu Glu Lys Ser Thr Gln Pro Lys
20 115 120 125
Gly Arg Lys Phe Lys Asp Phe Thr Ser Lys Phe Asn Ile Ala Ser Glu
130 135 140
Ala Lys Glu Asn Glu Pro Ile Ser Val Ile Gly Tyr Pro Asn Pro Asn
25 145 150 155 160
Gly Asn Lys Leu Gln Met Tyr Glu Ser Thr Gly Lys Val Leu Ser Val
165 170 175
Asn Gly Asn Ile Val Ser Ser Asp Ala Ile Ile Gln Pro Gly Ser Ser
30 180 185 190
Gly Ser Pro Ile Leu Asn Ser Lys His Glu Ala Ile Gly Val Ile Tyr
195 200 205
Ala Gly Asn Lys Pro Ser Gly Glu Ser Thr Arg Gly Phe Ala Val Tyr
35 210 215 220
Phe Ser Pro Glu Ile Lys Lys Phe Ile Ala Asp Asn Leu Asp Lys
225 230 235

<210> 116

<211> 238

<212> PRT

<213> Staphylococcus aureus

<400> 116

EP 2 510 947 B1

Met Asn Lys Asn Ile Ile Ile Lys Ser Ile Ala Ala Leu Thr Ile Leu
1 5 10 15
5 Thr Ser Val Thr Gly Val Gly Thr Thr Val Val Glu Gly Ile Gln Gln
20 25 30
Thr Ala Lys Ala Glu His Asn Val Lys Leu Ile Lys Asn Thr Asn Val
35 40 45
10 Ala Pro Tyr Asn Gly Val Val Ser Ile Gly Ser Gly Thr Gly Phe Ile
50 55 60
Val Gly Lys Asn Thr Ile Val Thr Asn Lys His Val Val Ala Gly Met
65 70 75 80
15 Glu Ile Gly Ala His Ile Ile Ala His Pro Asn Gly Glu Tyr Asn Asn
85 90 95
Gly Gly Phe Tyr Lys Val Lys Lys Ile Val Arg Tyr Ser Gly Gln Glu
100 105 110
20 Asp Ile Ala Ile Leu His Val Glu Asp Lys Ala Val His Pro Lys Asn
115 120 125
Arg Asn Phe Lys Asp Tyr Thr Gly Ile Leu Lys Ile Ala Ser Glu Ala
130 135 140
25 Lys Glu Asn Glu Arg Ile Ser Ile Val Gly Tyr Pro Glu Pro Tyr Ile
145 150 155 160
Asn Lys Phe Gln Met Tyr Glu Ser Thr Gly Lys Val Leu Ser Val Lys
165 170 175
30 Gly Asn Met Ile Ile Thr Asp Ala Phe Val Glu Pro Gly Asn Ser Gly
180 185 190
Ser Ala Val Phe Asn Ser Lys Tyr Glu Val Val Gly Val His Phe Gly
195 200 205
35 Gly Asn Gly Pro Gly Asn Lys Ser Thr Lys Gly Tyr Gly Val Tyr Phe
210 215 220
Ser Pro Glu Ile Lys Lys Phe Ile Ala Asp Asn Thr Asp Lys
225 230 235

<210> 117

<211> 239

<212> PRT

<213> Staphylococcus aureus

<400> 117

Met Asn Lys Asn Ile Val Ile Lys Ser Met Ala Ala Leu Ala Ile Leu
1 5 10 15
50 Thr Ser Val Thr Gly Ile Asn Ala Ala Val Val Glu Glu Thr Gln Gln
20 25 30
Ile Ala Asn Ala Glu Lys Asn Val Thr Gln Val Lys Asp Thr Asn Ile
35 40 45
55 Phe Pro Tyr Asn Gly Val Val Ser Phe Lys Asp Ala Thr Gly Phe Val
50 55 60

Ile Gly Lys Asn Thr Ile Ile Thr Asn Lys His Val Ser Lys Asp Tyr
 65 70 75 80
 5 Lys Val Gly Asp Arg Ile Thr Ala His Pro Asn Gly Asp Lys Gly Asn
 85 90 95
 Gly Gly Ile Tyr Lys Ile Lys Ser Ile Ser Asp Tyr Pro Gly Asp Glu
 100 105 110
 10 Asp Ile Ser Val Met Asn Ile Glu Glu Gln Ala Val Glu Arg Gly Pro
 115 120 125
 Lys Gly Phe Asn Phe Asn Glu Asn Val Gln Ala Phe Asn Phe Ala Lys
 130 135 140
 15 Asp Ala Lys Val Asp Asp Lys Ile Lys Val Ile Gly Tyr Pro Leu Pro
 145 150 155 160
 Ala Gln Asn Ser Phe Lys Gln Phe Glu Ser Thr Gly Thr Ile Lys Arg
 165 170 175
 20 Ile Lys Asp Asn Ile Leu Asn Phe Asp Ala Tyr Ile Glu Pro Gly Asn
 180 185 190
 Ser Gly Ser Pro Val Leu Asn Ser Asn Asn Glu Val Ile Gly Val Val
 195 200 205
 25 Tyr Gly Gly Ile Gly Lys Ile Gly Ser Glu Tyr Asn Gly Ala Val Tyr
 210 215 220
 Phe Thr Pro Gln Ile Lys Asp Phe Ile Gln Lys His Ile Glu Gln
 225 230 235

30 <210> 118
 <211> 240
 <212> PRT
 <213> Staphylococcus aureus

35 <400> 118

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EP 2 510 947 B1

Met Asn Lys Asn Val Val Ile Lys Ser Leu Ala Ala Leu Thr Ile Leu
1 5 10 15
Thr Ser Val Thr Gly Ile Gly Thr Thr Leu Val Glu Glu Val Gln Gln
5 20 25 30
Thr Ala Lys Ala Glu Asn Asn Val Thr Lys Val Lys Asp Thr Asn Ile
35 40 45
Phe Pro Tyr Thr Gly Val Val Ala Phe Lys Ser Ala Thr Gly Phe Val
10 50 55 60
Val Gly Lys Asn Thr Ile Leu Thr Asn Lys His Val Ser Lys Asn Tyr
65 70 75 80
Lys Val Gly Asp Arg Ile Thr Ala His Pro Asn Ser Asp Lys Gly Asn
15 85 90 95
Gly Gly Ile Tyr Ser Ile Lys Lys Ile Ile Asn Tyr Pro Gly Lys Glu
100 105 110
Asp Val Ser Val Ile Gln Val Glu Glu Arg Ala Ile Glu Arg Gly Pro
20 115 120 125
Lys Gly Phe Asn Phe Asn Asp Asn Val Thr Pro Phe Lys Tyr Ala Ala
130 135 140
Gly Ala Lys Ala Gly Glu Arg Ile Lys Val Ile Gly Tyr Pro His Pro
25 145 150 155 160
Tyr Lys Asn Lys Tyr Val Leu Tyr Glu Ser Thr Gly Pro Val Met Ser
165 170 175
30 Val Glu Gly Ser Ser Ile Val Tyr Ser Ala His Thr Glu Ser Gly Asn
180 185 190
Ser Gly Ser Pro Val Leu Asn Ser Asn Asn Glu Leu Val Gly Ile His
35 195 200 205
Phe Ala Ser Asp Val Lys Asn Asp Asp Asn Arg Asn Ala Tyr Gly Val
210 215 220
Tyr Phe Thr Pro Glu Ile Lys Lys Phe Ile Ala Glu Asn Ile Asp Lys
40 225 230 235 240

<210> 119

<211> 235

<212> PRT

<213> Staphylococcus aureus

<400> 119

EP 2 510 947 B1

Met Asn Lys Asn Val Met Val Lys Gly Leu Thr Ala Leu Thr Ile Leu
1 5 10 15
5 Thr Ser Leu Gly Phe Ala Glu Asn Ile Ser Asn Gln Pro His Ser Ile
20 25 30
Ala Lys Ala Glu Lys Asn Val Lys Glu Ile Thr Asp Ala Thr Lys Glu
35 40 45
10 Pro Tyr Asn Ser Val Val Ala Phe Val Gly Gly Thr Gly Val Val Val
50 55 60
Gly Lys Asn Thr Ile Val Thr Asn Lys His Ile Ala Lys Ser Asn Asp
65 70 75 80
15 Ile Phe Lys Asn Arg Val Ser Ala His His Ser Ser Lys Gly Lys Gly
85 90 95
Gly Gly Asn Tyr Asp Val Lys Asp Ile Val Glu Tyr Pro Gly Lys Glu
100 105 110
20 Asp Leu Ala Ile Val His Val His Glu Thr Ser Thr Glu Gly Leu Asn
115 120 125
Phe Asn Lys Asn Val Ser Tyr Thr Lys Phe Ala Asp Gly Ala Lys Val
130 135 140
25 Lys Asp Arg Ile Ser Val Ile Gly Tyr Pro Lys Gly Ala Gln Thr Lys
145 150 155 160
Tyr Lys Met Phe Glu Ser Thr Gly Thr Ile Asn His Ile Ser Gly Thr
165 170 175
30 Phe Met Glu Phe Asp Ala Tyr Ala Gln Pro Gly Asn Ser Gly Ser Pro
180 185 190
Val Leu Asn Ser Lys His Glu Leu Ile Gly Ile Leu Tyr Ala Gly Ser
195 200 205
35 Gly Lys Asp Glu Ser Glu Lys Asn Phe Gly Val Tyr Phe Thr Pro Gln
210 215 220
Leu Lys Glu Phe Ile Gln Asn Asn Ile Glu Lys
225 230 235

<210> 120

<211> 163

<212> PRT

<213> staphylococcus aureus

<400> 120

EP 2 510 947 B1

Met Leu Lys Arg Ser Leu Leu Phe Leu Thr Val Leu Leu Leu Leu Phe
1 5 10 15
Ser Phe Ser Ser Ile Thr Asn Glu Val Ser Ala Ser Ser Ser Phe Asp
5 20 25 30
Lys Gly Lys Tyr Lys Lys Gly Asp Asp Ala Ser Tyr Phe Glu Pro Thr
35 40 45
Gly Pro Tyr Leu Met Val Asn Val Thr Gly Val Asp Gly Lys Gly Asn
10 50 55 60
Glu Leu Leu Ser Pro His Tyr Val Glu Phe Pro Ile Lys Pro Gly Thr
65 70 75 80
Thr Leu Thr Lys Glu Lys Ile Glu Tyr Tyr Val Glu Trp Ala Leu Asp
15 85 90 95
Ala Thr Ala Tyr Lys Glu Phe Arg Val Val Glu Leu Asp Pro Ser Ala
100 105 110
Lys Ile Glu Val Thr Tyr Tyr Asp Lys Asn Lys Lys Lys Glu Glu Thr
20 115 120 125
Lys Ser Phe Pro Ile Thr Glu Lys Gly Phe Val Val Pro Asp Leu Ser
130 135 140
Glu His Ile Lys Asn Pro Gly Phe Asn Leu Ile Thr Lys Val Ile Ile
25 145 150 155 160
Glu Lys Lys

<210> 121

<211> 290

<212> PRT

<213> Staphylococcus aureus

<400> 121

Met Lys Lys Lys Ala Leu Leu Pro Leu Phe Leu Gly Ile Met Val Phe
35 1 5 10 15
Leu Ala Gly Cys Asp Tyr Ser Lys Pro Glu Lys Arg Ser Gly Phe Phe
20 25 30
Tyr Asn Thr Phe Val Asp Pro Met Lys Asn Val Leu Asp Trp Leu Gly
40 35 40 45
Asn Asn Leu Leu Asn Asp Asn Tyr Gly Leu Ala Ile Ile Ile Leu Val
50 55 60
Leu Val Ile Arg Ile Ile Leu Leu Pro Phe Met Leu Ser Asn Tyr Lys
45 65 70 75 80
Asn Ser His Met Met Arg Gln Lys Met Lys Val Ala Lys Pro Glu Val
85 90 95
Glu Lys Ile Gln Glu Lys Val Lys Arg Ala Arg Thr Gln Glu Glu Lys
50 100 105 110
Met Ala Ala Asn Gln Glu Leu Met Gln Val Tyr Lys Lys Tyr Asp Met
115 120 125
Asn Pro Ile Lys Ser Met Leu Gly Cys Leu Pro Met Leu Ile Gln Leu
55 130 135 140
Pro Ile Ile Met Gly Leu Tyr Phe Val Leu Lys Asp Gln Leu Val Asp
145 150 155 160

Gly Leu Phe Lys Tyr Pro His Phe Leu Trp Phe Asp Leu Gly Arg Pro
 165 170 175
 5 Asp Ile Trp Ile Thr Ile Ile Ala Gly Val Leu Tyr Phe Ile Gln Ala
 180 185 190
 Tyr Val Ser Ser Lys Thr Met Pro Asp Glu Gln Arg Gln Met Gly Tyr
 195 200 205
 10 Met Met Met Val Ile Ser Pro Ile Met Ile Ile Trp Ile Ser Leu Ser
 210 215 220
 Ser Ala Ser Ala Leu Gly Leu Tyr Trp Ser Val Ser Ala Ala Phe Leu
 225 230 235 240
 15 Val Val Gln Thr His Phe Ala Asn Ile Tyr Tyr Glu Lys Val Ala Lys
 245 250 255
 Lys Glu Val Gln Pro Phe Ile Glu Ala Tyr Glu Arg Glu His Asn Gly
 260 265 270
 20 Gly Ser Asn Lys Lys Gly Lys Asn Thr Gln Val Val Ser Lys Lys Lys
 275 280 285
 Lys Lys
 290

25 <210> 122
 <211> 460
 <212> PRT
 <213> Staphylococcus aureus

30 <400> 122

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EP 2 510 947 B1

Met Lys Ser Cys Pro Lys Cys Gly Gln Gln Ala Gln Asp Asp Val Gln
 1 5 10 15
 Ile Cys Thr Gln Cys Gly His Lys Phe Asp Ser Arg Gln Ala Leu Tyr
 5 20 25 30
 Arg Lys Ser Thr Asp Glu Asp Ile Gln Thr Asn Asn Ile Lys Met Arg
 35 40 45
 Lys Met Val Pro Trp Ala Ile Gly Phe Phe Ile Leu Ile Leu Ile Ile
 10 50 55 60
 Ile Leu Phe Phe Leu Leu Arg Asn Phe Asn Ser Pro Glu Ala Gln Thr
 65 70 75 80
 Lys Ile Leu Val Asn Ala Ile Glu Asn Asn Asp Lys Gln Lys Val Ala
 15 85 90 95
 Thr Leu Leu Ser Thr Lys Asp Asn Lys Val Asp Ser Glu Glu Ala Lys
 100 105 110
 Val Tyr Ile Asn Tyr Ile Lys Asp Glu Val Gly Leu Lys Gln Phe Val
 20 115 120 125
 Ser Asp Leu Lys Asn Thr Val His Lys Leu Asn Lys Ser Lys Thr Ser
 130 135 140
 Val Ala Ser Tyr Ile Gln Thr Arg Ser Gly Gln Asn Ile Leu Arg Val
 25 145 150 155 160
 Ser Lys Asn Gly Thr Arg Tyr Ile Phe Phe Asp Asn Met Ser Phe Thr
 165 170 175
 Ala Pro Thr Lys Gln Pro Ile Val Lys Pro Lys Glu Lys Thr Lys Tyr
 180 185 190
 30
 Glu Phe Lys Ser Gly Gly Lys Lys Lys Met Val Ile Ala Glu Ala Asn

EP 2 510 947 B1

	195	200	205
	Lys Val Thr Pro Ile Gly	Asn Phe Ile Pro Gly	Thr Tyr Arg Ile Pro
5	210	215	220
	Ala Met Lys Ser Thr Glu	Asn Gly Asp Phe Ala	Gly His Leu Lys Phe
	225	230	235
	Asp Phe Arg Gln Ser	Asn Ser Glu Thr Val	Asp Val Thr Glu Asp Phe
10	245	250	255
	Glu Glu Ala Asn Ile Ser Val Thr	Leu Lys Gly Asp Thr	Lys Leu Asn
	260	265	270
	Asp Ser Ser Lys Lys Val Thr	Ile Asn Asp His Glu	Met Ala Phe Ser
15	275	280	285
	Ser Ser Lys Thr Tyr Gly	Pro Tyr Pro Gln Asn	Lys Asp Ile Thr Ile
	290	295	300
	Ser Ala Ser Gly Lys Ala	Lys Asp Lys Thr Phe	Thr Thr Gln Thr Lys
20	305	310	315
	Thr Ile Lys Ala Ser Asp	Leu Lys Tyr Asn Thr	Glu Ile Thr Leu Asn
	325	330	335
	Phe Asp Ser Glu Asp Ile Glu	Asp Tyr Val Glu Lys Lys	Glu Lys Glu
25	340	345	350
	Glu Asn Ser Leu Lys Asn Lys	Leu Ile Glu Phe Phe	Ala Gly Tyr Ser
	355	360	365
	Leu Ala Asn Asn Ala Ala	Phe Asn Gln Ser Asp	Phe Asp Phe Val Ser
30	370	375	380
	Ser Tyr Ile Lys Lys Gly	Ser Ser Phe Tyr Asp	Asp Val Lys Lys Arg
	385	390	395
	Val Ser Lys Gly Ser Leu	Met Met Ile Ser	Ser Pro Gln Ile Ile Asp
	405	410	415
35	Ala Glu Lys His Gly Asp	Lys Ile Thr Ala Thr	Val Arg Leu Ile Asn
	420	425	430
	Glu Asn Gly Lys Gln Val	Asp Lys Glu Tyr Glu	Leu Glu Gln Gly Ser
	435	440	445
40	Gln Asp Arg Leu Gln Leu	Ile Lys Thr Ser Glu	Lys
	450	455	460

<210> 123

<211> 322

<212> PRT

<213> Staphylococcus aureus

<400> 123

EP 2 510 947 B1

Met Arg Lys Lys Trp Ser Thr Leu Ala Phe Gly Phe Leu Val Ala Ala
1 5 10 15
Tyr Ala His Ile Arg Ile Lys Glu Lys Arg Ser Val Lys Ser Tyr Met
5 20 25 30
Leu Glu Gln Gly Ile Arg Leu Ser Arg Ala Lys Arg Arg Phe Met Tyr
35 40 45
Lys Glu Glu Ala Met Lys Ala Leu Glu Lys Met Ala Pro Gln Thr Ala
10 50 55 60
Gly Glu Tyr Glu Gly Thr Asn Tyr Gln Phe Lys Met Pro Val Lys Val
65 70 75 80
Asp Lys His Phe Gly Ser Thr Val Tyr Thr Val Asn Asp Lys Gln Asp
15 85 90 95
Lys His Gln Arg Val Val Leu Tyr Ala His Gly Gly Ala Trp Phe Gln
100 105 110
Asp Pro Leu Lys Ile His Phe Glu Phe Ile Asp Glu Leu Ala Glu Thr
20 115 120 125
Leu Asn Ala Lys Val Ile Met Pro Val Tyr Pro Lys Ile Pro His Gln
130 135 140
Asp Tyr Gln Ala Thr Tyr Val Leu Phe Glu Lys Leu Tyr His Asp Leu
25 145 150 155 160
Leu Asn Gln Val Ala Asp Ser Lys Gln Ile Val Val Met Gly Asp Ser
165 170 175
Ala Gly Gly Gln Ile Ala Leu Ser Phe Ala Gln Leu Leu Lys Glu Lys
30 180 185 190
His Ile Val Gln Pro Gly His Ile Val Leu Ile Ser Pro Val Leu Asp
195 200 205
Ala Thr Met Gln His Pro Glu Ile Pro Asp Tyr Leu Lys Lys Asp Pro
35 210 215 220
Met Val Gly Val Asp Gly Ser Val Phe Leu Ala Glu Gln Trp Ala Gly
225 230 235 240
Asp Thr Pro Leu Asp Asn Tyr Lys Val Ser Pro Ile Asn Gly Asp Leu
40 245 250 255
Asp Gly Leu Gly Arg Ile Thr Leu Thr Val Gly Thr Lys Glu Val Leu
260 265 270
Tyr Pro Asp Ala Leu Asn Leu Ser Gln Leu Leu Ser Ala Lys Gly Ile
45 275 280 285
Glu His Asp Phe Ile Pro Gly Tyr Tyr Gln Phe His Ile Tyr Pro Val
290 295 300
Phe Pro Ile Pro Glu Arg Arg Arg Phe Leu Tyr Gln Val Lys Asn Ile
50 305 310 315 320
Ile Asn

<210> 124

<211> 143

<212> PRT

<213> Staphylococcus aureus

<400> 124

EP 2 510 947 B1

Met Glu Tyr Lys Lys Ile Leu Ile Arg Leu Leu Ile Ala Phe Ala Val
1 5 10 15
Leu Phe Ser Ala Asp Phe Thr Tyr Gln Ser Val Glu Gln Thr His Gln
5 20 25 30
Ser His Ala Ala Val Asn Tyr Tyr Ser Lys Asn Gln Cys Thr Trp Trp
35 40 45
Ala Phe Lys Arg Arg Ala Gln Val Gly Lys Pro Val Ser Asn Arg Trp
10 50 55 60
Gly Asn Ala Lys Asn Trp Tyr Tyr Asn Ala Arg Lys Ser Lys Tyr Ala
65 70 75 80
Thr Gly Arg Thr Pro Arg Lys Phe Ala Val Met Gln Ser Thr Ala Gly
15 85 90 95
Tyr Tyr Gly His Val Ala Val Val Glu Gln Val Tyr Lys Asn Gly Ser
100 105 110
Ile Lys Val Ser Glu Tyr Asn Phe Tyr Arg Pro Leu Lys Tyr Asn Thr
20 115 120 125
Arg Val Leu Ser Lys Lys Ala Ala Arg Asn Phe Asn Tyr Ile Tyr
130 135 140

25 <210> 125
<211> 255
<212> PRT
<213> staphylococcus aureus

30 <400> 125

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EP 2 510 947 B1

Met Lys Lys Ile Val Thr Ala Thr Ile Ala Thr Ala Gly Leu Ala Thr
1 5 10 15
Ile Ala Phe Ala Gly His Asp Ala Gln Ala Ala Glu Gln Asn Asn Asn
5 20 25 30
Gly Tyr Asn Ser Asn Asp Ala Gln Ser Tyr Ser Tyr Thr Tyr Thr Ile
35 40 45
Asp Ala Gln Gly Asn Tyr His Tyr Thr Trp Thr Gly Asn Trp Asn Pro
10 50 55 60
Ser Gln Leu Thr Gln Asn Asn Thr Tyr Tyr Tyr Asn Asn Tyr Asn Thr
65 70 75 80
Tyr Ser Tyr Asn Asn Ala Ser Tyr Asn Asn Tyr Tyr Asn His Ser Tyr
15 85 90 95
Gln Tyr Asn Asn Tyr Thr Asn Asn Ser Gln Thr Ala Thr Asn Asn Tyr
100 105 110
Tyr Thr Gly Gly Ser Gly Ala Ser Tyr Ser Thr Thr Ser Asn Asn Val
20 115 120 125
His Val Thr Thr Thr Ala Ala Pro Ser Ser Asn Gly Arg Ser Ile Ser
130 135 140
Asn Gly Tyr Ala Ser Gly Ser Asn Leu Tyr Thr Ser Gly Gln Cys Thr
25 145 150 155 160
Tyr Tyr Val Phe Asp Arg Val Gly Gly Lys Ile Gly Ser Thr Trp Gly
165 170 175
Asn Ala Ser Asn Trp Ala Asn Ala Ala Ala Ser Ser Gly Tyr Thr Val
30 180 185 190
Asn Asn Thr Pro Lys Val Gly Ala Ile Met Gln Thr Thr Gln Gly Tyr
195 200 205
Tyr Gly His Val Ala Tyr Val Glu Gly Val Asn Ser Asn Gly Ser Val
35 210 215 220
Arg Val Ser Glu Met Asn Tyr Gly His Gly Ala Gly Val Val Thr Ser
225 230 235 240
Arg Thr Ile Ser Ala Asn Gln Ala Gly Ser Tyr Asn Phe Ile His
40 245 250 255

<210> 126

<211> 131

<212> PRT

<213> staphylococcus aureus

<400> 126

EP 2 510 947 B1

Met Lys Lys Leu Ile Ile Ser Ile Met Ala Val Met Leu Phe Leu Thr
1 5 10 15
Gly Cys Gly Lys Ser Gln Glu Lys Ala Thr Leu Glu Lys Asp Ile Asp
5 20 25 30
Asn Leu Gln Lys Glu Asn Lys Glu Leu Lys Asp Lys Lys Glu Lys Leu
35 40 45
Gln Gln Glu Lys Glu Lys Leu Ala Asp Lys Gln Lys Asp Leu Glu Lys
10 50 55 60
Glu Val Lys Asp Leu Lys Pro Ser Lys Glu Asp Asn Lys Asp Asp Lys
65 70 75 80
Lys Asp Glu Asp Lys Asn Lys Asp Lys Asp Lys Asp Lys Glu Ala Ser
15 85 90 95
Gln Asp Lys Gln Ser Lys Asp Gln Thr Lys Ser Ser Asp Lys Asp Asn
100 105 110
His Lys Lys Pro Thr Ser Ala Asp Lys Asp Gln Lys Ala Asn Asp Lys
20 115 120 125
His Gln Ser
130

<210> 127

<211> 192

<212> PRT

<213> Staphylococcus aureus

<400> 127

EP 2 510 947 B1

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

<210> 128

<211> 505

<212> PRT

<213> Staphylococcus aureus

<400> 128

EP 2 510 947 B1

Met Thr Gln Gln Gln Asn Asp Lys Arg Thr Leu Lys Asn Lys His Thr
 1 5 10 15
 Tyr Gln Asn Glu Pro Leu Pro Asn Arg Lys Asp Phe Val Val Ser Phe
 5 20 25 30
 Ile Thr Gly Ala Leu Val Gly Ser Ala Leu Gly Leu Tyr Phe Lys Asn
 35 40 45
 Lys Val Tyr Gln Lys Ala Asp Asp Leu Lys Val Lys Glu Gln Glu Leu
 10 50 55 60
 Ser Gln Lys Phe Glu Glu Arg Lys Thr Gln Leu Glu Glu Thr Val Ala
 65 70 75 80
 Tyr Thr Lys Glu Arg Val Glu Gly Phe Leu Asn Lys Ser Lys Asn Glu
 15 85 90 95
 Gln Ala Ala Leu Lys Ala Gln Gln Ala Ala Ile Lys Glu Glu Ala Ser
 100 105 110
 Ala Asn Asn Leu Ser Asp Thr Ser Gln Glu Ala Gln Glu Ile Gln Glu
 20 115 120 125
 Ala Lys Arg Glu Ala Gln Ala Glu Ala Asp Lys Ser Val Ala Val Ser
 130 135 140
 Asn Lys Glu Ser Lys Ala Val Ala Leu Lys Ala Gln Gln Ala Ala Ile
 25 145 150 155 160
 Lys Glu Glu Ala Ser Ala Asn Asn Leu Ser Asp Thr Ser Gln Glu Ala
 165 170 175
 Gln Glu Ile Gln Glu Ala Lys Lys Glu Ala Gln Ala Glu Thr Asp Lys
 30 180 185 190
 Ser Ala Ala Val Ser Asn Glu Glu Pro Lys Ala Val Ala Leu Lys Ala
 195 200 205
 Gln Gln Ala Ala Ile Lys Glu Glu Ala Ser Ala Asn Asn Leu Ser Asp
 35 210 215 220
 Thr Ser Gln Glu Ala Gln Glu Val Gln Glu Ala Lys Lys Glu Ala Gln
 225 230 235 240
 Ala Glu Thr Asp Lys Ser Ala Ala Val Ser Asn Glu Glu Pro Lys Ala
 245 250 255
 Val Ala Leu Lys Ala Gln Gln Ala Ala Ile Lys Glu Glu Ala Ser Ala
 40 260 265 270
 Asn Asn Leu Ser Asp Ile Ser Gln Glu Ala Gln Glu Val Gln Glu Ala
 275 280 285
 Lys Lys Glu Ala Gln Ala Glu Lys Asp Ser Asp Thr Leu Thr Lys Asp
 45 290 295 300
 Ala Ser Ala Ala Lys Val Glu Val Ser Lys Pro Glu Ser Gln Ala Glu
 305 310 315 320
 Arg Leu Ala Asn Ala Ala Lys Gln Lys Gln Ala Lys Leu Thr Pro Gly
 50 325 330 335

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Ser Lys Glu Ser Gln Leu Thr Glu Ala Leu Phe Ala Glu Lys Pro Val
 340 345 350
 5 Ala Lys Asn Asp Leu Lys Glu Ile Pro Gln Leu Val Thr Lys Lys Asn
 355 360 365
 Asp Val Ser Glu Thr Glu Thr Val Asn Ile Asp Asn Lys Asp Thr Val
 370 375 380
 10 Lys Gln Lys Glu Ala Lys Phe Glu Asn Gly Val Ile Thr Arg Lys Ala
 385 390 395 400
 Asp Glu Lys Thr Thr Asn Asn Thr Ala Val Asp Lys Lys Ser Gly Lys
 405 410 415
 15 Gln Ser Lys Lys Thr Thr Pro Ser Asn Lys Arg Asn Ala Ser Lys Ala
 420 425 430
 Ser Thr Asn Lys Thr Ser Gly Gln Lys Lys Gln His Asn Lys Lys Ser
 435 440 445
 20 Ser Gln Gly Ala Lys Lys Gln Ser Ser Ser Ser Lys Ser Thr Gln Lys
 450 455 460
 Asn Asn Gln Thr Ser Asn Lys Asn Ser Lys Thr Thr Asn Ala Lys Ser
 465 470 475 480
 25 Ser Asn Ala Ser Lys Thr Pro Asn Ala Lys Val Glu Lys Ala Lys Ser
 485 490 495
 Lys Ile Glu Lys Arg Thr Phe Asn Asp
 500 505

30 <210> 129
 <211> 305
 <212> PRT
 <213> Staphylococcus aureus
 35 <400> 129

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EP 2 510 947 B1

Met Phe Lys Arg Thr Lys Leu Ile Leu Ile Ala Thr Leu Leu Leu Ser
 1 5 10 15
 Gly Cys Ser Thr Thr Asn Asn Glu Ser Asn Lys Glu Thr Lys Ser Val
 5 20 25 30
 Pro Glu Glu Met Glu Ala Ser Lys Tyr Val Gly Gln Gly Phe Gln Pro
 35 40 45
 Pro Ala Glu Lys Asp Val Val Glu Phe Ala Lys Lys His Lys Asp Lys
 10 50 55 60
 Ile Ala Lys Arg Gly Glu Gln Phe Phe Met Asp Asn Phe Gly Leu Lys
 65 70 75 80
 Val Lys Ala Thr Asn Val Val Gly Ser Gly Lys Gly Val Glu Val Phe
 15 85 90 95
 Val His Cys Asp Asp His Asp Ile Val Phe Asn Ala Ser Ile Pro Phe
 100 105 110
 Asp Lys Ser Ile Ile Glu Ser Asp Ser Ser Leu Arg Ser Glu Asp Lys
 20 115 120 125
 Gly Asp Asp Met Ser Thr Leu Val Gly Thr Val Leu Ser Gly Phe Glu
 130 135 140
 Tyr Arg Thr Gln Lys Glu Lys Tyr Asp Asn Leu Tyr Lys Phe Phe Lys
 25 145 150 155 160
 Asp Asn Glu Glu Lys Tyr Gln Tyr Thr Gly Phe Thr Lys Glu Ala Ile
 165 170 175
 Asn Lys Thr Gln Asn Val Gly Tyr Lys Asn Glu Tyr Phe Tyr Ile Thr
 30 180 185 190
 Tyr Ser Ser Arg Ser Leu Lys Glu Tyr Arg Lys Tyr Tyr Glu Pro Leu
 195 200 205
 Ile His Lys Asn Asp Lys Glu Phe Lys Glu Gly Met Glu Gln Ala Arg
 35 210 215 220
 Lys Glu Val Asn Tyr Ala Ala Asn Thr Asp Thr Val Thr Thr Leu Phe
 225 230 235 240
 Ser Thr Lys Glu Asn Phe Thr Lys Asp Asn Thr Val Asp Asp Val Ile
 40 245 250 255
 Glu Leu Ser Asp Lys Leu Tyr Asn Phe Lys Asn Lys Pro Glu Lys Ser
 260 265 270
 Thr Ile Thr Ile Gln Ile Gly Lys Pro Thr Ile Asn Thr Lys Lys Ala
 45 275 280 285
 Phe Tyr Asp Asp Asn Asp Pro Ile Glu Tyr Gly Val Tyr Arg Lys Asp
 290 295 300
 Glu
 50 305

<210> 130

<211> 226

55 <212> PRT

<213> Staphylococcus aureus

<400> 130

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[illegible]

<210> 131

<211> 231

<212> PRT

<213> Staphylococcus aureus

<400> 131

EP 2 510 947 B1

Met Lys Met Lys Asn Ile Ala Lys Ile Ser Leu Leu Leu Gly Ile Leu
1 5 10 15
Ala Thr Gly Val Asn Thr Thr Thr Glu Lys Pro Val His Ala Glu Lys
5 20 25 30
Lys Pro Ile Val Ile Ser Glu Asn Ser Lys Lys Leu Lys Ala Tyr Tyr
35 40 45
Asn Gln Pro Ser Ile Glu Tyr Lys Asn Val Thr Gly Tyr Ile Ser Phe
10 50 55 60
Ile Gln Pro Ser Ile Lys Phe Met Asn Ile Ile Asp Gly Asn Ser Val
65 70 75 80
Asn Asn Ile Ala Leu Ile Gly Lys Asp Lys Gln His Tyr His Thr Gly
15 85 90 95
Val His Arg Asn Leu Asn Ile Phe Tyr Val Asn Glu Asp Lys Arg Phe
100 105 110
Glu Gly Ala Lys Tyr Ser Ile Gly Gly Ile Thr Ser Ala Asn Asp Lys
20 115 120 125
Ala Val Asp Leu Ile Ala Glu Ala Arg Val Ile Lys Glu Asp His Thr
130 135 140
Gly Glu Tyr Asp Tyr Asp Phe Phe Pro Phe Lys Ile Asp Lys Glu Ala
25 145 150 155 160
Met Ser Leu Lys Glu Ile Asp Phe Lys Leu Arg Lys Tyr Leu Ile Asp
165 170 175
Asn Tyr Gly Leu Tyr Gly Glu Met Ser Thr Gly Lys Ile Thr Val Lys
30 180 185 190
Lys Lys Tyr Tyr Gly Lys Tyr Thr Phe Glu Leu Asp Lys Lys Leu Gln
195 200 205
Glu Asp Arg Met Ser Asp Val Ile Asn Val Thr Asp Ile Asp Arg Ile
35 210 215 220
Glu Ile Lys Val Ile Lys Ala
225 230

<210> 132

<211> 356

<212> PRT

<213> Staphylococcus aureus

<400> 132

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

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Thr Thr Gly Ala Ile Thr Val Thr Thr Gln Ser Val Lys Ala Glu Lys
 20 25 30
 Ile Gln Ser Thr Lys Val Asp Lys Val Pro Thr Leu Lys Ala Glu Arg
 5 35 40 45
 Leu Ala Met Ile Asn Ile Thr Ala Gly Ala Asn Ser Ala Thr Thr Gln
 50 55 60
 Ala Ala Asn Thr Arg Gln Glu Arg Thr Pro Lys Leu Glu Lys Ala Pro
 10 65 70 75 80
 Asn Thr Asn Glu Glu Lys Thr Ser Ala Ser Lys Ile Glu Lys Ile Ser
 85 90 95
 Gln Pro Lys Gln Glu Glu Gln Lys Thr Leu Asn Ile Ser Ala Thr Pro
 15 100 105 110
 Ala Pro Lys Gln Glu Gln Ser Gln Thr Thr Thr Glu Ser Thr Thr Pro
 115 120 125
 Lys Thr Lys Val Thr Thr Pro Pro Ser Thr Asn Thr Pro Gln Pro Met
 20 130 135 140
 Gln Ser Thr Lys Ser Asp Thr Pro Gln Ser Pro Thr Ile Lys Gln Ala
 145 150 155 160
 Gln Thr Asp Met Thr Pro Lys Tyr Glu Asp Leu Arg Ala Tyr Tyr Thr
 25 165 170 175
 Lys Pro Ser Phe Glu Phe Glu Lys Gln Phe Gly Phe Met Leu Lys Pro
 180 185 190
 Trp Thr Thr Val Arg Phe Met Asn Val Ile Pro Asn Arg Phe Ile Tyr
 30 195 200 205
 Lys Ile Ala Leu Val Gly Lys Asp Glu Lys Lys Tyr Lys Asp Gly Pro
 210 215 220
 Tyr Asp Asn Ile Asp Val Phe Ile Val Leu Glu Asp Asn Lys Tyr Gln
 35 225 230 235 240
 Leu Lys Lys Tyr Ser Val Gly Gly Ile Thr Lys Thr Asn Ser Lys Lys
 245 250 255
 Val Asn His Lys Val Glu Leu Ser Ile Thr Lys Lys Asp Asn Gln Gly
 40 260 265 270
 Met Ile Ser Arg Asp Val Ser Glu Tyr Met Ile Thr Lys Glu Glu Ile
 275 280 285
 Ser Leu Lys Glu Leu Asp Phe Lys Leu Arg Lys Gln Leu Ile Glu Lys
 45 290 295 300
 His Asn Leu Tyr Gly Asn Met Gly Ser Gly Thr Ile Val Ile Lys Met
 305 310 315 320
 Lys Asn Gly Gly Lys Tyr Thr Phe Glu Leu His Lys Lys Leu Gln Glu
 325 330 335
 His Arg Met Ala Asp Val Ile Asp Gly Thr Asn Ile Asp Asn Ile Glu
 50 340 345 350
 Val Asn Ile Lys
 355

<210> 133
 <211> 308
 <212> PRT

EP 2 510 947 B1

<213> Staphylococcus aureus

<400> 133

5 Met Lys Ile Thr Thr Ile Ala Lys Thr Ser Leu Ala Leu Gly Leu Leu
1 5 10 15
Thr Thr Gly Val Ile Thr Thr Thr Thr Gln Ala Ala Asn Ala Thr Thr
20 25 30
10 Leu Ser Ser Thr Lys Val Glu Ala Pro Gln Ser Thr Pro Pro Ser Thr
35 40 45
Lys Ile Glu Ala Pro Gln Ser Lys Pro Asn Ala Thr Thr Pro Pro Ser
50 55 60
15 Thr Lys Val Glu Ala Pro Gln Gln Thr Ala Asn Ala Thr Thr Pro Pro
65 70 75 80
Ser Thr Lys Val Thr Thr Pro Pro Ser Thr Asn Thr Pro Gln Pro Met
85 90 95
20 Gln Ser Thr Lys Ser Asp Thr Pro Gln Ser Pro Thr Thr Lys Gln Val
100 105 110
Pro Thr Glu Ile Asn Pro Lys Phe Lys Asp Leu Arg Ala Tyr Tyr Thr
115 120 125
25 Lys Pro Ser Leu Glu Phe Lys Asn Glu Ile Gly Ile Ile Leu Lys Lys
130 135 140
Trp Thr Thr Ile Arg Phe Met Asn Val Val Pro Asp Tyr Phe Ile Tyr
145 150 155 160
30 Lys Ile Ala Leu Val Gly Lys Asp Asp Lys Lys Tyr Gly Glu Gly Val
165 170 175
His Arg Asn Val Asp Val Phe Val Val Leu Glu Glu Asn Asn Tyr Asn
180 185 190
35 Leu Glu Lys Tyr Ser Val Gly Gly Ile Thr Lys Ser Asn Ser Lys Lys
195 200 205
Val Asp His Lys Ala Gly Val Arg Ile Thr Lys Glu Asp Asn Lys Gly
210 215 220
40 Thr Ile Ser His Asp Val Ser Glu Phe Lys Ile Thr Lys Glu Gln Ile
225 230 235 240
Ser Leu Lys Glu Leu Asp Phe Lys Leu Arg Lys Gln Leu Ile Glu Lys
245 250 255
45 Asn Asn Leu Tyr Gly Asn Val Gly Ser Gly Lys Ile Val Ile Lys Met
260 265 270
Lys Asn Gly Gly Lys Tyr Thr Phe Glu Leu His Lys Lys Leu Gln Glu
275 280 285
50 Asn Arg Met Ala Asp Val Ile Asp Gly Thr Asn Ile Asp Asn Ile Glu
290 295 300
Val Asn Ile Lys
305

55 <210> 134

<211> 234

<212> PRT

<213> Staphylococcus aureus

<400> 134

5 Met Lys Met Thr Ala Ile Ala Lys Ala Ser Leu Ala Leu Gly Ile Leu
 1 5 10
 Ala Thr Gly Thr Ile Thr Ser Leu His Gln Thr Val Asn Ala Ser Glu
 20 25 30
 10 His Lys Ala Lys Tyr Glu Asn Val Thr Lys Asp Ile Phe Asp Leu Arg
 35 40 45
 Asp Tyr Tyr Ser Gly Ala Ser Lys Glu Leu Lys Asn Val Thr Gly Tyr
 50 55 60
 15 Arg Tyr Ser Lys Gly Gly Lys His Tyr Leu Ile Phe Asp Lys Asn Arg
 65 70 75 80
 Lys Phe Thr Arg Val Gln Ile Phe Gly Lys Asp Ile Glu Arg Phe Lys
 85 90 95
 20 Ala Arg Lys Asn Pro Gly Leu Asp Ile Phe Val Val Lys Glu Ala Glu
 100 105 110
 Asn Arg Asn Gly Thr Val Phe Ser Tyr Gly Gly Val Thr Lys Lys Asn
 115 120 125
 25 Gln Asp Ala Tyr Tyr Asp Tyr Ile Asn Ala Pro Arg Phe Gln Ile Lys
 130 135 140
 Arg Asp Glu Gly Asp Gly Ile Ala Thr Tyr Gly Arg Val His Tyr Ile
 145 150 155 160
 30 Tyr Lys Glu Glu Ile Ser Leu Lys Glu Leu Asp Phe Lys Leu Arg Gln
 165 170 175
 Tyr Leu Ile Gln Asn Phe Asp Leu Tyr Lys Lys Phe Pro Lys Asp Ser
 180 185 190
 35 Lys Ile Lys Val Ile Met Lys Asp Gly Gly Tyr Tyr Thr Phe Glu Leu
 195 200 205
 Asn Lys Lys Leu Gln Thr Asn Arg Met Ser Asp Val Ile Asp Gly Arg
 210 215 220
 40 Asn Ile Glu Lys Ile Glu Ala Asn Ile Arg
 225 230

<210> 135

<211> 231

<212> PRT

45 <213> Staphylococcus aureus

<400> 135

50

55

EP 2 510 947 B1

Met Lys Leu Lys Thr Leu Ala Lys Ala Thr Leu Val Leu Gly Leu Leu
 1 5 10 15
 Ala Thr Gly Val Ile Thr Thr Glu Ser Gln Thr Val Lys Ala Ala Glu
 20 25 30
 Ser Thr Gln Gly Gln His Asn Tyr Lys Ser Leu Lys Tyr Tyr Tyr Ser
 35 40 45
 Lys Pro Ser Ile Glu Leu Lys Asn Leu Asp Gly Leu Tyr Arg Gln Lys
 50 55 60
 Val Thr Asp Lys Gly Val Tyr Val Trp Lys Asp Arg Lys Asp Tyr Phe
 65 70 75 80
 Val Gly Leu Leu Gly Lys Asp Ile Glu Lys Tyr Pro Gln Gly Glu His
 85 90 95
 Asp Lys Gln Asp Ala Phe Leu Val Ile Glu Glu Glu Thr Val Asn Gly
 100 105 110
 Arg Gln Tyr Ser Ile Gly Gly Leu Ser Lys Thr Asn Ser Lys Glu Phe
 115 120 125
 Ser Lys Glu Val Asp Val Lys Val Thr Arg Lys Ile Asp Glu Ser Ser
 130 135 140
 Glu Lys Ser Lys Asp Ser Lys Phe Lys Ile Thr Lys Glu Glu Ile Ser
 145 150 155 160
 Leu Lys Glu Leu Asp Phe Lys Leu Arg Lys Lys Leu Met Glu Glu Glu
 165 170 175
 Lys Leu Tyr Gly Ala Val Asn Asn Arg Lys Gly Lys Ile Val Val Lys
 180 185 190
 Met Glu Asp Asp Lys Phe Tyr Thr Phe Glu Leu Thr Lys Lys Leu Gln
 195 200 205
 Pro His Arg Met Gly Asp Thr Ile Asp Gly Thr Lys Ile Lys Glu Ile
 210 215 220
 Asn Val Glu Leu Glu Tyr Lys
 225 230

<210> 136
 <211> 231
 <212> PRT
 <213> Staphylococcus aureus

<400> 136

EP 2 510 947 B1

1 Met Lys Leu Lys Thr Leu Ala Lys Ala Thr Leu Ala Leu Gly Leu Leu
 5 Thr Thr Gly Val Ile Thr Ser Glu Gly Gln Ala Val Gln Ala Lys Glu
 Lys Gln Glu Arg Val Gln His Leu Tyr Asp Ile Lys Asp Leu His Arg
 10 Tyr Tyr Ser Ser Glu Ser Phe Glu Phe Ser Asn Ile Ser Gly Lys Val
 Glu Asn Tyr Asn Gly Ser Asn Val Val Arg Phe Asn Gln Glu Asn Gln
 15 Asn His Gln Leu Phe Leu Leu Gly Lys Asp Lys Glu Lys Tyr Lys Glu
 Gly Ile Glu Gly Lys Asp Val Phe Val Val Lys Glu Leu Ile Asp Pro
 20 Asn Gly Arg Leu Ser Thr Val Gly Gly Val Thr Lys Lys Asn Asn Lys
 Ser Ser Glu Thr Asn Thr His Leu Phe Val Asn Lys Val Tyr Gly Gly
 25 Asn Leu Asp Ala Ser Ile Asp Ser Phe Ser Ile Asn Lys Glu Glu Val
 Ser Leu Lys Glu Leu Asp Phe Lys Ile Arg Gln His Leu Val Lys Asn
 30 Tyr Gly Leu Tyr Lys Gly Thr Thr Lys Tyr Gly Lys Ile Thr Ile Asn
 Leu Lys Asp Gly Glu Lys Gln Glu Ile Asp Leu Gly Asp Lys Leu Gln
 Phe Glu Arg Met Gly Asp Val Leu Asn Ser Lys Asp Ile Asn Lys Ile
 35 210 215 220
 Glu Val Thr Leu Lys Gln Ile
 225 230

<210> 137
 <211> 232
 <212> PRT
 <213> Staphylococcus aureus

<400> 137

EP 2 510 947 B1

Met Lys Phe Thr Val Ile Ala Lys Ala Ile Phe Ile Leu Gly Ile Leu
1 5 10 15
5 Thr Thr Ser Val Met Ile Thr Glu Asn Gln Ser Val Asn Ala Lys Gly
20 25 30
Lys Tyr Glu Lys Met Asn Arg Leu Tyr Asp Thr Asn Lys Leu His Gln
35 40 45
10 Tyr Tyr Ser Gly Pro Ser Tyr Glu Leu Thr Asn Val Ser Gly Gln Ser
50 55 60
Gln Gly Tyr Tyr Asp Ser Asn Val Leu Leu Phe Asn Gln Gln Asn Gln
65 70 75 80
15 Lys Phe Gln Val Phe Leu Leu Gly Lys Asp Glu Asn Lys Tyr Lys Glu
85 90 95
Lys Thr His Gly Leu Asp Val Phe Ala Val Pro Glu Leu Val Asp Leu
100 105 110
20 Asp Gly Arg Ile Phe Ser Val Ser Gly Val Thr Lys Lys Asn Val Lys
115 120 125
Ser Ile Phe Glu Ser Leu Arg Thr Pro Asn Leu Leu Val Lys Lys Ile
130 135 140
25 Asp Asp Lys Asp Gly Phe Ser Ile Asp Glu Phe Phe Phe Ile Gln Lys
145 150 155 160
Glu Glu Val Ser Leu Lys Glu Leu Asp Phe Lys Ile Arg Lys Leu Leu
165 170 175
30 Ile Lys Lys Tyr Lys Leu Tyr Glu Gly Ser Ala Asp Lys Gly Arg Ile
180 185 190
Val Ile Asn Met Lys Asp Glu Asn Lys Tyr Glu Ile Asp Leu Ser Asp
195 200 205
35 Lys Leu Asp Phe Glu Arg Met Ala Asp Val Ile Asn Ser Glu Gln Ile
210 215 220
Lys Asn Ile Glu Val Asn Leu Lys
225 230

<210> 138

<211> 232

<212> PRT

<213> Staphylococcus aureus

<400> 138

Met Lys Leu Thr Thr Ile Ala Lys Ala Thr Leu Ala Leu Gly Ile Leu
1 5 10 15
50 Thr Thr Gly Val Phe Thr Ala Glu Ser Gln Thr Gly His Ala Lys Val
20 25 30
Glu Leu Asp Glu Thr Gln Arg Lys Tyr Tyr Ile Asn Met Leu His Gln
35 40 45

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

<210> 139

<211> 227

<212> PRT

<213> Staphylococcus aureus

<400> 139

EP 2 510 947 B1

Met Lys Phe Thr Ala Leu Ala Lys Ala Thr Leu Ala Leu Gly Ile Leu
 1 5 10 15
 Thr Thr Gly Thr Leu Thr Thr Glu Val His Ser Gly His Ala Lys Gln
 5 20 25 30
 Asn Gln Lys Ser Val Asn Lys His Asp Lys Glu Ala Leu Tyr Arg Tyr
 35 40 45
 Tyr Thr Gly Lys Thr Met Glu Met Lys Asn Ile Ser Ala Leu Lys His
 10 50 55 60
 Gly Lys Asn Asn Leu Arg Phe Lys Phe Arg Gly Ile Lys Ile Gln Val
 65 70 75 80
 Leu Leu Pro Gly Asn Asp Lys Ser Lys Phe Gln Gln Arg Ser Tyr Glu
 15 85 90 95
 Gly Leu Asp Val Phe Phe Val Gln Glu Lys Arg Asp Lys His Asp Ile
 100 105 110
 Phe Tyr Thr Val Gly Gly Val Ile Gln Asn Asn Lys Thr Ser Gly Val
 20 115 120 125
 Val Ser Ala Pro Ile Leu Asn Ile Ser Lys Glu Lys Gly Glu Asp Ala
 130 135 140
 Phe Val Lys Gly Tyr Pro Tyr Tyr Ile Lys Lys Glu Lys Ile Thr Leu
 25 145 150 155 160
 Lys Glu Leu Asp Tyr Lys Leu Arg Lys His Leu Ile Glu Lys Tyr Gly
 165 170 175
 Leu Tyr Lys Thr Ile Ser Lys Asp Gly Arg Val Lys Ile Ser Leu Lys
 30 180 185 190
 Asp Gly Ser Phe Tyr Asn Leu Asp Leu Arg Ser Lys Leu Lys Phe Lys
 195 200 205
 Tyr Met Gly Glu Val Ile Glu Ser Lys Gln Ile Lys Asp Ile Glu Val
 35 210 215 220
 Asn Leu Lys
 225

40 <210> 140
 <211> 225
 <212> PRT
 <213> Staphylococcus aureus

45 <400> 140

50

55

Met Lys Leu Lys Asn Ile Ala Lys Ala Ser Leu Ala Leu Gly Ile Leu
 1 5 10
 Thr Thr Gly Met Ile Thr Thr Thr Ala Gln Pro Val Lys Ala Ser Thr
 5 20 25 30
 Leu Glu Val Arg Ser Gln Ala Thr Gln Asp Leu Ser Glu Tyr Tyr Asn
 35 40 45
 Arg Pro Phe Phe Glu Tyr Thr Asn Gln Ser Gly Tyr Lys Glu Glu Gly
 10 50 55 60
 Lys Val Thr Phe Thr Pro Asn Tyr Gln Leu Ile Asp Val Thr Leu Thr
 65 70 75 80
 Gly Asn Glu Lys Gln Asn Phe Gly Glu Asp Ile Ser Asn Val Asp Ile
 15 85 90 95
 Phe Val Val Arg Glu Asn Ser Asp Arg Ser Gly Asn Thr Ala Ser Ile
 100 105 110
 Gly Gly Ile Thr Lys Thr Asn Gly Ser Asn Tyr Ile Asp Lys Val Lys
 20 115 120 125
 Asp Val Asn Leu Ile Ile Thr Lys Asn Ile Asp Ser Val Thr Ser Thr
 130 135 140
 Ser Thr Ser Ser Thr Tyr Thr Ile Asn Lys Glu Glu Ile Ser Leu Lys
 25 145 150 155 160
 Glu Leu Asp Phe Lys Leu Arg Lys His Leu Ile Asp Lys His Asn Leu
 165 170 175
 Tyr Lys Thr Glu Pro Lys Asp Ser Lys Ile Arg Ile Thr Met Lys Asp
 30 180 185 190
 Gly Gly Phe Tyr Thr Phe Glu Leu Asn Lys Lys Leu Gln Thr His Arg
 195 200 205
 Met Gly Asp Val Ile Asp Gly Arg Asn Ile Glu Lys Ile Glu Val Asn
 35 210 215 220
 Leu
 225

<210> 141

<211> 116

<212> PRT

<213> Staphylococcus aureus

<400> 141

EP 2 510 947 B1

Met Lys Phe Lys Lys Tyr Ile Leu Thr Gly Thr Leu Ala Leu Leu Leu
1 5 10 15
Ser Ser Thr Gly Ile Ala Thr Ile Glu Gly Asn Lys Ala Asp Ala Ser
5 20 25 30
Ser Leu Asp Lys Tyr Leu Thr Glu Ser Gln Phe His Asp Lys Arg Ile
35 40 45
Ala Glu Glu Leu Arg Thr Leu Leu Asn Lys Ser Asn Val Tyr Ala Leu
10 50 55 60
Ala Ala Gly Ser Leu Asn Pro Tyr Tyr Lys Arg Thr Ile Met Met Asn
65 70 75 80
Glu Tyr Arg Ala Lys Ala Ala Leu Lys Lys Asn Asp Phe Val Ser Met
15 85 90 95
Ala Asp Ala Lys Val Ala Leu Glu Lys Ile Tyr Lys Glu Ile Asp Glu
100 105 110
Ile Ile Asn Arg
20 115

<210> 142

<211> 508

<212> PRT

25 <213> Staphylococcus aureus

<400> 142

Met Lys Asn Lys Leu Leu Val Leu Ser Leu Gly Ala Leu Cys Val Ser
30 1 5 10 15
Gln Ile Trp Glu Ser Asn Arg Ala Ser Ala Val Val Ser Gly Glu Lys
20 25 30
Asn Pro Tyr Val Ser Glu Ser Leu Lys Leu Thr Asn Asn Lys Asn Lys
35 35 40 45
Ser Arg Thr Val Glu Glu Tyr Lys Lys Ser Leu Asp Asp Leu Ile Trp
50 55 60
Ser Phe Pro Asn Leu Asp Asn Glu Arg Phe Asp Asn Pro Glu Tyr Lys
40 65 70 75 80
Glu Ala Met Lys Lys Tyr Gln Gln Arg Phe Met Ala Glu Asp Glu Ala
85 90 95
Leu Lys Lys Phe Phe Ser Glu Glu Lys Lys Ile Lys Asn Gly Asn Thr
45 100 105 110
Asp Asn Leu Asp Tyr Leu Gly Leu Ser His Glu Arg Tyr Glu Ser Val
115 120 125
Phe Asn Thr Leu Lys Lys Gln Ser Glu Glu Phe Leu Lys Glu Ile Glu
50 130 135 140
Asp Ile Lys Lys Asp Asn Pro Glu Leu Lys Asp Phe Asn Glu Glu Glu
145 150 155 160
Gln Leu Lys Cys Asp Leu Glu Leu Asn Lys Leu Glu Asn Gln Ile Leu
55 165 170 175
Met Leu Gly Lys Thr Phe Tyr Gln Asn Tyr Arg Asp Asp Val Glu Ser
180 185 190

EP 2 510 947 B1

Leu Tyr Ser Lys Leu Asp Leu Ile Met Gly Tyr Lys Asp Glu Glu Arg
 195 200 205
 Ala Asn Lys Lys Ala Val Asn Lys Arg Met Leu Glu Asn Lys Lys Glu
 210 215 220
 Asp Leu Glu Thr Ile Ile Asp Glu Phe Phe Ser Asp Ile Asp Lys Thr
 225 230 235 240
 Arg Pro Asn Asn Ile Pro Val Leu Glu Asp Glu Lys Gln Glu Glu Lys
 245 250 255
 Asn His Lys Asn Met Ala Gln Leu Lys Ser Asp Thr Glu Ala Ala Lys
 260 265 270
 Ser Asp Glu Ser Lys Arg Ser Lys Arg Ser Lys Arg Ser Leu Asn Thr
 275 280 285
 Gln Asn His Lys Pro Ala Ser Gln Glu Val Ser Glu Gln Gln Lys Ala
 290 295 300
 Glu Tyr Asp Lys Arg Ala Glu Glu Arg Lys Ala Arg Phe Leu Asp Asn
 305 310 315 320
 Gln Lys Ile Lys Lys Thr Pro Val Val Ser Leu Glu Tyr Asp Phe Glu
 325 330 335
 His Lys Gln Arg Ile Asp Asn Glu Asn Asp Lys Lys Leu Val Val Ser
 340 345 350
 Ala Pro Thr Lys Lys Pro Thr Ser Pro Thr Thr Tyr Thr Glu Thr Thr
 355 360 365
 Thr Gln Val Pro Met Pro Thr Val Glu Arg Gln Thr Gln Gln Gln Ile
 370 375 380
 Ile Tyr Asn Ala Pro Lys Gln Leu Ala Gly Leu Asn Gly Glu Ser His
 385 390 395 400
 Asp Phe Thr Thr Thr His Gln Ser Pro Thr Thr Ser Asn His Thr His
 405 410 415
 Asn Asn Val Val Glu Phe Glu Glu Thr Ser Ala Leu Pro Gly Arg Lys
 420 425 430
 Ser Gly Ser Leu Val Gly Ile Ser Gln Ile Asp Ser Ser His Leu Thr
 435 440 445
 Glu Arg Glu Lys Arg Val Ile Lys Arg Glu His Val Arg Glu Ala Gln
 450 455 460
 Lys Leu Val Asp Asn Tyr Lys Asp Thr His Ser Tyr Lys Asp Arg Ile
 465 470 475 480
 Asn Ala Gln Gln Lys Val Asn Thr Leu Ser Glu Gly His Gln Lys Arg
 485 490 495
 Phe Asn Lys Gln Ile Asn Lys Val Tyr Asn Gly Lys
 500 505

<210> 143

<211> 208

<212> PRT

<213> Staphylococcus aureus

<400> 143

EP 2 510 947 B1

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

5 Leu Ala Gly Cys Thr Thr Asp Lys Lys Glu Ile Lys Ala Tyr Leu Lys
20 25 30

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

10 Lys Lys Ile Ala Glu Leu Asp Glu Lys Lys Lys Lys Leu Thr Glu Asp
50 55 60

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

15 Ile Lys Asn Ala Asp Asp Arg Leu Lys Glu Phe Glu Lys Glu Glu Asp
85 90 95

Ala Ile Lys Lys Ser Glu Gln Asp Phe Lys Lys Ala Lys Ser His Val
100 105 110

20 Asp Asn Ile Asp Asn Asp Val Lys Arg Lys Glu Val Lys Gln Leu Asp
115 120 125

Asp Val Leu Lys Glu Lys Tyr Lys Leu His Ser Asp Tyr Ala Lys Ala
130 135 140

25 Tyr Lys Lys Ala Val Asn Ser Glu Lys Thr Leu Phe Lys Tyr Leu Asn
145 150 155 160

Gln Asn Asp Ala Thr Gln Gln Gly Val Asn Glu Lys Ser Lys Ala Ile
165 170 175

30 Glu Gln Asn Tyr Lys Lys Leu Lys Glu Val Ser Asp Lys Tyr Thr Lys
180 185 190

Val Leu Asn Lys Val Gly Lys Glu Lys Gln Asp Val Asp Gln Phe Lys
195 200 205

35 <210> 144
<211> 109
<212> PRT
<213> Staphylococcus aureus

40 <400> 144

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

45 Ser Leu Thr Val Ser Thr Phe Ala Gly Glu Ser His Ala Gln Thr Lys
20 25 30

Asn Val Glu Ala Ala Lys Lys Tyr Asp Gln Tyr Gln Thr Asn Phe Lys
35 40 45

50 Lys Gln Val Asn Lys Lys Val Val Asp Ala Gln Lys Ala Val Asn Phe
50 55 60

Phe Lys Arg Thr Arg Thr Val Ala Thr His Arg Lys Ala Gln Arg Ala
65 70 75 80

55 Val Asn Leu Ile His Phe Gln His Ser Tyr Glu Lys Lys Lys Leu Gln
85 90 95

Arg Gln Ile Asp Leu Val Leu Lys Tyr Asn Thr Leu Lys
100 105

<210> 145
 <211> 116
 <212> PRT
 <213> Staphylococcus aureus

5

<400> 145

Met Lys Ile Arg Lys Ser Ile Leu Ala Gly Thr Leu Ala Ile Val Leu

10

1 5 10 15

Ala Ser Pro Leu Val Thr Asn Leu Asp Lys Asn Glu Ala Gln Ala Ser
 20 25 30

15

Thr Ser Leu Pro Thr Ser Asn Glu Tyr Gln Asn Glu Lys Leu Ala Asn
 35 40 45

Glu Leu Lys Ser Leu Leu Asp Glu Leu Asn Val Asn Glu Leu Ala Thr
 50 55 60

20

Gly Ser Leu Asn Thr Tyr Tyr Lys Arg Thr Ile Lys Ile Ser Gly Gln
 65 70 75 80

Lys Ala Met Tyr Ala Leu Lys Ser Lys Asp Phe Lys Lys Met Ser Glu
 85 90 95

25

Ala Lys Tyr Gln Leu Gln Lys Ile Tyr Asn Glu Ile Asp Glu Ala Leu
 100 105 110

Lys Ser Lys Tyr
 115

30

<210> 146
 <211> 149
 <212> PRT
 <213> Staphylococcus aureus

35

<400> 146

40

45

50

55

EP 2 510 947 B1

Met Lys Lys Lys Leu Ala Thr Thr Val Leu Ala Leu Ser Phe Leu Thr
1 5 10 15
Ala Gly Ile Ser Thr His His His Ser Ala Lys Ala Phe Thr Phe Glu
20 25 30
Pro Phe Pro Thr Asn Glu Glu Ile Glu Ser Asn Lys Lys Met Leu Glu
35 40 45
Lys Glu Lys Ala Tyr Lys Glu Ser Phe Lys Asn Ser Gly Leu Pro Thr
50 55 60
Thr Leu Gly Lys Leu Asp Glu Arg Leu Arg Asn Tyr Leu Lys Lys Gly
65 70 75 80
Thr Lys Asn Ser Ala Gln Phe Glu Lys Met Val Ile Leu Thr Glu Asn
85 90 95
Lys Gly Tyr Tyr Thr Val Tyr Leu Asn Thr Pro Leu Ala Glu Asp Arg
100 105 110
Lys Asn Val Glu Leu Leu Gly Lys Met Tyr Lys Thr Tyr Phe Phe Lys
115 120 125
Lys Gly Glu Ser Lys Ser Ser Tyr Val Ile Asn Gly Pro Gly Lys Thr
130 135 140
Asn Glu Tyr Ala Tyr
145

<210> 147

<211> 257

<212> PRT

<213> Staphylococcus aureus

<400> 147

Met Lys Lys Thr Ala Phe Ile Leu Leu Leu Phe Ile Ala Leu Thr Trp
1 5 10 15
Thr Thr Ser Pro Leu Val Asn Gly Ser Glu Lys Ser Glu Glu Ile Asn
20 25 30

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

Ser

<210> 148

<211> 154

<212> PRT

<213> Staphylococcus aureus

<400> 148

EP 2 510 947 B1

1 Met Lys Arg Leu 5 Leu Gly Leu Leu Leu Val 10 Ser Thr Leu Val 15 Leu Ser
 5 Ala Cys Gly Asn 20 Asp Glu Asn Gln 25 Glu Glu Ser Lys Lys 30 Glu Val Lys
 Ser Lys 35 Glu Lys Lys Ile Glu 40 Lys Glu Lys Glu Asn 45 Lys Ser Lys Lys
 10 Asp Lys 50 Glu Lys Glu Val 55 Ala Thr Gln Gln Gln 60 Pro Asp Asn Gln Thr
 Val 65 Glu Gln Pro Gln 70 Ser Gln Glu Gln Ser 75 Val Gln Gln Pro Gln Gln 80
 15 Gln Ile Pro Gln 85 Asn Ser Val Pro Gln 90 Gln Asn Val Gln Val 95 Gln Gln
 Asn Lys Lys Gln 100 Lys Val Asp Leu 105 Asn Asn Met Pro Pro Thr Asp Phe
 20 Ser Thr 115 Glu Gly Met Ser Glu 120 Gln Ala Gln Lys Gln 125 Ile Glu Glu Leu
 Ser Met 130 Gln Lys Asp Tyr His 135 Gly Leu Ser Gln Arg 140 Glu Tyr Asn Asp
 25 Arg Val 145 Ser Glu Ile Ile 150 Asn Asn Asp Asn

<210> 149

<211> 1501

<212> PRT

<213> Staphylococcus aureus

<400> 149

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Met Gln Met Arg Asp Lys Lys Gly Pro Val Asn Lys Arg Val Asp Phe
 1 5 10 15
 Leu Ser Asn Lys Leu Asn Lys Tyr Ser Ile Arg Lys Phe Thr Val Gly
 5 20 25 30
 Thr Ala Ser Ile Leu Ile Gly Ser Leu Met Tyr Leu Gly Thr Gln Gln
 35 40 45
 Glu Ala Glu Ala Ala Glu Asn Ile Glu Asn Pro Thr Thr Leu Lys
 10 50 55 60
 Asp Asn Val Gln Ser Lys Glu Val Lys Ile Glu Glu Val Thr Asn Lys
 65 70 75 80
 Asp Thr Ala Pro Gln Gly Val Glu Ala Lys Ser Glu Val Thr Ser Asn
 15 85 90 95
 Lys Asp Thr Ile Glu His Glu Pro Ser Val Lys Ala Glu Asp Ile Ser
 100 105 110
 Lys Lys Glu Asp Thr Pro Lys Glu Val Ala Asp Val Ala Glu Val Gln
 20 115 120 125
 Pro Lys Ser Ser Val Thr His Asn Ala Glu Thr Pro Lys Val Arg Lys
 130 135 140
 Ala Arg Ser Val Asp Glu Gly Ser Phe Asp Ile Thr Arg Asp Ser Lys
 25 145 150 155 160
 Asn Val Val Glu Ser Thr Pro Ile Thr Ile Gln Gly Lys Glu His Phe
 165 170 175
 Glu Gly Tyr Gly Ser Val Asp Ile Gln Lys Lys Pro Thr Asp Leu Gly
 30 180 185 190
 Val Ser Glu Val Thr Arg Phe Asn Val Gly Asn Glu Ser Asn Gly Leu
 195 200 205
 Ile Gly Ala Leu Gln Leu Lys Asn Lys Ile Asp Phe Ser Lys Asp Phe
 210 215 220
 Asn Phe Lys Val Arg Val Ala Asn Asn His Gln Ser Asn Thr Thr Gly
 35 225 230 235 240
 Ala Asp Gly Trp Gly Phe Leu Phe Ser Lys Gly Asn Ala Glu Glu Tyr
 245 250 255
 Leu Thr Asn Gly Gly Ile Leu Gly Asp Lys Gly Leu Val Asn Ser Gly
 40 260 265 270
 Gly Phe Lys Ile Asp Thr Gly Tyr Ile Tyr Thr Ser Ser Met Asp Lys
 45
 50
 55

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	275							280				285				
	Thr	Glu 290	Lys	Gln	Ala	Gly	Gln 295	Gly	Tyr	Arg	Gly	Tyr 300	Gly	Ala	Phe	Val
5	Lys 305	Asn	Asp	Ser	Ser	Gly 310	Asn	Ser	Gln	Met	Val 315	Gly	Glu	Asn	Ile	Asp 320
	Lys	Ser	Lys	Thr	Asn 325	Phe	Leu	Asn	Tyr	Ala 330	Asp	Asn	Ser	Thr	Asn 335	Thr
10	Ser	Asp	Gly	Lys 340	Phe	His	Gly	Gln	Arg 345	Leu	Asn	Asp	Val	Ile 350	Leu	Thr
	Tyr	Val	Ala 355	Ser	Thr	Gly	Lys	Met 360	Arg	Ala	Glu	Tyr	Ala 365	Gly	Lys	Thr
15	Trp	Glu 370	Thr	Ser	Ile	Thr	Asp 375	Leu	Gly	Leu	Ser	Lys 380	Asn	Gln	Ala	Tyr
	Asn 385	Phe	Leu	Ile	Thr	Ser 390	Ser	Gln	Arg	Trp	Gly 395	Leu	Asn	Gln	Gly	Ile 400
20	Asn	Ala	Asn	Gly	Trp 405	Met	Arg	Thr	Asp	Leu 410	Lys	Gly	Ser	Glu	Phe 415	Thr
	Phe	Thr	Pro	Glu 420	Ala	Pro	Lys	Thr	Ile 425	Thr	Glu	Leu	Glu	Lys 430	Lys	Val
25	Glu	Glu	Ile 435	Pro	Phe	Lys	Lys	Glu 440	Arg	Lys	Phe	Asn	Pro 445	Asp	Leu	Ala
	Pro	Gly 450	Thr	Glu	Lys	Val	Thr 455	Arg	Glu	Gly	Gln	Lys 460	Gly	Glu	Lys	Thr
30	Ile 465	Thr	Thr	Pro	Thr	Leu 470	Lys	Asn	Pro	Leu	Thr 475	Gly	Val	Ile	Ile	Ser 480
	Lys	Gly	Glu	Pro	Lys 485	Glu	Glu	Ile	Thr	Lys 490	Asp	Pro	Ile	Asn	Glu 495	Leu
35	Thr	Glu	Tyr	Gly 500	Pro	Glu	Thr	Ile	Ala 505	Pro	Gly	His	Arg	Asp 510	Glu	Phe
	Asp	Pro	Lys 515	Leu	Pro	Thr	Gly	Lys 520	Lys	Glu	Glu	Val	Pro 525	Gly	Lys	Pro
40	Gly	Ile 530	Lys	Asn	Pro	Glu	Thr 535	Gly	Asp	Val	Val	Arg 540	Pro	Pro	Val	Asp
	Ser 545	Val	Thr	Lys	Tyr	Gly 550	Pro	Val	Lys	Gly	Asp 555	Ser	Ile	Val	Glu	Lys 560
45	Glu	Glu	Ile	Pro	Phe 565	Glu	Lys	Glu	Arg	Lys 570	Phe	Asn	Pro	Asp	Leu 575	Ala
	Pro	Gly	Thr	Glu 580	Lys	Val	Thr	Arg	Glu 585	Gly	Gln	Lys	Gly	Glu 590	Lys	Thr
50	Ile	Thr	Thr 595	Pro	Thr	Leu	Lys	Asn 600	Pro	Leu	Thr	Gly	Glu 605	Ile	Ile	Ser
	Lys	Gly 610	Glu	Ser	Lys	Glu	Glu 615	Ile	Thr	Lys	Asp	Pro 620	Ile	Asn	Glu	Leu
55	Thr 625	Glu	Tyr	Gly	Pro	Glu 630	Thr	Ile	Thr	Pro	Gly 635	His	Arg	Asp	Glu	Phe 640
	Asp	Pro	Lys	Leu	Pro 645	Thr	Gly	Glu	Lys	Glu 650	Glu	Val	Pro	Gly	Lys 655	Pro

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Gly Ile Lys Asn Pro Glu Thr Gly Asp Val Val Arg Pro Pro Val Asp
 660 665 670
 Ser Val Thr Lys Tyr Gly Pro Val Lys Gly Asp Ser Ile Val Glu Lys
 5 675 680 685
 Glu Glu Ile Pro Phe Glu Lys Glu Arg Lys Phe Asn Pro Asp Leu Ala
 690 695 700
 Pro Gly Thr Glu Lys Val Thr Arg Glu Gly Gln Lys Gly Glu Lys Thr
 10 705 710 715 720
 Ile Thr Thr Pro Thr Leu Lys Asn Pro Leu Thr Gly Val Ile Ile Ser
 725 730 735
 Lys Gly Glu Pro Lys Glu Glu Ile Thr Lys Asp Pro Ile Asn Glu Leu
 15 740 745 750
 Thr Glu Tyr Gly Pro Glu Thr Ile Thr Pro Gly His Arg Asp Glu Phe
 755 760 765
 Asp Pro Lys Leu Pro Thr Gly Glu Lys Glu Glu Val Pro Gly Lys Pro
 20 770 775 780
 Gly Ile Lys Asn Pro Glu Thr Gly Asp Val Val Arg Pro Pro Val Asp
 785 790 795 800
 Ser Val Thr Lys Tyr Gly Pro Val Lys Gly Asp Ser Ile Val Glu Lys
 25 805 810 815
 Glu Glu Ile Pro Phe Lys Lys Glu Arg Lys Phe Asn Pro Asp Leu Ala
 820 825 830
 Pro Gly Thr Glu Lys Val Thr Arg Glu Gly Gln Lys Gly Glu Lys Thr
 30 835 840 845
 Ile Thr Thr Pro Thr Leu Lys Asn Pro Leu Thr Gly Glu Ile Ile Ser
 850 855 860
 Lys Gly Glu Ser Lys Glu Glu Ile Thr Lys Asp Pro Ile Asn Glu Leu
 35 865 870 875 880
 Thr Glu Tyr Gly Pro Glu Thr Ile Thr Pro Gly His Arg Asp Glu Phe
 885 890 895
 Asp Pro Lys Leu Pro Thr Gly Glu Lys Glu Glu Val Pro Gly Lys Pro
 40 900 905 910
 Gly Ile Lys Asn Pro Glu Thr Gly Asp Val Val Arg Pro Pro Val Asp
 915 920 925
 Ser Val Thr Lys Tyr Gly Pro Val Lys Gly Asp Ser Ile Val Glu Lys
 930 935 940
 Glu Glu Ile Pro Phe Lys Lys Glu Arg Lys Phe Asn Pro Asp Leu Ala
 45 945 950 955 960
 Pro Gly Thr Glu Lys Val Thr Arg Glu Gly Gln Lys Gly Glu Lys Thr
 965 970 975
 Ile Thr Thr Pro Thr Leu Lys Asn Pro Leu Thr Gly Glu Ile Ile Ser
 50 980 985 990
 Lys Gly Glu Ser Lys Glu Glu Ile Thr Lys Asp Pro Ile Asn Glu Leu
 995 1000 1005
 Thr Glu Tyr Gly Pro Glu Thr Ile Thr Pro Gly His Arg Asp Glu Phe
 55 1010 1015 1020

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Asp Pro Lys Leu Pro Thr Gly Glu Lys Glu Glu Val Pro Gly Lys Pro
 1025 1030 1035 1040
 Gly Ile Lys Asn Pro Glu Thr Gly Asp Val Val Arg Pro Pro Val Asp
 5 1045 1050 1055
 Ser Val Thr Lys Tyr Gly Pro Val Lys Gly Asp Ser Ile Val Glu Lys
 1060 1065 1070
 Glu Glu Ile Pro Phe Glu Lys Glu Arg Lys Phe Asn Pro Asp Leu Ala
 10 1075 1080 1085
 Pro Gly Thr Glu Lys Val Thr Arg Glu Gly Gln Lys Gly Glu Lys Thr
 1090 1095 1100
 Ile Thr Thr Pro Thr Leu Lys Asn Pro Leu Thr Gly Glu Ile Ile Ser
 15 1105 1110 1115 1120
 Lys Gly Glu Ser Lys Glu Glu Ile Thr Lys Asp Pro Ile Asn Glu Leu
 1125 1130 1135
 Thr Glu Tyr Gly Pro Glu Thr Ile Thr Pro Gly His Arg Asp Glu Phe
 20 1140 1145 1150
 Asp Pro Lys Leu Pro Thr Gly Glu Lys Glu Glu Val Pro Gly Lys Pro
 1155 1160 1165
 Gly Ile Lys Asn Pro Glu Thr Gly Asp Val Val Arg Pro Pro Val Asp
 25 1170 1175 1180
 Ser Val Thr Lys Tyr Gly Pro Val Lys Gly Asp Ser Ile Val Glu Lys
 1185 1190 1195 1200
 Glu Glu Ile Pro Phe Glu Lys Glu Arg Lys Phe Asn Pro Asp Leu Ala
 1205 1210 1215
 Pro Gly Thr Glu Lys Val Thr Arg Glu Gly Gln Lys Gly Glu Lys Thr
 30 1220 1225 1230
 Ile Thr Thr Pro Thr Leu Lys Asn Pro Leu Thr Gly Glu Ile Ile Ser
 1235 1240 1245
 Lys Gly Glu Ser Lys Glu Glu Ile Thr Lys Asp Pro Val Asn Glu Leu
 35 1250 1255 1260
 Thr Glu Phe Gly Gly Glu Lys Ile Pro Gln Gly His Lys Asp Ile Phe
 1265 1270 1275 1280
 Asp Pro Asn Leu Pro Thr Asp Gln Thr Glu Lys Val Pro Gly Lys Pro
 40 1285 1290 1295
 Gly Ile Lys Asn Pro Asp Thr Gly Lys Val Ile Glu Glu Pro Val Asp
 1300 1305 1310
 Asp Val Ile Lys His Gly Pro Lys Thr Gly Thr Pro Glu Thr Lys Thr
 45 1315 1320 1325
 Val Glu Ile Pro Phe Glu Thr Lys Arg Glu Phe Asn Pro Lys Leu Gln
 1330 1335 1340
 Pro Gly Glu Glu Arg Val Lys Gln Glu Gly Gln Pro Gly Ser Lys Thr
 50 1345 1350 1355 1360
 Ile Thr Thr Pro Ile Thr Val Asn Pro Leu Thr Gly Glu Lys Val Gly
 1365 1370 1375
 Glu Gly Gln Pro Thr Glu Glu Ile Thr Lys Gln Pro Val Asp Lys Ile
 55 1380 1385 1390
 Val Glu Phe Gly Gly Glu Lys Pro Lys Asp Pro Lys Gly Pro Glu Asn

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	1395	1400	1405
	Pro Glu Lys Pro Ser Arg	Pro Thr His Pro Ser Gly	Pro Val Asn Pro
	1410	1415	1420
5	Asn Asn Pro Gly Leu Ser Lys Asp Arg Ala Lys Pro Asn Gly Pro Val		
	1425	1430	1435 1440
	His Ser Met Asp Lys Asn Asp Lys Val Lys Lys Ser Lys Ile Ala Lys		
	1445	1450	1455
10	Glu Ser Val Ala Asn Gln Glu Lys Lys Arg Ala Glu Leu Pro Lys Thr		
	1460	1465	1470
	Gly Leu Glu Ser Thr Gln Lys Gly Leu Ile Phe Ser Ser Ile Ile Gly		
	1475	1480	1485
15	Ile Ala Gly Leu Met Leu Leu Ala Arg Arg Arg Lys Asn		
	1490	1495	1500

<210> 150

<211> 293

20 <212> PRT

<213> Staphylococcus aureus

<400> 150

25

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EP 2 510 947 B1

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
1 5 10 15
Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
20 25 30
Gly Met Leu Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
35 40 45
Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
50 55 60
Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
65 70 75 80
Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
85 90 95
Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
100 105 110
Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr Gly Asp Asp
115 120 125
Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser Ile Gly His
130 135 140
Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro
145 150 155 160
Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
165 170 175
Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
180 185 190
Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
195 200 205
Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe
210 215 220
Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
225 230 235 240
Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
245 250 255
Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp
260 265 270
Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
275 280 285
Glu Glu Met Thr Asn
290

<210> 151

<211> 207

<212> PRT

<213> Staphylococcus aureus

<400> 151

EP 2 510 947 B1

Met Ala Met Ile Lys Met Ser Pro Glu Glu Ile Arg Ala Lys Ser Gln
1 5 10
5 Ser Tyr Gly Gln Gly Ser Asp Gln Ile Arg Gln Ile Leu Ser Asp Leu
20 25 30
Thr Arg Ala Gln Gly Glu Ile Ala Ala Asn Trp Glu Gly Gln Ala Phe
35 40 45
10 Ser Arg Phe Glu Glu Gln Phe Gln Gln Leu Ser Pro Lys Val Glu Lys
50 55 60
Phe Ala Gln Leu Leu Glu Glu Ile Lys Gln Gln Leu Asn Ser Thr Ala
65 70 75 80
15 Asp Ala Val Gln Glu Gln Asp Gln Gln Leu Ser Asn Asn Phe Gly Leu
85 90 95
Gln Ala Ser Gly Gly Gly Ser Met Gly Gly Tyr Lys Gly Ile Lys Ala
100 105 110
20 Asp Gly Gly Lys Val Asp Gln Ala Lys Gln Leu Ala Ala Lys Thr Ala
115 120 125
Lys Asp Ile Glu Ala Cys Gln Lys Gln Thr Gln Gln Leu Ala Glu Tyr
130 135 140
25 Ile Glu Gly Ser Asp Trp Glu Gly Gln Phe Ala Asn Lys Val Lys Asp
145 150 155 160
Val Leu Leu Ile Met Ala Lys Phe Gln Glu Glu Leu Val Gln Pro Met
165 170 175
30 Ala Asp His Gln Lys Ala Ile Asp Asn Leu Ser Gln Asn Leu Ala Lys
180 185 190
Tyr Asp Thr Leu Ser Ile Lys Gln Gly Leu Asp Arg Val Asn Pro
195 200 205

<210> 152

<211> 207

<212> PRT

<213> Staphylococcus aureus

<400> 152

Met Gly Gly Tyr Lys Gly Ile Lys Ala Asp Gly Gly Lys Val Asp Gln
1 5 10
45 Ala Lys Gln Leu Ala Ala Lys Thr Ala Lys Asp Ile Glu Ala Cys Gln
20 25 30

EP 2 510 947 B1

Lys Gln Thr Gln Gln Leu Ala Glu Tyr Ile Glu Gly Ser Asp Trp Glu
 35 40 45
 Gly Gln Phe Ala Asn Lys Val Lys Asp Val Leu Leu Ile Met Ala Lys
 5 50 55 60
 Phe Gln Glu Glu Leu Val Gln Pro Met Ala Asp His Gln Lys Ala Ile
 65 70 75 80
 Asp Asn Leu Ser Gln Asn Leu Ala Lys Tyr Asp Thr Leu Ser Ile Lys
 10 85 90 95
 Gln Gly Leu Asp Arg Val Asn Pro Ala Ser Gly Gly Gly Ser Met Ala
 100 105 110
 Met Ile Lys Met Ser Pro Glu Glu Ile Arg Ala Lys Ser Gln Ser Tyr
 15 115 120 125
 Gly Gln Gly Ser Asp Gln Ile Arg Gln Ile Leu Ser Asp Leu Thr Arg
 130 135 140
 Ala Gln Gly Glu Ile Ala Ala Asn Trp Glu Gly Gln Ala Phe Ser Arg
 20 145 150 155 160
 Phe Glu Glu Gln Phe Gln Gln Leu Ser Pro Lys Val Glu Lys Phe Ala
 165 170 175
 Gln Leu Leu Glu Glu Ile Lys Gln Gln Leu Asn Ser Thr Ala Asp Ala
 25 180 185 190
 Val Gln Glu Gln Asp Gln Gln Leu Ser Asn Asn Phe Gly Leu Gln
 195 200 205

<210> 153

<211> 169

<212> PRT

<213> Staphylococcus aureus

<400> 153

EP 2 510 947 B1

5 Cys Gly Asn Asp Thr Pro Lys Asp Glu Thr Lys Ser Thr Glu Ser Asn
 1 5 10 15
 Thr Asn Gln Asp Thr Asn Thr Thr Lys Asp Val Ile Ala Leu Lys Asp
 20 25 30
 Val Lys Thr Ser Pro Glu Asp Ala Val Lys Lys Ala Glu Glu Thr Tyr
 35 40 45
 10 Lys Gly Gln Lys Leu Lys Gly Ile Ser Phe Glu Asn Ser Asn Gly Glu
 50 55 60
 Trp Ala Tyr Lys Val Thr Gln Gln Lys Ser Gly Glu Glu Ser Glu Val
 65 70 75 80
 15 Leu Val Ala Asp Lys Asn Lys Lys Val Ile Asn Lys Lys Thr Glu Lys
 85 90 95
 Glu Asp Thr Met Asn Glu Asn Asp Asn Phe Lys Tyr Ser Asp Ala Ile
 100 105 110
 20 Asp Tyr Lys Lys Ala Ile Lys Glu Gly Gln Lys Glu Phe Asp Gly Asp
 115 120 125
 Ile Lys Glu Trp Ser Leu Glu Lys Asp Asp Gly Lys Leu Val Tyr Asn
 130 135 140
 25 Ile Asp Leu Lys Lys Gly Asn Lys Lys Gln Glu Val Thr Val Asp Ala
 145 150 155 160
 Lys Asn Gly Lys Val Leu Lys Ser Glu

165

30

<210> 154

<211> 106

<212> PRT

35

<213> Staphylococcus aureus

<400> 154

40

Cys Gly Asn Asp Thr Pro Lys Asp Glu Thr Lys Ser Thr Glu Ser Asn
 1 5 10 15
 Thr Asn Gln Asp Thr Asn Thr Thr Lys Asp Val Ile Ala Leu Lys Asp
 20 25 30
 Val Lys Thr Ser Pro Glu Asp Ala Val Lys Lys Ala Glu Glu Thr Tyr
 35 40 45
 45 Lys Gly Gln Lys Leu Lys Gly Ile Ser Phe Glu Asn Ser Asn Gly Glu
 50 55 60
 Trp Ala Tyr Lys Val Thr Gln Gln Lys Ser Gly Glu Glu Ser Glu Val
 65 70 75 80
 Leu Val Ala Asp Lys Asn Lys Lys Val Ile Asn Lys Lys Thr Glu Lys
 85 90 95
 55 Glu Asp Thr Met Asn Glu Asn Asp Asn Phe
 100 105

55

<210> 155

<211> 580

EP 2 510 947 B1

<212> PRT

<213> Staphylococcus aureus

<400> 155

5

Ala Glu Asn Thr Ser Thr Glu Asn Ala Lys Gln Asp Asp Ala Thr Thr
1 5 10 15

10

Ser Asp Asn Lys Glu Val Val Ser Glu Thr Glu Asn Asn Ser Thr Thr
20 25 30

Glu Asn Asn Ser Thr Asn Pro Ile Lys Lys Glu Thr Asn Thr Asp Ser
35 40 45

15

Gln Pro Glu Ala Lys Lys Glu Ser Thr Ser Ser Thr Gln Lys Gln
50 55 60

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

20

Lys Glu Asn Val Lys Pro Ser Thr Asp Lys Thr Ala Thr Glu Asp Thr
85 90 95

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

25

Val Thr Thr Lys Pro Ser Thr Ser Glu Pro Ser Thr Ser Glu Ile Gln
115 120 125

Thr Lys Pro Thr Thr Pro Gln Glu Ser Thr Asn Ile Glu Asn Ser Gln
130 135 140

30

Pro Gln Pro Thr Pro Ser Lys Val Asp Asn Gln Val Thr Asp Ala Thr
145 150 155 160

Asn Pro Lys Glu Pro Val Asn Val Ser Lys Glu Glu Leu Lys Asn Asn
165 170 175

35

Pro Glu Lys Leu Lys Glu Leu Val Arg Asn Asp Ser Asn Thr Asp His
180 185 190

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Ser Thr Lys Pro Val Ala Thr Ala Pro Thr Ser Val Ala Pro Lys Arg
 195 200 205
 Val Asn Ala Lys Met Arg Phe Ala Val Ala Gln Pro Ala Ala Val Ala
 210 215 220
 Ser Asn Asn Val Asn Asp Leu Ile Lys Val Thr Lys Gln Thr Ile Lys
 225 230 235 240
 Val Gly Asp Gly Lys Asp Asn Val Ala Ala Ala His Asp Gly Lys Asp
 245 250 255
 Ile Glu Tyr Asp Thr Glu Phe Thr Ile Asp Asn Lys Val Lys Lys Gly
 260 265 270
 Asp Thr Met Thr Ile Asn Tyr Asp Lys Asn Val Ile Pro Ser Asp Leu
 275 280 285
 Thr Asp Lys Asn Asp Pro Ile Asp Ile Thr Asp Pro Ser Gly Glu Val
 290 295 300
 Ile Ala Lys Gly Thr Phe Asp Lys Ala Thr Lys Gln Ile Thr Tyr Thr
 305 310 315 320
 Phe Thr Asp Tyr Val Asp Lys Tyr Glu Asp Ile Lys Ser Arg Leu Thr
 325 330 335
 Leu Tyr Ser Tyr Ile Asp Lys Lys Thr Val Pro Asn Glu Thr Ser Leu
 340 345 350
 Asn Leu Thr Phe Ala Thr Ala Gly Lys Glu Thr Ser Gln Asn Val Thr
 355 360 365
 Val Asp Tyr Gln Asp Pro Met Val His Gly Asp Ser Asn Ile Gln Ser
 370 375 380
 Ile Phe Thr Lys Leu Asp Glu Asp Lys Gln Thr Ile Glu Gln Gln Ile
 385 390 395 400
 Tyr Val Asn Pro Leu Lys Lys Ser Ala Thr Asn Thr Lys Val Asp Ile
 405 410 415
 Ala Gly Ser Gln Val Asp Asp Tyr Gly Asn Ile Lys Leu Gly Asn Gly
 420 425 430
 Ser Thr Ile Ile Asp Gln Asn Thr Glu Ile Lys Val Tyr Lys Val Asn
 435 440 445
 Ser Asp Gln Gln Leu Pro Gln Ser Asn Arg Ile Tyr Asp Phe Ser Gln
 450 455 460
 Tyr Glu Asp Val Thr Ser Gln Phe Asp Asn Lys Lys Ser Phe Ser Asn
 465 470 475 480
 Asn Val Ala Thr Leu Asp Phe Gly Asp Ile Asn Ser Ala Tyr Ile Ile
 485 490 495
 Lys Val Val Ser Lys Tyr Thr Pro Thr Ser Asp Gly Glu Leu Asp Ile
 500 505 510
 Ala Gln Gly Thr Ser Met Arg Thr Thr Asp Lys Tyr Gly Tyr Tyr Asn
 515 520 525
 Tyr Ala Gly Tyr Ser Asn Phe Ile Val Thr Ser Asn Asp Thr Gly Gly
 530 535 540
 Gly Asp Gly Thr Val Lys Pro Glu Glu Lys Leu Tyr Lys Ile Gly Asp
 545 550 555 560

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Tyr Val Trp Glu Asp Val Asp Lys Asp Gly Val Gln Gly Thr Asp Ser
565 570 575

Lys Glu Lys Pro
580

5

<210> 156

<211> 540

<212> PRT

10 <213> Staphylococcus aureus

<400> 156

15

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25

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EP 2 510 947 B1

Ala Glu Ser Thr Asn Lys Glu Leu Asn Glu Ala Thr Thr Ser Ala Ser
1 5 10 15
Asp Asn Gln Ser Ser Asp Lys Val Asp Met Gln Gln Leu Asn Gln Glu
5 20 25 30
Asp Asn Thr Lys Asn Asp Asn Gln Lys Glu Met Val Ser Ser Gln Gly
35 40 45
Asn Glu Thr Thr Ser Asn Gly Asn Lys Leu Ile Glu Lys Glu Ser Val
10 50 55 60
Gln Ser Thr Thr Gly Asn Lys Val Glu Val Ser Thr Ala Lys Ser Asp
65 70 75 80
Glu Gln Ala Ser Pro Lys Ser Thr Asn Glu Asp Leu Asn Thr Lys Gln
15 85 90 95
Thr Ile Ser Asn Gln Glu Ala Leu Gln Pro Asp Leu Gln Glu Asn Lys
100 105 110
Ser Val Val Asn Val Gln Pro Thr Asn Glu Glu Asn Lys Lys Val Asp
20 115 120 125
Ala Lys Thr Glu Ser Thr Thr Leu Asn Val Lys Ser Asp Ala Ile Lys
130 135 140
Ser Asn Asp Glu Thr Leu Val Asp Asn Asn Ser Asn Ser Asn Asn Glu
25 145 150 155 160
Asn Asn Ala Asp Ile Ile Leu Pro Lys Ser Thr Ala Pro Lys Arg Leu
165 170 175
Asn Thr Arg Met Arg Ile Ala Ala Val Gln Pro Ser Ser Thr Glu Ala
30 180 185 190
Lys Asn Val Asn Asp Leu Ile Thr Ser Asn Thr Thr Leu Thr Val Val
195 200 205
Asp Ala Asp Lys Asn Asn Lys Ile Val Pro Ala Gln Asp Tyr Leu Ser
210 215 220
Leu Lys Ser Gln Ile Thr Val Asp Asp Lys Val Lys Ser Gly Asp Tyr
35 225 230 235 240
Phe Thr Ile Lys Tyr Ser Asp Thr Val Gln Val Tyr Gly Leu Asn Pro
245 250 255
Glu Asp Ile Lys Asn Ile Gly Asp Ile Lys Asp Pro Asn Asn Gly Glu
40 260 265 270
Thr Ile Ala Thr Ala Lys His Asp Thr Ala Asn Asn Leu Ile Thr Tyr
275 280 285
Thr Phe Thr Asp Tyr Val Asp Arg Phe Asn Ser Val Gln Met Gly Ile
45 290 295 300
Asn Tyr Ser Ile Tyr Met Asp Ala Asp Thr Ile Pro Val Ser Lys Asn

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	305		310		315		320									
	Asp	Val	Glu	Phe	Asn 325	Val	Thr	Ile	Gly	Asn 330	Thr	Thr	Thr	Lys	Thr 335	Thr
5	Ala	Asn	Ile	Gln 340	Tyr	Pro	Asp	Tyr	Val 345	Val	Asn	Glu	Lys	Asn 350	Ser	Ile
	Gly	Ser	Ala 355	Phe	Thr	Glu	Thr	Val 360	Ser	His	Val	Gly	Asn 365	Lys	Glu	Asn
10	Pro	Gly 370	Tyr	Tyr	Lys	Gln	Thr 375	Ile	Tyr	Val	Asn	Pro 380	Ser	Glu	Asn	Ser
	Leu 385	Thr	Asn	Ala	Lys	Leu 390	Lys	Val	Gln	Ala	Tyr 395	His	Ser	Ser	Tyr	Pro 400
15	Asn	Asn	Ile	Gly	Gln 405	Ile	Asn	Lys	Asp	Val 410	Thr	Asp	Ile	Lys	Ile 415	Tyr
	Gln	Val	Pro	Lys 420	Gly	Tyr	Thr	Leu	Asn 425	Lys	Gly	Tyr	Asp	Val 430	Asn	Thr
20	Lys	Glu	Leu 435	Thr	Asp	Val	Thr	Asn 440	Gln	Tyr	Leu	Gln	Lys 445	Ile	Thr	Tyr
	Gly	Asp 450	Asn	Asn	Ser	Ala	Val 455	Ile	Asp	Phe	Gly	Asn 460	Ala	Asp	Ser	Ala
25	Tyr 465	Val	Val	Met	Val	Asn 470	Thr	Lys	Phe	Gln	Tyr 475	Thr	Asn	Ser	Glu	Ser 480
	Pro	Thr	Leu	Val	Gln 485	Met	Ala	Thr	Leu	Ser 490	Ser	Thr	Gly	Asn	Lys 495	Ser
30	Val	Ser	Thr	Gly 500	Asn	Ala	Leu	Gly	Phe 505	Thr	Asn	Asn	Gln	Ser 510	Gly	Gly
	Ala	Gly	Gln 515	Glu	Val	Tyr	Lys	Ile 520	Gly	Asn	Tyr	Val	Trp 525	Glu	Asp	Thr
35	Asn	Lys 530	Asn	Gly	Val	Gln	Glu 535	Leu	Gly	Glu	Lys	Gly 540				

<210> 157

<211> 145

40 <212> PRT

<213> Staphylococcus aureus

<400> 157

45

50

55

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Asp Ser Gln Gln Val Asn Ala Ala Thr Glu Ala Thr Asn Ala Thr Asn
 1 5 10 15
 Asn Gln Ser Thr Gln Val Ser Gln Ala Thr Ser Gln Pro Ile Asn Phe
 5 20 25 30
 Gln Val Gln Lys Asp Gly Ser Ser Glu Lys Ser His Met Asp Asp Tyr
 35 40 45
 Met Gln His Pro Gly Lys Val Ile Lys Gln Asn Asn Lys Tyr Tyr Phe
 10 50 55 60
 Gln Thr Val Leu Asn Asn Ala Ser Phe Trp Lys Glu Tyr Lys Phe Tyr
 65 70 75 80
 Asn Ala Asn Asn Gln Glu Leu Ala Thr Thr Val Val Asn Asp Asn Lys
 15 85 90 95
 Lys Ala Asp Thr Arg Thr Ile Asn Val Ala Val Glu Pro Gly Tyr Lys
 100 105 110
 Ser Leu Thr Thr Lys Val His Ile Val Val Pro Gln Ile Asn Tyr Asn
 20 115 120 125
 His Arg Tyr Thr Thr His Leu Glu Phe Glu Lys Ala Ile Pro Thr Leu
 130 135 140
 Ala
 25 145

<210> 158

<211> 50

<212> PRT

30 <213> Staphylococcus aureus

<400> 158

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
 35 1 5 10 15
 Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
 20 25 30
 Gly Met Leu Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
 40 35 40 45
 Asn Lys
 50

45 <210> 159

<211> 63

<212> PRT

<213> Staphylococcus aureus

50 <400> 159

55

EP 2 510 947 B1

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
 1 5 10 15
 Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
 5 20 25 30
 Gly Met Leu Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
 35 40 45
 Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly
 10 50 55 60

<210> 160

<211> 50

<212> PRT

15 <213> Staphylococcus aureus

<400> 160

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
 20 1 5 10 15
 Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
 25 20 25 30
 Gly Met His Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
 35 40 45
 Asn Lys
 50

30 <210> 161

<211> 63

<212> PRT

<213> Staphylococcus aureus

35 <400> 161

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
 40 1 5 10 15
 Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
 20 25 30
 Gly Met His Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
 35 40 45
 Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly
 45 50 55 60

<210> 162

<211> 289

50 <212> PRT

<213> Staphylococcus aureus

<400> 162

55

EP 2 510 947 B1

Ala Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr Gln Val Leu Asn
1 5 10 15
Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser Leu
5 20 25 30
Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Gln Lys
35 40 45
Leu Asn Asp Ser Gln Ala Pro Lys Ala Asp Ala Gln Gln Asn Asn Phe
10 50 55 60
Asn Lys Asp Gln Gln Ser Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn
65 70 75 80
Leu Asn Glu Ala Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp
15 85 90 95
Pro Ser Gln Ser Thr Asn Val Leu Gly Glu Ala Lys Lys Leu Asn Glu
100 105 110
Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys Glu Gln Gln Asn
20 115 120 125
Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg
130 135 140
Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn
25 145 150 155 160
Leu Leu Ser Glu Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala
165 170 175
Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu
180 185 190
30 His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser
195 200 205
Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys
210 215 220
35 Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys
225 230 235 240
Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Thr
245 250 255
40 Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
260 265 270
Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln

45 275 280 285

Ala

50 <210> 163
<211> 508
<212> PRT
<213> Staphylococcus aureus

55 <400> 163

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1 Ser Glu Gln Ser Asn Asp Thr Thr Gln Ser Ser Lys Asn Asn Ala Ser
 5 Ala Asp Ser Glu Lys Asn Asn Met Ile Glu Thr Pro Gln Leu Asn Thr
 10 Thr Ala Asn Asp Thr Ser Asp Ile Ser Ala Asn Thr Asn Ser Ala Asn
 15 Val Asp Ser Thr Thr Lys Pro Met Ser Thr Gln Thr Ser Asn Thr Thr
 20 Thr Thr Glu Pro Ala Ser Thr Asn Glu Thr Pro Gln Pro Thr Ala Ile
 25 Lys Asn Gln Ala Thr Ala Ala Lys Met Gln Asp Gln Thr Val Pro Gln
 30 Glu Ala Asn Ser Gln Val Asp Asn Lys Thr Thr Asn Asp Ala Asn Ser
 35 Ile Ala Thr Asn Ser Glu Leu Lys Asn Ser Gln Thr Leu Asp Leu Pro
 40 Gln Ser Ser Pro Gln Thr Ile Ser Asn Ala Gln Gly Thr Ser Lys Pro
 45 Ser Val Arg Thr Arg Ala Val Arg Ser Leu Ala Val Ala Glu Pro Val
 50 Val Asn Ala Ala Asp Ala Lys Gly Thr Asn Val Asn Asp Lys Val Thr
 55 Ala Ser Asn Phe Lys Leu Glu Lys Thr Thr Phe Asp Pro Asn Gln Ser
 60 Gly Asn Thr Phe Met Ala Ala Asn Phe Thr Val Thr Asp Lys Val Lys
 65 Ser Gly Asp Tyr Phe Thr Ala Lys Leu Pro Asp Ser Leu Thr Gly Asn
 70 Gly Asp Val Asp Tyr Ser Asn Ser Asn Asn Thr Met Pro Ile Ala Asp
 75 Ile Lys Ser Thr Asn Gly Asp Val Val Ala Lys Ala Thr Tyr Asp Ile
 80 Leu Thr Lys Thr Tyr Thr Phe Val Phe Thr Asp Tyr Val Asn Asn Lys
 85 Glu Asn Ile Asn Gly Gln Phe Ser Leu Pro Leu Phe Thr Asp Arg Ala
 90 Lys Ala Pro Lys Ser Gly Thr Tyr Asp Ala Asn Ile Asn Ile Ala Asp
 95 Glu Met Phe Asn Asn Lys Ile Thr Tyr Asn Tyr Ser Ser Pro Ile Ala
 100 305 310 315 320

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Gly Ile Asp Lys Pro Asn Gly Ala Asn Ile Ser Ser Gln Ile Ile Gly
 325 330
 Val Asp Thr Ala Ser Gly Gln Asn Thr Tyr Lys Gln Thr Val Phe Val
 340 345
 Asn Pro Lys Gln Arg Val Leu Gly Asn Thr Trp Val Tyr Ile Lys Gly
 355 360 365
 Tyr Gln Asp Lys Ile Glu Glu Ser Ser Gly Lys Val Ser Ala Thr Asp
 370 375 380
 Thr Lys Leu Arg Ile Phe Glu Val Asn Asp Thr Ser Lys Leu Ser Asp
 385 390 395 400
 Ser Tyr Tyr Ala Asp Pro Asn Asp Ser Asn Leu Lys Glu Val Thr Asp
 405 410 415
 Gln Phe Lys Asn Arg Ile Tyr Tyr Glu His Pro Asn Val Ala Ser Ile
 420 425 430
 Lys Phe Gly Asp Ile Thr Lys Thr Tyr Val Val Leu Val Glu Gly His
 435 440 445
 Tyr Asp Asn Thr Gly Lys Asn Leu Lys Thr Gln Val Ile Gln Glu Asn
 450 455 460
 Val Asp Pro Val Thr Asn Arg Asp Tyr Ser Ile Phe Gly Trp Asn Asn
 465 470 475 480
 Glu Asn Val Val Arg Tyr Gly Gly Gly Ser Ala Asp Gly Asp Ser Ala
 485 490 495
 Val Asn Pro Lys Asp Pro Thr Pro Gly Pro Pro Val
 500 505

<210> 164

<211> 468

<212> PRT

<213> Staphylococcus aureus

<400> 164

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	Ala	Glu	His	Thr	Asn	Gly	Glu	Leu	Asn	Gln	Ser	Lys	Asn	Glu	Thr	Thr
	1				5					10					15	
5	Ala	Pro	Ser	Glu	Asn	Lys	Thr	Thr	Lys	Lys	Val	Asp	Ser	Arg	Gln	Leu
				20					25					30		
	Lys	Asp	Asn	Thr	Gln	Thr	Ala	Thr	Ala	Asp	Gln	Pro	Lys	Val	Thr	Met
			35				40						45			
10	Ser	Asp	Ser	Ala	Thr	Val	Lys	Glu	Thr	Ser	Ser	Asn	Met	Gln	Ser	Pro
		50					55					60				
	Gln	Asn	Ala	Thr	Ala	Asn	Gln	Ser	Thr	Thr	Lys	Thr	Ser	Asn	Val	Thr
	65				70						75					80
15	Thr	Asn	Asp	Lys	Ser	Ser	Thr	Thr	Tyr	Ser	Asn	Glu	Thr	Asp	Lys	Ser
					85					90					95	
	Asn	Leu	Thr	Gln	Ala	Lys	Asp	Val	Ser	Thr	Thr	Pro	Lys	Thr	Thr	Thr
				100					105					110		
20	Ile	Lys	Pro	Arg	Thr	Leu	Asn	Arg	Met	Ala	Val	Asn	Thr	Val	Ala	Ala
			115					120					125			
	Pro	Gln	Gln	Gly	Thr	Asn	Val	Asn	Asp	Lys	Val	His	Phe	Ser	Asn	Ile
		130					135					140				

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Asp Ile Ala Ile Asp Lys Gly His Val Asn Gln Thr Thr Gly Lys Thr
 145 150 155 160
 Glu Phe Trp Ala Thr Ser Ser Asp Val Leu Lys Leu Lys Ala Asn Tyr
 5 165 170 175
 Thr Ile Asp Asp Ser Val Lys Glu Gly Asp Thr Phe Thr Phe Lys Tyr
 180 185 190
 Gly Gln Tyr Phe Arg Pro Gly Ser Val Arg Leu Pro Ser Gln Thr Gln
 10 195 200 205
 Asn Leu Tyr Asn Ala Gln Gly Asn Ile Ile Ala Lys Gly Ile Tyr Asp
 210 215 220
 Ser Thr Thr Asn Thr Thr Thr Tyr Thr Phe Thr Asn Tyr Val Asp Gln
 15 225 230 235 240
 Tyr Thr Asn Val Arg Gly Ser Phe Glu Gln Val Ala Phe Ala Lys Arg
 245 250 255
 Lys Asn Ala Thr Thr Asp Lys Thr Ala Tyr Lys Met Glu Val Thr Leu
 20 260 265 270
 Gly Asn Asp Thr Tyr Ser Glu Glu Ile Ile Val Asp Tyr Gly Asn Lys
 275 280 285
 Lys Ala Gln Pro Leu Ile Ser Ser Thr Asn Tyr Ile Asn Asn Glu Asp
 25 290 295 300
 Leu Ser Arg Asn Met Thr Ala Tyr Val Asn Gln Pro Lys Asn Thr Tyr
 305 310 315 320
 Thr Lys Gln Thr Phe Val Thr Asn Leu Thr Gly Tyr Lys Phe Asn Pro
 30 325 330 335
 Asn Ala Lys Asn Phe Lys Ile Tyr Glu Val Thr Asp Gln Asn Gln Phe
 340 345 350
 Val Asp Ser Phe Thr Pro Asp Thr Ser Lys Leu Lys Asp Val Thr Asp
 35 355 360 365
 Gln Phe Asp Val Ile Tyr Ser Asn Asp Asn Lys Thr Ala Thr Val Asp
 370 375 380
 Leu Met Lys Gly Gln Thr Ser Ser Asn Lys Gln Tyr Ile Ile Gln Gln
 385 390 395 400
 Val Ala Tyr Pro Asp Asn Ser Ser Thr Asp Asn Gly Lys Ile Asp Tyr
 40 405 410 415
 Thr Leu Asp Thr Asp Lys Thr Lys Tyr Ser Trp Ser Asn Ser Tyr Ser
 420 425 430
 Asn Val Asn Gly Ser Ser Thr Ala Asn Gly Asp Gln Lys Lys Tyr Asn
 435 440 445
 Leu Gly Asp Tyr Val Trp Glu Asp Thr Asn Lys Asp Gly Lys Gln Asp
 450 455 460
 50 Ala Asn Glu Lys
 465

<210> 165

<211> 198

55 <212> PRT

<213> staphylococcus aureus

<400> 165

Met Ser Asn Asn Phe Lys Asp Asp Phe Glu Lys Asn Arg Gln Ser Ile

1 5 10 15
 5 Asp Thr Asn Ser His Gln Asp His Thr Glu Asp Val Glu Lys Asp Gln
 20 25 30
 10 Ser Glu Leu Glu His Gln Asp Thr Ile Glu Asn Thr Glu Gln Gln Phe
 35 40 45
 15 Pro Pro Arg Asn Ala Gln Arg Arg Lys Arg Arg Arg Asp Leu Ala Thr
 50 55 60
 20 Asn His Asn Lys Gln Val His Asn Glu Ser Gln Thr Ser Glu Asp Asn
 65 70 75 80
 25 Val Gln Asn Glu Ala Gly Thr Ile Asp Asp Arg Gln Val Glu Ser Ser
 85 90 95
 30 His Ser Thr Glu Ser Gln Glu Pro Ser His Gln Asp Ser Thr Pro Gln
 100 105 110
 35 His Glu Glu Glu Tyr Tyr Asn Lys Asn Ala Phe Ala Met Asp Lys Ser
 115 120 125
 40 His Pro Glu Pro Ile Glu Asp Asn Asp Lys His Asp Thr Ile Lys Asn
 130 135 140
 45 Ala Glu Asn Asn Thr Glu His Ser Thr Val Ser Asp Lys Ser Glu Ala
 145 150 155 160
 50 Glu Gln Ser Gln Gln Pro Lys Pro Tyr Phe Thr Thr Gly Ala Asn Gln
 165 170 175
 55 Ser Glu Thr Ser Lys Asn Glu His Asp Asn Asp Ser Val Lys Gln Asp
 180 185 190
 Gln Asp Glu Pro Lys Glu
 195

<210> 166

<211> 511

<212> PRT

<213> Staphylococcus aureus

<400> 166

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	Met	Gly	Gln	Asp	Lys	Glu	Ala	Ala	Ala	Ser	Glu	Gln	Lys	Thr	Thr	Thr
	1				5					10					15	
5	Val	Glu	Glu	Asn	Gly	Asn	Ser	Ala	Thr	Asp	Asn	Lys	Thr	Ser	Glu	Thr
				20					25					30		
	Gln	Thr	Thr	Ala	Thr	Asn	Val	Asn	His	Ile	Glu	Glu	Thr	Gln	Ser	Tyr
			35					40					45			
10	Asn	Ala	Thr	Val	Thr	Glu	Gln	Pro	Ser	Asn	Ala	Thr	Gln	Val	Thr	Thr
		50					55					60				
	Glu	Glu	Ala	Pro	Lys	Ala	Val	Gln	Ala	Pro	Gln	Thr	Ala	Gln	Pro	Ala
	65					70					75					80
15	Asn	Ile	Glu	Thr	Val	Lys	Glu	Glu	Val	Val	Lys	Glu	Glu	Ala	Lys	Pro
					85					90					95	
	Gln	Val	Lys	Glu	Thr	Thr	Gln	Ser	Gln	Asp	Asn	Ser	Gly	Asp	Gln	Arg
				100					105					110		
20	Gln	Val	Asp	Leu	Thr	Pro	Lys	Lys	Ala	Thr	Gln	Asn	Gln	Val	Ala	Glu
			115					120					125			
	Thr	Gln	Val	Glu	Val	Ala	Gln	Pro	Arg	Thr	Ala	Ser	Glu	Ser	Lys	Pro
		130					135					140				

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Arg Val Thr Arg Ser Ala Asp Val Ala Glu Ala Lys Glu Ala Ser Asn
 145 150 155 160
 Ala Lys Val Glu Thr Gly Thr Asp Val Thr Ser Lys Val Thr Val Glu
 5 165 170 175
 Ile Gly Ser Ile Glu Gly His Asn Asn Thr Asn Lys Val Glu Pro His
 180 185 190
 Ala Gly Gln Arg Ala Val Leu Lys Tyr Lys Leu Lys Phe Glu Asn Gly
 10 195 200 205
 Leu His Gln Gly Asp Tyr Phe Asp Phe Thr Leu Ser Asn Asn Val Asn
 210 215 220
 Thr His Gly Val Ser Thr Ala Arg Lys Val Pro Glu Ile Lys Asn Gly
 15 225 230 235 240
 Ser Val Val Met Ala Thr Gly Glu Val Leu Glu Gly Gly Lys Ile Arg
 245 250 255
 Tyr Thr Phe Thr Asn Asp Ile Glu Asp Lys Val Asp Val Thr Ala Glu
 20 260 265 270
 Leu Glu Ile Asn Leu Phe Ile Asp Pro Lys Thr Val Gln Thr Asn Gly
 275 280 285
 Asn Gln Thr Ile Thr Ser Thr Leu Asn Glu Glu Gln Thr Ser Lys Glu
 25 290 295 300
 Leu Asp Val Lys Tyr Lys Asp Gly Ile Gly Asn Tyr Tyr Ala Asn Leu
 305 310 315 320
 Asn Gly Ser Ile Glu Thr Phe Asn Lys Ala Asn Asn Arg Phe Ser His
 30 325 330 335
 Val Ala Phe Ile Lys Pro Asn Asn Gly Lys Thr Thr Ser Val Thr Val
 340 345 350
 Thr Gly Thr Leu Met Lys Gly Ser Asn Gln Asn Gly Asn Gln Pro Lys
 35 355 360 365
 Val Arg Ile Phe Glu Tyr Leu Gly Asn Asn Glu Asp Ile Ala Lys Ser
 370 375 380
 Val Tyr Ala Asn Thr Thr Asp Thr Ser Lys Phe Lys Glu Val Thr Ser
 385 390 395 400
 Asn Met Ser Gly Asn Leu Asn Leu Gln Asn Asn Gly Ser Tyr Ser Leu
 40 405 410 415
 Asn Ile Glu Asn Leu Asp Lys Thr Tyr Val Val His Tyr Asp Gly Glu
 420 425 430
 Tyr Leu Asn Gly Thr Asp Glu Val Asp Phe Arg Thr Gln Met Val Gly
 45 435 440 445
 His Pro Glu Gln Leu Tyr Lys Tyr Tyr Tyr Asp Arg Gly Tyr Thr Leu
 450 455 460
 Thr Trp Asp Asn Gly Leu Val Leu Tyr Ser Asn Lys Ala Asn Gly Asn
 50 465 470 475 480
 Glu Lys Asn Gly Pro Ile Ile Gln Asn Asn Lys Phe Glu Tyr Lys Glu
 485 490 495
 Asp Thr Ile Lys Glu Thr Leu Thr Gly Gln Tyr Asp Lys Asn Leu
 55 500 505 510

<210> 167

<211> 442
<212> PRT
<213> Staphylococcus aureus

5 <400> 167

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Val Thr Thr Val Glu Glu Glu Tyr Asp Ser Ser Thr Leu Asp Ile Asp
 1 5 10 15
 Tyr His Thr Ala Ile Asp Gly Gly Gly Tyr Val Asp Gly Tyr Ile
 20 25 30
 Glu Thr Ile Glu Glu Thr Asp Ser Ser Ala Ile Asp Ile Asp Tyr His
 35 40 45
 Thr Ala Val Asp Ser Glu Ala Gly His Val Gly Gly Tyr Thr Glu Ser
 50 55 60
 Ser Glu Glu Ser Asn Pro Ile Asp Phe Glu Glu Ser Thr His Glu Asn
 65 70 75 80
 Ser Lys His His Ala Asp Val Val Glu Tyr Glu Glu Asp Thr Asn Pro
 85 90 95
 Gly Gly Gly Gln Val Thr Thr Glu Ser Asn Leu Val Glu Phe Asp Glu
 100 105 110
 Glu Ser Thr Lys Gly Ile Val Thr Gly Ala Val Ser Asp His Thr Thr
 115 120 125
 Val Glu Asp Thr Lys Glu Tyr Thr Thr Glu Ser Asn Leu Ile Glu Leu
 130 135 140
 Val Asp Glu Leu Pro Glu Glu His Gly Gln Ala Gln Gly Pro Val Glu
 145 150 155 160
 Glu Ile Thr Lys Asn Asn His His Ile Ser His Ser Gly Leu Gly Thr
 165 170 175
 Glu Asn Gly His Gly Asn Tyr Asp Val Ile Glu Glu Ile Glu Glu Asn
 180 185 190
 Ser His Val Asp Ile Lys Ser Glu Leu Gly Tyr Glu Gly Gly Gln Asn
 195 200 205
 Ser Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Glu Asp Lys Pro Lys
 210 215 220
 Tyr Glu Gln Gly Gly Asn Ile Val Asp Ile Asp Phe Asp Ser Val Pro
 225 230 235 240
 Gln Ile His Gly Gln Asn Lys Gly Asn Gln Ser Phe Glu Glu Asp Thr
 245 250 255
 Glu Lys Asp Lys Pro Lys Tyr Glu His Gly Gly Asn Ile Ile Asp Ile
 260 265 270
 Asp Phe Asp Ser Val Pro His Ile His Gly Phe Asn Lys His Thr Glu
 275 280 285
 Ile Ile Glu Glu Asp Thr Asn Lys Asp Lys Pro Ser Tyr Gln Phe Gly
 290 295 300
 Gly His Asn Ser Val Asp Phe Glu Glu Asp Thr Leu Pro Lys Val Ser
 305 310 315 320
 Gly Gln Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp Thr Thr Pro Pro
 325 330 335
 Ile Val Pro Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu

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				340				345					350			
5	Thr	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ser	Glu	Pro	Glu	Thr	Pro
			355					360					365			
	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ser	Glu	Pro	Glu	Thr	Pro	Thr	Pro
		370					375					380				
10	Pro	Thr	Pro	Glu	Val	Pro	Ala	Glu	Pro	Gly	Lys	Pro	Val	Pro	Pro	Ala
	385					390					395					400
	Lys	Glu	Glu	Pro	Lys	Lys	Pro	Ser	Lys	Pro	Val	Glu	Gln	Gly	Lys	Val
					405					410					415	
15	Val	Thr	Pro	Val	Ile	Glu	Ile	Asn	Glu	Lys	Val	Lys	Ala	Val	Ala	Pro
				420					425					430		
	Thr	Lys	Lys	Pro	Gln	Ser	Lys	Lys	Ser	Glu						
			435					440								

<210> 168
 <211> 1126
 <212> PRT
 <213> Staphylococcus aureus

 <400> 168

EP 2 510 947 B1

	Ala	Glu	Asn	Thr	Ser	Thr	Glu	Asn	Ala	Lys	Gln	Asp	Asp	Ala	Thr	Thr
	1				5					10					15	
5	Ser	Asp	Asn	Lys	Glu	Val	Val	Ser	Glu	Thr	Glu	Asn	Asn	Ser	Thr	Thr
				20					25					30		
	Glu	Asn	Asn	Ser	Thr	Asn	Pro	Ile	Lys	Lys	Glu	Thr	Asn	Thr	Asp	Ser
			35				40						45			
10	Gln	Pro	Glu	Ala	Lys	Lys	Glu	Ser	Thr	Ser	Ser	Ser	Thr	Gln	Lys	Gln
		50					55						60			
	Gln	Asn	Asn	Val	Thr	Ala	Thr	Thr	Glu	Thr	Lys	Pro	Gln	Asn	Ile	Glu
	65					70					75					80
15	Lys	Glu	Asn	Val	Lys	Pro	Ser	Thr	Asp	Lys	Thr	Ala	Thr	Glu	Asp	Thr
				85						90					95	
	Ser	Val	Ile	Leu	Glu	Glu	Lys	Lys	Ala	Pro	Asn	Asn	Thr	Asn	Asn	Asp
				100					105					110		
20	Val	Thr	Thr	Lys	Pro	Ser	Thr	Ser	Glu	Pro	Ser	Thr	Ser	Glu	Ile	Gln
			115					120					125			
	Thr	Lys	Pro	Thr	Thr	Pro	Gln	Glu	Ser	Thr	Asn	Ile	Glu	Asn	Ser	Gln
		130					135					140				
25	Pro	Gln	Pro	Thr	Pro	Ser	Lys	Val	Asp	Asn	Gln	Val	Thr	Asp	Ala	Thr
	145					150					155					160
	Asn	Pro	Lys	Glu	Pro	Val	Asn	Val	Ser	Lys	Glu	Glu	Leu	Lys	Asn	Asn
				165						170					175	
30	Pro	Glu	Lys	Leu	Lys	Glu	Leu	Val	Arg	Asn	Asp	Ser	Asn	Thr	Asp	His
				180					185					190		
	Ser	Thr	Lys	Pro	Val	Ala	Thr	Ala	Pro	Thr	Ser	Val	Ala	Pro	Lys	Arg
			195				200						205			
35	Val	Asn	Ala	Lys	Met	Arg	Phe	Ala	Val	Ala	Gln	Pro	Ala	Ala	Val	Ala
		210					215					220				
	Ser	Asn	Asn	Val	Asn	Asp	Leu	Ile	Lys	Val	Thr	Lys	Gln	Thr	Ile	Lys
	225				230						235					240

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	Val	Gly	Asp	Gly	Lys	Asp	Asn	Val	Ala	Ala	Ala	His	Asp	Gly	Lys	Asp
					245					250					255	
5	Ile	Glu	Tyr	Asp	Thr	Glu	Phe	Thr	Ile	Asp	Asn	Lys	Val	Lys	Lys	Gly
				260					265					270		
	Asp	Thr	Met	Thr	Ile	Asn	Tyr	Asp	Lys	Asn	Val	Ile	Pro	Ser	Asp	Leu
			275					280					285			
10	Thr	Asp	Lys	Asn	Asp	Pro	Ile	Asp	Ile	Thr	Asp	Pro	Ser	Gly	Glu	Val
		290					295					300				
	Ile	Ala	Lys	Gly	Thr	Phe	Asp	Lys	Ala	Thr	Lys	Gln	Ile	Thr	Tyr	Thr
	305					310					315					320
15	Phe	Thr	Asp	Tyr	Val	Asp	Lys	Tyr	Glu	Asp	Ile	Lys	Ser	Arg	Leu	Thr
					325					330					335	
	Leu	Tyr	Ser	Tyr	Ile	Asp	Lys	Lys	Thr	Val	Pro	Asn	Glu	Thr	Ser	Leu
				340					345					350		
20	Asn	Leu	Thr	Phe	Ala	Thr	Ala	Gly	Lys	Glu	Thr	Ser	Gln	Asn	Val	Thr
			355					360					365			
	Val	Asp	Tyr	Gln	Asp	Pro	Met	Val	His	Gly	Asp	Ser	Asn	Ile	Gln	Ser
		370					375					380				
25	Ile	Phe	Thr	Lys	Leu	Asp	Glu	Asp	Lys	Gln	Thr	Ile	Glu	Gln	Gln	Ile
	385					390					395					400
	Tyr	Val	Asn	Pro	Leu	Lys	Lys	Ser	Ala	Thr	Asn	Thr	Lys	Val	Asp	Ile
					405					410					415	
30	Ala	Gly	Ser	Gln	Val	Asp	Asp	Tyr	Gly	Asn	Ile	Lys	Leu	Gly	Asn	Gly
				420					425					430		
	Ser	Thr	Ile	Ile	Asp	Gln	Asn	Thr	Glu	Ile	Lys	Val	Tyr	Lys	Val	Asn
			435					440					445			
35	Ser	Asp	Gln	Gln	Leu	Pro	Gln	Ser	Asn	Arg	Ile	Tyr	Asp	Phe	Ser	Gln
		450					455					460				
	Tyr	Glu	Asp	Val	Thr	Ser	Gln	Phe	Asp	Asn	Lys	Lys	Ser	Phe	Ser	Asn
	465					470					475					480
40	Asn	Val	Ala	Thr	Leu	Asp	Phe	Gly	Asp	Ile	Asn	Ser	Ala	Tyr	Ile	Ile
					485					490					495	
	Lys	Val	Val	Ser	Lys	Tyr	Thr	Pro	Thr	Ser	Asp	Gly	Glu	Leu	Asp	Ile
				500					505					510		
45	Ala	Gln	Gly	Thr	Ser	Met	Arg	Thr	Thr	Asp	Lys	Tyr	Gly	Tyr	Tyr	Asn
			515					520					525			
	Tyr	Ala	Gly	Tyr	Ser	Asn	Phe	Ile	Val	Thr	Ser	Asn	Asp	Thr	Gly	Gly
		530					535					540				
50	Gly	Asp	Gly	Thr	Val	Lys	Pro	Glu	Glu	Lys	Leu	Tyr	Lys	Ile	Gly	Asp
	545					550					555					560
	Tyr	Val	Trp	Glu	Asp	Val	Asp	Lys	Asp	Gly	Val	Gln	Gly	Thr	Asp	Ser
					565					570					575	
55	Lys	Glu	Lys	Pro	Ala	Ser	Gly	Gly	Gly	Ser	Ala	Glu	Ser	Thr	Asn	Lys
				580					585					590		
	Glu	Leu	Asn	Glu	Ala	Thr	Thr	Ser	Ala	Ser	Asp	Asn	Gln	Ser	Ser	Asp
			595					600					605			

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Lys Val Asp Met Gln Gln Leu Asn Gln Glu Asp Asn Thr Lys Asn Asp
 610 615 620
 Asn Gln Lys Glu Met Val Ser Ser Gln Gly Asn Glu Thr Thr Ser Asn
 5 625 630 635 640
 Gly Asn Lys Leu Ile Glu Lys Glu Ser Val Gln Ser Thr Thr Gly Asn
 645 650 655
 Lys Val Glu Val Ser Thr Ala Lys Ser Asp Glu Gln Ala Ser Pro Lys
 10 660 665 670
 Ser Thr Asn Glu Asp Leu Asn Thr Lys Gln Thr Ile Ser Asn Gln Glu
 675 680 685
 Ala Leu Gln Pro Asp Leu Gln Glu Asn Lys Ser Val Val Asn Val Gln
 15 690 695 700
 Pro Thr Asn Glu Glu Asn Lys Lys Val Asp Ala Lys Thr Glu Ser Thr
 705 710 715 720
 Thr Leu Asn Val Lys Ser Asp Ala Ile Lys Ser Asn Asp Glu Thr Leu
 20 725 730 735
 Val Asp Asn Asn Ser Asn Ser Asn Asn Glu Asn Asn Ala Asp Ile Ile
 740 745 750
 Leu Pro Lys Ser Thr Ala Pro Lys Arg Leu Asn Thr Arg Met Arg Ile
 25 755 760 765
 Ala Ala Val Gln Pro Ser Ser Thr Glu Ala Lys Asn Val Asn Asp Leu
 770 775 780
 Ile Thr Ser Asn Thr Thr Leu Thr Val Val Asp Ala Asp Lys Asn Asn
 785 790 795 800
 Lys Ile Val Pro Ala Gln Asp Tyr Leu Ser Leu Lys Ser Gln Ile Thr
 30 805 810 815
 Val Asp Asp Lys Val Lys Ser Gly Asp Tyr Phe Thr Ile Lys Tyr Ser
 820 825 830
 Asp Thr Val Gln Val Tyr Gly Leu Asn Pro Glu Asp Ile Lys Asn Ile
 35 835 840 845
 Gly Asp Ile Lys Asp Pro Asn Asn Gly Glu Thr Ile Ala Thr Ala Lys
 850 855 860
 His Asp Thr Ala Asn Asn Leu Ile Thr Tyr Thr Phe Thr Asp Tyr Val
 40 865 870 875 880
 Asp Arg Phe Asn Ser Val Gln Met Gly Ile Asn Tyr Ser Ile Tyr Met
 885 890 895
 Asp Ala Asp Thr Ile Pro Val Ser Lys Asn Asp Val Glu Phe Asn Val
 45 900 905 910
 Thr Ile Gly Asn Thr Thr Thr Lys Thr Thr Ala Asn Ile Gln Tyr Pro
 915 920 925
 Asp Tyr Val Val Asn Glu Lys Asn Ser Ile Gly Ser Ala Phe Thr Glu
 50 930 935 940
 Thr Val Ser His Val Gly Asn Lys Glu Asn Pro Gly Tyr Tyr Lys Gln
 945 950 955 960
 Thr Ile Tyr Val Asn Pro Ser Glu Asn Ser Leu Thr Asn Ala Lys Leu
 55 965 970 975
 Lys Val Gln Ala Tyr His Ser Ser Tyr Pro Asn Asn Ile Gly Gln Ile

980 985 990
 Asn Lys Asp Val Thr Asp Ile Lys Ile Tyr Gln Val Pro Lys Gly Tyr
 995 1000 1005
 5 Thr Leu Asn Lys Gly Tyr Asp Val Asn Thr Lys Glu Leu Thr Asp Val
 1010 1015 1020
 Thr Asn Gln Tyr Leu Gln Lys Ile Thr Tyr Gly Asp Asn Asn Ser Ala
 1025 1030 1035 1040
 10 Val Ile Asp Phe Gly Asn Ala Asp Ser Ala Tyr Val Val Met Val Asn
 1045 1050 1055
 Thr Lys Phe Gln Tyr Thr Asn Ser Glu Ser Pro Thr Leu Val Gln Met
 1060 1065 1070
 15 Ala Thr Leu Ser Ser Thr Gly Asn Lys Ser Val Ser Thr Gly Asn Ala
 1075 1080 1085
 Leu Gly Phe Thr Asn Asn Gln Ser Gly Gly Ala Gly Gln Glu Val Tyr
 1090 1095 1100
 20 Lys Ile Gly Asn Tyr Val Trp Glu Asp Thr Asn Lys Asn Gly Val Gln
 1105 1110 1115 1120
 Glu Leu Gly Glu Lys Gly
 1125

25 <210> 169
 <211> 618
 <212> DNA
 <213> Staphylococcus aureus
 30 <400> 169

35 atggcaatga ttaagatgag tccagaggaa atcagagcaa aatcgcaatc ttacggggcaa 60
 ggttcagacc aaatccgtca aattttatct gatttaacac gtgcacaagg tgaaattgca 120
 gcgaactggg aaggtcaagc tttcagccgt ttcgaagagc aattccaaca acttagtcct 180
 aaagtagaaa aatttgcaca attattagaa gaaattaaac aacaattgaa tagcactgct 240
 gatgccgttc aagaaCaaga ccaacaactt tctaataatt tcggtttgca agctagcggg 300
 ggcggatccg gtggatataa aggtattaaa gcagatgggtg gcaagggtga tcaagcgaaa 360
 caattagcgg caaaaacagc taaagatatt gaagcatgtc aaaagcaaac gcaacagctc 420
 40 gctgagtata tcgaaggtag tgattgggaa ggacagttcg ccaataagggt gaaagatgtg 480
 ttactcatta tggcaaagt tcaagaagaa ttagtacaac cgatggctga ccatcaaaaa 540
 gcaattgata acttaagtca aaatctagcg aaatacgata cattatcaat taagcaaggg 600
 cttgataggg tgaaccca 618

45 <210> 170
 <211> 239
 <212> PRT
 <213> Staphylococcus aureus
 50 <400> 170

55

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Met Asn Lys Asn Ile Ile Ile Lys Ser Ile Ala Ala Leu Thr Ile Leu
1 5 10 15
5 Thr Ser Ile Thr Gly Val Gly Thr Thr Val Val Asp Gly Ile Gln Gln
20 25 30
Thr Ala Lys Ala Glu Asn Ser Val Lys Leu Ile Thr Asn Thr Asn Val
35 40 45
10 Ala Pro Tyr Ser Gly Val Thr Trp Met Gly Ala Gly Thr Gly Phe Val
50 55 60
Val Gly Asn His Thr Ile Ile Thr Asn Lys His Val Thr Tyr His Met
65 70 75 80
15 Lys Val Gly Asp Glu Ile Lys Ala His Pro Asn Gly Phe Tyr Asn Asn
85 90 95
Gly Gly Gly Leu Tyr Lys Val Thr Lys Ile Val Asp Tyr Pro Gly Lys
100 105 110
20 Glu Asp Ile Ala Val Val Gln Val Glu Glu Lys Ser Thr Gln Pro Lys
115 120 125
Gly Arg Lys Phe Lys Asp Phe Thr Ser Lys Phe Asn Ile Ala Ser Glu
130 135 140
25 Ala Lys Glu Asn Glu Pro Ile Ser Val Ile Gly Tyr Pro Asn Pro Asn
145 150 155 160
Gly Asn Lys Leu Gln Met Tyr Glu Ser Thr Gly Lys Val Leu Ser Val
165 170 175
30 Asn Gly Asn Ile Val Thr Ser Asp Ala Val Val Gln Pro Gly Ser Ser
180 185 190
Gly Ser Pro Ile Leu Asn Ser Lys Arg Glu Ala Ile Gly Val Met Tyr
195 200 205
35 Ala Ser Asp Lys Pro Thr Gly Glu Ser Thr Arg Ser Phe Ala Val Tyr
210 215 220
Phe Ser Pro Glu Ile Lys Lys Phe Ile Ala Asp Asn Leu Asp Lys
225 230 235

40 <210> 171
<211> 6
<212> PRT
<213> Artificial sequence

45 <220>
<223> Peptide linker

<400> 171

50 gly ser gly gly gly gly
1 5

55 <210> 172
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

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<223> Peptide linker

<400> 172

5 Gly ser Gly ser Gly Gly Gly Gly
1 5

<210> 173

 $\langle 211 \rangle$ 6

10 <212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Peptide linker

15

<400> 173

Ala Ser Gly Gly Gly Ser
1 5

<210> 174

<211> 18

<212> DNA

25 <213> Artificial sequence

 $\langle 220 \rangle$

<223> Sequence encoding SEQ ID NO: 173

30

<400> 174

gctagcggtg gcggatcc 18

<210> 175

<211> 26

35 <212> DNA

<212> DNA

<213> Artificial Sequence

<220>

<223> immunostimulatory oligonucleotide

40

<220>

<221> misc feature

<222> 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25

<223> 'n' is INOSINE

45

<400> 175

nennennenn nennennenn nennenn 26

<210> 176

$\langle 211 \rangle$ 11

50

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

55

<223> polycationic oligopeptide

<400> 176

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Lys Leu Lys Leu Leu Leu Leu Lys Leu Lys
1 5 10

<210> 177
<211> 203
<212> PRT
<213> Staphylococcus aureus

<400> 177

Met Phe Lys Lys Tyr Asp Ser Lys Asn Ser Ile Val Leu Lys Ser Ile
1 5 10 15
Leu Ser Leu Gly Ile Ile Tyr Gly Gly Thr Phe Gly Ile Tyr Pro Lys
20 25 30
Ala Asp Ala Ser Thr Gln Asn Ser Ser Ser Val Gln Asp Lys Gln Leu
35 40 45
Gln Lys Val Glu Glu Val Pro Asn Asn Ser Glu Lys Ala Leu Val Lys
50 55 60
Lys Leu Tyr Asp Arg Tyr Ser Lys Asp Thr Ile Asn Gly Lys Ser Asn
65 70 75 80
Lys Ser Arg Asn Trp Val Tyr Ser Glu Arg Pro Leu Asn Glu Asn Gln
85 90 95
Val Arg Ile His Leu Glu Gly Thr Tyr Thr Val Ala Gly Arg Val Tyr
100 105 110
Thr Pro Lys Arg Asn Ile Thr Leu Asn Lys Glu Val Val Thr Leu Lys
115 120 125
Glu Leu Asp His Ile Ile Arg Phe Ala His Ile Ser Tyr Gly Leu Tyr
130 135 140
Met Gly Glu His Leu Pro Lys Gly Asn Ile Val Ile Asn Thr Lys Asp
145 150 155 160
Gly Gly Lys Tyr Thr Leu Glu Ser His Lys Glu Leu Gln Lys Asp Arg
165 170 175
Glu Asn Val Lys Ile Asn Thr Ala Asp Ile Lys Asn Val Thr Phe Lys
180 185 190
Leu Val Lys Ser Val Asn Asp Ile Glu Gln Val
195 200

<210> 178
<211> 146
<212> PRT
<213> Staphylococcus aureus

<400> 178

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Met Asn Thr Lys Tyr Phe Leu Ala Ala Gly Ala Val Ile Thr Thr Leu
1 5 10 15
Ala Leu Gly Ala Cys Gly Asn Ser Asn Ser Gln Asp Gln Gly Asn Lys
20 25 30
Thr Glu Gln Lys Thr Lys Ser Glu Asp Ser Asn Val Lys Thr Asp Lys
35 40 45
Thr Lys His Leu Thr Gly Thr Phe Ser Ser Lys Asn Gly Glu Thr Val
50 55 60
Glu Gly Lys Ala Glu Ile Lys Asn Gly Lys Leu Met Leu Thr Asn Tyr
65 70 75 80
Lys Ser Ser Lys Gly Pro Asp Leu Tyr Val Tyr Leu Thr Lys Asn Gly
85 90 95
Asp Ile Lys Asn Gly Lys Glu Ile Ala Met Val Asp Tyr Asp Lys Glu
100 105 110
Lys Gln Thr Phe Asp Leu Lys Asn Val Asp Leu Ser Lys Tyr Asp Glu
115 120 125
Val Thr Ile Tyr Cys Lys Lys Ala His Val Ile Phe Gly Gly Ala Lys
130 135 140
Leu Lys
145

<210> 179

<211> 619

<212> PRT

<213> Staphylococcus aureus

<400> 179

Met Pro Lys Asn Lys Ile Leu Ile Tyr Leu Leu Ser Thr Thr Leu Val
1 5 10 15
Leu Pro Thr Leu Val Ser Pro Thr Ala Tyr Ala Asp Thr Pro Gln Lys
20 25 30
Asp Thr Thr Ala Lys Thr Thr Ser His Asp Ser Lys Lys Ser Asn Asp
35 40 45
Asp Glu Thr Ser Lys Asp Thr Thr Ser Lys Asp Ile Asp Lys Ala Asp
50 55 60
Lys Asn Asn Thr Ser Asn Gln Asp Asn Asn Asp Lys Lys Phe Lys Thr
65 70 75 80
Ile Asp Asp Ser Thr Ser Asp Ser Asn Asn Ile Ile Asp Phe Ile Tyr
85 90 95
Lys Asn Leu Pro Gln Thr Asn Ile Asn Gln Leu Leu Thr Lys Asn Lys
100 105 110

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Tyr Asp Asp Asn Tyr Ser Leu Thr Thr Leu Ile Gln Asn Leu Phe Asn
 115 120 125
 5 Leu Asn Ser Asp Ile Ser Asp Tyr Glu Gln Pro Arg Asn Gly Glu Lys
 130 135 140
 Ser Thr Asn Asp Ser Asn Lys Asn Ser Asp Asn Ser Ile Lys Asn Asp
 145 150 155 160
 10 Thr Asp Thr Gln Ser Ser Lys Gln Asp Lys Ala Asp Asn Gln Lys Ala
 165 170 175
 Pro Lys Ser Asn Asn Thr Lys Pro Ser Thr Ser Asn Lys Gln Pro Asn
 180 185 190
 15 Ser Pro Lys Pro Thr Gln Pro Asn Gln Ser Asn Ser Gln Pro Ala Ser
 195 200 205
 Asp Asp Lys Ala Asn Gln Lys Ser Ser Ser Lys Asp Asn Gln Ser Met
 210 215 220
 20 Ser Asp Ser Ala Leu Asp Ser Ile Leu Asp Gln Tyr Ser Glu Asp Ala
 225 230 235 240
 Lys Lys Thr Gln Lys Asp Tyr Ala Ser Gln Ser Lys Lys Asp Lys Asn
 245 250 255
 25 Glu Lys Ser Asn Thr Lys Asn Pro Gln Leu Pro Thr Gln Asp Glu Leu
 260 265 270
 Lys His Lys Ser Lys Pro Ala Gln Ser Phe Asn Asn Asp Val Asn Gln
 275 280 285
 30 Lys Asp Thr Arg Ala Thr Ser Leu Phe Glu Thr Asp Pro Ser Ile Ser
 290 295 300
 Asn Asn Asp Asp Ser Gly Gln Phe Asn Val Val Asp Ser Lys Asp Thr
 305 310 315 320
 35 Arg Gln Phe Val Lys Ser Ile Ala Lys Asp Ala His Arg Ile Gly Gln
 325 330 335
 Asp Asn Asp Ile Tyr Ala Ser Val Met Ile Ala Gln Ala Ile Leu Glu
 340 345 350
 40 Ser Asp Ser Gly Arg Ser Ala Leu Ala Lys Ser Pro Asn His Asn Leu
 355 360 365
 Phe Gly Ile Lys Gly Ala Phe Glu Gly Asn Ser Val Pro Phe Asn Thr
 370 375 380
 45 Leu Glu Ala Asp Gly Asn Gln Leu Tyr Ser Ile Asn Ala Gly Phe Arg
 385 390 395 400
 Lys Tyr Pro Ser Thr Lys Glu Ser Leu Lys Asp Tyr Ser Asp Leu Ile
 405 410 415
 50 Lys Asn Gly Ile Asp Gly Asn Arg Thr Ile Tyr Lys Pro Thr Trp Lys
 420 425 430
 Ser Glu Ala Asp Ser Tyr Lys Asp Ala Thr Ser His Leu Ser Lys Thr
 435 440 445
 Tyr Ala Thr Asp Pro Asn Tyr Ala Lys Lys Leu Asn Ser Ile Ile Lys
 450 455 460
 55 His Tyr Gln Leu Thr Gln Phe Asp Asp Glu Arg Met Pro Asp Leu Asp
 465 470 475 480

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Lys Tyr Glu Arg Ser Ile Lys Asp Tyr Asp Asp Ser Ser Asp Glu Phe
 485 490 495
 Lys Pro Phe Arg Glu Val Ser Asp Ser Met Pro Tyr Pro His Gly Gln
 500 505 510
 Cys Thr Trp Tyr Val Tyr Asn Arg Met Lys Gln Phe Gly Thr Ser Ile
 515 520 525
 Ser Gly Asp Leu Gly Asp Ala His Asn Trp Asn Asn Arg Ala Gln Tyr
 530 535 540
 Arg Asp Tyr Gln Val Ser His Thr Pro Lys Arg His Ala Ala Val Val
 545 550 555 560
 Phe Glu Ala Gly Gln Phe Gly Ala Asp Gln His Tyr Gly His Val Ala
 565 570 575
 Phe Val Glu Lys Val Asn Ser Asp Gly Ser Ile Val Ile Ser Glu Ser
 580 585 590
 Asn Val Lys Gly Leu Gly Ile Ile Ser His Arg Thr Ile Asn Ala Ala
 595 600 605
 Ala Ala Glu Glu Leu Ser Tyr Ile Thr Gly Lys
 610 615

<210> 180

<211> 208

<212> PRT

<213> Staphylococcus aureus

<400> 180

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Met Lys Phe Gly Lys Thr Ile Ala Val Val Leu Ala Ser Ser Val Leu
1 5 10 15
Leu Ala Gly Cys Thr Thr Asp Lys Lys Glu Ile Lys Ala Tyr Leu Lys
5 20 25 30
Gln Val Asp Lys Ile Lys Asp Asp Glu Glu Pro Ile Lys Thr Val Gly
35 40 45
Lys Lys Ile Ala Glu Leu Asp Glu Lys Lys Lys Lys Leu Thr Glu Asp
10 50 55 60
Val Asn Ser Lys Asp Thr Ala Val Arg Gly Lys Ala Val Lys Asp Leu
65 70 75 80
Ile Lys Asn Ala Asp Asp Arg Leu Lys Glu Phe Glu Lys Glu Glu Asp
15 85 90 95
Ala Ile Lys Lys Ser Glu Gln Asp Phe Lys Lys Ala Lys Ser His Val
100 105 110
Asp Asn Ile Asp Asn Asp Val Lys Arg Lys Glu Val Lys Gln Leu Asp
20 115 120 125
Asp Val Leu Lys Glu Lys Tyr Lys Leu His Ser Asp Tyr Ala Lys Ala
130 135 140
Tyr Lys Lys Ala Val Asn Ser Glu Lys Thr Leu Phe Lys Tyr Leu Asn
25 145 150 155 160
Gln Asn Asp Ala Thr Gln Gln Gly Val Asn Glu Lys Ser Lys Ala Ile
165 170 175
Glu Gln Asn Tyr Lys Lys Leu Lys Glu Val Ser Asp Lys Tyr Thr Lys
30 180 185 190
Val Leu Asn Lys Val Gly Lys Glu Lys Gln Asp Val Asp Gln Phe Lys

35 195 200 205

<210> 181
<211> 105
<212> PRT
40 <213> Staphylococcus aureus
<400> 181

45

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55

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Met Asn Lys Leu Leu Gln Ser Leu Ser Ala Leu Gly Val Ser Ala Thr
1 5 10 15
Leu Val Thr Pro Asn Leu Asn Ala Asp Ala Thr Thr Asn Thr Thr Pro
5 20 25 30
Gln Ile Lys Gly Ala Asn Asp Ile Val Ile Lys Lys Gly Gln Asp Tyr
35 40 45
Asn Leu Leu Asn Gly Ile Ser Ala Phe Asp Lys Glu Asp Gly Asp Leu
10 50 55 60
Thr Asp Lys Ile Lys Val Asp Gly Gln Ile Asp Thr Ser Lys Ser Gly
65 70 75 80
Lys Tyr Gln Ile Lys Tyr His Val Thr Asp Ser Asp Gly Ala Ile Lys
15 85 90 95
Ile Ser Thr Arg Tyr Ile Glu Val Lys
100 105

<210> 182

<211> 312

<212> PRT

<213> Staphylococcus aureus

<400> 182

Met Lys Lys Leu Val Pro Leu Leu Leu Ala Leu Leu Leu Leu Val Ala
1 5 10 15
Ala Cys Gly Thr Gly Gly Lys Gln Ser Ser Asp Lys Ser Asn Gly Lys
30 20 25 30
Leu Lys Val Val Thr Thr Asn Ser Ile Leu Tyr Asp Met Ala Lys Asn
35 35 40 45
Val Gly Gly Asp Asn Val Asp Ile His Ser Ile Val Pro Val Gly Gln
50 55 60
Asp Pro His Glu Tyr Glu Val Lys Pro Lys Asp Ile Lys Lys Leu Thr
65 70 75 80
Asp Ala Asp Val Ile Leu Tyr Asn Gly Leu Asn Leu Glu Thr Gly Asn
40 85 90 95
Gly Trp Phe Glu Lys Ala Leu Glu Gln Ala Gly Lys Ser Leu Lys Asp
100 105 110
Lys Lys Val Ile Ala Val Ser Lys Asp Val Lys Pro Ile Tyr Leu Asn
45 115 120 125
Gly Glu Glu Gly Asn Lys Asp Lys Gln Asp Pro His Ala Trp Leu Ser
130 135 140
Leu Asp Asn Gly Ile Lys Tyr Val Lys Thr Ile Gln Gln Thr Phe Ile
50 145 150 155 160
Asp Asn Asp Lys Lys His Lys Ala Asp Tyr Glu Lys Gln Gly Asn Lys
165 170 175
Tyr Ile Ala Gln Leu Glu Lys Leu Asn Asn Asp Ser Lys Asp Ser Lys
55 180 185 190

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	Asp	Lys	Phe	Asn	Asp	Ile	Pro	Lys	Glu	Gln	Arg	Ala	Met	Ile	Thr	Ser
			195					200					205			
5	Glu	Gly	Ala	Phe	Lys	Tyr	Phe	Ser	Lys	Gln	Tyr	Gly	Ile	Thr	Pro	Gly
		210					215					220				
	Tyr	Ile	Trp	Glu	Ile	Asn	Thr	Glu	Lys	Gln	Gly	Thr	Pro	Glu	Gln	Met
	225					230					235					240
10	Arg	Gln	Ala	Ile	Glu	Phe	Val	Lys	Lys	His	Lys	Leu	Lys	His	Leu	Leu
					245					250					255	
	Val	Glu	Thr	Ser	Val	Asp	Lys	Lys	Ala	Met	Glu	Ser	Leu	Ser	Glu	Glu
				260					265					270		
15	Thr	Lys	Lys	Asp	Ile	Phe	Gly	Glu	Val	Tyr	Thr	Asp	Ser	Ile	Gly	Lys
			275					280					285			
	Glu	Gly	Thr	Lys	Gly	Asp	Ser	Tyr	Tyr	Lys	Met	Met	Lys	Ser	Asn	Ile
		290					295					300				
20	Glu	Thr	Val	His	Gly	Ser	Met	Lys								
	305					310										

<210> 183

<211> 646

<212> PRT

25 <213> Staphylococcus aureus

<400> 183

30

35

40

45

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	Met	Ser	Ser	Gln	Lys	Lys	Lys	Ile	Ser	Leu	Phe	Ala	Phe	Phe	Leu	Leu
	1				5					10					15	
5	Thr	Val	Ile	Thr	Ile	Thr	Leu	Lys	Thr	Tyr	Phe	Ser	Tyr	Tyr	Val	Asp
				20					25					30		
	Phe	Ser	Leu	Gly	Val	Lys	Gly	Leu	Val	Gln	Asn	Leu	Ile	Leu	Leu	Met
			35				40						45			
10	Asn	Pro	Tyr	Ser	Leu	Val	Ala	Leu	Val	Leu	Ser	Val	Phe	Leu	Phe	Phe
		50					55					60				
	Lys	Gly	Lys	Lys	Ala	Phe	Trp	Phe	Met	Phe	Ile	Gly	Gly	Phe	Leu	Leu
	65				70						75					80
15	Thr	Phe	Leu	Leu	Tyr	Ala	Asn	Val	Val	Tyr	Phe	Arg	Phe	Phe	Ser	Asp
					85					90					95	
	Phe	Leu	Thr	Phe	Ser	Thr	Leu	Asn	Gln	Val	Gly	Asn	Val	Glu	Ser	Met
				100					105					110		
20	Gly	Gly	Ala	Val	Ser	Ala	Ser	Phe	Lys	Trp	Tyr	Asp	Phe	Val	Tyr	Phe
			115					120					125			
	Ile	Asp	Thr	Leu	Val	Tyr	Leu	Phe	Ile	Leu	Ile	Phe	Lys	Thr	Lys	Trp
		130					135					140				
25	Leu	Asp	Thr	Lys	Ala	Phe	Ser	Lys	Lys	Phe	Val	Pro	Val	Val	Met	Ala
	145				150						155					160
	Ala	Ser	Val	Ala	Leu	Phe	Phe	Leu	Asn	Leu	Ala	Phe	Ala	Glu	Thr	Asp
					165					170					175	
30	Arg	Pro	Glu	Leu	Leu	Thr	Arg	Thr	Phe	Asp	His	Lys	Tyr	Leu	Val	Lys
				180					185					190		
	Tyr	Leu	Gly	Pro	Tyr	Asn	Phe	Thr	Val	Tyr	Asp	Gly	Val	Lys	Thr	Ile
			195					200					205			

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Glu Asn Asn Gln Gln Lys Ala Leu Ala Ser Glu Asp Asp Leu Thr Lys
 210 215 220
 Val Leu Asn Tyr Thr Lys Gln Arg Gln Thr Glu Pro Asn Pro Glu Tyr
 225 230 235 240
 Tyr Gly Val Ala Lys Lys Lys Asn Ile Ile Lys Ile His Leu Glu Ser
 245 250 255
 Phe Gln Thr Phe Leu Ile Asn Lys Lys Val Asn Gly Lys Glu Val Thr
 260 265 270
 Pro Phe Leu Asn Lys Leu Ser Ser Gly Lys Glu Gln Phe Thr Tyr Phe
 275 280 285
 Pro Asn Phe Phe His Gln Thr Gly Gln Gly Lys Thr Ser Asp Ser Glu
 290 295 300
 Phe Thr Met Asp Asn Ser Leu Tyr Gly Leu Pro Gln Gly Ser Ala Phe
 305 310 315 320
 Ser Leu Lys Gly Asp Asn Thr Tyr Gln Ser Leu Pro Ala Ile Leu Asp
 325 330 335
 Gln Lys Gln Gly Tyr Lys Ser Asp Val Met His Gly Asp Tyr Lys Thr
 340 345 350
 Phe Trp Asn Arg Asp Gln Val Tyr Lys His Phe Gly Ile Asp Lys Phe
 355 360 365
 Tyr Asp Ala Thr Tyr Tyr Asp Met Ser Asp Lys Asn Val Val Asn Leu
 370 375 380
 Gly Leu Lys Asp Lys Ile Phe Phe Lys Asp Ser Ala Asn Tyr Gln Ala
 385 390 395 400
 Lys Met Lys Ser Pro Phe Tyr Ser His Leu Ile Thr Leu Thr Asn His
 405 410 415
 Tyr Pro Phe Thr Leu Asp Glu Lys Asp Ala Thr Ile Glu Lys Ser Asn
 420 425 430
 Thr Gly Asp Ala Thr Val Asp Gly Tyr Ile Gln Thr Ala Arg Tyr Leu
 435 440 445
 Asp Glu Ala Leu Glu Glu Tyr Ile Asn Asp Leu Lys Lys Lys Gly Leu
 450 455 460
 Tyr Asp Asn Ser Val Ile Met Ile Tyr Gly Asp His Tyr Gly Ile Ser
 465 470 475 480
 Glu Asn His Asn Asn Ala Met Glu Lys Leu Leu Gly Glu Lys Ile Thr
 485 490 495
 Pro Ala Lys Phe Thr Asp Leu Asn Arg Thr Gly Phe Trp Ile Lys Ile
 500 505 510
 Pro Gly Lys Ser Gly Gly Ile Asn Asn Glu Tyr Ala Gly Gln Val Asp
 515 520 525
 Val Met Pro Thr Ile Leu His Leu Ala Gly Ile Asp Thr Lys Asn Tyr
 530 535 540
 Leu Met Phe Gly Thr Asp Leu Phe Ser Lys Gly His Asn Gln Val Val
 545 550 555 560
 Pro Phe Arg Asn Gly Asp Phe Ile Thr Lys Asp Tyr Lys Tyr Val Asn
 565 570 575
 Gly Lys Ile Tyr Ser Asn Lys Asn Asn Glu Leu Ile Thr Thr Gln Pro

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580 585 590

Ala Asp Phe Glu Lys Asn Lys Lys Gln Val Glu Lys Asp Leu Glu Met
595 600 605

5 Ser Asp Asn Val Leu Asn Gly Asp Leu Phe Arg Phe Tyr Lys Asn Pro
610 615 620

Asp Phe Lys Lys Val Asn Pro Ser Lys Tyr Lys Tyr Glu Thr Gly Pro
625 630 635 640

10 Lys Ala Asn Ser Lys Lys
645

<210> 184

<211> 173

15 <212> PRT

<213> Staphylococcus aureus

<400> 184

20 Met Ile Asn Ile Ile Ser Ala Ile Gly Ser Ile Gly Thr Phe Ile Met
1 5 10 15

Ala Leu Phe Tyr Phe Val Ser Val Ser Val Gln Leu Tyr Gln Met Lys
20 25 30

25 Ile Ser Phe Leu Pro Ala Leu Gly Phe Asn Gln Ile Leu Leu Glu Arg
35 40 45

Glu Glu Asp Gln Leu Asn Ile Met Asn Ser Ala Thr Glu Glu His His
50 55 60

30 His Lys Asp Tyr Ile Lys Leu Tyr Asn Leu Gly Gly Gly Ala Ala Lys
65 70 75 80

Lys Ile Ala Ile Glu Val Leu Leu Gly Lys Asp Lys Val Ile Gln Lys
85 90 95

35 Lys Tyr Val His Ile Leu Pro Ser Lys Glu Gly Tyr Met Leu Pro Ile
100 105 110

Asn Lys Asn Val Tyr Glu Glu Leu Glu Arg Thr Ile Glu Asn Asn Gly
115 120 125

40 His Glu Ala Asp Leu Asn Val Arg Met Thr Tyr Tyr His Asn Val Ser
130 135 140

Arg Lys Gln Gln Glu Val Ile Leu Lys Gly Gln Ile Asp Arg Phe Asn
145 150 155 160

45 Thr Tyr Asn Asn Lys Glu Ile Tyr Asp Leu Gln Phe Ile
165 170

<210> 185

<211> 156

50 <212> PRT

<213> Staphylococcus aureus

<400> 185

55

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Met Lys Arg Lys Val Leu Val Leu Thr Met Gly Val Ile Cys Ala Thr
1 5 10
Gln Leu Trp His Ser Asn His Ala Asn Ala Leu Val Thr Glu Ser Gly
5 20 25 30
Ala Asn Asp Thr Lys Gln Phe Thr Glu Ile Val Ser Glu Glu Lys Val
35 40 45
Ile Thr Val Glu His Ala Gln Ile Asn Ile Phe Gln Ser Asn Ser Asn
10 50 55 60
Ser Asn Leu Met Glu Phe Asn Ile Leu Thr Met Gly Gly Lys Ser Gly
65 70 75 80
Ala Met Val Gly Tyr Ser Glu Ile Asp Ser Ser His Phe Thr Asp Arg
15 85 90 95
Asp Lys Arg Val Ile Arg Arg Asp His Val Lys Glu Ala Gln Ser Leu
100 105 110
Val Glu Asn Tyr Lys Asp Thr Gln Ser Ala Asp Ala Arg Met Lys Ala
20 115 120 125
Lys Gln Lys Val Asn Thr Leu Ser Lys Pro His Gln Asn Tyr Phe Asn
130 135 140
Lys Gln Ile Asp Lys Val Tyr Asn Gly Leu Gln Arg
25 145 150 155

<210> 186

<211> 133

30 <212> PRT

<213> Staphylococcus aureus

<400> 186

Met Lys Lys Asn Ile Thr Lys Thr Ile Ile Ala Ser Thr Val Ile Ala
35 1 5 10
Ala Gly Leu Leu Thr Gln Thr Asn Asp Ala Lys Ala Phe Phe Ser Tyr
20 25 30
Glu Trp Lys Gly Leu Glu Ile Ala Lys Asn Leu Ala Asp Gln Ala Lys
40 35 40 45
Lys Asp Asp Glu Arg Ile Asp Lys Leu Met Lys Glu Ser Asp Lys Asn
50 55 60
Leu Thr Pro Tyr Lys Ala Glu Thr Val Asn Asp Leu Tyr Leu Ile Val
45 65 70 75 80
Lys Lys Leu Ser Gln Gly Asp Val Lys Lys Ala Val Val Arg Ile Lys
85 90 95
Asp Gly Gly Pro Arg Asp Tyr Tyr Thr Phe Asp Leu Thr Arg Pro Leu
50 100 105 110
Glu Glu Asn Arg Lys Asn Ile Lys Val Val Lys Asn Gly Glu Ile Asp
115 120 125
Ser Ile Thr Trp Tyr
55 130

<210> 187

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<211> 274
 <212> PRT
 <213> Staphylococcus aureus

5 <400> 187

	Met	Tyr	Pro	Asn	Trp	Gly	Gln	Tyr	Lys	Arg	Ala	Asp	Leu	Ile	Gly	Gln
	1				5					10					15	
10	Ser	Ser	Tyr	Ile	Lys	Asn	Asn	Asp	Val	Val	Ile	Phe	Asn	Glu	Ala	Phe
				20					25					30		
	Asp	Asn	Gly	Ala	Ser	Asp	Lys	Leu	Leu	Ser	Asn	Val	Lys	Lys	Glu	Tyr
			35					40					45			
15	Pro	Tyr	Gln	Thr	Pro	Val	Leu	Gly	Arg	Ser	Gln	Ser	Gly	Trp	Asp	Lys
		50					55					60				
	Thr	Glu	Gly	Ser	Tyr	Ser	Ser	Thr	Val	Ala	Glu	Asp	Gly	Gly	Val	Ala
20	65					70					75					80
	Ile	Val	Ser	Lys	Tyr	Pro	Ile	Lys	Glu	Lys	Ile	Gln	His	Val	Phe	Lys
					85					90					95	
	Ser	Gly	Cys	Gly	Phe	Asp	Asn	Asp	Ser	Asn	Lys	Gly	Phe	Val	Tyr	Thr
25				100					105					110		
	Lys	Ile	Glu	Lys	Asn	Gly	Lys	Asn	Val	His	Val	Ile	Gly	Thr	His	Thr
			115					120					125			
	Gln	Ser	Glu	Asp	Ser	Arg	Cys	Gly	Ala	Gly	His	Asp	Arg	Lys	Ile	Arg
30		130					135					140				
	Ala	Glu	Gln	Met	Lys	Glu	Ile	Ser	Asp	Phe	Val	Lys	Lys	Lys	Asn	Ile
	145					150					155					160
	Pro	Lys	Asp	Glu	Thr	Val	Tyr	Ile	Gly	Gly	Asp	Leu	Asn	Val	Asn	Lys
35					165					170					175	
	Gly	Thr	Pro	Glu	Phe	Lys	Asp	Met	Leu	Lys	Asn	Leu	Asn	Val	Asn	Asp
				180					185					190		
	Val	Leu	Tyr	Ala	Gly	His	Asn	Ser	Thr	Trp	Asp	Pro	Gln	Ser	Asn	Ser
40			195					200					205			
	Ile	Ala	Lys	Tyr	Asn	Tyr	Pro	Asn	Gly	Lys	Pro	Glu	His	Leu	Asp	Tyr
		210					215					220				
	Ile	Phe	Thr	Asp	Lys	Asp	His	Lys	Gln	Pro	Lys	Gln	Leu	Val	Asn	Glu
45	225					230					235					240
	Val	Val	Thr	Glu	Lys	Pro	Lys	Pro	Trp	Asp	Val	Tyr	Ala	Phe	Pro	Tyr
					245					250					255	
	Tyr	Tyr	Val	Tyr	Asn	Asp	Phe	Ser	Asp	His	Tyr	Pro	Ile	Lys	Ala	Tyr
50				260					265					270		
	Ser	Lys														

<210> 188
 <211> 390
 <212> PRT
 <213> Staphylococcus aureus

<400> 188

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Met Leu Glu Phe Glu Gln Gly Phe Asn His Leu Ala Thr Leu Lys Val
 1 5 10 15
 Ile Gly Val Gly Gly Gly Gly Asn Asn Ala Val Asn Arg Met Ile Asp
 5 20 25 30
 His Gly Met Asn Asn Val Glu Phe Ile Ala Ile Asn Thr Asp Gly Gln
 35 40 45
 Ala Leu Asn Leu Ser Lys Ala Glu Ser Lys Ile Gln Ile Gly Glu Lys
 10 50 55 60
 Leu Thr Arg Gly Leu Gly Ala Gly Ala Asn Pro Glu Ile Gly Lys Lys
 65 70 75 80
 Ala Ala Glu Glu Ser Arg Glu Gln Ile Glu Asp Ala Ile Gln Gly Ala
 15 85 90 95
 Asp Met Val Phe Val Thr Ser Gly Met Gly Gly Gly Thr Gly Thr Gly
 100 105 110
 Ala Ala Pro Val Val Ala Lys Ile Ala Lys Glu Met Gly Ala Leu Thr
 20
 25
 30
 35
 40
 45
 50
 55

EP 2 510 947 B1

	115		120		125												
	Val	Gly	Val	Val	Thr	Arg	Pro	Phe	Ser	Phe	Glu	Gly	Arg	Lys	Arg	Gln	
		130					135					140					
5	Thr	Gln	Ala	Ala	Ala	Gly	Val	Glu	Ala	Met	Lys	Ala	Ala	Val	Asp	Thr	
	145					150					155					160	
	Leu	Ile	Val	Ile	Pro	Asn	Asp	Arg	Leu	Leu	Asp	Ile	Val	Asp	Lys	Ser	
					165					170					175		
10	Thr	Pro	Met	Met	Glu	Ala	Phe	Lys	Glu	Ala	Asp	Asn	Val	Leu	Arg	Gln	
				180					185					190			
	Gly	Val	Gln	Gly	Ile	Ser	Asp	Leu	Ile	Ala	Val	Ser	Gly	Glu	Val	Asn	
			195					200					205				
15	Leu	Asp	Phe	Ala	Asp	Val	Lys	Thr	Ile	Met	Ser	Asn	Gln	Gly	Ser	Ala	
		210					215					220					
	Leu	Met	Gly	Ile	Gly	Val	Ser	Ser	Gly	Glu	Asn	Arg	Ala	Val	Glu	Ala	
	225					230					235					240	
20	Ala	Lys	Lys	Ala	Ile	Ser	Ser	Pro	Leu	Leu	Glu	Thr	Ser	Ile	Val	Gly	
					245					250					255		
	Ala	Gln	Gly	Val	Leu	Met	Asn	Ile	Thr	Gly	Gly	Glu	Ser	Leu	Ser	Leu	
				260					265					270			
25	Phe	Glu	Ala	Gln	Glu	Ala	Ala	Asp	Ile	Val	Gln	Asp	Ala	Ala	Asp	Glu	
			275					280					285				
	Asp	Val	Asn	Met	Ile	Phe	Gly	Thr	Val	Ile	Asn	Pro	Glu	Leu	Gln	Asp	
		290					295				300						
30	Glu	Ile	Val	Val	Thr	Val	Ile	Ala	Thr	Gly	Phe	Asp	Asp	Lys	Pro	Thr	
	305					310					315					320	
	Ser	His	Gly	Arg	Lys	Ser	Gly	Ser	Thr	Gly	Phe	Gly	Thr	Ser	Val	Asn	
					325					330					335		
35	Thr	Ser	Ser	Asn	Ala	Thr	Ser	Lys	Asp	Glu	Ser	Phe	Thr	Ser	Asn	Ser	
				340					345					350			
	Ser	Asn	Ala	Gln	Ala	Thr	Asp	Ser	Val	Ser	Glu	Arg	Thr	His	Thr	Thr	
			355					360					365				
40	Lys	Glu	Asp	Asp	Ile	Pro	Ser	Phe	Ile	Arg	Asn	Arg	Glu	Glu	Arg	Arg	
		370					375					380					
	Ser	Arg	Arg	Thr	Arg	Arg											
	385					390											

45 <210> 189
 <211> 258
 <212> PRT
 <213> Staphylococcus aureus

50 <400> 189

55

EP 2 510 947 B1

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
1 5 10 15
Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
5 20 25 30
Gly Met Leu Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
35 40 45
Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
10 50 55 60
Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
15 65 70 75 80
Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
85 90 95
Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Pro Ser Gly
20 100 105 110
Ser Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro Thr Asp Lys
115 120 125
Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn Gln Asn Trp
25 130 135 140
Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly Asn Gln Leu
145 150 155 160
Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp Asn Phe Leu
30 165 170 175
Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe Ser Pro Asp
180 185 190
Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys Gln Gln Thr
35 195 200 205
Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr Gln Leu His
210 215 220
Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp Lys Trp Ile
40 225 230 235 240
Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys Glu Glu Met
245 250 255

Thr Asn

45 <210> 190
<211> 306
<212> PRT
<213> Staphylococcus aureus

50 <400> 190

55

EP 2 510 947 B1

1 Lys Phe Val Val Pro Glu Ser Gly Ile Asn Lys Ile Ile Pro Ala Tyr
 5 Asp Glu Phe Lys Asn Ser Pro Lys Val Asn Val Ser Asn Leu Thr Asp
 Asn Lys Asn Phe Val Ala Ser Glu Asp Lys Leu Asn Lys Ile Ala Asp
 10 Ser Ser Ala Ala Ser Lys Ile Val Asp Lys Asn Phe Val Val Pro Glu
 Ser Lys Leu Gly Asn Ile Val Pro Glu Tyr Lys Glu Ile Asn Asn Arg
 15 Val Asn Val Ala Thr Asn Asn Pro Ala Ser Gln Gln Val Asp Lys His
 Phe Val Ala Lys Gly Pro Glu Val Asn Arg Phe Ile Thr Gln Asn Lys
 20 Val Asn His His Phe Ile Thr Thr Gln Thr His Tyr Lys Lys Val Ile
 Thr Ser Tyr Lys Ser Thr His Val His Lys His Val Asn His Ala Lys
 25 Asp Ser Ile Asn Lys His Phe Ile Val Lys Pro Ser Glu Ser Pro Arg
 Tyr Thr His Pro Ser Gln Ser Leu Ile Ile Lys His His Phe Ala Val
 30 Pro Gly Tyr His Ala His Lys Phe Val Thr Pro Gly His Ala Ser Ile
 Lys Ile Asn His Phe Cys Val Val Pro Gln Ile Asn Ser Phe Lys Val
 35 Ile Pro Pro Tyr Gly His Asn Ser His Arg Met His Val Pro Ser Phe
 Gln Asn Asn Thr Thr Ala Thr His Gln Asn Ala Lys Val Asn Lys Ala
 40 Tyr Asp Tyr Lys Tyr Phe Tyr Ser Tyr Lys Val Val Lys Gly Val Lys
 Lys Tyr Phe Ser Phe Ser Gln Ser Asn Gly Tyr Lys Ile Gly Lys Pro
 45 Ser Leu Asn Ile Lys Asn Val Asn Tyr Gln Tyr Ala Val Pro Ser Tyr
 Ser Pro Thr His Tyr Val Pro Glu Phe Lys Gly Ser Leu Pro Ala Pro
 50 Arg val
 305

<210> 191

<211> 308

<212> PRT

<213> Staphylococcus aureus

<400> 191

EP 2 510 947 B1

Ser Val Thr Glu Ser Val Asp Lys Lys Phe Val Val Pro Glu Ser Gly
 1 5 10 15
 Ile Asn Lys Ile Ile Pro Ala Tyr Asp Glu Phe Lys Asn Ser Pro Lys
 5 20 25 30
 Val Asn Val Ser Asn Leu Thr Asp Asn Lys Asn Phe Val Ala Ser Glu
 35 40 45
 Asp Lys Leu Asn Lys Ile Ala Asp Ser Ser Ala Ala Ser Lys Ile Val
 10 50 55 60
 Asp Lys Asn Phe Val Val Pro Glu Ser Lys Leu Gly Asn Ile Val Pro
 65 70 75 80
 Glu Tyr Lys Glu Ile Asn Asn Arg Val Asn Val Ala Thr Asn Asn Pro
 15 85 90 95
 Ala Ser Gln Gln Val Asp Lys His Phe Val Ala Lys Gly Pro Glu Val
 100 105 110
 Asn Arg Phe Ile Thr Gln Asn Lys Val Asn His His Phe Ile Thr Thr
 20 115 120 125
 Gln Thr His Tyr Lys Lys Val Ile Thr Ser Tyr Lys Ser Thr His Val
 130 135 140
 His Lys His Val Asn His Ala Lys Asp Ser Ile Asn Lys His Phe Ile
 25
 145 150 155 160
 Val Lys Pro Ser Glu Ser Pro Arg Tyr Thr His Pro Ser Gln Ser Leu
 165 170 175
 Ile Ile Lys His His Phe Ala Val Pro Gly Tyr His Ala His Lys Phe
 180 185 190
 Val Thr Pro Gly His Ala Ser Ile Lys Ile Asn His Phe Cys Val Val
 195 200 205
 35 Pro Gln Ile Asn Ser Phe Lys Val Ile Pro Pro Tyr Gly His Asn Ser
 210 215 220
 His Arg Met His Val Pro Ser Phe Gln Asn Asn Thr Thr Ala Thr His
 225 230 235 240
 40 Gln Asn Ala Lys Val Asn Lys Ala Tyr Asp Tyr Lys Tyr Phe Tyr Ser
 245 250 255
 Tyr Lys Val Val Lys Gly Val Lys Lys Tyr Phe Ser Phe Ser Gln Ser
 260 265 270
 45 Asn Gly Tyr Lys Ile Gly Lys Pro Ser Leu Asn Ile Lys Asn Val Asn
 275 280 285
 Tyr Gln Tyr Ala Val Pro Ser Tyr Ser Pro Thr His Tyr Val Pro Glu
 290 295 300
 50 Phe Lys Gly Ser
 305

<210> 192

<211> 300

<212> PRT

<213> Staphylococcus aureus

<400> 192

EP 2 510 947 B1

1 Lys Phe Val Val Pro Glu Ser Gly Ile Asn Lys Ile Ile Pro Ala Tyr
 5 Asp Glu Phe Lys Asn Ser Pro Lys Val Asn Val Ser Asn Leu Thr Asp
 10 Asn Lys Asn Phe Val Ala Ser Glu Asp Lys Leu Asn Lys Ile Ala Asp
 15 Ser Ser Ala Ala Ser Lys Ile Val Asp Lys Asn Phe Val Val Pro Glu
 20 Ser Lys Leu Gly Asn Ile Val Pro Glu Tyr Lys Glu Ile Asn Asn Arg
 25 Val Asn Val Ala Thr Asn Asn Pro Ala Ser Gln Gln Val Asp Lys His
 30 Phe Val Ala Lys Gly Pro Glu Val Asn Arg Phe Ile Thr Gln Asn Lys
 35 Val Asn His His Phe Ile Thr Thr Gln Thr His Tyr Lys Lys Val Ile
 40 Thr Ser Tyr Lys Ser Thr His Val His Lys His Val Asn His Ala Lys
 45 Asp Ser Ile Asn Lys His Phe Ile Val Lys Pro Ser Glu Ser Pro Arg
 50 Tyr Thr His Pro Ser Gln Ser Leu Ile Ile Lys His His Phe Ala Val
 55 Pro Gly Tyr His Ala His Lys Phe Val Thr Pro Gly His Ala Ser Ile
 60 Lys Ile Asn His Phe Cys Val Val Pro Gln Ile Asn Ser Phe Lys Val
 65 Ile Pro Pro Tyr Gly His Asn Ser His Arg Met His Val Pro Ser Phe
 70 Gln Asn Asn Thr Thr Ala Thr His Gln Asn Ala Lys Val Asn Lys Ala
 75 Tyr Asp Tyr Lys Tyr Phe Tyr Ser Tyr Lys Val Val Lys Gly Val Lys
 80 Lys Tyr Phe Ser Phe Ser Gln Ser Asn Gly Tyr Lys Ile Gly Lys Pro
 85 Ser Leu Asn Ile Lys Asn Val Asn Tyr Gln Tyr Ala Val Pro Ser Tyr
 90 Ser Pro Thr His Tyr Val Pro Glu Phe Lys Gly Ser
 95

<210> 193

<211> 121

<212> PRT

<213> Staphylococcus aureus

<400> 193

EP 2 510 947 B1

1 Ser Val Thr Glu 5 Ser Val Asp Lys Lys Phe Val Val Pro Glu Ser Gly
 10 Ile Asn Lys 20 Ile Ile Pro Ala Tyr Asp Glu Phe Lys Asn Ser Pro Lys
 5 Val Asn Val 35 Ser Asn Leu Thr Asp Asn Lys Asn Phe Val Ala Ser Glu
 10 Asp Lys Leu Asn Lys Ile Ala Asp Ser Ser Ala Ala Ser Lys Ile Val
 65 Asp Lys Asn Phe Val 70 Val Pro Glu Ser Lys Leu Gly Asn Ile Val Pro
 15 Glu Tyr Lys Glu 85 Ile Asn Asn Arg Val Asn Val Ala Thr Asn Asn Pro
 100 Ala Ser Gln Gln Val Asp Lys His Phe 105 Val Ala Lys Gly Pro Glu Val
 110 Asn Arg Phe 115 Ile Thr Gln Asn Lys 120 Val

<210> 194
 <211> 53
 <212> PRT
 <213> Staphylococcus aureus

25
 <400> 194

30 Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
 1 5 10 15
 Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
 20 25 30
 Gly Met His Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
 35 35 40 45
 Asn Lys Lys Leu Leu
 50

40
 <210> 195
 <211> 53
 <212> PRT
 <213> Staphylococcus aureus

45
 <400> 195

50 Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
 1 5 10 15
 Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
 20 25 30
 Gly Met Leu Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
 55 35 40 45
 Asn Lys Lys Leu Leu
 50

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<210> 196
 <211> 316
 <212> PRT
 <213> Staphylococcus aureus

5
 <400> 196

10	Ser	Glu	Gln	Ser	Asn	Asp	Thr	Thr	Gln	Ser	Ser	Lys	Asn	Asn	Ala	Ser
	1				5					10					15	
	Ala	Asp	Ser	Glu	Lys	Asn	Asn	Met	Ile	Glu	Thr	Pro	Gln	Leu	Asn	Thr
				20					25					30		
	Thr	Ala	Asn	Asp	Thr	Ser	Asp	Ile	Ser	Ala	Asn	Thr	Asn	Ser	Ala	Asn
15			35					40					45			
	Val	Asp	Ser	Thr	Thr	Lys	Pro	Met	Ser	Thr	Gln	Thr	Ser	Asn	Thr	Thr
		50					55					60				
	Thr	Thr	Glu	Pro	Ala	Ser	Thr	Asn	Glu	Thr	Pro	Gln	Pro	Thr	Ala	Ile
20	65					70					75					80
	Lys	Asn	Gln	Ala	Thr	Ala	Ala	Lys	Met	Gln	Asp	Gln	Thr	Val	Pro	Gln
					85					90					95	
	Glu	Ala	Asn	Ser	Gln	Val	Asp	Asn	Lys	Thr	Thr	Asn	Asp	Ala	Asn	Ser
25				100					105					110		
	Ile	Ala	Thr	Asn	Ser	Glu	Leu	Lys	Asn	Ser	Gln	Thr	Leu	Asp	Leu	Pro
			115					120					125			
	Gln	Ser	Ser	Pro	Gln	Thr	Ile	Ser	Asn	Ala	Gln	Gly	Thr	Ser	Lys	Pro
30							135					140				
	Ser	Val	Arg	Thr	Arg	Ala	Val	Arg	Ser	Leu	Ala	Val	Ala	Glu	Pro	Val
	145					150					155					160
	Val	Asn	Ala	Ala	Asp	Ala	Lys	Gly	Thr	Asn	Val	Asn	Asp	Lys	Val	Thr
					165					170					175	
35	Ala	Ser	Asn	Phe	Lys	Leu	Glu	Lys	Thr	Thr	Phe	Asp	Pro	Asn	Gln	Ser
				180					185					190		
	Gly	Asn	Thr	Phe	Met	Ala	Ala	Asn	Phe	Thr	Val	Thr	Asp	Lys	Val	Lys
			195					200					205			
40	Ser	Gly	Asp	Tyr	Phe	Thr	Ala	Lys	Leu	Pro	Asp	Ser	Leu	Thr	Gly	Asn
		210					215					220				
	Gly	Asp	Val	Asp	Tyr	Ser	Asn	Ser	Asn	Asn	Thr	Met	Pro	Ile	Ala	Asp
45																
	225						230					235				240
	Ile	Lys	Ser	Thr	Asn	Gly	Asp	Val	Val	Ala	Lys	Ala	Thr	Tyr	Asp	Ile
					245					250					255	
50	Leu	Thr	Lys	Thr	Tyr	Thr	Phe	Val	Phe	Thr	Asp	Tyr	Val	Asn	Asn	Lys
				260					265					270		
	Glu	Asn	Ile	Asn	Gly	Gln	Phe	Ser	Leu	Pro	Leu	Phe	Thr	Asp	Arg	Ala
			275					280					285			
55	Lys	Ala	Pro	Lys	Ser	Gly	Thr	Tyr	Asp	Ala	Asn	Ile	Asn	Ile	Ala	Asp
		290					295					300				
	Glu	Met	Phe	Asn	Asn	Lys	Ile	Thr	Tyr	Asn	Tyr	Ser				
		305				310					315					

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<210> 197
 <211> 331
 <212> PRT
 <213> Staphylococcus aureus

5

<400> 197

10

15

20

25

30

35

40

45

50

55

Gly Thr Asn Val Asn Asp Lys Val Thr Ala Ser Asn Phe Lys Leu Glu
 1 5 10 15
 Lys Thr Thr Phe Asp Pro Asn Gln Ser Gly Asn Thr Phe Met Ala Ala
 20
 Asn Phe Thr Val Thr Asp Lys Val Lys Ser Gly Asp Tyr Phe Thr Ala
 35 40 45
 Lys Leu Pro Asp Ser Leu Thr Gly Asn Gly Asp Val Asp Tyr Ser Asn
 50 55 60
 Ser Asn Asn Thr Met Pro Ile Ala Asp Ile Lys Ser Thr Asn Gly Asp
 65 70 75 80
 Val Val Ala Lys Ala Thr Tyr Asp Ile Leu Thr Lys Thr Tyr Thr Phe
 85 90 95
 Val Phe Thr Asp Tyr Val Asn Asn Lys Glu Asn Ile Asn Gly Gln Phe
 100 105 110
 Ser Leu Pro Leu Phe Thr Asp Arg Ala Lys Ala Pro Lys Ser Gly Thr
 115 120 125
 Tyr Asp Ala Asn Ile Asn Ile Ala Asp Glu Met Phe Asn Asn Lys Ile
 130 135 140
 Thr Tyr Asn Tyr Ser Ser Pro Ile Ala Gly Ile Asp Lys Pro Asn Gly
 145 150 155 160
 Ala Asn Ile Ser Ser Gln Ile Ile Gly Val Asp Thr Ala Ser Gly Gln
 165 170 175
 Asn Thr Tyr Lys Gln Thr Val Phe Val Asn Pro Lys Gln Arg Val Leu
 180 185 190
 Gly Asn Thr Trp Val Tyr Ile Lys Gly Tyr Gln Asp Lys Ile Glu Glu
 195 200 205
 Ser Ser Gly Lys Val Ser Ala Thr Asp Thr Lys Leu Arg Ile Phe Glu
 210 215 220
 Val Asn Asp Thr Ser Lys Leu Ser Asp Ser Tyr Tyr Ala Asp Pro Asn
 225 230 235 240
 Asp Ser Asn Leu Lys Glu Val Thr Asp Gln Phe Lys Asn Arg Ile Tyr
 245 250 255

EP 2 510 947 B1

5 Tyr Glu His Pro Asn Val Ala Ser Ile Lys Phe Gly Asp Ile Thr Lys
260 265 270
Thr Tyr Val Val Leu Val Glu Gly His Tyr Asp Asn Thr Gly Lys Asn
275 280 285
10 Leu Lys Thr Gln Val Ile Gln Glu Asn Val Asp Pro Val Thr Asn Arg
290 295 300
Asp Tyr Ser Ile Phe Gly Trp Asn Asn Glu Asn Val Val Arg Tyr Gly
305 310 315 320
Gly Gly Ser Ala Asp Gly Asp Ser Ala Val Asn
325 330

<210> 198

<211> 183

<212> PRT

<213> Staphylococcus aureus

<400> 198

20 Ser Ser Pro Ile Ala Gly Ile Asp Lys Pro Asn Gly Ala Asn Ile Ser
1 5 10 15
25 Ser Gln Ile Ile Gly Val Asp Thr Ala Ser Gly Gln Asn Thr Tyr Lys
20 25 30
Gln Thr Val Phe Val Asn Pro Lys Gln Arg Val Leu Gly Asn Thr Trp
35 40 45
30 Val Tyr Ile Lys Gly Tyr Gln Asp Lys Ile Glu Glu Ser Ser Gly Lys
50 55 60
Val Ser Ala Thr Asp Thr Lys Leu Arg Ile Phe Glu Val Asn Asp Thr
65 70 75 80
35 Ser Lys Leu Ser Asp Ser Tyr Tyr Ala Asp Pro Asn Asp Ser Asn Leu
85 90 95
Lys Glu Val Thr Asp Gln Phe Lys Asn Arg Ile Tyr Tyr Glu His Pro
100 105 110
40 Asn Val Ala Ser Ile Lys Phe Gly Asp Ile Thr Lys Thr Tyr Val Val
115 120 125
Leu Val Glu Gly His Tyr Asp Asn Thr Gly Lys Asn Leu Lys Thr Gln
130 135 140
45 Val Ile Gln Glu Asn Val Asp Pro Val Thr Asn Arg Asp Tyr Ser Ile
145 150 155 160
Phe Gly Trp Asn Asn Glu Asn Val Val Arg Tyr Gly Gly Gly Ser Ala
165 170 175
50 Asp Gly Asp Ser Ala Val Asn
180

<210> 199

<211> 199

<212> PRT

<213> Staphylococcus aureus

<400> 199

EP 2 510 947 B1

Pro Asp Tyr Val Val Asn Glu Lys Asn Ser Ile Gly Ser Ala Phe Thr
1 5 10 15
Glu Thr Val Ser His Val Gly Asn Lys Glu Asn Pro Gly Tyr Tyr Lys
5 20 25 30
Gln Thr Ile Tyr Val Asn Pro Ser Glu Asn Ser Leu Thr Asn Ala Lys
35 40 45
Leu Lys Val Gln Ala Tyr His Ser Ser Tyr Pro Asn Asn Ile Gly Gln
10 50 55 60
Ile Asn Lys Asp Val Thr Asp Ile Lys Ile Tyr Gln Val Pro Lys Gly
65 70 75 80
Tyr Thr Leu Asn Lys Gly Tyr Asp Val Asn Thr Lys Glu Leu Thr Asp
15 85 90 95
Val Thr Asn Gln Tyr Leu Gln Lys Ile Thr Tyr Gly Asp Asn Asn Ser
100 105 110
Ala Val Ile Asp Phe Gly Asn Ala Asp Ser Ala Tyr Val Val Met Val
20 115 120 125
Asn Thr Lys Phe Gln Tyr Thr Asn Ser Glu Ser Pro Thr Leu Val Gln
130 135 140
Met Ala Thr Leu Ser Ser Thr Gly Asn Lys Ser Val Ser Thr Gly Asn
25 145 150 155 160
Ala Leu Gly Phe Thr Asn Asn Gln Ser Gly Gly Ala Gly Gln Glu Val
165 170 175
Tyr Lys Ile Gly Asn Tyr Val Trp Glu Asp Thr Asn Lys Asn Gly Val
30 180 185 190
Gln Glu Leu Gly Glu Lys Gly
195

35 <210> 200
<211> 104
<212> PRT
<213> Staphylococcus aureus
40 <400> 200

Met Ala Ile Val Lys Val Thr Asp Ala Asp Phe Asp Ser Lys Val Glu
1 5 10 15
Ser Gly Val Gln Leu Val Asp Phe Trp Ala Thr Trp Cys Gly Pro Cys
45 20 25 30
Lys Met Ile Ala Pro Val Leu Glu Glu Leu Ala Ala Asp Tyr Glu Gly
35 40 45
Lys Ala Asp Ile Leu Lys Leu Asp Val Asp Glu Asn Pro Ser Thr Ala
50 50 55 60
Ala Lys Tyr Glu Val Met Ser Ile Pro Thr Leu Ile Val Phe Lys Asp
65 70 75 80
Gly Gln Pro Val Asp Lys Val Val Gly Phe Gln Pro Lys Glu Asn Leu
55 85 90 95
Ala Glu Val Leu Asp Lys His Leu
100

EP 2 510 947 B1

<210> 201
 <211> 189
 <212> PRT
 <213> Staphylococcus aureus

5

<400> 201

10

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

15

20 25 30
 Gly Ser Trp Ser Val Val Cys Phe Tyr Pro Ala Asp Phe Ser Phe Val
 35 40 45

20

Cys Pro Thr Glu Leu Glu Asp Leu Gln Asn Gln Tyr Glu Glu Leu Gln
 50 55 60
 Lys Leu Gly Val Asn Val Phe Ser Val Ser Thr Asp Thr His Phe Val
 65 70 75 80

25

His Lys Ala Trp His Asp His Ser Asp Ala Ile Ser Lys Ile Thr Tyr
 85 90 95
 Thr Met Ile Gly Asp Pro Ser Gln Thr Ile Thr Arg Asn Phe Asp Val
 100 105 110

30

Leu Asp Glu Ala Thr Gly Leu Ala Gln Arg Gly Thr Phe Ile Ile Asp
 115 120 125
 Pro Asp Gly Val Val Gln Ala Ser Glu Ile Asn Ala Asp Gly Ile Gly
 130 135 140

35

Arg Asp Ala Ser Thr Leu Ala His Lys Ile Lys Ala Ala Gln Tyr Val
 145 150 155 160
 Arg Lys Asn Pro Gly Glu Val Cys Pro Ala Lys Trp Glu Glu Gly Ala
 165 170 175

Lys Thr Leu Gln Pro Gly Leu Asp Leu Val Gly Lys Ile
 180 185

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<210> 202
 <211> 1054
 <212> PRT
 <213> Staphylococcus aureus

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<400> 202

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Ser Glu Gln Ser Asn Asp Thr Thr Gln Ser Ser Lys Asn Asn Ala Ser
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 Ala Asp Ser Glu Lys Asn Asn Met Ile Glu Thr Pro Gln Leu Asn Thr
 5 20 25 30
 Thr Ala Asn Asp Thr Ser Asp Ile Ser Ala Asn Thr Asn Ser Ala Asn
 35 40 45
 Val Asp Ser Thr Thr Lys Pro Met Ser Thr Gln Thr Ser Asn Thr Thr
 10 50 55 60
 Thr Thr Glu Pro Ala Ser Thr Asn Glu Thr Pro Gln Pro Thr Ala Ile
 65 70 75 80
 Lys Asn Gln Ala Thr Ala Ala Lys Met Gln Asp Gln Thr Val Pro Gln
 15 85 90 95
 Glu Ala Asn Ser Gln Val Asp Asn Lys Thr Thr Asn Asp Ala Asn Ser
 100 105
 Ile Ala Thr Asn Ser Glu Leu Lys Asn Ser Gln Thr Leu Asp Leu Pro
 20 115 120 125
 Gln Ser Ser Pro Gln Thr Ile Ser Asn Ala Gln Gly Thr Ser Lys Pro
 130 135 140
 Ser Val Arg Thr Arg Ala Val Arg Ser Leu Ala Val Ala Glu Pro Val
 25 145 150 155 160
 Val Asn Ala Ala Asp Ala Lys Gly Thr Asn Val Asn Asp Lys Val Thr
 165 170 175

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Ala Ser Asn Phe Lys Leu Glu Lys Thr Thr Phe Asp Pro Asn Gln Ser
 180 185 190
 Gly Asn Thr Phe Met Ala Ala Asn Phe Thr Val Thr Asp Lys Val Lys
 195 200 205
 Ser Gly Asp Tyr Phe Thr Ala Lys Leu Pro Asp Ser Leu Thr Gly Asn
 210 215 220
 Gly Asp Val Asp Tyr Ser Asn Ser Asn Thr Met Pro Ile Ala Asp
 225 230 235 240
 Ile Lys Ser Thr Asn Gly Asp Val Val Ala Lys Ala Thr Tyr Asp Ile
 245 250 255
 Leu Thr Lys Thr Tyr Thr Phe Val Phe Thr Asp Tyr Val Asn Asn Lys
 260 265 270
 Glu Asn Ile Asn Gly Gln Phe Ser Leu Pro Leu Phe Thr Asp Arg Ala
 275 280 285
 Lys Ala Pro Lys Ser Gly Thr Tyr Asp Ala Asn Ile Asn Ile Ala Asp
 290 295 300
 Glu Met Phe Asn Asn Lys Ile Thr Tyr Asn Tyr Ser Ser Pro Ile Ala
 305 310 315 320
 Gly Ile Asp Lys Pro Asn Gly Ala Asn Ile Ser Ser Gln Ile Ile Gly
 325 330 335
 Val Asp Thr Ala Ser Gly Gln Asn Thr Tyr Lys Gln Thr Val Phe Val
 340 345 350
 Asn Pro Lys Gln Arg Val Leu Gly Asn Thr Trp Val Tyr Ile Lys Gly
 355 360 365
 Tyr Gln Asp Lys Ile Glu Glu Ser Ser Gly Lys Val Ser Ala Thr Asp
 370 375 380
 Thr Lys Leu Arg Ile Phe Glu Val Asn Asp Thr Ser Lys Leu Ser Asp
 385 390 395 400
 Ser Tyr Tyr Ala Asp Pro Asn Asp Ser Asn Leu Lys Glu Val Thr Asp
 405 410 415
 Gln Phe Lys Asn Arg Ile Tyr Tyr Glu His Pro Asn Val Ala Ser Ile
 420 425 430
 Lys Phe Gly Asp Ile Thr Lys Thr Tyr Val Val Leu Val Glu Gly His
 435 440 445
 Tyr Asp Asn Thr Gly Lys Asn Leu Lys Thr Gln Val Ile Gln Glu Asn
 450 455 460
 Val Asp Pro Val Thr Asn Arg Asp Tyr Ser Ile Phe Gly Trp Asn Asn
 465 470 475 480
 Glu Asn Val Val Arg Tyr Gly Gly Gly Ser Ala Asp Gly Asp Ser Ala
 485 490 495
 Val Asn Pro Lys Asp Pro Thr Pro Gly Pro Pro Val Ala Ser Gly Gly
 500 505 510
 Gly Ser Ala Glu Ser Thr Asn Lys Glu Leu Asn Glu Ala Thr Thr Ser
 515 520 525
 Ala Ser Asp Asn Gln Ser Ser Asp Lys Val Asp Met Gln Gln Leu Asn
 530 535 540

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Gln Glu Asp Asn Thr Lys Asn Asp Asn Gln Lys Glu Met Val Ser Ser
 545 550 555 560
 Gln Gly Asn Glu Thr Thr Ser Asn Gly Asn Lys Leu Ile Glu Lys Glu
 565 570 575
 Ser Val Gln Ser Thr Thr Gly Asn Lys Val Glu Val Ser Thr Ala Lys
 580 585 590
 Ser Asp Glu Gln Ala Ser Pro Lys Ser Thr Asn Glu Asp Leu Asn Thr
 595 600 605
 Lys Gln Thr Ile Ser Asn Gln Glu Ala Leu Gln Pro Asp Leu Gln Glu
 610 615 620
 Asn Lys Ser Val Val Asn Val Gln Pro Thr Asn Glu Glu Asn Lys Lys
 625 630 635 640
 Val Asp Ala Lys Thr Glu Ser Thr Thr Leu Asn Val Lys Ser Asp Ala
 645 650 655
 Ile Lys Ser Asn Asp Glu Thr Leu Val Asp Asn Asn Ser Asn Ser Asn
 660 665 670
 Asn Glu Asn Asn Ala Asp Ile Ile Leu Pro Lys Ser Thr Ala Pro Lys
 675 680 685
 Arg Leu Asn Thr Arg Met Arg Ile Ala Ala Val Gln Pro Ser Ser Thr
 690 695 700
 Glu Ala Lys Asn Val Asn Asp Leu Ile Thr Ser Asn Thr Thr Leu Thr
 705 710 715 720
 Val Val Asp Ala Asp Lys Asn Asn Lys Ile Val Pro Ala Gln Asp Tyr
 725 730 735
 Leu Ser Leu Lys Ser Gln Ile Thr Val Asp Asp Lys Val Lys Ser Gly
 740 745 750
 Asp Tyr Phe Thr Ile Lys Tyr Ser Asp Thr Val Gln Val Tyr Gly Leu
 755 760 765
 Asn Pro Glu Asp Ile Lys Asn Ile Gly Asp Ile Lys Asp Pro Asn Asn
 770 775 780
 Gly Glu Thr Ile Ala Thr Ala Lys His Asp Thr Ala Asn Asn Leu Ile
 785 790 795 800
 Thr Tyr Thr Phe Thr Asp Tyr Val Asp Arg Phe Asn Ser Val Gln Met
 805 810 815
 Gly Ile Asn Tyr Ser Ile Tyr Met Asp Ala Asp Thr Ile Pro Val Ser
 820 825 830
 Lys Asn Asp Val Glu Phe Asn Val Thr Ile Gly Asn Thr Thr Thr Lys
 835 840 845
 Thr Thr Ala Asn Ile Gln Tyr Pro Asp Tyr Val Val Asn Glu Lys Asn
 850 855 860
 Ser Ile Gly Ser Ala Phe Thr Glu Thr Val Ser His Val Gly Asn Lys
 865 870 875 880
 Glu Asn Pro Gly Tyr Tyr Lys Gln Thr Ile Tyr Val Asn Pro Ser Glu
 885 890 895
 Asn Ser Leu Thr Asn Ala Lys Leu Lys Val Gln Ala Tyr His Ser Ser
 900 905 910
 Tyr Pro Asn Asn Ile Gly Gln Ile Asn Lys Asp Val Thr Asp Ile Lys

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915 920 925
 Ile Tyr Gln Val Pro Lys Gly Tyr Thr Leu Asn Lys Gly Tyr Asp Val
 930 935 940
 5 Asn Thr Lys Glu Leu Thr Asp Val Thr Asn Gln Tyr Leu Gln Lys Ile
 945 950 955 960
 Thr Tyr Gly Asp Asn Asn Ser Ala Val Ile Asp Phe Gly Asn Ala Asp
 965 970 975
 10 Ser Ala Tyr Val Val Met Val Asn Thr Lys Phe Gln Tyr Thr Asn Ser
 980 985 990
 Glu Ser Pro Thr Leu Val Gln Met Ala Thr Leu Ser Ser Thr Gly Asn
 995 1000 1005
 15 Lys Ser Val Ser Thr Gly Asn Ala Leu Gly Phe Thr Asn Asn Gln Ser
 1010 1015 1020
 Gly Gly Ala Gly Gln Glu Val Tyr Lys Ile Gly Asn Tyr Val Trp Glu
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 20 Asp Thr Asn Lys Asn Gly Val Gln Glu Leu Gly Glu Lys Gly
 1045 1050

<210> 203

<211> 1054

25 <212> PRT

<213> Staphylococcus aureus

<400> 203

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	Ala	Glu	Ser	Thr	Asn	Lys	Glu	Leu	Asn	Glu	Ala	Thr	Thr	Ser	Ala	Ser
	1				5					10					15	
5	Asp	Asn	Gln	Ser	Ser	Asp	Lys	Val	Asp	Met	Gln	Gln	Leu	Asn	Gln	Glu
				20					25					30		
	Asp	Asn	Thr	Lys	Asn	Asp	Asn	Gln	Lys	Glu	Met	Val	Ser	Ser	Gln	Gly
			35					40					45			
10	Asn	Glu	Thr	Thr	Ser	Asn	Gly	Asn	Lys	Leu	Ile	Glu	Lys	Glu	Ser	Val
		50					55					60				
	Gln	Ser	Thr	Thr	Gly	Asn	Lys	Val	Glu	Val	Ser	Thr	Ala	Lys	Ser	Asp
	65					70					75					80
15	Glu	Gln	Ala	Ser	Pro	Lys	Ser	Thr	Asn	Glu	Asp	Leu	Asn	Thr	Lys	Gln
					85					90					95	
	Thr	Ile	Ser	Asn	Gln	Glu	Ala	Leu	Gln	Pro	Asp	Leu	Gln	Glu	Asn	Lys
				100					105					110		
20	Ser	Val	Val	Asn	Val	Gln	Pro	Thr	Asn	Glu	Glu	Asn	Lys	Lys	Val	Asp
			115					120					125			
	Ala	Lys	Thr	Glu	Ser	Thr	Thr	Leu	Asn	Val	Lys	Ser	Asp	Ala	Ile	Lys
		130					135					140				
25	Ser	Asn	Asp	Glu	Thr	Leu	Val	Asp	Asn	Asn	Ser	Asn	Ser	Asn	Asn	Glu
	145					150					155					160
	Asn	Asn	Ala	Asp	Ile	Ile	Leu	Pro	Lys	Ser	Thr	Ala	Pro	Lys	Arg	Leu
					165					170					175	
30	Asn	Thr	Arg	Met	Arg	Ile	Ala	Ala	Val	Gln	Pro	Ser	Ser	Thr	Glu	Ala
				180					185					190		
	Lys	Asn	Val	Asn	Asp	Leu	Ile	Thr	Ser	Asn	Thr	Thr	Leu	Thr	Val	Val
			195					200					205			

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	Asp	Ala	Asp	Lys	Asn	Asn	Lys	Ile	Val	Pro	Ala	Gln	Asp	Tyr	Leu	Ser
	210						215					220				
5	Leu	Lys	Ser	Gln	Ile	Thr	Val	Asp	Asp	Lys	Val	Lys	Ser	Gly	Asp	Tyr
	225					230					235					240
	Phe	Thr	Ile	Lys	Tyr	Ser	Asp	Thr	Val	Gln	Val	Tyr	Gly	Leu	Asn	Pro
					245					250					255	
10	Glu	Asp	Ile	Lys	Asn	Ile	Gly	Asp	Ile	Lys	Asp	Pro	Asn	Asn	Gly	Glu
				260					265					270		
	Thr	Ile	Ala	Thr	Ala	Lys	His	Asp	Thr	Ala	Asn	Asn	Leu	Ile	Thr	Tyr
			275					280					285			
15	Thr	Phe	Thr	Asp	Tyr	Val	Asp	Arg	Phe	Asn	Ser	Val	Gln	Met	Gly	Ile
		290					295					300				
	Asn	Tyr	Ser	Ile	Tyr	Met	Asp	Ala	Asp	Thr	Ile	Pro	Val	Ser	Lys	Asn
	305					310					315					320
20	Asp	Val	Glu	Phe	Asn	Val	Thr	Ile	Gly	Asn	Thr	Thr	Thr	Lys	Thr	Thr
					325					330					335	
	Ala	Asn	Ile	Gln	Tyr	Pro	Asp	Tyr	Val	Val	Asn	Glu	Lys	Asn	Ser	Ile
				340					345					350		
25	Gly	Ser	Ala	Phe	Thr	Glu	Thr	Val	Ser	His	Val	Gly	Asn	Lys	Glu	Asn
			355					360					365			
	Pro	Gly	Tyr	Tyr	Lys	Gln	Thr	Ile	Tyr	Val	Asn	Pro	Ser	Glu	Asn	Ser
		370					375					380				
30	Leu	Thr	Asn	Ala	Lys	Leu	Lys	Val	Gln	Ala	Tyr	His	Ser	Ser	Tyr	Pro
	385					390					395					400
	Asn	Asn	Ile	Gly	Gln	Ile	Asn	Lys	Asp	Val	Thr	Asp	Ile	Lys	Ile	Tyr
					405					410					415	
35	Gln	Val	Pro	Lys	Gly	Tyr	Thr	Leu	Asn	Lys	Gly	Tyr	Asp	Val	Asn	Thr
				420					425					430		
	Lys	Glu	Leu	Thr	Asp	Val	Thr	Asn	Gln	Tyr	Leu	Gln	Lys	Ile	Thr	Tyr
			435				440					445				
40	Gly	Asp	Asn	Asn	Ser	Ala	Val	Ile	Asp	Phe	Gly	Asn	Ala	Asp	Ser	Ala
		450					455					460				
	Tyr	Val	Val	Met	Val	Asn	Thr	Lys	Phe	Gln	Tyr	Thr	Asn	Ser	Glu	Ser
	465					470					475					480
45	Pro	Thr	Leu	Val	Gln	Met	Ala	Thr	Leu	Ser	Ser	Thr	Gly	Asn	Lys	Ser
					485					490					495	
	Val	Ser	Thr	Gly	Asn	Ala	Leu	Gly	Phe	Thr	Asn	Asn	Gln	Ser	Gly	Gly
				500					505					510		
50	Ala	Gly	Gln	Glu	Val	Tyr	Lys	Ile	Gly	Asn	Tyr	Val	Trp	Glu	Asp	Thr
			515					520					525			
	Asn	Lys	Asn	Gly	Val	Gln	Glu	Leu	Gly	Glu	Lys	Gly	Ala	Ser	Gly	Gly
		530					535					540				
55	Gly	Ser	Ser	Glu	Gln	Ser	Asn	Asp	Thr	Thr	Gln	Ser	Ser	Lys	Asn	Asn
	545					550					555					560
	Ala	Ser	Ala	Asp	Ser	Glu	Lys	Asn	Asn	Met	Ile	Glu	Thr	Pro	Gln	Leu
					565					570					575	

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Asn Thr Thr Ala Asn Asp Thr Ser Asp Ile Ser Ala Asn Thr Asn Ser
 580 585 590
 Ala Asn Val Asp Ser Thr Thr Lys Pro Met Ser Thr Gln Thr Ser Asn
 595 600 605
 Thr Thr Thr Thr Glu Pro Ala Ser Thr Asn Glu Thr Pro Gln Pro Thr
 610 615 620
 Ala Ile Lys Asn Gln Ala Thr Ala Ala Lys Met Gln Asp Gln Thr Val
 625 630 635
 Pro Gln Glu Ala Asn Ser Gln Val Asp Asn Lys Thr Thr Asn Asp Ala
 645 650 655
 Asn Ser Ile Ala Thr Asn Ser Glu Leu Lys Asn Ser Gln Thr Leu Asp
 660 665 670
 Leu Pro Gln Ser Ser Pro Gln Thr Ile Ser Asn Ala Gln Gly Thr Ser
 675 680 685
 Lys Pro Ser Val Arg Thr Arg Ala Val Arg Ser Leu Ala Val Ala Glu
 690 695 700
 Pro Val Val Asn Ala Ala Asp Ala Lys Gly Thr Asn Val Asn Asp Lys
 705 710 715 720
 Val Thr Ala Ser Asn Phe Lys Leu Glu Lys Thr Thr Phe Asp Pro Asn
 725 730 735
 Gln Ser Gly Asn Thr Phe Met Ala Ala Asn Phe Thr Val Thr Asp Lys
 740 745 750
 Val Lys Ser Gly Asp Tyr Phe Thr Ala Lys Leu Pro Asp Ser Leu Thr
 755 760 765
 Gly Asn Gly Asp Val Asp Tyr Ser Asn Ser Asn Asn Thr Met Pro Ile
 770 775 780
 Ala Asp Ile Lys Ser Thr Asn Gly Asp Val Val Ala Lys Ala Thr Tyr
 785 790 795 800
 Asp Ile Leu Thr Lys Thr Tyr Thr Phe Val Phe Thr Asp Tyr Val Asn
 805 810 815
 Asn Lys Glu Asn Ile Asn Gly Gln Phe Ser Leu Pro Leu Phe Thr Asp
 820 825 830
 Arg Ala Lys Ala Pro Lys Ser Gly Thr Tyr Asp Ala Asn Ile Asn Ile
 835 840 845
 Ala Asp Glu Met Phe Asn Asn Lys Ile Thr Tyr Asn Tyr Ser Ser Pro
 850 855 860
 Ile Ala Gly Ile Asp Lys Pro Asn Gly Ala Asn Ile Ser Ser Gln Ile
 865 870 875 880
 Ile Gly Val Asp Thr Ala Ser Gly Gln Asn Thr Tyr Lys Gln Thr Val
 885 890 895
 Phe Val Asn Pro Lys Gln Arg Val Leu Gly Asn Thr Trp Val Tyr Ile
 900 905 910
 Lys Gly Tyr Gln Asp Lys Ile Glu Glu Ser Ser Gly Lys Val Ser Ala
 915 920 925
 Thr Asp Thr Lys Leu Arg Ile Phe Glu Val Asn Asp Thr Ser Lys Leu
 930 935 940
 Ser Asp Ser Tyr Tyr Ala Asp Pro Asn Asp Ser Asn Leu Lys Glu Val

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	945		950		955		960									
	Thr	Asp	Gln	Phe	Lys	Asn	Arg	Ile	Tyr	Tyr	Glu	His	Pro	Asn	Val	Ala
					965					970					975	
5	Ser	Ile	Lys	Phe	Gly	Asp	Ile	Thr	Lys	Thr	Tyr	Val	Val	Leu	Val	Glu
				980					985					990		
	Gly	His	Tyr	Asp	Asn	Thr	Gly	Lys	Asn	Leu	Lys	Thr	Gln	Val	Ile	Gln
			995					1000					1005			
10	Glu	Asn	Val	Asp	Pro	Val	Thr	Asn	Arg	Asp	Tyr	Ser	Ile	Phe	Gly	Trp
		1010					1015					1020				
	Asn	Asn	Glu	Asn	Val	Val	Arg	Tyr	Gly	Gly	Gly	Ser	Ala	Asp	Gly	Asp
	1025					1030					1035					1040
15	Ser	Ala	Val	Asn	Pro	Lys	Asp	Pro	Thr	Pro	Gly	Pro	Pro	Val		
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<210> 204

<211> 376

20 <212> PRT

<213> Staphylococcus aureus

<400> 204

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	Asp	Ser	Gln	Gln	Val	Asn	Ala	Ala	Thr	Glu	Ala	Thr	Asn	Ala	Thr	Asn
	1				5					10				15		
5	Asn	Gln	Ser	Thr	Gln	Val	Ser	Gln	Ala	Thr	Ser	Gln	Pro	Ile	Asn	Phe
				20					25					30		
	Gln	Val	Gln	Lys	Asp	Gly	Ser	Ser	Glu	Lys	Ser	His	Met	Asp	Asp	Tyr
			35					40					45			
10	Met	Gln	His	Pro	Gly	Lys	Val	Ile	Lys	Gln	Asn	Asn	Lys	Tyr	Tyr	Phe
	50						55					60				
	Gln	Thr	Val	Leu	Asn	Asn	Ala	Ser	Phe	Trp	Lys	Glu	Tyr	Lys	Phe	Tyr
	65				70						75					80
15	Asn	Ala	Asn	Asn	Gln	Glu	Leu	Ala	Thr	Thr	Val	Val	Asn	Asp	Asn	Lys
					85					90					95	
	Lys	Ala	Asp	Thr	Arg	Thr	Ile	Asn	Val	Ala	Val	Glu	Pro	Gly	Tyr	Lys
				100					105					110		
20	Ser	Leu	Thr	Thr	Lys	Val	His	Ile	Val	Val	Pro	Gln	Ile	Asn	Tyr	Asn
			115					120					125			
	His	Arg	Tyr	Thr	Thr	His	Leu	Glu	Phe	Glu	Lys	Ala	Ile	Pro	Thr	Leu
		130					135					140				
25	Ala	Asp	Ala	Ala	Lys	Pro	Asn	Asn	Val	Lys	Pro	Val	Gln	Pro	Lys	Pro
	145					150					155					160
	Ala	Gln	Pro	Lys	Thr	Pro	Thr	Glu	Gln	Thr	Lys	Pro	Val	Gln	Pro	Lys
					165					170					175	
30	Val	Glu	Lys	Val	Lys	Pro	Thr	Val	Thr	Thr	Thr	Ser	Lys	Val	Glu	Asp
				180					185					190		
	Asn	His	Ser	Thr	Lys	Val	Val	Ser	Thr	Asp	Thr	Thr	Lys	Asp	Gln	Thr
			195					200					205			
35	Lys	Thr	Gln	Thr	Ala	His	Thr	Val	Lys	Thr	Ala	Gln	Thr	Ala	Gln	Glu
		210					215					220				
	Gln	Asn	Lys	Val	Gln	Thr	Pro	Val	Lys	Asp	Val	Ala	Thr	Ala	Lys	Ser
	225					230					235					240

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Glu Ser Asn Asn Gln Ala Val Ser Asp Asn Lys Ser Gln Gln Thr Asn
 245 250 255
 Lys Val Thr Lys His Asn Glu Thr Pro Lys Gln Ala Ser Lys Ala Lys
 5 260 265 270
 Glu Ala Ser Gly Gly Gly Ser Met Ala Met Ile Lys Met Ser Pro Glu
 275 280 285
 Glu Ile Arg Ala Lys Ser Gln Ser Tyr Gly Gln Gly Ser Asp Gln Ile
 10 290 295 300
 Arg Gln Ile Leu Ser Asp Leu Thr Arg Ala Gln Gly Glu Ile Ala Ala
 305 310 315 320
 Asn Trp Glu Gly Gln Ala Phe Ser Arg Phe Glu Glu Gln Phe Gln Gln
 15 325 330 335
 Leu Ser Pro Lys Val Glu Lys Phe Ala Gln Leu Leu Glu Glu Ile Lys
 340 345 350
 Gln Gln Leu Asn Ser Thr Ala Asp Ala Val Gln Glu Gln Asp Gln Gln
 20 355 360 365
 Leu Ser Asn Asn Phe Gly Leu Gln
 370 375

<210> 205

<211> 613

<212> PRT

<213> Staphylococcus aureus

<400> 205

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Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
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 Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
 5 20 25 30
 Gly Met Leu Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
 35 40 45
 Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
 10 50 55 60
 Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
 65 70 75 80
 Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
 15 85 90 95
 Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
 100 105 110
 Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr Gly Asp Asp
 115 120 125
 20 Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser Ile Gly His
 130 135 140
 Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro
 145 150 155 160
 25 Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
 165 170 175
 Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
 180 185 190
 30
 35
 40
 45
 50
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Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
 195 200 205
 5 Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe
 210 215 220
 Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
 225 230 235 240
 10 Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
 245 250 255
 Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp
 260 265 270
 15 Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
 275 280 285
 Glu Glu Met Thr Asn Ala Ser Gly Gly Gly Ser Ser Val Thr Glu Ser
 290 295 300
 20 Val Asp Lys Lys Phe Val Val Pro Glu Ser Gly Ile Asn Lys Ile Ile
 305 310 315 320
 Pro Ala Tyr Asp Glu Phe Lys Asn Ser Pro Lys Val Asn Val Ser Asn
 325 330 335
 25 Leu Thr Asp Asn Lys Asn Phe Val Ala Ser Glu Asp Lys Leu Asn Lys
 340 345 350
 Ile Ala Asp Ser Ser Ala Ala Ser Lys Ile Val Asp Lys Asn Phe Val
 355 360 365
 Val Pro Glu Ser Lys Leu Gly Asn Ile Val Pro Glu Tyr Lys Glu Ile
 370 375 380
 30 Asn Asn Arg Val Asn Val Ala Thr Asn Asn Pro Ala Ser Gln Gln Val
 385 390 395 400
 Asp Lys His Phe Val Ala Lys Gly Pro Glu Val Asn Arg Phe Ile Thr
 405 410 415
 35 Gln Asn Lys Val Asn His His Phe Ile Thr Thr Gln Thr His Tyr Lys
 420 425 430
 Lys Val Ile Thr Ser Tyr Lys Ser Thr His Val His Lys His Val Asn
 435 440 445
 40 His Ala Lys Asp Ser Ile Asn Lys His Phe Ile Val Lys Pro Ser Glu
 450 455 460
 Ser Pro Arg Tyr Thr His Pro Ser Gln Ser Leu Ile Ile Lys His His
 465 470 475 480
 45 Phe Ala Val Pro Gly Tyr His Ala His Lys Phe Val Thr Pro Gly His
 485 490 495
 Ala Ser Ile Lys Ile Asn His Phe Cys Val Val Pro Gln Ile Asn Ser
 500 505 510
 50 Phe Lys Val Ile Pro Pro Tyr Gly His Asn Ser His Arg Met His Val
 515 520 525
 Pro Ser Phe Gln Asn Asn Thr Thr Ala Thr His Gln Asn Ala Lys Val
 530 535 540
 55 Asn Lys Ala Tyr Asp Tyr Lys Tyr Phe Tyr Ser Tyr Lys Val Val Lys
 545 550 555 560
 Gly Val Lys Lys Tyr Phe Ser Phe Ser Gln Ser Asn Gly Tyr Lys Ile

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				565					570					575		
	Gly	Lys	Pro	Ser	Leu	Asn	Ile	Lys	Asn	Val	Asn	Tyr	Gln	Tyr	Ala	Val
				580					585					590		
5	Pro	Ser	Tyr	Ser	Pro	Thr	His	Tyr	Val	Pro	Glu	Phe	Lys	Gly	Ser	Leu
			595					600					605			
	Pro	Ala	Pro	Arg	Val											
		610														
10																
	<210> 206															
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	<212> PRT															
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15																
	<400> 206															
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55																

EP 2 510 947 B1

	Ala	Asp	Ser	Asp	Ile	Asn	Ile	Lys	Thr	Gly	Thr	Thr	Asp	Ile	Gly	Ser
	1				5					10					15	
5	Asn	Thr	Thr	Val	Lys	Thr	Gly	Asp	Leu	Val	Thr	Tyr	Asp	Lys	Glu	Asn
				20					25					30		
	Gly	Met	His	Lys	Lys	Val	Phe	Tyr	Ser	Phe	Ile	Asp	Asp	Lys	Asn	His
			35					40					45			
10	Asn	Lys	Ala	Ser	Gly	Gly	Gly	Ser	Ser	Val	Thr	Glu	Ser	Val	Asp	Lys
		50					55					60				
	Lys	Phe	Val	Val	Pro	Glu	Ser	Gly	Ile	Asn	Lys	Ile	Ile	Pro	Ala	Tyr
	65					70					75					80
15	Asp	Glu	Phe	Lys	Asn	Ser	Pro	Lys	Val	Asn	Val	Ser	Asn	Leu	Thr	Asp
					85					90					95	
	Asn	Lys	Asn	Phe	Val	Ala	Ser	Glu	Asp	Lys	Leu	Asn	Lys	Ile	Ala	Asp
				100					105					110		
20	Ser	Ser	Ala	Ala	Ser	Lys	Ile	Val	Asp	Lys	Asn	Phe	Val	Val	Pro	Glu
			115					120					125			
	Ser	Lys	Leu	Gly	Asn	Ile	Val	Pro	Glu	Tyr	Lys	Glu	Ile	Asn	Asn	Arg
		130					135					140				
25	Val	Asn	Val	Ala	Thr	Asn	Asn	Pro	Ala	Ser	Gln	Gln	Val	Asp	Lys	His
	145					150					155					160
	Phe	Val	Ala	Lys	Gly	Pro	Glu	Val	Asn	Arg	Phe	Ile	Thr	Gln	Asn	Lys
					165					170					175	
30	Val	Asn	His	His	Phe	Ile	Thr	Thr	Gln	Thr	His	Tyr	Lys	Lys	Val	Ile
				180					185					190		
	Thr	Ser	Tyr	Lys	Ser	Thr	His	Val	His	Lys	His	Val	Asn	His	Ala	Lys
			195					200					205			
35	Asp	Ser	Ile	Asn	Lys	His	Phe	Ile	Val	Lys	Pro	Ser	Glu	Ser	Pro	Arg
		210					215					220				
	Tyr	Thr	His	Pro	Ser	Gln	Ser	Leu	Ile	Ile	Lys	His	His	Phe	Ala	Val
	225					230					235					240
40	Pro	Gly	Tyr	His	Ala	His	Lys	Phe	Val	Thr	Pro	Gly	His	Ala	Ser	Ile
					245					250					255	
	Lys	Ile	Asn	His	Phe	Cys	Val	Val	Pro	Gln	Ile	Asn	Ser	Phe	Lys	Val
				260					265					270		
45	Ile	Pro	Pro	Tyr	Gly	His	Asn	Ser	His	Arg	Met	His	Val	Pro	Ser	Phe
			275					280					285			

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	Gln	Asn	Asn	Thr	Thr	Ala	Thr	His	Gln	Asn	Ala	Lys	Val	Asn	Lys	Ala
		290					295					300				
5	Tyr	Asp	Tyr	Lys	Tyr	Phe	Tyr	Ser	Tyr	Lys	Val	Val	Lys	Gly	Val	Lys
	305					310					315					320
	Lys	Tyr	Phe	Ser	Phe	Ser	Gln	Ser	Asn	Gly	Tyr	Lys	Ile	Gly	Lys	Pro
					325					330					335	
10	Ser	Leu	Asn	Ile	Lys	Asn	Val	Asn	Tyr	Gln	Tyr	Ala	Val	Pro	Ser	Tyr
				340					345					350		
	Ser	Pro	Thr	His	Tyr	Val	Pro	Glu	Phe	Lys	Gly	Ser	Leu	Pro	Ala	Pro
			355					360					365			
15	Arg	Val														
		370														

<210> 207

<211> 370

<212> PRT

20 <213> Staphylococcus aureus

<400> 207

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Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
1 5 10 15
Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
5 20 25 30
Gly Met Leu Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
35 40 45
Asn Lys Ala Ser Gly Gly Gly Ser Ser Val Thr Glu Ser Val Asp Lys
10 50 55 60
Lys Phe Val Val Pro Glu Ser Gly Ile Asn Lys Ile Ile Pro Ala Tyr
65 70 75 80
Asp Glu Phe Lys Asn Ser Pro Lys Val Asn Val Ser Asn Leu Thr Asp
15 85 90 95
Asn Lys Asn Phe Val Ala Ser Glu Asp Lys Leu Asn Lys Ile Ala Asp
100 105 110
Ser Ser Ala Ala Ser Lys Ile Val Asp Lys Asn Phe Val Val Pro Glu
20 115 120 125
Ser Lys Leu Gly Asn Ile Val Pro Glu Tyr Lys Glu Ile Asn Asn Arg
130 135 140
Val Asn Val Ala Thr Asn Asn Pro Ala Ser Gln Gln Val Asp Lys His
25 145 150 155 160
Phe Val Ala Lys Gly Pro Glu Val Asn Arg Phe Ile Thr Gln Asn Lys
165 170 175
Val Asn His His Phe Ile Thr Thr Gln Thr His Tyr Lys Lys Val Ile
30 180 185 190
Thr Ser Tyr Lys Ser Thr His Val His Lys His Val Asn His Ala Lys
195 200 205
Asp Ser Ile Asn Lys His Phe Ile Val Lys Pro Ser Glu Ser Pro Arg
35 210 215 220
Tyr Thr His Pro Ser Gln Ser Leu Ile Ile Lys His His Phe Ala Val
225 230 235 240

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Pro Gly Tyr His Ala His Lys Phe Val Thr Pro Gly His Ala Ser Ile
245 250 255
Lys Ile Asn His Phe Cys Val Val Pro Gln Ile Asn Ser Phe Lys Val
5 260 265 270
Ile Pro Pro Tyr Gly His Asn Ser His Arg Met His Val Pro Ser Phe
275 280 285
Gln Asn Asn Thr Thr Ala Thr His Gln Asn Ala Lys Val Asn Lys Ala
10 290 295 300
Tyr Asp Tyr Lys Tyr Phe Tyr Ser Tyr Lys Val Val Lys Gly Val Lys
305 310 315 320
Lys Tyr Phe Ser Phe Ser Gln Ser Asn Gly Tyr Lys Ile Gly Lys Pro
15 325 330 335
Ser Leu Asn Ile Lys Asn Val Asn Tyr Gln Tyr Ala Val Pro Ser Tyr
340 345 350
Ser Pro Thr His Tyr Val Pro Glu Phe Lys Gly Ser Leu Pro Ala Pro
20 355 360 365
Arg Val
370

<210> 208
25 <211> 578
<212> PRT
<213> Staphylococcus aureus

<400> 208

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Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
1 5 10 15
Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
5 20 25 30
Gly Met Leu Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
35 40 45
Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
10 50 55 60
Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
65 70 75 80
Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
15 85 90 95
Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Pro Ser Gly
100 105 110
Ser Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro Thr Asp Lys
20 115 120 125
Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn Gln Asn Trp
130 135 140
Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly Asn Gln Leu
25 145 150 155 160
Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp Asn Phe Leu
165 170 175
Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe Ser Pro Asp
30 180 185 190
Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys Gln Gln Thr

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	195		200		205
	Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr Gln Leu His				
	210		215		220
5	Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp Lys Trp Ile				
	225		230		235
	Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys Glu Glu Met				
			245		250
10	Thr Asn Ala Ser Gly Gly Gly Ser Ser Val Thr Glu Ser Val Asp Lys				
			260		265
	Lys Phe Val Val Pro Glu Ser Gly Ile Asn Lys Ile Ile Pro Ala Tyr				
			275		280
15	Asp Glu Phe Lys Asn Ser Pro Lys Val Asn Val Ser Asn Leu Thr Asp				
			290		295
	Asn Lys Asn Phe Val Ala Ser Glu Asp Lys Leu Asn Lys Ile Ala Asp				
			305		310
20	Ser Ser Ala Ala Ser Lys Ile Val Asp Lys Asn Phe Val Val Pro Glu				
			325		330
	Ser Lys Leu Gly Asn Ile Val Pro Glu Tyr Lys Glu Ile Asn Asn Arg				
			340		345
25	Val Asn Val Ala Thr Asn Asn Pro Ala Ser Gln Gln Val Asp Lys His				
			355		360
	Phe Val Ala Lys Gly Pro Glu Val Asn Arg Phe Ile Thr Gln Asn Lys				
			370		375
30	Val Asn His His Phe Ile Thr Thr Gln Thr His Tyr Lys Lys Val Ile				
			385		390
	Thr Ser Tyr Lys Ser Thr His Val His Lys His Val Asn His Ala Lys				
			405		410
35	Asp Ser Ile Asn Lys His Phe Ile Val Lys Pro Ser Glu Ser Pro Arg				
			420		425
	Tyr Thr His Pro Ser Gln Ser Leu Ile Ile Lys His His Phe Ala Val				
			435		440
40	Pro Gly Tyr His Ala His Lys Phe Val Thr Pro Gly His Ala Ser Ile				
			450		455
	Lys Ile Asn His Phe Cys Val Val Pro Gln Ile Asn Ser Phe Lys Val				
			465		470
45	Ile Pro Pro Tyr Gly His Asn Ser His Arg Met His Val Pro Ser Phe				
			485		490
	Gln Asn Asn Thr Thr Ala Thr His Gln Asn Ala Lys Val Asn Lys Ala				
			500		505
50	Tyr Asp Tyr Lys Tyr Phe Tyr Ser Tyr Lys Val Val Lys Gly Val Lys				
			515		520
	Lys Tyr Phe Ser Phe Ser Gln Ser Asn Gly Tyr Lys Ile Gly Lys Pro				
			530		535
55	Ser Leu Asn Ile Lys Asn Val Asn Tyr Gln Tyr Ala Val Pro Ser Tyr				
			545		550
	Ser Pro Thr His Tyr Val Pro Glu Phe Lys Gly Ser Leu Pro Ala Pro				
			565		570
					575

Arg Val

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<210> 209

<211> 248

<212> PRT

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<213> Staphylococcus aureus

<400> 209

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Asp Ser Gln Gln Val Asn Ala Ala Thr Glu Ala Thr Asn Ala Thr Asn
1 5 10 15

Asn Gln Ser Thr Gln Val Ser Gln Ala Thr Ser Gln Pro Ile Asn Phe
20 25 30

20

Gln Val Gln Lys Asp Gly Ser Ser Glu Lys Ser His Met Asp Asp Tyr
35 40 45

Met Gln His Pro Gly Lys Val Ile Lys Gln Asn Asn Lys Tyr Tyr Phe
50 55 60

25

Gln Thr Val Leu Asn Asn Ala Ser Phe Trp Lys Glu Tyr Lys Phe Tyr
65 70 75 80

Asn Ala Asn Asn Gln Glu Leu Ala Thr Thr Val Val Asn Asp Asn Lys
85 90 95

30

Lys Ala Asp Thr Arg Thr Ile Asn Val Ala Val Glu Pro Gly Tyr Lys
100 105 110

Ser Leu Thr Thr Lys Val His Ile Val Val Pro Gln Ile Asn Tyr Asn
115 120 125

35

His Arg Tyr Thr Thr His Leu Glu Phe Glu Lys Ala Ile Pro Thr Leu
130 135 140

Ala Ala Ser Gly Gly Gly Ser Met Ala Met Ile Lys Met Ser Pro Glu
145 150 155 160

40

Glu Ile Arg Ala Lys Ser Gln Ser Tyr Gly Gln Gly Ser Asp Gln Ile
165 170 175

Arg Gln Ile Leu Ser Asp Leu Thr Arg Ala Gln Gly Glu Ile Ala Ala
180 185 190

45

Asn Trp Glu Gly Gln Ala Phe Ser Arg Phe Glu Glu Gln Phe Gln Gln
195 200 205

Leu Ser Pro Lys Val Glu Lys Phe Ala Gln Leu Leu Glu Glu Ile Lys
210 215 220

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Gln Gln Leu Asn Ser Thr Ala Asp Ala Val Gln Glu Gln Asp Gln Gln
225 230 235 240

Leu Ser Asn Asn Phe Gly Leu Gln
245

<210> 210

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<211> 358

<212> PRT

<213> Staphylococcus aureus

<400> 210

5	Asp	Ser	Gln	Gln	Val	Asn	Ala	Ala	Thr	Glu	Ala	Thr	Asn	Ala	Thr	Asn
	1				5					10					15	
	Asn	Gln	Ser	Thr	Gln	Val	Ser	Gln	Ala	Thr	Ser	Gln	Pro	Ile	Asn	Phe
				20					25					30		
10																
15																
20																
25																
30																
35																
40																
45																
50																
55																

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Gln Val Gln Lys Asp Gly Ser Ser Glu Lys Ser His Met Asp Asp Tyr
 35 40 45
 Met Gln His Pro Gly Lys Val Ile Lys Gln Asn Asn Lys Tyr Tyr Phe
 50 55 60
 Gln Thr Val Leu Asn Asn Ala Ser Phe Trp Lys Glu Tyr Lys Phe Tyr
 65 70 75 80
 Asn Ala Asn Asn Gln Glu Leu Ala Thr Thr Val Val Asn Asp Asn Lys
 85 90 95
 Lys Ala Asp Thr Arg Thr Ile Asn Val Ala Val Glu Pro Gly Tyr Lys
 100 105 110
 Ser Leu Thr Thr Lys Val His Ile Val Val Pro Gln Ile Asn Tyr Asn
 115 120 125
 His Arg Tyr Thr Thr His Leu Glu Phe Glu Lys Ala Ile Pro Thr Leu
 130 135 140
 Ala Ala Ser Gly Gly Gly Ser Met Ala Met Ile Lys Met Ser Pro Glu
 145 150 155 160
 Glu Ile Arg Ala Lys Ser Gln Ser Tyr Gly Gln Gly Ser Asp Gln Ile
 165 170 175
 Arg Gln Ile Leu Ser Asp Leu Thr Arg Ala Gln Gly Glu Ile Ala Ala
 180 185 190
 Asn Trp Glu Gly Gln Ala Phe Ser Arg Phe Glu Glu Gln Phe Gln Gln
 195 200 205
 Leu Ser Pro Lys Val Glu Lys Phe Ala Gln Leu Leu Glu Glu Ile Lys
 210 215 220
 Gln Gln Leu Asn Ser Thr Ala Asp Ala Val Gln Glu Gln Asp Gln Gln
 225 230 235 240
 Leu Ser Asn Asn Phe Gly Leu Gln Ala Ser Gly Gly Gly Ser Met Gly
 245 250 255
 Gly Tyr Lys Gly Ile Lys Ala Asp Gly Gly Lys Val Asp Gln Ala Lys
 260 265 270
 Gln Leu Ala Ala Lys Thr Ala Lys Asp Ile Glu Ala Cys Gln Lys Gln
 275 280 285
 Thr Gln Gln Leu Ala Glu Tyr Ile Glu Gly Ser Asp Trp Glu Gly Gln
 290 295 300
 Phe Ala Asn Lys Val Lys Asp Val Leu Leu Ile Met Ala Lys Phe Gln
 305 310 315 320
 Glu Glu Leu Val Gln Pro Met Ala Asp His Gln Lys Ala Ile Asp Asn
 325 330 335
 Leu Ser Gln Asn Leu Ala Lys Tyr Asp Thr Leu Ser Ile Lys Gln Gly
 340 345 350
 Leu Asp Arg Val Asn Pro
 355

<210> 211

<211> 388

<212> PRT

<213> Staphylococcus aureus

<400> 211

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Ser Ser Pro Ile Ala Gly Ile Asp Lys Pro Asn Gly Ala Asn Ile Ser

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	1		5		10		15									
	Ser	Gln	Ile	Ile	Gly	Val	Asp	Thr	Ala	Ser	Gly	Gln	Asn	Thr	Tyr	Lys
				20					25					30		
5	Gln	Thr	Val	Phe	Val	Asn	Pro	Lys	Gln	Arg	Val	Leu	Gly	Asn	Thr	Trp
			35					40					45			
	Val	Tyr	Ile	Lys	Gly	Tyr	Gln	Asp	Lys	Ile	Glu	Glu	Ser	Ser	Gly	Lys
		50					55					60				
10	Val	Ser	Ala	Thr	Asp	Thr	Lys	Leu	Arg	Ile	Phe	Glu	Val	Asn	Asp	Thr
	65					70					75					80
	Ser	Lys	Leu	Ser	Asp	Ser	Tyr	Tyr	Ala	Asp	Pro	Asn	Asp	Ser	Asn	Leu
					85					90					95	
15	Lys	Glu	Val	Thr	Asp	Gln	Phe	Lys	Asn	Arg	Ile	Tyr	Tyr	Glu	His	Pro
				100					105					110		
	Asn	Val	Ala	Ser	Ile	Lys	Phe	Gly	Asp	Ile	Thr	Lys	Thr	Tyr	Val	Val
			115					120					125			
20	Leu	Val	Glu	Gly	His	Tyr	Asp	Asn	Thr	Gly	Lys	Asn	Leu	Lys	Thr	Gln
		130					135					140				
	Val	Ile	Gln	Glu	Asn	Val	Asp	Pro	Val	Thr	Asn	Arg	Asp	Tyr	Ser	Ile
	145					150					155					160
25	Phe	Gly	Trp	Asn	Asn	Glu	Asn	Val	Val	Arg	Tyr	Gly	Gly	Gly	Ser	Ala
				165						170					175	
	Asp	Gly	Asp	Ser	Ala	Val	Asn	Ala	Ser	Gly	Gly	Gly	Ser	Pro	Asp	Tyr
				180					185					190		
30	Val	Val	Asn	Glu	Lys	Asn	Ser	Ile	Gly	Ser	Ala	Phe	Thr	Glu	Thr	Val
			195					200					205			
	Ser	His	Val	Gly	Asn	Lys	Glu	Asn	Pro	Gly	Tyr	Tyr	Lys	Gln	Thr	Ile
		210					215					220				
35	Tyr	Val	Asn	Pro	Ser	Glu	Asn	Ser	Leu	Thr	Asn	Ala	Lys	Leu	Lys	Val
	225					230					235					240
	Gln	Ala	Tyr	His	Ser	Ser	Tyr	Pro	Asn	Asn	Ile	Gly	Gln	Ile	Asn	Lys
				245						250					255	
40	Asp	Val	Thr	Asp	Ile	Lys	Ile	Tyr	Gln	Val	Pro	Lys	Gly	Tyr	Thr	Leu
				260					265					270		
	Asn	Lys	Gly	Tyr	Asp	Val	Asn	Thr	Lys	Glu	Leu	Thr	Asp	Val	Thr	Asn
			275					280					285			
45	Gln	Tyr	Leu	Gln	Lys	Ile	Thr	Tyr	Gly	Asp	Asn	Asn	Ser	Ala	Val	Ile
		290					295					300				
	Asp	Phe	Gly	Asn	Ala	Asp	Ser	Ala	Tyr	Val	Val	Met	Val	Asn	Thr	Lys
	305					310					315					320
50	Phe	Gln	Tyr	Thr	Asn	Ser	Glu	Ser	Pro	Thr	Leu	Val	Gln	Met	Ala	Thr
				325						330					335	
	Leu	Ser	Ser	Thr	Gly	Asn	Lys	Ser	Val	Ser	Thr	Gly	Asn	Ala	Leu	Gly
				340					345					350		
55	Phe	Thr	Asn	Asn	Gln	Ser	Gly	Gly	Ala	Gly	Gln	Glu	Val	Tyr	Lys	Ile
			355					360					365			
	Gly	Asn	Tyr	Val	Trp	Glu	Asp	Thr	Asn	Lys	Asn	Gly	Val	Gln	Glu	Leu
		370					375					380				

Gly Glu Lys Gly
385

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<210> 212

<211> 486

<212> PRT

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<213> Staphylococcus aureus

<400> 212

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	Asp	Ser	Gln	Gln	Val	Asn	Ala	Ala	Thr	Glu	Ala	Thr	Asn	Ala	Thr	Asn
	1				5					10				15		
5	Asn	Gln	Ser	Thr	Gln	Val	Ser	Gln	Ala	Thr	Ser	Gln	Pro	Ile	Asn	Phe
				20					25					30		
	Gln	Val	Gln	Lys	Asp	Gly	Ser	Ser	Glu	Lys	Ser	His	Met	Asp	Asp	Tyr
			35					40					45			
10	Met	Gln	His	Pro	Gly	Lys	Val	Ile	Lys	Gln	Asn	Asn	Lys	Tyr	Tyr	Phe
	50						55					60				
	Gln	Thr	Val	Leu	Asn	Asn	Ala	Ser	Phe	Trp	Lys	Glu	Tyr	Lys	Phe	Tyr
	65				70						75					80
15	Asn	Ala	Asn	Asn	Gln	Glu	Leu	Ala	Thr	Thr	Val	Val	Asn	Asp	Asn	Lys
					85					90					95	
	Lys	Ala	Asp	Thr	Arg	Thr	Ile	Asn	Val	Ala	Val	Glu	Pro	Gly	Tyr	Lys
				100					105					110		
20	Ser	Leu	Thr	Thr	Lys	Val	His	Ile	Val	Val	Pro	Gln	Ile	Asn	Tyr	Asn
			115					120					125			
	His	Arg	Tyr	Thr	Thr	His	Leu	Glu	Phe	Glu	Lys	Ala	Ile	Pro	Thr	Leu
		130					135					140				
25	Ala	Asp	Ala	Ala	Lys	Pro	Asn	Asn	Val	Lys	Pro	Val	Gln	Pro	Lys	Pro
	145					150					155					160
	Ala	Gln	Pro	Lys	Thr	Pro	Thr	Glu	Gln	Thr	Lys	Pro	Val	Gln	Pro	Lys
					165					170					175	
30	Val	Glu	Lys	Val	Lys	Pro	Thr	Val	Thr	Thr	Thr	Ser	Lys	Val	Glu	Asp
				180					185					190		
	Asn	His	Ser	Thr	Lys	Val	Val	Ser	Thr	Asp	Thr	Thr	Lys	Asp	Gln	Thr
			195					200					205			
35	Lys	Thr	Gln	Thr	Ala	His	Thr	Val	Lys	Thr	Ala	Gln	Thr	Ala	Gln	Glu
		210					215					220				
	Gln	Asn	Lys	Val	Gln	Thr	Pro	Val	Lys	Asp	Val	Ala	Thr	Ala	Lys	Ser
	225				230						235					240
40	Glu	Ser	Asn	Asn	Gln	Ala	Val	Ser	Asp	Asn	Lys	Ser	Gln	Gln	Thr	Asn
					245					250					255	
	Lys	Val	Thr	Lys	His	Asn	Glu	Thr	Pro	Lys	Gln	Ala	Ser	Lys	Ala	Lys
				260					265					270		
45	Glu	Ala	Ser	Gly	Gly	Gly	Ser	Met	Ala	Met	Ile	Lys	Met	Ser	Pro	Glu
			275					280					285			
	Glu	Ile	Arg	Ala	Lys	Ser	Gln	Ser	Tyr	Gly	Gln	Gly	Ser	Asp	Gln	Ile
		290					295					300				
50	Arg	Gln	Ile	Leu	Ser	Asp	Leu	Thr	Arg	Ala	Gln	Gly	Glu	Ile	Ala	Ala
	305					310					315					320

Asn Trp Glu Gly Gln Ala Phe Ser Arg Phe Glu Glu Gln Phe Gln Gln
 325 330 335
 5 Leu Ser Pro Lys Val Glu Lys Phe Ala Gln Leu Leu Glu Glu Ile Lys
 340 345 350
 Gln Gln Leu Asn Ser Thr Ala Asp Ala Val Gln Glu Gln Asp Gln Gln
 355 360 365
 10 Leu Ser Asn Asn Phe Gly Leu Gln Ala Ser Gly Gly Gly Ser Met Gly
 370 375 380
 Gly Tyr Lys Gly Ile Lys Ala Asp Gly Gly Lys Val Asp Gln Ala Lys
 385 390 395 400
 15 Gln Leu Ala Ala Lys Thr Ala Lys Asp Ile Glu Ala Cys Gln Lys Gln
 405 410 415
 Thr Gln Gln Leu Ala Glu Tyr Ile Glu Gly Ser Asp Trp Glu Gly Gln
 420 425 430
 20 Phe Ala Asn Lys Val Lys Asp Val Leu Leu Ile Met Ala Lys Phe Gln
 435 440 445
 Glu Glu Leu Val Gln Pro Met Ala Asp His Gln Lys Ala Ile Asp Asn
 450 455 460
 25 Leu Ser Gln Asn Leu Ala Lys Tyr Asp Thr Leu Ser Ile Lys Gln Gly
 465 470 475 480
 Leu Asp Arg Val Asn Pro
 485

<210> 213

<211> 256

<212> PRT

<213> Staphylococcus aureus

<400> 213

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Met Met Lys Arg Leu Asn Lys Leu Val Leu Gly Ile Ile Phe Leu Phe
1 5 10 15
Leu Val Ile Ser Ile Thr Ala Gly Cys Gly Ile Gly Lys Glu Ala Glu
5 20 25 30
Val Lys Lys Ser Phe Glu Lys Thr Leu Ser Met Tyr Pro Ile Lys Asn
35 40 45
Leu Glu Asp Leu Tyr Asp Lys Glu Gly Tyr Arg Asp Asp Gln Phe Asp
10 50 55 60
Lys Asn Asp Lys Gly Thr Trp Ile Ile Asn Ser Glu Met Val Ile Gln
65 70 75 80
Pro Asn Asn Glu Asp Met Val Ala Lys Gly Met Val Leu Tyr Met Asn
15 85 90 95
Arg Asn Thr Lys Thr Thr Asn Gly Tyr Tyr Tyr Val Asp Val Thr Lys
100 105 110
Asp Glu Asp Glu Gly Lys Pro His Asp Asn Glu Lys Arg Tyr Pro Val
20 115 120 125
Lys Met Val Asp Asn Lys Ile Ile Pro Thr Lys Glu Ile Lys Asp Glu
130 135 140
Lys Leu Lys Lys Glu Ile Glu Asn Phe Lys Phe Phe Val Gln Tyr Gly
25 145 150 155 160
Asp Phe Lys Asn Ile Lys Asn Tyr Lys Asp Gly Asp Ile Ser Tyr Asn
165 170 175
Pro Glu Val Pro Ser Tyr Ser Ala Lys Tyr Gln Leu Thr Asn Asp Asp
30 180 185 190
Tyr Asn Val Lys Gln Leu Arg Lys Arg Tyr Asp Ile Pro Thr Ser Lys
195 200 205
Ala Pro Lys Leu Leu Leu Lys Gly Ser Gly Asn Leu Lys Gly Ser Ser
35 210 215 220
Val Gly Tyr Lys Asp Ile Glu Phe Thr Phe Val Glu Lys Lys Glu Glu
225 230 235 240
Asn Ile Tyr Phe Ser Asp Ser Leu Asp Tyr Lys Lys Ser Gly Asp Val
40 245 250 255

<210> 214

<211> 256

<212> PRT

<213> Staphylococcus aureus

<400> 214

EP 2 510 947 B1

1 Met Met Lys Arg Leu Asn Lys Leu Val Leu Gly Ile Ile Phe Leu Phe
 5 Leu Val Ile Ser Ile Thr Ala Gly Cys Gly Ile Gly Lys Glu Ala Glu
 10 Val Lys Lys Ser Phe Glu Lys Thr Leu Ser Met Tyr Pro Ile Lys Asn
 15 Leu Glu Asp Leu Tyr Asp Lys Glu Gly Tyr Arg Asp Asp Gln Phe Asp
 20 Lys Asn Asp Lys Gly Thr Trp Ile Ile Asn Ser Glu Met Val Ile Gln
 25 Pro Asn Asn Glu Asp Met Val Ala Lys Gly Met Val Leu Tyr Met Asn
 30 Arg Asn Thr Lys Thr Thr Asn Gly Tyr Tyr Tyr Val Asp Val Thr Lys
 35 Asp Glu Asp Glu Gly Lys Pro His Asp Asn Glu Lys Arg Tyr Pro Val
 40 Lys Met Val Asp Asn Lys Ile Ile Pro Thr Lys Glu Ile Lys Asp Glu
 45 Lys Val Lys Lys Glu Ile Glu Asn Phe Lys Phe Phe Val Gln Tyr Gly
 50 Asp Phe Lys Asn Ile Lys Asn Tyr Lys Asp Gly Asp Ile Ser Tyr Asn
 55 Pro Glu Val Pro Ser Tyr Ser Ala Lys Tyr Gln Leu Thr Asn Asp Asp
 60 Tyr Asn Val Lys Gln Leu Arg Lys Arg Tyr Asp Ile Pro Thr Ser Lys
 65 Ala Pro Lys Leu Leu Leu Lys Gly Ser Gly Asn Leu Lys Gly Ser Ser
 70 Val Gly Tyr Lys Asp Ile Glu Phe Thr Phe Val Glu Lys Lys Glu Glu
 75 Asn Ile Tyr Phe Ser Asp Ser Leu Asp Tyr Lys Lys Ser Gly Asp Val
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<210> 215

<211> 256

<212> PRT

<213> Staphylococcus aureus

<400> 215

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Met Met Lys Arg Leu Asn Lys Leu Val Leu Gly Ile Ile Phe Leu Phe
 1 5 10 15
 Leu Val Ile Ser Ile Thr Ala Gly Cys Gly Ile Gly Lys Glu Ala Glu
 20 25 30
 Val Lys Lys Ser Phe Glu Lys Thr Leu Ser Met Tyr Pro Ile Lys Asn
 35 40 45
 Leu Glu Asp Leu Tyr Asp Lys Glu Gly Tyr Arg Asp Asp Gln Phe Asp
 50 55 60
 Lys Asn Asp Lys Gly Thr Trp Ile Ile Asn Ser Glu Met Val Ile Gln
 65 70 75 80
 Pro Asn Asn Glu Asp Met Val Ala Lys Gly Met Val Leu Tyr Met Asn
 85 90 95
 Arg Asn Thr Lys Thr Thr Asn Gly Tyr Tyr Tyr Val Asp Val Thr Lys
 100 105 110
 Asp Glu Asp Glu Gly Lys Pro His Asp Asn Glu Lys Arg Tyr Pro Val
 115 120 125
 Lys Met Val Asp Asn Lys Ile Ile Pro Thr Lys Glu Ile Lys Asp Glu
 130 135 140
 Lys Leu Lys Lys Glu Ile Glu Asn Phe Lys Phe Phe Val Gln Tyr Gly
 145 150 155 160
 Asp Phe Lys Asn Val Lys Asn Tyr Lys Asp Gly Asp Ile Ser Tyr Asn
 165 170 175
 Pro Glu Val Pro Ser Tyr Ser Ala Lys Tyr Gln Leu Thr Asn Asp Asp
 180 185 190
 Tyr Asn Val Lys Gln Leu Arg Lys Arg Tyr Asp Ile Pro Thr Ser Lys
 195 200 205
 Ala Pro Lys Leu Leu Leu Lys Gly Ser Gly Asn Leu Lys Gly Ser Ser
 210 215 220
 Val Gly Tyr Lys Asp Ile Glu Phe Thr Phe Val Glu Lys Lys Glu Glu
 225 230 235 240
 Asn Ile Tyr Phe Ser Asp Ser Leu Asp Tyr Lys Lys Ser Gly Asp Val
 245 250 255

<210> 216

<211> 258

<212> PRT

<213> Staphylococcus aureus

<400> 216

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
 1 5 10 15
 Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
 20 25 30
 Gly Met His Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
 35 40 45

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

<210> 217

<211> 40

<212> PRT

<213> Staphylococcus aureus

<400> 217

Lys Glu Tyr Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr
 1 5 10 15
 Gly Asp Asp Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser
 20 25 30
 Ile Gly His Thr Leu Lys Tyr Val
 35 40

<210> 218

<211> 109

<212> PRT

<213> Staphylococcus aureus

<400> 218

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Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
 1 5 10 15
 Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
 20 25 30
 Gly Met His Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
 35 40 45
 Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
 50 55 60
 Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
 65 70 75 80
 Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
 85 90 95
 Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr
 100 105

<210> 219

<211> 145

<212> PRT

<213> Staphylococcus aureus

<400> 219

Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro Thr Asp Lys Lys
 1 5 10 15
 Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn Gln Asn Trp Gly
 20 25 30
 Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly Asn Gln Leu Phe
 35 40 45
 Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp Asn Phe Leu Asp
 50 55 60
 Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe Ser Pro Asp Phe
 65 70 75 80
 Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys Gln Gln Thr Asn
 85 90 95
 Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr Gln Leu His Trp
 100 105 110
 Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp Lys Trp Ile Asp
 115 120 125
 Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys Glu Glu Met Thr
 130 135 140
 Asn
 145

<210> 220

<211> 506

<212> PRT

<213> Staphylococcus aureus

<400> 220

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	Ala	Asp	Ser	Asp	Ile	Asn	Ile	Lys	Thr	Gly	Thr	Thr	Asp	Ile	Gly	Ser
	1				5					10					15	
5	Asn	Thr	Thr	Val	Lys	Thr	Gly	Asp	Leu	Val	Thr	Tyr	Asp	Lys	Glu	Asn
				20					25					30		
	Gly	Met	Leu	Lys	Lys	Val	Phe	Tyr	Ser	Phe	Ile	Asp	Asp	Lys	Asn	His
			35					40					45			
10	Asn	Lys	Lys	Leu	Leu	Val	Ile	Arg	Thr	Lys	Gly	Thr	Ile	Ala	Gly	Gln
		50					55					60				
	Tyr	Arg	Val	Tyr	Ser	Glu	Glu	Gly	Ala	Asn	Lys	Ser	Gly	Leu	Ala	Trp
	65					70					75					80

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Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
 85 90 95
 5 Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
 100 105 110
 Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr Gly Asp Asp
 115 120 125
 10 Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser Ile Gly His
 130 135 140
 Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro
 145 150 155 160
 15 Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
 165 170 175
 Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
 180 185 190
 20 Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
 195 200 205
 Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe
 210 215 220
 25 Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
 225 230 235 240
 Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
 245 250 255
 30 Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp
 260 265 270
 Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
 275 280 285
 35 Glu Glu Met Thr Asn Ala Ser Gly Gly Gly Ser Met Ala Met Ile Lys
 290 295 300
 Met Ser Pro Glu Glu Ile Arg Ala Lys Ser Gln Ser Tyr Gly Gln Gly
 305 310 315 320
 Ser Asp Gln Ile Arg Gln Ile Leu Ser Asp Leu Thr Arg Ala Gln Gly
 325 330 335
 40 Glu Ile Ala Ala Asn Trp Glu Gly Gln Ala Phe Ser Arg Phe Glu Glu
 340 345 350
 Gln Phe Gln Gln Leu Ser Pro Lys Val Glu Lys Phe Ala Gln Leu Leu
 355 360 365
 45 Glu Glu Ile Lys Gln Gln Leu Asn Ser Thr Ala Asp Ala Val Gln Glu
 370 375 380
 Gln Asp Gln Gln Leu Ser Asn Asn Phe Gly Leu Gln Ala Ser Gly Gly
 385 390 395 400
 50 Gly Ser Met Gly Gly Tyr Lys Gly Ile Lys Ala Asp Gly Gly Lys Val
 405 410 415
 Asp Gln Ala Lys Gln Leu Ala Ala Lys Thr Ala Lys Asp Ile Glu Ala
 420 425 430
 55 Cys Gln Lys Gln Thr Gln Gln Leu Ala Glu Tyr Ile Glu Gly Ser Asp
 435 440 445

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Trp Glu Gly Gln Phe Ala Asn Lys Val Lys Asp Val Leu Leu Ile Met
450 455 460

Ala Lys Phe Gln Glu Glu Leu Val Gln Pro Met Ala Asp His Gln Lys
5 465 470 475 480

Ala Ile Asp Asn Leu Ser Gln Asn Leu Ala Lys Tyr Asp Thr Leu Ser
485 490 495

Ile Lys Gln Gly Leu Asp Arg Val Asn Pro
10 500 505

<210> 221

<211> 436

<212> PRT

15 <213> Staphylococcus aureus

<400> 221

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Asp Ser Gln Gln Val Asn Ala Ala Thr Glu Ala Thr Asn Ala Thr Asn
 1 5 10 15
 Asn Gln Ser Thr Gln Val Ser Gln Ala Thr Ser Gln Pro Ile Asn Phe
 5 20 25 30
 Gln Val Gln Lys Asp Gly Ser Ser Glu Lys Ser His Met Asp Asp Tyr
 35 40 45
 Met Gln His Pro Gly Lys Val Ile Lys Gln Asn Asn Lys Tyr Tyr Phe
 10 50 55 60
 Gln Thr Val Leu Asn Asn Ala Ser Phe Trp Lys Glu Tyr Lys Phe Tyr
 65 70 75 80
 Asn Ala Asn Asn Gln Glu Leu Ala Thr Thr Val Val Asn Asp Asn Lys
 15 85 90 95
 Lys Ala Asp Thr Arg Thr Ile Asn Val Ala Val Glu Pro Gly Tyr Lys
 100 105 110
 Ser Leu Thr Thr Lys Val His Ile Val Val Pro Gln Ile Asn Tyr Asn
 20 115 120 125
 His Arg Tyr Thr Thr His Leu Glu Phe Glu Lys Ala Ile Pro Thr Leu
 130 135 140
 Ala Ala Ser Gly Gly Gly Ser Cys Gly Asn Gln Gly Glu Lys Asn Asn
 25 145 150 155 160
 Lys Ala Glu Thr Lys Ser Tyr Lys Met Asp Asp Gly Lys Thr Val Asp
 165 170 175
 Ile Pro Lys Asp Pro Lys Arg Ile Ala Val Val Ala Pro Thr Tyr Ala
 30 180 185 190
 Gly Gly Leu Lys Lys Leu Gly Ala Asn Ile Val Ala Val Asn Gln Gln
 195 200 205
 Val Asp Gln Ser Lys Val Leu Lys Asp Lys Phe Lys Gly Val Thr Lys
 210 215 220
 Ile Gly Asp Gly Asp Val Glu Lys Val Ala Lys Glu Lys Pro Asp Leu
 35 225 230 235 240
 Ile Ile Val Tyr Ser Thr Asp Lys Asp Ile Lys Lys Tyr Gln Lys Val
 245 250 255
 Ala Pro Thr Val Val Val Asp Tyr Asn Lys His Lys Tyr Leu Glu Gln
 40 260 265 270
 Gln Glu Met Leu Gly Lys Ile Val Gly Lys Glu Asp Lys Val Lys Ala
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	275		280		285											
	Trp	Lys	Lys	Asp	Trp	Glu	Glu	Thr	Thr	Ala	Lys	Asp	Gly	Lys	Glu	Ile
		290					295					300				
5	Lys	Lys	Ala	Ile	Gly	Gln	Asp	Ala	Thr	Val	Ser	Leu	Phe	Asp	Glu	Phe
	305					310					315					320
	Asp	Lys	Lys	Leu	Tyr	Thr	Tyr	Gly	Asp	Asn	Trp	Gly	Arg	Gly	Gly	Glu
					325					330					335	
10	Val	Leu	Tyr	Gln	Ala	Phe	Gly	Leu	Lys	Met	Gln	Pro	Glu	Gln	Gln	Lys
				340					345					350		
	Leu	Thr	Ala	Lys	Ala	Gly	Trp	Ala	Glu	Val	Lys	Gln	Glu	Glu	Ile	Glu
			355					360					365			
15	Lys	Tyr	Ala	Gly	Asp	Tyr	Ile	Val	Ser	Thr	Ser	Glu	Gly	Lys	Pro	Thr
		370					375					380				
	Pro	Gly	Tyr	Glu	Ser	Thr	Asn	Met	Trp	Lys	Asn	Leu	Lys	Ala	Thr	Lys
	385					390					395					400
20	Glu	Gly	His	Ile	Val	Lys	Val	Asp	Ala	Gly	Thr	Tyr	Trp	Tyr	Asn	Asp
				405						410					415	
	Pro	Tyr	Thr	Leu	Asp	Phe	Met	Arg	Lys	Asp	Leu	Lys	Glu	Lys	Leu	Ile
				420					425					430		
25	Lys	Ala	Ala	Lys												
				435												

<210> 222

<211> 584

30 <212> PRT

<213> Staphylococcus aureus

<400> 222

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	Ala	Asp	Ser	Asp	Ile	Asn	Ile	Lys	Thr	Gly	Thr	Thr	Asp	Ile	Gly	Ser
	1				5					10					15	
5	Asn	Thr	Thr	Val	Lys	Thr	Gly	Asp	Leu	Val	Thr	Tyr	Asp	Lys	Glu	Asn
				20					25					30		
	Gly	Met	Leu	Lys	Lys	Val	Phe	Tyr	Ser	Phe	Ile	Asp	Asp	Lys	Asn	His
			35					40					45			
10	Asn	Lys	Lys	Leu	Leu	Val	Ile	Arg	Thr	Lys	Gly	Thr	Ile	Ala	Gly	Gln
		50					55					60				
	Tyr	Arg	Val	Tyr	Ser	Glu	Glu	Gly	Ala	Asn	Lys	Ser	Gly	Leu	Ala	Trp
	65					70					75					80
15	Pro	Ser	Ala	Phe	Lys	Val	Gln	Leu	Gln	Leu	Pro	Asp	Asn	Glu	Val	Ala
					85					90					95	
	Gln	Ile	Ser	Asp	Tyr	Tyr	Pro	Arg	Asn	Ser	Ile	Asp	Thr	Lys	Glu	Tyr
				100					105					110		
20	Met	Ser	Thr	Leu	Thr	Tyr	Gly	Phe	Asn	Gly	Asn	Val	Thr	Gly	Asp	Asp
			115					120					125			
	Thr	Gly	Lys	Ile	Gly	Gly	Leu	Ile	Gly	Ala	Asn	Val	Ser	Ile	Gly	His
		130					135					140				
25	Thr	Leu	Lys	Tyr	Val	Gln	Pro	Asp	Phe	Lys	Thr	Ile	Leu	Glu	Ser	Pro
	145					150					155					160
30	Thr	Asp	Lys	Lys	Val	Gly	Trp	Lys	Val	Ile	Phe	Asn	Asn	Met	Val	Asn
					165					170					175	

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	Gln	Asn	Trp	Gly	Pro	Tyr	Asp	Arg	Asp	Ser	Trp	Asn	Pro	Val	Tyr	Gly
				180					185					190		
5	Asn	Gln	Leu	Phe	Met	Lys	Thr	Arg	Asn	Gly	Ser	Met	Lys	Ala	Ala	Asp
			195					200					205			
	Asn	Phe	Leu	Asp	Pro	Asn	Lys	Ala	Ser	Ser	Leu	Leu	Ser	Ser	Gly	Phe
		210					215					220				
10	Ser	Pro	Asp	Phe	Ala	Thr	Val	Ile	Thr	Met	Asp	Arg	Lys	Ala	Ser	Lys
	225					230					235					240
	Gln	Gln	Thr	Asn	Ile	Asp	Val	Ile	Tyr	Glu	Arg	Val	Arg	Asp	Asp	Tyr
					245					250					255	
15	Gln	Leu	His	Trp	Thr	Ser	Thr	Asn	Trp	Lys	Gly	Thr	Asn	Thr	Lys	Asp
				260					265					270		
	Lys	Trp	Ile	Asp	Arg	Ser	Ser	Glu	Arg	Tyr	Lys	Ile	Asp	Trp	Glu	Lys
			275					280					285			
20	Glu	Glu	Met	Thr	Asn	Ala	Ser	Gly	Gly	Gly	Ser	Cys	Gly	Asn	Gln	Gly
		290					295					300				
	Glu	Lys	Asn	Asn	Lys	Ala	Glu	Thr	Lys	Ser	Tyr	Lys	Met	Asp	Asp	Gly
	305					310					315					320
25	Lys	Thr	Val	Asp	Ile	Pro	Lys	Asp	Pro	Lys	Arg	Ile	Ala	Val	Val	Ala
					325					330					335	
	Pro	Thr	Tyr	Ala	Gly	Gly	Leu	Lys	Lys	Leu	Gly	Ala	Asn	Ile	Val	Ala
				340					345					350		
30	Val	Asn	Gln	Gln	Val	Asp	Gln	Ser	Lys	Val	Leu	Lys	Asp	Lys	Phe	Lys
			355					360					365			
	Gly	Val	Thr	Lys	Ile	Gly	Asp	Gly	Asp	Val	Glu	Lys	Val	Ala	Lys	Glu
		370					375					380				
35	Lys	Pro	Asp	Leu	Ile	Ile	Val	Tyr	Ser	Thr	Asp	Lys	Asp	Ile	Lys	Lys
	385				390						395					400
	Tyr	Gln	Lys	Val	Ala	Pro	Thr	Val	Val	Val	Asp	Tyr	Asn	Lys	His	Lys
					405					410					415	
40	Tyr	Leu	Glu	Gln	Gln	Glu	Met	Leu	Gly	Lys	Ile	Val	Gly	Lys	Glu	Asp
				420					425					430		
	Lys	Val	Lys	Ala	Trp	Lys	Lys	Asp	Trp	Glu	Glu	Thr	Thr	Ala	Lys	Asp
			435					440					445			
45	Gly	Lys	Glu	Ile	Lys	Lys	Ala	Ile	Gly	Gln	Asp	Ala	Thr	Val	Ser	Leu
		450					455					460				
	Phe	Asp	Glu	Phe	Asp	Lys	Lys	Leu	Tyr	Thr	Tyr	Gly	Asp	Asn	Trp	Gly
	465					470					475					480
50	Arg	Gly	Gly	Glu	Val	Leu	Tyr	Gln	Ala	Phe	Gly	Leu	Lys	Met	Gln	Pro
					485					490					495	
	Glu	Gln	Gln	Lys	Leu	Thr	Ala	Lys	Ala	Gly	Trp	Ala	Glu	Val	Lys	Gln
				500					505					510		
55	Glu	Glu	Ile	Glu	Lys	Tyr	Ala	Gly	Asp	Tyr	Ile	Val	Ser	Thr	Ser	Glu
			515					520					525			
	Gly	Lys	Pro	Thr	Pro	Gly	Tyr	Glu	Ser	Thr	Asn	Met	Trp	Lys	Asn	Leu
		530					535					540				

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Lys Ala Thr Lys Glu Gly His Ile Val Lys Val Asp Ala Gly Thr Tyr
 545 550 555 560
 Trp Tyr Asn Asp Pro Tyr Thr Leu Asp Phe Met Arg Lys Asp Leu Lys
 565 570 575
 Glu Lys Leu Ile Lys Ala Ala Lys
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<210> 223

<211> 498

<212> PRT

<213> Staphylococcus aureus

<400> 223

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Cys Gly Asn Gln Gly Glu Lys Asn Asn Lys Ala Glu Thr Lys Ser Tyr
 1 5 10
 Lys Met Asp Asp Gly Lys Thr Val Asp Ile Pro Lys Asp Pro Lys Arg
 5 20 25 30
 Ile Ala Val Val Ala Pro Thr Tyr Ala Gly Gly Leu Lys Lys Leu Gly
 35 40 45
 Ala Asn Ile Val Ala Val Asn Gln Gln Val Asp Gln Ser Lys Val Leu
 10 50 55 60
 Lys Asp Lys Phe Lys Gly Val Thr Lys Ile Gly Asp Gly Asp Val Glu
 65 70 75 80
 Lys Val Ala Lys Glu Lys Pro Asp Leu Ile Ile Val Tyr Ser Thr Asp
 15 85 90 95
 Lys Asp Ile Lys Lys Tyr Gln Lys Val Ala Pro Thr Val Val Val Asp
 100 105 110
 Tyr Asn Lys His Lys Tyr Leu Glu Gln Gln Glu Met Leu Gly Lys Ile
 20 115 120 125
 Val Gly Lys Glu Asp Lys Val Lys Ala Trp Lys Lys Asp Trp Glu Glu
 130 135 140
 Thr Thr Ala Lys Asp Gly Lys Glu Ile Lys Lys Ala Ile Gly Gln Asp
 25 145 150 155 160
 Ala Thr Val Ser Leu Phe Asp Glu Phe Asp Lys Lys Leu Tyr Thr Tyr
 165 170 175
 Gly Asp Asn Trp Gly Arg Gly Gly Glu Val Leu Tyr Gln Ala Phe Gly
 30 180 185 190
 Leu Lys Met Gln Pro Glu Gln Gln Lys Leu Thr Ala Lys Ala Gly Trp
 195 200 205
 Ala Glu Val Lys Gln Glu Glu Ile Glu Lys Tyr Ala Gly Asp Tyr Ile
 35 210 215 220
 Val Ser Thr Ser Glu Gly Lys Pro Thr Pro Gly Tyr Glu Ser Thr Asn
 225 230 235 240
 Met Trp Lys Asn Leu Lys Ala Thr Lys Glu Gly His Ile Val Lys Val
 40 245 250 255
 Asp Ala Gly Thr Tyr Trp Tyr Asn Asp Pro Tyr Thr Leu Asp Phe Met
 260 265 270
 Arg Lys Asp Leu Lys Glu Lys Leu Ile Lys Ala Ala Lys Ala Ser Gly
 45 275 280 285
 Gly Gly Ser Met Ala Met Ile Lys Met Ser Pro Glu Glu Ile Arg Ala

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	290		295		300											
	Lys	Ser	Gln	Ser	Tyr	Gly	Gln	Gly	Ser	Asp	Gln	Ile	Arg	Gln	Ile	Leu
	305					310					315					320
5	Ser	Asp	Leu	Thr	Arg	Ala	Gln	Gly	Glu	Ile	Ala	Ala	Asn	Trp	Glu	Gly
					325					330					335	
	Gln	Ala	Phe	Ser	Arg	Phe	Glu	Glu	Gln	Phe	Gln	Gln	Leu	Ser	Pro	Lys
				340					345					350		
10	Val	Glu	Lys	Phe	Ala	Gln	Leu	Leu	Glu	Glu	Ile	Lys	Gln	Gln	Leu	Asn
			355					360					365			
	Ser	Thr	Ala	Asp	Ala	Val	Gln	Glu	Gln	Asp	Gln	Gln	Leu	Ser	Asn	Asn
		370					375					380				
15	Phe	Gly	Leu	Gln	Ala	Ser	Gly	Gly	Gly	Ser	Met	Gly	Gly	Tyr	Lys	Gly
	385					390					395					400
	Ile	Lys	Ala	Asp	Gly	Gly	Lys	Val	Asp	Gln	Ala	Lys	Gln	Leu	Ala	Ala
				405						410					415	
20	Lys	Thr	Ala	Lys	Asp	Ile	Glu	Ala	Cys	Gln	Lys	Gln	Thr	Gln	Gln	Leu
				420					425					430		
	Ala	Glu	Tyr	Ile	Glu	Gly	Ser	Asp	Trp	Glu	Gly	Gln	Phe	Ala	Asn	Lys
			435					440					445			
25	Val	Lys	Asp	Val	Leu	Leu	Ile	Met	Ala	Lys	Phe	Gln	Glu	Glu	Leu	Val
		450					455					460				
	Gln	Pro	Met	Ala	Asp	His	Gln	Lys	Ala	Ile	Asp	Asn	Leu	Ser	Gln	Asn
	465					470					475					480
30	Leu	Ala	Lys	Tyr	Asp	Thr	Leu	Ser	Ile	Lys	Gln	Gly	Leu	Asp	Arg	Val
				485						490					495	

Asn Pro

35 <210> 224
 <211> 520
 <212> PRT
 <213> Staphylococcus aureus
 40 <400> 224

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Ser Glu Asn Ser Val Thr Gln Ser Asp Ser Ala Ser Asn Glu Ser Lys
 1 5 10 15
 Ser Asn Asp Ser Ser Ser Val Ser Ala Ala Pro Lys Thr Asp Asp Thr
 5 20 25 30
 Asn Val Ser Asp Thr Lys Thr Ser Ser Asn Thr Asn Asn Gly Glu Thr
 35 40 45
 Ser Val Ala Gln Asn Pro Ala Gln Gln Glu Thr Thr Gln Ser Ser Ser
 10 50 55 60
 Thr Asn Ala Thr Thr Glu Glu Thr Pro Val Thr Gly Glu Ala Thr Thr
 65 70 75 80
 Thr Thr Thr Asn Gln Ala Asn Thr Pro Ala Thr Thr Gln Ser Ser Asn
 15 85 90 95
 Thr Asn Ala Glu Glu Leu Val Asn Gln Thr Ser Asn Glu Thr Thr Ser
 100 105 110
 Asn Asp Thr Asn Thr Val Ser Ser Val Asn Ser Pro Gln Asn Ser Thr
 20 115 120 125
 25
 30
 35
 40
 45
 50
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	Asn	Ala	Glu	Asn	Val	Ser	Thr	Thr	Gln	Asp	Thr	Ser	Thr	Glu	Ala	Thr
	130						135					140				
5	Pro	Ser	Asn	Asn	Glu	Ser	Ala	Pro	Gln	Ser	Thr	Asp	Ala	Ser	Asn	Lys
	145					150					155					160
	Asp	Val	Val	Asn	Gln	Ala	Val	Asn	Thr	Ser	Ala	Pro	Arg	Met	Arg	Ala
					165					170					175	
10	Phe	Ser	Leu	Ala	Ala	Val	Ala	Ala	Asp	Ala	Pro	Val	Ala	Gly	Thr	Asp
				180					185					190		
	Ile	Thr	Asn	Gln	Leu	Thr	Asn	Val	Thr	Val	Gly	Ile	Asp	Ser	Gly	Thr
			195					200					205			
15	Thr	Val	Tyr	Pro	His	Gln	Ala	Gly	Tyr	Val	Lys	Leu	Asn	Tyr	Gly	Phe
		210					215					220				
	Ser	Val	Pro	Asn	Ser	Ala	Val	Lys	Gly	Asp	Thr	Phe	Lys	Ile	Thr	Val
	225					230					235					240
20	Pro	Lys	Glu	Leu	Asn	Leu	Asn	Gly	Val	Thr	Ser	Thr	Ala	Lys	Val	Pro
					245					250					255	
	Pro	Ile	Met	Ala	Gly	Asp	Gln	Val	Leu	Ala	Asn	Gly	Val	Ile	Asp	Ser
				260					265					270		
25	Asp	Gly	Asn	Val	Ile	Tyr	Thr	Phe	Thr	Asp	Tyr	Val	Asn	Thr	Lys	Asp
			275					280					285			
	Asp	Val	Lys	Ala	Thr	Leu	Thr	Met	Pro	Ala	Tyr	Ile	Asp	Pro	Glu	Asn
		290					295					300				
30	Val	Lys	Lys	Thr	Gly	Asn	Val	Thr	Leu	Ala	Thr	Gly	Ile	Gly	Ser	Thr
	305					310					315					320
	Thr	Ala	Asn	Lys	Thr	Val	Leu	Val	Asp	Tyr	Glu	Lys	Tyr	Gly	Lys	Phe
					325					330					335	
35	Tyr	Asn	Leu	Ser	Ile	Lys	Gly	Thr	Ile	Asp	Gln	Ile	Asp	Lys	Thr	Asn
				340					345					350		
	Asn	Thr	Tyr	Arg	Gln	Thr	Ile	Tyr	Val	Asn	Pro	Ser	Gly	Asp	Asn	Val
			355					360					365			
40	Ile	Ala	Pro	Val	Leu	Thr	Gly	Asn	Leu	Lys	Pro	Asn	Thr	Asp	Ser	Asn
		370					375					380				
	Ala	Leu	Ile	Asp	Gln	Gln	Asn	Thr	Ser	Ile	Lys	Val	Tyr	Lys	Val	Asp
	385					390					395					400
45	Asn	Ala	Ala	Asp	Leu	Ser	Glu	Ser	Tyr	Phe	Val	Asn	Pro	Glu	Asn	Phe
					405					410					415	
	Glu	Asp	Val	Thr	Asn	Ser	Val	Asn	Ile	Thr	Phe	Pro	Asn	Pro	Asn	Gln
				420					425					430		
50	Tyr	Lys	Val	Glu	Phe	Asn	Thr	Pro	Asp	Asp	Gln	Ile	Thr	Thr	Pro	Tyr
			435					440					445			
	Ile	Val	Val	Val	Asn	Gly	His	Ile	Asp	Pro	Asn	Ser	Lys	Gly	Asp	Leu
		450					455					460				
55	Ala	Leu	Arg	Ser	Thr	Leu	Tyr	Gly	Tyr	Asn	Ser	Asn	Ile	Ile	Trp	Arg
	465					470					475					480
	Ser	Met	Ser	Trp	Asp	Asn	Glu	Val	Ala	Phe	Asn	Asn	Gly	Ser	Gly	Ser
					485					490					495	

Gly Asp Gly Ile Asp Lys Pro Val Val Pro Glu Gln Pro Asp Glu Pro
500 505 510

Gly Glu Ile Glu Pro Ile Pro Glu
515 520

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<210> 225

<211> 4

<212> PRT

10

<213> Artificial sequence

<220>

<223> Peptide linker

15

<400> 225

Pro Ser Gly Ser
1

20

<210> 226

<211> 6

<212> PRT

<213> Artificial Sequence

25

<220>

<223> Hexahistidine tag

<400> 226

30

His His His His His His
1 5

35

<210> 227

<211> 4

<212> PRT

<213> Artificial Sequence

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<220>

<223> Poly-glycine linker

<400> 227

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Gly Gly Gly Gly
1

<210> 228

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<211> 20

<212> PRT

<213> Staphylococcus aureus

<400> 228

55

EP 2 510 947 B1

Met Ser Gly Gly Ile Gly Asn Gln Tyr Ala Val Asp Pro Thr Ser Tyr
1 5 10 15

Leu Gln Ser Arg
20

<210> 229

<211> 23

<212> PRT

<213> Staphylococcus aureus

<400> 229

Ala Gly Asp Gln Ile Ala Tyr Ser Gly Ser Thr Gly Asn Ser Thr Ala
1 5 10 15

Pro His Val His Phe Gln Arg
20

<210> 230

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> tetrapeptide fragment of SEQ ID NO: 172

<400> 230

Gly Ser Gly Ser
1

<210> 231

<211> 293

<212> PRT

<213> Staphylococcus aureus

<400> 231

EP 2 510 947 B1

1 Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
 5 Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
 Gly Met His Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
 10 Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
 Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
 15 Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
 Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
 20 Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr Gly Asp Asp
 Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser Ile Gly His
 25 Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro
 Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
 30 Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
 Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
 35 Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe
 Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
 40 Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
 Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp
 45 Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
 Glu Glu Met Thr Asn
 290

<210> 232

<211> 296

<212> PRT

<213> Staphylococcus aureus

<400> 232

EP 2 510 947 B1

1 Met Ala Ser Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp
 5 Ile Gly Ser Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp
 Lys Glu Asn Gly Met Leu Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp
 10 Lys Asn His Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile
 Ala Gly Gln Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly
 15 Leu Ala Trp Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn
 Glu Val Ala Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr
 20 Lys Glu Tyr Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr
 Gly Asp Asp Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser
 25 Ile Gly His Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu
 Glu Ser Pro Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn
 30 Met Val Asn Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro
 Val Tyr Gly Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys
 35 Ala Ala Asp Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser
 Ser Gly Phe Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys
 40 Ala Ser Lys Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg
 Asp Asp Tyr Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn
 45 Thr Lys Asp Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp
 Trp Glu Lys Glu Glu Met Thr Asn

<210> 233

<211> 888

<212> DNA

<213> Staphylococcus aureus

<400> 233

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	atggctagcg	cagatttctga	tattaatatt	aaaaccggta	ctacagatat	tggaagcaat	60
	actacagtaa	aaacaggtga	tttagtcact	tatgataaag	aaaatggcat	gttaaaaaaa	120
	gtattttata	gttttatcga	tgataaaaaat	cataataaaa	aactgctagt	tattagaacg	180
5	aaaggtagca	ttgctgggtca	atatagaggtt	tatagcggaag	aagggtgctaa	caaaagtggg	240
	ttagcctggc	cttcagcctt	taagggtacag	ttgcaactac	ctgataatga	agtagctcaa	300
	atatctgatt	actatccaag	aaattcgatt	gatacaaaaag	agtatatgag	tactttaact	360
	tatggattca	acggtaatgt	tactgggtgat	gatacaggaa	aaattggcgg	ccttattggg	420
	gcaaatgttt	cgattgggtca	tacactgaaa	tatgttcaac	ctgatttcaa	aacaatttta	480
	gagagcccaa	ctgataaaaa	agtaggctgg	aaagtgatat	ttaacaatat	ggtagaatcaa	540
10	aattggggac	catatgatag	agattcttgg	aaccgggtat	atggcaatca	acttttcattg	600
	aaaactagaa	atggctctat	gaaagcagca	gataacttcc	ttgatcctaa	caaagcaagt	660
	tctctattat	cttcagggtt	ttcaccagac	ttcgctacag	ttattactat	ggatagaaaa	720
	gcatccaaac	aacaaacaaa	tatagatgta	atatacgaac	gagttcgtga	tgactaccaa	780
	ttgcaactgga	cttcaacaaa	ttggaaagggt	accaatacta	aagataaatg	gatagatcgt	840
	tcttcagaaa	gatataaaaat	cgattgggaa	aaagaagaaa	tgacaaat		888

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<210> 234

<211> 306

<212> PRT

<213> Staphylococcus epidermidis

20

<400> 234

25

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EP 2 510 947 B1

1 Met Lys Lys Leu 5 Leu Leu Pro Leu Ile Ala 10 Leu Ile Leu Val 15 Leu Ala
 5 Ala Cys Gly Asn 20 Asn Ser Asp Ser Gly 25 Ser Lys Asp Ser 30 Asp Lys Lys
 Ala Glu Thr 35 Lys Ser Tyr Lys 40 Thr Asp Asp Gly Lys 45 Thr Ile Lys Val
 10 Pro Lys 50 Asn Pro Lys Arg Ile 55 Ala Val Val Ala 60 Pro Ser Tyr Ala Gly
 Gly Ile Lys Lys Leu 70 Gly Gly Asn Val Val 75 Ala Val Ser Asn Gln Val 80
 15 Asp Gln Ser Ser 85 Ile Leu Lys Asp Lys 90 Phe Lys Gly Val Thr 95 Lys Val
 Gly Asp Asp 100 Asp Val Glu Lys Val 105 Ala Lys Gln Lys Pro 110 Asp Leu Ile
 20 Ile Val 115 Leu Asp Gln Asn Lys 120 Asn Ile Lys Lys Tyr 125 Lys Lys Ile Ala
 Ala Thr 130 Val Pro Phe Asn 135 Tyr Gln Lys His Lys 140 Tyr Leu Glu Gln Gln
 25 Glu Glu Leu Gly Lys 150 Leu Gly Lys Glu 155 Asp Glu Val Lys Lys Trp 160
 Glu Lys Gln Trp 165 Lys Asp Gln Thr Ala 170 Lys Asp Gly Lys Glu 175 Ile Lys
 30 Asn Lys Ile 180 Gly Ala Asp Ser Thr 185 Val Ser Ile Phe Asp 190 Glu Phe Asp
 Lys Lys Leu 195 Tyr Thr Tyr Gly 200 Asp Asn Trp Gly Arg 205 Gly Gly Glu Val
 35 Leu Tyr 210 Gln Ala Phe Gly Leu 215 Lys Met Ser Lys 220 Gly Gln His Asp Leu
 Thr 225 Lys Lys Ala Gly Trp 230 Ala Glu Val Asn 235 Gln Glu Gln Ile Glu Lys 240
 40 Val Ala Gly Asp 245 Tyr Ile Val Ser Thr 250 Ser Ala Gly Lys Ser 255 Thr Pro
 Gly Tyr Glu 260 Lys Thr Asn Ile Trp 265 Lys Asn Leu Pro Ala Val 270 Lys Lys
 45 Gly His Val 275 Ile Lys Val Lys 280 Ala Glu Thr Phe Trp Tyr 285 Asn Asp Pro
 Tyr Thr 290 Leu Asp Phe Met Arg 295 Lys Asp Leu Lys 300 Lys Lys Leu Met Asp
 50 Ala Lys 305

<210> 235

<211> 253

<212> PRT

55 <213> Staphylococcus epidermidis

<400> 235

EP 2 510 947 B1

Met Arg Tyr Leu Lys Lys Val Thr Ile Tyr Ile Ser Leu Leu Ile Leu
1 5 10 15
Val Ser Gly Cys Gly Asn Gly Lys Glu Thr Glu Ile Lys Gln Asn Phe
20 25 30
Asn Lys Met Leu Asp Met Tyr Pro Thr Lys Asn Leu Glu Asp Phe Tyr
35 40 45
Asp Lys Glu Gly Tyr Arg Asp Glu Glu Phe Asp Lys Lys Asp Lys Gly
50 55 60
Thr Trp Ile Val Gly Ser Thr Met Thr Ile Glu Pro Lys Gly Lys Tyr
65 70 75 80
Met Glu Ser Arg Gly Met Phe Leu Tyr Ile Asn Arg Asn Thr Arg Thr
85 90 95
Thr Lys Gly Tyr Tyr Tyr Val Arg Lys Thr Thr Asp Asp Ser Lys Gly
100 105 110
Arg Leu Lys Asp Asp Glu Lys Arg Tyr Pro Val Lys Met Glu His Asn
115 120 125
Lys Ile Ile Pro Thr Lys Pro Ile Pro Asn Asp Lys Leu Lys Lys Glu
130 135 140
Ile Glu Asn Phe Lys Phe Phe Val Gln Tyr Gly Asp Phe Lys Asn Leu
145 150 155 160
Lys Asp Tyr Lys Asp Gly Asp Ile Ser Tyr Asn Pro Asn Val Pro Ser
165 170 175
Tyr Ser Ala Lys Tyr Gln Leu Ser Asn Asn Asp Tyr Asn Val Lys Gln
180 185 190
Leu Arg Lys Arg Tyr Asp Ile Pro Thr Asn Gln Ala Pro Lys Leu Leu
195 200 205
Leu Lys Gly Asp Gly Asp Leu Lys Gly Ser Ser Ile Gly Ser Lys Ser
210 215 220
Leu Glu Phe Thr Phe Ile Glu Asn Lys Glu Glu Asn Ile Phe Phe Ser
225 230 235 240
Asp Gly Val Gln Phe Thr Pro Ser Glu Asp Ser Glu Ser
245 250

<210> 236

<211> 531

<212> PRT

<213> Staphylococcus aureus

<400> 236

EP 2 510 947 B1

1 Val Gly Asn Val Thr Val Thr Val Phe Asp Asn Asn Thr Asn Thr Lys
 5 Val Gly Glu Ala Val Thr Lys Glu Asp Gly Ser Tyr Leu Ile Pro Asn
 10 Leu Pro Asn Gly Asp Tyr Arg Val Glu Phe Ser Asn Leu Pro Lys Gly
 Tyr Glu Val Thr Pro Ser Lys Gln Gly Asn Asn Glu Glu Leu Asp Ser
 15 Asn Gly Leu Ser Ser Val Ile Thr Val Asn Gly Lys Asp Asn Leu Ser
 Ala Asp Leu Gly Ile Tyr Lys Pro Lys Tyr Asn Leu Gly Asp Tyr Val
 20 Trp Glu Asp Thr Asn Lys Asn Gly Ile Gln Asp Gln Asp Glu Lys Gly
 Ile Ser Gly Val Thr Val Thr Leu Lys Asp Glu Asn Gly Asn Val Leu
 25 Lys Thr Val Thr Thr Asp Ala Asp Gly Lys Tyr Lys Phe Thr Asp Leu
 Asp Asn Gly Asn Tyr Lys Val Glu Phe Thr Thr Pro Glu Gly Tyr Thr
 30 Pro Thr Thr Val Thr Ser Gly Ser Asp Ile Glu Lys Asp Ser Asn Gly
 Leu Thr Thr Thr Gly Val Ile Asn Gly Ala Asp Asn Met Thr Leu Asp
 35 Ser Gly Phe Tyr Lys Thr Pro Lys Tyr Asn Leu Gly Asn Tyr Val Trp
 Glu Asp Thr Asn Lys Asp Gly Lys Gln Asp Ser Thr Glu Lys Gly Ile
 40 Ser Gly Val Thr Val Thr Leu Lys Asn Glu Asn Gly Glu Val Leu Gln
 Thr Thr Lys Thr Asp Lys Asp Gly Lys Tyr Gln Phe Thr Gly Leu Glu
 45 Asn Gly Thr Tyr Lys Val Glu Phe Glu Thr Pro Ser Gly Tyr Thr Pro
 Thr Gln Val Gly Ser Gly Thr Asp Glu Gly Ile Asp Ser Asn Gly Thr
 50 Ser Thr Thr Gly Val Ile Lys Asp Lys Asp Asn Asp Thr Ile Asp Ser
 Gly Phe Tyr Lys Pro Thr Tyr Asn Leu Gly Asp Tyr Val Trp Glu Asp
 55 Thr Asn Lys Asn Gly Val Gln Asp Lys Asp Glu Lys Gly Ile Ser Gly
 Val Thr Val Thr Leu Lys Asp Glu Asn Asp Lys Val Leu Lys Thr Val
 Thr Thr Asp Glu Asn Gly Lys Tyr Gln Phe Thr Asp Leu Asn Asn Gly

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Thr Tyr Lys Val Glu Phe Glu Thr Pro Ser Gly Tyr Thr Pro Thr Ser
 370 375 380
 Val Thr Ser Gly Asn Asp Thr Glu Lys Asp Ser Asn Gly Leu Thr Thr
 385 390 395 400
 Thr Gly Val Ile Lys Asp Ala Asp Asn Met Thr Leu Asp Ser Gly Phe
 405 410 415
 Tyr Lys Thr Pro Lys Tyr Ser Leu Gly Asp Tyr Val Trp Tyr Asp Ser
 420 425 430
 Asn Lys Asp Gly Lys Gln Asp Ser Thr Glu Lys Gly Ile Lys Asp Val
 435 440 445
 Lys Val Thr Leu Leu Asn Glu Lys Gly Glu Val Ile Gly Thr Thr Lys
 450 455 460
 Thr Asp Glu Asn Gly Lys Tyr Cys Phe Asp Asn Leu Asp Ser Gly Lys
 465 470 475 480
 Tyr Lys Val Ile Phe Glu Lys Pro Ala Gly Leu Thr Gln Thr Val Thr
 485 490 495
 Asn Thr Thr Glu Asp Asp Lys Asp Ala Asp Gly Gly Glu Val Asp Val
 500 505 510
 Thr Ile Thr Asp His Asp Asp Phe Thr Leu Asp Asn Gly Tyr Phe Glu
 515 520 525
 Glu Asp Thr
 530

<210> 237

<211> 504

<212> PRT

<213> Staphylococcus aureus

<400> 237

EP 2 510 947 B1

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
1 5 10 15
Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
5 20 25 30
Gly Met Leu Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
35 40 45
Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
10 50 55 60
Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
65 70 75 80
Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
15 85 90 95
Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
100 105 110
Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr Gly Asp Asp
20 115 120 125
Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser Ile Gly His
130 135 140
Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro
25 145 150 155 160

EP 2 510 947 B1

Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
 165 170 175
 5 Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
 180 185 190
 Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
 195 200 205
 10 Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe
 210 215 220
 Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
 225 230 235 240
 15 Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
 245 250 255
 Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp
 260 265 270
 20 Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
 275 280 285
 Glu Glu Met Thr Asn Ala Pro Thr Ala Arg Gly Ala Met Ile Lys Met
 290 295 300
 25 Ser Pro Glu Glu Ile Arg Ala Lys Ser Gln Ser Tyr Gly Gln Gly Ser
 305 310 315 320
 Asp Gln Ile Arg Gln Ile Leu Ser Asp Leu Thr Arg Ala Gln Gly Glu
 325 330 335
 30 Ile Ala Ala Asn Trp Glu Gly Gln Ala Phe Ser Arg Phe Glu Glu Gln
 340 345 350
 Phe Gln Gln Leu Ser Pro Lys Val Glu Lys Phe Ala Gln Leu Leu Glu
 355 360 365
 35 Glu Ile Lys Gln Gln Leu Asn Ser Thr Ala Asp Ala Val Gln Glu Gln
 370 375 380
 Asp Gln Gln Leu Ser Asn Asn Phe Gly Leu Gln Ala Ser Gly Gly Gly
 385 390 395 400
 40 Ser Gly Gly Tyr Lys Gly Ile Lys Ala Asp Gly Gly Lys Val Asp Gln
 405 410 415
 Ala Lys Gln Leu Ala Ala Lys Thr Ala Lys Asp Ile Glu Ala Cys Gln
 420 425 430
 45 Lys Gln Thr Gln Gln Leu Ala Glu Tyr Ile Glu Gly Ser Asp Trp Glu
 435 440 445
 Gly Gln Phe Ala Asn Lys Val Lys Asp Val Leu Leu Ile Met Ala Lys
 450 455 460
 50 Phe Gln Glu Glu Leu Val Gln Pro Met Ala Asp His Gln Lys Ala Ile
 465 470 475 480
 Asp Asn Leu Ser Gln Asn Leu Ala Lys Tyr Asp Thr Leu Ser Ile Lys
 485 490 495
 55 Gln Gly Leu Asp Arg Val Asn Pro
 500

<210> 238
 <211> 496
 <212> PRT

<213> Staphylococcus aureus

<400> 238

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EP 2 510 947 B1

1 Cys Gly Asn Gln Gly Glu Lys Asn Asn Lys Ala Glu Thr Lys Ser Tyr
 5 Lys Met Asp Asp Gly Lys Thr Val Asp Ile Pro Lys Asp Pro Lys Arg
 10 Ile Ala Val Val Ala Pro Thr Tyr Ala Gly Gly Leu Lys Lys Leu Gly
 15 Lys Asp Lys Phe Lys Gly Val Thr Lys Ile Gly Asp Gly Asp Val Glu
 20 Lys Val Ala Lys Glu Lys Pro Asp Leu Ile Ile Val Tyr Ser Thr Asp
 25 Lys Asp Ile Lys Lys Tyr Gln Lys Val Ala Pro Thr Val Val Val Asp
 30 Tyr Asn Lys His Lys Tyr Leu Glu Gln Gln Glu Met Leu Gly Lys Ile
 35 Val Gly Lys Glu Asp Lys Val Lys Ala Trp Lys Lys Asp Trp Glu Glu
 40 Thr Thr Ala Lys Asp Gly Lys Glu Ile Lys Lys Ala Ile Gly Gln Asp
 45 Ala Thr Val Ser Leu Phe Asp Glu Phe Asp Lys Lys Leu Tyr Thr Tyr
 50 Gly Asp Asn Trp Gly Arg Gly Gly Glu Val Leu Tyr Gln Ala Phe Gly
 55 Leu Lys Met Gln Pro Glu Gln Gln Lys Leu Thr Ala Lys Ala Gly Trp
 60 Ala Glu Val Lys Gln Glu Glu Ile Glu Lys Tyr Ala Gly Asp Tyr Ile
 65 Val Ser Thr Ser Glu Gly Lys Pro Thr Pro Gly Tyr Glu Ser Thr Asn
 70 Met Trp Lys Asn Leu Lys Ala Thr Lys Glu Gly His Ile Val Lys Val
 75 Asp Ala Gly Thr Tyr Trp Tyr Asn Asp Pro Tyr Thr Leu Asp Phe Met
 80 Arg Lys Asp Leu Lys Glu Lys Leu Ile Lys Ala Ala Lys Ala Pro Thr
 85 Ala Arg Gly Ala Met Ile Lys Met Ser Pro Glu Glu Ile Arg Ala Lys
 90 Ser Gln Ser Tyr Gly Gln Gly Ser Asp Gln Ile Arg Gln Ile Leu Ser
 95 Asp Leu Thr Arg Ala Gln Gly Glu Ile Ala Ala Asn Trp Glu Gly Gln
 100 Ala Phe Ser Arg Phe Glu Glu Gln Phe Gln Gln Leu Ser Pro Lys Val
 105 Glu Lys Phe Ala Gln Leu Leu Glu Glu Ile Lys Gln Gln Leu Asn Ser
 110

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Thr Ala Asp Ala Val Gln Glu Gln Asp Gln Gln Leu Ser Asn Asn Phe
 370 375 380
 5 Gly Leu Gln Ala Ser Gly Gly Gly Ser Gly Gly Tyr Lys Gly Ile Lys
 385 390 395
 Ala Asp Gly Gly Lys Val Asp Gln Ala Lys Gln Leu Ala Ala Lys Thr
 405 410 415
 10 Ala Lys Asp Ile Glu Ala Cys Gln Lys Gln Thr Gln Gln Leu Ala Glu
 420 425 430
 Tyr Ile Glu Gly Ser Asp Trp Glu Gly Gln Phe Ala Asn Lys Val Lys
 435 440 445
 15 Asp Val Leu Leu Ile Met Ala Lys Phe Gln Glu Glu Leu Val Gln Pro
 450 455 460
 Met Ala Asp His Gln Lys Ala Ile Asp Asn Leu Ser Gln Asn Leu Ala
 465 470 475 480
 20 Lys Tyr Asp Thr Leu Ser Ile Lys Gln Gly Leu Asp Arg Val Asn Pro
 485 490 495

<210> 239

<211> 6

<212> PRT

<213> Peptide linker

<400> 239

Ala Pro Thr Ala Arg Gly
1 5

<210> 240

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> N-terminal sequence

<400> 240

Met Gly Ser Ser His His His His His His Glu Asn Leu Tyr Phe Gln
1 5 10 15

Gly

<210> 241

<211> 205

<212> PRT

<213> Staphylococcus aureus

<400> 241

EP 2 510 947 B1

Ala Met Ile Lys Met Ser Pro Glu Glu Ile Arg Ala Lys Ser Gln Ser
1 5 10 15
Tyr Gly Gln Gly Ser Asp Gln Ile Arg Gln Ile Leu Ser Asp Leu Thr
5 20 25 30
Arg Ala Gln Gly Glu Ile Ala Ala Asn Trp Glu Gly Gln Ala Phe Ser
35 40 45
Arg Phe Glu Glu Gln Phe Gln Gln Leu Ser Pro Lys Val Glu Lys Phe
10 50 55 60
Ala Gln Leu Leu Glu Glu Ile Lys Gln Gln Leu Asn Ser Thr Ala Asp
65 70 75 80
Ala Val Gln Glu Gln Asp Gln Gln Leu Ser Asn Asn Phe Gly Leu Gln
15 85 90 95
Ala Ser Gly Gly Gly Ser Gly Gly Tyr Lys Gly Ile Lys Ala Asp Gly
100 105 110
Gly Lys Val Asp Gln Ala Lys Gln Leu Ala Ala Lys Thr Ala Lys Asp
20 115 120 125
Ile Glu Ala Cys Gln Lys Gln Thr Gln Gln Leu Ala Glu Tyr Ile Glu
130 135 140
Gly Ser Asp Trp Glu Gly Gln Phe Ala Asn Lys Val Lys Asp Val Leu
25 145 150 155 160
Leu Ile Met Ala Lys Phe Gln Glu Glu Leu Val Gln Pro Met Ala Asp
165 170 175
His Gln Lys Ala Ile Asp Asn Leu Ser Gln Asn Leu Ala Lys Tyr Asp
30 180 185 190
Thr Leu Ser Ile Lys Gln Gly Leu Asp Arg Val Asn Pro
195 200 205

35 <210> 242
<211> 293
<212> PRT
<213> Staphylococcus aureus
40 <400> 242
45
50
55

EP 2 510 947 B1

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
1 5 10 15
Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
20 25 30
Gly Met His Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
35 40 45
Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
50 55 60
Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
65 70 75 80
Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
85 90 95
Gln Ile Ser Asp Leu Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
100 105 110
Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr Gly Asp Asp
115 120 125
Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser Ile Gly His
130 135 140
Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro
145 150 155 160
Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
165 170 175
Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
180 185 190
Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
195 200 205
Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe
210 215 220
Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
225 230 235 240
Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
245 250 255
Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp
260 265 270
Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
275 280 285
Glu Glu Met Thr Asn
290

<210> 243

<211> 293

<212> PRT

<213> Staphylococcus aureus

<400> 243

EP 2 510 947 B1

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
1 5 10 15
Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
5 20 25 30
Gly Met His Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
35 40 45
Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
10 50 55 60
Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
65 70 75 80
Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
15 85 90 95
Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
100 105 110
Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr Gly Asp Asp
20 115 120 125
Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser Ile Gly His
130 135 140
Thr Leu Lys Tyr Val Gln Pro Leu Phe Lys Thr Ile Leu Glu Ser Pro
25 145 150 155 160
Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
165 170 175
Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
30 180 185 190
Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
195 200 205
Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe
35 210 215 220
Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
225 230 235 240
Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
40 245 250 255
Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp
260 265 270
Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
45 275 280 285
Glu Glu Met Thr Asn
290

<210> 244

<211> 293

<212> PRT

<213> Staphylococcus aureus

<400> 244

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Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
225 230 235 240
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 40 Thr Thr Ala Lys Asp Gly Lys Glu Ile Lys Lys Ala Ile Gly Gln Asp
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 Ser Ala Lys Tyr Gln Leu Thr Asn Asp Asp Tyr Asn Val Lys Gln Leu
 30 Arg Lys Arg Tyr Asp Ile Pro Thr Ser Lys Ala Pro Lys Leu Leu Leu
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 Glu Gly Ser Asp Trp Glu Gly Gln Phe Ala Asn Lys Val Lys Asp Val
 25 145 150 155 160
 Leu Leu Ile Met Ala Lys Phe Gln Glu Glu Leu Val Gln Pro Met Ala
 165 170 175
 Asp His Gln Lys Ala Ile Asp Asn Leu Ser Gln Asn Leu Ala Lys Tyr
 180 185 190
 Asp Thr Leu Ser Ile Lys Gln Gly Leu Asp Arg Val Asn Pro
 195 200 205

Claims

1. A vaccine comprising sta006 antigen for use in a method for protecting against *S. aureus* infection in a mammal, wherein the sta006 antigen comprises an amino acid sequence: (i) (a) having 70% or more identity to SEQ ID NO: 42; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 42, wherein 'n' is 7 or more; and (ii) wherein the sta006 antigen can elicit an antibody that recognises SEQ ID NO: 42.
2. The vaccine for use according to claim 1, further comprising an adjuvant.
3. A vaccine comprising a sta006 antigen and an adjuvant, wherein the sta006 antigen comprises an amino acid sequence: (i) (a) having 70% or more identity to SEQ ID NO: 42; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 42, wherein 'n' is 7 or more; and (ii) wherein the sta006 antigen can elicit an antibody that recognises SEQ ID NO: 42.
4. The vaccine for use according to claim 1 and claims dependent thereto, or according to claim 3 and claims dependent thereto, wherein the sta006 antigen comprises an amino acid sequence having 80%, 90% or more identity to SEQ ID NO: 42.
5. The vaccine for use according to claim 1 and claims dependent thereto, or according to claim 3 and claims dependent thereto, wherein the sta006 antigen comprises an amino acid sequence having 90% or more identity to SEQ ID NO: 246.
6. The vaccine for use according to claim 1 and claims dependent thereto, or according to claim 3 and claims dependent thereto, wherein the sta006 antigen comprises an amino acid sequence having 99% or more identity to SEQ ID NO:

248.

7. The vaccine for use according to claim 2 and claims dependent thereto, or according to claim 3 and claims dependent thereto, wherein the adjuvant is aluminium hydroxide.
8. The vaccine for use according to claim 1 and claims dependent thereto, or according to claim 3 and claims dependent thereto, wherein the vaccine includes a histidine buffer or a phosphate buffer.
9. The vaccine for use according to claim 1 and claims dependent thereto, or according to claim 3 and claims dependent thereto, further comprising one or more conjugates of a *S.aureus* exopolysaccharide and a carrier protein.
10. The vaccine for the use according to claims 1,2,4-8, or according to claims 3-8, further comprising one or more conjugates of a *S.aureus* capsular polysaccharide and a carrier protein.
11. The vaccine for use according to claim 1 and claims dependent thereto, or according to claim 3 and claims dependent thereto, in lyophilized form.
12. The vaccine for use according to claims 1,2,4-10, or according to claims 3-10, in aqueous form.
13. A method for preparing the vaccine of claim 12, by reconstituting the vaccine of claim 11 with aqueous material.
14. A vaccine for use according to claim 1 and claims dependent thereto, or according to claim 3 and claims dependent thereto, further comprising a pharmaceutical carrier and/or an excipient.

Patentansprüche

1. Vakzin umfassend sta006-Antigen, zur Verwendung in einem Verfahren zum Schutz vor *S. aureus*-Infektion bei einem Säuger, wobei das sta006-Antigen eine Aminosäuresequenz umfasst: (i) (a) mit 70 % oder mehr Identität zu SEQ ID NO: 42; und/oder (b) umfassend ein Fragment aus mindestens 'n' aufeinanderfolgenden Aminosäuren von SEQ ID NO: 42, wobei 'n' 7 oder mehr ist; und (ii) wobei das sta006-Antigen die Bildung eines Antikörpers, der SEQ ID NO: 42 erkennt, auslösen kann.
2. Vakzin zur Verwendung gemäß Anspruch 1, ferner umfassend ein Adjuvans.
3. Vakzin umfassend ein sta006-Antigen und ein Adjuvans, wobei das sta006-Antigen eine Aminosäuresequenz umfasst:
(i) (a) mit 70 % oder mehr Identität zu SEQ ID NO: 42; und/oder (b) umfassend ein Fragment aus mindestens 'n' aufeinanderfolgenden Aminosäuren von SEQ ID NO: 42, wobei 'n' 7 oder mehr ist; und (ii) wobei das sta006-Antigen die Bildung eines Antikörpers, der SEQ ID NO: 42 erkennt, auslösen kann.
4. Vakzin zur Verwendung gemäß Anspruch 1 und den davon abhängigen Ansprüchen oder gemäß Anspruch 3 und den davon abhängigen Ansprüchen, wobei das sta006-Antigen eine Aminosäuresequenz mit 80 %, 90 % oder mehr Identität zu SEQ ID NO: 42 umfasst.
5. Vakzin zur Verwendung gemäß Anspruch 1 und den davon abhängigen Ansprüchen oder gemäß Anspruch 3 und den davon abhängigen Ansprüchen, wobei das sta006-Antigen eine Aminosäuresequenz mit 90 % oder mehr Identität zu SEQ ID NO: 246 umfasst.
6. Vakzin zur Verwendung gemäß Anspruch 1 und den davon abhängigen Ansprüchen oder gemäß Anspruch 3 und den davon abhängigen Ansprüchen, wobei das sta006-Antigen eine Aminosäuresequenz mit 99 % oder mehr Identität zu SEQ ID NO: 248 umfasst.
7. Vakzin zur Verwendung gemäß Anspruch 2 und den davon abhängigen Ansprüchen oder gemäß Anspruch 3 und den davon abhängigen Ansprüchen, wobei das Adjuvans Aluminiumhydroxid ist.

8. Vakzin zur Verwendung gemäß Anspruch 1 und den davon abhängigen Ansprüchen, oder gemäß Anspruch 3 und den davon abhängigen Ansprüchen, wobei das Vakzin einen Histidin-Puffer oder einen Phosphat-Puffer enthält.
9. Vakzin zur Verwendung gemäß Anspruch 1 und den davon abhängigen Ansprüchen oder gemäß Anspruch 3 und den davon abhängigen Ansprüchen, ferner umfassend ein oder mehrere Konjugat(e) eines *S.aureus*-Exopolysaccharids und eines Trägerproteins.
10. Vakzin zur Verwendung gemäß Ansprüchen 1, 2, 4-8 oder gemäß Ansprüchen 3-8, ferner umfassend ein oder mehrere Konjugat(e) eines *S. aureus*-Kapselpolysaccharids und eines Trägerproteins.
11. Vakzin zur Verwendung gemäß Anspruch 1 und den davon abhängigen Ansprüchen oder gemäß Anspruch 3 und den davon abhängigen Ansprüchen in lyophilisierter Form.
12. Vakzin zur Verwendung gemäß Ansprüchen 1, 2, 4-10 oder gemäß Ansprüchen 3-10 in wässriger Form.
13. Verfahren zur Herstellung des Vakzins gemäß Anspruch 12 durch Rekonstitution des Vakzins gemäß Anspruch 11 mit wässrigem Material.
14. Vakzin zur Verwendung gemäß Anspruch 1 und den davon abhängigen Ansprüchen oder gemäß Anspruch 3 und den davon abhängigen Ansprüchen, ferner umfassend einen pharmazeutischen Träger und/oder einen Hilfsstoff.

Revendications

1. Vaccin comprenant l'antigène sta006 pour une utilisation dans un procédé de protection contre une infection par *S. aureus* chez un mammifère, l'antigène sta006 comprenant une séquence d'acides aminés : (i) (a) présentant 70 % ou plus d'identité avec SEQ ID NO : 42 ; et/ou (b) comprenant un fragment d'au moins « n » acides aminés consécutifs de SEQ ID NO : 42, où « n » vaut 7 ou plus ; et (ii) l'antigène sta006 pouvant déclencher un anticorps qui reconnaît SEQ ID NO : 42.
2. Vaccin pour une utilisation selon la revendication 1, comprenant en outre un adjuvant.
3. Vaccin comprenant un antigène sta006 et un adjuvant, l'antigène sta006 comprenant une séquence d'acides aminés : (i) (a) présentant 70 % ou plus d'identité avec SEQ ID NO : 42 ; et/ou (b) comprenant un fragment d'au moins « n » acides aminés consécutifs de SEQ ID NO : 42, où « n » vaut 7 ou plus ; et (ii) l'antigène sta006 pouvant déclencher un anticorps qui reconnaît SEQ ID NO : 42.
4. Vaccin pour une utilisation selon la revendication 1 et les revendications qui en dépendent, ou selon la revendication 3 et les revendications qui en dépendent, dans lequel l'antigène sta006 comprend une séquence d'acides aminés présentant 80 %, 90 % ou plus d'identité avec SEQ ID NO : 42.
5. Vaccin pour une utilisation selon la revendication 1 et les revendications qui en dépendent, ou selon la revendication 3 et les revendications qui en dépendent, dans lequel l'antigène sta006 comprend une séquence d'acides aminés présentant 90 % ou plus d'identité avec SEQ ID NO : 246.
6. Vaccin pour une utilisation selon la revendication 1 et les revendications qui en dépendent, ou selon la revendication 3 et les revendications qui en dépendent, dans lequel l'antigène sta006 comprend une séquence d'acides aminés présentant 99 % ou plus d'identité avec SEQ ID NO : 248.
7. Vaccin pour une utilisation selon la revendication 2 et les revendications qui en dépendent, ou selon la revendication 3 et les revendications qui en dépendent, dans lequel l'adjuvant est l'hydroxyde d'aluminium.
8. Vaccin pour une utilisation selon la revendication 1 et les revendications qui en dépendent, ou selon la revendication 3 et les revendications qui en dépendent, le vaccin comprenant un tampon histidine ou un tampon phosphate.
9. Vaccin pour une utilisation selon la revendication 1 et les revendications qui en dépendent, ou selon la revendication 3 et les revendications qui en dépendent, comprenant en outre un ou plusieurs conjugués d'un exopolysaccharide de *S. aureus* et d'une protéine de support.

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10. Vaccin pour l'utilisation selon les revendications 1, 2, 4 à 8, selon les revendications 3 à 8, comprenant en outre un ou plusieurs conjugués d'un polysaccharide capsulaire de *S. aureus* et d'une protéine de support.

5 11. Vaccin pour une utilisation selon la revendication 1 et les revendications qui en dépendent, ou selon la revendication 3 et les revendications qui en dépendent, sous forme lyophilisée.

12. Vaccin pour une utilisation selon les revendications 1, 2, 4 à 10, ou selon les revendications 3 à 10, sous forme aqueuse.

10 13. Procédé de préparation du vaccin selon la revendication 12, par reconstitution du vaccin selon la revendication 11 avec un matériau aqueux.

15 14. Vaccin pour une utilisation selon la revendication 1 et les revendications qui en dépendent, ou selon la revendication 3 et les revendications qui en dépendent, comprenant en outre un support et/ou un excipient pharmaceutique.

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FIGURE 1

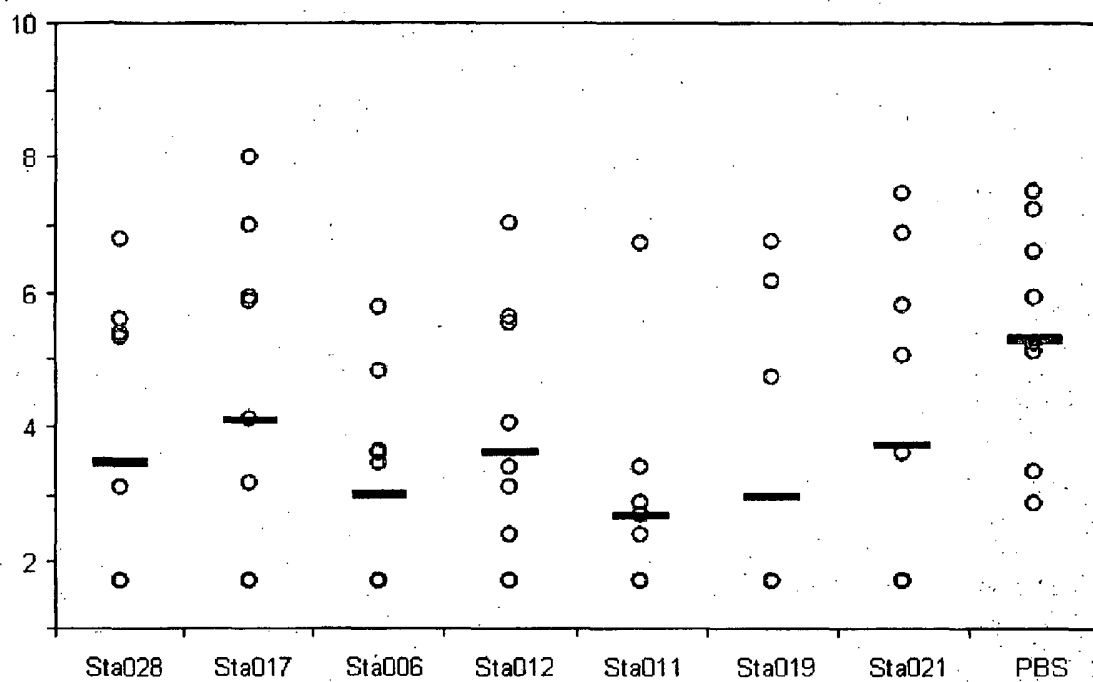


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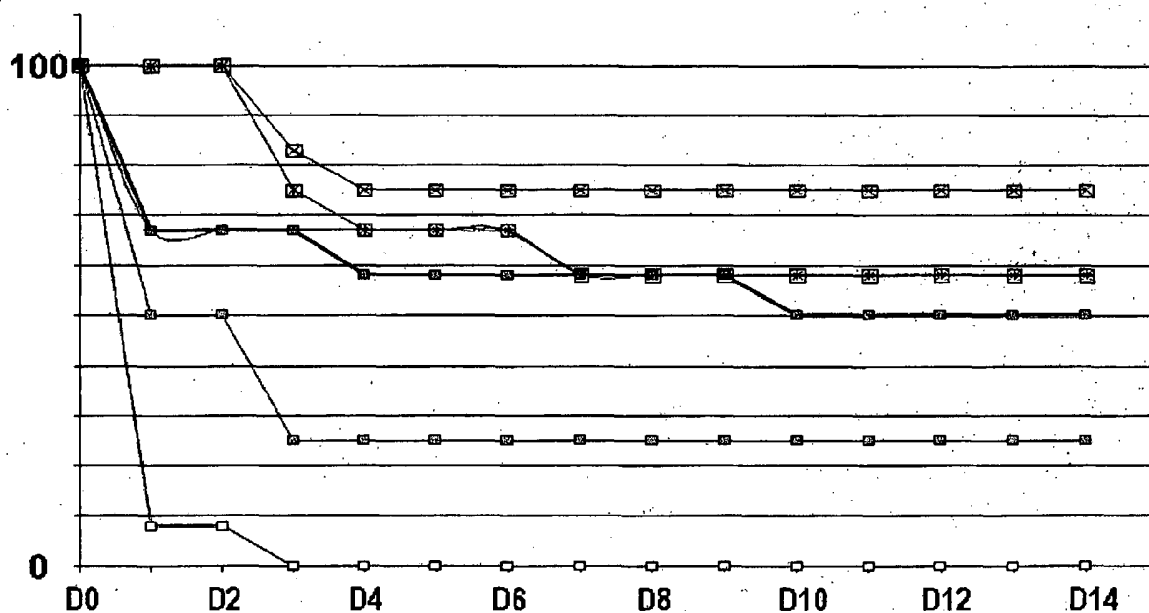


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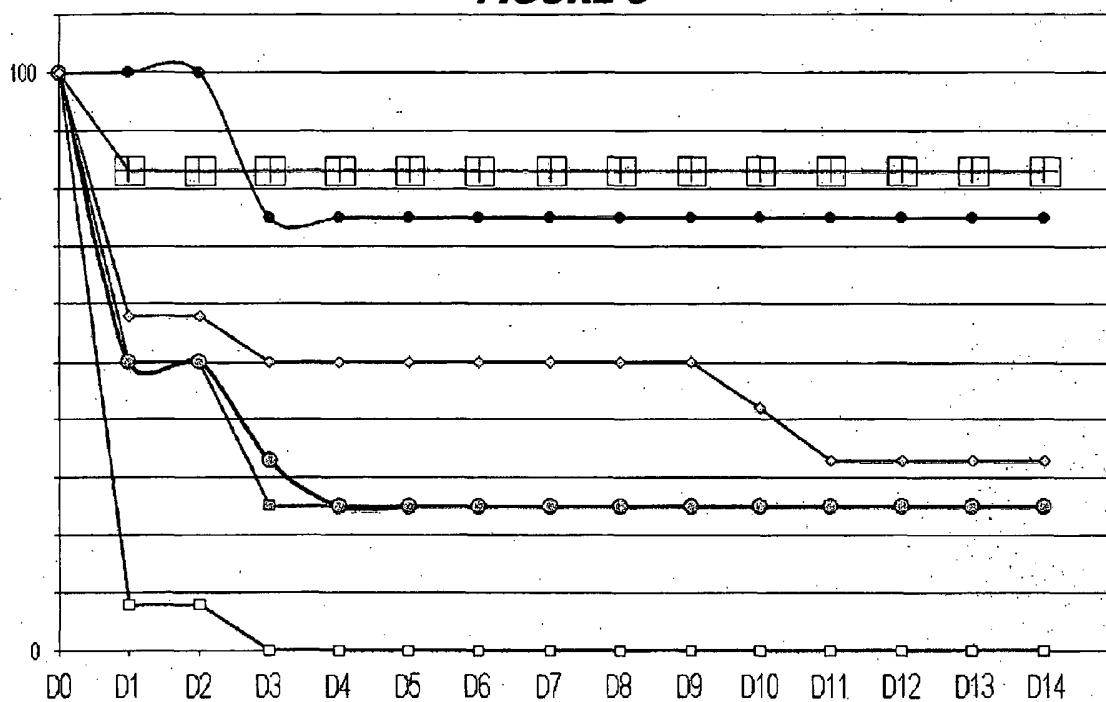


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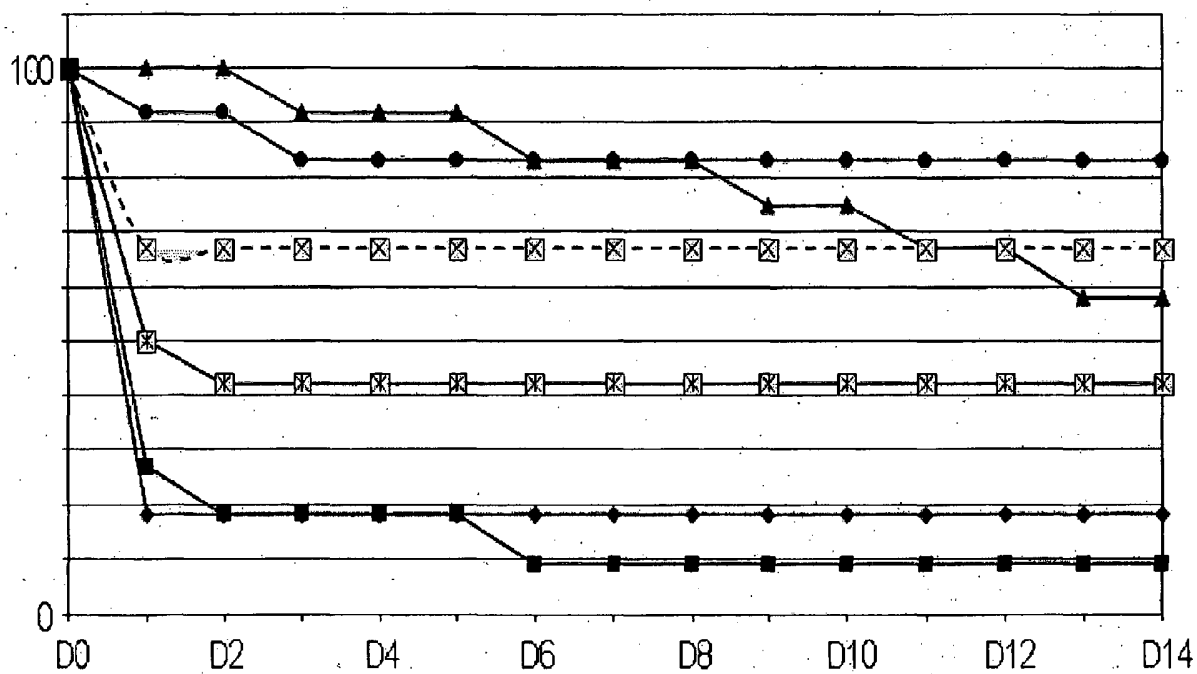


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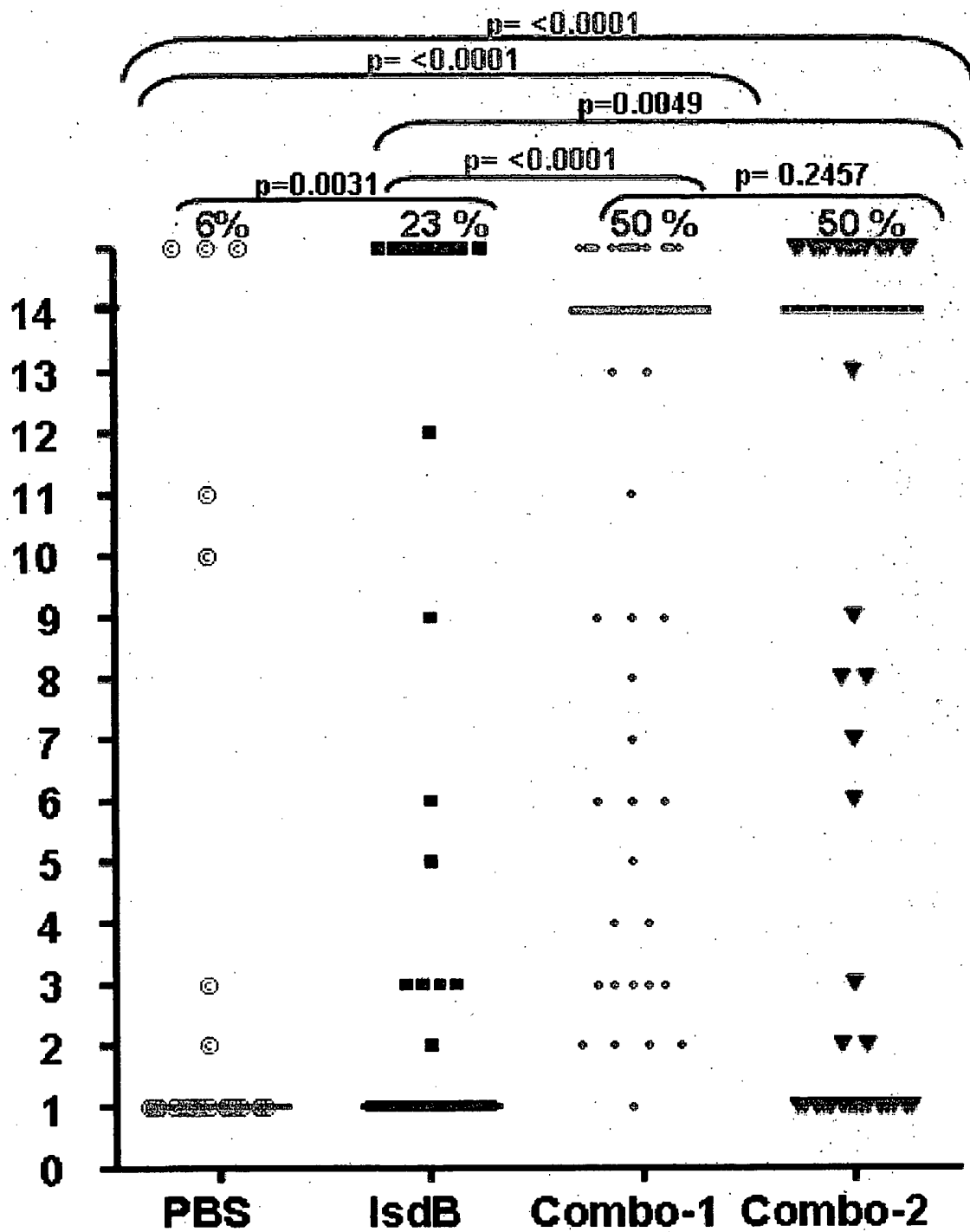


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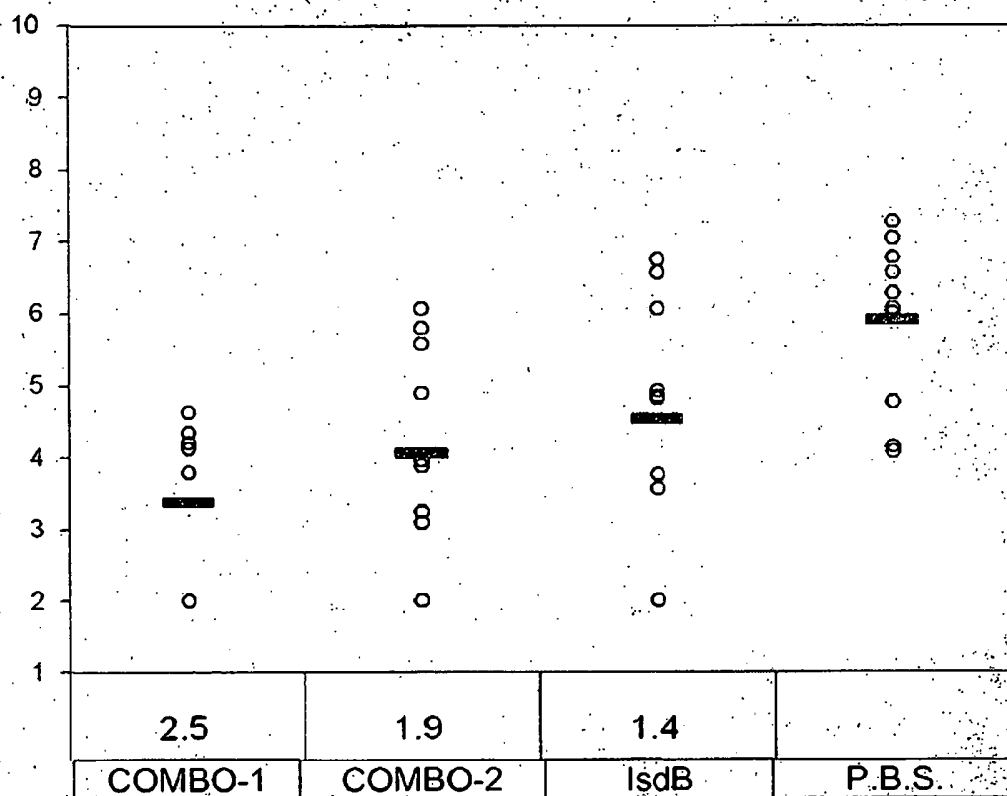


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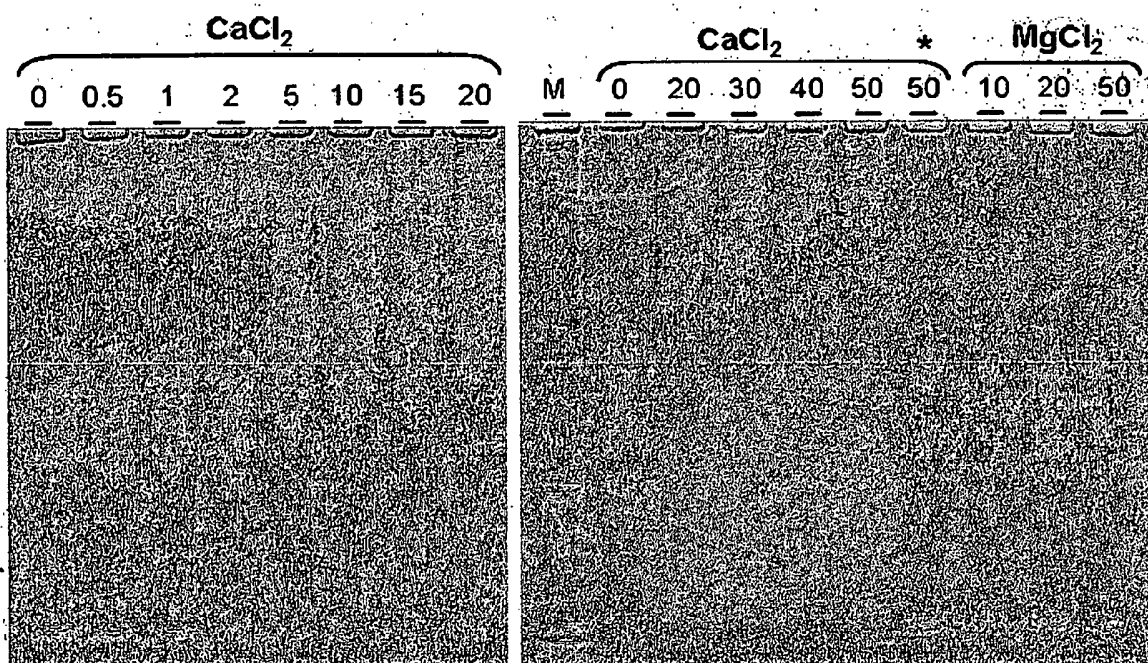


FIGURE 7

FIGURE 7A

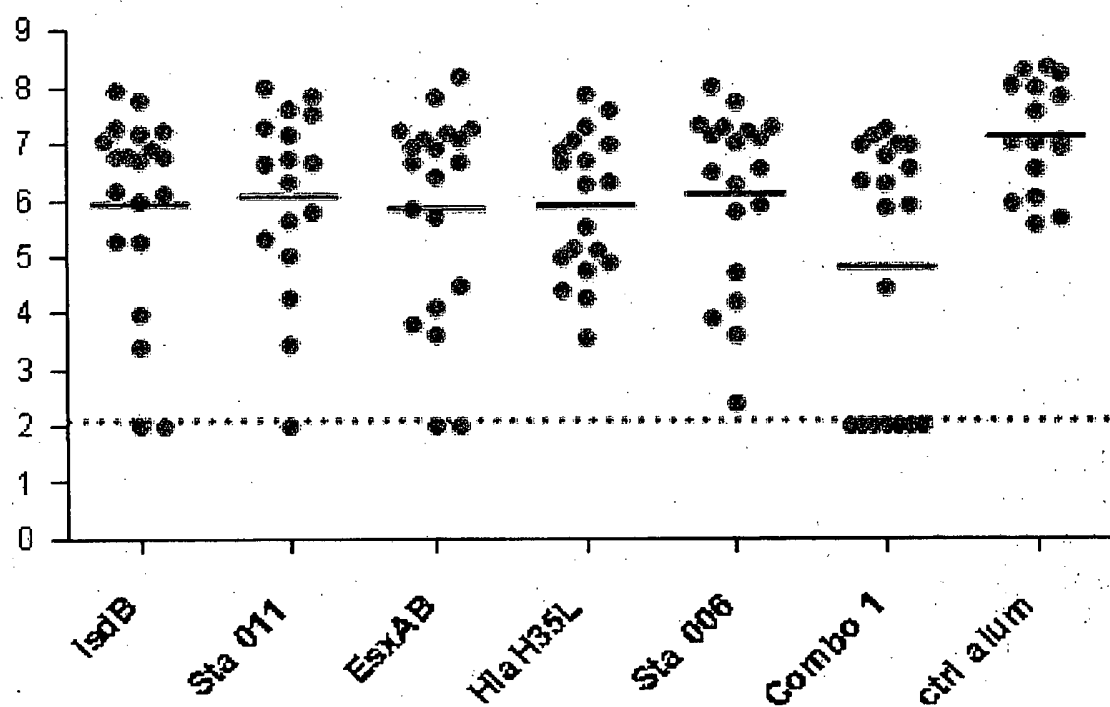


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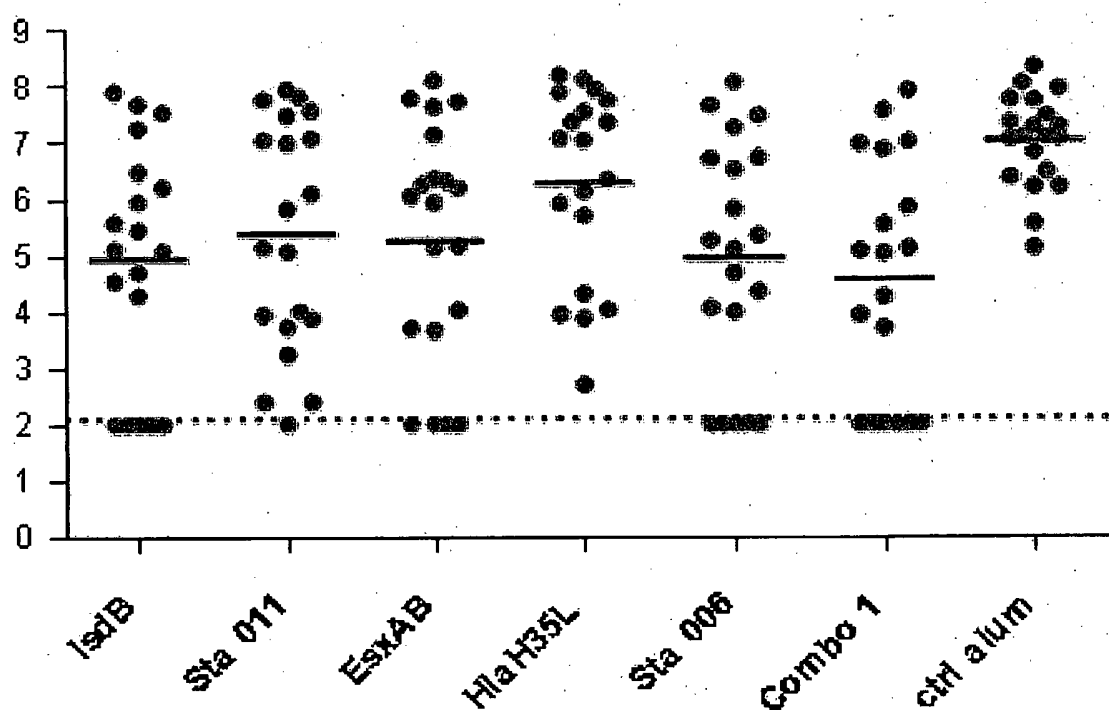


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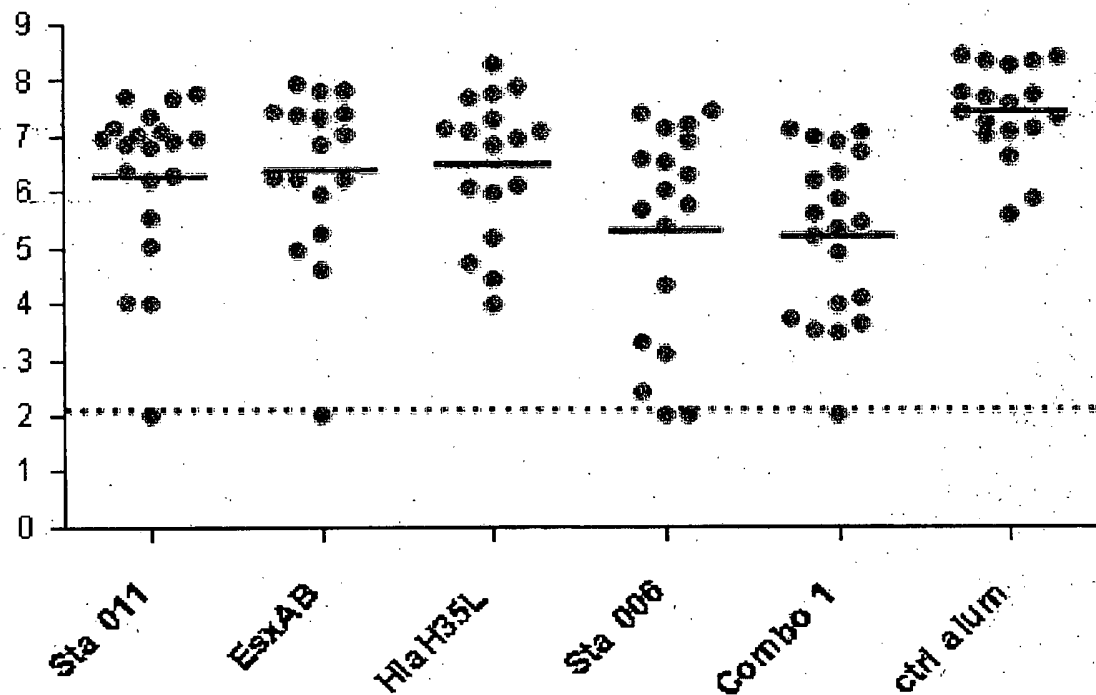


FIGURE 7D

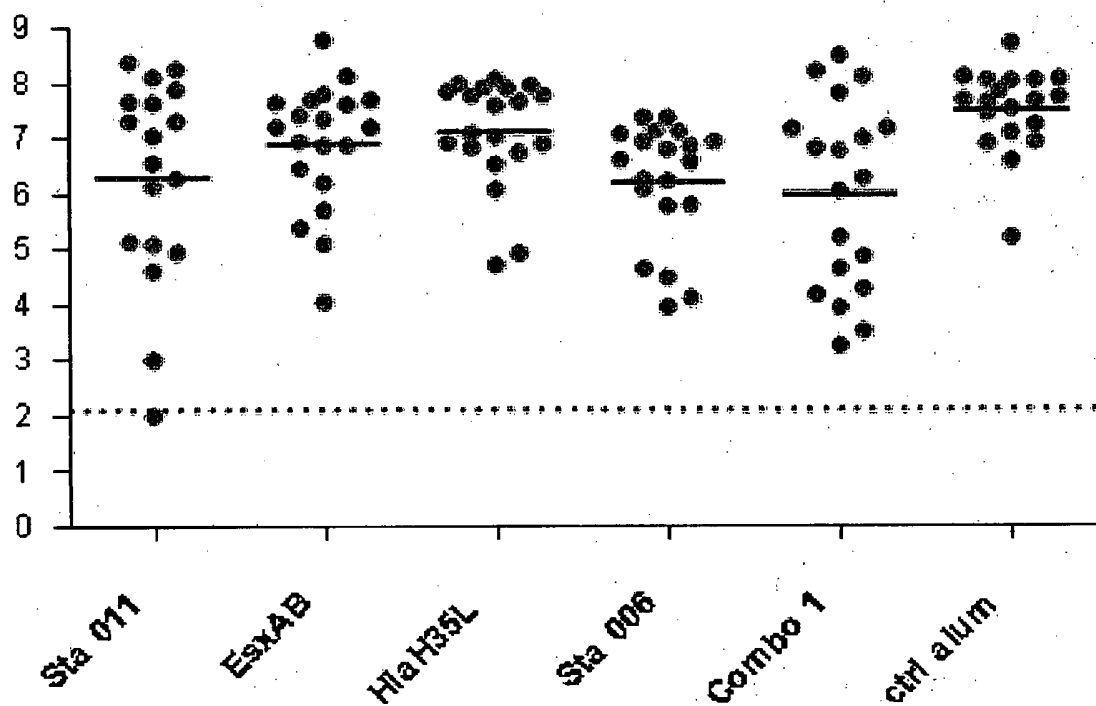


FIGURE 9

FIGURE 9A

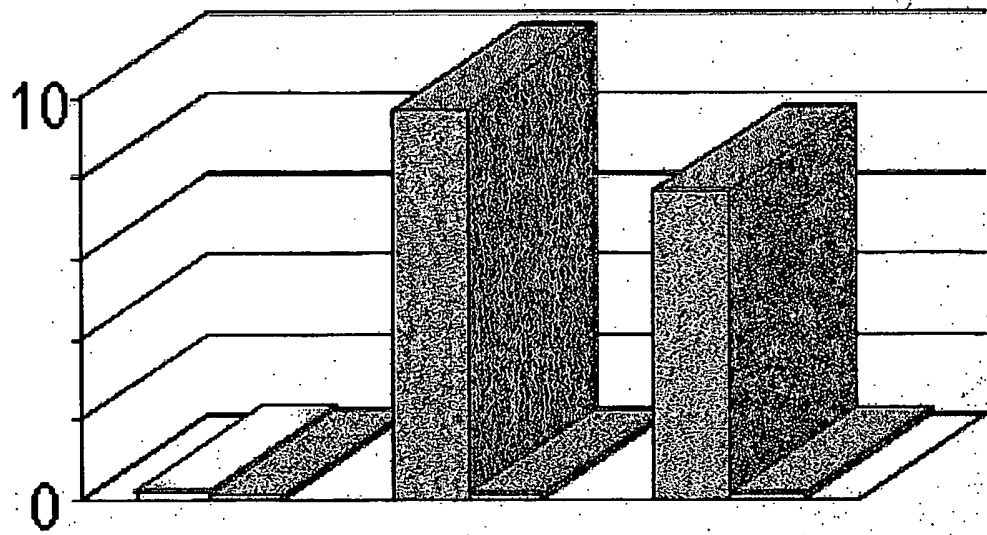


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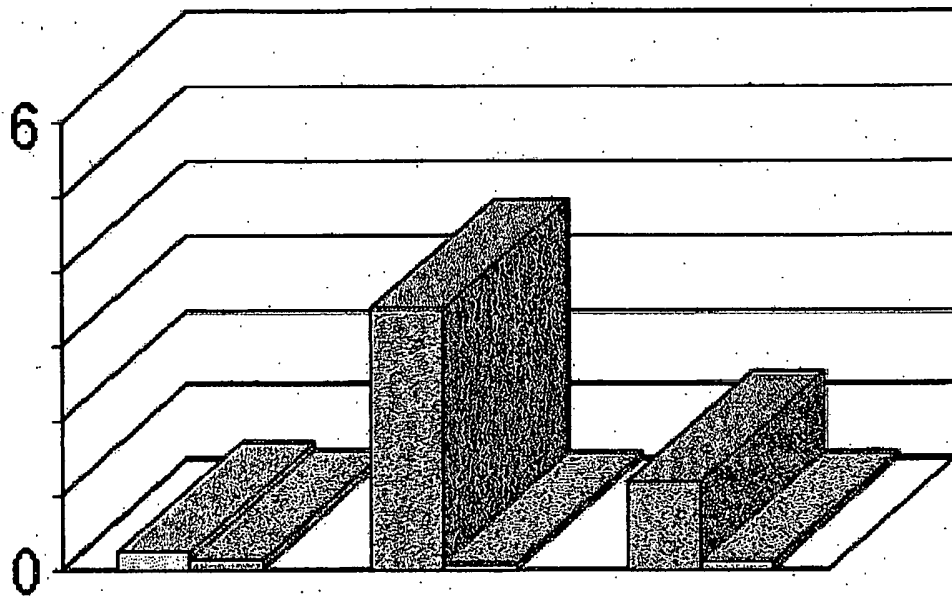


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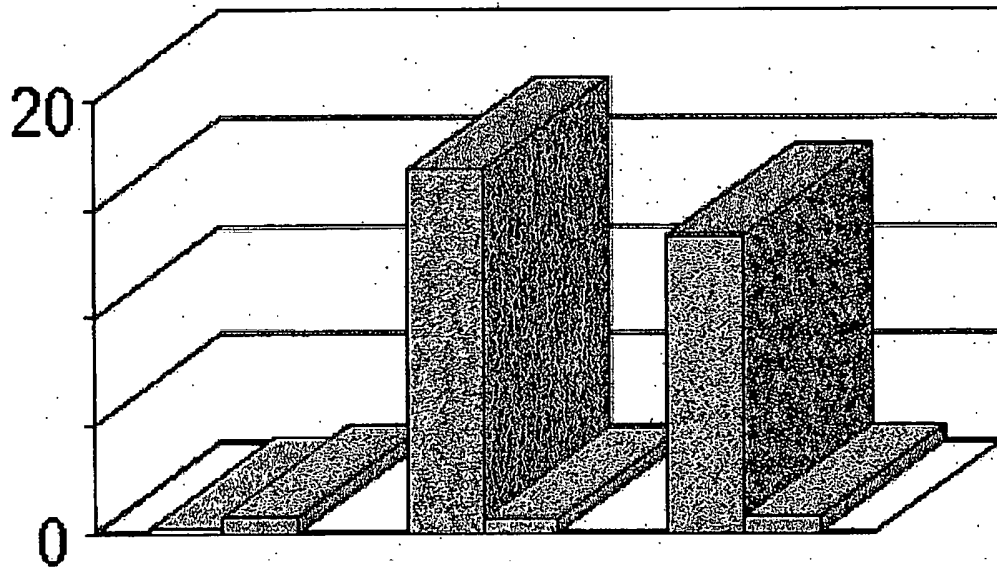


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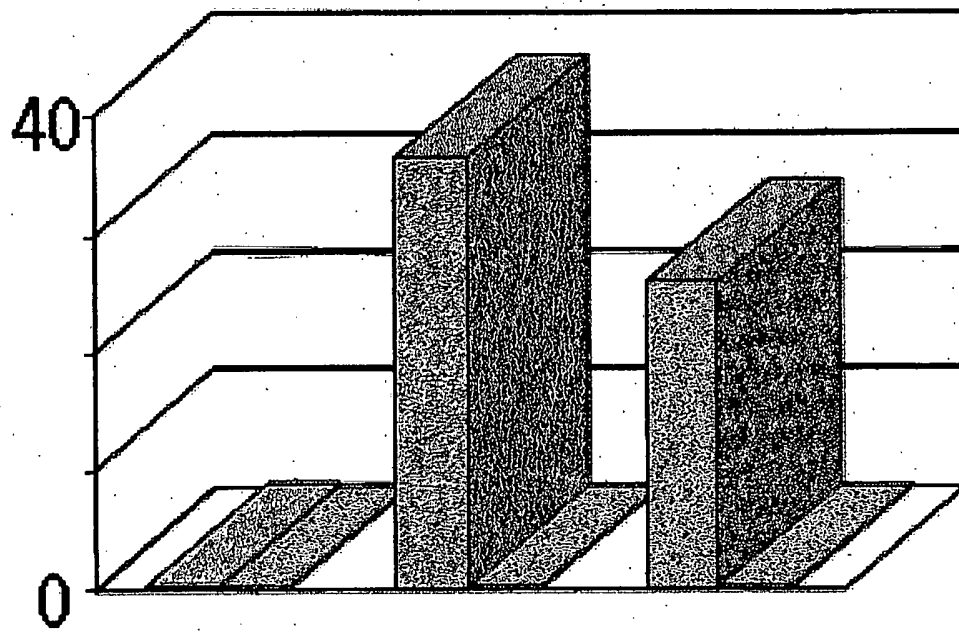


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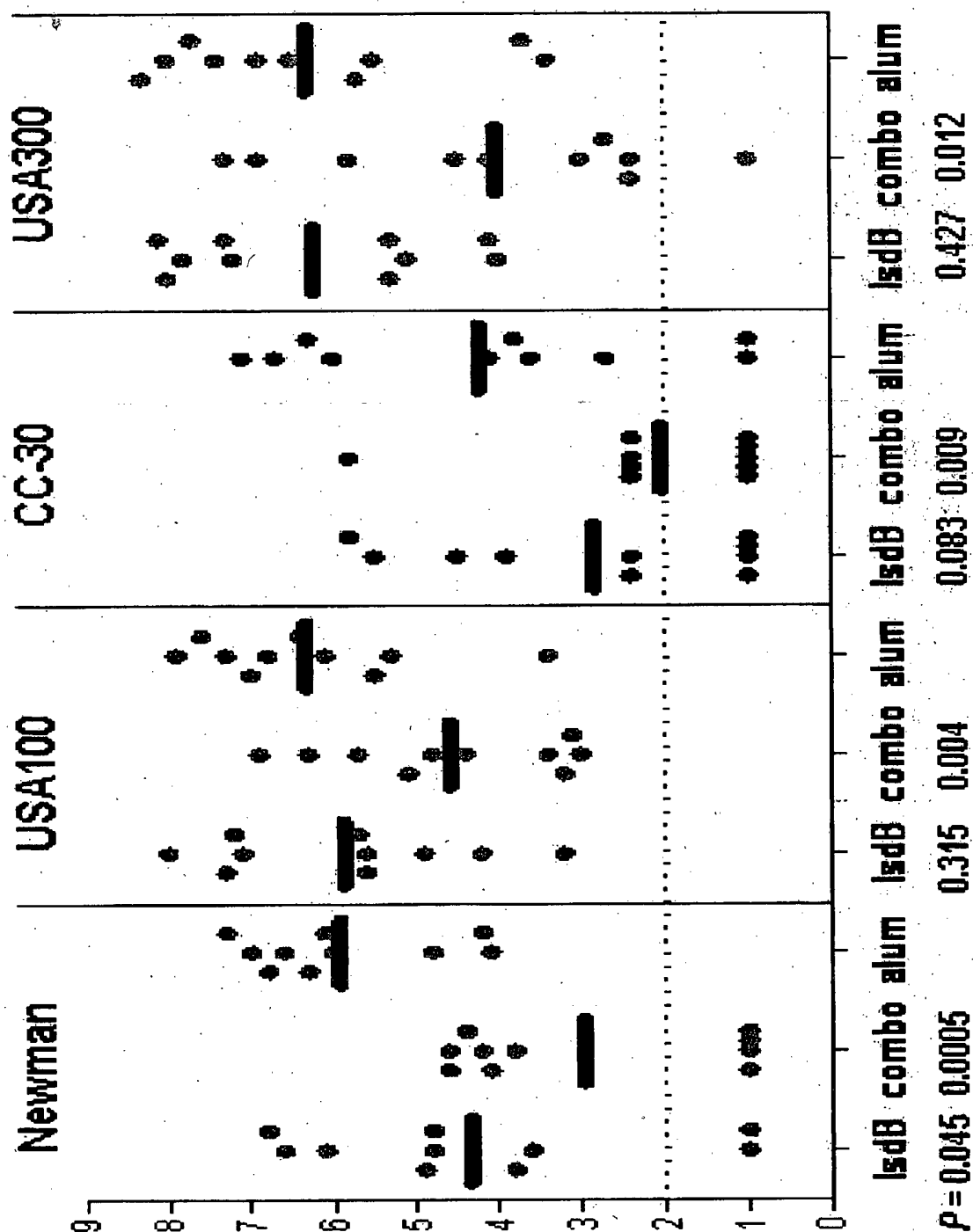


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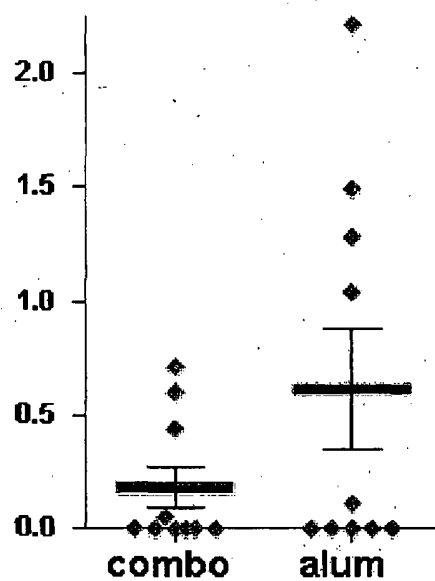
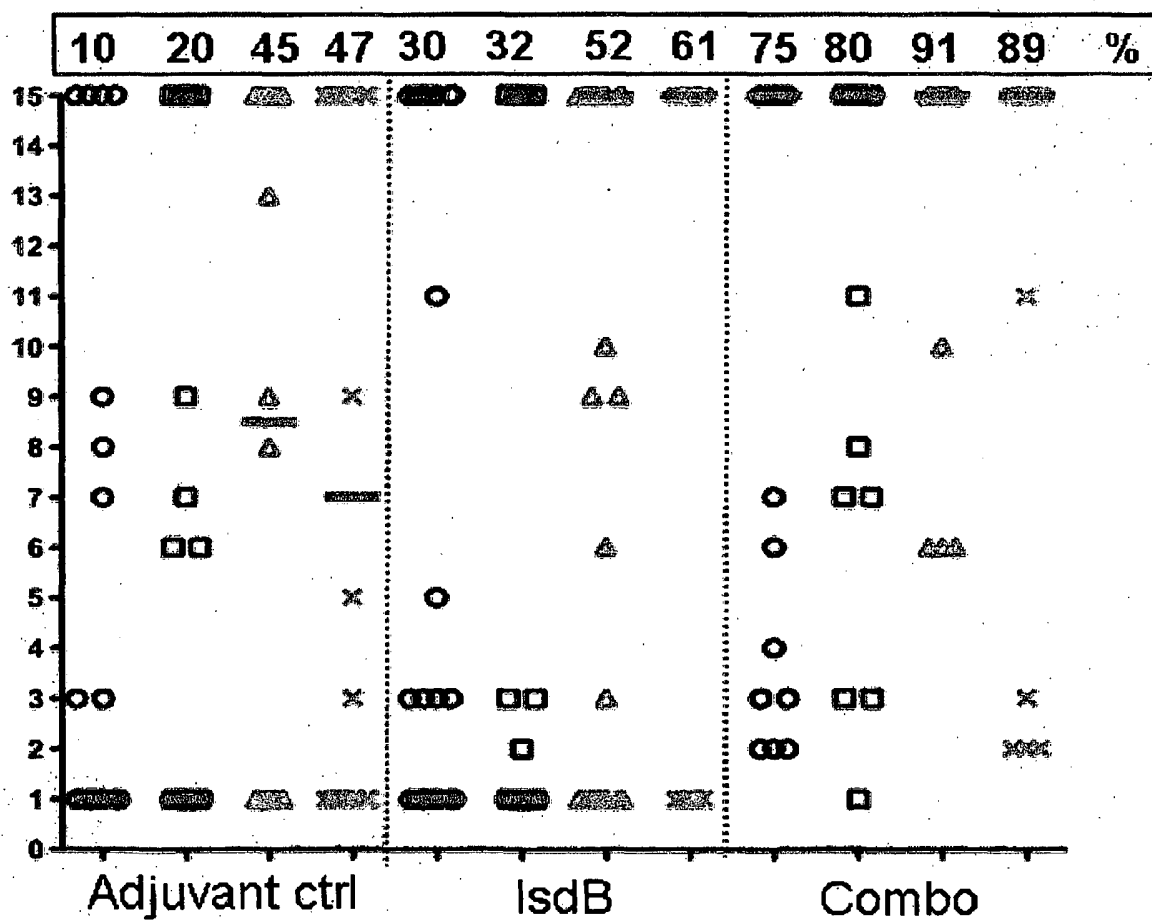


FIGURE 12





REFERENCES CITED IN THE DESCRIPTION

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Szabadalmi igénypontok

1. Oltóanyag, amely tartalmaz sta006 antigént, emlősben *S. aureus* fertőzés elleni védekezésre szolgáló eljárásban történő alkalmazásra, ahol a sta006 antigén tartalmaz olyan aminosav-szekvenciát, amely (i) (a) a SEQ ID NO: 42 szerinti szekvenciával 70%-ban vagy nagyobb mértékben azonos és/vagy (b) tartalmaz egy, a SEQ ID NO: 42 szerinti szekvencia legalább 'n' egymást követő aminosavaiból álló fragmenst, ahol 'n' értéke 7 vagy több és (ii) ahol a sta006 antigén képes kiváltani a SEQ ID NO: 42 szerinti szekvenciát felismerő ellenanyag képződését.

2. Az 1. igénypont szerinti oltóanyag az ott meghatározott alkalmazásra, amely tartalmaz adjuvánst is.

3. Oltóanyag, amely tartalmaz sta006 antigént és adjuvánst, ahol az sta006 antigén tartalmaz olyan aminosav-szekvenciát, amely (i) (a) a SEQ ID NO: 42 szerinti szekvenciával 70%-ban vagy nagyobb mértékben azonos és/vagy (b) tartalmaz egy, a SEQ ID NO: 42 szerinti szekvencia legalább 'n' egymást követő aminosavaiból álló fragmenst, ahol 'n' értéke 7 vagy több és (ii) ahol a sta006 antigén képes kiváltani a SEQ ID NO: 42 szerinti szekvenciát felismerő ellenanyag képződését.

4. Az 1. igénypont és az attól függő igénypontok bármelyike szerinti oltóanyag az ott meghatározott alkalmazásra vagy a 3. igénypont és az attól függő igénypontok bármelyike szerinti oltóanyag, ahol a sta006 antigén tartalmaz egy, a SEQ ID NO: 42 szerinti szekvenciával 80%-ban, 90%-ban vagy nagyobb mértékben azonos aminosav-szekvenciát.

5. Az 1. igénypont és az attól függő igénypontok bármelyike szerinti oltóanyag az ott meghatározott alkalmazásra vagy a 3. igénypont és az attól függő igénypontok bármelyike szerinti oltóanyag, ahol a sta006 antigén tartalmaz egy, a SEQ ID NO: 246 szerinti szekvenciával 90%-ban vagy nagyobb mértékben azonos aminosav-szekvenciát.

6. Az 1. igénypont és az attól függő igénypontok bármelyike szerinti oltóanyag az ott meghatározott alkalmazásra vagy a 3. igénypont és az attól függő igénypontok bármelyike szerinti oltóanyag, ahol a sta006 antigén tartalmaz egy, a SEQ ID NO: 248 szerinti szekvenciával 99%-ban vagy nagyobb mértékben azonos aminosav-szekvenciát.

7. A 2. igénypont és az attól függő igénypontok bármelyike szerinti oltóanyag az ott meghatározott alkalmazásra vagy a 3. igénypont és az attól függő igénypontok bármelyike szerinti oltóanyag, ahol az adjuváns alumínium-hidroxid.

8. Az 1. igénypont és az attól függő igénypontok bármelyike szerinti oltóanyag az ott meghatározott alkalmazásra vagy a 3. igénypont és az attól függő igénypontok bármelyike szerinti oltóanyag, ahol az oltóanyag tartalmaz hisztidimpuffert vagy foszfátpuffert.

9. Az 1. igénypont és az attól függő igénypontok bármelyike szerinti oltóanyag az ott meghatározott alkalmazásra vagy a 3. igénypont és az attól függő igénypontok bármelyike szerinti oltóanyag, amely tartalmazza továbbá egy vagy több *S. aureus* exopoliszacharid és hordozófehérje konjugátumát.

10. Az 1., 2., 4-8. igénypontok bármelyike szerinti oltóanyag az ott meghatározott alkalmazásra vagy a 3-8. igénypontok bármelyike szerinti oltóanyag, amely tartalmazza továbbá egy vagy több *S. aureus* kapszuláris poliszacharid és hordozófehérje konjugátumát.

11. Az 1. igénypont és az attól függő igénypontok bármelyike szerinti oltóanyag az ott meghatározott alkalmazásra vagy a 3. igénypont és az attól függő igénypontok bármelyike szerinti oltóanyag, liofilizált formában.

12. Az 1., 2., 4-10. igénypontok bármelyike szerinti oltóanyag az ott meghatározott alkalmazásra vagy a 3-10. igénypontok bármelyike szerinti oltóanyag, vizes formában.

13. Eljárás a 12. igénypont szerinti oltóanyag előállítására, a 11. igénypont szerinti oltóanyag vizes anyagban történő felvétele útján.

14. Az 1. igénypont és az attól függő igénypontok bármelyike szerinti oltóanyag az ott meghatározott alkalmazásra vagy a 3. igénypont és az attól függő igénypontok bármelyike szerinti oltóanyag, amely tartalmaz gyógyászati hordozót és/vagy segédanyagot is.

A meghatalmazott:

DANUBIA

Szabadalmi és Jogi Iroda Kft.

Dr. Fethő Árpád

szabadalmi ügyvivő