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(54) Title: COMPOSITIONS FOR IMMUNISING AGAINST STAPHYLOCOCCUS AERUS

(57) Abstract: An effective *Staphylococcus aureus* vaccine may require several antigenic components, and so various combinations of *S. aureus* antigens are identified for use in immunisation. These polypeptides may optionally be used in combination with *S.aureus* saccharides.



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COMPOSITIONS FOR IMMUNISING AGAINST STAPHYLOCOCCUS AUREUS**TECHNICAL FIELD**

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

BACKGROUND ART

- 5 *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.
- 10 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.

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.

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

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.

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.

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.

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, sta120, 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.

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

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.

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.

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.

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.

5 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.

10 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.

15 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.

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.

20 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.

25 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.

30 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
35 is sometimes referred to herein as the 'sixth antigen group'.

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.

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.

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.

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).

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.

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: 151; 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.

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.

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).

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.

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

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)
- Laminin receptor
- MAP
- MntC (also known as SitC)
- MRPII
- Npase
- ORF0594
- ORF0657n
- ORF0826
- PBP4
- RAP (RNA III activating protein)

- Sai-1
- SasK
- SBI
- SdrG
- 5 • SdrH
- SSP-1
- SSP-2
- Vitronectin-binding protein

Combinations with saccharides

10 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

15 (2) one or more conjugates of a *S.aureus* exopolysaccharide and a carrier protein.

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.

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.

30 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 FucNAc in their repeat unit as well as ManNAcA which can be used to introduce a sulfhydryl 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 $\rightarrow$.
 5 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].

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;
- 10 (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.

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
 15 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],
 20 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.

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

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

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
 30 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
 35 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].

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.

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

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*.

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

First antigen group*clfA*

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).

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.

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

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).

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

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).

- 10 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

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).

- 25 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

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).

- Useful ebhA antigens can elicit an antibody (*e.g.* when administered to a human) that recognises
- 5 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.
- 10 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
- 15 protein domains.

ebpS

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).

- 20 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,
- 25 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 (*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
- 30 protein domains.

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

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).

- 5 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, 10 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

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).

- 20 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, 25 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 30 of SEQ ID NO: 8 can usefully be omitted. Other fragments omit one or more protein domains.

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

- 35 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).

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

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).

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

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).

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

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.

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.

SEQ ID NOs: 166 ('FnBA₁₋₅₁₁') and 167 ('FnBA₅₁₂₋₉₅₃') are useful fragments of SEQ ID NO: 12. These fragments are more easily used at an industrial scale.

FnBB

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).

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

The 'Hla' antigen is the 'alpha-hemolysin precursor' also known as 'alpha toxin' or simply 'hemolysin'.

- 5 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.
- 10 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, 15 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.

- 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.
- 30 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).
- 35 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).

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

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.

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.

10 *hlgB*

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).

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

25 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).

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

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).

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.

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.

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.

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

isdB

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.

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 18.

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

In some embodiments, compositions of the invention do not include an *isdB* antigen.

isdC

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).

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, 60, 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.

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

isdG

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).

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

- 10 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.

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.

- 25 Reference 59 discloses antigens which usefully include epitopes from both IsdB and IsdH.

isdI

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).

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

- 5 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).

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%,
10 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
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: 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.

20 *lukE*

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).

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%,
25 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
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: 24 while retaining at least one epitope of SEQ ID NO: 24. Other fragments omit one or more protein domains.

lukF

- 35 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

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).

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

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).

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.

5 *sasA*

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).

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.

20 *sasB*

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

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

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).

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

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).

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 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 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

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).

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 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 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

- 10 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).

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 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 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.

SEQ ID NO: 164 is a useful fragment of SEQ ID NO: 33 ('SdrC₅₁₋₅₁₈'). 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.

sdrD

- 30 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).

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.*

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

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).

Useful sdrE2 antigens can elicit an antibody (*e.g.* when administered to a human) that recognises 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.*

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

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 anti-parallel 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.

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.

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

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.

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).

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 peptides.

Second antigen group

sta001

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.

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

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).

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.

- 10 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

- 15 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).

- 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

- 30 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).

- 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

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).

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

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).

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.

5 *sta007*

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.

- 10 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, 15 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-
20 terminal amino acids of SEQ ID NO: 43 can usefully be omitted. Other fragments omit one or more protein domains.

sta008

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
25 strain it is nwmn_2270 (GI:151222482).

- 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, 30 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
35 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

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).

- 5 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

- 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.

- 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

- 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).

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.

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.

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

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).

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

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).

- 5 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, 10 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 15 omit one or more protein domains.

sta014

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).

- Useful sta014 antigens can elicit an antibody (*e.g.* when administered to a human) that recognises 20 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. 25 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 30 protein domains.

sta015

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).

- 35 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.

- 5 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
10 protein domains.

sta016

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).

- Useful sta016 antigens can elicit an antibody (e.g. when administered to a human) that recognises
15 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.
20 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

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).

- Useful sta017 antigens can elicit an antibody (e.g. when administered to a human) that recognises
30 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.
35 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

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).

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

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).

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.

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

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).

Useful sta020 antigens can elicit an antibody (e.g. when administered to a human) that recognises
 5 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.

10 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
 15 protein domains.

sta021

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).

Useful sta021 antigens can elicit an antibody (e.g. when administered to a human) that recognises
 20 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.

25 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 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
 30 protein domains.

sta022

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).

Useful sta022 antigens can elicit an antibody (e.g. when administered to a human) that recognises
 35 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.

sta023

- 10 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).

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.

sta024

- 25 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).

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.

sta025

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

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
10 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
15 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

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).

20 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,
25 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-
30 terminal amino acids of SEQ ID NO: 62 can usefully be omitted. Other fragments omit one or more
protein domains.

sta027

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).

35 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.

- 5 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
10 protein domains.

sta028

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).

- 15 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,
20 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-
25 terminal amino acids of SEQ ID NO: 64 can usefully be omitted. Other fragments omit one or more protein domains.

sta029

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).

- 30 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,
35 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.

5 *sta030*

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).

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.* 10 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 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: 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

20 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).

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.* 25 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- 30 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

35 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).

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

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).

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

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).

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.

5 *sta035*

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).

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.

20 *sta036*

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).

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

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

- 5 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

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

- 20 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

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).

- 35 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

- 10 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).

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

- 25 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).

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

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).

Useful sta042 antigens can elicit an antibody (*e.g.* when administered to a human) that recognises

- 5 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.
- 10 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
- 15 protein domains.

sta043

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).

Useful sta043 antigens can elicit an antibody (*e.g.* when administered to a human) that recognises

- 20 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.
- 25 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
- 30 protein domains.

sta044

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).

Useful sta044 antigens can elicit an antibody (*e.g.* when administered to a human) that recognises

- 35 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 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.

10 *sta045*

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).

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 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.

sta046

25 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).

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 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.

sta047

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).

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 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.

sta048

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).

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

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).

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.

10 *sta050*

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).

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.

25 *sta051*

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).

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

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

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

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).

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

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

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).

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

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).

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.

5 *sta057*

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).

Useful sta057 antigens can elicit an antibody (*e.g.* when administered to a human) that recognises
 10 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
 15 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.

20 *sta058*

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).

Useful sta058 antigens can elicit an antibody (*e.g.* when administered to a human) that recognises
 25 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
 30 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

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).

- Useful sta059 antigens can elicit an antibody (*e.g.* when administered to a human) that recognises
- 5 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.
- 10 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
- 15 protein domains.

sta060

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).

- 20 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.
- 25 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
- 30 protein domains.

sta061

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).

- 35 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.

- 5 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
10 protein domains.

sta062

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).

Useful sta062 antigens can elicit an antibody (e.g. when administered to a human) that recognises
15 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.

- 20 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
25 protein domains.

sta063

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).

Useful sta063 antigens can elicit an antibody (e.g. when administered to a human) that recognises
30 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.

- 35 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 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).

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
10 (*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
15 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.

20 *sta065*

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).

Useful sta065 antigens can elicit an antibody (*e.g.* when administered to a human) that recognises
25 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
30 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
35 more protein domains.

sta066

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).

Useful sta066 antigens can elicit an antibody (e.g. when administered to a human) that recognises
 5 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
 10 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
 15 more protein domains.

sta067

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).

Useful sta067 antigens can elicit an antibody (e.g. when administered to a human) that recognises
 20 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
 25 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 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
 30 more protein domains.

sta068

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).

Useful sta068 antigens can elicit an antibody (e.g. when administered to a human) that recognises
 35 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 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.

sta069

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).

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 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.

sta070

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).

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 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.

5 *sta071*

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).

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
 10 (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, 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
 15 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.

20 *sta072*

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).

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
 25 (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
 30 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

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.

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.

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

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

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).

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

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).

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

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).

Useful sta076 antigens can elicit an antibody (e.g. when administered to a human) that recognises 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

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.

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

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).

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

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

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

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

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
10 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
15 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

20 The 'sta081' antigen is annotated as 'serine protease SplD (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).

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
25 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
30 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

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

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

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).

Useful sta083 antigens can elicit an antibody (e.g. when administered to a human) that recognises 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 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 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

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).

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) 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 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

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).

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) 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 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

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).

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) 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.

sta087

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).

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.

sta088

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).

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.

sta089

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).

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.

sta090

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).

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.

sta091

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).

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.

sta092

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).

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.

sta093

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).

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.

sta094

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).

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: 129 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

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).

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

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).

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.

5 *sta097*

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).

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
10 (*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
15 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.

20 *sta098*

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).

Useful sta098 antigens can elicit an antibody (*e.g.* when administered to a human) that recognises
25 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
30 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
35 more protein domains.

sta099

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).

Useful sta099 antigens can elicit an antibody (e.g. when administered to a human) that recognises
 5 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:
 10 134. 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
 15 more protein domains.

sta100

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).

Useful sta100 antigens can elicit an antibody (e.g. when administered to a human) that recognises
 20 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:
 25 135. 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
 30 more protein domains.

sta101

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 nwmm_0394 (GI:151220606).

35 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

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).

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

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).

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

- 5 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).

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%, 10 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 15 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

- 20 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).

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%, 25 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 30 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

- 35 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).

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) 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 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

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).

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) 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 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

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).

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) 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 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

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).

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) 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 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.

sta110

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).

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.

sta111

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).

- Useful sta111 antigens can elicit an antibody (*e.g.* when administered to a human) that recognises
- 5 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.
- 10 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
- 15 more protein domains.

sta112

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).

- 20 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
- 25 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
- 30 17 N-terminal amino acids of SEQ ID NO: 182 can usefully be omitted. Other fragments omit one or more protein domains.

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

sta113

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

Useful *stal13* 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, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These *stal13* 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.

stal14

The '*stal14*' antigen is annotated as 'hypothetical protein'. In the NCTC 8325 strain *stal14* is SAOUHSC_00810 and has amino acid sequence SEQ ID NO: 184 (GI:88194570).

Useful *stal14* 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 *stal14* 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.

stal15

The '*stal15*' antigen is annotated as 'hypothetical protein'. In the NCTC 8325 strain *stal15* is SAOUHSC_00817 and has amino acid sequence SEQ ID NO: 185 (GI:88194576).

Useful *stal15* 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 *stal15* 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.

5 *sta116*

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).

Useful *sta116* antigens can elicit an antibody (*e.g.* when administered to a human) that recognises
 10 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.
 15 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
 20 more protein domains.

sta117

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).

Useful *sta117* antigens can elicit an antibody (*e.g.* when administered to a human) that recognises
 25 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
 30 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

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).

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

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).

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

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).

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

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).

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

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).

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

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).

Useful NW_10 antigens can elicit an antibody (*e.g.* when administered to a human) that recognises

- 5 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.
- 10 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
- 15 more protein domains.

NW_7

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).

Useful NW_7 antigens can elicit an antibody (*e.g.* when administered to a human) that recognises

- 20 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.
- 25 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
- 30 more protein domains.

NW_8

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).

Useful NW_8 antigens can elicit an antibody (*e.g.* when administered to a human) that recognises

- 35 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.

10 NW_2

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).

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.

25 NW_1

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).

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

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

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
10 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
15 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

Antigens used in the invention may be present in the composition as individual separate
20 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
25 only one expression and purification need be employed in order to produce two polypeptides which are both antigenically useful.

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
30 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.

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,
35 or five antigens are preferred, such as two or three antigens.

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.

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

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.

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-.

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.

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).

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).

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).

Another hybrid polypeptide of the invention may include both IsdA and EsxA antigens. These may be in either order, N- to C- terminus. SEQ ID NO: 204 ('IsdA-EsxA') is an example of such a hybrid, having a hexapeptide linker ASGGGS (SEQ ID NO: 173). SEQ ID NO: 209 ('isdA40-184-esxA') is another example of such a hybrid, in which IsdA₄₀₋₁₈₄ is joined to EsxA via linker ASGGGS (SEQ ID NO: 173).

Another hybrid polypeptide of the invention may include both IsdA and sta006 antigens. These may be in either order, N- to C- terminus. SEQ ID NO: 221 ('isdA40-184-sta006') is an example of such a hybrid, in which IsdA₄₀₋₁₈₄ is joined to Sta006 via hexapeptide linker ASGGGS (SEQ ID NO: 173).

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).

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).

Another hybrid polypeptide of the invention may include IsdA and EsxA and EsxB antigens. These may be in any order, N- to C- terminus. SEQ ID NO: 210 ('isdA40-184-esxAB') is an example of such a triple hybrid, in which IsdA₄₀₋₁₈₄ 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 ('IsdA-esxAB') is another example of such a triple hybrid, in which IsdA is joined to EsxAB via linker ASGGGS (SEQ ID NO: 173).

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.

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.

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 IsdA and wild-type EsxA, or which recognise both wild-type IsdA 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

IsdA 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

5 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.*).

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.

10 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 staphylococcal 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
15 antigens in the compositions are separated from the whole organism with which the molecule is expressed.

Polypeptides used with the invention are preferably staphylococcal polypeptides.

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
20 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
25 can occur as single chains or associated chains.

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
30 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).

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
35 induce polypeptide expression.

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*,
5 *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.

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.

10 **Nucleic acids**

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.

The invention also provides nucleic acid comprising nucleotide sequences having sequence identity
15 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.

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
20 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%;
25 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.).

In some embodiments, nucleic acid of the invention hybridizes to a target under low stringency
30 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.

35 The invention includes nucleic acid comprising sequences complementary to these sequences (e.g. for antisense or probing, or for use as primers).

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.

5 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.

10 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.

15 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.*

20 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.

25 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.

30 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
35 "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.

- 5 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.

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).

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.

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.

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

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

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).

- 25 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).

30 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

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.

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.*

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.

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].

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) $X_1=X_2 \neq X_3$ (iii) $X_1 \neq X_2=X_3$ (iv) $X_1 \neq X_2 \neq X_3$ or (v) $X_1=X_3 \neq X_2$, etc.

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.

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

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%.

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.

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

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.

10 ***Immunogenic compositions and medicaments***

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.

- 15 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.

- 20 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.

- 25 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.

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

- 30 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.*

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.

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.

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.

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.

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.

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.

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.

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).

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.

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

A. *Mineral-containing compositions*

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].

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.

A fibrous morphology (*e.g.* as seen in transmission electron micrographs) is typical for aluminium hydroxide adjuvants. The pI 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.

Aluminium phosphate adjuvants generally have a PO_4/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 PO_4/Al molar ratio between 0.84 and 0.92, included at $0.6\text{mg Al}^{3+}/\text{ml}$. 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 $0.5\text{-}20\mu\text{m}$ (*e.g.* about $5\text{-}10\mu\text{m}$) after any antigen adsorption. Adsorptive capacities of between $0.7\text{-}1.5\text{ mg protein per mg Al}^{+++}$ at pH 7.4 have been reported for aluminium phosphate adjuvants.

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.

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.

- 5 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.
- 10 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. $\geq 5:1$, $\geq 6:1$, $\geq 7:1$, $\geq 8:1$, $\geq 9:1$, etc.

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
 15 between 0.3 and 1mg/ml. A maximum of 0.85mg/dose is preferred.

B. Oil Emulsions

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
 20 adjuvant (CFA) and incomplete Freund's adjuvant (IFA) may also be used.

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 μ m in diameter, and ideally have a sub-micron diameter, with these small sizes being achieved with a microfluidiser to provide
 25 stable emulsions. Droplets with a size less than 220nm are preferred as they can be subjected to filter sterilization.

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
 30 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
 35 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.

Surfactants can be classified by their 'HLB' (hydrophile/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 DOWFAX™ 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 Tergitol™ 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.

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.

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%.

Preferred emulsion adjuvants have an average droplets size of <1µm *e.g.* ≤750nm, ≤500nm, ≤400nm, ≤300nm, ≤250nm, ≤220nm, ≤200nm, or smaller. These droplet sizes can conveniently be achieved by techniques such as microfluidisation.

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 squalane, 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% squalane, 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% squalane, 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].

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.

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.

5 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
10 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]

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
15 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™.

20 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].

Combinations of saponins and cholesterol can be used to form unique particles called
25 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].

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

D. Virosomes and virus-like particles

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
35 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, ϕ -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

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.

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].

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.

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.

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 analogue substitutions *e.g.* replacement of guanosine with 2'-deoxy-7-deazaguanosine. The adjuvant effect of CpG oligonucleotides is further discussed in refs. 123-128.

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.

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.

A useful CpG adjuvant is CpG7909, also known as ProMuneTM (Coley Pharmaceutical Group, Inc.). Another is CpG1826. 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.

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) CpI 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.

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, specifically incorporated herein by reference in its entirety.

F. Human immunomodulators

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

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*

Microparticles may also be used as adjuvants in the invention. Microparticles (*i.e.* a particle of
5 ~100nm to ~150µm in diameter, more preferably ~200nm to ~30µm in diameter, and most preferably
~500nm to ~10µm 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
10 detergent, such as CTAB).

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

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

J. *Polyoxyethylene ether and polyoxyethylene ester formulations*

Adjuvants suitable for use in the invention include polyoxyethylene ethers and polyoxyethylene
15 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-
20 lauryl ether, polyoxyethylene-35-lauryl ether, and polyoxyethylene-23-lauryl ether.

K. *Phosphazenes*

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

L. *Muramyl peptides*

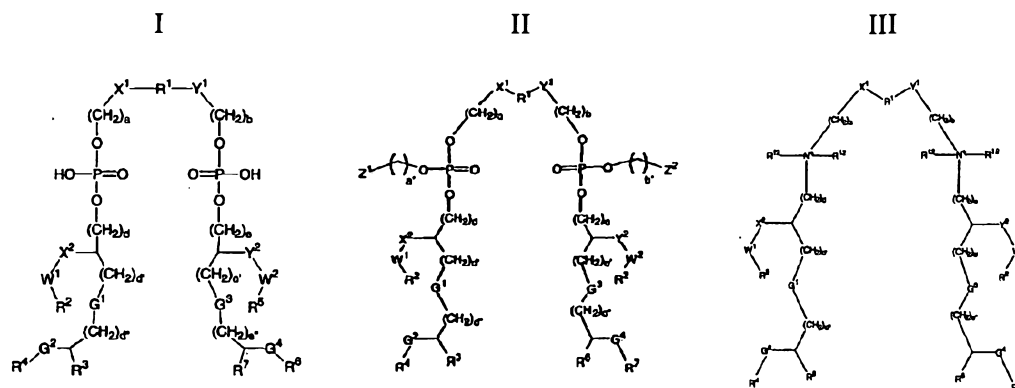
25 Examples of muramyl peptides suitable for use as adjuvants in the invention include N-acetyl-
muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine
(nor-MDP), and N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-*sn*-
glycero-3-hydroxyphosphoryloxy)-ethylamine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

M. *Imidazoquinolone Compounds.*

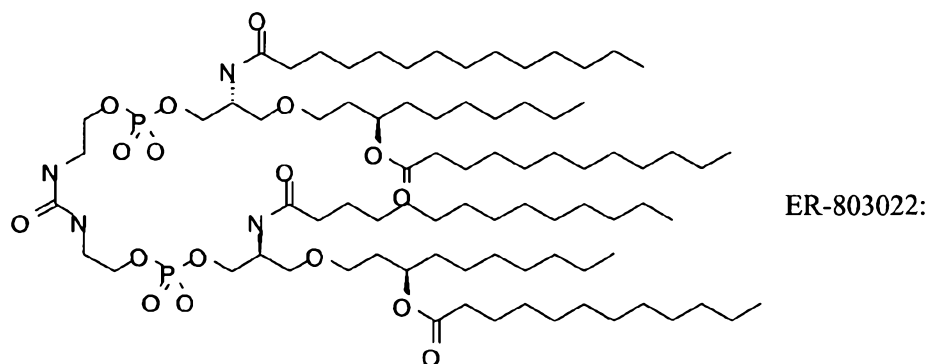
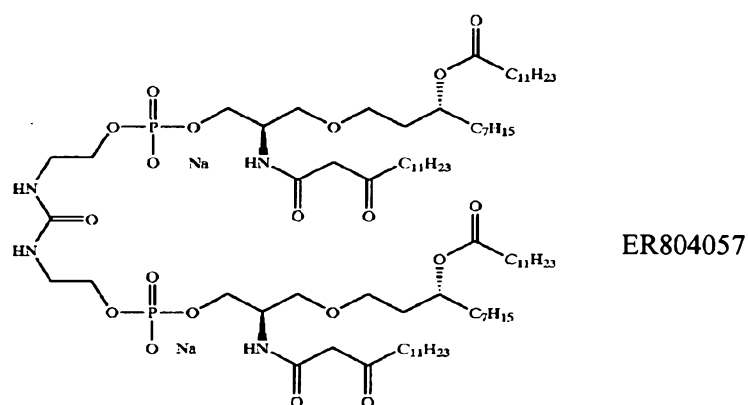
30 Examples of imidazoquinolone compounds suitable for use adjuvants in the invention include
Imiquimod ("R-837") [164,165], Resiquimod ("R-848") [166], and their analogs; and salts thereof
(*e.g.* the hydrochloride salts). Further details about immunostimulatory imidazoquinolines can be
found in references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

N. *Substituted ureas*

35 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.:



5 O. Further adjuvants

Further adjuvants that may be used with the invention include:

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

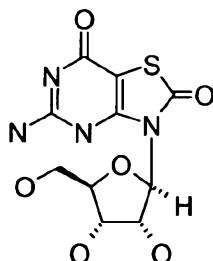
Cyclic diguanylate ('c-di-GMP'), which has been reported as a useful adjuvant for *S.aureus* vaccines [175].

- 10 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 .

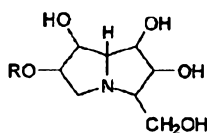
A tryptanthrin compound, such as those disclosed in reference 177. Methods of formulating, manufacturing, and screening for active compounds are also described in reference 177. The thiosemicarbazones are particularly effective in the stimulation of human peripheral blood mononuclear cells for the production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

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



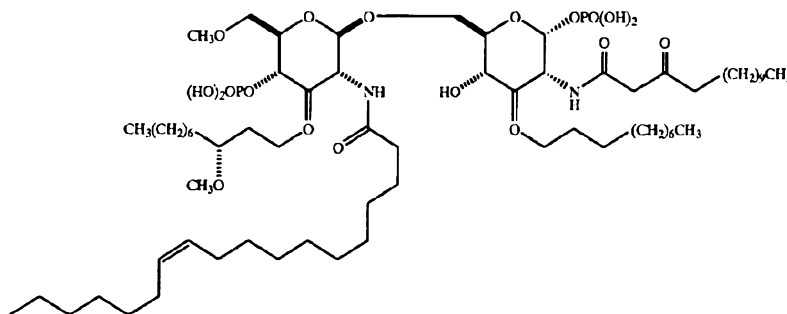
and prodrugs thereof; (b) ANA975; (c) ANA-025-1; (d) ANA380; (e) the compounds disclosed in references 178 to 180 Loxoribine (7-allyl-8-oxoguanosine) [181].

- Compounds disclosed in reference 182, including: Acylpiperazine compounds, Indoleione compounds, Tetrahydroisoquinoline (THIQ) compounds, Benzocyclodione 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.*
- 5 • A gamma inulin [201] or derivative thereof, such as algammulin.



Adjuvant combinations

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% squalane, 0.4% Tween 80TM, 5% pluronic-block polymer L121, and thr-MDP, either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion. (7) RibiTM 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 (DetoxTM); and (8) one or more mineral salts (such as an aluminum salt) + a non-toxic derivative of LPS (such as 3dMPL).

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

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.

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.

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 recognized or interact with antigens displayed on MHC Class I molecules.

- 5 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
10 subsets: TH1 phenotype and TH2 phenotypes which differ in their cytokine and effector function.

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
15 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.

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
20 future protection.

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

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
25 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.

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
30 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.

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.

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.

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).

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.

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.

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.

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.

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.

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').

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

5 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.

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.

10 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.

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
15 endocarditis, toxic shock syndrome, and/or septicaemia.

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
20 comprising one or more of the following: instructions, syringe or other delivery device, adjuvant, or pharmaceutically acceptable formulating solution.

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

25 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.

30 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.

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.

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.

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.

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

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.

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.*).

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.

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

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.).

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.

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.

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.

The vector of the invention is preferably an autonomously replicating episomal or extrachromosomal vector, such as a plasmid.

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

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.

The vector of the invention 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.

The vector of the invention may comprise a multiple cloning site

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.

The vector of the invention 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.

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.

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).

- 5 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; 10 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.

- Non-viral delivery vehicles and methods can also be employed, including, but not limited to, 15 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 20 described in references 258 & 259.

- 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 25 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].

- 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 30 detergent, such as CTAB).

S.epidermidis

- 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 35 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.

5 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, 10 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, 15 60, 70, 80, 90, 100, 150, 200, 250 or more).

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

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.

More generally, the invention provides the use of the sta006 and/or sta011 homolog from any 25 *Staphylococcus* species for immunising a mammal against that species.

Antibodies

Antibodies against *S.aureus* antigens can be used for passive immunisation. Thus the invention provides an antibody which is specific for an antigen in the first, second, third or fourth antigen groups. The invention also provides the use of such antibodies in therapy. The invention also 30 provides the use of such antibodies in the manufacture of a medicament. The invention also provides 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.

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

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.*

“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.

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”.

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.*

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.

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

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

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), IsdB, 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), IsdB, 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 IsdB 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 IsdB.

Figure 5 shows collected data on mouse survival from four different experiments after challenge of mice previously immunised with various compositions (PBS negative control; IsdB 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 Combo1 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 IsdB 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 (x) 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, IsdB or Combo1.

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

10 *Antigen selection*

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

IsdA 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-IsdA antibodies revealed extracellular structures. These structures were seen in a variety of growth and infection conditions, including iron positive conditions (in which IsdA 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 IsdA-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 IsdA 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.

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.

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.

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.

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.

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 5µg 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.

Surface digestion [302] and/or analysis of secreted proteins revealed peptide fragments from ClfA, ClfB, coA, eap, ebhA, ebpS, efb, emp, FnBA, FnBB, hla, IsdA, IsdB, IsdH, 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,

stal12, stal13, stal15, stal16, stal17, stal18, stal20, 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.

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

5 **Strain coverage**

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.

Genes encoding IsdA, 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.

The encoded IsdA 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.

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

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

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

The analysis of the potential cellular cytotoxicity by *S.aureus* recombinant antigens Hla, Hla-H35L, IsdA, IsdB, 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 (10µg/ml, 1µg/ml, 0.1µg/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.

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

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.

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.

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%.

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.

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

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.

- 5 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 100µg/ml, or as combinations at 50µg/ml each. Capsular saccharide conjugates from type 5 or type 8 strains are added at 5µg/ml, 10µg/ml or 25µg/ml. Aluminium hydroxide was used at 2mg/ml, in a 10mM histidine buffer (pH 6.5) and with 9mg/ml NaCl.
- 10 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.

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

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

- 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.

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.

- 25 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.

30 **Efficacy testing**

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.

Further individual antigens were tested: (i) NW_10; (ii) IsdA₄₀₋₁₈₄; (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%.

- 5 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%.

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

Experiment SA-10-a tested the efficacy of antigen combinations. Six groups of twelve CD-1 mice received a negative control (PBS), IsdB, 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 + IsdA₄₀₋₁₈₄ + 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).

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 + IsdA₄₀₋₁₈₄ + Sta006 + EsxAB; or (iv) SdrD₅₃₋₅₉₂ + IsdA₄₀₋₁₈₄ + 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).

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 IsdB as a positive control [2].

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 + IsdA₄₀₋₁₈₄ + 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%.

Experiment SA-12 tested: (i) Hla-H35L + IsdA₄₀₋₁₈₄ + Sta006 + Sta011; (ii) Hla-H35L + EsxAB + Sta006 + Sta011; (iii) EsxAB + IsdA₄₀₋₁₈₄ + Sta006 + Sta011; (iv) EsxAB + IsdA + 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%.

Experiment SA-14 tested: (i) EsxAB + Hla-H35L + Sta006 + Sta011; (ii) EsxAB + IsdA₄₀₋₁₈₄ + 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.

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).

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%.

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 IsdB. "Combo-1" was EsxAB+Hla-H35L+Sta006+Sta011 (with polypeptides comprising SEQ ID NOs: 241, 150, 246 & 247). "Combo-2" was EsxAB+IsdA₄₀₋₁₈₄+Sta006+Sta011. The median survival times for each group of 48 mice after 14 days were compared. Whereas the PBS and IsdB 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 IsdB group ($p < 0.0001$); survival in the "Combo-2" group was statistically superior to both the PBS group ($p < 0.0001$) and the IsdB group ($p = 0.0049$). These data are shown in Figure 5.

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 IsdB 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 IsdB group was not included.

Further experiments compared protection achieved with Combo-1, IsdB 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 IsdB; and P3 compared PBS with IsdB:

	Staph-19		FPR3757		Lac	
Survival	%	Days	%	Days	%	Days
PBS	20	1	45	8	47	7
IsdB	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	-

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 IsdB. 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).

Further experiments showed that Combo1 is highly protective against clinically relevant strains in the sepsis model, and always achieved a higher survival % than IsdB. 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 IsdB-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

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

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-IsdB serum was used. Pre-immune and negative control sera showed no killing of Newman strain in this assay. In a first experiment: anti-IsdB 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-IsdB serum performed slightly better; all single or multi-polypeptide sera using the Combo-1 polypeptides showed at least 26% killing.

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 EsxA-B, Hla-H35L, Sta006, Sta011; a fifth group received 50µl of each serum (200µl in total). Two other groups received serum from IsdB-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	IsdB	-ve ctrl
Survival	5%	26%	0%	15%	25%	10%	5%

In further experiments the level of specific antibodies induced in CD1 mice were examined to assess the immunogenicity of the four polypeptides in Combo1. Compositions included either 20µg of each of the four single polypeptides, or 4x10µg 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 when it was administered in the combination than when administered alone (compare middle and right pairs).

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

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.

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 Combo1 combination gave a median survival of the full 15 days, with 59% of mice surviving this long (*cf.* only 35% with IsdB).

It will be understood that the invention has been described by way of example only and modifications may be made whilst remaining within the scope and spirit of the invention.

5 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	88196585	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	-	-
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	-	-
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_1733	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	-	-
95	sta059	SAOUHSC_02708	88196348	-	-
96	sta060	SAOUHSC_02767	88196403	-	-
97	sta061	SAOUHSC_02783	88196419	-	-
98	sta062	SAOUHSC_02788	88196424	-	-
99	sta063	SAOUHSC_02971	88196592	-	-
100	sta064	SAOUHSC_03006	88196625	NWMN_2569	151222781
101	sta065	SAOUHSC_00051	88193871	-	-
102	sta066	SAOUHSC_00172	88193982	-	-
103	sta067	SAOUHSC_00176	88193986	-	-
104	sta068	SAOUHSC_00327	88194127	-	-
105	sta069	SAOUHSC_00427	88194219	-	-
106	sta070	SAOUHSC_00773	88194535	-	-
107	sta071	SAOUHSC_00854	88194612	-	-
108	sta072	SAOUHSC_00872	88194629	-	-
109	sta073	SAOUHSC_00994	88194750	NWMN_0922	151221134
110	sta074	SAOUHSC_01220	88194956	-	-
111	sta075	SAOUHSC_01256	88194989	-	-
112	sta076	SAOUHSC_01263	88194996	-	-
113	sta077	SAOUHSC_01317	88195047	-	-
114	sta078	SAOUHSC_01857	88195555	-	-
115	sta079	SAOUHSC_01935	88195630	-	-
116	sta080	SAOUHSC_01936	88195631	-	-
170	sta081	SAOUHSC_01938	88195633		
117	sta082	SAOUHSC_01939	88195634	-	-
118	sta083	SAOUHSC_01941	88195635	-	-
119	sta084	SAOUHSC_01942	88195636	-	-
120	sta085	SAOUHSC_02171	88195848	-	-
121	sta086	SAOUHSC_02327	88195993	-	-

122	sta087	SAOUHSC_02635	88196276	-	-
123	sta088	SAOUHSC_02844	88196477	-	-
124	sta089	SAOUHSC_02855	88196486	-	-
125	sta090	SAOUHSC_02883	88196512	-	-
126	sta091	SAOUHSC_00685	88194450	-	-
127	sta092	SAOUHSC_00174	88193984	-	-
128	sta093	SAOUHSC_01854	88195552	-	-
129	sta094	SAOUHSC_01512	88195226	-	-
130	sta095	SAOUHSC_00383	88194180	NWMN_0388	151220600
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

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
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
combo1	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
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
Sta003	alum	Newman	1.0E+07	1.32
EsxAB + Sta019 + Sta006 + Sta011	alum	Newman	9.0E+06	3.04
combo1	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
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
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
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
EsxAB + HlaH35L + Sta006 + Sta017	alum	Newman	1.0E+07	1.88
EsxAB + Hla ₂₇₋₇₆ + 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
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
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
Combo1	alum	Mu-50	3.8E+07	1.73
IsdB	alum	USA 200	2.0E+07	1.17
Combo1	alum	USA 200	2.0E+07	1.87

IsdB	alum	USA 300	3.0E+07	0.09
Combo1	alum	USA 300	3.0E+07	2.19
IsdB	alum	Staph19	2.7E+07	0.66
Combo1	alum	Staph19	2.7E+07	0.46
IsdB	alum	Mu-50	4.5E+07	0.98
Combo1	alum	Mu-50	4.5E+07	0.76
IsdB	alum	USA 200	1.6E+07	0.18
Combo1	alum	USA 200	1.6E+07	0.19
IsdB	alum	USA 300	2.2E+07	-0.21
Combo1	alum	USA 300	2.2E+07	-0.29
IsdB	alum	Staph19	2.3E+07	0.57
Combo1	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
Combo1	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
Combo1	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
Combo1	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
Combo1	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
Combo1	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
Combo1	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
Combo1	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 CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. An immunogenic composition comprising a combination of antigens or antigenic peptides, said combination of antigens or antigenic peptides comprising:
 - (1) sta006 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 42; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 42 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 42 having at least 50% sequence identity to SEQ ID NO: 42 and comprising a B-cell epitope thereof; and
 - (2) sta011 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 47; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 47 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 47 having at least 50% sequence identity to SEQ ID NO: 47 and comprising a B-cell epitope thereof.

2. Use of a combination of antigens or antigenic peptides to treat or prevent infection by *S. aureus*, said combination of antigens or antigenic peptides comprising:
 - (1) sta006 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 42; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 42 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 42 having at least 50% sequence identity to SEQ ID NO: 42 and comprising a B-cell epitope thereof; and
 - (2) sta011 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 47; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 47 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 47 having at least 50% sequence identity to SEQ ID NO: 47 and comprising a B-cell epitope thereof.

3. Use of a combination of antigens or antigenic peptides in the preparation of a medicament for treatment or prevention of infection by *S. aureus*, said combination of antigens or antigenic peptides comprising:
 - (1) sta006 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 42; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 42 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 42 having at least 50% sequence identity to SEQ ID NO: 42 and comprising a B-cell epitope thereof; and
 - (2) sta011 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 47; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 47 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 47 having at least 50% sequence identity to SEQ ID NO: 47 and comprising a B-cell epitope thereof.

47 having at least 50% sequence identity to SEQ ID NO: 47 and comprising a B-cell epitope thereof.

4. The immunogenic composition according to claim 1 or the use according to claim 2 or 3, wherein the combination of antigens or antigenic peptides further comprises at least one staphylococcal antigen or antigenic peptide thereof selected from:
 - (3) esxA having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 10; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 10 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 10 having at least 50% sequence identity to SEQ ID NO: 10 and comprising a B-cell epitope thereof;
 - (4) esxB having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 11; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 11 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 11 having at least 50% sequence identity to SEQ ID NO: 11 and comprising a B-cell epitope thereof;
 - (5) hla having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 14; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 14 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 14 having at least 50% sequence identity to SEQ ID NO: 14 and comprising a B-cell epitope thereof;
 - (6) ebpS having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 6; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 6 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 6 having at least 50% sequence identity to SEQ ID NO: 6 and comprising a B-cell epitope thereof;
 - (7) efb having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 7; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 7 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 7 having at least 50% sequence identity to SEQ ID NO: 7 and comprising a B-cell epitope thereof;
 - (8) emp having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 8; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 8 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 8 having at least 50% sequence identity to SEQ ID NO: 8 and comprising a B-cell epitope thereof;
 - (9) esaC having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 9; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 9 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 9

- having at least 50% sequence identity to SEQ ID NO: 9 and comprising a B-cell epitope thereof;
- (10) coA having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 3; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 3 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 3 having at least 50% sequence identity to SEQ ID NO: 3 and comprising a B-cell epitope thereof;
 - (11) eap having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 4; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 4 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 4 having at least 50% sequence identity to SEQ ID NO: 4 and comprising a B-cell epitope thereof;
 - (12) FnBA having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 12; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 12 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 12 having at least 50% sequence identity to SEQ ID NO: 12 and comprising a B-cell epitope thereof;
 - (13) FnBB having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 13; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 13 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 13 having at least 50% sequence identity to SEQ ID NO: 13 and comprising a B-cell epitope thereof;
 - (14) ebhA having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 5; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 5 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 5 having at least 50% sequence identity to SEQ ID NO: 5 and comprising a B-cell epitope thereof;
 - (15) hlgB having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 15; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 15 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 15 having at least 50% sequence identity to SEQ ID NO: 15 and comprising a B-cell epitope thereof;
 - (16) hlgC having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 16; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 16 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 16 having at least 50% sequence identity to SEQ ID NO: 16 and comprising a B-cell epitope thereof;
 - (17) isdA having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 17; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 17 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 17

- having at least 50% sequence identity to SEQ ID NO: 17 and comprising a B-cell epitope thereof;
- (18) isdB having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 18; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 18 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 18 having at least 50% sequence identity to SEQ ID NO: 18 and comprising a B-cell epitope thereof;
 - (19) isdC having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 19; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 19 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 19 having at least 50% sequence identity to SEQ ID NO: 19 and comprising a B-cell epitope thereof;
 - (20) isdG having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 20; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 20 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 20 having at least 50% sequence identity to SEQ ID NO: 20 and comprising a B-cell epitope thereof;
 - (21) isdH having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 21; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 21 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 21 having at least 50% sequence identity to SEQ ID NO: 21 and comprising a B-cell epitope thereof;
 - (22) isdI having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 22; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 22 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 22 having at least 50% sequence identity to SEQ ID NO: 22 and comprising a B-cell epitope thereof;
 - (23) lukD having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 23; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 23 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 23 having at least 50% sequence identity to SEQ ID NO: 23 and comprising a B-cell epitope thereof;
 - (24) lukE having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 24; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 25 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 24 having at least 50% sequence identity to SEQ ID NO: 24 and comprising a B-cell epitope thereof;
 - (25) lukF having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 25; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 25 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 25

- having at least 50% sequence identity to SEQ ID NO: 25 and comprising a B-cell epitope thereof;
- (26) lukS having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 26; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 26 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 26 having at least 50% sequence identity to SEQ ID NO: 26 and comprising a B-cell epitope thereof;
 - (27) nuc having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 27; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 27 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 27 having at least 50% sequence identity to SEQ ID NO: 27 and comprising a B-cell epitope thereof;
 - (28) sasA having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 28; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 28 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 28 having at least 50% sequence identity to SEQ ID NO: 28 and comprising a B-cell epitope thereof;
 - (29) sasB having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 29; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 29 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 29 having at least 50% sequence identity to SEQ ID NO: 29 and comprising a B-cell epitope thereof;
 - (30) sasC having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 30; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 30 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 30 having at least 50% sequence identity to SEQ ID NO: 30 and comprising a B-cell epitope thereof;
 - (31) sasD having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 31; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 31 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 31 having at least 50% sequence identity to SEQ ID NO: 31 and comprising a B-cell epitope thereof;
 - (32) sasF having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 32; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 32 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 32 having at least 50% sequence identity to SEQ ID NO: 32 and comprising a B-cell epitope thereof;
 - (33) sdrC having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 33; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 33 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 33

- having at least 50% sequence identity to SEQ ID NO: 33 and comprising a B-cell epitope thereof;
- (34) sdrD having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 34; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 34 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 34 having at least 50% sequence identity to SEQ ID NO: 34 and comprising a B-cell epitope thereof;
- (35) sdrE2 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 35; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 35 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 35 having at least 50% sequence identity to SEQ ID NO: 35 and comprising a B-cell epitope thereof;
- (36) spa having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 36; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 36 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 36 having at least 50% sequence identity to SEQ ID NO: 36 and comprising a B-cell epitope thereof;
- (37) clfA having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 1; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 1 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 1 having at least 50% sequence identity to SEQ ID NO: 1 and comprising a B-cell epitope thereof;
- (38) clfB having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 2; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 2 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 2 having at least 50% sequence identity to SEQ ID NO: 2 and comprising a B-cell epitope thereof;
- (39) sta001 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 37; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 37 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 37 having at least 50% sequence identity to SEQ ID NO: 37 and comprising a B-cell epitope thereof;
- (40) sta002 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 38; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 38 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 38 having at least 50% sequence identity to SEQ ID NO: 38 and comprising a B-cell epitope thereof;
- (41) sta003 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 39; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 39 that include a B-cell epitope thereof; and a variant of SEQ ID NO:

- 39 having at least 50% sequence identity to SEQ ID NO: 39 and comprising a B-cell epitope thereof;
- (42) sta004 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 40; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 40 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 40 having at least 50% sequence identity to SEQ ID NO: 40 and comprising a B-cell epitope thereof;
- (43) sta005 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 41; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 41 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 41 having at least 50% sequence identity to SEQ ID NO: 41 and comprising a B-cell epitope thereof;
- (44) sta007 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 43; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 43 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 43 having at least 50% sequence identity to SEQ ID NO: 43 and comprising a B-cell epitope thereof;
- (45) sta008 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 44; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 44 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 44 having at least 50% sequence identity to SEQ ID NO: 44 and comprising a B-cell epitope thereof;
- (46) sta009 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 45; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 45 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 45 having at least 50% sequence identity to SEQ ID NO: 45 and comprising a B-cell epitope thereof;
- (47) sta010 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 46; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 46 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 46 having at least 50% sequence identity to SEQ ID NO: 46 and comprising a B-cell epitope thereof;
- (48) sta012 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 48; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 48 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 48 having at least 50% sequence identity to SEQ ID NO: 48 and comprising a B-cell epitope thereof;
- (49) sta013 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 49; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 49 that include a B-cell epitope thereof; and a variant of SEQ ID NO:

- 49 having at least 50% sequence identity to SEQ ID NO: 49 and comprising a B-cell epitope thereof;
- (50) sta014 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 50; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 50 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 50 having at least 50% sequence identity to SEQ ID NO: 50 and comprising a B-cell epitope thereof;
- (51) sta015 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 51; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 51 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 51 having at least 50% sequence identity to SEQ ID NO: 51 and comprising a B-cell epitope thereof;
- (52) sta016 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 52; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 52 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 52 having at least 50% sequence identity to SEQ ID NO: 52 and comprising a B-cell epitope thereof;
- (53) sta017 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 53; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 53 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 53 having at least 50% sequence identity to SEQ ID NO: 53 and comprising a B-cell epitope thereof;
- (54) sta018 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 54; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 54 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 54 having at least 50% sequence identity to SEQ ID NO: 54 and comprising a B-cell epitope thereof;
- (55) sta019 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 55; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 55 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 55 having at least 50% sequence identity to SEQ ID NO: 55 and comprising a B-cell epitope thereof;
- (56) sta020 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 56; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 56 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 56 having at least 50% sequence identity to SEQ ID NO: 56 and comprising a B-cell epitope thereof;
- (57) sta021 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 57; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 57 that include a B-cell epitope thereof; and a variant of SEQ ID NO:

- 57 having at least 50% sequence identity to SEQ ID NO: 57 and comprising a B-cell epitope thereof;
- (58) sta022 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 58; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 58 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 58 having at least 50% sequence identity to SEQ ID NO: 58 and comprising a B-cell epitope thereof;
- (59) sta023 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 59; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 59 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 59 having at least 50% sequence identity to SEQ ID NO: 59 and comprising a B-cell epitope thereof;
- (60) sta024 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 60; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 60 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 60 having at least 50% sequence identity to SEQ ID NO: 60 and comprising a B-cell epitope thereof;
- (61) sta025 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 61; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 61 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 61 having at least 50% sequence identity to SEQ ID NO: 61 and comprising a B-cell epitope thereof;
- (62) sta026 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 62; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 62 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 62 having at least 50% sequence identity to SEQ ID NO: 62 and comprising a B-cell epitope thereof;
- (63) sta027 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 63; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 63 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 63 having at least 50% sequence identity to SEQ ID NO: 63 and comprising a B-cell epitope thereof;
- (64) sta028 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 64; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 64 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 64 having at least 50% sequence identity to SEQ ID NO: 64 and comprising a B-cell epitope thereof;
- (65) sta029 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 65; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 65 that include a B-cell epitope thereof; and a variant of SEQ ID NO:

- 65 having at least 50% sequence identity to SEQ ID NO: 65 and comprising a B-cell epitope thereof;
- (66) sta030 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 66; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 66 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 66 having at least 50% sequence identity to SEQ ID NO: 66 and comprising a B-cell epitope thereof;
- (67) sta031 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 67; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 67 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 67 having at least 50% sequence identity to SEQ ID NO: 67 and comprising a B-cell epitope thereof;
- (68) sta032 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 68; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 68 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 68 having at least 50% sequence identity to SEQ ID NO: 68 and comprising a B-cell epitope thereof;
- (69) sta033 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 69; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 69 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 69 having at least 50% sequence identity to SEQ ID NO: 69 and comprising a B-cell epitope thereof;
- (70) sta034 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 70; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 70 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 70 having at least 50% sequence identity to SEQ ID NO: 70 and comprising a B-cell epitope thereof;
- (71) sta035 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 71; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 71 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 71 having at least 50% sequence identity to SEQ ID NO: 71 and comprising a B-cell epitope thereof;
- (72) sta036 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 72; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 72 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 72 having at least 50% sequence identity to SEQ ID NO: 72 and comprising a B-cell epitope thereof;
- (73) sta037 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 73; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 73 that include a B-cell epitope thereof; and a variant of SEQ ID NO:

- 73 having at least 50% sequence identity to SEQ ID NO: 73 and comprising a B-cell epitope thereof;
- (74) sta038 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 74; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 74 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 74 having at least 50% sequence identity to SEQ ID NO: 74 and comprising a B-cell epitope thereof;
- (75) sta039 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 75; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 75 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 75 having at least 50% sequence identity to SEQ ID NO: 75 and comprising a B-cell epitope thereof;
- (76) sta040 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 76; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 76 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 76 having at least 50% sequence identity to SEQ ID NO: 76 and comprising a B-cell epitope thereof;
- (77) sta041 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 77; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 77 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 77 having at least 50% sequence identity to SEQ ID NO: 77 and comprising a B-cell epitope thereof;
- (78) sta042 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 78; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 78 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 78 having at least 50% sequence identity to SEQ ID NO: 78 and comprising a B-cell epitope thereof;
- (79) sta043 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 79; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 79 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 79 having at least 50% sequence identity to SEQ ID NO: 79 and comprising a B-cell epitope thereof;
- (80) sta044 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 80; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 80 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 80 having at least 50% sequence identity to SEQ ID NO: 80 and comprising a B-cell epitope thereof;
- (81) having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 81; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 81 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 81

- having at least 50% sequence identity to SEQ ID NO: 81 and comprising a B-cell epitope thereof;
- (82) sta046 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 82; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 82 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 82 having at least 50% sequence identity to SEQ ID NO: 82 and comprising a B-cell epitope thereof;
- (83) sta047 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 83; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 83 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 83 having at least 50% sequence identity to SEQ ID NO: 83 and comprising a B-cell epitope thereof;
- (84) sta048 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 84; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 84 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 84 having at least 50% sequence identity to SEQ ID NO: 84 and comprising a B-cell epitope thereof;
- (85) sta049 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 85; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 85 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 85 having at least 50% sequence identity to SEQ ID NO: 85 and comprising a B-cell epitope thereof;
- (86) sta050 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 86; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 86 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 86 having at least 50% sequence identity to SEQ ID NO: 86 and comprising a B-cell epitope thereof;
- (87) sta051 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 87; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 87 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 87 having at least 50% sequence identity to SEQ ID NO: 87 and comprising a B-cell epitope thereof;
- (88) sta052 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 88; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 88 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 88 having at least 50% sequence identity to SEQ ID NO: 88 and comprising a B-cell epitope thereof;
- (89) sta053 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 89; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 89 that include a B-cell epitope thereof; and a variant of SEQ ID NO:

- 89 having at least 50% sequence identity to SEQ ID NO: 89 and comprising a B-cell epitope thereof;
- (90) sta054 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 90; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 90 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 90 having at least 50% sequence identity to SEQ ID NO: 90 and comprising a B-cell epitope thereof;
- (91) sta055 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 91; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 91 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 91 having at least 50% sequence identity to SEQ ID NO: 91 and comprising a B-cell epitope thereof;
- (92) sta056 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 92; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 92 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 92 having at least 50% sequence identity to SEQ ID NO: 92 and comprising a B-cell epitope thereof;
- (93) sta057 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 93; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 93 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 93 having at least 50% sequence identity to SEQ ID NO: 93 and comprising a B-cell epitope thereof;
- (94) sta058 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 94; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 94 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 94 having at least 50% sequence identity to SEQ ID NO: 94 and comprising a B-cell epitope thereof;
- (95) sta059 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 95; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 95 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 95 having at least 50% sequence identity to SEQ ID NO: 95 and comprising a B-cell epitope thereof;
- (96) sta060 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 96; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 96 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 96 having at least 50% sequence identity to SEQ ID NO: 96 and comprising a B-cell epitope thereof;
- (97) sta061 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 97; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 97 that include a B-cell epitope thereof; and a variant of SEQ ID NO:

- 97 having at least 50% sequence identity to SEQ ID NO: 97 and comprising a B-cell epitope thereof;
- (98) sta062 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 98; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 98 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 98 having at least 50% sequence identity to SEQ ID NO: 98 and comprising a B-cell epitope thereof;
- (99) sta063 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 99; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 99 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 99 having at least 50% sequence identity to SEQ ID NO: 99 and comprising a B-cell epitope thereof;
- (100) sta064 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 100; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 100 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 100 having at least 50% sequence identity to SEQ ID NO: 100 and comprising a B-cell epitope thereof;
- (101) sta065 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 101; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 101 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 101 having at least 50% sequence identity to SEQ ID NO: 101 and comprising a B-cell epitope thereof;
- (102) sta066 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 102; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 102 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 102 having at least 50% sequence identity to SEQ ID NO: 102 and comprising a B-cell epitope thereof;
- (103) sta067 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 103; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 103 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 103 having at least 50% sequence identity to SEQ ID NO: 103 and comprising a B-cell epitope thereof;
- (104) sta068 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 104; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 104 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 104 having at least 50% sequence identity to SEQ ID NO: 104 and comprising a B-cell epitope thereof;
- (105) sta069 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 105; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 105 that include a B-cell epitope thereof; and a variant of SEQ ID NO:

- 105 having at least 50% sequence identity to SEQ ID NO: 105 and comprising a B-cell epitope thereof;
- (106) sta070 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 106; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 106 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 106 having at least 50% sequence identity to SEQ ID NO: 106 and comprising a B-cell epitope thereof;
- (107) sta071 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 107; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 107 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 107 having at least 50% sequence identity to SEQ ID NO: 107 and comprising a B-cell epitope thereof;
- (108) sta072 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 108; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 108 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 108 having at least 50% sequence identity to SEQ ID NO: 108 and comprising a B-cell epitope thereof;
- (109) sta073 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 109; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 109 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 109 having at least 50% sequence identity to SEQ ID NO: 109 and comprising a B-cell epitope thereof;
- (110) sta074 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 110; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 110 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 110 having at least 50% sequence identity to SEQ ID NO: 110 and comprising a B-cell epitope thereof;
- (111) sta075 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 111; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 111 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 111 having at least 50% sequence identity to SEQ ID NO: 111 and comprising a B-cell epitope thereof;
- (112) sta076 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 112; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 112 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 112 having at least 50% sequence identity to SEQ ID NO: 112 and comprising a B-cell epitope thereof;
- (113) sta077 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 113; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 113 that include a B-cell epitope thereof; and a variant of SEQ ID NO:

- 113 having at least 50% sequence identity to SEQ ID NO: 113 and comprising a B-cell epitope thereof;
- (114) sta078 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 114; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 114 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 114 having at least 50% sequence identity to SEQ ID NO: 114 and comprising a B-cell epitope thereof;
- (115) sta079 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 115; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 115 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 115 having at least 50% sequence identity to SEQ ID NO: 115 and comprising a B-cell epitope thereof;
- (116) sta080 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 116; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 116 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 116 having at least 50% sequence identity to SEQ ID NO: 116 and comprising a B-cell epitope thereof;
- (117) sta082 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 117; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 117 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 117 having at least 50% sequence identity to SEQ ID NO: 117 and comprising a B-cell epitope thereof;
- (118) sta083 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 118; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 118 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 118 having at least 50% sequence identity to SEQ ID NO: 118 and comprising a B-cell epitope thereof;
- (119) sta084 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 119; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 119 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 119 having at least 50% sequence identity to SEQ ID NO: 119 and comprising a B-cell epitope thereof;
- (120) sta085 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 120; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 120 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 120 having at least 50% sequence identity to SEQ ID NO: 120 and comprising a B-cell epitope thereof;
- (121) sta086 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 121; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 121 that include a B-cell epitope thereof; and a variant of SEQ ID NO:

- 121 having at least 50% sequence identity to SEQ ID NO: 121 and comprising a B-cell epitope thereof;
- (122) sta087 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 122; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 122 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 122 having at least 50% sequence identity to SEQ ID NO: 122 and comprising a B-cell epitope thereof;
- (123) sta088 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 123; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 123 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 123 having at least 50% sequence identity to SEQ ID NO: 123 and comprising a B-cell epitope thereof;
- (124) sta089 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 124; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 124 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 124 having at least 50% sequence identity to SEQ ID NO: 124 and comprising a B-cell epitope thereof;
- (125) sta090 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 125; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 125 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 125 having at least 50% sequence identity to SEQ ID NO: 125 and comprising a B-cell epitope thereof;
- (126) sta091 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 126; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 126 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 126 having at least 50% sequence identity to SEQ ID NO: 126 and comprising a B-cell epitope thereof;
- (127) sta092 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 127; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 127 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 127 having at least 50% sequence identity to SEQ ID NO: 127 and comprising a B-cell epitope thereof;
- (128) sta093 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 128; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 128 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 128 having at least 50% sequence identity to SEQ ID NO: 128 and comprising a B-cell epitope thereof;
- (129) sta094 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 129; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 129 that include a B-cell epitope thereof; and a variant of SEQ ID NO:

- 129 having at least 50% sequence identity to SEQ ID NO: 129 and comprising a B-cell epitope thereof;
- (130) sta095 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 130; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 130 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 130 having at least 50% sequence identity to SEQ ID NO: 130 and comprising a B-cell epitope thereof;
- (131) sta096 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 131; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 131 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 131 having at least 50% sequence identity to SEQ ID NO: 131 and comprising a B-cell epitope thereof;
- (132) sta097 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 132; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 132 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 132 having at least 50% sequence identity to SEQ ID NO: 132 and comprising a B-cell epitope thereof;
- (133) sta098 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 133; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 133 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 133 having at least 50% sequence identity to SEQ ID NO: 133 and comprising a B-cell epitope thereof;
- (134) sta099 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 134; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 134 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 134 having at least 50% sequence identity to SEQ ID NO: 134 and comprising a B-cell epitope thereof;
- (135) sta100 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 135; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 135 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 135 having at least 50% sequence identity to SEQ ID NO: 135 and comprising a B-cell epitope thereof;
- (136) sta101 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 136; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 136 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 136 having at least 50% sequence identity to SEQ ID NO: 136 and comprising a B-cell epitope thereof;
- (137) sta102 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 137; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 137 that include a B-cell epitope thereof; and a variant of SEQ ID NO:

- 137 having at least 50% sequence identity to SEQ ID NO: 137 and comprising a B-cell epitope thereof;
- (138) sta103 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 138; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 138 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 138 having at least 50% sequence identity to SEQ ID NO: 138 and comprising a B-cell epitope thereof;
- (139) sta104 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 139; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 139 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 139 having at least 50% sequence identity to SEQ ID NO: 139 and comprising a B-cell epitope thereof;
- (140) sta105 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 140; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 140 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 140 having at least 50% sequence identity to SEQ ID NO: 140 and comprising a B-cell epitope thereof;
- (141) sta106 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 141; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 141 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 141 having at least 50% sequence identity to SEQ ID NO: 141 and comprising a B-cell epitope thereof;
- (142) sta107 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 177; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 177 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 177 having at least 50% sequence identity to SEQ ID NO: 177 and comprising a B-cell epitope thereof;
- (143) sta108 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 178; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 178 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 178 having at least 50% sequence identity to SEQ ID NO: 178 and comprising a B-cell epitope thereof;
- (144) sta109 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 179; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 179 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 179 having at least 50% sequence identity to SEQ ID NO: 179 and comprising a B-cell epitope thereof;
- (145) sta110 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 180; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 180 that include a B-cell epitope thereof; and a variant of SEQ ID NO:

- 180 having at least 50% sequence identity to SEQ ID NO: 180 and comprising a B-cell epitope thereof;
- (146) sta111 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 181; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 181 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 181 having at least 50% sequence identity to SEQ ID NO: 181 and comprising a B-cell epitope thereof;
- (147) sta112 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 182; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 182 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 182 having at least 50% sequence identity to SEQ ID NO: 182 and comprising a B-cell epitope thereof;
- (148) sta113 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 183; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 183 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 183 having at least 50% sequence identity to SEQ ID NO: 183 and comprising a B-cell epitope thereof;
- (149) sta114 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 184; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 184 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 184 having at least 50% sequence identity to SEQ ID NO: 184 and comprising a B-cell epitope thereof;
- (150) sta115 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 185; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 185 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 185 having at least 50% sequence identity to SEQ ID NO: 185 and comprising a B-cell epitope thereof;
- (151) sta116 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 186; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 186 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 186 having at least 50% sequence identity to SEQ ID NO: 186 and comprising a B-cell epitope thereof;
- (152) sta117 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 187; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 187 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 187 having at least 50% sequence identity to SEQ ID NO: 187 and comprising a B-cell epitope thereof;
- (153) sta118 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 188; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 188 that include a B-cell epitope thereof; and a variant of SEQ ID NO:

- 188 having at least 50% sequence identity to SEQ ID NO: 188 and comprising a B-cell epitope thereof;
- (154) sta119 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 200; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 200 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 200 having at least 50% sequence identity to SEQ ID NO: 200 and comprising a B-cell epitope thereof;
- (155) sta120 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 201; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 201 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 201 having at least 50% sequence identity to SEQ ID NO: 201 and comprising a B-cell epitope thereof;
- (156) NW_6 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 142; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 142 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 142 having at least 50% sequence identity to SEQ ID NO: 142 and comprising a B-cell epitope thereof;
- (157) NW_9 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 143; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 143 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 143 having at least 50% sequence identity to SEQ ID NO: 143 and comprising a B-cell epitope thereof;
- (158) NW_10 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 144; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 144 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 144 having at least 50% sequence identity to SEQ ID NO: 144 and comprising a B-cell epitope thereof;
- (159) NW_7 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 145; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 145 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 145 having at least 50% sequence identity to SEQ ID NO: 145 and comprising a B-cell epitope thereof;
- (160) NW_8 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 146; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 146 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 146 having at least 50% sequence identity to SEQ ID NO: 146 and comprising a B-cell epitope thereof;
- (161) NW_2 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 147; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 147 that include a B-cell epitope thereof; and a variant of SEQ ID NO:

- 147 having at least 50% sequence identity to SEQ ID NO: 147 and comprising a B-cell epitope thereof;
- (162) NW_1 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 148; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 148 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 148 having at least 50% sequence identity to SEQ ID NO: 148 and comprising a B-cell epitope thereof;
- (163) sta081 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 170; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 170 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 170 having at least 50% sequence identity to SEQ ID NO: 170 and comprising a B-cell epitope thereof; and
- (164) NW_5 having an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 149; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 149 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 149 having at least 50% sequence identity to SEQ ID NO: 149 and comprising a B-cell epitope thereof.
5. The immunogenic composition according to claim 1 or 4 or the use according to any one of claims 2 to 4, wherein:
- (1) sta006 comprises an amino acid sequence having at least 60% identity to an amino acid set forth in SEQ ID NO: 42 and comprising a B-cell epitope thereof; and
 - (2) 2sta011 comprises an amino acid sequence having at least 60% identity to an amino acid set forth in SEQ ID NO: 47 and comprising a B-cell epitope thereof.
6. The immunogenic composition according to claim 1 or 4 or the use according to any one of claims 2 to 4, wherein:
- (1) sta006 comprises an amino acid sequence having at least 70% identity to an amino acid set forth in SEQ ID NO: 42 and comprising a B-cell epitope thereof; and
 - (2) sta011 comprises an amino acid sequence having at least 70% identity to an amino acid set forth in SEQ ID NO: 47 and comprising a B-cell epitope thereof.
7. The immunogenic composition according to claim 1 or 4 or the use according to any one of claims 2 to 4, wherein:
- (1) sta006 comprises an amino acid sequence having at least 80% identity to an amino acid set forth in SEQ ID NO: 42 and comprising a B-cell epitope thereof; and
 - (2) sta011 comprises an amino acid sequence having at least 80% identity to an amino acid set forth in SEQ ID NO: 47 and comprising a B-cell epitope thereof.

8. The immunogenic composition according to claim 1 or 4 or the use according to any one of claims 2 to 4, wherein:
 - (1) sta006 comprises an amino acid sequence having at least 90% identity to an amino acid set forth in SEQ ID NO: 42 and comprising a B-cell epitope thereof; and
 - (2) sta011 comprises an amino acid sequence having at least 90% identity to an amino acid set forth in SEQ ID NO: 47 and comprising a B-cell epitope thereof.
9. The immunogenic composition according to claim 1 or 4 or the use according to any one of claims 2 to 4, wherein:
 - (1) sta006 comprises an amino acid sequence set forth in SEQ ID NO: 42; and
 - (2) sta011 comprises an amino acid sequence set forth in SEQ ID NO: 47.
10. The immunogenic composition or use according to any one of claims 4 to 9, wherein the combination of antigens or antigenic peptides comprises:
 - (i) at least one antigen or antigenic peptide selected from (37), (38), (8), (9), (3), (4), (5), (17), (18), (19), (31), (32), (33), (34), (35) and (36); and
 - (ii) at least one antigen or antigenic peptide selected from (40), (1), (43), (2), (64), (96), (133) and (147).
11. The immunogenic composition or use according to any one of claims 4 to 9, wherein the combination of antigens or antigenic peptides comprises one or more antigens or antigenic peptides selected from: (37), (38), (35), (33), (32), (8), (34), (36), (9), (3), (4), (19), (5), (17) and (18)
12. The immunogenic composition or use according to any one of claims 4 to 9, wherein the combination of antigens or antigenic peptides comprises one or more antigens or antigenic peptides selected from: (3), (4) and (5) .
13. The immunogenic composition or use according to any one of claims 4 to 9, wherein the combination of antigens or antigenic peptides comprises (3), (4), (1), (5) and (2).
14. The immunogenic composition according to claim 1 or the use according to claim 2 or 3, wherein the combination or antigens or antigenic peptides comprises:
 - (3) an esxA antigen having an amino acid sequence having at least 60% identity to an amino acid set forth in SEQ ID NO: 10 and comprising a B-cell epitope thereof;
 - (4) an esxB antigen having an amino acid sequence having at least 60% identity to an amino acid set forth in SEQ ID NO: 11 and comprising a B-cell epitope thereof;
 - (1) a sta006 antigen having an amino acid sequence having at least 60% identity to an amino acid set forth in SEQ ID NO: 42 and comprising a B-cell epitope thereof;

- (5) a hla antigen having an amino acid sequence having at least 60% identity to an amino acid set forth in SEQ ID NO: 14 and comprising a B-cell epitope thereof; and
 - (2) a sta011 antigen having an amino acid sequence having at least 60% identity to an amino acid set forth in SEQ ID NO: 47 and comprising a B-cell epitope thereof.
15. The immunogenic composition according to claim 1 or the use according to claim 2 or 3, wherein the combination or antigens or antigenic peptides comprises:
- (3) an esxA antigen having an amino acid sequence having at least 70% identity to an amino acid set forth in SEQ ID NO: 10 and comprising a B-cell epitope thereof;
 - (4) an esxB antigen having an amino acid sequence having at least 70% identity to an amino acid set forth in SEQ ID NO: 11 and comprising a B-cell epitope thereof;
 - (1) a sta006 antigen having an amino acid sequence having at least 70% identity to an amino acid set forth in SEQ ID NO: 42 and comprising a B-cell epitope thereof;
 - (5) a hla antigen having an amino acid sequence having at least 70% identity to an amino acid set forth in SEQ ID NO: 14 and comprising a B-cell epitope thereof; and
 - (2) a sta011 antigen having an amino acid sequence having at least 70% identity to an amino acid set forth in SEQ ID NO: 47 and comprising a B-cell epitope thereof.
16. The immunogenic composition according to claim 1 or the use according to claim 2 or 3, wherein the combination or antigens or antigenic peptides comprises:
- (3) an esxA antigen having an amino acid sequence having at least 80% identity to an amino acid set forth in SEQ ID NO: 10 and comprising a B-cell epitope thereof;
 - (4) an esxB antigen having an amino acid sequence having at least 80% identity to an amino acid set forth in SEQ ID NO: 11 and comprising a B-cell epitope thereof;
 - (1) a sta006 antigen having an amino acid sequence having at least 80% identity to an amino acid set forth in SEQ ID NO: 42 and comprising a B-cell epitope thereof;
 - (5) a hla antigen having an amino acid sequence having at least 80% identity to an amino acid set forth in SEQ ID NO: 14 and comprising a B-cell epitope thereof; and
 - (2) a sta011 antigen having an amino acid sequence having at least 80% identity to an amino acid set forth in SEQ ID NO: 47 and comprising a B-cell epitope thereof.
17. The immunogenic composition according to claim 1 or the use according to claim 2 or 3, wherein the combination or antigens or antigenic peptides comprises:
- (3) an esxA antigen having an amino acid sequence having at least 90% identity to an amino acid set forth in SEQ ID NO: 10 and comprising a B-cell epitope thereof;
 - (4) an esxB antigen having an amino acid sequence having at least 90% identity to an amino acid set forth in SEQ ID NO: 11 and comprising a B-cell epitope thereof;

- (1) a sta006 antigen having an amino acid sequence having at least 90% identity to an amino acid set forth in SEQ ID NO: 42 and comprising a B-cell epitope thereof;
 - (5) a hla antigen having an amino acid sequence having at least 90% identity to an amino acid set forth in SEQ ID NO: 14 and comprising a B-cell epitope thereof; and
 - (2) a sta011 antigen having an amino acid sequence having at least 90% identity to an amino acid set forth in SEQ ID NO: 47 and comprising a B-cell epitope thereof.
18. The immunogenic composition according to claim 1 or the use according to claim 2 or 3, wherein the combination of antigens or antigenic peptides comprises:
- (3) an esxA antigen having an amino acid sequence set forth in SEQ ID NO: 10;
 - (4) an esxB antigen having an amino acid sequence set forth in SEQ ID NO: 11;
 - (1) a sta006 antigen having an amino acid sequence set forth in SEQ ID NO: 42;
 - (5) a hla antigen having an amino acid sequence set forth in SEQ ID NO: 14; and
 - (2) a sta011 antigen having an amino acid sequence set forth in SEQ ID NO: 47.
19. The immunogenic composition according to any one of claims 1 or 4 to 18 or the use according to any one of claims 2 to 18, wherein one or more of the antigens or antigenic peptides is adsorbed to an aluminium hydroxide adjuvant.
20. The immunogenic composition according to any one of claims 1 or 4 to 19, wherein said composition comprises a histidine buffer.
21. The immunogenic composition according to any one of claims 1 or 4 to 20, further comprising: one or more conjugates of (i) a *S.aureus* exopolysaccharide and (ii) a carrier protein.
22. The immunogenic composition according to any one of claims 1 or 4 to 20, further comprising: one or more conjugates of (i) a *S.aureus* capsular polysaccharide and (ii) a carrier protein.
23. A pharmaceutical composition comprising the immunogenic compositions according to any one of claims 1 or 4 to 22 and a pharmaceutically acceptable diluent, carrier or excipient.
24. A method of raising an immune response in a mammal comprising administering to the mammal an effective amount of the immunogenic composition according to any one of claims 1 or 4 to 22 or the pharmaceutical composition according to claim 23.
25. The use according to claim 3 or any one of claims 4 to 19 when dependent on claim 3, wherein the medicament comprises a histidine buffer.

26. The use according to claim 3 or any one of claims 4 to 19 when dependent on claim 3, wherein the medicament further comprises one or more conjugates of (i) a *S.aureus* exopolysaccharide and (ii) a carrier protein.
27. The use according to claim 3 or any one of claims 4 to 19 when dependent on claim 3, wherein the medicament further comprises: one or more conjugates of (i) a *S.aureus* capsular polysaccharide and (ii) a carrier protein.
28. An isolated or purified antigen or antigenic peptide when used in the preparation of an immunogenic composition according to any one of claims 1 or 4 to 22 or a pharmaceutical composition according to claim 23, said antigen or antigenic peptide comprising:
 - (i) an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 42; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 42 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 42 having at least 50% sequence identity to SEQ ID NO: 42 and comprising a B-cell epitope thereof; or
 - (ii) an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 47; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 47 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 47 having at least 50% sequence identity to SEQ ID NO: 47 and comprising a B-cell epitope thereof.
29. An isolated or purified polynucleotide when used in the preparation of an immunogenic composition according to any one of claims 1 or 4 to 22 or a pharmaceutical composition according to claim 23, said isolated or purified polynucleotide comprising:
 - (i) a polynucleotide encoding an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 42; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 42 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 42 having at least 50% sequence identity to SEQ ID NO: 42 and comprising a B-cell epitope thereof; or
 - (ii) a polynucleotide encoding an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 47; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 47 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 47 having at least 50% sequence identity to SEQ ID NO: 47 and comprising a B-cell epitope thereof.
30. A kit when used to prepare an immunogenic composition according to any one of claims 1 or 4 to 22, said kit comprising:
 - (i) a first container containing an antigen or antigenic peptide comprising an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 42; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 42 that include a

- B-cell epitope thereof; and a variant of SEQ ID NO: 42 having at least 50% sequence identity to SEQ ID NO: 42 and comprising a B-cell epitope thereof; and
- (ii) a second container containing an antigen or antigenic peptide comprising an amino acid sequence selected from: an amino acid sequence set forth in SEQ ID NO: 47; an amino acid sequence comprising at least 7 consecutive residues of SEQ ID NO: 47 that include a B-cell epitope thereof; and a variant of SEQ ID NO: 47 having at least 50% sequence identity to SEQ ID NO: 47 and comprising a B-cell epitope thereof.
31. The kit according to claim 30, wherein:
- the first container contains an antigen or antigenic peptide comprising an amino acid sequence set forth in SEQ ID NO: 42; and
- the second container contains an antigen or antigenic peptide comprising an amino acid sequence set forth in SEQ ID NO: 47.
32. The immunogenic composition according to any one of claims 1 or 4 to 22 or the use according to any one of claims 2 to 19 or 25 to 27 of the pharmaceutical composition according to claim 23 or method according to claim 24 or the antigen or antigenic peptide when used according to claim 28 or the polynucleotide when used according to claim 29 or the kit when used according to claim 30 or 31 substantially as hereinbefore described with reference to the Figures and/or Examples.

DATED this TWENTY SECOND day of SEPTEMBER, 2014

Novartis AG

By the patent attorneys for the applicant:

FB Rice

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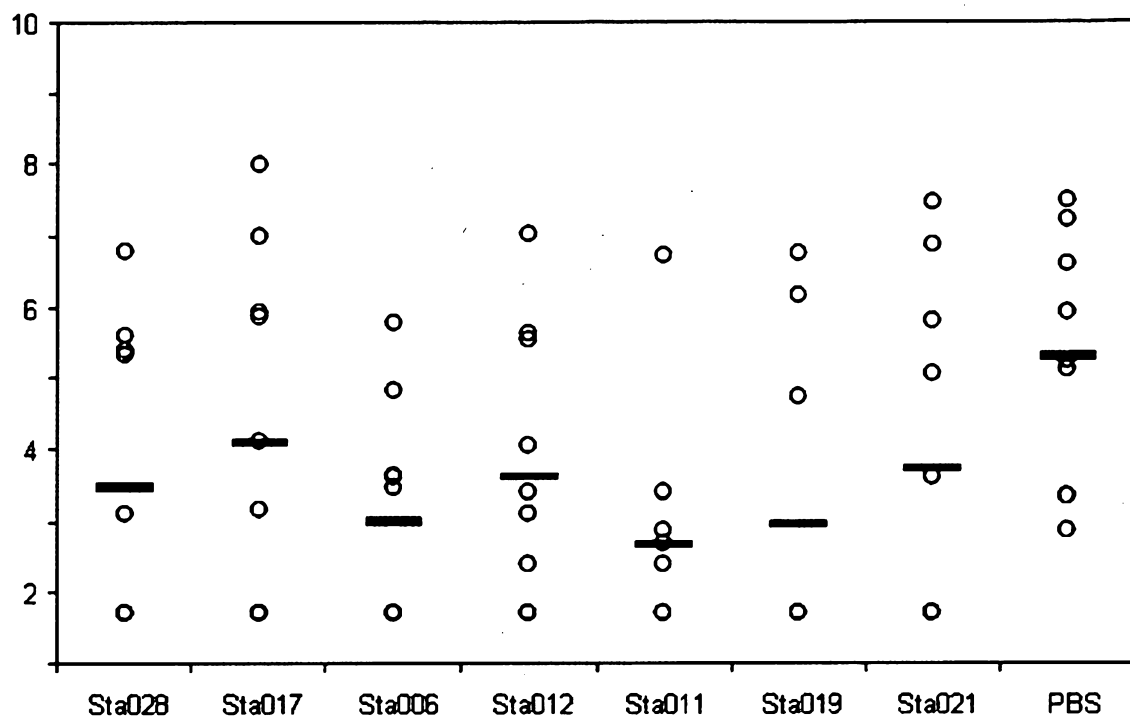
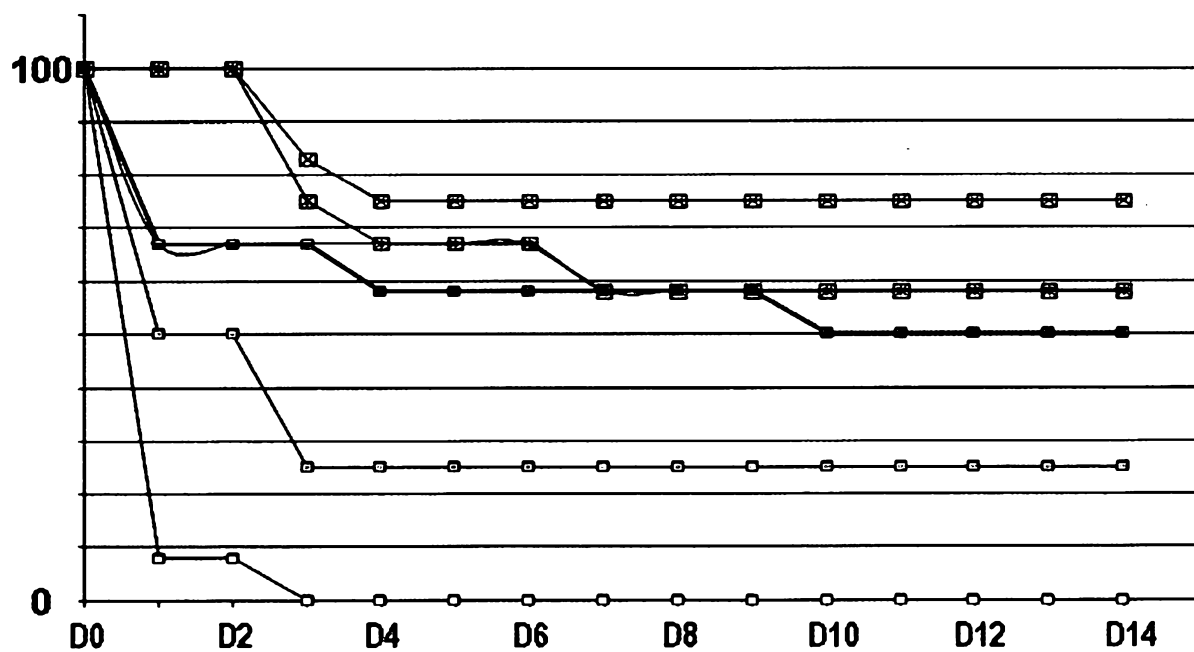
FIGURE 1**FIGURE 2**

FIGURE 3

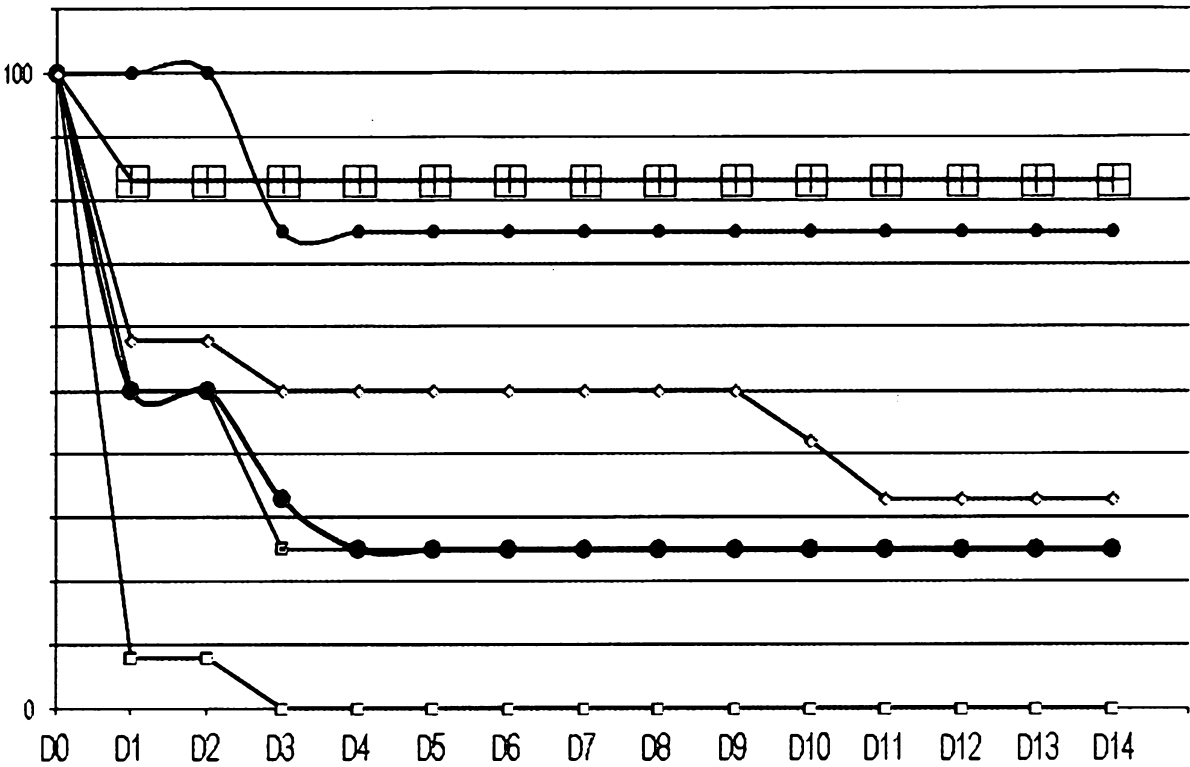
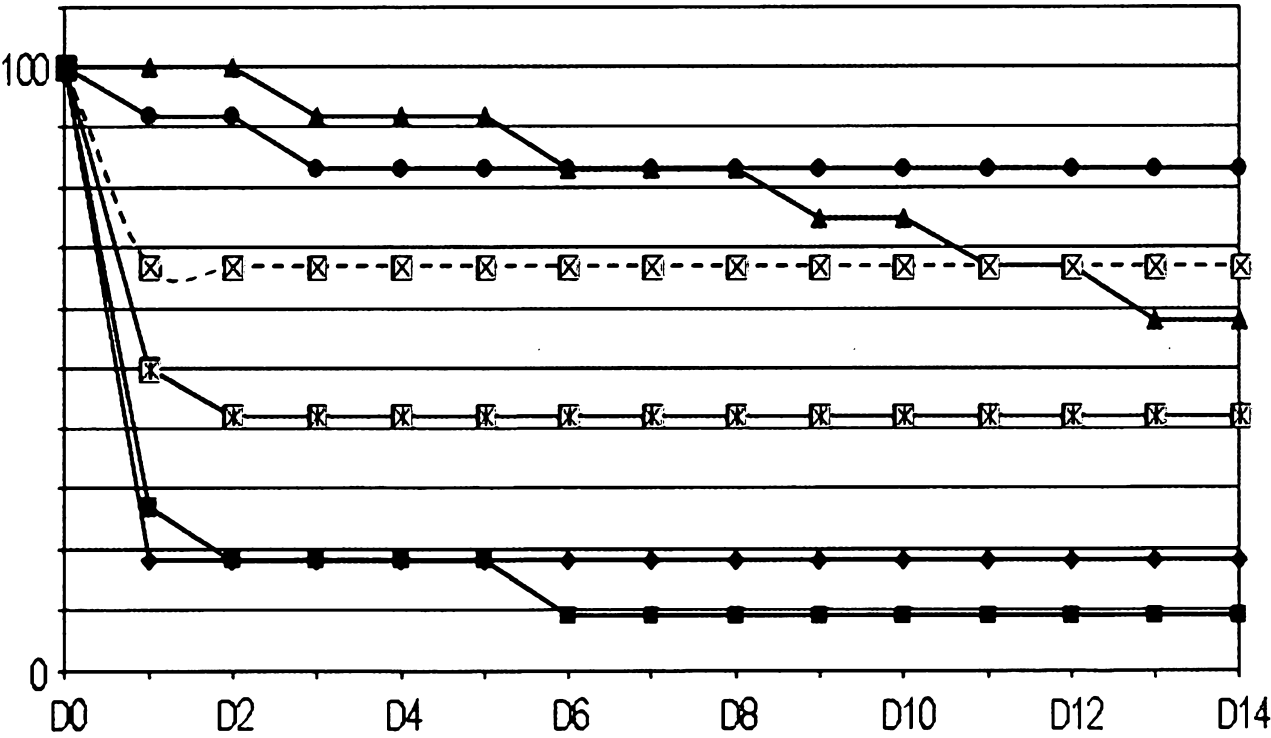


FIGURE 4



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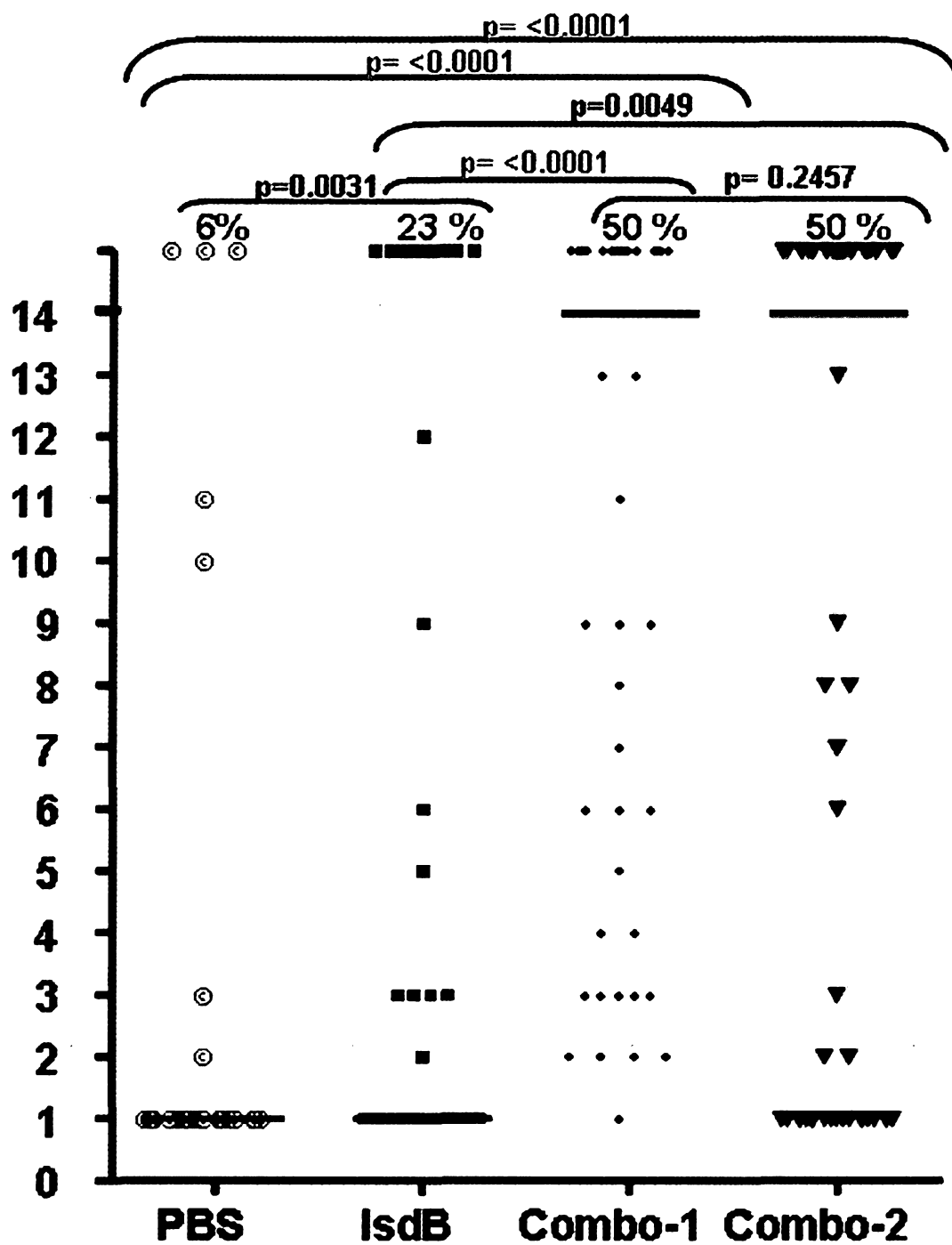
FIGURE 5

FIGURE 6

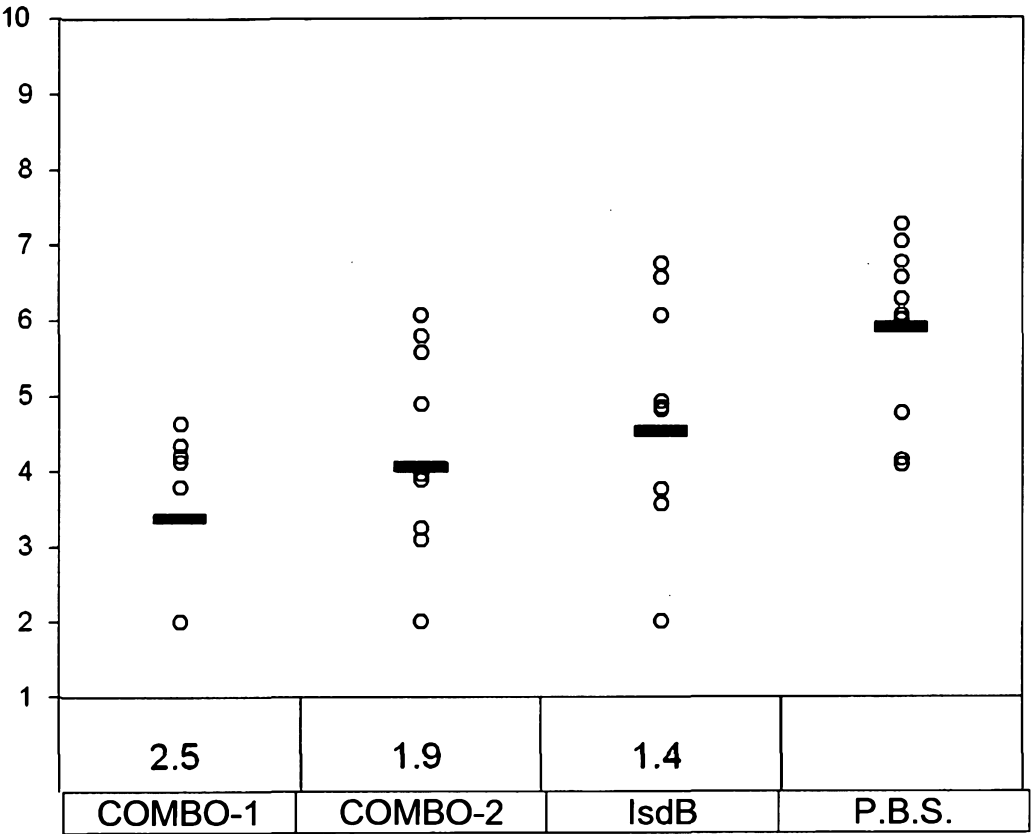
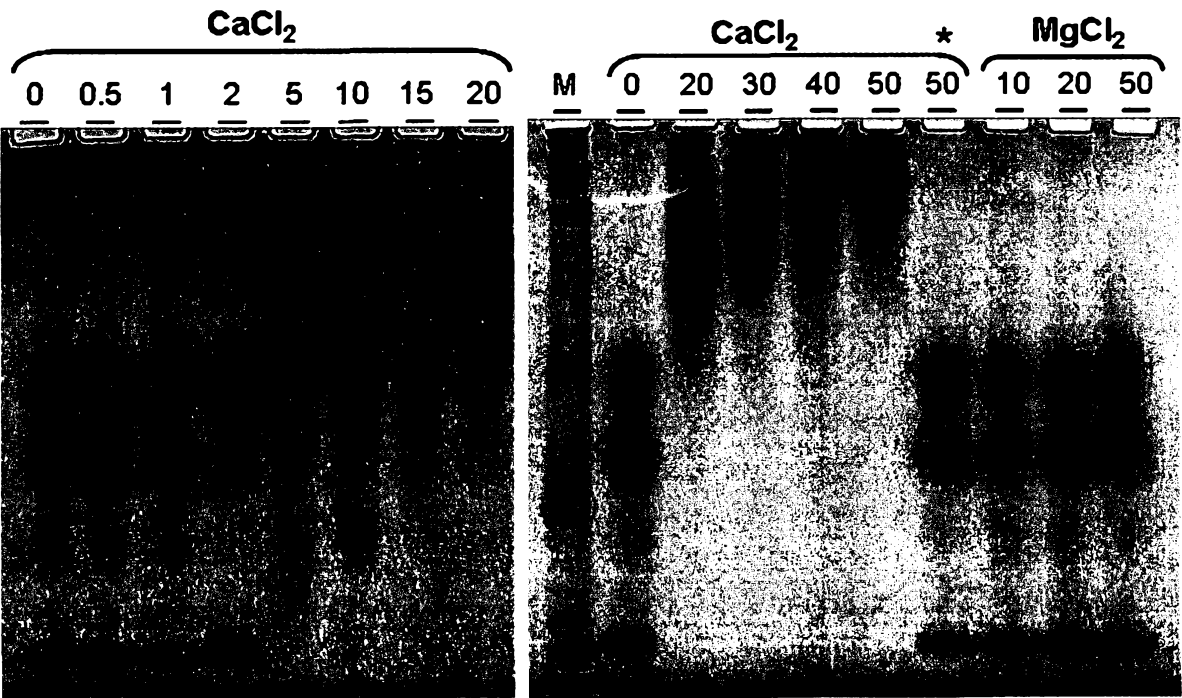


FIGURE 8



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FIGURE 7

FIGURE 7A

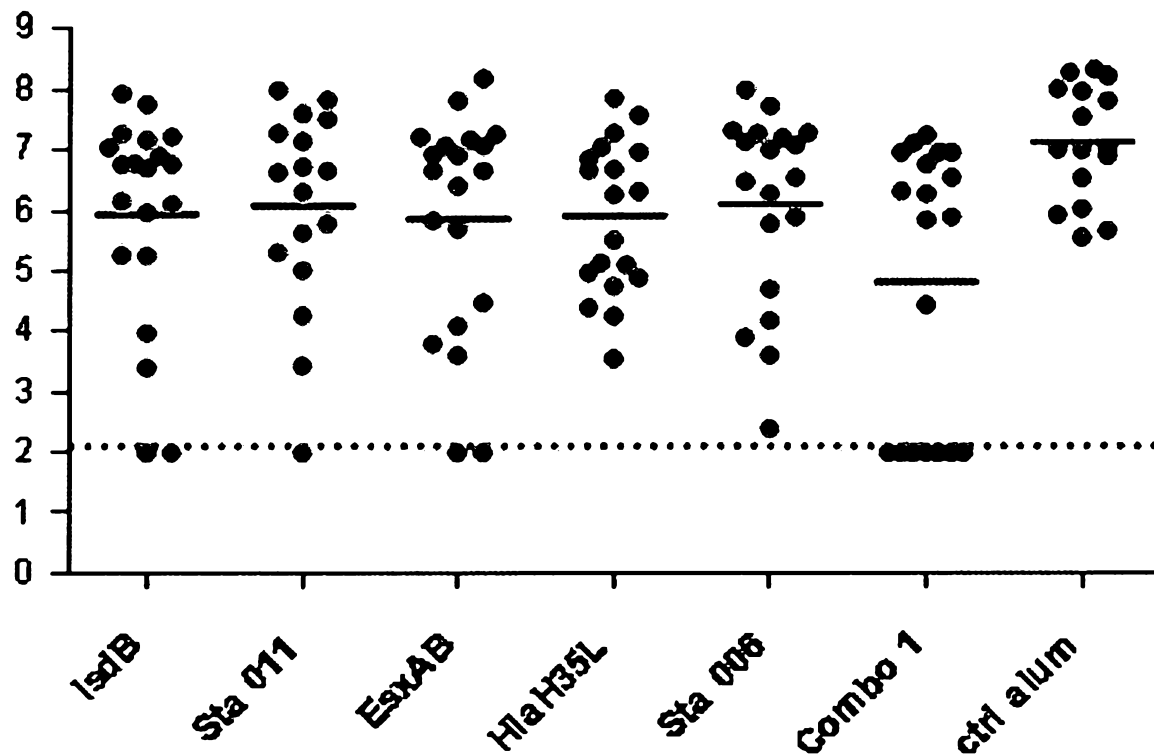
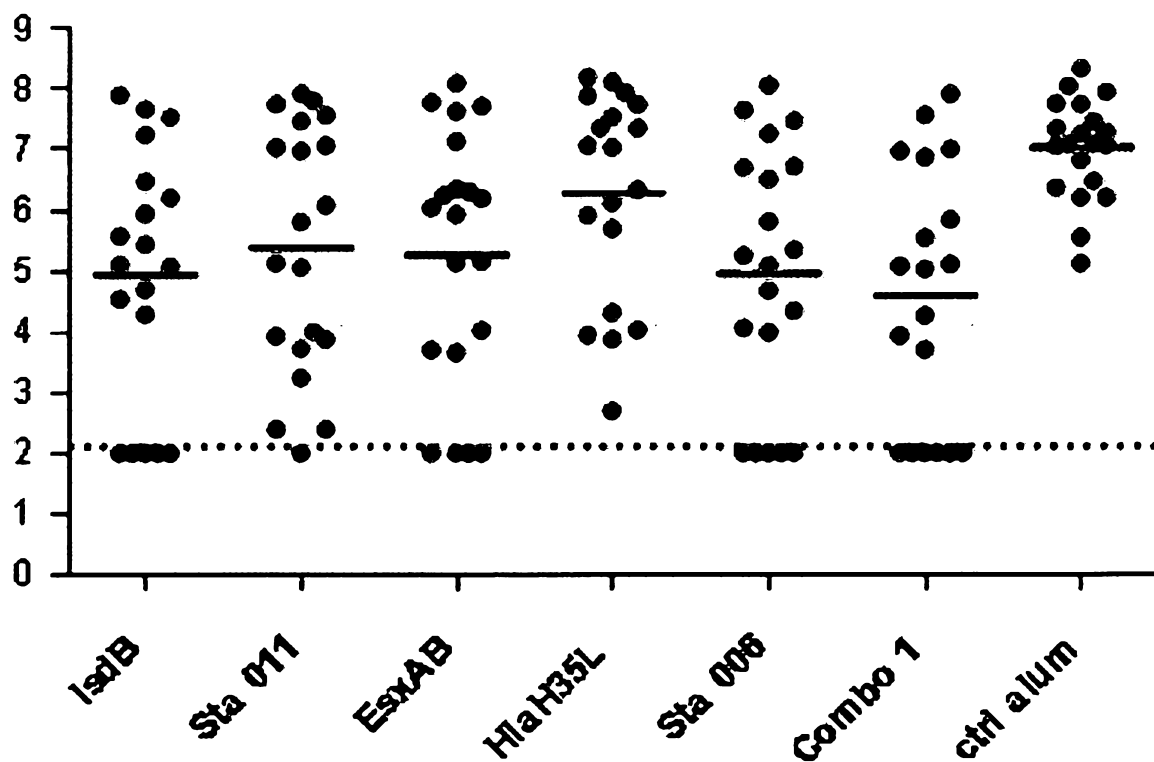
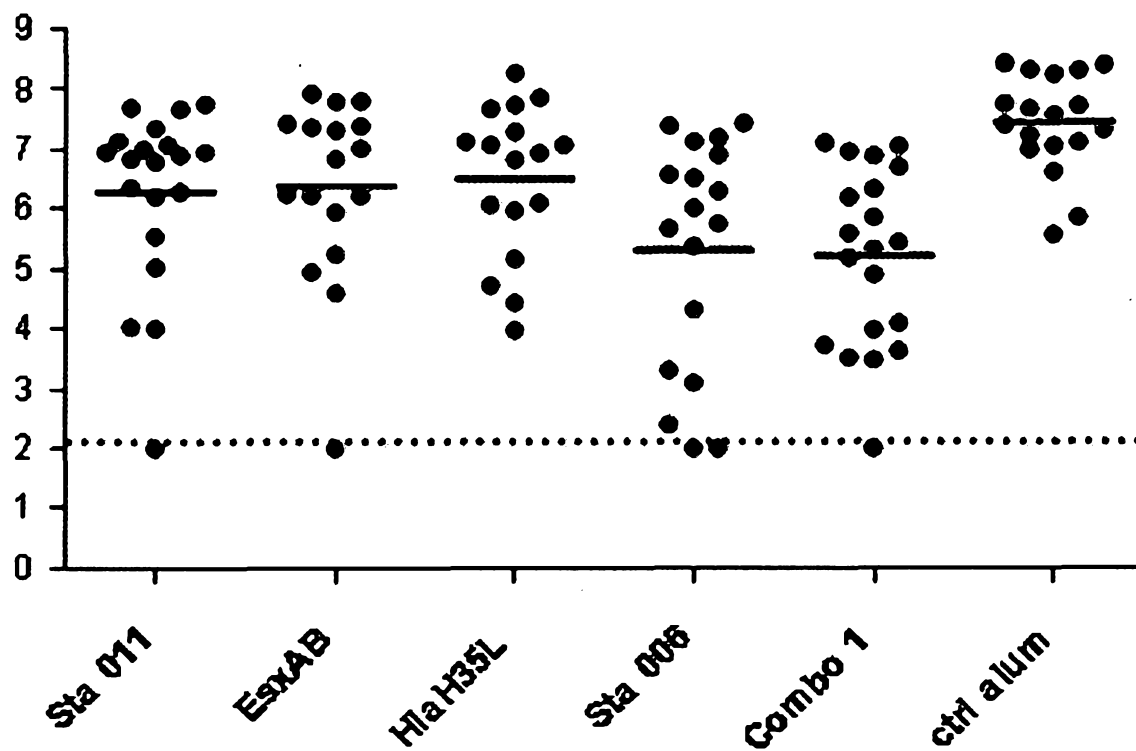
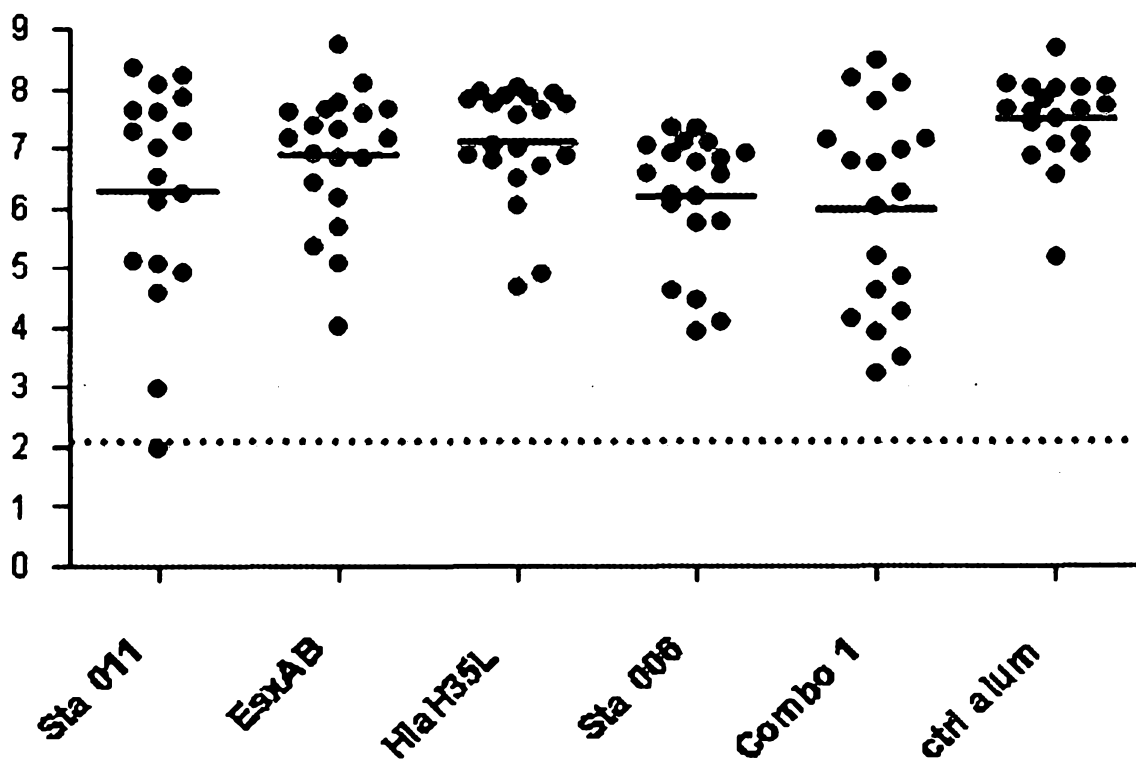


FIGURE 7B



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FIGURE 7C**FIGURE 7D**

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FIGURE 9

FIGURE 9A

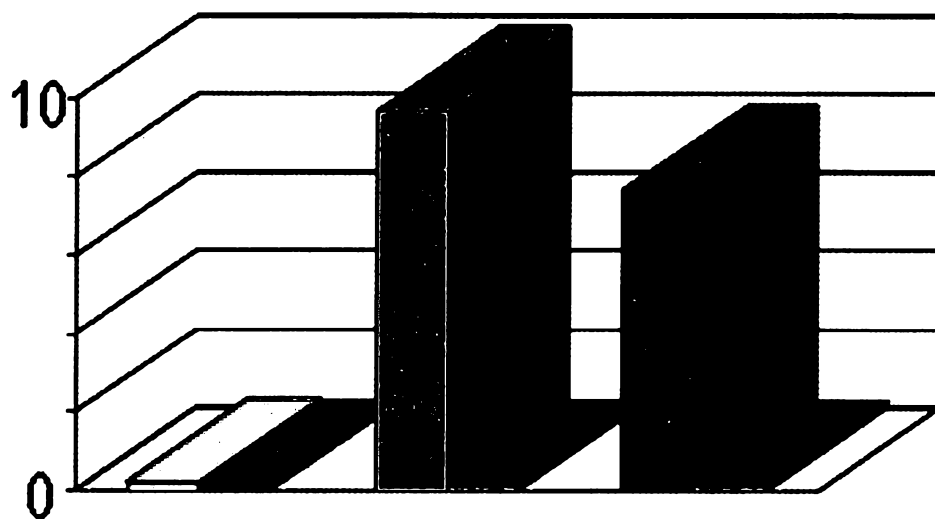
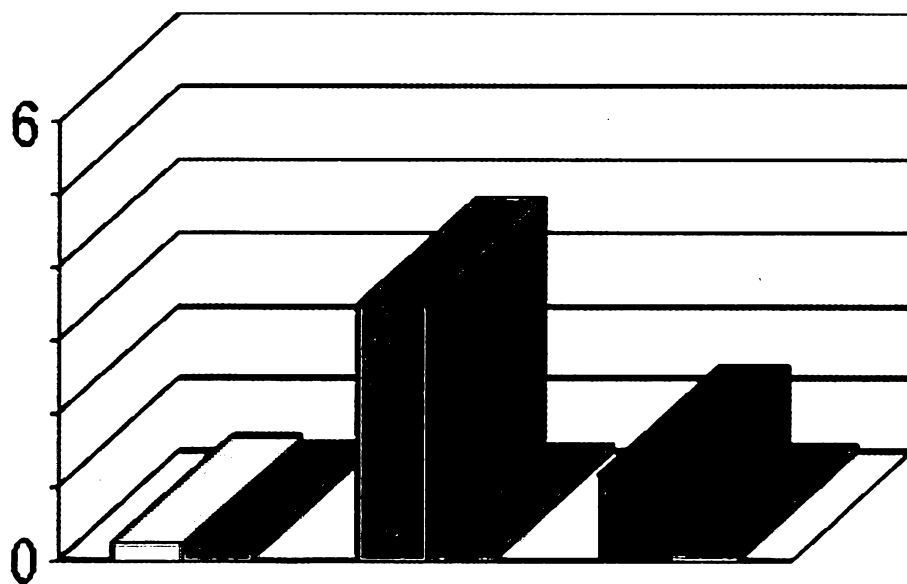


FIGURE 9B



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FIGURE 9C

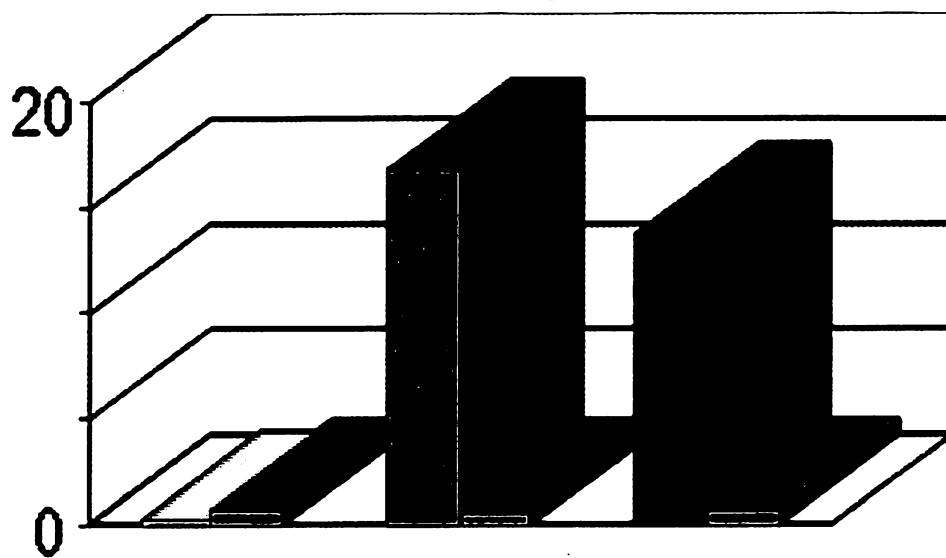
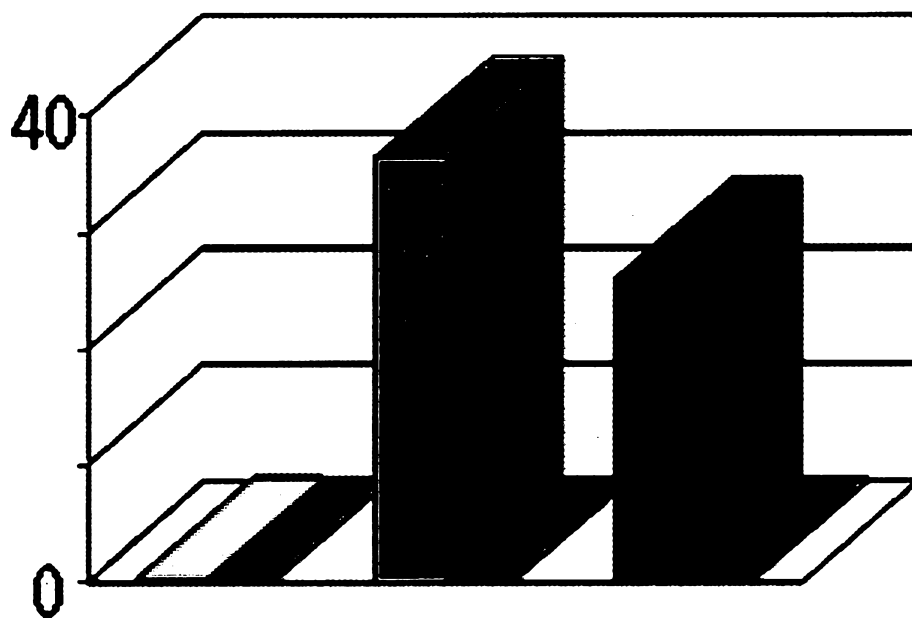


FIGURE 9D



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FIGURE 10

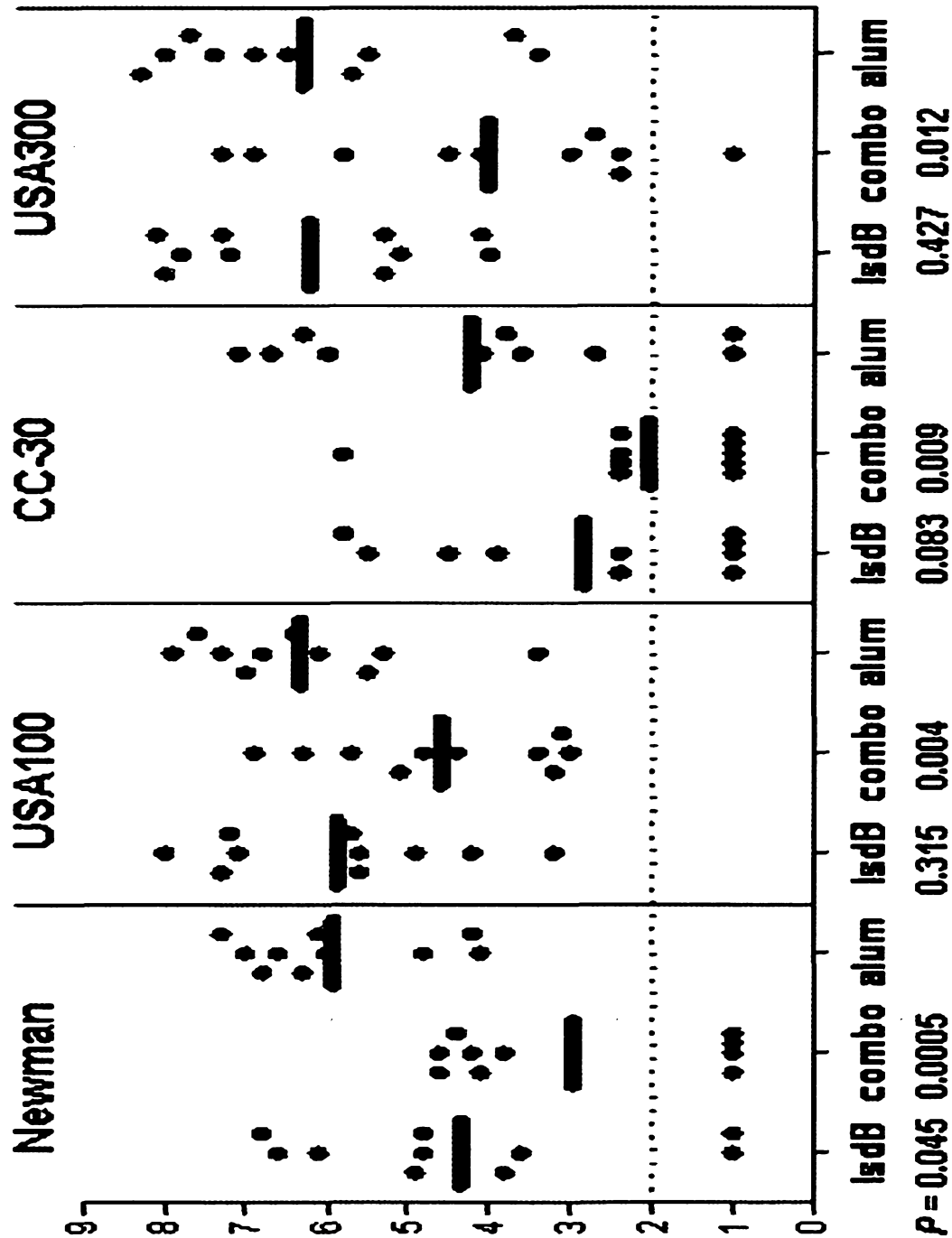
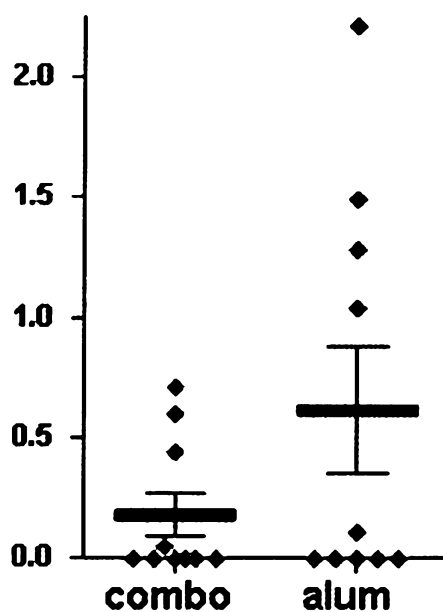
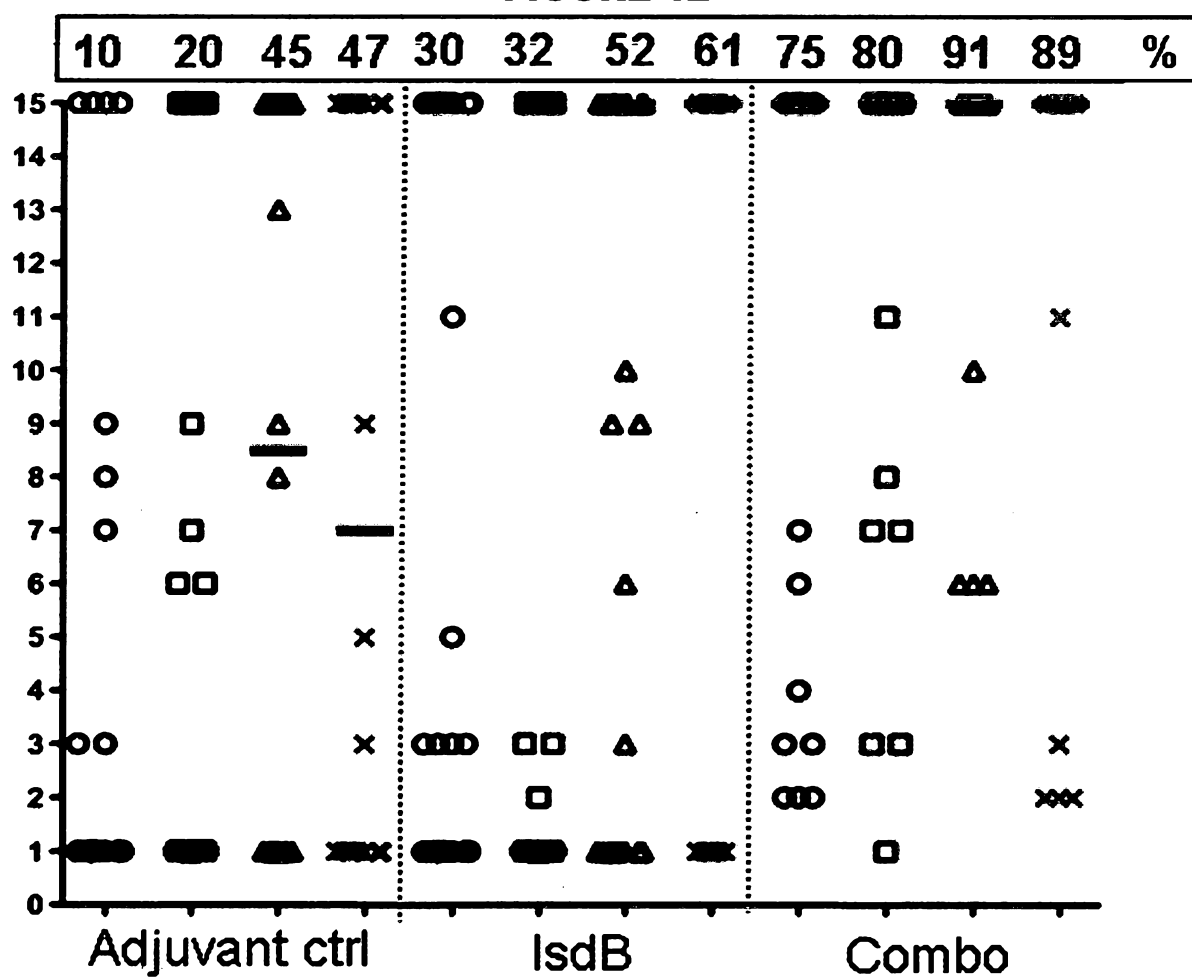
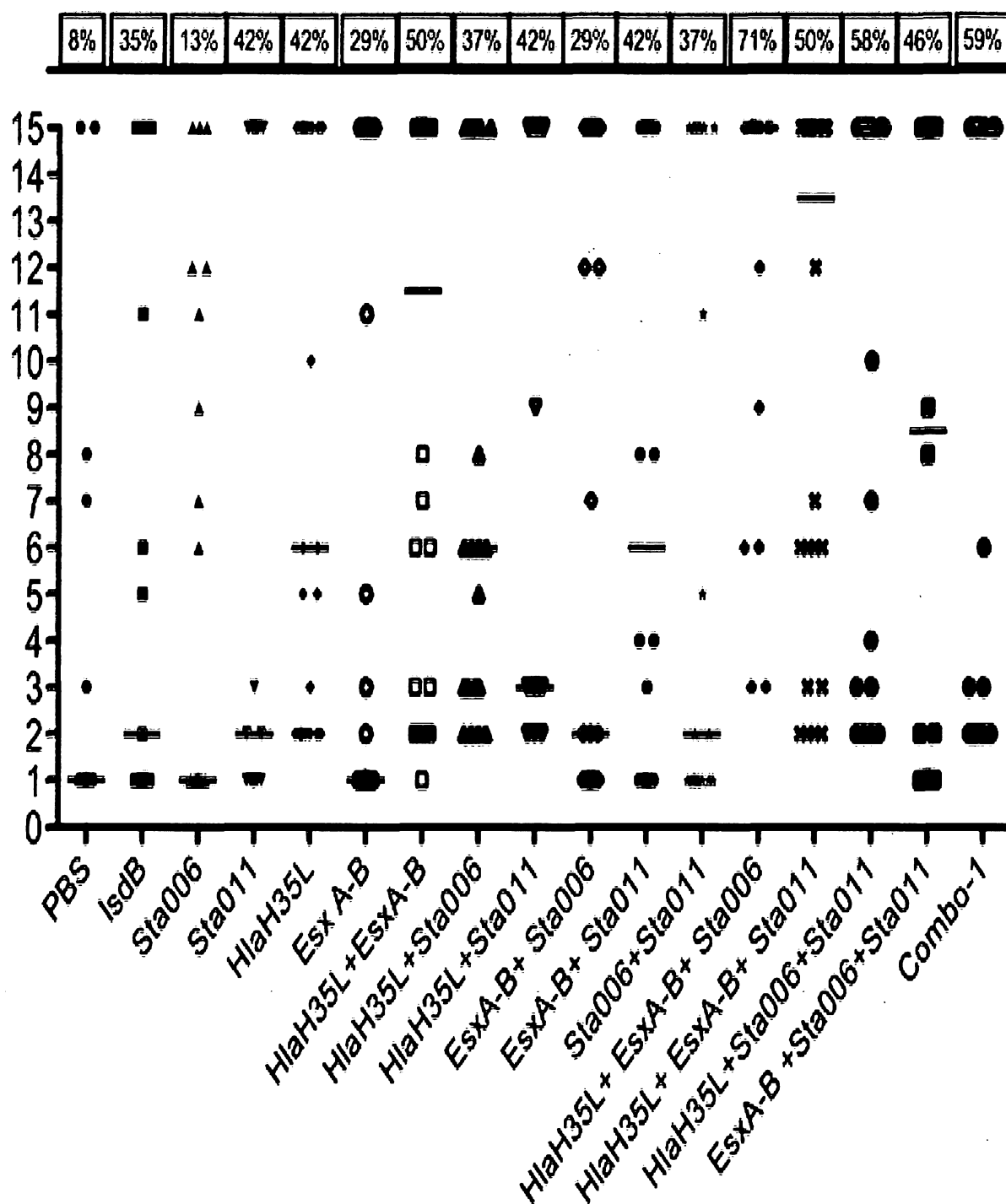


FIGURE 11**FIGURE 12**

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FIGURE 13

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<151> 2009-04-14

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<151> 2009-08-14

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Val Thr Gly Glu Ala Thr Thr Thr Thr Thr Asn Gln Ala Asn Thr Pro
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Asn Ser Pro Gln Asn Ser Thr Asn Ala Glu Asn Val Ser Thr Thr Gln

2010238255

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 Thr Lys Pro Met Ser Thr Gln Thr Ser Asn Thr Thr Thr Thr Glu Pro
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 Ala Ser Thr Asn Glu Thr Pro Gln Pro Thr Ala Ile Lys Asn Gln Ala
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 Phe Thr Ala Lys Leu Pro Asp Ser Leu Thr Gly Asn Gly Asp Val Asp
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Glu	Pro	Ser	Pro	Asp	Pro	Asp	Pro	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
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 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 675 680 685
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 690 695 700
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
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 740 745 750
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 755 760 765
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 770 775 780
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 His Lys Thr Asp Ala Leu Pro Glu Thr Gly Asp Lys Ser Glu Asn Thr
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Asp Ser Arg Tyr Leu Asn Ser Ala Leu Tyr Tyr Leu Glu Asp Tyr Ile
50          55          60

Ile Tyr Ala Ile Gly Leu Thr Asn Lys Tyr Glu Tyr Gly Asp Asn Ile
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Tyr Lys Glu Ala Lys Asp Arg Leu Leu Glu Lys Val Leu Arg Glu Asp
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Gln Tyr Leu Leu Glu Arg Lys Lys Ser Gln Tyr Glu Asp Tyr Lys Gln
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Trp Tyr Ala Asn Tyr Lys Lys Glu Asn Pro Arg Thr Asp Leu Lys Met
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Lys	Lys	Pro	Ser	Glu	Thr	Asn	Ala	Tyr	Asn	Val	Thr	Thr	His	Ala	Asn	530	535	540
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Val His Val Pro Tyr Ala Ile Thr Val Asn Gly Thr Ser Gln Asn Ile
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85          90          95

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Lys Asn Gly Thr Lys Lys Val Ile Asp Leu Lys Ala Gly Ile Tyr Thr
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Val Asp Leu Arg Leu Ser Lys Gln Ala Lys Tyr Thr Val Asn Phe Lys
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Asn Gly Thr Lys Lys Val Ile Asp Leu Lys Ser Gly Ile Tyr Thr Ala
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Asn Leu Ile Asn Ser Ser Asp Ile Lys Ser Ile Asn Ile Asn Val Asp
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Thr Lys Lys His Ile Glu Asn Lys Ala Lys Arg Asn Tyr Gln Val Pro
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Tyr Ser Ile Asn Leu Asn Gly Thr Ser Thr Asn Ile Leu Ser Asn Leu
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Ser Phe Ser Asn Lys Pro Trp Thr Asn Tyr Lys Asn Leu Thr Ser Gln
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Ile Lys Ser Val Leu Lys His Asp Arg Gly Ile Ser Glu Gln Asp Leu
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Lys Tyr Ala Lys Lys Ala Tyr Tyr Thr Val Tyr Phe Lys Asn Gly Gly
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Lys Ala Lys Ala Asp Arg Tyr Val Pro Tyr Thr Ile Ala Val Asn Gly
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Asp Arg Gly Ile Gly Glu Arg Glu Leu Lys Tyr Ala Lys Lys Ala Thr
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Tyr Thr Val His Phe Lys Asn Gly Thr Lys Lys Val Ile Asn Ile Asn
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Ile Asp Ile Asp Val Lys Thr Gly Thr Lys Ala Lys Ala Asp Ser Tyr
465                      470                      475                      480

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

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

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

Tyr Thr Lys Ser Lys Lys Asn Lys
                    580

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<213> Staphylococcus aureus
<223> ebhA

<400> 5

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1                      5                      10                      15

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

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

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

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

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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
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		
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				
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	
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			
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
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			
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
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				
			420					425					430						
Thr	Val	His	Ile	Tyr	Ser	Leu	Glu	Asp	Leu	Ser	Arg	Ala	Ser	Asp	Tyr				
		435					440					445							
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				
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						
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								
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					
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							
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				
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						
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
 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
 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
 Lys Glu Gln Leu Phe Glu Ile Arg Val Lys Pro His Thr Pro Thr Ile
 785 790 795 800
 Thr Thr Thr Ala Glu Gln Leu Arg Gly Thr Ala Leu Gln Lys Val Pro
 805 810 815
 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
 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
 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
 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
 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

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
Ser Ile His Val Gly Lys Ile Ser Glu Asp Ala His Pro Ile Val	1010	1015	1020
Leu Gly Asn Thr Glu Lys Val Val Val Val Asn Pro Thr Ala Val	1025	1030	1035
Ser Asn Asp Glu Lys Gln Ser Ile Ile Thr Ala Phe Met Asn Lys	1040	1045	1050
Asn Gln Asn Ile Arg Gly Tyr Leu Ala Ser Thr Asp Pro Val Thr	1055	1060	1065
Val Asp Asn Asn Gly Asn Val Thr Leu His Tyr Arg Asp Gly Ser	1070	1075	1080
Ser Thr Thr Leu Asp Ala Thr Asn Val Met Thr Tyr Glu Pro Val	1085	1090	1095
Val Lys Pro Glu Tyr Gln Thr Val Asn Ala Ala Lys Thr Ala Thr	1100	1105	1110
Val Thr Ile Ala Lys Gly Gln Ser Phe Ser Ile Gly Asp Ile Lys	1115	1120	1125
Gln Tyr Phe Thr Leu Ser Asn Gly Gln Pro Ile Pro Ser Gly Thr	1130	1135	1140
Phe Thr Asn Ile Thr Ser Asp Arg Thr Ile Pro Thr Ala Gln Glu	1145	1150	1155
Val Ser Gln Met Asn Ala Gly Thr Gln Leu Tyr His Ile Thr Ala	1160	1165	1170
Thr Asn Ala Tyr His Lys Asp Ser Glu Asp Phe Tyr Ile Ser Leu	1175	1180	1185
Lys Ile Ile Asp Val Lys Gln Pro Glu Gly Asp Gln Arg Val Tyr	1190	1195	1200
Arg Thr Ser Thr Tyr Asp Leu Thr Thr Asp Glu Ile Ser Lys Val	1205	1210	1215
Lys Gln Ala Phe Ile Asn Ala Asn Arg Asp Val Ile Thr Leu Ala	1220	1225	1230
Glu Gly Asp Ile Ser Val Thr Asn Thr Pro Asn Gly Ala Asn Val	1235	1240	1245

Ser Thr 1250	Ile Thr Val Asn 1255	Ile Asn Lys Gly Arg 1260	Leu Thr Lys Ser
Phe Ala 1265	Ser Asn Leu Ala Asn 1270	Met Asn Phe Leu Arg 1275	Trp Val Asn
Phe Pro 1280	Gln Asp Tyr Thr Val 1285	Thr Trp Thr Asn Ala 1290	Lys Ile Ala
Asn Arg 1295	Pro Thr Asp Gly Gly 1300	Leu Ser Trp Ser Asp 1305	Asp His Lys
Ser Leu 1310	Ile Tyr Arg Tyr Asp 1315	Ala Thr Leu Gly Thr 1320	Gln Ile Thr
Thr Asn 1325	Asp Ile Leu Thr Met 1330	Leu Lys Ala Thr Thr 1335	Thr Val Pro
Gly Leu 1340	Arg Asn Asn Ile Thr 1345	Gly Asn Glu Lys Ser 1350	Gln Ala Glu
Ala Gly 1355	Gly Arg Pro Asn Phe 1360	Arg Thr Thr Gly Tyr 1365	Ser Gln Ser
Asn Ala 1370	Thr Thr Asp Gly Gln 1375	Arg Gln Phe Thr Leu 1380	Asn Gly Gln
Val Ile 1385	Gln Val Leu Asp Ile 1390	Ile Asn Pro Ser Asn 1395	Gly Tyr Gly
Gly Gln 1400	Pro Val Thr Asn Ser 1405	Asn Thr Arg Ala Asn 1410	His Ser Asn
Ser Thr 1415	Val Val Asn Val Asn 1420	Glu Pro Ala Ala Asn 1425	Gly Ala Gly
Ala Phe 1430	Thr Ile Asp His Val 1435	Val Lys Ser Asn Ser 1440	Thr His Asn
Ala Ser 1445	Asp Ala Val Tyr Lys 1450	Ala Gln Leu Tyr Leu 1455	Thr Pro Tyr
Gly Pro 1460	Lys Gln Tyr Val Glu 1465	His Leu Asn Gln Asn 1470	Thr Gly Asn
Thr Thr 1475	Asp Ala Ile Asn Ile 1480	Tyr Phe Val Pro Ser 1485	Asp Leu Val
Asn Pro 1490	Thr Ile Ser Val Gly 1495	Asn Tyr Thr Asn His 1500	Gln Val Phe
Ser Gly	Glu Thr Phe Thr Asn	Thr Ile Thr Ala Asn	Asp Asn Phe

1505						1510						1515			
Gly Val	Gln Ser	Val Thr	Val	Pro Asn	Thr Ser	Gln	Ile Thr	Gly							
1520						1525						1530			
Thr Val	Asp Asn	Asn His	Gln	His Val	Ser Ala	Thr	Ala Pro	Asn							
1535						1540						1545			
Val Thr	Ser Ala	Thr Asn	Lys	Thr Ile	Asn Leu	Leu	Ala Thr	Asp							
1550						1555						1560			
Thr Ser	Gly Asn	Thr Ala	Thr	Thr Ser	Phe Asn	Val	Thr Val	Lys							
1565						1570						1575			
Pro Leu	Arg Asp	Lys Tyr	Arg	Val Gly	Thr Ser	Ser	Thr Ala	Ala							
1580						1585						1590			
Asn Pro	Val Arg	Ile Ala	Asn	Ile Ser	Asn Asn	Ala	Thr Val	Ser							
1595						1600						1605			
Gln Ala	Asp Gln	Thr Thr	Ile	Ile Asn	Ser Leu	Thr	Phe Thr	Glu							
1610						1615						1620			
Thr Val	Pro Asn	Arg Ser	Tyr	Ala Arg	Ala Ser	Ala	Asn Glu	Ile							
1625						1630						1635			
Thr Ser	Lys Thr	Val Ser	Asn	Val Ser	Arg Thr	Gly	Asn Asn	Ala							
1640						1645						1650			
Asn Val	Thr Val	Thr Val	Thr	Tyr Gln	Asp Gly	Thr	Thr Ser	Thr							
1655						1660						1665			
Val Thr	Val Pro	Val Lys	His	Val Ile	Pro Glu	Ile	Val Ala	His							
1670						1675						1680			
Ser His	Tyr Thr	Val Gln	Gly	Gln Asp	Phe Pro	Ala	Gly Asn	Gly							
1685						1690						1695			
Ser Ser	Ala Ser	Asp Tyr	Phe	Lys Leu	Ser Asn	Gly	Ser Asp	Ile							
1700						1705						1710			
Ala Asp	Ala Thr	Ile Thr	Trp	Val Ser	Gly Gln	Ala	Pro Asn	Lys							
1715						1720						1725			
Asp Asn	Thr Arg	Ile Gly	Glu	Asp Ile	Thr Val	Thr	Ala His	Ile							
1730						1735						1740			
Leu Ile	Asp Gly	Glu Thr	Thr	Pro Ile	Thr Lys	Thr	Ala Thr	Tyr							
1745						1750						1755			
Lys Val	Val Arg	Thr Val	Pro	Lys His	Val Phe	Glu	Thr Ala	Arg							
1760						1765						1770			

Gly Val 1775	Leu Tyr Pro Gly Val 1780	Ser Asp Met Tyr Asp 1785	Ala Lys Gln
Tyr Val 1790	Lys Pro Val Asn Asn 1795	Ser Trp Ser Thr Asn 1800	Ala Gln His
Met Asn 1805	Phe Gln Phe Val Gly 1810	Thr Tyr Gly Pro Asn 1815	Lys Asp Val
Val Gly 1820	Ile Ser Thr Arg Leu 1825	Ile Arg Val Thr Tyr 1830	Asp Asn Arg
Gln Thr 1835	Glu Asp Leu Thr Ile 1840	Leu Ser Lys Val Lys 1845	Pro Asp Pro
Pro Arg 1850	Ile Asp Ala Asn Ser 1855	Val Thr Tyr Lys Ala 1860	Gly Leu Thr
Asn Gln 1865	Glu Ile Lys Val Asn 1870	Asn Val Leu Asn Asn 1875	Ser Ser Val
Lys Leu 1880	Phe Lys Ala Asp Asn 1885	Thr Pro Leu Asn Val 1890	Thr Asn Ile
Thr His 1895	Gly Ser Gly Phe Ser 1900	Ser Val Val Thr Val 1905	Ser Asp Ala
Leu Pro 1910	Asn Gly Gly Ile Lys 1915	Ala Lys Ser Ser Ile 1920	Ser Met Asn
Asn Val 1925	Thr Tyr Thr Thr Gln 1930	Asp Glu His Gly Gln 1935	Val Val Thr
Val Thr 1940	Arg Asn Glu Ser Val 1945	Asp Ser Asn Asp Ser 1950	Ala Thr Val
Thr Val 1955	Thr Pro Gln Leu Gln 1960	Ala Thr Thr Glu Gly 1965	Ala Val Phe
Ile Lys 1970	Gly Gly Asp Gly Phe 1975	Asp Phe Gly His Val 1980	Glu Arg Phe
Ile Gln 1985	Asn Pro Pro His Gly 1990	Ala Thr Val Ala Trp 1995	His Asp Ser
Pro Asp 2000	Thr Trp Lys Asn Thr 2005	Val Gly Asn Thr His 2010	Lys Thr Ala
Val Val 2015	Thr Leu Pro Asn Gly 2020	Gln Gly Thr Arg Asn 2025	Val Glu Val
Pro Val 2030	Lys Val Tyr Pro Val 2035	Ala Asn Ala Lys Ala 2040	Pro Ser Arg

Asp Val 2045	Lys Gly Gln Asn Leu	Thr Asn Gly Thr Asp	Ala Met Asn 2055
Tyr Ile 2060	Thr Phe Asp Pro Asn	Thr Asn Thr Asn Gly	Ile Thr Ala 2070
Ala Trp 2075	Ala Asn Arg Gln Gln	Pro Asn Asn Gln Gln	Ala Gly Val 2085
Gln His 2090	Leu Asn Val Asp Val	Thr Tyr Pro Gly Ile	Ser Ala Ala 2100
Lys Arg 2105	Val Pro Val Thr Val	Asn Val Tyr Gln Phe	Glu Phe Pro 2115
Gln Thr 2120	Thr Tyr Thr Thr Thr	Val Gly Gly Thr Leu	Ala Ser Gly 2130
Thr Gln 2135	Ala Ser Gly Tyr Ala	His Met Gln Asn Ala	Thr Gly Leu 2145
Pro Thr 2150	Asp Gly Phe Thr Tyr	Lys Trp Asn Arg Asp	Thr Thr Gly 2160
Thr Asn 2165	Asp Ala Asn Trp Ser	Ala Met Asn Lys Pro	Asn Val Ala 2175
Lys Val 2180	Val Asn Ala Lys Tyr	Asp Val Ile Tyr Asn	Gly His Thr 2190
Phe Ala 2195	Thr Ser Leu Pro Ala	Lys Phe Val Val Lys	Asp Val Gln 2205
Pro Ala 2210	Lys Pro Thr Val Thr	Glu Thr Ala Ala Gly	Ala Ile Thr 2220
Ile Ala 2225	Pro Gly Ala Asn Gln	Thr Val Asn Thr His	Ala Gly Asn 2235
Val Thr 2240	Thr Tyr Ala Asp Lys	Leu Val Ile Lys Arg	Asn Gly Asn 2250
Val Val 2255	Thr Thr Phe Thr Arg	Arg Asn Asn Thr Ser	Pro Trp Val 2265
Lys Glu 2270	Ala Ser Ala Ala Thr	Val Ala Gly Ile Ala	Gly Thr Asn 2280
Asn Gly 2285	Ile Thr Val Ala Ala	Gly Thr Phe Asn Pro	Ala Asp Thr 2295
Ile Gln 2300	Val Val Ala Thr Gln	Gly Ser Gly Glu Thr	Val Ser Asp 2310

Glu	Gln	Arg	Ser	Asp	Asp	Phe	Thr	Val	Val	Ala	Pro	Gln	Pro	Asn	
2315						2320					2325				
Gln	Ala	Thr	Thr	Lys	Ile	Trp	Gln	Asn	Gly	His	Ile	Asp	Ile	Thr	
2330						2335					2340				
Pro	Asn	Asn	Pro	Ser	Gly	His	Leu	Ile	Asn	Pro	Thr	Gln	Ala	Met	
2345						2350					2355				
Asp	Ile	Ala	Tyr	Thr	Glu	Lys	Val	Gly	Asn	Gly	Ala	Glu	His	Ser	
2360						2365					2370				
Lys	Thr	Ile	Asn	Val	Val	Arg	Gly	Gln	Asn	Asn	Gln	Trp	Thr	Ile	
2375						2380					2385				
Ala	Asn	Lys	Pro	Asp	Tyr	Val	Thr	Leu	Asp	Ala	Gln	Thr	Gly	Lys	
2390						2395					2400				
Val	Thr	Phe	Asn	Ala	Asn	Thr	Ile	Lys	Pro	Asn	Ser	Ser	Ile	Thr	
2405						2410					2415				
Ile	Thr	Pro	Lys	Ala	Gly	Thr	Gly	His	Ser	Val	Ser	Ser	Asn	Pro	
2420						2425					2430				
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	
2450						2455					2460				
Asn	Ala	Val	Gln	Val	Ala	Asn	Lys	Arg	Thr	Ala	Thr	Ile	Lys	Asn	
2465						2470					2475				
Gly	Thr	Ala	Met	Pro	Thr	Asn	Leu	Ala	Gly	Gly	Ser	Thr	Thr	Thr	
2480						2485					2490				
Ile	Pro	Val	Thr	Val	Thr	Tyr	Asn	Asp	Gly	Ser	Thr	Glu	Glu	Val	
2495						2500					2505				
Gln	Glu	Ser	Ile	Phe	Thr	Lys	Ala	Asp	Lys	Arg	Glu	Leu	Ile	Thr	
2510						2515					2520				
Ala	Lys	Asn	His	Leu	Asp	Asp	Pro	Val	Ser	Thr	Glu	Gly	Lys	Lys	
2525						2530					2535				
Pro	Gly	Thr	Ile	Thr	Gln	Tyr	Asn	Asn	Ala	Met	His	Asn	Ala	Gln	
2540						2545					2550				
Gln	Gln	Ile	Asn	Thr	Ala	Lys	Thr	Glu	Ala	Gln	Gln	Val	Ile	Asn	
2555						2560					2565				
Asn	Glu	Arg	Ala	Thr	Pro	Gln	Gln	Val	Ser	Asp	Ala	Leu	Thr	Lys	

2570	2575	2580
Val Arg Ala Ala Gln Thr Lys Ile Asp Gln Ala Lys Ala Leu Leu 2585 2590 2595		
Gln Asn Lys Glu Asp Asn Ser Gln Leu Val Thr Ser Lys Asn Asn 2600 2605 2610		
Leu Gln Ser Ser Val Asn Gln Val Pro Ser Thr Ala Gly Met Thr 2615 2620 2625		
Gln Gln Ser Ile Asp Asn Tyr Asn Ala Lys Lys Arg Glu Ala Glu 2630 2635 2640		
Thr Glu Ile Thr Ala Ala Gln Arg Val Ile Asp Asn Gly Asp Ala 2645 2650 2655		
Thr Ala Gln Gln Ile Ser Asp Glu Lys His Arg Val Asp Asn Ala 2660 2665 2670		
Leu Thr Ala Leu Asn Gln Ala Lys His Asp Leu Thr Ala Asp Thr 2675 2680 2685		
His Ala Leu Glu Gln Ala Val Gln Gln Leu Asn Arg Thr Gly Thr 2690 2695 2700		
Thr Thr Gly Lys Lys Pro Ala Ser Ile Thr Ala Tyr Asn Asn Ser 2705 2710 2715		
Ile Arg Ala Leu Gln Ser Asp Leu Thr Ser Ala Lys Asn Ser Ala 2720 2725 2730		
Asn Ala Ile Ile Gln Lys Pro Ile Arg Thr Val Gln Glu Val Gln 2735 2740 2745		
Ser Ala Leu Thr Asn Val Asn Arg Val Asn Glu Arg Leu Thr Gln 2750 2755 2760		
Ala Ile Asn Gln Leu Val Pro Leu Ala Asp Asn Ser Ala Leu Lys 2765 2770 2775		
Thr Ala Lys Thr Lys Leu Asp Glu Glu Ile Asn Lys Ser Val Thr 2780 2785 2790		
Thr Asp Gly Met Thr Gln Ser Ser Ile Gln Ala Tyr Glu Asn Ala 2795 2800 2805		
Lys Arg Ala Gly Gln Thr Glu Ser Thr Asn Ala Gln Asn Val Ile 2810 2815 2820		
Asn Asn Gly Asp Ala Thr Asp Gln Gln Ile Ala Ala Glu Lys Thr 2825 2830 2835		

Lys Val	Glu Glu Lys Tyr	Asn Ser Leu Lys Gln	Ala Ile Ala Gly
2840		2845	2850
Leu Thr	Pro Asp Leu Ala	Pro Leu Gln Thr Ala	Lys Thr Gln Leu
2855		2860	2865
Gln Asn	Asp Ile Asp Gln	Pro Thr Ser Thr Thr	Gly Met Thr Ser
2870		2875	2880
Ala Ser	Ile Ala Ala Phe	Asn Glu Lys Leu Ser	Ala Ala Arg Thr
2885		2890	2895
Lys Ile	Gln Glu Ile Asp	Arg Val Leu Ala Ser	His Pro Asp Val
2900		2905	2910
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
2930		2935	2940
Leu Glu	Asn Ala Lys Asn	Gln Leu Gln His Ser	Ile Asp Thr Gln
2945		2950	2955
Thr Ser	Thr Thr Gly Met	Thr Gln Asp Ser Ile	Asn Ala Tyr Asn
2960		2965	2970
Ala Lys	Leu Thr Ala Ala	Arg Asn Lys Ile Gln	Gln Ile Asn Gln
2975		2980	2985
Val Leu	Ala Gly Ser Pro	Thr Val Glu Gln Ile	Asn Thr Asn Thr
2990		2995	3000
Ser Thr	Ala Asn Gln Ala	Lys Ser Asp Leu Asp	His Ala Arg Gln
3005		3010	3015
Ala Leu	Thr Pro Asp Lys	Ala Pro Leu Gln Thr	Ala Lys Thr Gln
3020		3025	3030
Leu Glu	Gln Ser Ile Asn	Gln Pro Thr Asp Thr	Thr Gly Met Thr
3035		3040	3045
Thr Ala	Ser Leu Asn Ala	Tyr Asn Gln Lys Leu	Gln Ala Ala Arg
3050		3055	3060
Gln Lys	Leu Thr Glu Ile	Asn Gln Val Leu Asn	Gly Asn Pro Thr
3065		3070	3075
Val Gln	Asn Ile Asn Asp	Lys Val Thr Glu Ala	Asn Gln Ala Lys
3080		3085	3090
Asp Gln	Leu Asn Thr Ala	Arg Gln Gly Leu Thr	Leu Asp Arg Gln
3095		3100	3105

Pro Ala	Leu Thr Thr	Leu His	Gly Ala Ser Asn	Leu Asn Gln Ala
3110		3115		3120
Gln Gln	Asn Asn Phe Thr	Gln Gln Ile Asn Ala	Ala Gln Asn His	
3125		3130		3135
Ala Ala	Leu Glu Thr Ile	Lys Ser Asn Ile Thr	Ala Leu Asn Thr	
3140		3145		3150
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	
3170		3175		3180
Ala Tyr	Asp Asn Ala Val	Asn Ala Ala Lys Gly	Val Ile Gly Glu	
3185		3190		3195
Thr Thr	Asn Pro Thr Met	Asp Val Asn Thr Val	Asn Gln Lys Ala	
3200		3205		3210
Ala Ser	Val Lys Ser Thr	Lys Asp Ala Leu Asp	Gly Gln Gln Asn	
3215		3220		3225
Leu Gln	Arg Ala Lys Thr	Glu Ala Thr Asn Ala	Ile Thr His Ala	
3230		3235		3240
Ser Asp	Leu Asn Gln Ala	Gln Lys Asn Ala Leu Thr	Gln Gln Val	
3245		3250		3255
Asn Ser	Ala Gln Asn Val	Gln Ala Val Asn Asp	Ile Lys Gln Thr	
3260		3265		3270
Thr Gln	Ser Leu Asn Thr	Ala Met Thr Gly Leu	Lys Arg Gly Val	
3275		3280		3285
Ala Asn	His Asn Gln Val	Val Gln Ser Asp Asn	Tyr Val Asn Ala	
3290		3295		3300
Asp Thr	Asn Lys Lys Asn	Asp Tyr Asn Asn Ala	Tyr Asn His Ala	
3305		3310		3315
Asn Asp	Ile Ile Asn Gly	Asn Ala Gln His Pro	Val Ile Thr Pro	
3320		3325		3330
Ser Asp	Val Asn Asn Ala	Leu Ser Asn Val Thr	Ser Lys Glu His	
3335		3340		3345
Ala Leu	Asn Gly Glu Ala	Lys Leu Asn Ala Ala	Lys Gln Glu Ala	
3350		3355		3360
Asn Thr	Ala Leu Gly His	Leu Asn Asn Leu Asn	Asn Ala Gln Arg	
3365		3370		3375

Gln Asn	Leu Gln Ser Gln	Ile Asn Gly Ala His	Gln Ile Asp Ala
3380		3385	3390
Val Asn	Thr Ile Lys Gln	Asn Ala Thr Asn Leu	Asn Ser Ala Met
3395		3400	3405
Gly Asn	Leu Arg Gln Ala	Val Ala Asp Lys Asp	Gln Val Lys Arg
3410		3415	3420
Thr Glu	Asp Tyr Ala Asp	Ala Asp Thr Ala Lys	Gln Asn Ala Tyr
3425		3430	3435
Asn Ser	Ala Val Ser Ser	Ala Glu Thr Ile Ile	Asn Gln Thr Thr
3440		3445	3450
Asn Pro	Thr Met Ser Val	Asp Asp Val Asn Arg	Ala Thr Ser Ala
3455		3460	3465
Val Thr	Ser Asn Lys Asn	Ala Leu Asn Gly Tyr	Glu Lys Leu Ala
3470		3475	3480
Gln Ser	Lys Thr Asp Ala	Ala Arg Ala Ile Asp	Ala Leu Pro His
3485		3490	3495
Leu Asn	Asn Ala Gln Lys	Ala Asp Val Lys Ser	Lys Ile Asn Ala
3500		3505	3510
Ala Ser	Asn Ile Ala Gly	Val Asn Thr Val Lys	Gln Gln Gly Thr
3515		3520	3525
Asp Leu	Asn Thr Ala Met	Gly Asn Leu Gln Gly	Ala Ile Asn Asp
3530		3535	3540
Glu Gln	Thr Thr Leu Asn	Ser Gln Asn Tyr Gln	Asp Ala Thr Pro
3545		3550	3555
Ser Lys	Lys Thr Ala Tyr	Thr Asn Ala Val Gln	Ala Ala Lys Asp
3560		3565	3570
Ile Leu	Asn Lys Ser Asn	Gly Gln Asn Lys Thr	Lys Asp Gln Val
3575		3580	3585
Thr Glu	Ala Met Asn Gln	Val Asn Ser Ala Lys	Asn Asn Leu Asp
3590		3595	3600
Gly Thr	Arg Leu Leu Asp	Gln Ala Lys Gln Thr	Ala Lys Gln Gln
3605		3610	3615
Leu Asn	Asn Met Thr His	Leu Thr Thr Ala Gln	Lys Thr Asn Leu
3620		3625	3630
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 3650 3655 3660		
Arg Gln Ser Ile Ala Asn Lys Asp Ala Thr Lys Ala Ser Glu Asp 3665 3670 3675		
Tyr Val Asp Ala Asn Asn Asp Lys Gln Thr Ala Tyr Asn Asn Ala 3680 3685 3690		
Val Ala Ala Ala Glu Thr Ile Ile Asn Ala Asn Ser Asn Pro Glu 3695 3700 3705		
Met Asn Pro Ser Thr Ile Thr Gln Lys Ala Glu Gln Val Asn Ser 3710 3715 3720		
Ser Lys Thr Ala Leu Asn Gly Asp Glu Asn Leu Ala Ala Ala Lys 3725 3730 3735		
Gln Asn Ala Lys Thr Tyr Leu Asn Thr Leu Thr Ser Ile Thr Asp 3740 3745 3750		
Ala Gln Lys Asn Asn Leu Ile Ser Gln Ile Thr Ser Ala Thr Arg 3755 3760 3765		
Val Ser Gly Val Asp Thr Val Lys Gln Asn Ala Gln His Leu Asp 3770 3775 3780		
Gln Ala Met Ala Ser Leu Gln Asn Gly Ile Asn Asn Glu Ser Gln 3785 3790 3795		
Val Lys Ser Ser Glu Lys Tyr Arg Asp Ala Asp Thr Asn Lys Gln 3800 3805 3810		
Gln Glu Tyr Asp Asn Ala Ile Thr Ala Ala Lys Ala Ile Leu Asn 3815 3820 3825		
Lys Ser Thr Gly Pro Asn Thr Ala Gln Asn Ala Val Glu Ala Ala 3830 3835 3840		
Leu Gln Arg Val Asn Asn Ala Lys Asp Ala Leu Asn Gly Asp Ala 3845 3850 3855		
Lys Leu Ile Ala Ala Gln Asn Ala Ala Lys Gln His Leu Gly Thr 3860 3865 3870		
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 3890 3895 3900		

Asn Ala 3905	Asn Ser Leu Asp Gly 3910	Ala Met Gly Asn Leu 3915	Gln Thr Ala
Ile Asn 3920	Asp Lys Ser Gly Thr 3925	Leu Ala Ser Gln Asn 3930	Phe Leu Asp
Ala Asp 3935	Glu Gln Lys Arg Asn 3940	Ala Tyr Asn Gln Ala 3945	Val Ser Ala
Ala Glu 3950	Thr Ile Leu Asn Lys 3955	Gln Thr Gly Pro Asn 3960	Thr Ala Lys
Thr Ala 3965	Val Glu Gln Ala Leu 3970	Asn Asn Val Asn Asn 3975	Ala Lys His
Ala Leu 3980	Asn Gly Thr Gln Asn 3985	Leu Asn Asn Ala Lys 3990	Gln Ala Ala
Ile Thr 3995	Ala Ile Asn Gly Ala 4000	Ser Asp Leu Asn Gln 4005	Lys Gln Lys
Asp Ala 4010	Leu Lys Ala Gln Ala 4015	Asn Gly Ala Gln Arg 4020	Val Ser Asn
Ala Gln 4025	Asp Val Gln His Asn 4030	Ala Thr Glu Leu Asn 4035	Thr Ala Met
Gly Thr 4040	Leu Lys His Ala Ile 4045	Ala Asp Lys Thr Asn 4050	Thr Leu Ala
Ser Ser 4055	Lys Tyr Val Asn Ala 4060	Asp Ser Thr Lys Gln 4065	Asn Ala Tyr
Thr Thr 4070	Lys Val Thr Asn Ala 4075	Glu His Ile Ile Ser 4080	Gly Thr Pro
Thr Val 4085	Val Thr Thr Pro Ser 4090	Glu Val Thr Ala Ala 4095	Ala Asn Gln
Val Asn 4100	Ser Ala Lys Gln Glu 4105	Leu Asn Gly Asp Glu 4110	Arg Leu Arg
Glu Ala 4115	Lys Gln Asn Ala Asn 4120	Thr Ala Ile Asp Ala 4125	Leu Thr Gln
Leu Asn 4130	Thr Pro Gln Lys Ala 4135	Lys Leu Lys Glu Gln 4140	Val Gly Gln
Ala Asn 4145	Arg Leu Glu Asp Val 4150	Gln Thr Val Gln Thr 4155	Asn Gly Gln
Ala Leu 4160	Asn Asn Ala Met Lys 4165	Gly Leu Arg Asp Ser 4170	Ile Ala Asn

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Glu	Thr	Thr	Val	Lys	Thr	Ser	Gln	Asn	Tyr	Thr	Asp	Ala	Ser	Pro
4175						4180					4185			
Asn	Asn	Gln	Ser	Thr	Tyr	Asn	Ser	Ala	Val	Ser	Asn	Ala	Lys	Gly
4190						4195					4200			
Ile	Ile	Asn	Gln	Thr	Asn	Asn	Pro	Thr	Met	Asp	Thr	Ser	Ala	Ile
4205						4210					4215			
Thr	Gln	Ala	Thr	Thr	Gln	Val	Asn	Asn	Ala	Lys	Asn	Gly	Leu	Asn
4220						4225					4230			
Gly	Ala	Glu	Asn	Leu	Arg	Asn	Ala	Gln	Asn	Thr	Ala	Lys	Gln	Asn
4235						4240					4245			
Leu	Asn	Thr	Leu	Ser	His	Leu	Thr	Asn	Asn	Gln	Lys	Ser	Ala	Ile
4250						4255					4260			
Ser	Ser	Gln	Ile	Asp	Arg	Ala	Gly	His	Val	Ser	Glu	Val	Thr	Ala
4265						4270					4275			
Thr	Lys	Asn	Ala	Ala	Thr	Glu	Leu	Asn	Thr	Gln	Met	Gly	Asn	Leu
4280						4285					4290			
Glu	Gln	Ala	Ile	His	Asp	Gln	Asn	Thr	Val	Lys	Gln	Ser	Val	Lys
4295						4300					4305			
Phe	Thr	Asp	Ala	Asp	Lys	Ala	Lys	Arg	Asp	Ala	Tyr	Thr	Asn	Ala
4310						4315					4320			
Val	Ser	Arg	Ala	Glu	Ala	Ile	Leu	Asn	Lys	Thr	Gln	Gly	Ala	Asn
4325						4330					4335			
Thr	Ser	Lys	Gln	Asp	Val	Glu	Ala	Ala	Ile	Gln	Asn	Val	Ser	Ser
4340						4345					4350			
Ala	Lys	Asn	Ala	Leu	Asn	Gly	Asp	Gln	Asn	Val	Thr	Asn	Ala	Lys
4355						4360					4365			
Asn	Ala	Ala	Lys	Asn	Ala	Leu	Asn	Asn	Leu	Thr	Ser	Ile	Asn	Asn
4370						4375					4380			
Ala	Gln	Lys	Arg	Asp	Leu	Thr	Thr	Lys	Ile	Asp	Gln	Ala	Thr	Thr
4385						4390					4395			
Val	Ala	Gly	Val	Glu	Ala	Val	Ser	Asn	Thr	Ser	Thr	Gln	Leu	Asn
4400						4405					4410			
Thr	Ala	Met	Ala	Asn	Leu	Gln	Asn	Gly	Ile	Asn	Asp	Lys	Thr	Asn
4415						4420					4425			
Thr	Leu	Ala	Ser	Glu	Asn	Tyr	His	Asp	Ala	Asp	Ser	Asp	Lys	Lys
4430						4435					4440			

Thr	Ala	Tyr	Thr	Gln	Ala	Val	Thr	Asn	Ala	Glu	Asn	Ile	Leu	Asn
4445						4450					4455			
Lys	Asn	Ser	Gly	Ser	Asn	Leu	Asp	Lys	Thr	Ala	Val	Glu	Asn	Ala
4460						4465					4470			
Leu	Ser	Gln	Val	Ala	Asn	Ala	Lys	Gly	Ala	Leu	Asn	Gly	Asn	His
4475						4480					4485			
Asn	Leu	Glu	Gln	Ala	Lys	Ser	Asn	Ala	Asn	Thr	Thr	Ile	Asn	Gly
4490						4495					4500			
Leu	Gln	His	Leu	Thr	Thr	Ala	Gln	Lys	Asp	Lys	Leu	Lys	Gln	Gln
4505						4510					4515			
Val	Gln	Gln	Ala	Gln	Asn	Val	Ala	Gly	Val	Asp	Thr	Val	Lys	Ser
4520						4525					4530			
Ser	Ala	Asn	Thr	Leu	Asn	Gly	Ala	Met	Gly	Thr	Leu	Arg	Asn	Ser
4535						4540					4545			
Ile	Gln	Asp	Asn	Thr	Ala	Thr	Lys	Asn	Gly	Gln	Asn	Tyr	Leu	Asp
4550						4555					4560			
Ala	Thr	Glu	Arg	Asn	Lys	Thr	Asn	Tyr	Asn	Asn	Ala	Val	Asp	Ser
4565						4570					4575			
Ala	Asn	Gly	Val	Ile	Asn	Ala	Thr	Ser	Asn	Pro	Asn	Met	Asp	Ala
4580						4585					4590			
Asn	Ala	Ile	Asn	Gln	Ile	Ala	Thr	Gln	Val	Thr	Ser	Thr	Lys	Asn
4595						4600					4605			
Ala	Leu	Asp	Gly	Thr	His	Asn	Leu	Thr	Gln	Ala	Lys	Gln	Thr	Ala
4610						4615					4620			
Thr	Asn	Ala	Ile	Asp	Gly	Ala	Thr	Asn	Leu	Asn	Lys	Ala	Gln	Lys
4625						4630					4635			
Asp	Ala	Leu	Lys	Ala	Gln	Val	Thr	Ser	Ala	Gln	Arg	Val	Ala	Asn
4640						4645					4650			
Val	Thr	Ser	Ile	Gln	Gln	Thr	Ala	Asn	Glu	Leu	Asn	Thr	Ala	Met
4655						4660					4665			
Gly	Gln	Leu	Gln	His	Gly	Ile	Asp	Asp	Glu	Asn	Ala	Thr	Lys	Gln
4670						4675					4680			
Thr	Gln	Lys	Tyr	Arg	Asp	Ala	Glu	Gln	Ser	Lys	Lys	Thr	Ala	Tyr
4685						4690					4695			
Asp	Gln	Ala	Val	Ala	Ala	Ala	Lys	Ala	Ile	Leu	Asn	Lys	Gln	Thr

4700		4705		4710
Gly Ser Asn Ser Asp Lys	Ala 4720	Ala Val Asp Arg	Ala 4725	Leu Gln Gln
Val Thr Ser Thr Lys Asp	Ala 4735	Leu Asn Gly Asp	Ala 4740	Lys Leu Ala
Glu Ala Lys Ala Ala Ala	Lys 4750	Gln Asn Leu Gly Thr	Leu 4755	Asn His
Ile Thr Asn Ala Gln Arg	Thr 4765	Asp Leu Glu Gly Gln	Ile 4770	Asn Gln
Ala Thr Thr Val Asp Gly	Val 4780	Asn Thr Val Lys Thr	Asn 4785	Ala Asn
Thr Leu Asp Gly Ala Met	Asn 4795	Ser Leu Gln Gly Ser	Ile 4800	Asn Asp
Lys Asp Ala Thr Leu Arg	Asn 4810	Gln Asn Tyr Leu Asp	Ala 4815	Asp Glu
Ser Lys Arg Asn Ala Tyr	Thr 4825	Gln Ala Val Thr Ala	Ala 4830	Glu Gly
Ile Leu Asn Lys Gln Thr	Gly 4840	Gly Asn Thr Ser Lys	Ala 4845	Asp Val
Asp Asn Ala Leu Asn Ala	Val 4855	Thr Arg Ala Lys Ala	Ala 4860	Leu Asn
Gly Ala Asp Asn Leu Arg	Asn 4870	Ala Lys Thr Ser Ala	Thr 4875	Asn Thr
Ile Asp Gly Leu Pro Asn	Leu 4885	Thr Gln Leu Gln Lys	Asp 4890	Asn Leu
Lys His Gln Val Glu Gln	Ala 4900	Gln Asn Val Ala Gly	Val 4905	Asn Gly
Val Lys Asp Lys Gly Asn	Thr 4915	Leu Asn Thr Ala Met	Gly 4920	Ala Leu
Arg Thr Ser Ile Gln Asn	Asp 4930	Asn Thr Thr Lys Thr	Ser 4935	Gln Asn
Tyr Leu Asp Ala Ser Asp	Ser 4945	Asn Lys Asn Asn Tyr	Asn 4950	Thr Ala
Val Asn Asn Ala Asn Gly	Val 4960	Ile Asn Ala Thr Asn	Asn 4965	Pro Asn

Met Asp 4970	Ala Asn Ala Ile Asn 4975	Gly Met Ala Asn Gln 4980	Val Asn Thr
Thr Lys 4985	Ala Ala Leu Asn Gly 4990	Ala Gln Asn Leu Ala 4995	Gln Ala Lys
Thr Asn 5000	Ala Thr Asn Thr Ile 5005	Asn Asn Ala His Asp 5010	Leu Asn Gln
Lys Gln 5015	Lys Asp Ala Leu Lys 5020	Thr Gln Val Asn Asn 5025	Ala Gln Arg
Val Ser 5030	Asp Ala Asn Asn Val 5035	Gln His Thr Ala Thr 5040	Glu Leu Asn
Ser Ala 5045	Met Thr Ala Leu Lys 5050	Ala Ala Ile Ala Asp 5055	Lys Glu Arg
Thr Lys 5060	Ala Ser Gly Asn Tyr 5065	Val Asn Ala Asp Gln 5070	Glu Lys Arg
Gln Ala 5075	Tyr Asp Ser Lys Val 5080	Thr Asn Ala Glu Asn 5085	Ile Ile Ser
Gly Thr 5090	Pro Asn Ala Thr Leu 5095	Thr Val Asn Asp Val 5100	Asn Ser Ala
Ala Ser 5105	Gln Val Asn Ala Ala 5110	Lys Thr Ala Leu Asn 5115	Gly Asp Asn
Asn Leu 5120	Arg Val Ala Lys Glu 5125	His Ala Asn Asn Thr 5130	Ile Asp Gly
Leu Ala 5135	Gln Leu Asn Asn Ala 5140	Gln Lys Ala Lys Leu 5145	Lys Glu Gln
Val Gln 5150	Ser Ala Thr Thr Leu 5155	Asp Gly Val Gln Thr 5160	Val Lys Asn
Ser Ser 5165	Gln Thr Leu Asn Thr 5170	Ala Met Lys Gly Leu 5175	Arg Asp Ser
Ile Ala 5180	Asn Glu Ala Thr Ile 5185	Lys Ala Gly Gln Asn 5190	Tyr Thr Asp
Ala Ser 5195	Pro Asn Asn Arg Asn 5200	Glu Tyr Asp Ser Ala 5205	Val Thr Ala
Ala Lys 5210	Ala Ile Ile Asn Gln 5215	Thr Ser Asn Pro Thr 5220	Met Glu Pro
Asn Thr 5225	Ile Thr Gln Val Thr 5230	Ser Gln Val Thr Thr 5235	Lys Glu Gln

Ala	Leu	Asn	Gly	Ala	Arg	Asn	Leu	Ala	Gln	Ala	Lys	Thr	Thr	Ala
5240						5245					5250			
Lys	Asn	Asn	Leu	Asn	Asn	Leu	Thr	Ser	Ile	Asn	Asn	Ala	Gln	Lys
5255						5260					5265			
Asp	Ala	Leu	Thr	Arg	Ser	Ile	Asp	Gly	Ala	Thr	Thr	Val	Ala	Gly
5270						5275					5280			
Val	Asn	Gln	Glu	Thr	Ala	Lys	Ala	Thr	Glu	Leu	Asn	Asn	Ala	Met
5285						5290					5295			
His	Ser	Leu	Gln	Asn	Gly	Ile	Asn	Asp	Glu	Thr	Gln	Thr	Lys	Gln
5300						5305					5310			
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
5330						5335					5340			
Gly	Gln	Asn	Val	Asp	Lys	Ala	Ala	Val	Glu	Gln	Ala	Leu	Gln	Asn
5345						5350					5355			
Val	Asn	Ser	Thr	Lys	Thr	Ala	Leu	Asn	Gly	Asp	Ala	Lys	Leu	Asn
5360						5365					5370			
Glu	Ala	Lys	Ala	Ala	Ala	Lys	Gln	Thr	Leu	Gly	Thr	Leu	Thr	His
5375						5380					5385			
Ile	Asn	Asn	Ala	Gln	Arg	Thr	Ala	Leu	Asp	Asn	Glu	Ile	Thr	Gln
5390						5395					5400			
Ala	Thr	Asn	Val	Glu	Gly	Val	Asn	Thr	Val	Lys	Ala	Lys	Ala	Gln
5405						5410					5415			
Gln	Leu	Asp	Gly	Ala	Met	Gly	Gln	Leu	Glu	Thr	Ser	Ile	Arg	Asp
5420						5425					5430			
Lys	Asp	Thr	Thr	Leu	Gln	Ser	Gln	Asn	Tyr	Gln	Asp	Ala	Asp	Asp
5435						5440					5445			
Ala	Lys	Arg	Thr	Ala	Tyr	Ser	Gln	Ala	Val	Asn	Ala	Ala	Ala	Thr
5450						5455					5460			
Ile	Leu	Asn	Lys	Thr	Ala	Gly	Gly	Asn	Thr	Pro	Lys	Ala	Asp	Val
5465						5470					5475			
Glu	Arg	Ala	Met	Gln	Ala	Val	Thr	Gln	Ala	Asn	Thr	Ala	Leu	Asn
5480						5485					5490			
Gly	Ile	Gln	Asn	Leu	Asp	Arg	Ala	Lys	Gln	Ala	Ala	Asn	Thr	Ala
5495						5500					5505			

Ile Thr	Asn Ala Ser Asp	Leu	Asn Thr Lys Gln Lys	Glu Ala Leu
5510		5515		5520
Lys Ala	Gln Val Thr Ser	Ala	Gly Arg Val Ser	Ala Ala Asn Gly
5525		5530		5535
Val Glu	His Thr Ala Thr	Glu	Leu Asn Thr Ala	Met Thr Ala Leu
5540		5545		5550
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
5570		5575		5580
Val Thr	Ala Ala Glu Asn	Ile	Val Ser Gly Thr	Pro Thr Pro Thr
5585		5590		5595
Leu Thr	Pro Ala Asp Val	Thr	Asn Ala Ala Thr	Gln Val Thr Asn
5600		5605		5610
Ala Lys	Thr Gln Leu Asn	Gly	Asn His Asn Leu	Glu Val Ala Lys
5615		5620		5625
Gln Asn	Ala Asn Thr Ala	Ile	Asp Gly Leu Thr	Ser Leu Asn Gly
5630		5635		5640
Pro Gln	Lys Ala Lys Leu	Lys	Glu Gln Val Gly	Gln Ala Thr Thr
5645		5650		5655
Leu Pro	Asn Val Gln Thr	Val	Arg Asp Asn Ala	Gln Thr Leu Asn
5660		5665		5670
Thr Ala	Met Lys Gly Leu	Arg	Asp Ser Ile Ala	Asn Glu Ala Thr
5675		5680		5685
Ile Lys	Ala Gly Gln Asn	Tyr	Thr Asp Ala Ser	Gln Asn Lys Gln
5690		5695		5700
Thr Asp	Tyr Asn Ser Ala	Val	Thr Ala Ala Lys	Ala Ile Ile Gly
5705		5710		5715
Gln Thr	Thr Ser Pro Ser	Met	Asn Ala Gln Glu	Ile Asn Gln Ala
5720		5725		5730
Lys Asp	Gln Val Thr Ala	Lys	Gln Gln Ala Leu	Asn Gly Gln Glu
5735		5740		5745
Asn Leu	Arg Thr Ala Gln	Thr	Asn Ala Lys Gln	His Leu Asn Gly
5750		5755		5760
Leu Ser	Asp Leu Thr Asp	Ala	Gln Lys Asp Ala	Val Lys Arg Gln

5765						5770								5775
Ile Glu Gly Ala Thr His Val Asn Glu Val Thr Gln Ala Gln Asn	5780					5785								5790
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	5810					5815								5820
Ala Asp Glu Ala Lys Arg Asn Ala Tyr Thr Asn Ala Val Thr Gln	5825					5830								5835
Ala Glu Gln Ile Leu Asn Lys Ala Gln Gly Pro Asn Thr Ser Lys	5840					5845								5850
Asp Gly Val Glu Thr Ala Leu Glu Asn Val Gln Arg Ala Lys Asn	5855					5860								5865
Glu Leu Asn Gly Asn Gln Asn Val Ala Asn Ala Lys Thr Thr Ala	5870					5875								5880
Lys Asn Ala Leu Asn Asn Leu Thr Ser Ile Asn Asn Ala Gln Lys	5885					5890								5895
Glu Ala Leu Lys Ser Gln Ile Glu Gly Ala Thr Thr Val Ala Gly	5900					5905								5910
Val Asn Gln Val Ser Thr Thr Ala Ser Glu Leu Asn Thr Ala Met	5915					5920								5925
Ser Asn Leu Gln Asn Gly Ile Asn Asp Glu Ala Ala Thr Lys Ala	5930					5935								5940
Ala Leu Asn Gly Thr Gln Asn Leu Glu Lys Ala Lys Gln His Ala	5945					5950								5955
Asn Thr Ala Ile Asp Gly Leu Ser His Leu Thr Asn Ala Gln Lys	5960					5965								5970
Glu Ala Leu Lys Gln Leu Val Gln Gln Ser Thr Thr Val Ala Glu	5975					5980								5985
Ala Gln Gly Asn Glu Gln Lys Ala Asn Asn Val Asp Ala Ala Met	5990					5995								6000
Asp Lys Leu Arg Gln Ser Ile Ala Asp Asn Ala Thr Thr Lys Gln	6005					6010								6015
Asn Gln Asn Tyr Thr Asp Ala Ser Gln Asn Lys Lys Asp Ala Tyr	6020					6025								6030

Asn	Asn	Ala	Val	Thr	Thr	Ala	Gln	Gly	Ile	Ile	Asp	Gln	Thr	Thr
6035						6040					6045			
Ser	Pro	Thr	Leu	Asp	Pro	Thr	Val	Ile	Asn	Gln	Ala	Ala	Gly	Gln
6050						6055					6060			
Val	Ser	Thr	Thr	Lys	Asn	Ala	Leu	Asn	Gly	Asn	Glu	Asn	Leu	Glu
6065						6070					6075			
Ala	Ala	Lys	Gln	Gln	Ala	Ser	Gln	Ser	Leu	Gly	Ser	Leu	Asp	Asn
6080						6085					6090			
Leu	Asn	Asn	Ala	Gln	Lys	Gln	Thr	Val	Thr	Asp	Gln	Ile	Asn	Gly
6095						6100					6105			
Ala	His	Thr	Val	Asp	Glu	Ala	Asn	Gln	Ile	Lys	Gln	Asn	Ala	Gln
6110						6115					6120			
Asn	Leu	Asn	Thr	Ala	Met	Gly	Asn	Leu	Lys	Gln	Ala	Ile	Ala	Asp
6125						6130					6135			
Lys	Asp	Ala	Thr	Lys	Ala	Thr	Val	Asn	Phe	Thr	Asp	Ala	Asp	Gln
6140						6145					6150			
Ala	Lys	Gln	Gln	Ala	Tyr	Asn	Thr	Ala	Val	Thr	Asn	Ala	Glu	Asn
6155						6160					6165			
Ile	Ile	Ser	Lys	Ala	Asn	Gly	Gly	Asn	Ala	Thr	Gln	Ala	Glu	Val
6170						6175					6180			
Glu	Gln	Ala	Ile	Lys	Gln	Val	Asn	Ala	Ala	Lys	Gln	Ala	Leu	Asn
6185						6190					6195			
Gly	Asn	Ala	Asn	Val	Gln	His	Ala	Lys	Asp	Glu	Ala	Thr	Ala	Leu
6200						6205					6210			
Ile	Asn	Ser	Ser	Asn	Asp	Leu	Asn	Gln	Ala	Gln	Lys	Asp	Ala	Leu
6215						6220					6225			
Lys	Gln	Gln	Val	Gln	Asn	Ala	Thr	Thr	Val	Ala	Gly	Val	Asn	Asn
6230						6235					6240			
Val	Lys	Gln	Thr	Ala	Gln	Glu	Leu	Asn	Asn	Ala	Met	Thr	Gln	Leu
6245						6250					6255			
Lys	Gln	Gly	Ile	Ala	Asp	Lys	Glu	Gln	Thr	Lys	Ala	Asp	Gly	Asn
6260						6265					6270			
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
6290						6295					6300			

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Val	Thr	Pro	Ser	Glu	Ile	Thr	Ala	Ala	Leu	Asn	Lys	Val	Thr	Gln
	6305					6310					6315			
Ala	Lys	Asn	Asp	Leu	Asn	Gly	Asn	Thr	Asn	Leu	Ala	Thr	Ala	Lys
	6320					6325					6330			
Gln	Asn	Val	Gln	His	Ala	Ile	Asp	Gln	Leu	Pro	Asn	Leu	Asn	Gln
	6335					6340					6345			
Ala	Gln	Arg	Asp	Glu	Tyr	Ser	Lys	Gln	Ile	Thr	Gln	Ala	Thr	Leu
	6350					6355					6360			
Val	Pro	Asn	Val	Asn	Ala	Ile	Gln	Gln	Ala	Ala	Thr	Thr	Leu	Asn
	6365					6370					6375			
Asp	Ala	Met	Thr	Gln	Leu	Lys	Gln	Gly	Ile	Ala	Asn	Lys	Ala	Gln
	6380					6385					6390			
Ile	Lys	Gly	Ser	Glu	Asn	Tyr	His	Asp	Ala	Asp	Thr	Asp	Lys	Gln
	6395					6400					6405			
Thr	Ala	Tyr	Asp	Asn	Ala	Val	Thr	Lys	Ala	Glu	Glu	Leu	Leu	Lys
	6410					6415					6420			
Gln	Thr	Thr	Asn	Pro	Thr	Met	Asp	Pro	Asn	Thr	Ile	Gln	Gln	Ala
	6425					6430					6435			
Leu	Thr	Lys	Val	Asn	Asp	Thr	Asn	Gln	Ala	Leu	Asn	Gly	Asn	Gln
	6440					6445					6450			
Lys	Leu	Ala	Asp	Ala	Lys	Gln	Asp	Ala	Lys	Thr	Thr	Leu	Gly	Thr
	6455					6460					6465			
Leu	Asp	His	Leu	Asn	Asp	Ala	Gln	Lys	Gln	Ala	Leu	Thr	Thr	Gln
	6470					6475					6480			
Val	Glu	Gln	Ala	Pro	Asp	Ile	Ala	Thr	Val	Asn	Asn	Val	Lys	Gln
	6485					6490					6495			
Asn	Ala	Gln	Asn	Leu	Asn	Asn	Ala	Met	Thr	Asn	Leu	Asn	Asn	Ala
	6500					6505					6510			
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
	6530					6535					6540			
Ala	Glu	Gly	Ile	Leu	Ser	Lys	Ala	Asn	Gly	Ser	Asn	Ala	Ser	Gln
	6545					6550					6555			
Thr	Glu	Val	Glu	Gln	Ala	Met	Gln	Arg	Val	Asn	Glu	Ala	Lys	Gln
	6560					6565					6570			

Ala Leu	Asn Gly	Asn Asp	Asn Val	Gln Arg	Ala Lys	Asp Ala	Ala
6575			6580		6585		
Lys Gln	Val Ile	Thr Asn	Ala Asn	Asp Leu	Asn Gln	Ala Met	Thr
6590			6595		6600		
Gln Leu	Lys Gln	Gly Ile	Ala Asp	Lys Asp	Gln Thr	Lys Ala	Asn
6605			6610		6615		
Gly Asn	Phe Val	Asn Ala	Asp Thr	Asp Lys	Gln Asn	Ala Tyr	Asn
6620			6625		6630		
Asn Ala	Val Ala	His Ala	Glu Gln	Ile Ile	Ser Gly	Thr Pro	Asn
6635			6640		6645		
Ala Asn	Val Asp	Pro Gln	Gln Val	Ala Gln	Ala Leu	Gln Gln	Val
6650			6655		6660		
Asn Gln	Ala Lys	Gly Asp	Leu Asn	Gly Asn	His Asn	Leu Gln	Val
6665			6670		6675		
Ala Lys	Asp Asn	Ala Asn	Thr Ala	Ile Asp	Gln Leu	Pro Asn	Leu
6680			6685		6690		
Asn Gln	Pro Gln	Lys Thr	Ala Leu	Lys Asp	Gln Val	Ser His	Ala
6695			6700		6705		
Glu Leu	Val Thr	Gly Val	Asn Ala	Ile Lys	Gln Asn	Ala Asp	Ala
6710			6715		6720		
Leu Asn	Asn Ala	Met Gly	Thr Leu	Lys Gln	Gln Ile	Gln Ala	Asn
6725			6730		6735		
Ser Gln	Val Pro	Gln Ser	Val Asp	Phe Thr	Gln Ala	Asp Gln	Asp
6740			6745		6750		
Lys Gln	Gln Ala	Tyr Asn	Asn Ala	Ala Asn	Gln Ala	Gln Gln	Ile
6755			6760		6765		
Ala Asn	Gly Ile	Pro Thr	Pro Val	Leu Thr	Pro Asp	Thr Val	Thr
6770			6775		6780		
Gln Ala	Val Thr	Thr Met	Asn Gln	Ala Lys	Asp Ala	Leu Asn	Gly
6785			6790		6795		
Asp Glu	Lys Leu	Ala Gln	Ala Lys	Gln Glu	Ala Leu	Ala Asn	Leu
6800			6805		6810		
Asp Thr	Leu Arg	Asp Leu	Asn Gln	Pro Gln	Arg Asp	Ala Leu	Arg
6815			6820		6825		
Asn Gln	Ile Asn	Gln Ala	Gln Ala	Leu Ala	Thr Val	Glu Gln	Thr

6830		6835		6840
Lys Gln Asn Ala Gln Asn Val Asn Thr Ala Met Ser Asn Leu Lys				
6845		6850		6855
Gln Gly Ile Ala Asn Lys Asp Thr Val Lys Ala Ser Glu Asn Tyr				
6860		6865		6870
His Asp Ala Asp Ala Asp Lys Gln Thr Ala Tyr Thr Asn Ala Val				
6875		6880		6885
Ser Gln Ala Glu Gly Ile Ile Asn Gln Thr Thr Asn Pro Thr Leu				
6890		6895		6900
Asn Pro Asp Glu Ile Thr Arg Ala Leu Thr Gln Val Thr Asp Ala				
6905		6910		6915
Lys Asn Gly Leu Asn Gly Glu Ala Lys Leu Ala Thr Glu Lys Gln				
6920		6925		6930
Asn Ala Lys Asp Ala Val Ser Gly Met Thr His Leu Asn Asp Ala				
6935		6940		6945
Gln Lys Gln Ala Leu Lys Gly Gln Ile Asp Gln Ser Pro Glu Ile				
6950		6955		6960
Ala Thr Val Asn Gln Val Lys Gln Thr Ala Thr Ser Leu Asp Gln				
6965		6970		6975
Ala Met Asp Gln Leu Ser Gln Ala Ile Asn Asp Lys Ala Gln Thr				
6980		6985		6990
Leu Ala Asp Gly Asn Tyr Leu Asn Ala Asp Pro Asp Lys Gln Asn				
6995		7000		7005
Ala Tyr Lys Gln Ala Val Ala Lys Ala Glu Ala Leu Leu Asn Lys				
7010		7015		7020
Gln Ser Gly Thr Asn Glu Val Gln Ala Gln Val Glu Ser Ile Thr				
7025		7030		7035
Asn Glu Val Asn Ala Ala Lys Gln Ala Leu Asn Gly Asn Asp Asn				
7040		7045		7050
Leu Ala Asn Ala Lys Gln Gln Ala Lys Gln Gln Leu Ala Asn Leu				
7055		7060		7065
Thr His Leu Asn Asp Ala Gln Lys Gln Ser Phe Glu Ser Gln Ile				
7070		7075		7080
Thr Gln Ala Pro Leu Val Thr Asp Val Thr Thr Ile Asn Gln Lys				
7085		7090		7095

Ala Gln Thr Leu Asp His Ala Met Glu Leu Leu Arg Asn Ser Val 7100 7105 7110
Ala Asp Asn Gln Thr Thr Leu Ala Ser Glu Asp Tyr His Asp Ala 7115 7120 7125
Thr Ala Gln Arg Gln Asn Asp Tyr Asn Gln Ala Val Thr Ala Ala 7130 7135 7140
Asn Asn Ile Ile Asn Gln Thr Thr Ser Pro Thr Met Asn Pro Asp 7145 7150 7155
Asp Val Asn Gly Ala Thr Thr Gln Val Asn Asn Thr Lys Val Ala 7160 7165 7170
Leu Asp Gly Asp Glu Asn Leu Ala Ala Ala Lys Gln Gln Ala Asn 7175 7180 7185
Asn Arg Leu Asp Gln Leu Asp His Leu Asn Asn Ala Gln Lys Gln 7190 7195 7200
Gln Leu Gln Ser Gln Ile Thr Gln Ser Ser Asp Ile Ala Ala Val 7205 7210 7215
Asn Gly His Lys Gln Thr Ala Glu Ser Leu Asn Thr Ala Met Gly 7220 7225 7230
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 7250 7255 7260
Thr Ala Val Asn Glu Ala Ala Ala Met Ile Asn Lys Gln Thr Gly 7265 7270 7275
Gln Asn Ala Asn Gln Thr Glu Val Glu Gln Ala Ile Thr Lys Val 7280 7285 7290
Gln Thr Thr Leu Gln Ala Leu Asn Gly Asp His Asn Leu Gln Val 7295 7300 7305
Ala Lys Thr Asn Ala Thr Gln Ala Ile Asp Ala Leu Thr Ser Leu 7310 7315 7320
Asn Asp Pro Gln Lys Thr Ala Leu Lys Asp Gln Val Thr Ala Ala 7325 7330 7335
Thr Leu Val Thr Ala Val His Gln Ile Glu Gln Asn Ala Asn Thr 7340 7345 7350
Leu Asn Gln Ala Met His Gly Leu Arg Gln Ser Ile Gln Asp Asn 7355 7360 7365

Ala Ala	Thr Lys	Ala Asn	Ser	Lys Tyr	Ile Asn	Glu	Asp Gln	Pro	
7370			7375			7380			
Glu Gln	Gln Asn	Tyr Asp	Gln	Ala Val	Gln Ala	Ala	Asn Asn	Ile	
7385			7390			7395			
Ile Asn	Glu Gln	Thr Ala	Thr	Leu Asp	Asn Asn	Ala	Ile Asn	Gln	
7400			7405			7410			
Ala Ala	Thr Thr	Val Asn	Thr	Thr Lys	Ala Ala	Leu	His Gly	Asp	
7415			7420			7425			
Val Lys	Leu Gln	Asn Asp	Lys	Asp His	Ala Lys	Gln	Thr Val	Ser	
7430			7435			7440			
Gln Leu	Ala His	Leu Asn	Asn	Ala Gln	Lys His	Met	Glu Asp	Thr	
7445			7450			7455			
Leu Ile	Asp Ser	Glu Thr	Thr	Arg Thr	Ala Val	Lys	Gln Asp	Leu	
7460			7465			7470			
Thr Glu	Ala Gln	Ala Leu	Asp	Gln Leu	Met Asp	Ala	Leu Gln	Gln	
7475			7480			7485			
Ser Ile	Ala Asp	Lys Asp	Ala	Thr Arg	Ala Ser	Ser	Ala Tyr	Val	
7490			7495			7500			
Asn Ala	Glu Pro	Asn Lys	Lys	Gln Ser	Tyr Asp	Glu	Ala Val	Gln	
7505			7510			7515			
Asn Ala	Glu Ser	Ile Ile	Ala	Gly Leu	Asn Asn	Pro	Thr Ile	Asn	
7520			7525			7530			
Lys Gly	Asn Val	Ser Ser	Ala	Thr Gln	Ala Val	Ile	Ser Ser	Lys	
7535			7540			7545			
Asn Ala	Leu Asp	Gly Val	Glu	Arg Leu	Ala Gln	Asp	Lys Gln	Thr	
7550			7555			7560			
Ala Gly	Asn Ser	Leu Asn	His	Leu Asp	Gln Leu	Thr	Pro Ala	Gln	
7565			7570			7575			
Gln Gln	Ala Leu	Glu Asn	Gln	Ile Asn	Asn Ala	Thr	Thr Arg	Asp	
7580			7585			7590			
Lys Val	Ala Glu	Ile Ile	Ala	Gln Ala	Gln Ala	Leu	Asn Glu	Ala	
7595			7600			7605			
Met Lys	Ala Leu	Lys Glu	Ser	Ile Lys	Asp Gln	Pro	Gln Thr	Glu	
7610			7615			7620			
Ala Ser	Ser Lys	Phe Ile	Asn	Glu Asp	Gln Ala	Gln	Lys Asp	Ala	
7625			7630			7635			

Tyr Thr	Gln Ala Val	Gln His	Ala Lys Asp	Leu Ile	Asn Lys Thr	
7640		7645		7650		
Thr Asp	Pro Thr Leu	Ala Lys	Ser Ile Ile	Asp Gln	Ala Thr Gln	
7655		7660		7665		
Ala Val	Thr Asp Ala	Lys Asn	Asn Leu His	Gly Asp	Gln Lys Leu	
7670		7675		7680		
Ala Gln	Asp Lys Gln	Arg Ala	Thr Glu Thr	Leu Asn	Asn Leu Ser	
7685		7690		7695		
Asn Leu	Asn Thr Pro	Gln Arg	Gln Ala Leu	Glu Asn	Gln Ile Asn	
7700		7705		7710		
Asn Ala	Ala Thr Arg	Gly Glu	Val Ala Gln	Lys Leu	Thr Glu Ala	
7715		7720		7725		
Gln Ala	Leu Asn Gln	Ala Met	Glu Ala Leu	Arg Asn	Ser Ile Gln	
7730		7735		7740		
Asp Gln	Gln Gln Thr	Glu Ala	Gly Ser Lys	Phe Ile	Asn Glu Asp	
7745		7750		7755		
Lys Pro	Gln Lys Asp	Ala Tyr	Gln Ala Ala	Val Gln	Asn Ala Lys	
7760		7765		7770		
Asp Leu	Ile Asn Gln	Thr Asn	Asn Pro Thr	Leu Asp	Lys Ala Gln	
7775		7780		7785		
Val Glu	Gln Leu Thr	Gln Ala	Val Asn Gln	Ala Lys	Asp Asn Leu	
7790		7795		7800		
His Gly	Asp Gln Lys	Leu Ala	Asp Asp Lys	Gln His	Ala Val Thr	
7805		7810		7815		
Asp Leu	Asn Gln Leu	Asn Gly	Leu Asn Asn	Pro Gln	Arg Gln Ala	
7820		7825		7830		
Leu Glu	Ser Gln Ile	Asn Asn	Ala Ala Thr	Arg Gly	Glu Val Ala	
7835		7840		7845		
Gln Lys	Leu Ala Glu	Ala Lys	Ala Leu Asp	Gln Ala	Met Gln Ala	
7850		7855		7860		
Leu Arg	Asn Ser Ile	Gln Asp	Gln Gln Gln	Thr Glu	Ser Gly Ser	
7865		7870		7875		
Lys Phe	Ile Asn Glu	Asp Lys	Pro Gln Lys	Asp Ala	Tyr Gln Ala	
7880		7885		7890		
Ala Val	Gln Asn Ala	Lys Asp	Leu Ile Asn	Gln Thr	Gly Asn Pro	

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7895					7900					7905				
Thr	Leu	Asp	Lys	Ser	Gln	Val	Glu	Gln	Leu	Thr	Gln	Ala	Val	Thr
7910					7915					7920				
Thr	Ala	Lys	Asp	Asn	Leu	His	Gly	Asp	Gln	Lys	Leu	Ala	Arg	Asp
7925					7930					7935				
Gln	Gln	Gln	Ala	Val	Thr	Thr	Val	Asn	Ala	Leu	Pro	Asn	Leu	Asn
7940					7945					7950				
His	Ala	Gln	Gln	Gln	Ala	Leu	Thr	Asp	Ala	Ile	Asn	Ala	Ala	Pro
7955					7960					7965				
Thr	Arg	Thr	Glu	Val	Ala	Gln	His	Val	Gln	Thr	Ala	Thr	Glu	Leu
7970					7975					7980				
Asp	His	Ala	Met	Glu	Thr	Leu	Lys	Asn	Lys	Val	Asp	Gln	Val	Asn
7985					7990					7995				
Thr	Asp	Lys	Ala	Gln	Pro	Asn	Tyr	Thr	Glu	Ala	Ser	Thr	Asp	Lys
8000					8005					8010				
Lys	Glu	Ala	Val	Asp	Gln	Ala	Leu	Gln	Ala	Ala	Glu	Ser	Ile	Thr
8015					8020					8025				
Asp	Pro	Thr	Asn	Gly	Ser	Asn	Ala	Asn	Lys	Asp	Ala	Val	Asp	Gln
8030					8035					8040				
Val	Leu	Thr	Lys	Leu	Gln	Glu	Lys	Glu	Asn	Glu	Leu	Asn	Gly	Asn
8045					8050					8055				
Glu	Arg	Val	Ala	Glu	Ala	Lys	Thr	Gln	Ala	Lys	Gln	Thr	Ile	Asp
8060					8065					8070				
Gln	Leu	Thr	His	Leu	Asn	Ala	Asp	Gln	Ile	Ala	Thr	Ala	Lys	Gln
8075					8080					8085				
Asn	Ile	Asp	Gln	Ala	Thr	Lys	Leu	Gln	Pro	Ile	Ala	Glu	Leu	Val
8090					8095					8100				
Asp	Gln	Ala	Thr	Gln	Leu	Asn	Gln	Ser	Met	Asp	Gln	Leu	Gln	Gln
8105					8110					8115				
Ala	Val	Asn	Glu	His	Ala	Asn	Val	Glu	Gln	Thr	Val	Asp	Tyr	Thr
8120					8125					8130				
Gln	Ala	Asp	Ser	Asp	Lys	Gln	Asn	Ala	Tyr	Lys	Gln	Ala	Ile	Ala
8135					8140					8145				
Asp	Ala	Glu	Asn	Val	Leu	Lys	Gln	Asn	Ala	Asn	Lys	Gln	Gln	Val
8150					8155					8160				

Asp	Gln	Ala	Leu	Gln	Asn	Ile	Leu	Asn	Ala	Lys	Gln	Ala	Leu	Asn
8165						8170					8175			
Gly	Asp	Glu	Arg	Val	Ala	Leu	Ala	Lys	Thr	Asn	Gly	Lys	His	Asp
8180						8185					8190			
Ile	Asp	Gln	Leu	Asn	Ala	Leu	Asn	Asn	Ala	Gln	Gln	Asp	Gly	Phe
8195						8200					8205			
Lys	Gly	Arg	Ile	Asp	Gln	Ser	Asn	Asp	Leu	Asn	Gln	Ile	Gln	Gln
8210						8215					8220			
Ile	Val	Asp	Glu	Ala	Lys	Ala	Leu	Asn	Arg	Ala	Met	Asp	Gln	Leu
8225						8230					8235			
Ser	Gln	Glu	Ile	Thr	Asp	Asn	Glu	Gly	Arg	Thr	Lys	Gly	Ser	Thr
8240						8245					8250			
Asn	Tyr	Val	Asn	Ala	Asp	Thr	Gln	Val	Lys	Gln	Val	Tyr	Asp	Glu
8255						8260					8265			
Thr	Val	Asp	Lys	Ala	Lys	Gln	Ala	Leu	Asp	Lys	Ser	Thr	Gly	Gln
8270						8275					8280			
Asn	Leu	Thr	Ala	Lys	Gln	Val	Ile	Lys	Leu	Asn	Asp	Ala	Val	Thr
8285						8290					8295			
Ala	Ala	Lys	Lys	Ala	Leu	Asn	Gly	Glu	Glu	Arg	Leu	Asn	Asn	Arg
8300						8305					8310			
Lys	Ala	Glu	Ala	Leu	Gln	Arg	Leu	Asp	Gln	Leu	Thr	His	Leu	Asn
8315						8320					8325			
Asn	Ala	Gln	Arg	Gln	Leu	Ala	Ile	Gln	Gln	Ile	Asn	Asn	Ala	Glu
8330						8335					8340			
Thr	Leu	Asn	Lys	Ala	Ser	Arg	Ala	Ile	Asn	Arg	Ala	Thr	Lys	Leu
8345						8350					8355			
Asp	Asn	Ala	Met	Gly	Ser	Val	Gln	Gln	Tyr	Ile	Asp	Glu	Gln	His
8360						8365					8370			
Leu	Gly	Val	Ile	Ser	Ser	Thr	Asn	Tyr	Ile	Asn	Ala	Asp	Asp	Asn
8375						8380					8385			
Leu	Lys	Ala	Asn	Tyr	Asp	Asn	Ala	Ile	Ala	Asn	Ala	Ala	His	Glu
8390						8395					8400			
Leu	Asp	Lys	Val	Gln	Gly	Asn	Ala	Ile	Ala	Lys	Ala	Glu	Ala	Glu
8405						8410					8415			
Gln	Leu	Lys	Gln	Asn	Ile	Ile	Asp	Ala	Gln	Asn	Ala	Leu	Asn	Gly
8420						8425					8430			

Asp Gln	Asn Leu	Ala Asn	Ala	Lys Asp	Lys Ala	Asn	Ala Phe	Val	
8435			8440			8445			
Asn Ser	Leu Asn	Gly Leu	Asn	Gln Gln	Gln Gln	Asp	Leu Ala	His	
8450			8455			8460			
Lys Ala	Ile Asn	Asn Ala	Asp	Thr Val	Ser Asp	Val	Thr Asp	Ile	
8465			8470			8475			
Val Asn	Asn Gln	Ile Asp	Leu	Asn Asp	Ala Met	Glu	Thr Leu	Lys	
8480			8485			8490			
His Leu	Val Asp	Asn Glu	Ile	Pro Asn	Ala Glu	Gln	Thr Val	Asn	
8495			8500			8505			
Tyr Gln	Asn Ala	Asp Asp	Asn	Ala Lys	Thr Asn	Phe	Asp Asp	Ala	
8510			8515			8520			
Lys Arg	Leu Ala	Asn Thr	Leu	Leu Asn	Ser Asp	Asn	Thr Asn	Val	
8525			8530			8535			
Asn Asp	Ile Asn	Gly Ala	Ile	Gln Ala	Val Asn	Asp	Ala Ile	His	
8540			8545			8550			
Asn Leu	Asn Gly	Asp Gln	Arg	Leu Gln	Asp Ala	Lys	Asp Lys	Ala	
8555			8560			8565			
Ile Gln	Ser Ile	Asn Gln	Ala	Leu Ala	Asn Lys	Leu	Lys Glu	Ile	
8570			8575			8580			
Glu Ala	Ser Asn	Ala Thr	Asp	Gln Asp	Lys Leu	Ile	Ala Lys	Asn	
8585			8590			8595			
Lys Ala	Glu Glu	Leu Ala	Asn	Ser Ile	Ile Asn	Asn	Ile Asn	Lys	
8600			8605			8610			
Ala Thr	Ser Asn	Gln Ala	Val	Ser Gln	Val Gln	Thr	Ala Gly	Asn	
8615			8620			8625			
His Ala	Ile Glu	Gln Val	His	Ala Asn	Glu Ile	Pro	Lys Ala	Lys	
8630			8635			8640			
Ile Asp	Ala Asn	Lys Asp	Val	Asp Lys	Gln Val	Gln	Ala Leu	Ile	
8645			8650			8655			
Asp Glu	Ile Asp	Arg Asn	Pro	Asn Leu	Thr Asp	Lys	Glu Lys	Gln	
8660			8665			8670			
Ala Leu	Lys Asp	Arg Ile	Asn	Gln Ile	Leu Gln	Gln	Gly His	Asn	
8675			8680			8685			
Gly Ile	Asn Asn	Ala Met	Thr	Lys Glu	Glu Ile	Glu	Gln Ala	Lys	
8690			8695			8700			

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Ala	Gln	Leu	Ala	Gln	Ala	Leu	Gln	Asp	Ile	Lys	Asp	Leu	Val	Lys
8705						8710					8715			
Ala	Lys	Glu	Asp	Ala	Lys	Gln	Asp	Val	Asp	Lys	Gln	Val	Gln	Ala
8720						8725					8730			
Leu	Ile	Asp	Glu	Ile	Asp	Gln	Asn	Pro	Asn	Leu	Thr	Asp	Lys	Glu
8735						8740					8745			
Lys	Gln	Ala	Leu	Lys	Asp	Arg	Ile	Asn	Gln	Ile	Leu	Gln	Gln	Gly
8750						8755					8760			
His	Asn	Asp	Ile	Asn	Asn	Ala	Met	Thr	Lys	Glu	Ala	Ile	Glu	Gln
8765						8770					8775			
Ala	Lys	Glu	Arg	Leu	Ala	Gln	Ala	Leu	Gln	Asp	Ile	Lys	Asp	Leu
8780						8785					8790			
Val	Lys	Ala	Lys	Glu	Asp	Ala	Lys	Asn	Asp	Ile	Asp	Lys	Arg	Val
8795						8800					8805			
Gln	Ala	Leu	Ile	Asp	Glu	Ile	Asp	Gln	Asn	Pro	Asn	Leu	Thr	Asp
8810						8815					8820			
Lys	Glu	Lys	Gln	Ala	Leu	Lys	Asp	Arg	Ile	Asn	Gln	Ile	Leu	Gln
8825						8830					8835			
Gln	Gly	His	Asn	Asp	Ile	Asn	Asn	Ala	Leu	Thr	Lys	Glu	Glu	Ile
8840						8845					8850			
Glu	Gln	Ala	Lys	Ala	Gln	Leu	Ala	Gln	Ala	Leu	Gln	Asp	Ile	Lys
8855						8860					8865			
Asp	Leu	Val	Lys	Ala	Lys	Glu	Asp	Ala	Lys	Asn	Ala	Ile	Lys	Ala
8870						8875					8880			
Leu	Ala	Asn	Ala	Lys	Arg	Asp	Gln	Ile	Asn	Ser	Asn	Pro	Asp	Leu
8885						8890					8895			
Thr	Pro	Glu	Gln	Lys	Ala	Lys	Ala	Leu	Lys	Glu	Ile	Asp	Glu	Ala
8900						8905					8910			
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
8930						8935					8940			
Thr	His	Val	Trp	Glu	Val	Asp	Glu	Gln	Pro	Ala	Val	Asn	Glu	Ile
8945						8950					8955			
Phe	Glu	Ala	Thr	Pro	Glu	Gln	Ile	Leu	Val	Asn	Gly	Glu	Leu	Ile
8960						8965					8970			

8960		8965		8970
Val His Arg Asp Asp Ile Ile Thr Glu Gln Asp Ile Leu Ala His				
8975		8980		8985
Ile Asn Leu Ile Asp Gln Leu Ser Ala Glu Val Ile Asp Thr Pro				
8990		8995		9000
Ser Thr Ala Thr Ile Ser Asp Ser Leu Thr Ala Lys Val Glu Val				
9005		9010		9015
Thr Leu Leu Asp Gly Ser Lys Val Ile Val Asn Val Pro Val Lys				
9020		9025		9030
Val Val Glu Lys Glu Leu Ser Val Val Lys Gln Gln Ala Ile Glu				
9035		9040		9045
Ser Ile Glu Asn Ala Ala Gln Gln Lys Ile Asn Glu Ile Asn Asn				
9050		9055		9060
Ser Val Thr Leu Thr Leu Glu Gln Lys Glu Ala Ala Ile Ala Glu				
9065		9070		9075
Val Asn Lys Leu Lys Gln Gln Ala Ile Asp His Val Asn Asn Ala				
9080		9085		9090
Pro Asp Val His Ser Val Glu Glu Ile Gln Gln Gln Glu Gln Ala				
9095		9100		9105
His Ile Glu Gln Phe Asn Pro Glu Gln Phe Thr Ile Glu Gln Ala				
9110		9115		9120
Lys Ser Asn Ala Ile Lys Ser Ile Glu Asp Ala Ile Gln His Met				
9125		9130		9135
Ile Asp Glu Ile Lys Ala Arg Thr Asp Leu Thr Asp Lys Glu Lys				
9140		9145		9150
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				
9170		9175		9180
Leu Glu Gln Phe Lys Ala Gln Met Lys Ala Ala Asn Pro Thr Ala				
9185		9190		9195
Lys Glu Leu Ala Lys Arg Lys Gln Glu Ala Ile Ser Arg Ile Lys				
9200		9205		9210
Asp Phe Ser Asn Glu Lys Ile Asn Ser Ile Arg Asn Ser Glu Ile				
9215		9220		9225

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Gly	Thr	Ala	Asp	Glu	Lys	Gln	Ala	Ala	Met	Asn	Gln	Ile	Asn	Glu
9230						9235					9240			
Ile	Val	Leu	Glu	Thr	Ile	Arg	Asp	Ile	Asn	Asn	Ala	His	Thr	Leu
9245						9250					9255			
Gln	Gln	Val	Glu	Ala	Ala	Leu	Asn	Asn	Gly	Ile	Ala	Arg	Ile	Ser
9260						9265					9270			
Ala	Val	Gln	Ile	Val	Thr	Ser	Asp	Arg	Ala	Lys	Gln	Ser	Ser	Ser
9275						9280					9285			
Thr	Gly	Asn	Glu	Ser	Asn	Ser	His	Leu	Thr	Ile	Gly	Tyr	Gly	Thr
9290						9295					9300			
Ala	Asn	His	Pro	Phe	Asn	Ser	Ser	Thr	Ile	Gly	His	Lys	Lys	Lys
9305						9310					9315			
Leu	Asp	Glu	Asp	Asp	Asp	Ile	Asp	Pro	Leu	His	Met	Arg	His	Phe
9320						9325					9330			
Ser	Asn	Asn	Phe	Gly	Asn	Val	Ile	Lys	Asn	Ala	Ile	Gly	Val	Val
9335						9340					9345			
Gly	Ile	Ser	Gly	Leu	Leu	Ala	Ser	Phe	Trp	Phe	Phe	Ile	Ala	Lys
9350						9355					9360			
Arg	Arg	Arg	Lys	Glu	Asp	Glu	Glu	Glu	Glu	Leu	Glu	Ile	Arg	Asp
9365						9370					9375			
Asn	Asn	Lys	Asp	Ser	Ile	Lys	Glu	Thr	Leu	Asp	Asp	Thr	Lys	His
9380						9385					9390			
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
9410						9415					9420			
Leu	Asp	Lys	Val	Lys	His	Thr	Pro	Phe	Phe	Leu	Pro	Lys	Arg	Arg
9425						9430					9435			
Arg	Lys	Glu	Asp	Glu	Glu	Asp	Val	Glu	Val	Thr	Asn	Glu	Asn	Thr
9440						9445					9450			
Asp	Glu	Lys	Val	Leu	Lys	Asp	Asn	Glu	His	Ser	Pro	Leu	Leu	Phe
9455						9460					9465			
Ala	Lys	Arg	Arg	Lys	Asp	Lys	Glu	Glu	Asp	Val	Glu	Thr	Thr	Thr
9470						9475					9480			
Ser	Ile	Glu	Ser	Lys	Asp	Glu	Asp	Val	Pro	Leu	Leu	Leu	Ala	Lys
9485						9490					9495			

Lys Lys Asn Gln Lys Asp Asn Gln Ser Lys Asp Lys Lys Ser Ala
9500 9505 9510

Ser Lys Asn Thr Ser Lys Lys Val Ala Ala Lys Lys Lys Lys Lys
9515 9520 9525

Lys Ala Lys Lys Asn Lys Lys
9530 9535

<210> 6
<211> 486
<212> PRT
<213> Staphylococcus aureus
<223> ebpS

<400> 6

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
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
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
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

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

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

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

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

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

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

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

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

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 Gln Arg
420 425 430

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

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

485

<210> 7
 <211> 165
 <212> PRT
 <213> Staphylococcus aureus
 <223> efb

<400> 7

Met Lys Asn Lys Leu Ile Ala Lys Ser Leu Leu Thr Leu Ala Ala Ile
 1 5 10 15

Gly Ile Thr Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly
 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
 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
 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
 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
 145 150 155 160

Gln Gly Leu Val Lys
 165

<210> 8
 <211> 340
 <212> PRT
 <213> Staphylococcus aureus
 <223> emp

<400> 8

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
 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
 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
 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
 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
 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
 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
 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
 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
 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
 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
 340

<210> 9
 <211> 130
 <212> PRT
 <213> Staphylococcus aureus
 <223> esaC

<400> 9

Met Asn Phe Asn Asp Ile Glu Thr Met Val Lys Ser Lys Phe Lys Asp
 1 5 10 15

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

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

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

Ala Lys Glu Ile Ala Gly Glu Lys Ala Ser Glu Tyr Phe Asn Lys Ala
 115 120 125

Met Asn
 130

<210> 10
 <211> 97
 <212> PRT
 <213> Staphylococcus aureus
 <223> esxA

<400> 10

Met Ala Met Ile Lys Met Ser Pro Glu Glu Ile Arg Ala Lys Ser Gln
 1 5 10 15

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

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

Asp Ala Val Gln Glu Gln Asp Gln Gln Leu Ser Asn Asn Phe Gly Leu
85 90 95

Gln

<210> 11
<211> 104
<212> PRT
<213> Staphylococcus aureus
<223> esxB

<400> 11

Met Gly Gly Tyr Lys Gly Ile Lys Ala Asp Gly Gly Lys Val Asp Gln
1 5 10 15

Ala Lys Gln Leu Ala Ala Lys Thr Ala Lys Asp Ile Glu Ala Cys Gln
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
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
85 90 95

Gln Gly Leu Asp Arg Val Asn Pro
100

<210> 12
<211> 990
<212> PRT
<213> Staphylococcus aureus
<223> FnBA

<400> 12

Met Gly Gln Asp Lys Glu Ala Ala Ala Ser Glu Gln Lys Thr Thr Thr
1 5 10 15

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																	
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				
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						
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								
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					
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							
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				
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						
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				
						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
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
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
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
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
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 Val
500 505 510

Thr Thr Val Glu Glu Glu Tyr Asp Ser Ser Thr Leu Asp Ile Asp Tyr
515 520 525

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

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

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

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

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

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

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

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

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

Gln Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp Thr Thr Pro Pro Ile
835 840 845

Val Pro Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr
850 855 860

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

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

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

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
980 985 990

<210> 13
<211> 917
<212> PRT
<213> Staphylococcus aureus
<223> FnBB

<400> 13

Met Ile Val Val Gly Met Gly Gln Glu Lys Glu Ala Ala Ala Ser Glu
1 5 10 15

Gln Asn Asn Thr Thr Val Glu Glu Ser Gly Ser Ser Ala Thr Glu Ser
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
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
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

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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

Phe Thr Leu Ser Asp Asn Val Glu Thr His Gly Ile Ser Thr Leu Arg
      195                      200                      205

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

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

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

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

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

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

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

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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

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

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

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
  565                                570                                575

Asp His Thr Thr Ile Glu Asp Thr Lys Glu Tyr Thr Thr Glu Ser Asn
  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

Gly Leu Gly Thr Glu Asn Gly His Gly Asn Tyr Gly Val Ile Glu Glu
  625                                630                                635                                640

Ile Glu Glu Asn Ser His Val Asp Ile Lys Ser Glu Leu Gly Tyr Glu
  645                                650                                655

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

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

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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

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

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

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

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

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

Lys Asn His Lys Ala
      915

<210> 14
<211> 319
<212> PRT
<213> Staphylococcus aureus
<223> hla

<400> 14

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

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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
100 105 110

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

<210> 15


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<211> 325
<212> PRT
<213> Staphylococcus aureus
<223> hlgB

<400> 15

Met Lys Met Asn Lys Leu Val Lys Ser Ser Val Ala Thr Ser Met Ala
1          5          10          15

Leu Leu Leu Leu Ser Gly Thr Ala Asn Ala Glu Gly Lys Ile Thr Pro
20          25          30

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

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

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

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

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

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

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

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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

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

Thr Glu Asn Asn Lys
325

<210> 16
<211> 315
<212> PRT
<213> Staphylococcus aureus
<223> hlgC

<400> 16

Met Leu Lys Asn Lys Ile Leu Thr Thr Thr Leu Ser Val Ser Leu Leu
1 5 10 15

Ala Pro Leu Ala Asn Pro Leu Leu Glu Asn Ala Lys Ala Ala Asn Asp
20 25 30

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

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

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

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

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

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

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

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

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
<211> 350
<212> PRT
<213> Staphylococcus aureus
<223> isdA

<400> 17

Met Thr Lys His Tyr Leu Asn Ser Lys Tyr Gln Ser Glu Gln Arg Ser
1 5 10 15

Ser Ala Met Lys Lys Ile Thr Met Gly Thr Ala Ser Ile Ile Leu Gly
20 25 30

Ser Leu Val Tyr Ile Gly Ala Asp Ser Gln Gln Val Asn Ala Ala Thr
35 40 45

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

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

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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

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

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

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

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

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

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

Gly Ser Leu Ser Leu Leu Leu Phe Lys Arg Lys Glu Ser Lys
                    340                                345                    350

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<210> 18
<211> 645
<212> PRT
<213> Staphylococcus aureus
<223> isdB

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<400> 18

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Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys

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1	5	10	15
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 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
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
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
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
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	385	390	395
Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile	405	410	415
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
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
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
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
Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys	545	550	555
Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys	565	570	575

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

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
625 630 635 640

Arg Lys Arg Lys Asn
645

<210> 19

<211> 227

<212> PRT

<213> Staphylococcus aureus

<223> isdC

<400> 19

Met Lys Asn Ile Leu Lys Val Phe Asn Thr Thr Ile Leu Ala Leu Ile
1 5 10 15

Ile Ile Ile Ala Thr Phe Ser Asn Ser Ala Asn Ala Ala Asp Ser Gly
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
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
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
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
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
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
210 215 220

Asn Val Glu
225

<210> 20
<211> 107
<212> PRT
<213> Staphylococcus aureus
<223> isdG

<400> 20

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
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
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
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
<223> isdH

<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

Thr Ser Gln His Gln Ala Gln Ala Ala Glu Asn Thr Asn Thr Ser Asp

35	40	45																	
Lys	Ile	Ser	Glu	Asn	Gln	Asn	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				
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						
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								
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					
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							
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				
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						
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								
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		
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				
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	
				405					410					415		
Ser	Asp	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Pro	Val	Ser	Asn	Gly	Thr	
			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	
465					470					475					480	
Leu	Ala	Pro	Tyr	His	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	
				485					490					495		
Leu	Glu	Lys	Leu	Gln	Glu	Lys	Leu	Pro	Glu	Lys	Tyr	Lys	Ala	Glu	Tyr	
			500					505					510			
Lys	Lys	Lys	Leu	Asp	Gln	Thr	Arg	Val	Glu	Leu	Ala	Asp	Gln	Val	Lys	
		515					520					525				
Ser	Ala	Val	Thr	Glu	Phe	Glu	Asn	Val	Thr	Pro	Thr	Asn	Asp	Gln	Leu	
	530					535					540					
Thr	Asp	Leu	Gln	Glu	Ala	His	Phe	Val	Val	Phe	Glu	Ser	Glu	Glu	Asn	
545					550					555					560	
Ser	Glu	Ser	Val	Met	Asp	Gly	Phe	Val	Glu	His	Pro	Phe	Tyr	Thr	Ala	
				565					570					575		
Thr	Leu	Asn	Gly	Gln	Lys	Tyr	Val	Val	Met	Lys	Thr	Lys	Asp	Asp	Ser	
			580					585					590			
Tyr	Trp	Lys	Asp	Leu	Ile	Val	Glu	Gly	Lys	Arg	Val	Thr	Thr	Val	Ser	
		595					600					605				

Lys Asp Pro Lys Asn Asn Ser Arg Thr Leu Ile Phe Pro Tyr Ile Pro
 610 615 620
 Asp Lys Ala Val Tyr Asn Ala Ile Val Lys Val Val Val Ala Asn Ile
 625 630 635 640
 Gly Tyr Glu Gly Gln Tyr His Val Arg Ile Ile Asn Gln Asp Ile Asn
 645 650 655
 Thr Lys Asp Asp Asp Thr Ser Gln Asn Asn Thr Ser Glu Pro Leu Asn
 660 665 670
 Val Gln Thr Gly Gln Glu Gly Lys Val Ala Asp Thr Asp Val Ala Glu
 675 680 685
 Asn Ser Ser Thr Ala Thr Asn Pro Lys Asp Ala Ser Asp Lys Ala Asp
 690 695 700
 Val Ile Glu Pro Glu Ser Asp Val Val Lys Asp Ala Asp Asn Asn Ile
 705 710 715 720
 Asp Lys Asp Val Gln His Asp Val Asp His Leu Ser Asp Met Ser Asp
 725 730 735
 Asn Asn His Phe Asp Lys Tyr Asp Leu Lys Glu Met Asp Thr Gln Ile
 740 745 750
 Ala Lys Asp Thr Asp Arg Asn Val Asp Lys Asp Ala Asp Asn Ser Val
 755 760 765
 Gly Met Ser Ser Asn Val Asp Thr Asp Lys Asp Ser Asn Lys Asn Lys
 770 775 780
 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
 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
 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

<210> 22
<211> 108
<212> PRT
<213> Staphylococcus aureus
<223> isdI

<400> 22

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 40 45

Asp Glu Val Lys Ile Leu Thr Ile Trp Glu Ser Glu Asp Ser Phe Asn
50 55 60

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

<210> 23
<211> 327
<212> PRT
<213> Staphylococcus aureus
<223> lukD

<400> 23

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

2010238255

[illegible]

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<210> 24
<211> 301
<212> PRT
<213> Staphylococcus aureus
<223> lukE
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<400> 24

Met Ser Val Gly Leu Ile Ala Pro Leu Ala Ser Pro Ile Gln Glu Ser
1 5 10 15

04 Jun 2014

Arg	Ala	Asn	Thr	Asn	Ile	Glu	Asn	Ile	Gly	Asp	Gly	Ala	Glu	Val	Ile
			20					25					30		
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				
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	
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			
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
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		
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				
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	
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			
Asn	Trp	Lys	Thr	His	Glu	Ile	Lys	Val	Lys	Gly	His	Asn			
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<210> 25
<211> 338
<212> PRT
<213> Staphylococcus aureus
<223> lukF

<400> 25

Met Ile Lys Gln Leu Cys Lys Asn Ile Thr Ile Cys Thr Leu Ala Leu
1          5          10          15

Ser Thr Thr Phe Thr Val Leu Pro Ala Thr Ser Phe Ala Lys Ile Asn
          20          25          30

Ser Glu Ile Lys Gln Val Ser Glu Lys Asn Leu Asp Gly Asp Thr Lys
          35          40          45

Met Tyr Thr Arg Thr Ala Thr Thr Ser Asp Ser Gln Lys Asn Ile Thr
50          55          60

Gln Ser Leu Gln Phe Asn Phe Leu Thr Glu Pro Asn Tyr Asp Lys Glu
65          70          75          80

Thr Val Phe Ile Lys Ala Lys Gly Thr Ile Gly Ser Gly Leu Arg Ile
          85          90          95

Leu Asp Pro Asn Gly Tyr Trp Asn Ser Thr Leu Arg Trp Pro Gly Ser
          100          105          110

Tyr Ser Val Ser Ile Gln Asn Val Asp Asp Asn Asn Asn Thr Asn Val
          115          120          125

Thr Asp Phe Ala Pro Lys Asn Gln Asp Glu Ser Arg Glu Val Lys Tyr
130          135          140

Thr Tyr Gly Tyr Lys Thr Gly Gly Asp Phe Ser Ile Asn Arg Gly Gly
145          150          155          160

Leu Thr Gly Asn Ile Thr Lys Glu Ser Asn Tyr Ser Glu Thr Ile Ser
          165          170          175

Tyr Gln Gln Pro Ser Tyr Arg Thr Leu Leu Asp Gln Ser Thr Ser His
          180          185          190

Lys Gly Val Gly Trp Lys Val Glu Ala His Leu Ile Asn Asn Met Gly
          195          200          205

His Asp His Thr Arg Gln Leu Thr Asn Asp Ser Asp Asn Arg Thr Lys
210          215          220

Ser Glu Ile Phe Ser Leu Thr Arg Asn Gly Asn Leu Trp Ala Lys Asp
225          230          235          240

Asn Phe Thr Pro Lys Asp Lys Met Pro Val Thr Val Ser Glu Gly Phe
          245          250          255

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Asn Pro Glu Phe Leu Ala Val Met Ser His Asp Lys Lys Asp Lys Gly
260 265 270

Lys Ser Gln Phe Val Val His Tyr Lys Arg Ser Met Asp Glu Phe Lys
275 280 285

Ile Asp Trp Asn Arg His Gly Phe Trp Gly Tyr Trp Ser Gly Glu Asn
290 295 300

His Val Asp Lys Lys Glu Glu Lys Leu Ser Ala Leu Tyr Glu Val Asp
305 310 315 320

Trp Lys Thr His Asn Val Lys Phe Val Lys Val Leu Asn Asp Asn Glu
325 330 335

Lys Lys

<210> 26

<211> 351

<212> PRT

<213> Staphylococcus aureus

<223> lukS

<400> 26

Met Lys Asn Lys Lys Arg Val Leu Ile Ala Ser Ser Leu Ser Cys Ala
1 5 10 15

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

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

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

Ser Ile His Ser Asn Leu Lys Phe Glu Ser His Lys Glu Glu Lys Asn
115 120 125

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


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145              150              155              160

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

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

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

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

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

Arg Leu Ile Val Thr Tyr Glu Val Asp Trp Lys Asn Lys Thr Val Lys
              325              330              335

Val Val Asp Lys Tyr Ser Asp Asp Asn Lys Pro Tyr Lys Glu Gly
              340              345              350

<210> 27
<211> 177
<212> PRT
<213> Staphylococcus aureus
<223> nuc

<400> 27

Met Lys Ser Asn Lys Ser Leu Ala Met Ile Val Val Ala Ile Ile Ile
1              5              10              15

Val Gly Val Leu Ala Phe Gln Phe Met Asn His Thr Gly Pro Phe Lys
              20              25              30

Lys Gly Thr Asn His Glu Thr Val Gln Asp Leu Asn Gly Lys Asp Lys
              35              40              45

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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
<223> sasA

<400> 28

Met Ser Lys Arg Gln Lys Ala Phe His Asp Ser Leu Ala Asn Glu Lys
1 5 10 15

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

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

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

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
Glu	Lys	Ser	Glu	Lys	Val	Thr	Ser	Thr	Thr	Asn	Ser	Thr	Ser	Asn	Gln	145	150	155
Gln	Glu	Lys	Leu	Thr	Ser	Thr	Ser	Glu	Ser	Thr	Ser	Ser	Lys	Asn	Thr	165	170	175
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
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
Ala	Met	Ser	Thr	Phe	Ala	Ser	Ala	Ala	Thr	Thr	Thr	Ala	Val	Thr	Ala	245	250	255
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
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

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
 Asn Ser Ile Ile Gly Thr Pro Thr Lys Ile Gly Gln Ser Thr Val Thr
 625 630 635 640
 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
 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
Ser Gly Leu Thr Phe Asp Ser Thr Asn Asn Thr Ile Ser Gly Thr Pro		
705	710	715
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
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
Gly Ser Ile Val Val Ser Thr Ser Ala Ser Thr Ser Lys Ser Thr Ser		
785	790	795
Val Ser Leu Ser Asp Ser Val Ser Ala Ser Lys Ser Leu Ser Thr Ser		
805	810	815
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
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
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
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
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
 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
 995 1000 1005
 Glu Ile Val Ser Asp Ser Ile Ser Thr Ser Gly Ser Leu Ser Ala
 1010 1015 1020
 Ser Asp Ser Lys Ser Met Ser Val Ser Ser Ser Met Ser Thr Ser
 1025 1030 1035
 Gln Ser Gly Ser Thr Ser Glu Ser Leu Ser Asp Ser Gln Ser Thr
 1040 1045 1050
 Ser Asp Ser Asp Ser Lys Ser Leu Ser Gln Ser Thr Ser Gln Ser
 1055 1060 1065
 Gly Ser Thr Ser Thr Ser Thr Ser Thr Ser Ala Ser Val Arg Thr
 1070 1075 1080
 Ser Glu Ser Gln Ser Thr Ser Gly Ser Met Ser Ala Ser Gln Ser
 1085 1090 1095
 Asp Ser Met Ser Ile Ser Thr Ser Phe Ser Asp Ser Thr Ser Asp
 1100 1105 1110
 Ser Lys Ser Ala Ser Thr Ala Ser Ser Glu Ser Ile Ser Gln Ser
 1115 1120 1125
 Ala Ser Thr Ser Thr Ser Gly Ser Val Ser Thr Ser Thr Ser Leu
 1130 1135 1140
 Ser Thr Ser Asn Ser Glu Arg Thr Ser Thr Ser Met Ser Asp Ser
 1145 1150 1155
 Thr Ser Leu Ser Thr Ser Glu Ser Asp Ser Ile Ser Glu Ser Thr
 1160 1165 1170
 Ser Thr Ser Asp Ser Ile Ser Glu Ala Ile Ser Ala Ser Glu Ser
 1175 1180 1185
 Thr Phe Ile Ser Leu Ser Glu Ser Asn Ser Thr Ser Asp Ser Glu
 1190 1195 1200
 Ser Gln Ser Ala Ser Ala Phe Leu Ser Glu Ser Leu Ser Glu Ser
 1205 1210 1215
 Thr Ser Glu Ser Thr Ser Glu Ser Val Ser Ser Ser Thr Ser Glu
 1220 1225 1230

Ser Thr 1235	Ser Leu Ser Asp Ser 1240	Thr Ser Glu Ser Gly 1245	Ser Thr Ser
Thr Ser 1250	Leu Ser Asn Ser 1255	Ser Gly Ser Thr Ser 1260	Ile Ser Thr
Ser Thr 1265	Ser Ile Ser Glu Ser 1270	Thr Ser Thr Phe Lys 1275	Ser Glu Ser
Val Ser 1280	Thr Ser Leu Ser Met 1285	Ser Thr Ser Thr Ser 1290	Leu Ser Asp
Ser Thr 1295	Ser Leu Ser Thr Ser 1300	Leu Ser Asp Ser Thr 1305	Ser Asp Ser
Lys Ser 1310	Asp Ser Leu Ser Thr 1315	Ser Met Ser Thr Ser 1320	Asp Ser Ile
Ser Thr 1325	Ser Lys Ser Asp Ser 1330	Ile Ser Thr Ser Thr 1335	Ser Leu Ser
Gly Ser 1340	Thr Ser Glu Ser Glu 1345	Ser Asp Ser Thr Ser 1350	Ser Ser Glu
Ser Lys 1355	Ser Asp Ser Thr Ser 1360	Met Ser Ile Ser Met 1365	Ser Gln Ser
Thr Ser 1370	Gly Ser Thr Ser Thr 1375	Ser Thr Ser Thr Ser 1380	Leu Ser Asp
Ser Thr 1385	Ser Thr Ser Leu Ser 1390	Leu Ser Ala Ser Met 1395	Asn Gln Ser
Gly Val 1400	Asp Ser Asn Ser Ala 1405	Ser Gln Ser Ala Ser 1410	Asn Ser Thr
Ser Thr 1415	Ser Thr Ser Glu Ser 1420	Asp Ser Gln Ser Thr 1425	Ser Ser Tyr
Thr Ser 1430	Gln Ser Thr Ser Gln 1435	Ser Glu Ser Thr Ser 1440	Thr Ser Thr
Ser Leu 1445	Ser Asp Ser Thr Ser 1450	Ile Ser Lys Ser Thr 1455	Ser Gln Ser
Gly Ser 1460	Val Ser Thr Ser Ala 1465	Ser Leu Ser Gly Ser 1470	Glu Ser Glu
Ser Asp 1475	Ser Gln Ser Ile Ser 1480	Thr Ser Ala Ser Glu 1485	Ser Thr Ser
Glu Ser 1490	Ala Ser Thr Ser Leu 1495	Ser Asp Ser Thr Ser 1500	Thr Ser Asn

Ser Gly 1505	Ser Ala	Ser Thr	Ser	Thr	Ser Leu	Asn	Asn	Ser Ala	Ser	
			1510				1515			
Ala Ser 1520	Glu Ser	Asp Leu	Ser	Ser Thr	Ser Leu	Ser	Asp Ser	Thr		
			1525				1530			
Ser Ala 1535	Ser Met	Gln Ser	Ser	Glu Ser	Asp Ser	Gln	Ser Thr	Ser		
			1540				1545			
Ala Ser 1550	Leu Ser	Asp Ser	Leu	Ser Thr	Ser Thr	Ser	Asn Arg	Met		
			1555				1560			
Ser Thr 1565	Ile Ala	Ser Leu	Ser	Thr Ser	Val Ser	Thr	Ser Glu	Ser		
			1570				1575			
Gly Ser 1580	Thr Ser	Glu Ser	Thr	Ser Glu	Ser Asp	Ser	Thr Ser	Thr		
			1585				1590			
Ser Leu 1595	Ser Asp	Ser Gln	Ser	Thr Ser	Arg Ser	Thr	Ser Ala	Ser		
			1600				1605			
Gly Ser 1610	Ala Ser	Thr Ser	Thr	Ser Thr	Ser Asp	Ser	Arg Ser	Thr		
			1615				1620			
Ser Ala 1625	Ser Thr	Ser Thr	Ser	Met Arg	Thr Ser	Thr	Ser Asp	Ser		
			1630				1635			
Gln Ser 1640	Met Ser	Leu Ser	Thr	Ser Thr	Ser Thr	Ser	Met Ser	Asp		
			1645				1650			
Ser Thr 1655	Ser Leu	Ser Asp	Ser	Val Ser	Asp Ser	Thr	Ser Asp	Ser		
			1660				1665			
Thr Ser 1670	Ala Ser	Thr Ser	Gly	Ser Met	Ser Val	Ser	Ile Ser	Leu		
			1675				1680			
Ser Asp 1685	Ser Thr	Ser Thr	Ser	Thr Ser	Ala Ser	Glu	Val Met	Ser		
			1690				1695			
Ala Ser 1700	Ile Ser	Asp Ser	Gln	Ser Met	Ser Glu	Ser	Val Asn	Asp		
			1705				1710			
Ser Glu 1715	Ser Val	Ser Glu	Ser	Asn Ser	Glu Ser	Asp	Ser Lys	Ser		
			1720				1725			
Met Ser 1730	Gly Ser	Thr Ser	Val	Ser Asp	Ser Gly	Ser	Leu Ser	Val		
			1735				1740			
Ser Thr 1745	Ser Leu	Arg Lys	Ser	Glu Ser	Val Ser	Glu	Ser Ser	Ser		
			1750				1755			
Leu Ser	Cys Ser	Gln Ser	Met	Ser Asp	Ser Val	Ser	Thr Ser	Asp		

1760		1765		1770
Ser Ser 1775	Ser Leu Ser Val	Ser Thr Ser Leu Arg 1780	Ser Ser Glu Ser 1785	
Val Ser 1790	Glu Ser Asp Ser	Leu Ser Asp Ser Lys 1795	Ser Thr Ser Gly 1800	
Ser Thr 1805	Ser Thr Ser Thr	Ser Gly Ser Leu Ser 1810	Ser Thr Ser 1815	
Leu Ser 1820	Gly Ser Glu Ser	Val Ser Glu Ser Thr 1825	Ser Leu Ser Asp 1830	
Ser Ile 1835	Ser Met Ser Asp	Ser Thr Ser Thr Ser 1840	Ser Asp Ser 1845	
Leu Ser 1850	Gly Ser Ile Ser	Leu Ser Gly Ser Thr 1855	Ser Leu Ser Thr 1860	
Ser Asp 1865	Ser Leu Ser Asp	Ser Lys Ser Leu Ser 1870	Ser Ser Gln Ser 1875	
Met Ser 1880	Gly Ser Glu Ser	Thr Ser Thr Ser Val 1885	Ser Asp Ser Gln 1890	
Ser Ser 1895	Ser Thr Ser Asn	Ser Gln Phe Asp Ser 1900	Met Ser Ile Ser 1905	
Ala Ser 1910	Glu Ser Asp Ser	Met Ser Thr Ser Asp 1915	Ser Ser Ile 1920	
Ser Gly 1925	Ser Asn Ser Thr	Ser Thr Ser Leu Ser 1930	Ser Asp Ser 1935	
Met Ser 1940	Gly Ser Val Ser	Val Ser Thr Ser Thr 1945	Ser Leu Ser Asp 1950	
Ser Ile 1955	Ser Gly Ser Thr	Ser Val Ser Asp Ser 1960	Ser Ser Thr Ser 1965	
Thr Ser 1970	Thr Ser Leu Ser	Asp Ser Met Ser Gln 1975	Ser Gln Ser Thr 1980	
Ser Thr 1985	Ser Ala Ser Gly	Ser Leu Ser Thr Ser 1990	Ile Ser Thr Ser 1995	
Met Ser 2000	Met Ser Ala Ser	Thr Ser Ser Ser Gln 2005	Ser Thr Ser Val 2010	
Ser Thr 2015	Ser Leu Ser Thr	Ser Asp Ser Ile Ser 2020	Ser Thr Ser 2025	

Ile Ser 2030	Ile Ser Gly Ser 2035	Gln Ser Thr Val Glu Ser 2040	Glu Ser Thr
Ser Asp 2045	Ser Thr Ser Ile Ser 2050	Asp Ser Glu Ser Leu 2055	Ser Thr Ser
Asp Ser 2060	Asp Ser Thr Ser Thr 2065	Ser Thr Ser Asp Ser 2070	Thr Ser Gly
Ser Thr 2075	Ser Thr Ser Ile Ser 2080	Glu Ser Leu Ser Thr 2085	Ser Gly Ser
Gly Ser 2090	Thr Ser Val Ser Asp 2095	Ser Thr Ser Met Ser 2100	Glu Ser Asn
Ser Ser 2105	Ser Val Ser Met Ser 2110	Gln Asp Lys Ser Asp 2115	Ser Thr Ser
Ile Ser 2120	Asp Ser Glu Ser Val 2125	Ser Thr Ser Thr Ser 2130	Thr Ser Leu
Ser Thr 2135	Ser Asp Ser Thr Ser 2140	Thr Ser Glu Ser Leu 2145	Ser Thr Ser
Met Ser 2150	Gly Ser Gln Ser Ile 2155	Ser Asp Ser Thr Ser 2160	Thr Ser Met
Ser Gly 2165	Ser Thr Ser Thr Ser 2170	Glu Ser Asn Ser Met 2175	His Pro Ser
Asp Ser 2180	Met Ser Met His His 2185	Thr His Ser Thr Ser 2190	Thr Ser Arg
Leu Ser 2195	Ser Glu Ala Thr Thr 2200	Ser Thr Ser Glu Ser 2205	Gln Ser Thr
Leu Ser 2210	Ala Thr Ser Glu Val 2215	Thr Lys His Asn Gly 2220	Thr Pro Ala
Gln Ser 2225	Glu Lys Arg Leu Pro 2230	Asp Thr Gly Asp Ser 2235	Ile Lys Gln
Asn Gly 2240	Leu Leu Gly Gly Val 2245	Met Thr Leu Leu Val 2250	Gly Leu Gly
Leu Met 2255	Lys Arg Lys Lys Lys 2260	Lys Asp Glu Asn Asp 2265	Gln Asp Asp
Ser Gln 2270	Ala		

<210> 29
 <211> 2478
 <212> PRT

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<213> Staphylococcus aureus
<223> sasB

<400> 29

Met Asn Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val
1                               5                               10                               15

Gly Ile Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn
                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
  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
          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

Asp Asp Pro Ala Ile Ser Thr Asp Glu Asn Arg Gln Asp Pro Thr Val
      195                      200                      205

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

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

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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

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

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

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

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

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

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

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

Gln Gln Val Asn Ser Gln Val Asp Asn Ser His Tyr Thr Thr Ala Ser

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545                               550                               555                               560

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

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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
 930 935 940
 Gln Ala Ala Tyr Thr Glu Leu Asp Thr Lys Lys Gln Glu Ala Arg Thr
 945 950 955 960
 Asn Leu Asp Ala Ala Asn Thr Asn Ser Asp Val Thr Thr Ala Lys Asp
 965 970 975
 Asn Ser Ile Ala Ala Ile Asn Gln Val Gln Ala Ala Thr Thr Lys Lys
 980 985 990
 Ser Asp Ala Lys Ala Glu Ile Ala Gln Lys Ala Ser Glu Arg Lys Thr
 995 1000 1005
 Ala Ile Glu Ala Met Asn Asp Ser Thr Thr Glu Glu Gln Gln Ala
 1010 1015 1020
 Ala Lys Asp Lys Val Asp Gln Ala Val Val Thr Ala Asn Ala Asp
 1025 1030 1035
 Ile Asp Asn Ala Ala Ala Asn Asn Asp Val Asp Asn Ala Lys Thr
 1040 1045 1050
 Thr Asn Glu Ala Thr Ile Ala Ala Ile Thr Pro Asp Ala Asn Val
 1055 1060 1065
 Lys Pro Ala Ala Lys Gln Ala Ile Ala Asp Lys Val Gln Ala Gln
 1070 1075 1080
 Glu Thr Ala Ile Asp Gly Asn Asn Gly Ser Thr Thr Glu Glu Lys
 1085 1090 1095
 Ala Ala Ala Lys Gln Gln Val Gln Thr Glu Lys Thr Thr Ala Asp
 1100 1105 1110

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Ala	Ala	Ile	Asp	Ala	Ala	His	Thr	Asn	Ala	Glu	Val	Glu	Ala	Ala
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Lys	Lys	Ala	Ala	Ile	Ala	Lys	Ile	Glu	Ala	Ile	Gln	Pro	Ala	Thr
1130						1135					1140			
Thr	Thr	Lys	Asp	Asn	Ala	Lys	Glu	Ala	Ile	Ala	Thr	Lys	Ala	Asn
1145						1150					1155			
Glu	Arg	Lys	Thr	Ala	Ile	Ala	Gln	Thr	Gln	Asp	Ile	Thr	Ala	Glu
1160						1165					1170			
Glu	Ile	Ala	Ala	Ala	Asn	Ala	Asp	Val	Asp	Asn	Ala	Val	Thr	Gln
1175						1180					1185			
Ala	Asn	Ser	Asn	Ile	Glu	Ala	Ala	Asn	Ser	Gln	Asn	Asp	Val	Asp
1190						1195					1200			
Gln	Ala	Lys	Thr	Thr	Gly	Glu	Asn	Ser	Ile	Asp	Gln	Val	Thr	Pro
1205						1210					1215			
Thr	Val	Asn	Lys	Lys	Ala	Thr	Ala	Arg	Asn	Glu	Ile	Thr	Ala	Ile
1220						1225					1230			
Leu	Asn	Asn	Lys	Leu	Gln	Glu	Ile	Gln	Ala	Thr	Pro	Asp	Ala	Thr
1235						1240					1245			
Asp	Glu	Glu	Lys	Gln	Ala	Ala	Asp	Ala	Glu	Ala	Asn	Thr	Glu	Asn
1250						1255					1260			
Gly	Lys	Ala	Asn	Gln	Ala	Ile	Ser	Ala	Ala	Thr	Thr	Asn	Ala	Gln
1265						1270					1275			
Val	Asp	Glu	Ala	Lys	Ala	Asn	Ala	Glu	Ala	Ala	Ile	Asn	Ala	Val
1280						1285					1290			
Thr	Pro	Lys	Val	Val	Lys	Lys	Gln	Ala	Ala	Lys	Asp	Glu	Ile	Asp
1295						1300					1305			
Gln	Leu	Gln	Ala	Thr	Gln	Thr	Asn	Val	Ile	Asn	Asn	Asp	Gln	Asn
1310						1315					1320			
Ala	Thr	Thr	Glu	Glu	Lys	Glu	Ala	Ala	Ile	Gln	Gln	Leu	Ala	Thr
1325						1330					1335			
Ala	Val	Thr	Asp	Ala	Lys	Asn	Asn	Ile	Thr	Ala	Ala	Thr	Asp	Asp
1340						1345					1350			
Asn	Gly	Val	Asp	Gln	Ala	Lys	Asp	Ala	Gly	Lys	Asn	Ser	Ile	Gln
1355						1360					1365			
Ser	Thr	Gln	Pro	Ala	Thr	Ala	Val	Lys	Ser	Asn	Ala	Lys	Asn	Asp
1370						1375					1380			

Val	Asp	Gln	Ala	Val	Thr	Thr	Gln	Asn	Gln	Ala	Ile	Asp	Asn	Thr	1385	1390	1395
Thr	Gly	Ala	Thr	Thr	Glu	Glu	Lys	Asn	Ala	Ala	Lys	Asp	Leu	Val	1400	1405	1410
Leu	Lys	Ala	Lys	Glu	Lys	Ala	Tyr	Gln	Asp	Ile	Leu	Asn	Ala	Gln	1415	1420	1425
Thr	Thr	Asn	Asp	Val	Thr	Gln	Ile	Lys	Asp	Gln	Ala	Val	Ala	Asp	1430	1435	1440
Ile	Gln	Gly	Ile	Thr	Ala	Asp	Thr	Thr	Ile	Lys	Asp	Val	Ala	Lys	1445	1450	1455
Asp	Glu	Leu	Ala	Thr	Lys	Ala	Asn	Glu	Gln	Lys	Ala	Leu	Ile	Ala	1460	1465	1470
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	1490	1495	1500
Ala	Gln	Ser	Ile	Asp	Asp	Val	Asn	Thr	Ala	Lys	Asp	Asn	Ala	Ile	1505	1510	1515
Gln	Ala	Ile	Asp	Pro	Ile	Gln	Ala	Ser	Thr	Asp	Val	Lys	Thr	Asn	1520	1525	1530
Ala	Arg	Ala	Glu	Leu	Leu	Thr	Glu	Met	Gln	Asn	Lys	Ile	Thr	Glu	1535	1540	1545
Ile	Leu	Asn	Asn	Asn	Glu	Thr	Thr	Asn	Glu	Glu	Lys	Gly	Asn	Asp	1550	1555	1560
Ile	Gly	Pro	Val	Arg	Ala	Ala	Tyr	Glu	Glu	Gly	Leu	Asn	Asn	Ile	1565	1570	1575
Asn	Ala	Ala	Thr	Thr	Thr	Gly	Asp	Val	Thr	Thr	Ala	Lys	Asp	Thr	1580	1585	1590
Ala	Val	Gln	Lys	Val	Gln	Gln	Leu	His	Ala	Asn	Pro	Val	Lys	Lys	1595	1600	1605
Pro	Ala	Gly	Lys	Lys	Glu	Leu	Asp	Gln	Ala	Ala	Ala	Asp	Lys	Lys	1610	1615	1620
Thr	Gln	Ile	Glu	Gln	Thr	Pro	Asn	Ala	Ser	Gln	Gln	Glu	Ile	Asn	1625	1630	1635
Asp	Ala	Lys	Gln	Glu	Val	Asp	Thr	Glu	Leu	Asn	Gln	Ala	Lys	Thr			

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Asn Val 1655	Asp Gln Ser Ser	Thr 1660	Asn Glu Tyr Val	Asp 1665
Lys Glu 1670	Gly Lys Ala Lys	Ile 1675	Asn Ala Val Lys	Thr 1680
Tyr Lys 1685	Lys Asp Ala Leu	Ala 1690	Lys Ile Glu Asp	Ala 1695
Lys Val 1700	Asn Glu Ala Asp	Asn 1705	Ser Asn Ala Ser	Thr 1710
Ile Ala 1715	Glu Ala Lys Gln	Lys 1720	Leu Ala Glu Leu	Lys 1725
Asp Gln 1730	Asn Val Asn Gln	Ala 1735	Thr Ser Lys Asp	Asp 1740
Gln Ile 1745	His Asn Asp Leu	Asp 1750	Asn Ile Asn Asp	Tyr 1755
Thr Gly 1760	Lys Lys Glu Ser	Ala 1765	Thr Thr Asp Leu	Tyr 1770
Asp Gln 1775	Lys Lys Asn Asn	Ile 1780	Ser Ala Asp Thr	Asn 1785
Asp Glu 1790	Lys Gln Gln Ala	Ile 1795	Lys Gln Val Asp	Gln 1800
Thr Ala 1805	Leu Glu Ser Ile	Asn 1810	Asn Gly Val Asp	Asn 1815
Asp Asp 1820	Ala Leu Thr Gln	Gly 1825	Lys Ala Ala Ile	Asp 1830
Val Asp 1835	Ala Thr Val Lys	Pro 1840	Lys Ala Asn Gln	Ala 1845
Lys Ala 1850	Glu Asp Thr Lys	Glu 1855	Ser Ile Asp Gln	Ser 1860
Thr Ala 1865	Glu Glu Lys Thr	Glu 1870	Ala Leu Ala Met	Ile 1875
Thr Asp 1880	Gln Ala Lys Gln	Gly 1885	Ile Thr Asp Ala	Thr 1890
Glu Val 1895	Glu Lys Ala Lys	Ala 1900	Gln Gly Leu Glu	Ala 1905

Ile Gln 1910	Ile Asp Ser Thr 1915	Glu Lys Gln Lys Ala 1920	Ile Glu Glu Leu 1925
Glu Thr 1925	Ala Leu Asp Gln 1930	Ile Glu Ala Gly Val 1935	Asn Val Asn Ala 1940
Asp Ala 1940	Thr Thr Glu Glu 1945	Lys Glu Ala Phe Thr 1950	Asn Ala Leu Glu 1955
Asp Ile 1955	Leu Ser Lys Ala 1960	Thr Glu Asp Ile Ser 1965	Asp Gln Thr Thr 1970
Asn Ala 1970	Glu Ile Ala Thr 1975	Val Lys Asn Ser Ala 1980	Leu Glu Gln Leu 1985
Lys Ala 1985	Gln Arg Ile Asn 1990	Pro Glu Val Lys Lys 1995	Asn Ala Leu Glu 2000
Ala Ile 2000	Arg Glu Val Val 2005	Asn Lys Gln Ile Glu 2010	Ile Ile Lys Asn 2015
Ala Asp 2015	Ala Asp Ala Ser 2020	Ala Lys Glu Ile Ala 2025	Arg Thr Asp Leu 2030
Gly Arg 2030	Tyr Phe Asp Arg 2035	Phe Ala Asp Lys Leu 2040	Asp Lys Thr Gln 2045
Thr Asn 2045	Ala Glu Val Ala 2050	Glu Leu Gln Asn Val 2055	Thr Ile Pro Ala 2060
Ile Glu 2060	Ala Ile Val Pro 2065	Gln Asn Asp Pro Asp 2070	Ala Asn Asp Thr 2075
Asn Asn 2075	Gly Ile Asp Asn 2080	Asn Asp Ala Thr Ala 2085	Asn Ser Asn Ala 2090
Asn Ala 2090	Thr Pro Glu Asn 2095	Thr Gly Gln Pro Asn 2100	Val Ser Glu Thr 2105
Thr Ala 2105	Asn Gly Lys Ala 2110	Asp Ala Ser Pro Thr 2115	Thr Pro Asn Asn 2120
Ser Asp 2120	Ala Ala Thr Gly 2125	Glu Thr Thr Ala Thr 2130	Ser Ala Thr Asp 2135
Asp Ala 2135	Asn Asp Lys Pro 2140	Gln Ala Asn Asn Asn 2145	Ser Ser Val Asp 2150
Ala Ser 2150	Thr Asn Ser Pro 2155	Thr Met Asp Asn Asp 2160	Val Thr Ser Lys 2165
Pro Glu 2165	Val Glu Ser Thr 2170	Asn Asn Gly Thr Thr 2175	Asp Lys Pro Val 2180

Thr Glu 2180	Thr Asp Asn Ala 2185	Thr Pro Ala Glu Ser 2190	Thr Asn Asn
Asn Ser 2195	Thr Thr Thr Ala 2200	Asn Glu Asn Ala 2205	Pro Thr Gly Ser
Thr Ala 2210	Thr Ala Pro Thr 2215	Ala Ser Thr Glu 2220	Ala Ser Ser
Ala Asp 2225	Ser Lys Asp Asn 2230	Ser Val Asn Asp 2235	Lys Gln Asn
Ala Glu 2240	Val Asn Asn Ser 2245	Glu Ser Gln Ser 2250	Thr Asn Asp Lys
Val Ala 2255	Gln Pro Lys Ser 2260	Asn Lys Ala Lys 2265	Ala Glu Lys Asp
Gly Ser 2270	Asp Ser Thr Asn 2275	Gln Ser Met Val 2280	Thr Thr Glu
Thr Leu 2285	Pro Ser Ala Asp 2290	Ile Thr Glu Pro 2295	Val Pro Ser Asn
Thr Ser 2300	Lys Asp Lys Glu 2305	Glu Ser Thr Thr 2310	Asn Gln Thr Asp Ala
Gly Gln 2315	Leu Lys Ser Glu 2320	Thr Asn Val Ala 2325	Ser Asn Glu Ala Asp
Lys Ser 2330	Pro Ser Lys Ala 2335	Asp Thr Glu Val 2340	Ser Asn Lys Pro Ser
Thr Ser 2345	Ala Ser Ser Glu 2350	Ala Lys Glu Lys 2355	Met Thr Ser Thr Asn
Val Ser 2360	Gln Lys Asp Asp 2365	Thr Ala Thr Ala 2370	Asp Thr Asn Asp Thr
Gln Lys 2375	Ser Val Gly Ser 2380	Ala Ala Asn Asn 2385	Lys Ala Thr Gln Asn
Asp Gly 2390	Ala Asn Ala Ser 2395	Pro Ala Thr Val 2400	Ser Asn Gly Ser Asn
Ser Ala 2405	Asn Gln Asp Met 2410	Leu Asn Val Thr 2415	Asn Thr Asp Asp His
Gln Ala 2420	Lys Thr Lys Ser 2425	Ala Gln Gln Gly 2430	Lys Val Asn Lys Ala
Lys Gln 2435	Gln Ala Lys Thr 2440	Leu Pro Asp Thr 2445	Gly Met Ser His Asn

Asp Asp Leu Pro Tyr Ala Glu Leu Ala Leu Gly Ala Gly Met Ala
 2450 2455 2460

Phe Leu Ile Arg Arg Phe Thr Lys Lys Asp Gln Gln Thr Glu Glu
 2465 2470 2475

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 <211> 2186
 <212> PRT
 <213> Staphylococcus aureus
 <223> sasC

<400> 30

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
 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
 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
 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
 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
 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
 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

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	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	275	280	285	
Arg Thr Ser Met Phe Asp Ser Gly Asp Asn Lys Asn Tyr Gln Ala Gln	290	295	300	
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	
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	
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
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	
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	
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	

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

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

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

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

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
660 665 670

Glu Asp Leu Val Asn Gln Asn Asp Glu Leu Thr Asp Glu Glu Lys Gln
675 680 685

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

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

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

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
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
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
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
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
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
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
Ala Lys Gln Asn Ile Asn Ala Ala Asp Thr Asn Gln Glu Val Ala	1010		1015	1020
Gln Ala Lys Asp Gln Gly Thr Gln Asn Ile Val Val Ile Gln Pro	1025		1030	1035
Ala Thr Gln Val Lys Thr Asp Thr Arg Asn Val Val Asn Asp Lys	1040		1045	1050
Ala Arg Glu Ala Ile Thr Asn Ile Asn Ala Thr Thr Gly Ala Thr	1055		1060	1065

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Arg	Glu	Glu	Lys	Gln	Glu	Ala	Ile	Asn	Arg	Val	Asn	Thr	Leu	Lys
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Asn	Arg	Ala	Leu	Thr	Asp	Ile	Gly	Val	Thr	Ser	Thr	Thr	Ala	Met
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Val	Asn	Ser	Ile	Arg	Asp	Asp	Ala	Val	Asn	Gln	Ile	Gly	Ala	Val
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Gln	Pro	His	Val	Thr	Lys	Lys	Gln	Thr	Ala	Thr	Gly	Val	Leu	Asn
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Asp	Leu	Ala	Thr	Ala	Lys	Lys	Gln	Glu	Ile	Asn	Gln	Asn	Thr	Asn
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Ala	Thr	Thr	Glu	Glu	Lys	Gln	Val	Ala	Leu	Asn	Gln	Val	Asp	Gln
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Glu	Leu	Ala	Thr	Ala	Ile	Asn	Asn	Ile	Asn	Gln	Ala	Asp	Thr	Asn
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Ala	Glu	Val	Asp	Gln	Ala	Gln	Gln	Leu	Gly	Thr	Lys	Ala	Ile	Asn
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Ala	Ile	Gln	Pro	Asn	Ile	Val	Lys	Lys	Pro	Ala	Ala	Leu	Ala	Gln
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Ile	Asn	Gln	His	Tyr	Asn	Ala	Lys	Leu	Ala	Glu	Ile	Asn	Ala	Thr
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Pro	Asp	Ala	Thr	Asn	Asp	Glu	Lys	Asn	Ala	Ala	Ile	Asn	Thr	Leu
122012251230														
Asn	Gln	Asp	Arg	Gln	Gln	Ala	Ile	Glu	Ser	Ile	Lys	Gln	Ala	Asn
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Thr	Asn	Ala	Glu	Val	Asp	Gln	Ala	Ala	Thr	Val	Ala	Glu	Asn	Asn
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Ile	Asp	Ala	Val	Gln	Val	Asp	Val	Val	Lys	Lys	Gln	Ala	Ala	Arg
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Asp	Lys	Ile	Thr	Ala	Glu	Val	Ala	Lys	Arg	Ile	Glu	Ala	Val	Lys
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Gln	Thr	Pro	Asn	Ala	Thr	Asp	Glu	Glu	Lys	Gln	Ala	Ala	Val	Asn
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Gln	Ile	Asn	Gln	Leu	Lys	Asp	Gln	Ala	Ile	Asn	Gln	Ile	Asn	Gln
131013151320														
Asn	Gln	Thr	Asn	Asp	Gln	Val	Asp	Thr	Thr	Thr	Asn	Gln	Ala	Val

1325		1330		1335
Asn Ala Ile Asp Asn Val Glu Ala Glu Val Val Ile Lys Thr Lys				
1340		1345		1350
Ala Ile Ala Asp Ile Glu Lys Ala Val Lys Glu Lys Gln Gln Gln				
1355		1360		1365
Ile Asp Asn Ser Leu Asp Ser Thr Asp Asn Glu Lys Glu Val Ala				
1370		1375		1380
Ser Gln Ala Leu Ala Lys Glu Lys Glu Lys Ala Leu Ala Ala Ile				
1385		1390		1395
Asp Gln Ala Gln Thr Asn Ser Gln Val Asn Gln Ala Ala Thr Asn				
1400		1405		1410
Gly Val Ser Ala Ile Lys Ile Ile Gln Pro Glu Thr Lys Val Lys				
1415		1420		1425
Pro Ala Ala Arg Glu Lys Ile Asn Gln Lys Ala Asn Glu Leu Arg				
1430		1435		1440
Ala Lys Ile Asn Gln Asp Lys Glu Ala Thr Ala Glu Glu Arg Gln				
1445		1450		1455
Val Ala Leu Asp Lys Ile Asn Glu Phe Val Asn Gln Ala Met Thr				
1460		1465		1470
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				
1490		1495		1500
Val Arg Ala Ala Ala Arg Asp Ala Val Lys Gln Gln Tyr Glu Ala				
1505		1510		1515
Lys Lys Arg Glu Ile Glu Gln Ala Glu His Ala Thr Asp Glu Glu				
1520		1525		1530
Lys Gln Val Ala Leu Asn Gln Leu Ala Asn Asn Glu Lys Arg Ala				
1535		1540		1545
Leu Gln Asn Ile Asp Gln Ala Ile Ala Asn Asn Asp Val Lys Arg				
1550		1555		1560
Val Glu Thr Asn Gly Ile Ala Thr Leu Lys Gly Val Gln Pro His				
1565		1570		1575
Ile Val Ile Lys Pro Glu Ala Gln Gln Ala Ile Lys Ala Ser Ala				
1580		1585		1590

Glu Asn	Gln Val	Glu Ser	Ile	Lys Asp	Thr Pro	His	Ala Thr	Val	
1595			1600			1605			
Asp Glu	Leu Asp	Glu Ala	Asn	Gln Leu	Ile Ser	Asp	Thr Leu	Lys	
1610			1615			1620			
Gln Ala	Gln Gln	Glu Ile	Glu	Asn Thr	Asn Gln	Asp	Ala Ala	Val	
1625			1630			1635			
Thr Asp	Val Arg	Asn Gln	Thr	Ile Lys	Ala Ile	Glu	Gln Ile	Lys	
1640			1645			1650			
Pro Lys	Val Arg	Arg Lys	Arg	Ala Ala	Leu Asp	Ser	Ile Glu	Glu	
1655			1660			1665			
Asn Asn	Lys Asn	Gln Leu	Asp	Ala Ile	Arg Asn	Thr	Leu Asp	Thr	
1670			1675			1680			
Thr Gln	Asp Glu	Arg Asp	Val	Ala Ile	Asp Thr	Leu	Asn Lys	Ile	
1685			1690			1695			
Val Asn	Thr Ile	Lys Asn	Asp	Ile Ala	Gln Asn	Lys	Thr Asn	Ala	
1700			1705			1710			
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	
1730			1735			1740			
Gly Val	Lys Ala	Glu Ala	Gln	Asn Ala	Leu Ile	Asp	Gln Ser	Asp	
1745			1750			1755			
Leu Ser	Thr Glu	Glu Glu	Arg	Leu Ala	Ala Lys	His	Leu Val	Glu	
1760			1765			1770			
Gln Ala	Leu Asn	Gln Ala	Ile	Asp Gln	Ile Asn	His	Ala Asp	Lys	
1775			1780			1785			
Thr Ala	Gln Val	Asn Gln	Asp	Ser Ile	Asn Ala	Gln	Asn Ile	Ile	
1790			1795			1800			
Ser Lys	Ile Lys	Pro Ala	Thr	Thr Val	Lys Ala	Thr	Ala Leu	Gln	
1805			1810			1815			
Gln Ile	Gln Asn	Ile Ala	Thr	Asn Lys	Ile Asn	Leu	Ile Lys	Ala	
1820			1825			1830			
Asn Asn	Glu Ala	Thr Asp	Glu	Glu Gln	Asn Ile	Ala	Ile Ala	Gln	
1835			1840			1845			
Val Glu	Lys Glu	Leu Ile	Lys	Ala Lys	Gln Gln	Ile	Ala Ser	Ala	
1850			1855			1860			

Val 1865	Thr	Asn	Ala	Asp	Val	Ala 1870	Tyr	Leu	Leu	His	Asp 1875	Glu	Lys	Asn
Glu 1880	Ile	Arg	Glu	Ile	Glu	Pro 1885	Val	Ile	Asn	Arg	Lys 1890	Ala	Ser	Ala
Arg 1895	Glu	Gln	Leu	Thr	Thr	Leu 1900	Phe	Asn	Asp	Lys	Lys 1905	Gln	Ala	Ile
Glu 1910	Ala	Asn	Ile	Gln	Ala	Thr 1915	Val	Glu	Glu	Arg	Asn 1920	Ser	Ile	Leu
Ala 1925	Gln	Leu	Gln	Asn	Ile	Tyr 1930	Asp	Thr	Ala	Ile	Gly 1935	Gln	Ile	Asp
Gln 1940	Asp	Arg	Ser	Asn	Ala	Gln 1945	Val	Asp	Lys	Thr	Ala 1950	Ser	Leu	Asn
Leu 1955	Gln	Thr	Ile	His	Asp	Leu 1960	Asp	Val	His	Pro	Ile 1965	Lys	Lys	Pro
Asp 1970	Ala	Glu	Lys	Thr	Ile	Asn 1975	Asp	Asp	Leu	Ala	Arg 1980	Val	Thr	Ala
Leu 1985	Val	Gln	Asn	Tyr	Arg	Lys 1990	Val	Ser	Asn	Arg	Asn 1995	Lys	Ala	Asp
Ala 2000	Leu	Lys	Ala	Ile	Thr	Ala 2005	Leu	Lys	Leu	Gln	Met 2010	Asp	Glu	Glu
Leu 2015	Lys	Thr	Ala	Arg	Thr	Asn 2020	Ala	Asp	Val	Asp	Ala 2025	Val	Leu	Lys
Arg 2030	Phe	Asn	Val	Ala	Leu	Ser 2035	Asp	Ile	Glu	Ala	Val 2040	Ile	Thr	Glu
Lys 2045	Glu	Asn	Ser	Leu	Leu	Arg 2050	Ile	Asp	Asn	Ile	Ala 2055	Gln	Gln	Thr
Tyr 2060	Ala	Lys	Phe	Lys	Ala	Ile 2065	Ala	Thr	Pro	Glu	Gln 2070	Leu	Ala	Lys
Val 2075	Lys	Val	Leu	Ile	Asp	Gln 2080	Tyr	Val	Ala	Asp	Gly 2085	Asn	Arg	Met
Ile 2090	Asp	Glu	Asp	Ala	Thr	Leu 2095	Asn	Asp	Ile	Lys	Gln 2100	His	Thr	Gln
Phe 2105	Ile	Val	Asp	Glu	Ile	Leu 2110	Ala	Ile	Lys	Leu	Pro 2115	Ala	Glu	Ala
Thr 2120	Lys	Val	Ser	Pro	Lys	Glu 2125	Ile	Gln	Pro	Ala	Pro 2130	Lys	Val	Cys

Thr Pro Ile Lys Lys Glu Glu Thr His Glu Ser Arg Lys Val Glu
2135 2140 2145

Lys Glu Leu Pro Asn Thr Gly Ser Glu Gly Met Asp Leu Pro Leu
2150 2155 2160

Lys Glu Phe Ala Leu Ile Thr Gly Ala Ala Leu Leu Ala Arg Arg
2165 2170 2175

Arg Thr Lys Asn Glu Lys Glu Ser
2180 2185

<210> 31
<211> 199
<212> PRT
<213> Staphylococcus aureus
<223> sasD

<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

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180
Lys Ser Ser Asn Glu Pro Lys
195

<210> 32
<211> 635
<212> PRT
<213> Staphylococcus aureus
<223> sasF

<400> 32

Met Ala Lys Tyr Arg Gly Lys Pro Phe Gln Leu Tyr Val Lys Leu Ser
1 5 10 15

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

Ile Leu Ser Lys Gln Asp Leu Leu Asp Lys Val Asp Lys Ala Ile Arg
50 55 60

Gln Ile Glu Gln Leu Lys Gln Leu Ser Ala Ser Ser Lys Glu His Tyr
65 70 75 80

Lys Ala Gln Leu Asn Glu Ala Lys Thr Ala Ser Gln Ile Asp Glu Ile
85 90 95

Ile Lys Arg Ala Asn Glu Leu Asp Ser Lys Asp Asn Lys Ser Ser His
100 105 110

Thr Glu Met Asn Gly Gln Ser Asp Ile Asp Ser Lys Leu Asp Gln Leu
115 120 125

Leu Lys Asp Leu Asn Glu Val Ser Ser Asn Val Asp Arg Gly Gln Gln
130 135 140

Ser Gly Glu Asp Asp Leu Asn Ala Met Lys Asn Asp Met Ser Gln Thr
145 150 155 160

Ala Thr Thr Lys His Gly Glu Lys Asp Asp Lys Asn Asp Glu Ala Met
165 170 175

Val Asn Lys Ala Leu Glu Asp Leu Asp His Leu Asn Gln Gln Ile His
180 185 190

Lys Ser Lys Asp Ala Ser Lys Asp Thr Ser Glu Asp Pro Ala Val Ser
195 200 205

Thr Thr Asp Asn Asn His Glu Val Ala Lys Thr Pro Asn Asn Asp Gly
210 215 220

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Ser Gly His Val Val Leu Asn Lys Phe Leu Ser Asn Glu Glu Asn Gln
225                               230                               235                               240

Ser His Ser Asn Arg Leu Thr Asp Lys Leu Gln Gly Ser Asp Lys Ile
                               245                               250                               255

Asn His Ala Met Ile Glu Lys Leu Ala Lys Ser Asn Ala Ser Thr Gln
                               260                               265                               270

His Tyr Thr Tyr His Lys Leu Asn Thr Leu Gln Ser Leu Asp Gln Arg
275                               280                               285

Ile Ala Asn Thr Gln Leu Pro Lys Asn Gln Lys Ser Asp Leu Met Ser
290                               295                               300

Glu Val Asn Lys Thr Lys Glu Arg Ile Lys Ser Gln Arg Asn Ile Ile
305                               310                               315                               320

Leu Glu Glu Leu Ala Arg Thr Asp Asp Lys Lys Tyr Ala Thr Gln Ser
                               325                               330                               335

Ile Leu Glu Ser Ile Phe Asn Lys Asp Glu Ala Val Lys Ile Leu Lys
340                               345                               350

Asp Ile Arg Val Asp Gly Lys Thr Asp Gln Gln Ile Ala Asp Gln Ile
355                               360                               365

Thr Arg His Ile Asp Gln Leu Ser Leu Thr Thr Ser Asp Asp Leu Leu
370                               375                               380

Thr Ser Leu Ile Asp Gln Ser Gln Asp Lys Ser Leu Leu Ile Ser Gln
385                               390                               395                               400

Ile Leu Gln Thr Lys Leu Gly Lys Ala Glu Ala Asp Lys Leu Ala Lys
405                               410                               415

Asp Trp Thr Asn Lys Gly Leu Ser Asn Arg Gln Ile Val Asp Gln Leu
420                               425                               430

Lys Lys His Phe Ala Ser Thr Gly Asp Thr Ser Ser Asp Asp Ile Leu
435                               440                               445

Lys Ala Ile Leu Asn Asn Ala Lys Asp Lys Lys Gln Ala Ile Glu Thr
450                               455                               460

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

Lys Ser Ala Leu Asn Gly Lys Ala Asp Asp Leu Leu Asn Leu Gln Lys
500                               505                               510

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Arg Leu Asn Gln Thr Lys Lys Asp Ile Asp Tyr Ile Leu Ser Pro Ile
   515                               520                               525

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

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

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

Leu Ser Arg Arg Asn Lys Leu Lys Asn Lys Ala
   625                               630                               635

<210> 33
<211> 995
<212> PRT
<213> Staphylococcus aureus
<223> sdrC

<400> 33

Met Asn Asn Lys Lys Thr Ala Thr Asn Arg Lys Gly Met Ile Pro Asn
 1                               5                               10                               15

Arg Leu Asn Lys Phe Ser Ile Arg Lys Tyr Ser Val Gly Thr Ala Ser
   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
   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
   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
   115                              120                              125

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Val	Thr	Thr	Asn	Asp	Lys	Ser	Ser	Thr	Thr	Tyr	Ser	Asn	Glu	Thr	Asp	130	135	140
Lys	Ser	Asn	Leu	Thr	Gln	Ala	Lys	Asp	Val	Ser	Thr	Thr	Pro	Lys	Thr	145	150	155
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
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
Asn	Tyr	Thr	Ile	Asp	Asp	Ser	Val	Lys	Glu	Gly	Asp	Thr	Phe	Thr	Phe	225	230	235
Lys	Tyr	Gly	Gln	Tyr	Phe	Arg	Pro	Gly	Ser	Val	Arg	Leu	Pro	Ser	Gln	245	250	255
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
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
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
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
Asn	Pro	Asn	Ala	Lys	Asn	Phe	Lys	Ile	Tyr	Glu	Val	Thr	Asp	Gln	Asn	385	390	395
Gln	Phe	Val	Asp	Ser	Phe	Thr	Pro	Asp	Thr	Ser	Lys	Leu	Lys	Asp	Val			

				405						410						415			
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							
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					
Tyr	Asn	Leu	Gly	Asp	Tyr	Val	Trp	Glu	Asp	Thr	Asn	Lys	Asp	Gly	Lys				
			500					505					510						
Gln	Asp	Ala	Asn	Glu	Lys	Gly	Ile	Lys	Gly	Val	Tyr	Val	Ile	Leu	Lys				
		515					520					525							
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				
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						
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								
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					
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							

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
 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
 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
 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
 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
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser 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
 885 890 895
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 900 905 910
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 915 920 925
 Asp Ser Asp Ser Asp Ser Asp Ala Gly Lys His Thr Pro Ala Lys Pro
 930 935 940
 Met Ser Thr Val Lys Asp Gln His Lys Thr Ala Lys Ala Leu Pro Glu
 945 950 955 960
 Thr Gly Ser Glu Asn Asn Asn Ser Asn Asn Gly Thr Leu Phe Gly Gly
 965 970 975

Leu Phe Ala Ala Leu Gly Ser Leu Leu Leu Phe Gly Arg Arg Lys Lys
 980 985 990

Gln Asn Lys
 995

<210> 34
 <211> 1349
 <212> PRT
 <213> Staphylococcus aureus
 <223> sdrD

<400> 34

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
 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
 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
 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
 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
 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
 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

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

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

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

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

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

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

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

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

Lys Ile Thr Tyr Gly Asp Asn Asn Ser Ala Val Ile Asp Phe Gly Asn

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500	505	510
Ala Asp Ser 515	Ala Tyr Val Val Met 520	Val Asn Thr Lys Phe Gln Tyr Thr 525
Asn Ser Glu 530	Ser Pro Thr Leu Val 535	Gln Met Ala Thr Leu Ser Ser Thr 540
Gly Asn Lys 545	Ser Val Ser Thr 550	Gly Asn Ala Leu Gly Phe Thr Asn Asn 555 560
Gln Ser Gly 565	Gly Ala Gly Gln Glu Val 570	Tyr Lys Ile Gly Asn Tyr Val 575
Trp Glu Asp 580	Thr Asn Lys Asn Gly 585	Val Gln Glu Leu Gly Glu Lys Gly 590
Val Gly Asn 595	Val Thr Val Thr 600	Phe Asp Asn Asn Thr Asn Thr Lys 605
Val Gly Glu 610	Ala Val Thr Lys 615	Glu Asp Gly Ser Tyr Leu Ile Pro Asn 620
Leu Pro Asn 625	Gly Asp Tyr Arg Val 630	Glu Phe Ser Asn Leu Pro Lys Gly 635 640
Tyr Glu Val 645	Thr Pro Ser Lys 650	Gln Gly Asn Asn Glu Glu Leu Asp Ser 655
Asn Gly Leu 660	Ser Ser Val Ile Thr 665	Val Asn Gly Lys Asp Asn Leu Ser 670
Ala Asp Leu 675	Gly Ile Tyr Lys 680	Pro Lys Tyr Asn Leu Gly Asp Tyr Val 685
Trp Glu Asp 690	Thr Asn Lys Asn Gly 695	Ile Gln Asp Gln Asp Glu Lys Gly 700
Ile Ser Gly 705	Val Thr Val Thr 710	Leu Lys Asp Glu Asn Gly Asn Val Leu 715 720
Lys Thr Val 725	Thr Thr Asp Ala Asp 730	Gly Lys Tyr Lys Phe Thr Asp Leu 735
Asp Asn Gly 740	Asn Tyr Lys Val Glu 745	Phe Thr Thr Pro Glu Gly Tyr Thr 750
Pro Thr Thr 755	Val Thr Ser Gly 760	Ser Asp Ile Glu Lys Asp Ser Asn Gly 765
Leu Thr Thr 770	Thr Gly Val Ile 775	Asn Gly Ala Asp Asn Met Thr Leu Asp 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

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

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

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

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
930 935 940

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
965 970 975

Val Thr Ser Gly Asn Asp Thr Glu Lys Asp Ser Asn Gly Leu Thr Thr
980 985 990

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
1010 1015 1020

Ser Asn Lys Asp Gly Lys Gln Asp Ser Thr Glu Lys Gly Ile Lys
1025 1030 1035

Asp Val Lys Val Thr Leu Leu Asn Glu Lys Gly Glu Val Ile Gly
1040 1045 1050

Thr Thr Lys Thr Asp Glu Asn Gly Lys Tyr Cys Phe Asp Asn Leu
1055 1060 1065

Asp 1070	Ser	Gly	Lys	Tyr	Lys	Val 1075	Ile	Phe	Glu	Lys	Pro 1080	Ala	Gly	Leu
Thr 1085	Gln	Thr	Val	Thr	Asn	Thr 1090	Thr	Glu	Asp	Asp	Lys 1095	Asp	Ala	Asp
Gly 1100	Gly	Glu	Val	Asp	Val	Thr 1105	Ile	Thr	Asp	His	Asp 1110	Asp	Phe	Thr
Leu 1115	Asp	Asn	Gly	Tyr	Phe	Glu 1120	Glu	Asp	Thr	Ser	Asp 1125	Ser	Asp	Ser
Asp 1130	Ser	Asp	Ser	Asp	Ser	Asp 1135	Ser	Asp	Ser	Asp	Ser 1140	Asp	Ser	Asp
Ser 1145	Asp	Ser	Asp	Ser	Asp	Ser 1150	Asp	Ser	Asp	Ser	Asp 1155	Ser	Asp	Ser
Asp 1160	Ser	Asp	Ser	Asp	Ser	Asp 1165	Ser	Asp	Ser	Asp	Ser 1170	Asp	Ser	Asp
Ser 1175	Asp	Ser	Asp	Ser	Asp	Ser 1180	Asp	Ser	Asp	Ser	Asp 1185	Ser	Asp	Ser
Asp 1190	Ser	Asp	Ser	Asp	Ser	Asp 1195	Ser	Asp	Ser	Asp	Ser 1200	Asp	Ser	Asp
Ser 1205	Asp	Ser	Asp	Ser	Asp	Ser 1210	Asp	Ser	Asp	Ser	Asp 1215	Ser	Asp	Ser
Asp 1220	Ser	Asp	Ser	Asp	Ser	Asp 1225	Ser	Asp	Ser	Asp	Ser 1230	Asp	Ser	Asp
Ser 1235	Asp	Ser	Asp	Ser	Asp	Ser 1240	Asp	Ser	Asp	Ser	Asp 1245	Ser	Asp	Ser
Asp 1250	Ser	Asp	Ser	Asp	Ser	Asp 1255	Ser	Asp	Ser	Asp	Ser 1260	Asp	Ser	Asp
Ser 1265	Asp	Ser	Asp	Ser	Asp	Ser 1270	Asp	Ser	Asp	Ser	Asp 1275	Ser	Asp	Ser
Asp 1280	Ser	Asp	Ser	Asp	Ser	Asp 1285	Ser	Asp	Ser	Asp	Ala 1290	Gly	Lys	His
Thr 1295	Pro	Val	Lys	Pro	Met	Ser 1300	Thr	Thr	Lys	Asp	His 1305	His	Asn	Lys
Ala 1310	Lys	Ala	Leu	Pro	Glu	Thr 1315	Gly	Ser	Glu	Asn	Asn 1320	Gly	Ser	Asn
Asn 1325	Ala	Thr	Leu	Phe	Gly	Gly 1330	Leu	Phe	Ala	Ala	Leu 1335	Gly	Ser	Leu

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Leu Leu Phe Gly Arg Arg Lys Lys Gln Asn Lys
1340                      1345

<210> 35
<211> 1166
<212> PRT
<213> Staphylococcus aureus
<223> sdrE2

<400> 35

Met Ile Asn Arg Asp Asn Lys Lys Ala Ile Thr Lys Lys Gly Met Ile
1                      5                      10                      15

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

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

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

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

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

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

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

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225		230		235		240
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	
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	
Asp Gly Lys Asp Ile Glu Tyr Asp Thr Glu Phe Thr Ile Asp Asn Lys						
305		310		315		320
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
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
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	690	695	700
Gly	Lys	Asp	Asp	Met	Ser	Leu	Asp	Thr	Gly	Phe	Tyr	Lys	Glu	Pro	Lys	705	710	715
Tyr	Asn	Leu	Gly	Asp	Tyr	Val	Trp	Glu	Asp	Thr	Asn	Lys	Asp	Gly	Ile	725	730	735
Gln	Asp	Ala	Asn	Glu	Pro	Gly	Ile	Lys	Asp	Val	Lys	Val	Thr	Leu	Lys	740	745	750
Asp	Ser	Thr	Gly	Lys	Val	Ile	Gly	Thr	Thr	Thr	Thr	Asp	Ala	Ser	Gly	755	760	765
Lys	Tyr	Lys	Phe	Thr	Asp	Leu	Asp	Asn	Gly	Asn	Tyr	Thr	Val	Glu	Phe	770	775	780
Glu	Thr	Pro	Ala	Gly	Tyr	Thr	Pro	Thr	Val	Lys	Asn	Thr	Thr	Ala	Asp	785	790	795

Asp Lys Asp Ser Asn Gly Leu Thr Thr Thr Gly Val Ile Lys Asp Ala
 805 810 815
 Asp Asn Met Thr Leu Asp Arg Gly Phe Tyr Lys Thr Pro Lys Tyr Ser
 820 825 830
 Leu Gly Asp Tyr Val Trp Tyr Asp Ser Asn Lys Asp Gly Lys Gln Asp
 835 840 845
 Ser Thr Glu Lys Gly Ile Lys Asp Val Thr Val Thr Leu Gln Asn Glu
 850 855 860
 Lys Gly Glu Val Ile Gly Thr Thr Lys Thr Asp Glu Asn Gly Lys Tyr
 865 870 875 880
 Arg Phe Asp Asn Leu Asp Ser Gly Lys Tyr Lys Val Ile Phe Glu Lys
 885 890 895
 Pro Ala Gly Leu Thr Gln Thr Val Thr Asn Thr Thr Glu Asp Asp Lys
 900 905 910
 Asp Ala Asp Gly Gly Glu Val Asp Val Thr Ile Thr Asp His Asp Asp
 915 920 925
 Phe Thr Leu Asp Asn Gly Tyr Phe Glu Glu Asp Thr Ser Asp Ser Asp
 930 935 940
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 945 950 955 960
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 965 970 975
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 980 985 990
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 995 1000 1005
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 1010 1015 1020
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 1025 1030 1035
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 1040 1045 1050
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 1055 1060 1065
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 1070 1075 1080

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
1085 1090 1095

Ser Asp Ser Asp Ser Asp Ser Asp Ala Gly Lys His Thr Pro Val
1100 1105 1110

Lys Pro Met Ser Thr Thr Lys Asp His His Asn Lys Ala Lys Ala
1115 1120 1125

Leu Pro Glu Thr Gly Ser Glu Asn Asn Gly Ser Asn Asn Ala Thr
1130 1135 1140

Leu Phe Gly Gly Leu Phe Ala Ala Leu Gly Ser Leu Leu Leu Phe
1145 1150 1155

Gly Arg Arg Lys Lys Gln Asn Lys
1160 1165

<210> 36
<211> 516
<212> PRT
<213> Staphylococcus aureus
<223> spa

<400> 36

Met Lys Lys Lys Asn Ile Tyr Ser Ile Arg Lys Leu Gly Val Gly Ile
1 5 10 15

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

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

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

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

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
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
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
Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu	245			250		255
Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn	260			265		270
Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu	275			280		285
Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys	290			295		300
Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu	305			310		315
Asn Asp Ala Gln Ala Pro Lys Glu Glu Asp Asn Asn Lys Pro Gly Lys	325			330		335
Glu Asp Asn Asn Lys Pro Gly Lys Glu Asp Asn Asn Lys Pro Gly Lys	340			345		350
Glu Asp Asn Asn Lys Pro Gly Lys Glu Asp Asn Asn Lys Pro Gly Lys	355			360		365
Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Asn Lys Lys Pro Gly Lys	370			375		380
Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Asn Lys Lys Pro Gly Lys	385			390		395
Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro Gly Lys	405			410		415
Glu Asp Gly Asn Gly Val His Val Val Lys Pro Gly Asp Thr Val Asn	420			425		430

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Asp Ile Ala Lys Ala Asn Gly Thr Thr Ala Asp Lys Ile Ala Ala Asp
  435                                440                                445

Asn Lys Leu Ala Asp Lys Asn Met Ile Lys Pro Gly Gln Glu Leu Val
  450                                455                                460

Val Asp Lys Lys Gln Pro Ala Asn His Ala Asp Ala Asn Lys Ala Gln
  465                                470                                475                                480

Ala Leu Pro Glu Thr Gly Glu Glu Asn Pro Phe Ile Gly Thr Thr Val
                                485                                490                                495

Phe Gly Gly Leu Ser Leu Ala Leu Gly Ala Ala Leu Leu Ala Gly Arg
  500                                505                                510

Arg Arg Glu Leu
  515

<210> 37
<211> 772
<212> PRT
<213> Staphylococcus aureus
<223> sta001

<400> 37

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
  50                                55                                60

Glu Ala Ala Thr Asn Val Ser Ala Ser Ala Gln Gly Thr Ala Asp Asp
  65                                70                                75                                80

Thr Asn Ser Lys Val Thr Ser Asn Ala Pro Ser Asn Lys Pro Ser Thr
                                85                                90                                95

Val Val Ser Thr Lys Val Asn Glu Thr Arg Asp Val Asp Thr Gln Gln
  100                                105                                110

Ala Ser Thr Gln Lys Pro Thr His Thr Ala Thr Phe Lys Leu Ser Asn
  115                                120                                125

Ala Lys Thr Ala Ser Leu Ser Pro Arg Met Phe Ala Ala Asn Ala Pro
  130                                135                                140

Gln Thr Thr Thr His Lys Ile Leu His Thr Asn Asp Ile His Gly Arg
  145                                150                                155                                160

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Leu Ala Glu Glu Lys Gly Arg Val Ile Gly Met Ala Lys Leu Lys Thr
 165 170 175
 Val Lys Glu Gln Glu Lys Pro Asp Leu Met Leu Asp Ala Gly Asp Ala
 180 185 190
 Phe Gln Gly Leu Pro Leu Ser Asn Gln Ser Lys Gly Glu Glu Met Ala
 195 200 205
 Lys Ala Met Asn Ala Val Gly Tyr Asp Ala Met Ala Val Gly Asn His
 210 215 220
 Glu Phe Asp Phe Gly Tyr Asp Gln Leu Lys Lys Leu Glu Gly Met Leu
 225 230 235 240
 Asp Phe Pro Met Leu Ser Thr Asn Val Tyr Lys Asp Gly Lys Arg Ala
 245 250 255
 Phe Lys Pro Ser Thr Ile Val Thr Lys Asn Gly Ile Arg Tyr Gly Ile
 260 265 270
 Ile Gly Val Thr Thr Pro Glu Thr Lys Thr Lys Thr Arg Pro Glu Gly
 275 280 285
 Ile Lys Gly Val Glu Phe Arg Asp Pro Leu Gln Ser Val Thr Ala Glu
 290 295 300
 Met Met Arg Ile Tyr Lys Asp Val Asp Thr Phe Val Val Ile Ser His
 305 310 315 320
 Leu Gly Ile Asp Pro Ser Thr Gln Glu Thr Trp Arg Gly Asp Tyr Leu
 325 330 335
 Val Lys Gln Leu Ser Gln Asn Pro Gln Leu Lys Lys Arg Ile Thr Val
 340 345 350
 Ile Asp Gly His Ser His Thr Val Leu Gln Asn Gly Gln Ile Tyr Asn
 355 360 365
 Asn Asp Ala Leu Ala Gln Thr Gly Thr Ala Leu Ala Asn Ile Gly Lys
 370 375 380
 Ile Thr Phe Asn Tyr Arg Asn Gly Glu Val Ser Asn Ile Lys Pro Ser
 385 390 395 400
 Leu Ile Asn Val Lys Asp Val Glu Asn Val Thr Pro Asn Lys Ala Leu
 405 410 415
 Ala Glu Gln Ile Asn Gln Ala Asp Gln Thr Phe Arg Ala Gln Thr Ala
 420 425 430
 Glu Val Ile Ile Pro Asn Asn Thr Ile Asp Phe Lys Gly Glu Arg Asp
 435 440 445

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

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

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

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

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

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

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

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

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


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              725              730              735
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

Arg Lys Ala Ser
      770

<210> 38
<211> 190
<212> PRT
<213> Staphylococcus aureus
<223> sta002

<400> 38
Met Lys Leu Lys Ser Leu Ala Val Leu Ser Met Ser Ala Val Val Leu
 1          5          10          15

Thr Ala Cys Gly Asn Asp Thr Pro Lys Asp Glu Thr Lys Ser Thr Glu
      20          25          30

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

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

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

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

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

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<210> 39
<211> 502
<212> PRT
<213> Staphylococcus aureus
<223> sta003

<400> 39

Met Arg Glu Asn Phe Lys Leu Arg Lys Met Lys Val Gly Leu Val Ser
1                               10                      15

Val Ala Ile Thr Met Leu Tyr Ile Met Thr Asn Gly Gln Ala Glu Ala
                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
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
                        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
130                      135                      140

Ser Asp Pro Tyr Leu Gly Asp Asp Glu Glu Asp Glu Glu Val Glu Glu
145                      150                      155                      160

Thr Ser Thr Glu Glu Val Gly Ala Glu Glu Glu Ser Thr Glu Ala Lys
                165                170                175

Ala Thr Tyr Thr Thr Pro Arg Tyr Glu Lys Ala Tyr Glu Ile Pro Lys
                180                185                190

Glu Gln Leu Lys Glu Lys Asp Gly His His Gln Val Phe Ile Glu Pro
          195                      200                      205

Ile Thr Glu Gly Ser Gly Ile Ile Lys Gly His Thr Ser Val Lys Gly
210                      215                      220

Lys Val Ala Leu Ser Ile Asn Asn Lys Phe Ile Asn Phe Glu Thr Asn
225                      230                      235                      240

Ala Asn Gly Gly Pro Asn Lys Glu Glu Ala Lys Ser Gly Ser Glu Gly
                245                250                255

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Ile Trp Met Pro Ile Asp Asp Lys Gly Tyr Phe Asn Phe Asp Phe Lys
    260                               265                               270

Thr Lys Arg Phe Asp Asp Leu Glu Leu Lys Lys Asn Asp Glu Ile Ser
    275                               280                               285

Leu Thr Phe Ala Pro Asp Asp Glu Asp Glu Ala Leu Lys Ser Leu Ile
    290                               295                               300

Phe Lys Thr Lys Val Thr Ser Leu Glu Asp Ile Asp Lys Ala Glu Thr
    305                               310                               315                               320

Lys Tyr Asp His Thr Lys Val Glu Lys Val Lys Val Leu Lys Asp Val
    325                               330                               335

Lys Glu Asp Leu His Val Asp Glu Ile Tyr Gly Ser Leu Tyr His Thr
    340                               345                               350

Glu Lys Gly Lys Gly Ile Leu Asp Lys Glu Gly Thr Lys Val Ile Lys
    355                               360                               365

Gly Lys Thr Lys Phe Ala Asn Ala Val Val Lys Val Asp Ser Glu Leu
    370                               375                               380

Gly Glu Gly Gln Glu Phe Pro Asp Leu Gln Val Asp Glu Lys Gly Glu
    385                               390                               395                               400

Phe Ser Phe Asp Val Asp His Ala Gly Phe Arg Leu Gln Asn Gly Glu
    405                               410                               415

Thr Leu Asn Phe Thr Val Val Asp Pro Ile Thr Gly Glu Leu Leu Ser
    420                               425                               430

Gly Asn Phe Val Ser Lys Asn Ile Asp Ile Tyr Glu Ser Pro Glu Glu
    435                               440                               445

Lys Ala Asp Arg Glu Phe Asp Glu Arg Met Glu Asn Thr Pro Ala Tyr
    450                               455                               460

His Lys Leu His Gly Asp Lys Ile Val Gly Tyr Asp Thr Asn Gly Phe
    465                               470                               475                               480

Pro Ile Thr Trp Phe Tyr Pro Leu Gly Glu Lys Lys Val Glu Arg Lys
    485                               490                               495

Ala Pro Lys Leu Glu Lys
    500

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<210> 40
<211> 342
<212> PRT
<213> Staphylococcus aureus
<223> sta004

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<400> 40

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 30

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

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                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 Thr Ile Lys Gln Ile Glu Glu
      325                      330                      335

Leu Asp Lys Val Val Lys
      340

<210>  41
<211>  241
<212>  PRT
<213>  Staphylococcus aureus
<223>  sta005

<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

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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

<210> 42
<211> 302
<212> PRT
<213> Staphylococcus aureus
<223> sta006

<400> 42

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
20 25 30

Tyr Lys Met Asp Asp Gly Lys Thr Val Asp Ile Pro Lys Asp Pro Lys
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
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
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
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
165 170 175

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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 Gly Glu Val Leu Tyr Gln Ala Phe
    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
    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
    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
    290                      295                      300

<210> 43
<211> 267
<212> PRT
<213> Staphylococcus aureus
<223> sta007

<400> 43

Met Lys Lys Ile Ala Thr Ala Thr Ile Ala Thr Ala Gly Phe Ala Thr
1      5      10      15

Ile Ala Ile Ala Ser Gly Asn Gln Ala His Ala Ser Glu Gln Asp Asn
    20      25      30

Tyr Gly Tyr Asn Pro Asn Asp Pro Thr Ser Tyr Ser Tyr Thr Tyr Thr
    35      40      45

Ile Asp Ala Gln Gly Asn Tyr His Tyr Thr Trp Lys Gly Asn Trp His
    50      55      60

Pro Ser Gln Leu Asn Gln Asp Asn Gly Tyr Tyr Ser Tyr Tyr Tyr Tyr
    65      70      75      80

Asn Gly Tyr Asn Asn Tyr Asn Asn Tyr Asn Asn Gly Tyr Ser Tyr Asn
    85      90      95

Asn Tyr Ser Arg Tyr Asn Asn Tyr Ser Asn Asn Asn Gln Ser Tyr Asn
    100     105     110

Tyr Asn Asn Tyr Asn Ser Tyr Asn Thr Asn Ser Tyr Arg Thr Gly Gly
    115     120     125

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Leu Gly Ala Ser Tyr Ser Thr Ser Ser Asn Asn Val Gln Val Thr Thr
130                      135                      140

Thr Met Ala Pro Ser Ser Asn Gly Arg Ser Ile Ser Ser Gly Tyr Thr
145                      150                      155                      160

Ser Gly Arg Asn Leu Tyr Thr Ser Gly Gln Cys Thr Tyr Tyr Val Phe
165                      170                      175

Asp Arg Val Gly Gly Lys Ile Gly Ser Thr Trp Gly Asn Ala Ser Asn
180                      185                      190

Trp Ala Asn Ala Ala Ala Arg Ala Gly Tyr Thr Val Asn Asn Thr Pro
195                      200                      205

Lys Ala Gly Ala Ile Met Gln Thr Thr Gln Gly Ala Tyr Gly His Val
210                      215                      220

Ala Tyr Val Glu Ser Val Asn Ser Asn Gly Ser Val Arg Val Ser Glu
225                      230                      235                      240

Met Asn Tyr Gly Tyr Gly Pro Gly Val Val Thr Ser Arg Thr Ile Ser
245                      250                      255

Ala Ser Gln Ala Ala Gly Tyr Asn Phe Ile His
260                      265

<210> 44
<211> 209
<212> PRT
<213> Staphylococcus aureus
<223> sta008

<400> 44

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
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
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
85                      90                      95

Asn Asn Gln Ala Asn Asn Asn Gln Lys Ser Ser Tyr Val Ala Pro Tyr

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				100					105					110					
Tyr	Gly	Gln	Asn	Ala	Ala	Pro	Val	Ala	Arg	Gln	Ile	Tyr	Pro	Phe	Asn				
		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				
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				
			180					185						190					
Thr	Val	Asp	Tyr	Thr	Gly	Gln	Ala	Met	Val	Thr	Asp	Pro	Asn	Tyr	Gln				
		195					200					205							

Gln

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<210> 45
<211> 436
<212> PRT
<213> Staphylococcus aureus
<223> sta009
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<400> 45

Met Lys Asn Lys Tyr Ile Ser Lys Leu Leu Val Gly Ala Ala Thr Ile
1 5 10 15

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

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

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

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
 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
 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
 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
 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
 260 265 270
 Gln Ile Gln Ser Pro Gln Ile Glu Lys Pro Lys Val Glu Ser Pro Lys
 275 280 285
 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
 305 310 315 320
 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
 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
 Ala Gln Val Arg Asn Tyr Val Thr Glu Ser Ile Asn Thr Gly Lys Val
 385 390 395 400
 Leu Tyr Thr Phe Tyr Gln Asn Pro Thr Leu Val Lys Thr Ala Ile Lys
 405 410 415

Ala Gln Glu Thr Ala Ser Ser Ile Lys Asn Thr Leu Ser Asn Leu Leu
420 425 430

Ser Phe Trp Lys
435

<210> 46
<211> 233
<212> PRT
<213> Staphylococcus aureus
<223> sta010

<400> 46

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
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
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
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
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
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
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
210 215 220

Ala Gln Gly Leu Gly Ala Trp Gly Phe
225 230

<210> 47
<211> 256
<212> PRT
<213> Staphylococcus aureus
<223> sta011

<400> 47

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 Ile Lys Lys Glu Ile Glu Asn Phe Lys Phe Phe Val Gln Tyr Gly
145 150 155 160

Asp Phe Lys Asn Leu 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

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225                      230                      235                      240

Asn Ile Tyr Phe Ser Asp Ser Leu Asp Tyr Lys Lys Ser Gly Asp Val
      245                      250                      255

<210>  48
<211>  514
<212>  PRT
<213>  Staphylococcus aureus
<223>  sta012

<400>  48

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
      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
 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
      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
      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
      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
      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
      210              215              220

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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
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

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

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
340 345 350

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

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

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

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

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

<210> 49
 <211> 511
 <212> PRT
 <213> Staphylococcus aureus
 <223> sta013

<400> 49

Met Ser Asn Ile Ala Phe Tyr Val Val Ser Asp Val His Gly Tyr Ile
 1 5 10 15

Phe Pro Thr Asp Phe Thr Ser Arg Asn Gln Tyr Gln Pro Met Gly Leu
 20 25 30

Leu Leu Ala Asn His Val Ile Glu Gln Asp Arg Arg Gln Tyr Asp Gln
 35 40 45

Ser Phe Lys Ile Asp Asn Gly Asp Phe Leu Gln Gly Ser Pro Phe Cys
 50 55 60

Asn Tyr Leu Ile Ala His Ser Gly Ser Ser Gln Pro Leu Val Asp Phe
 65 70 75 80

Tyr Asn Arg Met Ala Phe Asp Phe Gly Thr Leu Gly Asn His Glu Phe
 85 90 95

Asn Tyr Gly Leu Pro Tyr Leu Lys Asp Thr Leu Arg Arg Leu Asn Tyr
 100 105 110

Pro Val Leu Cys Ala Asn Ile Tyr Glu Asn Asp Ser Thr Leu Thr Asp
 115 120 125

Asn Gly Val Lys Tyr Phe Gln Val Gly Asp Gln Thr Val Gly Val Ile
 130 135 140

Gly Leu Thr Thr Gln Phe Ile Pro His Trp Glu Gln Pro Glu His Ile
 145 150 155 160

Gln Ser Leu Thr Phe His Ser Ala Phe Glu Ile Leu Gln Gln Tyr Leu
 165 170 175

Pro Glu Met Lys Arg His Ala Asp Ile Ile Val Val Cys Tyr His Gly
 180 185 190

Gly Phe Glu Lys Asp Leu Glu Ser Gly Thr Pro Thr Glu Val Leu Thr
 195 200 205

Gly Glu Asn Glu Gly Tyr Ala Met Leu Glu Ala Phe Ser Lys Asp Ile
 210 215 220

Asp Ile Phe Ile Thr Gly His Gln His Arg Gln Ile Ala Glu Arg Phe
 225 230 235 240

Lys Gln Thr Ala Val Ile Gln Pro Gly Thr Arg Gly Thr Thr Val Gly
245 250 255

Arg Val Val Leu Ser Thr Asp Glu Tyr Glu Asn Leu Ser Val Glu Ser
260 265 270

Cys Glu Leu Leu Pro Val Ile Asp Asp Ser Thr Phe Thr Ile Asp Glu
275 280 285

Asp Asp Gln His Leu Arg Lys Gln Leu Glu Asp Trp Leu Asp Tyr Glu
290 295 300

Ile Thr Thr Leu Pro Tyr Asp Met Thr Ile Asn His Ala Phe Glu Ala
305 310 315 320

Arg Val Ala Pro His Pro Phe Thr Asn Phe Met Asn Tyr Ala Leu Leu
325 330 335

Glu Lys Ser Asp Ala Asp Val Ala Cys Thr Ala Leu Phe Asp Ser Ala
340 345 350

Ser Gly Phe Lys Gln Val Val Thr Met Arg Asp Val Ile Asn Asn Tyr
355 360 365

Pro Phe Pro Asn Thr Phe Lys Val Leu Ala Val Ser Gly Ala Lys Leu
370 375 380

Lys Glu Ala Ile Glu Arg Ser Ala Glu Tyr Phe Asp Val Lys Asn Asp
385 390 395 400

Glu Val Ser Val Ser Ala Asp Phe Leu Glu Pro Lys Pro Gln His Phe
405 410 415

Asn Tyr Asp Ile Tyr Gly Gly Val Ser Tyr Thr Ile His Val Gly Arg
420 425 430

Pro Lys Gly Gln Arg Val Ser Asn Met Met Ile Gln Gly His Ala Val
435 440 445

Asp Leu Lys Gln Thr Tyr Thr Ile Cys Val Asn Asn Tyr Arg Ala Val
450 455 460

Gly Gly Gly Gln Tyr Asp Met Tyr Ile Asp Ala Pro Val Val Lys Asp
465 470 475 480

Ile Gln Val Glu Gly Ala Gln Leu Leu Ile Asp Phe Leu Ser Asn Asn
485 490 495

Asn Leu Met Arg Ile Pro Gln Val Val Asp Phe Lys Val Glu Lys
500 505 510

<210> 50


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<211> 324
<212> PRT
<213> Staphylococcus aureus
<223> sta014

<400> 50

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

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

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

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

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

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

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

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

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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
 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
 Ala Ser Arg Ser
 <210> 51
 <211> 591
 <212> PRT
 <213> Staphylococcus aureus
 <223> sta015
 <400> 51
 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
 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
 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
 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
 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
 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				
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
<223> sta016

<400> 52

Met Val Ile Asn Leu Asn Asp Lys Gln Thr Lys Thr Ser Lys Glu Gly
1 5 10 15

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

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

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

Thr Val Ala Val Pro Ala Ile Pro Lys Leu Phe Asp Tyr Ile His Lys

115	120	125																	
Arg Tyr Ala Lys Leu Ser Leu Glu Asp Leu Ile Asn Pro Ala Ile Glu																			
130	135	140																	
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
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
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
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
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
Arg Ala Gln Tyr Leu Ala Asp Asp Asn Phe His Glu Val Pro Val Gln																			
	305	310																	320
Ser Leu Ile Asp Asp Asp Tyr Leu Lys Ala Arg Ser Thr Leu Ile Asp																			
	325	330																	335
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
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																	400

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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

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

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
      485                      490                      495

Ile Leu Ala Leu Ile Ala His Gly His Ala Met Glu His Lys Pro Asp
      500                      505                      510

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

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

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

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

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

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<210> 53
<211> 322
<212> PRT

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<213> Staphylococcus aureus
<223> sta017

<400> 53

Met Lys Ser Lys Ile Tyr Ile Leu Leu Leu Phe Leu Ile Phe Leu Ser
1 5 10 15

Ala Cys Ala Asn Thr Arg His Ser Glu Ser Asp Lys Asn Val Leu Thr
20 25 30

Val Tyr Ser Pro Tyr Gln Ser Asn Leu Ile Arg Pro Ile Leu Asn Glu
35 40 45

Phe Glu Lys Gln Glu His Val Lys Ile Glu Ile Lys His Gly Ser Thr
50 55 60

Gln Val Leu Leu Ser Asn Leu His Asn Glu Asp Phe Ser Glu Arg Gly
65 70 75 80

Asp Val Phe Met Gly Gly Val Leu Ser Glu Thr Ile Asp His Pro Glu
85 90 95

Asp Phe Val Pro Tyr Gln Asp Thr Ser Val Thr Gln Gln Leu Glu Asp
100 105 110

Tyr Arg Ser Asn Asn Lys Tyr Val Thr Ser Phe Leu Leu Met Pro Thr
115 120 125

Val Ile Val Val Asn Ser Asp Leu Gln Gly Asp Ile Lys Ile Arg Gly
130 135 140

Tyr Gln Asp Leu Leu Gln Pro Ile Leu Lys Gly Lys Ile Ala Tyr Ser
145 150 155 160

Asn Pro Asn Thr Thr Thr Thr Gly Tyr Gln His Met Arg Ala Ile Tyr
165 170 175

Ser Met His His Arg Val Ser Asp Val His Gln Phe Gln Asn His Ala
180 185 190

Met Gln Leu Ser Lys Thr Ser Lys Val Ile Glu Asp Val Ala Lys Gly
195 200 205

Lys Tyr Tyr Ala Gly Leu Ser Tyr Glu Gln Asp Ala Arg Thr Trp Lys
210 215 220

Asn Lys Gly Tyr Pro Val Ser Ile Val Tyr Pro Ile Glu Gly Thr Met
225 230 235 240

Leu Asn Val Asp Gly Ile Ala Leu Val Lys Asn Ala His Pro His Pro
245 250 255

Lys Arg Lys Lys Leu Val Gln Tyr Leu Thr Ser Arg Ser Val Gln Gln
260 265 270

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Arg Leu Val Ala Glu Phe Asp Ala Lys Ser Ile Arg Lys Asp Val Ser
275 280 285

Glu Gln Ser Asp Gln Ser Ile Glu Asn Leu Lys Asn Ile Pro Leu Ile
290 295 300

Pro Lys Ser Lys Leu Pro Asp Ile Pro His His Lys Phe Leu Glu Met
305 310 315 320

Ile Gln

<210> 54
<211> 470
<212> PRT
<213> Staphylococcus aureus
<223> sta018

<400> 54

Met His Ser Ser Gly Lys Asp Leu Asn Ile Ser Leu Pro Leu Lys Thr
1 5 10 15

Lys Ser Ile Ala Pro Tyr Glu Thr Asp Val Pro Val Lys Ile Gly Ala
20 25 30

Ala Glu Ser Leu Phe Lys Thr Asn Asp Gln Gly Lys Ile Glu Lys Ala
35 40 45

Leu Val Lys Ser Tyr His Gln Pro Asn Asp Thr Thr Leu Asp Ile Glu
50 55 60

Leu Lys Asp Asn Ile Lys Phe Gln Asn Gly Gln Lys Leu Thr Ala Glu
65 70 75 80

Lys Val Lys Ser Ser Leu Glu Asn Ser Met Lys Lys Ser Asp Leu Val
85 90 95

Lys Tyr Ser Leu Pro Ile Ser Ser Ile Thr Ala Lys Gly Gln Lys Leu
100 105 110

Thr Ile Lys Thr Asn Ser Ala Tyr Pro Glu Leu Val Ser Glu Leu Ala
115 120 125

Asn Pro Phe Met Ala Ile Tyr Asp Thr Asp Ala Lys Ser Asp Val Asn
130 135 140

Gln Thr Pro Val Gly Thr Gly Pro Tyr Gln Ile Lys Asp Tyr Lys Gln
145 150 155 160

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

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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
<223> sta019

<400> 55

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
20 25 30

Gln Ala His Thr Gln Met Ser Thr Gln Ser Gln Asp Val Ser Tyr Gly
35 40 45

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

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

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

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

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

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

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

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

Tyr Ala Val Asp Pro Thr Ser Tyr Leu Gln Ser Arg
305 310 315

<210> 56
<211> 507
<212> PRT
<213> Staphylococcus aureus
<223> sta020

<400> 56

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

Lys Asp Tyr Phe Asn Asp Arg Phe Glu Asn Glu Val Lys Phe Gln Glu
50 55 60

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

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

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

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			
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					
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		
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				
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		
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				
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	
Lys	Arg	Gln	Asp	Lys	Gly	Lys	Ile	Thr	Val	Ala	Leu	Asp	Lys	Tyr	Ser	
				405					410					415		
Asp	Glu	Asn	Glu	Phe	Thr	Phe	Glu	Asn	Asn	Ile	Asp	Ser	Asp	Val	Lys	
			420					425					430			
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	

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450                               455                               460

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

Met Phe Glu Ser Ile Leu Lys Lys Ala Ser Lys
500                               505

<210> 57
<211> 297
<212> PRT
<213> Staphylococcus aureus
<223> sta021

<400> 57

Met Lys Lys Thr Ile Leu Leu Thr Met Thr Thr Leu Thr Leu Phe Ser
1                               5                               10                               15

Met Ser Pro Asn Ser Ala Gln Ala Tyr Thr Asn Asp Ser Lys Thr Leu
20                               25                               30

Glu Glu Ala Lys Lys Ala His Pro Asn Ala Gln Phe Lys Val Asn Lys
35                               40                               45

Asp Thr Gly Ala Tyr Thr Tyr Thr Tyr Asp Lys Asn Asn Thr Pro Asn
50                               55                               60

Asn Asn His Gln Asn Gln Ser Arg Thr Asn Asp Asn His Gln His Ala
65                               70                               75                               80

Asn Gln Arg Asp Leu Asn Asn Asn Gln Tyr His Ser Ser Leu Ser Gly
85                               90                               95

Gln Tyr Thr His Ile Asn Asp Ala Ile Asp Ser His Thr Pro Pro Gln
100                              105                              110

Thr Ser Pro Ser Asn Pro Leu Thr Pro Ala Ile Pro Asn Val Glu Asp
115                              120                              125

Asn Asp Asp Glu Leu Asn Asn Ala Phe Ser Lys Asp Asn Lys Gly Leu
130                              135                              140

Ile Thr Gly Ile Asp Leu Asp Glu Leu Tyr Asp Glu Leu Gln Ile Ala
145                              150                              155                              160

Glu Phe Asn Asp Lys Ala Lys Thr Ala Asp Gly Lys Pro Leu Ala Leu
165                              170                              175

Gly Asn Gly Lys Ile Ile Asp Gln Pro Leu Ile Thr Ser Lys Asn Asn
180                              185                              190

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Leu Tyr Thr Ala Gly Gln Cys Thr Trp Tyr Val Phe Asp Lys Arg Ala
195 200 205

Lys Asp Gly His Thr Ile Ser Thr Phe Trp Gly Asp Ala Lys Asn Trp
210 215 220

Ala Gly Gln Ala Ser Ser Asn Gly Phe Lys Val Asp Arg His Pro Thr
225 230 235 240

Arg Gly Ser Ile Leu Gln Thr Val Asn Gly Pro Phe Gly His Val Ala
245 250 255

Tyr Val Glu Lys Val Asn Ile Asp Gly Ser Ile Leu Ile Ser Glu Met
260 265 270

Asn Trp Ile Gly Glu Tyr Ile Val Ser Ser Arg Thr Ile Ser Ala Ser
275 280 285

Glu Val Ser Ser Tyr Asn Tyr Ile His
290 295

<210> 58
<211> 124
<212> PRT
<213> Staphylococcus aureus
<223> sta022

<400> 58

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
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
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
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
115 120

<210> 59
<211> 296
<212> PRT

<213> Staphylococcus aureus

<223> sta023

<400> 59

Met Asn Lys Ile Ser Lys Tyr Ile Ala Ile Ala Ser Leu Ser Val Ala
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 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
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
100 105 110

Pro Tyr Gln Gly Tyr Ala Ser Ile His Asn Lys Pro Phe Pro Glu Gly
115 120 125

Trp His Glu Trp Val Gln Ala Ala Lys Ala Lys Pro Val Tyr Gly Ala
130 135 140

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

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

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

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

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

<210> 60
 <211> 690
 <212> PRT
 <213> Staphylococcus aureus
 <223> sta024

<400> 60

Met Leu Arg Gly Gln Glu Glu Arg Lys Tyr Ser Ile Arg Lys Tyr Ser
 1 5 10 15

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

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

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

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

Asn Thr His His Ala Glu Arg Asn Gly Ser Gln Ser Thr Thr Ser Gln
 145 150 155 160

Ser Asn Asp Val Asp Lys Ser Gln Pro Ser Ile Pro Ala Gln Lys Val
 165 170 175

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

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
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
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
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
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
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
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
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
Arg Lys Ile Met Phe Ala Leu Asn Arg Phe Met Gly Asn Lys Tyr Ser		
	485	490 495

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Asn Ile Asp Leu Gly Leu Thr Gln Trp Gly Phe Lys Gln Leu Pro Asn
    500                                505                                510

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
    530                                535                                540

Lys Leu Asn Asn Met Thr Ser Met Asn Pro Asn Ile Thr Tyr Thr Thr
    545                                550                                555                                560

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

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

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

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

Ala Ser
    690

<210> 61
<211> 208
<212> PRT
<213> Staphylococcus aureus
<223> sta025

<400> 61

Met Lys Lys Arg Leu Leu Leu Ser Thr Phe Leu Ala Ser Thr Leu Ile
1                                5                                10                                15

Leu Thr Gly Cys Ala Ser Asp Gln Ser Asp Asn Glu Asp His His Thr
20                                25                                30

Ser Thr Gly Ile His Ala Pro Lys Ser Ala Lys Lys Leu Glu Thr Lys
35                                40                                45

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Asp Ile Phe Asn Ser Asp Lys Lys Asn Ser Asp Ile Ser Asp Ala Glu
50                      55                      60

Met Lys Gln Ala Ile Glu Lys Tyr Leu Ser Val Asn Ser Asp Ile Leu
65                      70                      75                      80

Asp Asn Lys Tyr Ile Met Gln His Lys Leu Asp Lys Gln Ile Asp Ser
85                      90                      95

Gln Thr Lys Val Thr Glu Lys Gln Ala Glu Thr Leu Ser His Leu Ser
100                    105                    110

Asn Leu Ala Val Lys Asn Asp Leu His Phe Lys Lys Phe Val Thr Glu
115                    120                    125

Asn Asn Ile Pro Lys Glu Tyr Lys Lys Pro Val Glu Leu Met Met Asn
130                    135                    140

Tyr Phe Lys Ala Leu Asn Ser Thr Ile Ala Asn Val Asp Glu Asp Ile
145                    150                    155                    160

Glu Lys Leu Ser Tyr Gln Pro Gln Asn Lys Ile Asn Val Val Asp Val
165                    170                    175

Pro Thr Lys Tyr Ala Gly Asp Val Asn Lys Lys Gln Gln Asp Lys Ile
180                    185                    190

Lys Asp Phe Leu Lys Ser Lys Gly Ile Lys Ser Asp Val Ile Asp Lys
195                    200                    205

<210> 62
<211> 261
<212> PRT
<213> Staphylococcus aureus
<223> sta026

<400> 62

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
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
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
85                    90                    95

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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
      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
      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
      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
      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
      245                      250                      255

Pro Ser Glu Asp Lys
      260

<210> 63
<211> 347
<212> PRT
<213> Staphylococcus aureus
<223> sta027

<400> 63

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
      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
      50                      55                      60

Asn Ser Lys Leu Asp Ile Ile Thr Pro Val Asp Met Ser Ser Asn Ala

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65				70				75				80					
Lys	Leu	Pro	Val	Ile	Phe	Trp	Met	His	Gly	Gly	Gly	Tyr	Ile	Ala	Gly		
				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		
				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		
				145					150					155			
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		
				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		
				210					215					220			
Tyr	Thr	Gly	Glu	Glu	Asp	Trp	Glu	Lys	Ser	Phe	Lys	Asn	Ile	Ser	Gln		
				225					230					235			
Met	Ser	Thr	Val	Lys	Gln	Ser	Thr	Lys	Asn	Tyr	Pro	Pro	Thr	Phe	Leu		
				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		
				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		
				305					310					315			
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								

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<210> 64
<211> 265
<212> PRT
<213> Staphylococcus aureus
<223> sta028

<400> 64

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

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

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

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

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

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

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

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

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Glu Val Ser Ser Tyr Ala Phe Ile His
260 265

<210> 65
<211> 292
<212> PRT
<213> Staphylococcus aureus
<223> sta029

<400> 65

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
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
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
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
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
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
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
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
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
275 280 285

Leu Glu Glu Lys
290

<210> 66
<211> 242
<212> PRT
<213> Staphylococcus aureus
<223> sta030

<400> 66

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
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
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
85 90 95

Ala Lys Lys Asp Asp Lys Asp Leu Asn Pro Ser Ser Ile Ser His Asp
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

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

Ser Glu Asp Lys Thr Val Asp Ser Lys Ser Phe Lys Phe Ser Lys Leu


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180              185              190
Lys Thr Glu Asp Phe Ser His Arg Ala Glu Thr Arg Glu Glu Val Glu
195              200              205

Lys Lys Glu Lys Glu Phe 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

Glu Val

<210> 67
<211> 439
<212> PRT
<213> Staphylococcus aureus
<223> sta031

<400> 67

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
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
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
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

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

Gln Arg Gly Lys Phe Asp Val Leu Ile Val Leu Ser His Cys Gly Ile
165             170             175

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Phe Phe Asp Glu Thr Leu Cys Gln Glu Leu Pro Glu Ile Asp Val Ile
180 185 190

Phe Gly Ser His Thr His His Tyr Phe Glu His Gly Glu Ile Asn Asn
195 200 205

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

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

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

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

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

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

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

Lys Glu Lys Leu Leu Glu Tyr
435

<210> 68
<211> 774
<212> PRT

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<213> Staphylococcus aureus
<223> sta032

<400> 68

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

Arg Asp Val Asn Glu Asn Lys Ala Glu Glu Ser Lys Ser Asn Gln Asp
85 90 95

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

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

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

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

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

Glu Gln Thr Lys Thr Tyr Thr Tyr Gly Asp Ser Glu Gln Asn Asp Lys
260 265 270

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Ser Asn His Glu Asn Asp Leu Ser His His Ile Pro Ser Ile Ser Asp
 275                                280                285

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

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

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

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

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

Ala Gln Lys Tyr Thr Thr Thr Met Lys Asn Ala Asn Asn Thr Val Lys
 450                                455                460

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

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

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

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545                      550                      555                      560

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

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

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

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

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

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

Ile Asn Ile Lys Leu Lys
      770

<210> 69
<211> 393
<212> PRT
<213> Staphylococcus aureus
<223> sta033

<400> 69

Met Asn Ser Ser Cys Lys Ser Arg Val Phe Asn Ile Ile Ser Ile Ile
1          5          10          15

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Met Val Ser Met Leu Ile Leu Ser Leu Gly Ala Phe Ala Asn Asn Asn
 20 25 30
 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
 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
 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
 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
 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
 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
 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
 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
 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

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

Gln Asp Ala Asp Ser Ser Leu Leu His Leu Ser Phe Asn Arg Asp Tyr
370 375 380

Asn Trp Tyr Gly Ser Met Ile Gly Tyr
385 390

<210> 70
<211> 336
<212> PRT
<213> Staphylococcus aureus
<223> sta034

<400> 70

Met Lys Gly Lys Phe Leu Lys Val Ser Ser Leu Phe Val Ala Thr Leu
1 5 10 15

Thr Thr Ala Thr Leu Val Ser Ser Pro Ala Ala Asn Ala Leu Ser Ser
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
50 55 60

Glu His Ala Asn Val Ile Leu Pro Asn Asn Asp Arg His Gln Ile Thr
65 70 75 80

Asp Thr Thr Asn Gly His Tyr Ala Pro Val Thr Tyr Ile Gln Val Glu
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
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
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
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
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
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
275 280 285

Pro Asn Asn Pro Asp Asn Pro Asp Asn Pro Asn Asn Pro Asp Asn Pro
290 295 300

Asn Asn Pro Asp Glu Pro Asn Asn Pro Asp Asn Pro Asn Asn Pro Asp
305 310 315 320

Asn Pro Asp Asn Gly Asp Asn Asn Asn Ser Asp Asn Pro Asp Ala Ala
325 330 335

<210> 71
<211> 397
<212> PRT
<213> Staphylococcus aureus
<223> sta035

<400> 71

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

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
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			
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					
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		
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				
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		
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			
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					
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	
				325					330					335		
Pro	Thr	Leu	Asn	Arg	Leu	Asn	Gly	Gly	Phe	Phe	Gly	Gln	Val	Phe	Thr	
			340					345					350			

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
 Gln Asn Lys Pro Tyr Asn Thr Lys Gly Val Ile Val Gln
 385 390 395
 <210> 72
 <211> 358
 <212> PRT
 <213> Staphylococcus aureus
 <223> sta036
 <400> 72
 Met Arg Asn Val Lys Gln Ile Ala Thr Lys Ser Ile Ile Ala Ile Ile
 1 5 10 15
 Ser Leu Gly Ile Leu Thr Tyr Thr Thr Met Ile Gly Ser Val Leu Ala
 20 25 30
 Asp Glu Ile Lys Tyr Pro Ser Ala Lys Phe Asn Gln Pro Glu Ala Lys
 35 40 45
 Asp Lys Thr Glu Leu Thr Thr Ser Ile Phe Asp Glu Lys Ile Lys Glu
 50 55 60
 Asn Lys Ala Leu Glu Leu Leu Ile Phe Asn Gln Glu Asn Lys Asn Val
 65 70 75 80
 Thr Glu Glu Gln Gln Leu Val Asp Glu Lys Ala Gln Leu Ile Ser Asp
 85 90 95
 Met Thr Gly Lys Ile Tyr Leu Gln Val Lys Leu Lys Gly Gln Ile Asp
 100 105 110
 Lys Glu Gln Leu Val Phe Gln Asn Asp Lys Asn Glu Glu Phe Pro Phe
 115 120 125
 Val Ile Lys Asp Glu Lys Asp Asp Thr Ile Val Arg Ile Leu Ile Glu
 130 135 140
 Gln His Met Asp Lys Ile Asn Met His Val Lys Thr Leu Ala Glu Lys
 145 150 155 160
 Lys Asn Leu Asp Asn Lys Glu Met Val Tyr Ser Ile His Phe Lys Glu
 165 170 175
 Lys Lys Val Gln His Asp Asp Ala Lys Glu Val Pro Ser Lys His Gln
 180 185 190
 Asn Gln Glu Asn Asn Gln Asp Gln Leu Lys Lys Asp Ile Asp Asp Lys
 195 200 205

Lys Asp Ser Gln Lys Ser Asp Thr Lys Glu Arg Arg Thr Ser Leu Phe
210 215 220

Thr Glu Lys Gly Leu Asn Asp Ile Pro Val Gln Lys Asp Lys Val Gln
225 230 235 240

Gln Asp Ser Asn Lys Lys Ile Glu Asn Glu Arg Pro Lys Ala Ser Gly
245 250 255

Thr Leu Lys Val Glu Asn Ser Pro Pro Thr Ile Lys Lys Val Glu Asn
260 265 270

Asn His Lys Glu Gln Pro Lys His Lys Asp Glu Lys Ser Lys Lys Glu
275 280 285

Lys Lys Lys Val Val Glu Lys Glu Lys Ala Leu Pro Ala Phe Asn Arg
290 295 300

Asp Asp Asp Ser Lys Asn Ser Ser Gln Leu Ser Ser Asp Ile Lys Glu
305 310 315 320

Leu Asp Glu Pro Asn His Lys Lys Gln Tyr Met Leu Phe Ala Ala Gly
325 330 335

Ile Val Leu Ala Thr Ile Leu Leu Ile Ser Ala His Leu Tyr Ser Arg
340 345 350

Lys Arg Gly Asn Gln Val
355

<210> 73
<211> 282
<212> PRT
<213> Staphylococcus aureus
<223> sta037

<400> 73

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

<210> 74
<211> 244
<212> PRT
<213> Staphylococcus aureus
<223> sta038

<400> 74

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

Leu Met Ser Lys His Gln Glu His Val Arg Pro Gln Phe Glu Ser Leu

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50              55              60

Glu Lys Ile Asn Lys Asp Ile Val Gly Trp Ile Lys Leu Ser Gly Thr
65              70              75              80

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

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

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

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

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

Ile Lys Val Ser

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<210> 75
<211> 238
<212> PRT
<213> Staphylococcus aureus
<223> sta039

<400> 75

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Met Ser Lys Asn Ile Thr Lys Asn Ile Ile Leu Thr Thr Thr Leu Leu
1              5              10              15

Leu Leu Gly Thr Val Leu Pro Gln Asn Gln Lys Pro Val Phe Ser Phe
20            25            30

Tyr Ser Glu Ala Lys Ala Tyr Ser Ile Gly Gln Asp Glu Thr Asn Ile
35            40            45

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Asn Glu Leu Ile Lys Tyr Tyr Thr Gln Pro His Phe Ser Phe Ser Asn
 50                      55                      60

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

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

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

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

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

Val Lys Asn Pro Asn Lys Ile Thr Val Asp Val Leu Phe Asp
      225                      230                      235

<210> 76
<211> 241
<212> PRT
<213> Staphylococcus aureus
<223> sta040

<400> 76

Met Asn Asn Asn Ile Thr Lys Lys Ile Ile Leu Ser Thr Thr Leu Leu
 1                      5                      10                      15

Leu Leu Gly Thr Ala Ser Thr Gln Phe Pro Asn Thr Pro Ile Asn Ser
      20                      25                      30

Ser Ser Glu Ala Lys Ala Tyr Tyr Ile Asn Gln Asn Glu Thr Asn Val
      35                      40                      45

Asn Glu Leu Thr Lys Tyr Tyr Ser Gln Lys Tyr Leu Thr Phe Ser Asn
      50                      55                      60

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Ser Thr Leu Trp Gln Lys Asp Asn Gly Thr Ile His Ala Thr Leu Leu
65              70              75              80

Gln Phe Ser Trp Tyr Ser His Ile Gln Val Tyr Gly Pro Glu Ser Trp
85              90              95

Gly Asn Ile Asn Gln Leu Arg Asn Lys Ser Val Asp Ile Phe Gly Ile
100            105            110

Lys Asp Gln Glu Thr Ile Asp Ser Phe Ala Leu Ser Gln Glu Thr Phe
115            120            125

Thr Gly Gly Val Thr Pro Ala Ala Thr Ser Asn Asp Lys His Tyr Lys
130            135            140

Leu Asn Val Thr Tyr Lys Asp Lys Ala Glu Thr Phe Thr Gly Gly Phe
145            150            155            160

Pro Val Tyr Glu Gly Asn Lys Pro Val Leu Thr Leu Lys Glu Leu Asp
165            170            175

Phe Arg Ile Arg Gln Thr Leu Ile Lys Ser Lys Lys Leu Tyr Asn Asn
180            185            190

Ser Tyr Asn Lys Gly Gln Ile Lys Ile Thr Gly Ala Asp Asn Asn Tyr
195            200            205

Thr Ile Asp Leu Ser Lys Arg Leu Pro Ser Thr Asp Ala Asn Arg Tyr
210            215            220

Val Lys Lys Pro Gln Asn Ala Lys Ile Glu Val Ile Leu Glu Lys Ser
225            230            235            240

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Asn

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<210>  77
<211> 565
<212>  PRT
<213>  Staphylococcus aureus
<223>  sta041

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<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
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
50            55            60

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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	
			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			
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	

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[illegible]

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<210> 78
<211> 317
<212> PRT
<213> Staphylococcus aureus
<223> sta042
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<400> 78

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
 20 25 30
 Glu Glu Ser Lys Gln Glu Thr Val Lys Lys Glu Ser Glu Glu Glu Lys
 35 40 45
 Asp Pro Asp Leu Glu Lys Tyr Glu Glu Ile Glu Lys Lys Met Lys Gly
 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
 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
 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
 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
 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
 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
 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
 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
305 310 315

<210> 79
<211> 372
<212> PRT
<213> Staphylococcus aureus
<223> sta043

<400> 79

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
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
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
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
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
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
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
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
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
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
325 330 335

Leu Asp Gln Asn Trp Asn Asn Gly Gly Trp Arg Lys Ala Glu Val Ala
340 345 350

His Lys Val Val His Asn Tyr Glu Asn Asp Met Ile Phe Ile Arg Pro
355 360 365

Phe Lys Lys Ala
370

<210> 80
<211> 304
<212> PRT
<213> Staphylococcus aureus
<223> sta044

<400> 80

Met Leu Lys Lys Ala Lys Phe Ile Leu Met Ala Thr Ile Leu Leu Ser
1 5 10 15

Gly Cys Ser Thr Thr Asn Asn Glu Ser Asn Lys Glu Thr Lys Ser Val
20 25 30

Pro Glu Glu Met Asp Ala Ser Lys Tyr Val Gly Gln Gly Phe Gln Pro
35 40 45

Pro Ala Glu Lys Asp Ala Ile Glu Phe Ala Lys Lys His Lys Asp Lys
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 Ile Gly Ser Gly Asp Gly Val Glu Val Phe
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 Asp Ser Asp Ser Ser Leu Arg Ser Lys Asp Lys		
115	120	125
Gly Asp Asp Met Ser Thr Leu Val Gly Ala Val Leu Ser Gly Phe Glu		
130	135	140
Tyr Arg Ala Gln Lys Glu Lys Tyr Asp Lys Leu Tyr Lys Phe Phe Lys		
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 Ser Gly Tyr Glu Asn Glu Tyr Phe Tyr Ile Ser		
180	185	190
Ala Ile Pro Tyr Asn Leu Ala Glu Tyr Arg Asp Tyr Phe Glu Pro Leu		
195	200	205
Leu Asn Lys Ser Asp Ser Glu Phe Ser Lys Glu Leu Ser Asn Val Lys		
210	215	220
Lys Gln Leu Lys Asp Lys Ser Lys Val Ser Val Thr Thr Thr Leu Phe		
225	230	235
240		
Ser Lys Lys Lys Asn Tyr Thr Lys Lys Ser Asn Ser Glu Asn Val Ile		
245	250	255
Lys Met Ala Glu Glu Ile Lys Lys Asp Lys Glu Ile Pro Asn Gly Ile		
260	265	270
Glu Leu Ser Ile Lys Phe Ser Asp Asn Lys Ile Asn Thr Val Lys Pro		
275	280	285
Asn Phe Asn Gly Glu Ser Thr Ser Glu Tyr Gly Val Phe Asp Gln Glu		
290	295	300
<210> 81		
<211> 193		
<212> PRT		
<213> Staphylococcus aureus		
<223> sta045		
<400> 81		
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		
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
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
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
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
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
180 185 190

Ser

<210> 82
<211> 216
<212> PRT
<213> Staphylococcus aureus
<223> sta046

<400> 82

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

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

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

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
<223> sta047

<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

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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
<223> sta048

<400> 84

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
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
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
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

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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									
		355					360					365												
Glu	Gly	Tyr	Met	His	Lys	Glu	Asn	Ile	Leu	Thr	Thr	Ala	Asn	Asn	Gly									
	370					375					380													
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										
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												

Leu Asn Val Ala Asn Gln Lys Ala Ser
450 455

<210> 85
<211> 320
<212> PRT
<213> Staphylococcus aureus
<223> sta049

<400> 85

Met Lys Met Ile Asn Lys Leu Ile Val Pro Val Thr Ala Ser Ala Leu
1 5 10 15

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

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

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

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

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

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

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

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

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

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
<213> Staphylococcus aureus
<223> sta050

<400> 86

Met Lys Arg Asn Phe Pro Lys Leu Ile Ala Leu Ser Leu Ile Phe Ser
1 5 10 15

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

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

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

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

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

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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

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

Tyr Thr Met Ser Glu Leu Leu Asn Ala Thr Tyr Asn Thr Asn Lys Tyr
      245                      250                      255

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
<223> sta051

<400> 87

Met Lys Lys Phe Phe Phe Ile Gly Leu Leu Val Phe Val Val Phe Phe
  1                      5                      10                      15

Thr Ala Ala Thr Ile Ile Trp Phe Ser Tyr Asp Lys Asn Lys Tyr Gly

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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		
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		
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		
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		
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		
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		
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		
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		
275	280	

<210> 88
 <211> 303
 <212> PRT
 <213> Staphylococcus aureus

<223> sta052

<400> 88

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
<223> sta053

<400> 89

Met Ser Tyr His Trp Phe Lys Lys Met Leu Leu Ser Thr Ser Ile Leu
1 5 10 15

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

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

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

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

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

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

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

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

Lys Asp Tyr Gly Glu Val Thr Asp Glu Asp Ile Tyr Asn Ile Ile Arg
275 280 285

Lys Gln Asn Phe Ser Gly Asn Ala Tyr Leu Asn Gly Leu Gln Gln Gln
290 295 300

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

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

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

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
<223> sta054

<400> 90

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
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		
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		
				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		
	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		
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		
			180					185					190				
Ser	Val	Ala	Pro	Ala	Lys	Tyr	Lys	Gly	Val	Ser	Pro	Ala	Asn	Ala	Pro		
	195						200					205					
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											
225					230												
<210>	91																
<211>	294																
<212>	PRT																
<213>	Staphylococcus aureus																
<223>	sta055																
<400>	91																
Met	Gly	Val	Lys	Ser	Val	Lys	Lys	Ile	Phe	Val	Ile	Ile	Thr	Thr	Leu		
1				5					10					15			
Leu	Ala	Val	Ala	Ile	Ile	Ile	Gly	Ser	Ile	Ile	Met	Val	Val	Phe	Ser		
			20					25					30				
Gln	Arg	Gln	Ala	Gln	Thr	Phe	Lys	Ile	Gln	Gln	Gln	Gln	Phe	Val	Lys		
	35						40					45					

Lys Pro Ile Pro Thr Leu Phe Leu His Gly Phe Gly Gly Ser Ala Asn
50 55 60

Ser Glu Lys Phe Met Val Lys Gln Ala Glu Lys Arg Gly Val Thr Lys
65 70 75 80

Asp Ile Ile Thr Ala Tyr Val Ser Lys Asp Gly Ala Val Thr Phe Lys
85 90 95

Gly Lys Leu Arg Lys Asp Ala Val Asn Pro Ile Val Lys Ile Glu Leu
100 105 110

Glu Asn Asn Arg Gln Gly Tyr Leu Asp Lys Asn Ala Ala Trp Phe Lys
115 120 125

Asn Val Leu Thr Lys Leu Gln Ser Glu Tyr Asn Phe Asp Lys Phe Asn
130 135 140

Phe Val Gly His Ser Met Gly Asn Leu Thr Phe Ala Gln Tyr Met Met
145 150 155 160

Thr Tyr Gly Asn Asp Lys Ser Leu Pro Gln Leu Asn Lys Gln Val Asn
165 170 175

Ile Ala Gly Thr Phe Asn Gly Val Leu Asn Met Asn Glu Asp Val Asn
180 185 190

Glu Ile Thr Val Asp Lys Asp Gly Lys Pro Ser Arg Met Asn Gln Pro
195 200 205

Tyr Gln Gln Leu Arg Val Leu Lys Asp Ile Tyr Lys Gly Lys Gly Ile
210 215 220

Glu Val Leu Asn Ile Tyr Gly Asp Leu Lys Asp Gly Thr His Ser Asp
225 230 235 240

Gly Arg Val Ser Asn Ser Ser Ser Lys Ser Leu Lys Tyr Leu Leu Gly
245 250 255

Asn Ser Pro Lys Ser Tyr Arg Glu Ser Lys Tyr Glu Gly Glu Pro Ala
260 265 270

Gln His Ser Gln Leu His Glu Asn Glu Asn Val Ala Asn Glu Leu Ile
275 280 285

Asp Phe Leu Trp Lys Lys
290

<210> 92
<211> 807
<212> PRT
<213> Staphylococcus aureus
<223> sta056

<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

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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
 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

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                    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
                    705                      710                      715                      720

Glu Ser Val Trp Ala Gly Val Asn Tyr Ser Asn Ser Thr Gln Thr Phe
                    725                      730                      735

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

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

Val His Phe Glu Leu Thr Lys
                    805

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<210> 93
<211> 166
<212> PRT
<213> Staphylococcus aureus
<223> sta057

<400> 93

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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

Asn Tyr Asn Asn Tyr Asn Tyr Asn Thr Thr Gln 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

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

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

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

Tyr Asn Tyr Ile His Ile
165

<210> 94
<211> 516
<212> PRT
<213> Staphylococcus aureus
<223> sta058

<400> 94

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

Val Thr Ile Lys Thr Thr Val Tyr Pro Leu Gln Ser Phe Ala Glu Gln
35 40 45

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

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

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

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

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

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

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

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

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

Arg Glu Leu Ser Asp Tyr Ala Gly Glu Trp Gln Ser Val Tyr Pro Tyr
355 360 365

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Leu Lys Asp Gly Thr Leu Asp Glu Val Met Glu His Lys Ala Glu Asn
 370                      375                      380

Asp Pro Lys Lys Ser Ala Lys Asp Leu Lys Ala Tyr Tyr Asp Lys Gly
385                      390                      395                      400

Tyr Lys Thr Asp Ile Thr Asn Ile Asp Ile Lys Gly Asn Glu Ile Thr
                      405                      410                      415

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

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

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

Met Leu Ala His
 515

<210> 95
<211> 309
<212> PRT
<213> Staphylococcus aureus
<223> sta059

<400> 95

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
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
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

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[illegible]

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<210> 96
<211> 532
<212> PRT
<213> Staphylococcus aureus
<223> sta060
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<400> 96

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	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	50	55	60
Pro	Leu	Val	Arg	Asn	Thr	Lys	Asp	Gly	Ile	Lys	Pro	Leu	Leu	Ala	Lys	65	70	75
Lys	Trp	Asp	Val	Ser	Glu	Asp	Gly	Lys	Thr	Tyr	Thr	Phe	His	Leu	Arg	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	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	145	150	155
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	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	210	215	220
Lys	Val	Met	Pro	Ala	Gly	Glu	Thr	Ala	Phe	Leu	Ser	Met	Lys	Lys	Gly	225	230	235
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

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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
<223> sta061

<400> 97

Met Ile His Ser Lys Lys Leu Thr Leu Gly Ile Cys Leu Val Leu Leu
1                      5                      10                      15

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Ile Ile Leu Ile Val Gly Tyr Val Ile Met Thr Lys Thr Asn Gly Arg
      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
      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
      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
      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
      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
      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
      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
      245                     250                     255

Glu Asp Thr Arg Tyr Glu Ser Asn
      260

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<210> 98
<211> 261
<212> PRT
<213> Staphylococcus aureus
<223> sta062

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<400> 98

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
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
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
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
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
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
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
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
245 250 255

Glu Asp Asp Lys Ser
260

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<210> 99
<211> 498
<212> PRT
<213> Staphylococcus aureus
<223> sta063

<400> 99

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
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
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
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
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
145 150 155 160

Tyr Val Tyr Asn Val Glu Leu Ile Thr Val Thr Pro Glu Ile Ser His
165 170 175

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

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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
<223> sta064

<400> 100

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Met Lys Ser Gln Asn Lys Tyr Ser Ile Arg Lys Phe Ser Val Gly Ala
1          5          10          15

Ser Ser Ile Leu Ile Ala Thr Leu Leu Phe Leu Ser Gly Gly Gln Ala
          20          25          30

Gln Ala Ala Glu Lys Gln Val Asn Met Gly Asn Ser Gln Glu Asp Thr
          35          40          45

Val Thr Ala Gln Ser Ile Gly Asp Gln Gln Thr Arg Glu Asn Ala Asn
50          55          60

Tyr Gln Arg Glu Asn Gly Val Asp Glu Gln Gln His Thr Glu Asn Leu
65          70          75          80

Thr Lys Asn Leu His Asn Asp Lys Thr Ile Ser Glu Glu Asn His Arg
          85          90          95

Lys Thr Asp Asp Leu Asn Lys Asp Gln Leu Lys Asp Asp Lys Lys Ser
          100          105          110

Ser Leu Asn Asn Lys Asn Ile Gln Arg Asp Thr Thr Lys Asn Asn Asn
          115          120          125

Ala Asn Pro Ser Asp Val Asn Gln Gly Leu Glu Gln Ala Ile Asn Asp
130          135          140

Gly Lys Gln Ser Lys Val Ala Ser Gln Gln Gln Ser Lys Glu Ala Asp
145          150          155          160

Asn Ser Gln Asp Ser Asn Ala Asn Asn Asn Leu Pro Ser Gln Ser Arg
          165          170          175

Ile Lys Glu Ala Pro Ser Leu Asn Lys Leu Asp Gln Thr Ser Gln Arg
          180          185          190

Glu Ile Val Asn Glu Thr Glu Ile Glu Lys Val Gln Pro Gln Gln Asn
195          200          205

Asn Gln Ala Asn Asp Lys Ile Thr Asn Tyr Asn Phe Asn Asn Glu Gln
210          215          220

Glu Val Lys Pro Gln Lys Asp Glu Lys Thr Leu Ser Val Ser Asp Leu
225          230          235          240

Lys Asn Asn Gln Lys Ser Pro Val Glu Pro Thr Lys Asp Asn Asp Lys
          245          250          255

Lys Asn Gly Leu Asn Leu Leu Lys Ser Ser Ala Val Ala Thr Leu Pro
          260          265          270

Asn Lys Gly Thr Lys Glu Leu Thr Ala Lys Ala Lys Asp Asp Gln Thr

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275	280	285
Asn Lys Val Ala Lys Gln Gly Gln Tyr Lys Asn Gln Asp Pro Ile Val		
290	295	300
Leu Val His Gly Phe Asn Gly Phe Thr Asp Asp Ile Asn Pro Ser Val		
305	310	315
320		
Leu Ala His Tyr Trp Gly Gly Asn Lys Met Asn Ile Arg Gln Asp Leu		
325	330	335
Glu Glu Asn Gly Tyr Lys Ala Tyr Glu Ala Ser Ile Ser Ala Phe Gly		
340	345	350
Ser Asn Tyr Asp Arg Ala Val Glu Leu Tyr Tyr Tyr Ile Lys Gly Gly		
355	360	365
Arg Val Asp Tyr Gly Ala Ala His Ala Ala Lys Tyr Gly His Glu Arg		
370	375	380
Tyr Gly Lys Thr Tyr Glu Gly Ile Tyr Lys Asp Trp Lys Pro Gly Gln		
385	390	395
400		
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
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
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
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
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		

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

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

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

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

<210> 101
<211> 328
<212> PRT
<213> Staphylococcus aureus
<223> sta065

<400> 101

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
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
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
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
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
 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
 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
 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
 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
 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
 305 310 315 320
 Ser Glu Ile Ile Asp Ser Asn Lys
 325

<210> 102
 <211> 257
 <212> PRT
 <213> Staphylococcus aureus
 <223> sta066

<400> 102

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
 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

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

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

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

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

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

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
<223> sta067

<400> 103

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

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2010238255

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

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Val Arg Gly Trp Tyr Leu Ser Glu Tyr Ser Lys His Lys Tyr Trp Ala
305                      310                      315                      320

Lys Asp Leu Met Leu Tyr Ile Thr Ser Lys Asp Thr Leu Gln Lys Tyr
                      325                      330                      335

Thr Asp Glu Met Ser Glu Ile Thr Gly Arg Val Asp Val Lys Ser Ser
                      340                      345                      350

Asn Pro Asn Leu Lys Val Phe Glu Lys Gln Ala Arg His Ala Glu Pro
                      355                      360                      365

Met Pro Asn Ile Pro Glu Met Arg Gln Val Trp Glu Pro Met Gly Asn
370                      375                      380

Ala Ser Ile Phe Ile Ser Asn Gly Lys Asn Pro Lys Gln Ala Leu Asp
385                      390                      395                      400

Glu Ala Thr Asn Asp Ile Thr Gln Asn Ile Lys Ile Leu His Pro Ser
                      405                      410                      415

Gln Asn Asp Lys Lys Gly Asp
420

<210> 104
<211> 560
<212> PRT
<213> Staphylococcus aureus
<223> sta068

<400> 104

Met Leu Ile Thr Ala Ala Met Val Cys Ser Phe Gly Leu Leu Lys Ser
1                      5                      10                      15

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
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
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
100                     105                     110

Gly Ser Lys Ile Lys Leu Leu Gln Gln Gln Val Asp Ala Lys Asp Ala
115                     120                     125

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Ala	Met	Thr	Lys	Ala	Ile	Lys	Asp	Lys	Asn	Lys	Ala	Glu	Leu	Glu	Ser	
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	
				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	
		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	
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	
		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	
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	
			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	
	370					375					380					
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
<223> sta069

<400> 105

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
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
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
85 90 95

Ala Gly Asp Ser Leu Ser Leu Ile Ala Ser Lys Tyr Gly Thr Thr Tyr

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[illegible]

Ala Leu Asn Asn Ala Ala His Ala Gln Gln His Gly Thr Gln Val Lys
20 25 30

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

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

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

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

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

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

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

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
<211> 346
<212> PRT

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<213> Staphylococcus aureus
<223> sta071

<400> 107

Met Ile Ile Ala Ile Ile Ile Leu Ile Phe Ile Ser Phe Phe Phe Ser
1 5 10 15

Gly Ser Glu Thr Ala Leu Thr Ala Ala Asn Lys Thr Lys Phe Lys Thr
20 25 30

Glu Ala Asp Lys Gly Asp Lys Lys Ala Lys Gly Ile Val Lys Leu Leu
35 40 45

Glu Lys Pro Ser Glu Phe Ile Thr Thr Ile Leu Ile Gly Asn Asn Val
50 55 60

Ala Asn Ile Leu Leu Pro Thr Leu Val Thr Ile Met Ala Leu Arg Trp
65 70 75 80

Gly Ile Ser Val Gly Ile Ala Ser Ala Val Leu Thr Val Val Ile Ile
85 90 95

Leu Ile Ser Glu Val Ile Pro Lys Ser Val Ala Ala Thr Phe Pro Asp
100 105 110

Lys Ile Thr Arg Leu Val Tyr Pro Ile Ile Asn Ile Cys Val Ile Val
115 120 125

Phe Arg Pro Ile Thr Leu Leu Leu Asn Lys Leu Thr Asp Ser Ile Asn
130 135 140

Arg Ser Leu Ser Lys Gly Gln Pro Gln Glu His Gln Phe Ser Lys Glu
145 150 155 160

Glu Phe Lys Thr Met Leu Ala Ile Ala Gly His Glu Gly Ala Leu Asn
165 170 175

Glu Ile Glu Thr Ser Arg Leu Glu Gly Val Ile Asn Phe Glu Asn Leu
180 185 190

Lys Val Lys Asp Val Asp Thr Thr Pro Arg Ile Asn Val Thr Ala Phe
195 200 205

Ala Ser Asn Ala Thr Tyr Glu Glu Val Tyr Glu Thr Val Met Asn Lys
210 215 220

Pro Tyr Thr Arg Tyr Pro Val Tyr Glu Gly Asp Ile Asp Asn Ile Ile
225 230 235 240

Gly Val Phe His Ser Lys Tyr Leu Leu Ala Trp Ser Asn Lys Lys Glu
245 250 255

Asn Gln Ile Thr Asn Tyr Ser Ala Lys Pro Leu Phe Val Asn Glu His
260 265 270

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Asn Lys Ala Glu Trp Val Leu Arg Lys Met Thr Ile Ser Arg Lys His
275 280 285

Leu Ala Ile Val Leu Asp Glu Phe Gly Gly Thr Glu Ala Ile Val Ser
290 295 300

His Glu Asp Leu Ile Glu Glu Leu Leu Gly Met Glu Ile Glu Asp Glu
305 310 315 320

Met Asp Lys Lys Glu Lys Glu Lys Leu Ser Gln Gln Gln Ile Gln Phe
325 330 335

Gln Gln Arg Lys Asn Arg Asn Val Ser Ile
340 345

<210> 108

<211> 391

<212> PRT

<213> Staphylococcus aureus

<223> sta072

<400> 108

Met Lys Leu Lys Pro Phe Leu Pro Ile Leu Ile Ser Gly Ala Val Phe
1 5 10 15

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

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 Asp Pro Phe Asn Pro
65 70 75 80

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

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

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

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[illegible]

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<210> 109
<211> 1256
<212> PRT
<213> Staphylococcus aureus
<223> sta073
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<400> 109

Met Ala Lys Lys Phe Asn Tyr Lys Leu Pro Ser Met Val Ala Leu Thr
1 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
 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
 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
 Lys Thr Asn Thr Asn Val Thr Asn Ala Gly Tyr Ser Leu Val Asp Asp
 130 135 140
 Glu Asp Asp Asn Ser Glu Asn Gln Ile Asn Pro Glu Leu Ile Lys Ser
 145 150 155 160
 Ala Ala Lys Pro Ala Ala Leu Glu Thr Gln Tyr Lys Thr Ala Ala Pro
 165 170 175
 Lys Ala Ala Thr Thr Ser Ala Pro Lys Ala Lys Thr Glu Ala Thr Pro
 180 185 190
 Lys Val Thr Thr Phe Ser Ala Ser Ala Gln Pro Arg Ser Val Ala Ala
 195 200 205
 Thr Pro Lys Thr Ser Leu Pro Lys Tyr Lys Pro Gln Val Asn Ser Ser
 210 215 220
 Ile Asn Asp Tyr Ile Cys Lys Asn Asn Leu Lys Ala Pro Lys Ile Glu
 225 230 235 240
 Glu Asp Tyr Thr Ser Tyr Phe Pro Lys Tyr Ala Tyr Arg Asn Gly Val
 245 250 255
 Gly Arg Pro Glu Gly Ile Val Val His Asp Thr Ala Asn Asp Arg Ser
 260 265 270
 Thr Ile Asn Gly Glu Ile Ser Tyr Met Lys Asn Asn Tyr Gln Asn Ala
 275 280 285
 Phe Val His Ala Phe Val Asp Gly Asp Arg Ile Ile Glu Thr Ala Pro
 290 295 300

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


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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
      900              905              910

Val Tyr Leu Tyr Gly Thr Ile Asn Asn Arg Thr Gly Trp Val Asn Ala
      915              920              925

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              960

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

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
      1010              1015              1020

Met Thr Leu Asn Gln Val Ala Gln Ile Gln Ala Gly Leu Gln Tyr
      1025              1030              1035

Lys Pro Gln Val Gln Arg Val Pro Gly Lys Trp Thr Asp Ala Lys
      1040              1045              1050

Phe Asn Asp Val Lys His Ala Met Asp Thr Lys Arg Leu Ala Gln
      1055              1060              1065

Asp Pro Ala Leu Lys Tyr Gln Phe Leu Arg Leu Asp Gln Pro Gln
      1070              1075              1080

Asn Ile Ser Ile Asp Lys Ile Asn Gln Phe Leu Lys Gly Lys Gly
      1085              1090              1095

Val Leu Glu Asn Gln Gly Ala Ala Phe Asn Lys Ala Ala Gln Met
      1100              1105              1110

Tyr Gly Ile Asn Glu Val Tyr Leu Ile Ser His Ala Leu Leu Glu
      1115              1120              1125

Thr Gly Asn Gly Thr Ser Gln Leu Ala Lys Gly Ala Asp Val Val
      1130              1135              1140

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Asn Asn  Lys Val Val Thr Asn  Ser Asn Thr Lys Tyr  His Asn Val
1145                                1150                        1155

Phe Gly  Ile Ala Ala Tyr Asp  Asn Asp Pro Leu Arg  Glu Gly Ile
1160                                1165                        1170

Lys Tyr  Ala Lys Gln Ala Gly  Trp Asp Thr Val Ser  Lys Ala Ile
1175                                1180                        1185

Val Gly  Gly Ala Lys Phe Ile  Gly Asn Ser Tyr Val  Lys Ala Gly
1190                                1195                        1200

Gln Asn  Thr Leu Tyr Lys Met  Arg Trp Asn Pro Ala  His Pro Gly
1205                                1210                        1215

Thr His  Gln Tyr Ala Thr Asp  Val Asp Trp Ala Asn  Ile Asn Ala
1220                                1225                        1230

Lys Ile  Ile Lys Gly Tyr Tyr  Asp Lys Ile Gly Glu  Val Gly Lys
1235                                1240                        1245

Tyr Phe  Asp Ile Pro Gln Tyr  Lys
1250                                1255

<210>  110
<211>  414
<212>  PRT
<213>  Staphylococcus aureus
<223>  sta074

<400>  110

Met Lys Phe Ser Thr Leu Ser Glu Glu Glu Phe Thr Asn Tyr Thr Lys
1          5          10          15

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

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

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

Asn Leu Arg Asp Ala Asn Gly Arg Ile Ile Lys Asn Tyr Asn Asn Ser
115         120         125

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Val	Ile	Val	Lys	Met	Leu	Gly	Lys	Ile	Gly	Tyr	Leu	His	Gln	Gly	Tyr	130	135	140
Thr	Thr	Gly	Tyr	Ser	Asn	Lys	Ser	Gln	Ile	Arg	Trp	Ile	Ser	Val	Leu	145	150	155
Asp	Leu	Lys	Asp	Lys	Asp	Glu	Asn	Gln	Leu	Leu	Lys	Glu	Met	Glu	Tyr	165	170	175
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
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
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
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
Glu	Asp	Gly	Pro	Val	Leu	Asp	Leu	Ala	Ala	Ala	Leu	Phe	Ile	Cys	Thr	305	310	315
Asp	Asp	Glu	Val	Tyr	Tyr	Leu	Ser	Ser	Gly	Ser	Asn	Pro	Lys	Tyr	Asn	325	330	335
Gln	Tyr	Met	Gly	Ala	Tyr	His	Leu	Gln	Trp	His	Met	Ile	Lys	Tyr	Ala	340	345	350
Lys	Ser	His	Asn	Ile	Asn	Arg	Tyr	Asn	Phe	Tyr	Gly	Ile	Thr	Gly	Val	355	360	365
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
Arg	Pro	Ile	Leu	Tyr	Lys	Phe	Ala	Lys	Leu	Ile	Tyr	Lys	Val			405	410	

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<210> 111
<211> 428
<212> PRT
<213> Staphylococcus aureus
<223> sta075

<400> 111

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
          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
          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
          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
          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
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
          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
225          230          235          240

Glu Asp Val Lys Glu Ala Phe Val Thr Glu Ser Met Lys Ile Gln Ser

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[illegible]

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
 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
 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
 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
 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
 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
 Lys His Ser Ile Glu Val Ala His Leu Ala Ser Met Leu Ala Ala Glu
 340 345 350

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Leu Gly Glu Asp Glu Thr Leu Ala Lys Arg Ala Gly Leu Leu His Asp
   355                               360                               365

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

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

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

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

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
<211> 284
<212> PRT
<213> Staphylococcus aureus
<223> sta077

<400> 113

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

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

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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

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

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

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

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

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

Lys Glu Gln Val Asp Gln Ile Thr Ala Ile Phe Lys
      275                      280

<210> 114
<211> 1274
<212> PRT
<213> Staphylococcus aureus
<223> sta078

<400> 114

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
      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				
50						55					60								
Glu	Asn	Val	Glu	Gln	Ser	Ala	Asp	Thr	Ile	Ser	Asp	Glu	Lys	Glu	Gln				
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				
								105						110					
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								
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					
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							
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				
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						
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								
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
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
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	400
Leu	Asn	Gln	Val	Ser	Thr	Thr	Lys	Gln	Leu	Ser	Asp	Asp	Glu	Val	Thr	405	410	415
Val	Ser	Asn	Val	Thr	Ser	Gln	His	Gln	Ser	Ala	Leu	Gln	His	Asn	Val	420	425	430
Glu	Val	Asn	Asp	Lys	Asp	Glu	Leu	Lys	Asn	Gln	Ser	Arg	Leu	Ile	Ala	435	440	445
Asp	Ser	Glu	Glu	Asp	Gly	Ala	Thr	Asn	Lys	Glu	Glu	Tyr	Ser	Gly	Ser	450	455	460
Gln	Ile	Asp	Asp	Ala	Glu	Phe	Tyr	Glu	Leu	Asn	Asp	Thr	Glu	Val	Asp	465	470	475
Glu	Asp	Thr	Thr	Ser	Asn	Ile	Glu	Asp	Asn	Thr	Asn	Arg	Asn	Ala	Ser	485	490	495
Glu	Met	His	Val	Asp	Ala	Pro	Lys	Thr	Gln	Glu	Tyr	Ala	Val	Thr	Glu	500	505	510
Ser	Gln	Val	Asn	Asn	Ile	Asp	Lys	Thr	Val	Asp	Asn	Glu	Ile	Glu	Leu	515	520	525
Ala	Pro	Arg	His	Lys	Lys	Asp	Asp	Gln	Thr	Asn	Leu	Ser	Val	Asn	Ser	530	535	540
Leu	Lys	Thr	Asn	Asp	Val	Asn	Asp	Asn	His	Val	Val	Glu	Asp	Ser	Ser	545	550	555
Met	Asn	Glu	Ile	Glu	Lys	Asn	Asn	Ala	Glu	Ile	Thr	Glu	Asn	Val	Gln	565	570	575
Asn	Glu	Ala	Ala	Glu	Ser	Glu	Gln	Asn	Val	Glu	Glu	Lys	Thr	Ile	Glu	580	585	590
Asn	Val	Asn	Pro	Lys	Lys	Gln	Thr	Glu	Lys	Val	Ser	Thr	Leu	Ser	Lys	595	600	605

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Arg 610	Pro	Phe	Asn	Val	Val	Met 615	Thr	Pro	Ser	Asp	Lys 620	Lys	Arg	Met	Met
Asp 625	Arg	Lys	Lys	His	Ser 630	Lys	Val	Asn	Val	Pro 635	Glu	Leu	Lys	Pro	Val 640
Gln	Ser	Lys	Gln	Ala 645	Val	Ser	Glu	Arg	Met 650	Pro	Ala	Ser	Gln	Ala	Thr 655
Pro	Ser	Ser	Arg 660	Ser	Asp	Ser	Gln	Glu 665	Ser	Asn	Thr	Asn	Ala 670	Tyr	Lys
Thr	Asn	Asn	Met 675	Thr	Ser	Asn	Asn	Val 680	Glu	Asn	Asn	Gln	Leu	Ile	Gly
His 690	Ala	Glu	Thr	Glu	Asn	Asp 695	Tyr	Gln	Asn	Ala	Gln 700	Gln	Tyr	Ser	Glu
Gln 705	Lys	Pro	Ser	Val	Asp 710	Ser	Thr	Gln	Thr	Glu 715	Ile	Phe	Glu	Glu	Ser 720
Gln	Asp	Asp	Asn	Gln 725	Leu	Glu	Asn	Glu	Gln 730	Val	Asp	Gln	Ser	Thr	Ser 735
Ser	Ser	Val	Ser 740	Glu	Val	Ser	Asp	Ile 745	Thr	Glu	Glu	Ser	Glu 750	Glu	Thr
Thr	His 755	Pro	Asn	Asn	Thr	Ser	Gly 760	Gln	Gln	Asp	Asn 765	Asp	Asp	Gln	Gln
Lys 770	Asp	Leu	Gln	Ser	Ser	Phe 775	Ser	Asn	Lys	Asn	Glu 780	Asp	Thr	Ala	Asn
Glu 785	Asn	Arg	Pro	Arg	Thr 790	Asn	Gln	Gln	Asp	Val 795	Ala	Thr	Asn	Gln	Ala 800
Val	Gln	Thr	Ser	Lys 805	Pro	Met	Ile	Arg	Lys 810	Gly	Pro	Asn	Ile	Lys 815	Leu
Pro	Ser	Val	Ser 820	Leu	Leu	Glu	Glu	Pro 825	Gln	Val	Ile	Glu	Ser 830	Asp	Glu
Asp	Trp 835	Ile	Thr	Asp	Lys	Lys	Lys 840	Glu	Leu	Asn	Asp	Ala 845	Leu	Phe	Tyr
Phe 850	Asn	Val	Pro	Ala	Glu	Val 855	Gln	Asp	Val	Thr	Glu 860	Gly	Pro	Ser	Val
Thr 865	Arg	Phe	Glu	Leu	Ser 870	Val	Glu	Lys	Gly	Val 875	Lys	Val	Ser	Arg	Ile 880
Thr	Ala	Leu	Gln	Asp 885	Asp	Ile	Lys	Met	Ala 890	Leu	Ala	Ala	Lys	Asp 895	Ile

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Arg Ile Glu Ala Pro Ile Pro Gly Thr Ser Arg Val Gly Ile Glu Val
      900                      905                      910

Pro Asn Gln Asn Pro Thr Thr Val Asn Leu Arg Ser Ile Ile Glu Ser
      915                      920                      925

Pro Ser Phe Lys Asn Ala Glu Ser Lys Leu Thr Val Ala Met Gly Tyr
      930                      935                      940

Arg Ile Asn Asn Glu Pro Leu Leu Met Asp Ile Ala Lys Thr Pro His
      945                      950                      955                      960

Ala Leu Ile Ala Gly Ala Thr Gly Ser Gly Lys Ser Val Cys Ile Asn
      965                      970                      975

Ser Ile Leu Met Ser Leu Leu Tyr Lys Asn His Pro Glu Glu Leu Arg
      980                      985                      990

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
      1010                      1015                      1020

Thr Gln Ser Leu Lys Trp Ala Val Glu Glu Met Glu Arg Arg Tyr
      1025                      1030                      1035

Lys Leu Phe Ala His Tyr His Val Arg Asn Ile Thr Ala Phe Asn
      1040                      1045                      1050

Lys Lys Ala Pro Tyr Asp Glu Arg Met Pro Lys Ile Val Ile Val
      1055                      1060                      1065

Ile Asp Glu Leu Ala Asp Leu Met Met Met Ala Pro Gln Glu Val
      1070                      1075                      1080

Glu Gln Ser Ile Ala Arg Ile Ala Gln Lys Ala Arg Ala Cys Gly
      1085                      1090                      1095

Ile His Met Leu Val Ala Thr Gln Arg Pro Ser Val Asn Val Ile
      1100                      1105                      1110

Thr Gly Leu Ile Lys Ala Asn Ile Pro Thr Arg Ile Ala Phe Met
      1115                      1120                      1125

Val Ser Ser Ser Val Asp Ser Arg Thr Ile Leu Asp Ser Gly Gly
      1130                      1135                      1140

Ala Glu Arg Leu Leu Gly Tyr Gly Asp Met Leu Tyr Leu Gly Ser
      1145                      1150                      1155

Gly Met Asn Lys Pro Ile Arg Val Gln Gly Thr Phe Val Ser Asp

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1160                      1165                      1170
Asp Glu  Ile Asp Asp Val Val  Asp Phe Ile Lys Gln  Gln Arg Glu
1175                      1180                      1185

Pro Asp  Tyr Leu Phe Glu Glu  Lys Glu Leu Leu Lys  Lys Thr Gln
1190                      1195                      1200

Thr Gln  Ser Gln Asp Glu Leu  Phe Asp Asp Val Cys  Ala Phe Met
1205                      1210                      1215

Val Asn  Glu Gly His Ile Ser  Thr Ser Leu Ile Gln  Arg His Phe
1220                      1225                      1230

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
1250                      1255                      1260

Val Tyr  Val Thr Glu Ala Asp  Leu Asn Lys Glu
1265                      1270

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<210> 115
<211> 239
<212> PRT
<213> Staphylococcus aureus
<223> sta079

```

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<400> 115

```

```

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
          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
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
          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
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
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
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
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
<223> sta080

<400> 116

Met Asn Lys Asn Ile Ile Ile Lys Ser Ile Ala Ala Leu Thr Ile Leu
1 5 10 15

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

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

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

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

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

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

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
<223> sta082

<400> 117

Met Asn Lys Asn Ile Val Ile Lys Ser Met Ala Ala Leu Ala Ile Leu
1 5 10 15

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

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

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

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

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

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

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

<210> 118
<211> 240
<212> PRT
<213> Staphylococcus aureus
<223> sta083

<400> 118

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
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
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
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
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
145 150 155 160

Tyr Lys Asn Lys Tyr Val Leu Tyr Glu Ser Thr Gly Pro Val Met Ser


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165              170              175
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
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
225              230              235              240

<210> 119
<211> 235
<212> PRT
<213> Staphylococcus aureus
<223> sta084

<400> 119

Met Asn Lys Asn Val Met Val Lys Gly Leu Thr Ala Leu Thr Ile Leu
1              5              10              15

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

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

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

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

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

```

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

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
<223> sta085

<400> 120

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
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
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
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
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
145 150 155 160

Glu Lys Lys

<210> 121
<211> 290
<212> PRT

<213> Staphylococcus aureus

<223> sta086

<400> 121

Met Lys Lys Lys Ala Leu Leu Pro Leu Phe Leu Gly Ile Met Val Phe
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
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
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
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
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

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

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

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

Gly Ser Asn Lys Lys Gly Lys Asn Thr Gln Val Val Ser Lys Lys Lys
275 280 285

Lys Lys
290

<210> 122
<211> 460
<212> PRT
<213> Staphylococcus aureus
<223> sta087

<400> 122

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
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
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
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
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
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

Glu Phe Lys Ser Gly Gly Lys Lys Lys Met Val Ile Ala Glu Ala Asn
195 200 205

Lys Val Thr Pro Ile Gly Asn Phe Ile Pro Gly Thr Tyr Arg Ile Pro

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210                215                220
Ala Met Lys Ser Thr Glu Asn Gly Asp Phe Ala Gly His Leu Lys Phe
225                230                235                240

Asp Phe Arg Gln Ser Asn Ser Glu Thr Val Asp Val Thr Glu Asp Phe
                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
                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
305                310                315                320

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
                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
                370                375                380

Ser Tyr Ile Lys Lys Gly Ser Ser Phe Tyr Asp Asp Val Lys Lys Arg
385                390                395                400

Val Ser Lys Gly Ser Leu Met Met Ile Ser Ser Pro Gln Ile Ile Asp
                405                410                415

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

Gln Asp Arg Leu Gln Leu Ile Lys Thr Ser Glu Lys
                450                455                460

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<210> 123
<211> 322
<212> PRT
<213> Staphylococcus aureus
<223> sta088

<400> 123

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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		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		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		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		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		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		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		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		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		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
305 310 315 320

Ile Asn

<210> 124
<211> 143
<212> PRT
<213> Staphylococcus aureus
<223> sta089

<400> 124

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
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
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
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
115 120 125

Arg Val Leu Ser Lys Lys Ala Ala Arg Asn Phe Asn Tyr Ile Tyr
130 135 140

<210> 125
<211> 255
<212> PRT
<213> Staphylococcus aureus
<223> sta090

<400> 125

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
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
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
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
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
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
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
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
245 250 255

<210> 126
<211> 131
<212> PRT
<213> Staphylococcus aureus
<223> sta091

<400> 126

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

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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				
	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				
				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				
		115					120					125							
His	Gln	Ser																	
	130																		
<210>	127																		
<211>	192																		
<212>	PRT																		
<213>	Staphylococcus aureus																		
<223>	sta092																		
<400>	127																		
Met	Thr	Lys	Arg	Pro	Lys	Arg	Ile	Leu	Ala	Thr	Ile	Ile	Ile	Phe	Leu				
1				5					10					15					
Ser	Leu	Leu	Phe	Thr	Ile	Ile	Tyr	Ile	Asp	Asp	Ile	Gln	Lys	Trp	Phe				
			20					25					30						
Asn	Gln	Tyr	Thr	Asp	Lys	Leu	Thr	Gln	Asn	His	Lys	Gly	Gln	Gly	His				
		35					40					45							
Ser	Lys	Trp	Glu	Asp	Phe	Phe	Arg	Gly	Ser	Arg	Ile	Thr	Glu	Thr	Phe				
	50					55					60								
Gly	Lys	Tyr	Gln	His	Ser	Pro	Phe	Asp	Gly	Lys	His	Tyr	Gly	Ile	Asp				
65					70					75					80				
Phe	Ala	Leu	Pro	Lys	Gly	Thr	Pro	Ile	Lys	Ala	Pro	Thr	Asn	Gly	Lys				
				85					90					95					
Val	Thr	Arg	Ile	Phe	Asn	Asn	Glu	Leu	Gly	Gly	Lys	Val	Leu	Gln	Ile				
			100					105					110						
Ala	Glu	Asp	Asn	Gly	Glu	Tyr	His	Gln	Trp	Tyr	Leu	His	Leu	Asp	Lys				
		115					120					125							

Tyr Asn Val Lys Val Gly Asp Arg Val Lys Ala Gly Asp Ile Ile Ala
 130 135 140

Tyr Ser Gly Asn Thr Gly Ile Gln Thr Thr Gly Ala His Leu His Phe
 145 150 155 160

Gln Arg Met Lys Gly Gly Val Gly Asn Ala Tyr Ala Glu Asp Pro Lys
 165 170 175

Pro Phe Ile Asp Gln Leu Pro Asp Gly Glu Arg Ser Leu Tyr Asp Leu
 180 185 190

<210> 128
 <211> 505
 <212> PRT
 <213> Staphylococcus aureus
 <223> sta093

<400> 128

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
 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
 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
 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
 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
 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
 180 185 190

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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
 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
 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
 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
 325                                330                        335

Ser Lys Glu Ser Gln Leu Thr Glu Ala Leu Phe Ala Glu Lys Pro Val
 340                                345                        350

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

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

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

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

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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

<210> 129
 <211> 305
 <212> PRT
 <213> Staphylococcus aureus
 <223> sta094

<400> 129

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
 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
 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
 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
 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
 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
 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

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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
                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
                275                280                285

Phe Tyr Asp Asp Asn Asp Pro Ile Glu Tyr Gly Val Tyr Arg Lys Asp
290                295                300

Glu
305

<210> 130
<211> 226
<212> PRT
<213> Staphylococcus aureus
<223> sta095

<400> 130

Met Lys Phe Lys Ala Ile Ala Lys Ala Ser Leu Ala Leu Gly Met Leu
1                5                10                15

Ala Thr Gly Val Ile Thr Ser Asn Val Gln Ser Val Gln Ala Lys Ala
                20                25                30

Glu Val Lys Gln Gln Ser Glu Ser Glu Leu Lys His Tyr Tyr Asn Lys
35                40                45

Pro Ile Leu Glu Arg Lys Asn Val Thr Gly Phe Lys Tyr Thr Asp Glu
50                55                60

Gly Lys His Tyr Leu Glu Val Thr Val Gly Gln Gln His Ser Arg Ile
65                70                75                80

Thr Leu Leu Gly Ser Asp Lys Asp Lys Phe Lys Asp Gly Glu Asn Ser
85                90                95

Asn Ile Asp Val Phe Ile Leu Arg Glu Gly Asp Ser Arg Gln Ala Thr
100               105               110

Asn Tyr Ser Ile Gly Gly Val Thr Lys Ser Asn Ser Val Gln Tyr Ile
115               120               125

Asp Tyr Ile Asn Thr Pro Ile Leu Glu Ile Lys Lys Asp Asn Glu Asp
130               135               140

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Val Leu Lys Asp Phe Tyr Tyr Ile Ser Lys Glu Asp Ile Ser Leu Lys
145                      150                      155                      160

Glu Leu Asp Tyr Arg Leu Arg Glu Arg Ala Ile Lys Gln His Gly Leu
                      165                      170                      175

Tyr Ser Asn Gly Leu Lys Gln Gly Gln Ile Thr Ile Thr Met Asn Asp
                      180                      185                      190

Gly Thr Thr His Thr Ile Asp Leu Ser Gln Lys Leu Glu Lys Glu Arg
                      195                      200                      205

Met Gly Glu Ser Ile Asp Gly Thr Lys Ile Asn Lys Ile Leu Val Glu
210                      215                      220

Met Lys
225

<210> 131
<211> 231
<212> PRT
<213> Staphylococcus aureus
<223> sta096

<400> 131

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
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
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
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
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
145                     150                     155                     160

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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
      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
      210                      215                      220

Glu Ile Lys Val Ile Lys Ala
225                      230

<210> 132
<211> 356
<212> PRT
<213> Staphylococcus aureus
<223> sta097

<400> 132

Met Lys Met Arg Thr Ile Ala Lys Thr Ser Leu Ala Leu Gly Leu Leu
1                      5                      10                      15

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
      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
      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
      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
      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
      165                     170                     175

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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
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
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
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
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
340 345 350

Val Asn Ile Lys
355

<210> 133
<211> 308
<212> PRT
<213> Staphylococcus aureus
<223> sta098

<400> 133

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

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
Thr Lys Val Glu Ala Pro Gln Gln Thr Ala Asn Ala Thr Thr Pro Pro		
65	70	75
Ser Thr Lys Val Thr Thr Pro Pro Ser Thr Asn Thr Pro Gln Pro Met		
	85	90
Gln Ser Thr Lys Ser Asp Thr Pro Gln Ser Pro Thr Thr Lys Gln Val		
	100	105
Pro Thr Glu Ile Asn Pro Lys Phe Lys Asp Leu Arg Ala Tyr Tyr Thr		
	115	120
Lys Pro Ser Leu Glu Phe Lys Asn Glu Ile Gly Ile Ile Leu Lys Lys		
	130	135
Trp Thr Thr Ile Arg Phe Met Asn Val Val Pro Asp Tyr Phe Ile Tyr		
	145	150
Lys Ile Ala Leu Val Gly Lys Asp Asp Lys Lys Tyr Gly Glu Gly Val		
	165	170
His Arg Asn Val Asp Val Phe Val Val Leu Glu Glu Asn Asn Tyr Asn		
	180	185
Leu Glu Lys Tyr Ser Val Gly Gly Ile Thr Lys Ser Asn Ser Lys Lys		
	195	200
Val Asp His Lys Ala Gly Val Arg Ile Thr Lys Glu Asp Asn Lys Gly		
	210	215
Thr Ile Ser His Asp Val Ser Glu Phe Lys Ile Thr Lys Glu Gln Ile		
	225	230
Ser Leu Lys Glu Leu Asp Phe Lys Leu Arg Lys Gln Leu Ile Glu Lys		
	245	250
Asn Asn Leu Tyr Gly Asn Val Gly Ser Gly Lys Ile Val Ile Lys Met		
	260	265
Lys Asn Gly Gly Lys Tyr Thr Phe Glu Leu His Lys Lys Leu Gln Glu		
	275	280
Asn Arg Met Ala Asp Val Ile Asp Gly Thr Asn Ile Asp Asn Ile Glu		
	290	300
Val Asn Ile Lys		
305		

<210> 134
 <211> 234
 <212> PRT
 <213> Staphylococcus aureus

<223> sta099

<400> 134

Met Lys Met Thr Ala Ile Ala Lys Ala Ser Leu Ala Leu Gly Ile Leu
1 5 10 15

Ala Thr Gly Thr Ile Thr Ser Leu His Gln Thr Val Asn Ala Ser Glu
20 25 30

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

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

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

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

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

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

Asn Ile Glu Lys Ile Glu Ala Asn Ile Arg
225 230

<210> 135

<211> 231

<212> PRT

<213> Staphylococcus aureus

<223> stal00

<400> 135

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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
<223> stal01

<400> 136

Met Lys Leu Lys Thr Leu Ala Lys Ala Thr Leu Ala Leu Gly Leu Leu
1          5          10          15

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Thr Thr Gly Val Ile Thr Ser Glu Gly Gln Ala Val Gln Ala Lys Glu
    20                      25                      30

Lys Gln Glu Arg Val Gln His Leu Tyr Asp Ile Lys Asp Leu His Arg
    35                      40                      45

Tyr Tyr Ser Ser Glu Ser Phe Glu Phe Ser Asn Ile Ser Gly Lys Val
    50                      55                      60

Glu Asn Tyr Asn Gly Ser Asn Val Val Arg Phe Asn Gln Glu Asn Gln
    65                      70                      75                      80

Asn His Gln Leu Phe Leu Leu Gly Lys Asp Lys Glu Lys Tyr Lys Glu
    85                      90                      95

Gly Ile Glu Gly Lys Asp Val Phe Val Val Lys Glu Leu Ile Asp Pro
    100                    105                    110

Asn Gly Arg Leu Ser Thr Val Gly Gly Val Thr Lys Lys Asn Asn Lys
    115                    120                    125

Ser Ser Glu Thr Asn Thr His Leu Phe Val Asn Lys Val Tyr Gly Gly
    130                    135                    140

Asn Leu Asp Ala Ser Ile Asp Ser Phe Ser Ile Asn Lys Glu Glu Val
    145                    150                    155                    160

Ser Leu Lys Glu Leu Asp Phe Lys Ile Arg Gln His Leu Val Lys Asn
    165                    170                    175

Tyr Gly Leu Tyr Lys Gly Thr Thr Lys Tyr Gly Lys Ile Thr Ile Asn
    180                    185                    190

Leu Lys Asp Gly Glu Lys Gln Glu Ile Asp Leu Gly Asp Lys Leu Gln
    195                    200                    205

Phe Glu Arg Met Gly Asp Val Leu Asn Ser Lys Asp Ile Asn Lys Ile
    210                    215                    220

Glu Val Thr Leu Lys Gln Ile
    225                    230

<210> 137
<211> 232
<212> PRT
<213> Staphylococcus aureus
<223> stal02

<400> 137

Met Lys Phe Thr Val Ile Ala Lys Ala Ile Phe Ile Leu Gly Ile Leu
  1                      5                      10                      15

Thr Thr Ser Val Met Ile Thr Glu Asn Gln Ser Val Asn Ala Lys Gly

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20					25					30					
Lys	Tyr	Glu	Lys	Met	Asn	Arg	Leu	Tyr	Asp	Thr	Asn	Lys	Leu	His	Gln
		35					40					45			
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
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	
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			
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	
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			
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										

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<210> 138
<211> 232
<212> PRT
<213> Staphylococcus aureus
<223> sta103
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<400> 138

Met Lys Leu Thr Thr Ile Ala Lys Ala Thr Leu Ala Leu Gly Ile Leu
1 5 10 15

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

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
<223> stal04

<400> 139

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
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
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
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
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
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
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
210 215 220

Asn Leu Lys
225

<210> 140
<211> 225
<212> PRT
<213> Staphylococcus aureus
<223> stal05

<400> 140

Met Lys Leu Lys Asn Ile Ala Lys Ala Ser Leu Ala Leu Gly Ile Leu
1 5 10 15

Thr Thr Gly Met Ile Thr Thr Thr Ala Gln Pro Val Lys Ala Ser Thr
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
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
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
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
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
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
210 215 220

Leu
225

<210> 141
<211> 116
<212> PRT
<213> Staphylococcus aureus
<223> stal06

<400> 141

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
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
50 55 60

Ala Ala Gly Ser Leu Asn Pro Tyr Tyr Lys Arg Thr Ile Met Met Asn


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65              70              75              80

Glu Tyr Arg Ala Lys Ala Ala Leu Lys Lys Asn Asp Phe Val Ser Met
            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
            115

<210> 142
<211> 508
<212> PRT
<213> Staphylococcus aureus
<223> NW_6

<400> 142

Met Lys Asn Lys Leu Leu Val Leu Ser Leu Gly Ala Leu Cys Val Ser
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             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
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
            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
            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
            165            170            175

Met Leu Gly Lys Thr Phe Tyr Gln Asn Tyr Arg Asp Asp Val Glu Ser
            180            185            190

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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
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
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
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

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
<223> NW_9

<400> 143

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
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
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
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
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
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
180 185 190

Val Leu Asn Lys Val Gly Lys Glu Lys Gln Asp Val Asp Gln Phe Lys
195 200 205

<210> 144
<211> 109

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<212>  PRT
<213>  Staphylococcus aureus
<223>  NW_10

<400>  144

Met Lys Lys Asn Phe Ile Gly Lys Ser Ile Leu Ser Ile Ala Ala Ile
1          5          10          15

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

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

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
<223>  NW_7

<400>  145

Met Lys Ile Arg Lys Ser Ile Leu Ala Gly Thr Leu Ala Ile Val Leu
1          5          10          15

Ala Ser Pro Leu Val Thr Asn Leu Asp Lys Asn Glu Ala Gln Ala Ser
          20          25          30

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

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

Ala Lys Tyr Gln Leu Gln Lys Ile Tyr Asn Glu Ile Asp Glu Ala Leu
          100          105          110

Lys Ser Lys Tyr

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115

<210> 146
 <211> 149
 <212> PRT
 <213> Staphylococcus aureus
 <223> NW_8

<400> 146

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
 <223> NW_2

<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

Glu Lys Asp Leu Arg Lys Lys Ser Glu Leu Gln Gly Ala Ala Leu Gly
 35 40 45

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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

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

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

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

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

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

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
<223> NW_1

<400> 148

Met Lys Arg Leu Leu Gly Leu Leu Leu Val Ser Thr Leu Val Leu Ser
 1                      5                      10                      15

Ala Cys Gly Asn Asp Glu Asn Gln Glu Glu Ser Lys Lys Glu Val Lys
          20                      25                      30

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Ser Lys Glu Lys Lys Ile Glu Lys Glu Lys Glu Asn Lys Ser Lys Lys
 35                                40                                45

Asp Lys Glu Lys Glu Val Ala Thr Gln Gln Gln Pro Asp Asn Gln Thr
 50                                55                                60

Val Glu Gln Pro Gln Ser Gln Glu Gln Ser Val Gln Gln Pro Gln Gln
 65                                70                                75                                80

Gln Ile Pro Gln Asn Ser Val Pro Gln Gln Asn Val Gln Val Gln Gln
                        85                                90                                95

Asn Lys Lys Gln Lys Val Asp Leu Asn Asn Met Pro Pro Thr Asp Phe
      100                                105                                110

Ser Thr Glu Gly Met Ser Glu Gln Ala Gln Lys Gln Ile Glu Glu Leu
 115                                120                                125

Ser Met Gln Lys Asp Tyr His Gly Leu Ser Gln Arg Glu Tyr Asn Asp
 130                                135                                140

Arg Val Ser Glu Ile Ile Asn Asn Asp Asn
 145                                150

<210> 149
<211> 1501
<212> PRT
<213> Staphylococcus aureus
<223> NW_5

<400> 149

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
      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 Asn Ile Glu Asn Pro Thr Thr Leu Lys
      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
      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
      115                                120                                125

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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
 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
                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
 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
                260                               265                      270

Gly Phe Lys Ile Asp Thr Gly Tyr Ile Tyr Thr Ser Ser Met Asp Lys
      275                               280                      285

Thr Glu Lys Gln Ala Gly Gln Gly Tyr Arg Gly Tyr Gly Ala Phe Val
 290                               295                      300

Lys Asn Asp Ser Ser Gly Asn Ser Gln Met Val Gly Glu Asn Ile Asp
 305                               310                      315                      320

Lys Ser Lys Thr Asn Phe Leu Asn Tyr Ala Asp Asn Ser Thr Asn Thr
                325                               330                      335

Ser Asp Gly Lys Phe His Gly Gln Arg Leu Asn Asp Val Ile Leu Thr
                340                               345                      350

Tyr Val Ala Ser Thr Gly Lys Met Arg Ala Glu Tyr Ala Gly Lys Thr
      355                               360                      365

Trp Glu Thr Ser Ile Thr Asp Leu Gly Leu Ser Lys Asn Gln Ala Tyr
 370                               375                      380

Asn Phe Leu Ile Thr Ser Ser Gln Arg Trp Gly Leu Asn Gln Gly Ile
 385                               390                      395                      400

Asn Ala Asn Gly Trp Met Arg Thr Asp Leu Lys Gly Ser Glu Phe Thr

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				405						410						415	
Phe	Thr	Pro	Glu	Ala	Pro	Lys	Thr	Ile	Thr	Glu	Leu	Glu	Lys	Lys	Val		
			420					425					430				
Glu	Glu	Ile	Pro	Phe	Lys	Lys	Glu	Arg	Lys	Phe	Asn	Pro	Asp	Leu	Ala		
		435					440					445					
Pro	Gly	Thr	Glu	Lys	Val	Thr	Arg	Glu	Gly	Gln	Lys	Gly	Glu	Lys	Thr		
	450					455					460						
Ile	Thr	Thr	Pro	Thr	Leu	Lys	Asn	Pro	Leu	Thr	Gly	Val	Ile	Ile	Ser		
465					470					475					480		
Lys	Gly	Glu	Pro	Lys	Glu	Glu	Ile	Thr	Lys	Asp	Pro	Ile	Asn	Glu	Leu		
				485					490					495			
Thr	Glu	Tyr	Gly	Pro	Glu	Thr	Ile	Ala	Pro	Gly	His	Arg	Asp	Glu	Phe		
			500					505					510				
Asp	Pro	Lys	Leu	Pro	Thr	Gly	Lys	Lys	Glu	Glu	Val	Pro	Gly	Lys	Pro		
		515					520					525					
Gly	Ile	Lys	Asn	Pro	Glu	Thr	Gly	Asp	Val	Val	Arg	Pro	Pro	Val	Asp		
	530					535					540						
Ser	Val	Thr	Lys	Tyr	Gly	Pro	Val	Lys	Gly	Asp	Ser	Ile	Val	Glu	Lys		
545					550					555					560		
Glu	Glu	Ile	Pro	Phe	Glu	Lys	Glu	Arg	Lys	Phe	Asn	Pro	Asp	Leu	Ala		
				565					570					575			
Pro	Gly	Thr	Glu	Lys	Val	Thr	Arg	Glu	Gly	Gln	Lys	Gly	Glu	Lys	Thr		
			580					585					590				
Ile	Thr	Thr	Pro	Thr	Leu	Lys	Asn	Pro	Leu	Thr	Gly	Glu	Ile	Ile	Ser		
	595						600					605					
Lys	Gly	Glu	Ser	Lys	Glu	Glu	Ile	Thr	Lys	Asp	Pro	Ile	Asn	Glu	Leu		
	610					615				620							
Thr	Glu	Tyr	Gly	Pro	Glu	Thr	Ile	Thr	Pro	Gly	His	Arg	Asp	Glu	Phe		
625					630					635				640			
Asp	Pro	Lys	Leu	Pro	Thr	Gly	Glu	Lys	Glu	Glu	Val	Pro	Gly	Lys	Pro		
				645					650					655			
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		
	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
 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
 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
 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
 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
 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
 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
 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
 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	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	1010	1015	1020
Phe Asp Pro Lys Leu Pro Thr Gly Glu Lys Glu Glu Val Pro Gly	1025	1030	1035
Lys Pro Gly Ile Lys Asn Pro Glu Thr Gly Asp Val Val Arg Pro	1040	1045	1050
Pro Val Asp Ser Val Thr Lys Tyr Gly Pro Val Lys Gly Asp Ser	1055	1060	1065
Ile Val Glu Lys Glu Glu Ile Pro Phe Glu Lys Glu Arg Lys Phe	1070	1075	1080
Asn Pro Asp Leu Ala Pro Gly Thr Glu Lys Val Thr Arg Glu Gly	1085	1090	1095
Gln Lys Gly Glu Lys Thr Ile Thr Thr Pro Thr Leu Lys Asn Pro	1100	1105	1110
Leu Thr Gly Glu Ile Ile Ser Lys Gly Glu Ser Lys Glu Glu Ile	1115	1120	1125
Thr Lys Asp Pro Ile Asn Glu Leu Thr Glu Tyr Gly Pro Glu Thr	1130	1135	1140
Ile Thr Pro Gly His Arg Asp Glu Phe Asp Pro Lys Leu Pro Thr	1145	1150	1155
Gly Glu Lys Glu Glu Val Pro Gly Lys Pro Gly Ile Lys Asn Pro	1160	1165	1170
Glu Thr Gly Asp Val Val Arg Pro Pro Val Asp Ser Val Thr Lys	1175	1180	1185
Tyr Gly Pro Val Lys Gly Asp Ser Ile Val Glu Lys Glu Glu Ile	1190	1195	1200
Pro Phe Glu Lys Glu Arg Lys Phe Asn Pro Asp Leu Ala Pro Gly	1205	1210	1215
Thr Glu Lys Val Thr Arg Glu Gly Gln Lys Gly Glu Lys Thr Ile	1220	1225	1230
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
1250 1255 1260

Leu Thr Glu Phe Gly Gly Glu Lys Ile Pro Gln Gly His Lys Asp
1265 1270 1275

Ile Phe Asp Pro Asn Leu Pro Thr Asp Gln Thr Glu Lys Val Pro
1280 1285 1290

Gly Lys Pro Gly Ile Lys Asn Pro Asp Thr Gly Lys Val Ile Glu
1295 1300 1305

Glu Pro Val Asp Asp Val Ile Lys His Gly Pro Lys Thr Gly Thr
1310 1315 1320

Pro Glu Thr Lys Thr Val Glu Ile Pro Phe Glu Thr Lys Arg Glu
1325 1330 1335

Phe Asn Pro Lys Leu Gln Pro Gly Glu Glu Arg Val Lys Gln Glu
1340 1345 1350

Gly Gln Pro Gly Ser Lys Thr Ile Thr Thr Pro Ile Thr Val Asn
1355 1360 1365

Pro Leu Thr Gly Glu Lys Val Gly Glu Gly Gln Pro Thr Glu Glu
1370 1375 1380

Ile Thr Lys Gln Pro Val Asp Lys Ile Val Glu Phe Gly Gly Glu
1385 1390 1395

Lys Pro Lys Asp Pro Lys Gly Pro Glu Asn Pro Glu Lys Pro Ser
1400 1405 1410

Arg Pro Thr His Pro Ser Gly Pro Val Asn Pro Asn Asn Pro Gly
1415 1420 1425

Leu Ser Lys Asp Arg Ala Lys Pro Asn Gly Pro Val His Ser Met
1430 1435 1440

Asp Lys Asn Asp Lys Val Lys Lys Ser Lys Ile Ala Lys Glu Ser
1445 1450 1455

Val Ala Asn Gln Glu Lys Lys Arg Ala Glu Leu Pro Lys Thr Gly
1460 1465 1470

Leu Glu Ser Thr Gln Lys Gly Leu Ile Phe Ser Ser Ile Ile Gly
1475 1480 1485

Ile Ala Gly Leu Met Leu Leu Ala Arg Arg Arg Lys Asn
1490 1495 1500

<210> 150

<211> 293
<212> PRT
<213> Staphylococcus aureus

<400> 150

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
 Met Ala Met Ile Lys Met Ser Pro Glu Glu Ile Arg Ala Lys Ser Gln
 1 5 10 15
 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
 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
 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
 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
 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
 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 15

Ala Lys Gln Leu Ala Ala Lys Thr Ala Lys Asp Ile Glu Ala Cys Gln
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
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
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
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
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
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

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

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

Glu Asp Thr Met Asn Glu Asn Asp Asn Phe Lys Tyr Ser Asp Ala Ile
100 105 110

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

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

<210> 154
<211> 106
<212> PRT
<213> Staphylococcus aureus
<400> 154

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

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

Glu Asp Thr Met Asn Glu Asn Asp Asn Phe
100 105


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<210> 155
<211> 580
<212> PRT
<213> Staphylococcus aureus

<400> 155

Ala Glu Asn Thr Ser Thr Glu Asn Ala Lys Gln Asp Asp Ala Thr Thr
1          5          10          15

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

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

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

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

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

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

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

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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
 Tyr Val Trp Glu Asp Val Asp Lys Asp Gly Val Gln Gly Thr Asp Ser
 565 570 575
 Lys Glu Lys Pro
 580
 <210> 156
 <211> 540
 <212> PRT
 <213> Staphylococcus aureus
 <400> 156
 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
 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
 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
 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
 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
 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
 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		
225	230	235
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		
	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		
	290	295
		300
Asn Tyr Ser Ile Tyr Met Asp Ala Asp Thr Ile Pro Val Ser Lys Asn		
305	310	315
		320
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
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
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
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
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

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

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
530 535 540

<210> 157
<211> 145
<212> PRT
<213> Staphylococcus aureus

<400> 157

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

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
145

<210> 158
<211> 50
<212> PRT
<213> Staphylococcus aureus

<400> 158

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser

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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
      50

<210> 159
<211> 63
<212> PRT
<213> Staphylococcus aureus

<400> 159

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
      50              55              60

<210> 160
<211> 50
<212> PRT
<213> Staphylococcus aureus

<400> 160

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
      50

<210> 161
<211> 63
<212> PRT
<213> Staphylococcus aureus

<400> 161

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
 50 55 60
 <210> 162
 <211> 289
 <212> PRT
 <213> Staphylococcus aureus
 <400> 162
 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
 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
 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
 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
 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
 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
 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

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

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
275 280 285

Ala

<210> 163
<211> 508
<212> PRT
<213> Staphylococcus aureus

<400> 163

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
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
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
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
130 135 140

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
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	Asn	Thr	Met	Pro	Ile	Ala	Asp		225	230	235
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
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
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

Ala Glu His Thr Asn Gly Glu Leu Asn Gln Ser Lys Asn Glu Thr Thr
1 5 10 15

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

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

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

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

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
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
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
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
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
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
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
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
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

Ala Asn Glu Lys

465

<210> 165
<211> 198
<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

Asp Thr Asn Ser His Gln Asp His Thr Glu Asp Val Glu Lys Asp Gln
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
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
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

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

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

Gln Asp Glu Pro Lys Glu
195

<210> 166
<211> 511
<212> PRT
<213> Staphylococcus aureus

<400> 166

Met Gly Gln Asp Lys Glu Ala Ala Ala Ser Glu Gln Lys Thr Thr Thr
1 5 10 15

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	
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
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	
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	
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	
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	
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
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	
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		
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	
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	
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	
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	
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	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	500	505	510	
<210> 167				
<211> 442				
<212> PRT				
<213> Staphylococcus aureus				
<400> 167				
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				

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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

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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
340 345 350

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

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

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

Ala Glu Asn Thr Ser Thr Glu Asn Ala Lys Gln Asp Asp Ala Thr Thr
1 5 10 15

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

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

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

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
Pro	Gln	Pro	Thr	Pro	Ser	Lys	Val	Asp	Asn	Gln	Val	Thr	Asp	Ala	Thr	145	150	155
Asn	Pro	Lys	Glu	Pro	Val	Asn	Val	Ser	Lys	Glu	Glu	Leu	Lys	Asn	Asn	165	170	175
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
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
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
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
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
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
Tyr Val Trp Glu Asp Val Asp Lys Asp Gly Val Gln Gly Thr Asp Ser	565	570	575
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
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	625	630	635
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	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	690	695	700

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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
                               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
                               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
                               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
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
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
                               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
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
                               965                               970                               975

Lys Val Gln Ala Tyr His Ser Ser Tyr Pro Asn Asn Ile Gly Gln Ile

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          980          985          990
Asn Lys Asp Val Thr Asp Ile Lys Ile Tyr Gln Val Pro Lys Gly Tyr
  995          1000          1005

Thr Leu Asn Lys Gly Tyr Asp Val Asn Thr Lys Glu Leu Thr Asp
 1010          1015          1020

Val Thr Asn Gln Tyr Leu Gln Lys Ile Thr Tyr Gly Asp Asn Asn
 1025          1030          1035

Ser Ala Val Ile Asp Phe Gly Asn Ala Asp Ser Ala Tyr Val Val
 1040          1045          1050

Met Val Asn Thr Lys Phe Gln Tyr Thr Asn Ser Glu Ser Pro Thr
 1055          1060          1065

Leu Val Gln Met Ala Thr Leu Ser Ser Thr Gly Asn Lys Ser Val
 1070          1075          1080

Ser Thr Gly Asn Ala Leu Gly Phe Thr Asn Asn Gln Ser Gly Gly
 1085          1090          1095

Ala Gly Gln Glu Val Tyr Lys Ile Gly Asn Tyr Val Trp Glu Asp
 1100          1105          1110

Thr Asn Lys Asn Gly Val Gln Glu Leu Gly Glu Lys Gly
 1115          1120          1125

<210> 169
<211> 618
<212> PRT
<213> Staphylococcus aureus

<400> 169

Ala Thr Gly Gly Cys Ala Ala Thr Gly Ala Thr Thr Ala Ala Gly Ala
 1          5          10          15

Thr Gly Ala Gly Thr Cys Cys Ala Gly Ala Gly Gly Ala Ala Ala Thr
 20          25          30

Cys Ala Gly Ala Gly Cys Ala Ala Ala Ala Thr Cys Gly Cys Ala Ala
 35          40          45

Thr Cys Thr Thr Ala Cys Gly Gly Gly Cys Ala Ala Gly Gly Thr Thr
 50          55          60

Cys Ala Gly Ala Cys Cys Ala Ala Ala Thr Cys Cys Gly Thr Cys Ala
 65          70          75          80

Ala Ala Thr Thr Thr Thr Ala Thr Cys Thr Gly Ala Thr Thr Thr Ala
 85          90          95

Ala Cys Ala Cys Gly Thr Gly Cys Ala Cys Ala Ala Gly Gly Thr Gly

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100								105				110							
Ala	Ala	Ala	Thr	Thr	Gly	Cys	Ala	Gly	Cys	Gly	Ala	Ala	Cys	Thr	Gly				
		115					120						125						
Gly	Gly	Ala	Ala	Gly	Gly	Thr	Cys	Ala	Ala	Gly	Cys	Thr	Thr	Thr	Cys				
	130					135					140								
Ala	Gly	Cys	Cys	Gly	Thr	Thr	Thr	Cys	Gly	Ala	Ala	Gly	Ala	Gly	Cys				
145					150					155					160				
Ala	Ala	Thr	Thr	Cys	Cys	Ala	Ala	Cys	Ala	Ala	Cys	Thr	Thr	Ala	Gly				
				165					170					175					
Thr	Cys	Cys	Thr	Ala	Ala	Ala	Gly	Thr	Ala	Gly	Ala	Ala	Ala	Ala	Ala				
			180					185					190						
Thr	Thr	Thr	Gly	Cys	Ala	Cys	Ala	Ala	Thr	Thr	Ala	Thr	Thr	Ala	Gly				
		195					200					205							
Ala	Ala	Gly	Ala	Ala	Ala	Thr	Thr	Ala	Ala	Ala	Cys	Ala	Ala	Cys	Ala				
	210					215					220								
Ala	Thr	Thr	Gly	Ala	Ala	Thr	Ala	Gly	Cys	Ala	Cys	Thr	Gly	Cys	Thr				
225					230					235					240				
Gly	Ala	Thr	Gly	Cys	Cys	Gly	Thr	Thr	Cys	Ala	Ala	Gly	Ala	Ala	Cys				
				245					250					255					
Ala	Ala	Gly	Ala	Cys	Cys	Ala	Ala	Cys	Ala	Ala	Cys	Thr	Thr	Thr	Cys				
			260					265					270						
Thr	Ala	Ala	Thr	Ala	Ala	Thr	Thr	Thr	Cys	Gly	Gly	Thr	Thr	Thr	Gly				
		275					280					285							
Cys	Ala	Ala	Gly	Cys	Thr	Ala	Gly	Cys	Gly	Gly	Thr	Gly	Gly	Cys	Gly				
	290					295					300								
Gly	Ala	Thr	Cys	Cys	Gly	Gly	Thr	Gly	Gly	Ala	Thr	Ala	Thr	Ala	Ala				
305					310					315					320				
Ala	Gly	Gly	Thr	Ala	Thr	Thr	Ala	Ala	Ala	Gly	Cys	Ala	Gly	Ala	Thr				
				325					330					335					
Gly	Gly	Thr	Gly	Gly	Cys	Ala	Ala	Gly	Gly	Thr	Thr	Gly	Ala	Thr	Cys				
			340					345					350						
Ala	Ala	Gly	Cys	Gly	Ala	Ala	Ala	Cys	Ala	Ala	Thr	Thr	Ala	Gly	Cys				
		355					360					365							
Gly	Gly	Cys	Ala	Ala	Ala	Ala	Ala	Cys	Ala	Gly	Cys	Thr	Ala	Ala	Ala				
	370				375						380								

Gly Ala Thr Ala Thr Thr Gly Ala Ala Gly Cys Ala Thr Gly Thr Cys
385 390 395 400

Ala Ala Ala Ala Gly Cys Ala Ala Ala Cys Gly Cys Ala Ala Cys Ala
405 410 415

Gly Cys Thr Cys Gly Cys Thr Gly Ala Gly Thr Ala Thr Ala Thr Cys
420 425 430

Gly Ala Ala Gly Gly Thr Ala Gly Thr Gly Ala Thr Thr Gly Gly Gly
435 440 445

Ala Ala Gly Gly Ala Cys Ala Gly Thr Thr Cys Gly Cys Cys Ala Ala
450 455 460

Thr Ala Ala Gly Gly Thr Gly Ala Ala Ala Gly Ala Thr Gly Thr Gly
465 470 475 480

Thr Thr Ala Cys Thr Cys Ala Thr Thr Ala Thr Gly Gly Cys Ala Ala
485 490 495

Ala Gly Thr Thr Thr Cys Ala Ala Gly Ala Ala Gly Ala Ala Thr Thr
500 505 510

Ala Gly Thr Ala Cys Ala Ala Cys Cys Gly Ala Thr Gly Gly Cys Thr
515 520 525

Gly Ala Cys Cys Ala Thr Cys Ala Ala Ala Ala Ala Gly Cys Ala Ala
530 535 540

Thr Thr Gly Ala Thr Ala Ala Cys Thr Thr Ala Ala Gly Thr Cys Ala
545 550 555 560

Ala Ala Ala Thr Cys Thr Ala Gly Cys Gly Ala Ala Ala Thr Ala Cys
565 570 575

Gly Ala Thr Ala Cys Ala Thr Thr Ala Thr Cys Ala Ala Thr Thr Ala
580 585 590

Ala Gly Cys Ala Ala Gly Gly Gly Cys Thr Thr Gly Ala Thr Ala Gly
595 600 605

Gly Gly Thr Gly Ala Ala Cys Cys Cys Ala
610 615

<210> 170
<211> 239
<212> PRT
<213> Staphylococcus aureus
<223> sta081

<400> 170

Met Asn Lys Asn Ile Ile Ile Lys Ser Ile Ala Ala Leu Thr Ile Leu
1 5 10 15

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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

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

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

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

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

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

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

<210> 171
<211> 6
<212> PRT
<213> Staphylococcus aureus

<400> 171

Gly Ser Gly Gly Gly Gly
1      5

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<210> 172
<211> 8
<212> PRT

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<213> Staphylococcus aureus

<400> 172

Gly Ser Gly Ser Gly Gly Gly Gly
1 5

<210> 173

<211> 6

<212> PRT

<213> Staphylococcus aureus

<400> 173

Ala Ser Gly Gly Gly Ser
1 5

<210> 174

<211> 18

<212> PRT

<213> Staphylococcus aureus

<400> 174

Gly Cys Thr Ala Gly Cys Gly Gly Thr Gly Gly Cys Gly Gly Ala Thr
1 5 10 15

Cys Cys

<210> 175

<211> 26

<212> PRT

<213> Staphylococcus aureus

<400> 175

Ile Cys Ile Cys Ile Cys Ile Cys Ile Cys Ile Cys Ile Cys Ile Cys
1 5 10 15

Ile Cys Ile Cys Ile Cys Ile Cys Ile Cys
20 25

<210> 176

<211> 11

<212> PRT

<213> Staphylococcus aureus

<400> 176

Lys Leu Lys Leu Leu Leu Leu Lys Leu Lys
1 5 10

<210> 177

<211> 203

<212> PRT

<213> Staphylococcus aureus

<223> sta107

<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
 <223> stal08
 <400> 178
 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
<223> stal09

<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

Tyr Asp Asp Asn Tyr Ser Leu Thr Thr Leu Ile Gln Asn Leu Phe Asn
115 120 125

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

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145              150              155              160

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

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

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

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

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

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

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

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

Lys Asn Gly Ile Asp Gly Asn Arg Thr Ile Tyr Lys Pro Thr Trp Lys
      420              425              430

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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

His Tyr Gln Leu Thr Gln Phe Asp Asp Glu Arg Met Pro Asp Leu Asp
465 470 475 480

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
<223> stall0

<400> 180

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
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
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
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
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
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
180 185 190

Val Leu Asn Lys Val Gly Lys Glu Lys Gln Asp Val Asp Gln Phe Lys
195 200 205

<210> 181
<211> 105
<212> PRT
<213> Staphylococcus aureus
<223> stall1

<400> 181

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
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
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
85 90 95

Ile Ser Thr Arg Tyr Ile Glu Val Lys
100 105

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<210> 182
<211> 312
<212> PRT
<213> Staphylococcus aureus
<223> stall2

<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
20 25 30

Leu Lys Val Val Thr Thr Asn Ser Ile Leu Tyr Asp Met Ala Lys Asn
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
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
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
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
180 185 190

Asp Lys Phe Asn Asp Ile Pro Lys Glu Gln Arg Ala Met Ile Thr Ser
195 200 205

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

Arg Gln Ala Ile Glu Phe Val Lys Lys His Lys Leu Lys His Leu Leu

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                245                250                255
Val Glu Thr Ser Val Asp Lys Lys Ala Met Glu Ser Leu Ser Glu Glu
      260                265                270

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

Glu Thr Val His Gly Ser Met Lys
305                310

<210> 183
<211> 646
<212> PRT
<213> Staphylococcus aureus
<223> stall3

<400> 183

Met Ser Ser Gln Lys Lys Lys Ile Ser Leu Phe Ala Phe Phe Leu Leu
1      5      10      15

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

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

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

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

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

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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
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
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
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
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
580 585 590

Ala Asp Phe Glu Lys Asn Lys Lys Gln Val Glu Lys Asp Leu Glu Met
595 600 605

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

Lys Ala Asn Ser Lys Lys
645

<210> 184
<211> 173
<212> PRT
<213> Staphylococcus aureus
<223> stall4

<400> 184

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

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

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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

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

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

Thr Tyr Asn Asn Lys Glu Ile Tyr Asp Leu Gln Phe Ile
                165                170

<210> 185
<211> 156
<212> PRT
<213> Staphylococcus aureus
<223> stall5

<400> 185

Met Lys Arg Lys Val Leu Val Leu Thr Met Gly Val Ile Cys Ala Thr
1                      5                      10                      15

Gln Leu Trp His Ser Asn His Ala Asn Ala Leu Val Thr Glu Ser Gly
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
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
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
115                120                125

Lys Gln Lys Val Asn Thr Leu Ser Lys Pro His Gln Asn Tyr Phe Asn

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130                               135                               140

Lys Gln Ile Asp Lys Val Tyr Asn Gly Leu Gln Arg
145                               150                               155

<210> 186
<211> 133
<212> PRT
<213> Staphylococcus aureus
<223> stall6

<400> 186

Met Lys Lys Asn Ile Thr Lys Thr Ile Ile Ala Ser Thr Val Ile Ala
1                               5                               10                               15

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
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
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
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
130

<210> 187
<211> 274
<212> PRT
<213> Staphylococcus aureus
<223> stall7

<400> 187

Met Tyr Pro Asn Trp Gly Gln Tyr Lys Arg Ala Asp Leu Ile Gly Gln
1                               5                               10                               15

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

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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
 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
      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
      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
      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
      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
 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
      260                               265                               270

Ser Lys

<210> 188
<211> 390
<212> PRT
<213> Staphylococcus aureus
<223> stall8

<400> 188

Met Leu Glu Phe Glu Gln Gly Phe Asn His Leu Ala Thr Leu Lys Val
 1                               5                               10                               15

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Ile	Gly	Val	Gly	Gly	Gly	Gly	Asn	Asn	Ala	Val	Asn	Arg	Met	Ile	Asp	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	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	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	115	120	125	
Val	Gly	Val	Val	Thr	Arg	Pro	Phe	Ser	Phe	Glu	Gly	Arg	Lys	Arg	Gln	130	135	140	
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	
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	
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
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	
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	

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

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

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

<210> 189
<211> 258
<212> PRT
<213> Staphylococcus aureus

<400> 189

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 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

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

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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

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

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> 190
<211> 306
<212> PRT
<213> Staphylococcus aureus

<400> 190

Lys Phe Val Val Pro Glu Ser Gly Ile Asn Lys Ile Ile Pro Ala Tyr
1      5                      10                      15

Asp Glu Phe Lys Asn Ser Pro Lys Val Asn Val Ser Asn Leu Thr Asp
      20                      25                      30

Asn Lys Asn Phe Val Ala Ser Glu Asp Lys Leu Asn Lys Ile Ala Asp
      35                      40                      45

Ser Ser Ala Ala Ser Lys Ile Val Asp Lys Asn Phe Val Val Pro Glu
      50                      55                      60

Ser Lys Leu Gly Asn Ile Val Pro Glu Tyr Lys Glu Ile Asn Asn Arg
      65                      70                      75                      80

Val Asn Val Ala Thr Asn Asn Pro Ala Ser Gln Gln Val Asp Lys His
      85                      90                      95

Phe Val Ala Lys Gly Pro Glu Val Asn Arg Phe Ile Thr Gln Asn Lys
      100                     105                     110

Val Asn His His Phe Ile Thr Thr Gln Thr His Tyr Lys Lys Val Ile
      115                     120                     125

Thr Ser Tyr Lys Ser Thr His Val His Lys His Val Asn His Ala Lys
      130                     135                     140

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Asp Ser Ile Asn Lys His Phe Ile Val Lys Pro Ser Glu Ser Pro Arg
145 150 155 160

Tyr Thr His Pro Ser Gln Ser Leu Ile Ile Lys His His Phe Ala Val
165 170 175

Pro Gly Tyr His Ala His Lys Phe Val Thr Pro Gly His Ala Ser Ile
180 185 190

Lys Ile Asn His Phe Cys Val Val Pro Gln Ile Asn Ser Phe Lys Val
195 200 205

Ile Pro Pro Tyr Gly His Asn Ser His Arg Met His Val Pro Ser Phe
210 215 220

Gln Asn Asn Thr Thr Ala Thr His Gln Asn Ala Lys Val Asn Lys Ala
225 230 235 240

Tyr Asp Tyr Lys Tyr Phe Tyr Ser Tyr Lys Val Val Lys Gly Val Lys
245 250 255

Lys Tyr Phe Ser Phe Ser Gln Ser Asn Gly Tyr Lys Ile Gly Lys Pro
260 265 270

Ser Leu Asn Ile Lys Asn Val Asn Tyr Gln Tyr Ala Val Pro Ser Tyr
275 280 285

Ser Pro Thr His Tyr Val Pro Glu Phe Lys Gly Ser Leu Pro Ala Pro
290 295 300

Arg Val
305

<210> 191
<211> 308
<212> PRT
<213> Staphylococcus aureus

<400> 191

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
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
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
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
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
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

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

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

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

Phe Lys Gly Ser
305

<210> 192
<211> 300
<212> PRT
<213> Staphylococcus aureus

<400> 192

Lys Phe Val Val Pro Glu Ser Gly Ile Asn Lys Ile Ile Pro Ala Tyr
1 5 10 15

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

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290                                295                                300

<210>  193
<211>  121
<212>  PRT
<213>  Staphylococcus aureus

<400>  193

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
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
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
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
115                              120

<210>  194
<211>  53
<212>  PRT
<213>  Staphylococcus aureus

<400>  194

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
50

<210>  195
<211>  53
<212>  PRT
<213>  Staphylococcus aureus

<400>  195

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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 Leu Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
35 40 45

Asn Lys Lys Leu Leu
50

<210> 196
<211> 316
<212> PRT
<213> Staphylococcus aureus

<400> 196

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
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
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
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
130 135 140

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

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 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
305 310 315

<210> 197
<211> 331
<212> PRT
<213> Staphylococcus aureus

<400> 197

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 25 30

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

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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

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

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

Ser Ser Pro Ile Ala Gly Ile Asp Lys Pro Asn Gly Ala Asn Ile Ser
1                      5                      10                      15

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

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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

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

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

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

Asp Gly Asp Ser Ala Val Asn
180

<210> 199
<211> 199
<212> PRT
<213> Staphylococcus aureus

<400> 199

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
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
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
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
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
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
180 185 190

Gln Glu Leu Gly Glu Lys Gly
195

<210> 200
<211> 104
<212> PRT
<213> Staphylococcus aureus
<223> stal19

<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
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 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
85 90 95

Ala Glu Val Leu Asp Lys His Leu
100

<210> 201
<211> 189
<212> PRT
<213> Staphylococcus aureus
<223> stal20

<400> 201

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
20 25 30

Gly Ser Trp Ser Val Val Cys Phe Tyr Pro Ala Asp Phe Ser Phe Val
35 40 45

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

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

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

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

<210> 202
<211> 1054
<212> PRT
<213> Staphylococcus aureus
<400> 202

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
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
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
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
130 135 140

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

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 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
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
 915 920 925

Ile Tyr Gln Val Pro Lys Gly Tyr Thr Leu Asn Lys Gly Tyr Asp Val
930 935 940

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

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

Lys Ser Val Ser Thr Gly Asn Ala Leu Gly Phe Thr Asn Asn Gln
1010 1015 1020

Ser Gly Gly Ala Gly Gln Glu Val Tyr Lys Ile Gly Asn Tyr Val
1025 1030 1035

Trp Glu Asp Thr Asn Lys Asn Gly Val Gln Glu Leu Gly Glu Lys
1040 1045 1050

Gly

<210> 203
<211> 1054
<212> PRT
<213> Staphylococcus aureus

<400> 203

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
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
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
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
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
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
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
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
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
290 295 300

Asn Tyr Ser Ile Tyr Met Asp Ala Asp Thr Ile Pro Val Ser Lys Asn
305 310 315 320

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

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

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

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

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

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

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

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

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
625 630 635 640

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

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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		
						935					940						
Ser	Asp	Ser	Tyr	Tyr	Ala	Asp	Pro	Asn	Asp	Ser	Asn	Leu	Lys	Glu	Val		
945					950					955					960		


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Thr Asp Gln Phe Lys Asn Arg Ile Tyr Tyr Glu His Pro Asn Val Ala
          965                      970                      975

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

Glu Asn Val Asp Pro Val Thr Asn Arg Asp Tyr Ser Ile Phe Gly
          1010                      1015                      1020

Trp Asn Asn Glu Asn Val Val Arg Tyr Gly Gly Gly Ser Ala Asp
          1025                      1030                      1035

Gly Asp Ser Ala Val Asn Pro Lys Asp Pro Thr Pro Gly Pro Pro
          1040                      1045                      1050

Val

<210> 204
<211> 376
<212> PRT
<213> Staphylococcus aureus

<400> 204

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

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

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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	
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	
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
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	
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	
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	
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	
Leu	Ser	Asn	Asn	Phe	Gly	Leu	Gln	370	375										
<210> 205																			
<211> 613																			
<212> PRT																			
<213> Staphylococcus aureus																			
<400> 205																			
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	Ala	Ser	Gly	Gly	Gly	Ser	Ser	Val	Thr	Glu	Ser	290	295	300	

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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

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

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

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

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

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

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

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
565                      570                      575

Gly Lys Pro Ser Leu Asn Ile Lys Asn Val Asn Tyr Gln Tyr Ala Val
580                      585                      590

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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

<210> 206

<211> 370

<212> PRT

<213> Staphylococcus aureus

<400> 206

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 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

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

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

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

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

Asp Ser Ile Asn Lys His Phe Ile Val Lys Pro Ser Glu Ser Pro Arg
210 215 220

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Tyr Thr His Pro Ser Gln Ser Leu Ile Ile Lys His His Phe Ala Val
225                230                235                240

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

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
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
                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
355                360                365

Arg Val
370

<210> 207
<211> 370
<212> PRT
<213> Staphylococcus aureus

<400> 207

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 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

Asp Glu Phe Lys Asn Ser Pro Lys Val Asn Val Ser Asn Leu Thr Asp
85                90                95

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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
    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
    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
    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
    210                                215                        220

Tyr Thr His Pro Ser Gln Ser Leu Ile Ile Lys His His Phe Ala Val
    225                                230                        235                        240

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

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
    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
    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
    355                                360                        365

Arg Val

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370

<210> 208
<211> 578
<212> PRT
<213> Staphylococcus aureus

<400> 208

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 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

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

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

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

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

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245									250					255			
Thr	Asn	Ala	Ser	Gly	Gly	Gly	Ser	Ser	Val	Thr	Glu	Ser	Val	Asp	Lys		
			260					265					270				
Lys	Phe	Val	Val	Pro	Glu	Ser	Gly	Ile	Asn	Lys	Ile	Ile	Pro	Ala	Tyr		
		275					280					285					
Asp	Glu	Phe	Lys	Asn	Ser	Pro	Lys	Val	Asn	Val	Ser	Asn	Leu	Thr	Asp		
		290					295					300					
Asn	Lys	Asn	Phe	Val	Ala	Ser	Glu	Asp	Lys	Leu	Asn	Lys	Ile	Ala	Asp		
305					310					315					320		
Ser	Ser	Ala	Ala	Ser	Lys	Ile	Val	Asp	Lys	Asn	Phe	Val	Val	Pro	Glu		
				325					330					335			
Ser	Lys	Leu	Gly	Asn	Ile	Val	Pro	Glu	Tyr	Lys	Glu	Ile	Asn	Asn	Arg		
			340					345					350				
Val	Asn	Val	Ala	Thr	Asn	Asn	Pro	Ala	Ser	Gln	Gln	Val	Asp	Lys	His		
		355					360					365					
Phe	Val	Ala	Lys	Gly	Pro	Glu	Val	Asn	Arg	Phe	Ile	Thr	Gln	Asn	Lys		
		370					375					380					
Val	Asn	His	His	Phe	Ile	Thr	Thr	Gln	Thr	His	Tyr	Lys	Lys	Val	Ile		
385					390					395					400		
Thr	Ser	Tyr	Lys	Ser	Thr	His	Val	His	Lys	His	Val	Asn	His	Ala	Lys		
				405					410					415			
Asp	Ser	Ile	Asn	Lys	His	Phe	Ile	Val	Lys	Pro	Ser	Glu	Ser	Pro	Arg		
			420					425					430				
Tyr	Thr	His	Pro	Ser	Gln	Ser	Leu	Ile	Ile	Lys	His	His	Phe	Ala	Val		
		435					440					445					
Pro	Gly	Tyr	His	Ala	His	Lys	Phe	Val	Thr	Pro	Gly	His	Ala	Ser	Ile		
		450					455					460					
Lys	Ile	Asn	His	Phe	Cys	Val	Val	Pro	Gln	Ile	Asn	Ser	Phe	Lys	Val		
465					470					475					480		
Ile	Pro	Pro	Tyr	Gly	His	Asn	Ser	His	Arg	Met	His	Val	Pro	Ser	Phe		
				485					490					495			
Gln	Asn	Asn	Thr	Thr	Ala	Thr	His	Gln	Asn	Ala	Lys	Val	Asn	Lys	Ala		
			500					505					510				
Tyr	Asp	Tyr	Lys	Tyr	Phe	Tyr	Ser	Tyr	Lys	Val	Val	Lys	Gly	Val	Lys		
		515					520					525					

Lys Tyr Phe Ser Phe Ser Gln Ser Asn Gly Tyr Lys Ile Gly Lys Pro
530 535 540

Ser Leu Asn Ile Lys Asn Val Asn Tyr Gln Tyr Ala Val Pro Ser Tyr
545 550 555 560

Ser Pro Thr His Tyr Val Pro Glu Phe Lys Gly Ser Leu Pro Ala Pro
565 570 575

Arg Val

<210> 209
<211> 248
<212> PRT
<213> Staphylococcus aureus

<400> 209

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

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

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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
245

<210> 210
<211> 358
<212> PRT
<213> Staphylococcus aureus

<400> 210

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

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

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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

Ser Ser Pro Ile Ala Gly Ile Asp Lys Pro Asn Gly Ala Asn Ile Ser
1                                5                                10                                15

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

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

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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

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

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

Asp Gly Asp Ser Ala Val Asn Ala Ser Gly Gly Gly Ser Pro Asp Tyr
180 185 190

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

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

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

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

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

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

<210> 212
<211> 486
<212> PRT
<213> Staphylococcus aureus

<400> 212

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

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 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

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

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

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

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

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

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

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

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

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

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

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<212>  PRT
<213>  Staphylococcus aureus

<400>  213

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 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
      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>  214
<211>  256

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<212>  PRT
<213>  Staphylococcus aureus

<400>  214

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 Val Lys Lys Glu Ile Glu Asn Phe Lys Phe Phe Val Gln Tyr Gly
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
      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>  215
<211>  256

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<212>  PRT
<213>  Staphylococcus aureus

<400>  215

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

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<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

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 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

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

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

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

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

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<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

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

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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

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 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
 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
 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
 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

Cys Gln Lys Gln Thr Gln Gln Leu Ala Glu Tyr Ile Glu Gly Ser Asp
435 440 445

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
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
500 505

<210> 221
<211> 436
<212> PRT
<213> Staphylococcus aureus

<400> 221

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

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 Cys Gly Asn Gln Gly Glu Lys Asn Asn
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
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
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
260 265 270

Gln Glu Met Leu Gly Lys Ile Val Gly Lys Glu Asp Lys Val Lys Ala
275 280 285

Trp Lys Lys Asp Trp Glu Glu Thr Thr Ala Lys Asp Gly Lys Glu Ile
290 295 300

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

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

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

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

Lys Ala Ala Lys
435


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<210> 222
<211> 584
<212> PRT
<213> Staphylococcus aureus

<400> 222

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

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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	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	
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			
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					
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		
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				
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	
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			
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	

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530
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
580

<210> 223
<211> 498
<212> PRT
<213> Staphylococcus aureus

<400> 223

Cys Gly Asn Gln Gly Glu Lys Asn Asn Lys Ala Glu Thr Lys Ser Tyr
1          5          10          15

Lys Met Asp Asp Gly Lys Thr Val Asp Ile Pro Lys Asp Pro Lys Arg
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
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
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
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
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
180         185         190

Leu Lys Met Gln Pro Glu Gln Gln Lys Leu Thr Ala Lys Ala Gly Trp

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195	200	205
Ala Glu Val Lys Gln Glu Glu Ile Glu Lys Tyr Ala Gly Asp Tyr Ile 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 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 275 280 285		
Gly Gly Ser Met Ala Met Ile Lys Met Ser Pro Glu Glu Ile Arg Ala 290 295 300		
Lys Ser Gln Ser Tyr Gly Gln Gly Ser Asp Gln Ile Arg Gln Ile Leu 305 310 315 320		
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		
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		
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		
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		
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		

Leu Ala Lys Tyr Asp Thr Leu Ser Ile Lys Gln Gly Leu Asp Arg Val
 485 490 495

Asn Pro

<210> 224
 <211> 520
 <212> PRT
 <213> Staphylococcus aureus

<400> 224

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
 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
 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
 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
 115 120 125

Asn Ala Glu Asn Val Ser Thr Thr Gln Asp Thr Ser Thr Glu Ala Thr
 130 135 140

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

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

Thr Val Tyr Pro His Gln Ala Gly Tyr Val Lys Leu Asn Tyr Gly Phe
 210 215 220

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Ser Val Pro Asn Ser Ala Val Lys Gly Asp Thr Phe Lys Ile Thr Val
225                               230                               235                               240

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

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

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

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

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

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

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

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

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Gly Glu Ile Glu Pro Ile Pro Glu
515 520

<210> 225
<211> 4
<212> PRT
<213> Staphylococcus aureus

<400> 225

Pro Ser Gly Ser
1

<210> 226
<211> 6
<212> PRT
<213> Staphylococcus aureus

<400> 226

His His His His His His
1 5

<210> 227
<211> 4
<212> PRT
<213> Staphylococcus aureus

<400> 227

Gly Gly Gly Gly
1

<210> 228
<211> 20
<212> PRT
<213> Staphylococcus aureus

<400> 228

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> Staphylococcus aureus

<400> 230

Gly Ser Gly Ser
1

<210> 231

<211> 293

<212> PRT

<213> Staphylococcus aureus

<400> 231

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 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


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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> 232
<211> 296
<212> PRT
<213> Staphylococcus aureus

<400> 232

Met Ala Ser Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp
1              5                   10           15

Ile Gly Ser Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp
                20                   25           30

Lys Glu Asn Gly Met Leu Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp
                35                   40           45

Lys Asn His Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile
50              55                   60

Ala Gly Gln Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly
65              70                   75           80

Leu Ala Trp Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn
                85                   90           95

Glu Val Ala Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr
100             105                   110

Lys Glu Tyr Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr
115             120                   125

Gly Asp Asp Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser
130             135                   140

Ile Gly His Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu
145             150                   155           160

Glu Ser Pro Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn
165             170                   175

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Met Val Asn Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro
      180                      185                      190

Val Tyr Gly Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys
      195                      200                      205

Ala Ala Asp Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser
      210                      215                      220

Ser Gly Phe Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys
      225                      230                      235                      240

Ala Ser Lys Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg
      245                      250                      255

Asp Asp Tyr Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn
      260                      265                      270

Thr Lys Asp Lys Trp Ile Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp
      275                      280                      285

Trp Glu Lys Glu Glu Met Thr Asn
      290                      295

<210> 233
<211> 888
<212> PRT
<213> Staphylococcus aureus

<400> 233

Ala Thr Gly Gly Cys Thr Ala Gly Cys Gly Cys Ala Gly Ala Thr Thr
  1                      5                      10                      15

Cys Thr Gly Ala Thr Ala Thr Thr Ala Ala Thr Ala Thr Thr Ala Ala
      20                      25                      30

Ala Ala Cys Cys Gly Gly Thr Ala Cys Thr Ala Cys Ala Gly Ala Thr
      35                      40                      45

Ala Thr Thr Gly Gly Ala Ala Gly Cys Ala Ala Thr Ala Cys Thr Ala
      50                      55                      60

Cys Ala Gly Thr Ala Ala Ala Ala Cys Ala Gly Gly Thr Gly Ala
      65                      70                      75                      80

Thr Thr Thr Ala Gly Thr Cys Ala Cys Thr Thr Ala Thr Gly Ala Thr
      85                      90                      95

Ala Ala Ala Gly Ala Ala Ala Ala Thr Gly Gly Cys Ala Thr Gly Thr
      100                      105                      110

Thr Ala Ala Ala Ala Ala Ala Ala Gly Thr Ala Thr Thr Thr Thr Ala
      115                      120                      125

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Thr Ala Gly Thr Thr Thr Thr Ala Thr Cys Gly Ala Thr Gly Ala Thr
 130 135 140
 Ala Ala Ala Ala Ala Thr Cys Ala Thr Ala Ala Thr Ala Ala Ala Ala
 145 150 155 160
 Ala Ala Cys Thr Gly Cys Thr Ala Gly Thr Thr Ala Thr Thr Ala Gly
 165 170 175
 Ala Ala Cys Gly Ala Ala Ala Gly Gly Thr Ala Cys Cys Ala Thr Thr
 180 185 190
 Gly Cys Thr Gly Gly Thr Cys Ala Ala Thr Ala Thr Ala Gly Ala Gly
 195 200 205
 Thr Thr Thr Ala Thr Ala Gly Cys Gly Ala Ala Gly Ala Ala Gly Gly
 210 215 220
 Thr Gly Cys Thr Ala Ala Cys Ala Ala Ala Ala Gly Thr Gly Gly Thr
 225 230 235 240
 Thr Thr Ala Gly Cys Cys Thr Gly Gly Cys Cys Thr Thr Cys Ala Gly
 245 250 255
 Cys Cys Thr Thr Thr Ala Ala Gly Gly Thr Ala Cys Ala Gly Thr Thr
 260 265 270
 Gly Cys Ala Ala Cys Thr Ala Cys Cys Thr Gly Ala Thr Ala Ala Thr
 275 280 285
 Gly Ala Ala Gly Thr Ala Gly Cys Thr Cys Ala Ala Ala Thr Ala Thr
 290 295 300
 Cys Thr Gly Ala Thr Thr Ala Cys Thr Ala Thr Cys Cys Ala Ala Gly
 305 310 315 320
 Ala Ala Ala Thr Thr Cys Gly Ala Thr Thr Gly Ala Thr Ala Cys Ala
 325 330 335
 Ala Ala Ala Gly Ala Gly Thr Ala Thr Ala Thr Gly Ala Gly Thr Ala
 340 345 350
 Cys Thr Thr Thr Ala Ala Cys Thr Thr Ala Thr Gly Gly Ala Thr Thr
 355 360 365
 Cys Ala Ala Cys Gly Gly Thr Ala Ala Thr Gly Thr Thr Ala Cys Thr
 370 375 380
 Gly Gly Thr Gly Ala Thr Gly Ala Thr Ala Cys Ala Gly Gly Ala Ala
 385 390 395 400
 Ala Ala Ala Thr Thr Gly Gly Cys Gly Gly Cys Cys Thr Thr Ala Thr
 405 410 415

Thr Gly Gly Thr Gly Cys Ala Ala Ala Thr Gly Thr Thr Thr Cys Gly	420	425	430
Ala Thr Thr Gly Gly Thr Cys Ala Thr Ala Cys Ala Cys Thr Gly Ala	435	440	445
Ala Ala Thr Ala Thr Gly Thr Thr Cys Ala Ala Cys Cys Thr Gly Ala	450	455	460
Thr Thr Thr Cys Ala Ala Ala Ala Cys Ala Ala Thr Thr Thr Thr Ala	465	470	475
Gly Ala Gly Ala Gly Cys Cys Cys Ala Ala Cys Thr Gly Ala Thr Ala	485	490	495
Ala Ala Ala Ala Ala Gly Thr Ala Gly Gly Cys Thr Gly Gly Ala Ala	500	505	510
Ala Gly Thr Gly Ala Thr Ala Thr Thr Thr Ala Ala Cys Ala Ala Thr	515	520	525
Ala Thr Gly Gly Thr Gly Ala Ala Thr Cys Ala Ala Ala Ala Thr Thr	530	535	540
Gly Gly Gly Gly Ala Cys Cys Ala Thr Ala Thr Gly Ala Thr Ala Gly	545	550	555
Ala Gly Ala Thr Thr Cys Thr Thr Gly Gly Ala Ala Cys Cys Cys Gly	565	570	575
Gly Thr Ala Thr Ala Thr Gly Gly Cys Ala Ala Thr Cys Ala Ala Cys	580	585	590
Thr Thr Thr Thr Cys Ala Thr Gly Ala Ala Ala Ala Cys Thr Ala Gly	595	600	605
Ala Ala Ala Thr Gly Gly Cys Thr Cys Thr Ala Thr Gly Ala Ala Ala	610	615	620
Gly Cys Ala Gly Cys Ala Gly Ala Thr Ala Ala Cys Thr Thr Cys Cys	625	630	635
Thr Thr Gly Ala Thr Cys Cys Thr Ala Ala Cys Ala Ala Ala Gly Cys	645	650	655
Ala Ala Gly Thr Thr Cys Thr Cys Thr Ala Thr Thr Ala Thr Cys Thr	660	665	670
Thr Cys Ala Gly Gly Gly Thr Thr Thr Thr Cys Ala Cys Cys Ala Gly	675	680	685
Ala Cys Thr Thr Cys Gly Cys Thr Ala Cys Ala Gly Thr Thr Ala Thr	690	695	700

Thr Ala Cys Thr Ala Thr Gly Gly Ala Thr Ala Gly Ala Ala Ala Ala
705 710 715 720

Gly Cys Ala Thr Cys Cys Ala Ala Ala Cys Ala Ala Cys Ala Ala Ala
725 730 735

Cys Ala Ala Ala Thr Ala Thr Ala Gly Ala Thr Gly Thr Ala Ala Thr
740 745 750

Ala Thr Ala Cys Gly Ala Ala Cys Gly Ala Gly Thr Thr Cys Gly Thr
755 760 765

Gly Ala Thr Gly Ala Cys Thr Ala Cys Cys Ala Ala Thr Thr Gly Cys
770 775 780

Ala Cys Thr Gly Gly Ala Cys Thr Thr Cys Ala Ala Cys Ala Ala Ala
785 790 795 800

Thr Thr Gly Gly Ala Ala Ala Gly Gly Thr Ala Cys Cys Ala Ala Thr
805 810 815

Ala Cys Thr Ala Ala Ala Gly Ala Thr Ala Ala Ala Thr Gly Gly Ala
820 825 830

Thr Ala Gly Ala Thr Cys Gly Thr Thr Cys Thr Thr Cys Ala Gly Ala
835 840 845

Ala Ala Gly Ala Thr Ala Thr Ala Ala Ala Thr Cys Gly Ala Thr
850 855 860

Thr Gly Gly Gly Ala Ala Ala Ala Gly Ala Ala Gly Ala Ala Ala
865 870 875 880

Thr Gly Ala Cys Ala Ala Ala Thr
885

<210> 234
<211> 306
<212> PRT
<213> Staphylococcus aureus

<400> 234

Met Lys Lys Leu Leu Leu Pro Leu Ile Ala Leu Ile Leu Val Leu Ala
1 5 10 15

Ala Cys Gly Asn Asn Ser Asp Ser Gly Ser Lys Asp Ser Asp Lys Lys
20 25 30

Ala Glu Thr Lys Ser Tyr Lys Thr Asp Asp Gly Lys Thr Ile Lys Val
35 40 45

Pro Lys Asn Pro Lys Arg Ile Ala Val Val Ala Pro Ser Tyr Ala Gly
50 55 60

Gly	Ile	Lys	Lys	Leu	Gly	Gly	Asn	Val	Val	Ala	Val	Ser	Asn	Gln	Val				
65					70					75					80				
Asp	Gln	Ser	Ser	Ile	Leu	Lys	Asp	Lys	Phe	Lys	Gly	Val	Thr	Lys	Val				
				85					90					95					
Gly	Asp	Asp	Asp	Val	Glu	Lys	Val	Ala	Lys	Gln	Lys	Pro	Asp	Leu	Ile				
			100					105					110						
Ile	Val	Leu	Asp	Gln	Asn	Lys	Asn	Ile	Lys	Lys	Tyr	Lys	Lys	Ile	Ala				
		115					120					125							
Ala	Thr	Val	Pro	Phe	Asn	Tyr	Gln	Lys	His	Lys	Tyr	Leu	Glu	Gln	Gln				
	130					135					140								
Glu	Glu	Leu	Gly	Lys	Leu	Leu	Gly	Lys	Glu	Asp	Glu	Val	Lys	Lys	Trp				
145					150					155					160				
Glu	Lys	Gln	Trp	Lys	Asp	Gln	Thr	Ala	Lys	Asp	Gly	Lys	Glu	Ile	Lys				
				165					170					175					
Asn	Lys	Ile	Gly	Ala	Asp	Ser	Thr	Val	Ser	Ile	Phe	Asp	Glu	Phe	Asp				
			180					185					190						
Lys	Lys	Leu	Tyr	Thr	Tyr	Gly	Asp	Asn	Trp	Gly	Arg	Gly	Gly	Glu	Val				
		195					200					205							
Leu	Tyr	Gln	Ala	Phe	Gly	Leu	Lys	Met	Ser	Lys	Gly	Gln	His	Asp	Leu				
	210					215					220								
Thr	Lys	Lys	Ala	Gly	Trp	Ala	Glu	Val	Asn	Gln	Glu	Gln	Ile	Glu	Lys				
225					230					235					240				
Val	Ala	Gly	Asp	Tyr	Ile	Val	Ser	Thr	Ser	Ala	Gly	Lys	Ser	Thr	Pro				
				245					250					255					
Gly	Tyr	Glu	Lys	Thr	Asn	Ile	Trp	Lys	Asn	Leu	Pro	Ala	Val	Lys	Lys				
			260					265					270						
Gly	His	Val	Ile	Lys	Val	Lys	Ala	Glu	Thr	Phe	Trp	Tyr	Asn	Asp	Pro				
	275						280					285							
Tyr	Thr	Leu	Asp	Phe	Met	Arg	Lys	Asp	Leu	Lys	Lys	Lys	Leu	Met	Asp				
	290					295					300								
Ala	Lys																		
305																			
<210>	235																		
<211>	253																		
<212>	PRT																		
<213>	Staphylococcus aureus																		

<400> 235

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

Val	Gly	Asn	Val	Thr	Val	Thr	Val	Phe	Asp	Asn	Asn	Thr	Asn	Thr	Lys	
1				5					10						15	
Val	Gly	Glu	Ala	Val	Thr	Lys	Glu	Asp	Gly	Ser	Tyr	Leu	Ile	Pro	Asn	
			20					25					30			
Leu	Pro	Asn	Gly	Asp	Tyr	Arg	Val	Glu	Phe	Ser	Asn	Leu	Pro	Lys	Gly	
		35					40					45				
Tyr	Glu	Val	Thr	Pro	Ser	Lys	Gln	Gly	Asn	Asn	Glu	Glu	Leu	Asp	Ser	
	50					55					60					
Asn	Gly	Leu	Ser	Ser	Val	Ile	Thr	Val	Asn	Gly	Lys	Asp	Asn	Leu	Ser	
65					70					75					80	
Ala	Asp	Leu	Gly	Ile	Tyr	Lys	Pro	Lys	Tyr	Asn	Leu	Gly	Asp	Tyr	Val	
				85					90					95		
Trp	Glu	Asp	Thr	Asn	Lys	Asn	Gly	Ile	Gln	Asp	Gln	Asp	Glu	Lys	Gly	
			100					105						110		
Ile	Ser	Gly	Val	Thr	Val	Thr	Leu	Lys	Asp	Glu	Asn	Gly	Asn	Val	Leu	
		115					120					125				
Lys	Thr	Val	Thr	Thr	Asp	Ala	Asp	Gly	Lys	Tyr	Lys	Phe	Thr	Asp	Leu	
		130				135					140					
Asp	Asn	Gly	Asn	Tyr	Lys	Val	Glu	Phe	Thr	Thr	Pro	Glu	Gly	Tyr	Thr	
145					150					155					160	
Pro	Thr	Thr	Val	Thr	Ser	Gly	Ser	Asp	Ile	Glu	Lys	Asp	Ser	Asn	Gly	
				165					170					175		
Leu	Thr	Thr	Thr	Gly	Val	Ile	Asn	Gly	Ala	Asp	Asn	Met	Thr	Leu	Asp	
			180					185					190			
Ser	Gly	Phe	Tyr	Lys	Thr	Pro	Lys	Tyr	Asn	Leu	Gly	Asn	Tyr	Val	Trp	
		195					200					205				
Glu	Asp	Thr	Asn	Lys	Asp	Gly	Lys	Gln	Asp	Ser	Thr	Glu	Lys	Gly	Ile	
	210					215					220					
Ser	Gly	Val	Thr	Val	Thr	Leu	Lys	Asn	Glu	Asn	Gly	Glu	Val	Leu	Gln	
225					230					235					240	
Thr	Thr	Lys	Thr	Asp	Lys	Asp	Gly	Lys	Tyr	Gln	Phe	Thr	Gly	Leu	Glu	
				245					250					255		
Asn	Gly	Thr	Tyr	Lys	Val	Glu	Phe	Glu	Thr	Pro	Ser	Gly	Tyr	Thr	Pro	
			260					265					270			
Thr	Gln	Val	Gly	Ser	Gly	Thr	Asp	Glu	Gly	Ile	Asp	Ser	Asn	Gly	Thr	

275	280	285
Ser Thr Thr Gly Val Ile Lys Asp Lys Asp Asn Asp Thr Ile Asp Ser		
290	295	300
Gly Phe Tyr Lys Pro Thr Tyr Asn Leu Gly Asp Tyr Val Trp Glu Asp		
305	310	315
Thr Asn Lys Asn Gly Val Gln Asp Lys Asp Glu Lys Gly Ile Ser Gly		
	325	330
Val Thr Val Thr Leu Lys Asp Glu Asn Asp Lys Val Leu Lys Thr Val		
	340	345
Thr Thr Asp Glu Asn Gly Lys Tyr Gln Phe Thr Asp Leu Asn Asn Gly		
	355	360
Thr Tyr Lys Val Glu Phe Glu Thr Pro Ser Gly Tyr Thr Pro Thr Ser		
	370	380
Val Thr Ser Gly Asn Asp Thr Glu Lys Asp Ser Asn Gly Leu Thr Thr		
385	390	395
Thr Gly Val Ile Lys Asp Ala Asp Asn Met Thr Leu Asp Ser Gly Phe		
	405	410
Tyr Lys Thr Pro Lys Tyr Ser Leu Gly Asp Tyr Val Trp Tyr Asp Ser		
	420	425
Asn Lys Asp Gly Lys Gln Asp Ser Thr Glu Lys Gly Ile Lys Asp Val		
	435	440
Lys Val Thr Leu Leu Asn Glu Lys Gly Glu Val Ile Gly Thr Thr Lys		
	450	455
Thr Asp Glu Asn Gly Lys Tyr Cys Phe Asp Asn Leu Asp Ser Gly Lys		
465	470	475
Tyr Lys Val Ile Phe Glu Lys Pro Ala Gly Leu Thr Gln Thr Val Thr		
	485	490
Asn Thr Thr Glu Asp Asp Lys Asp Ala Asp Gly Gly Glu Val Asp Val		
	500	505
Thr Ile Thr Asp His Asp Asp Phe Thr Leu Asp Asn Gly Tyr Phe Glu		
	515	520
Glu Asp Thr		
530		

<210> 237
 <211> 504
 <212> PRT
 <213> Staphylococcus aureus

<400> 237

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

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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

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

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

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

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

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

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

Gln Gly Leu Asp Arg Val Asn Pro
  500

<210> 238
<211> 496
<212> PRT
<213> Staphylococcus aureus

<400> 238

Cys Gly Asn Gln Gly Glu Lys Asn Asn Lys Ala Glu Thr Lys Ser Tyr
  1                                5                                10                                15

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Lys Met Asp Asp Gly Lys Thr Val Asp Ile Pro Lys Asp Pro Lys Arg
 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
 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
 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
 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
 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
 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
 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
 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 Pro Thr
 275 280 285
 Ala Arg Gly Ala Met Ile Lys Met Ser Pro Glu Glu Ile Arg Ala Lys
 290 295 300

Ser Gln Ser Tyr Gly Gln Gly Ser Asp Gln Ile Arg Gln Ile Leu Ser
305 310 315 320

Asp Leu Thr Arg Ala Gln Gly Glu Ile Ala Ala Asn Trp Glu Gly Gln
325 330 335

Ala Phe Ser Arg Phe Glu Glu Gln Phe Gln Gln Leu Ser Pro Lys Val
340 345 350

Glu Lys Phe Ala Gln Leu Leu Glu Glu Ile Lys Gln Gln Leu Asn Ser
355 360 365

Thr Ala Asp Ala Val Gln Glu Gln Asp Gln Gln Leu Ser Asn Asn Phe
370 375 380

Gly Leu Gln Ala Ser Gly Gly Gly Ser Gly Gly Tyr Lys Gly Ile Lys
385 390 395 400

Ala Asp Gly Gly Lys Val Asp Gln Ala Lys Gln Leu Ala Ala Lys Thr
405 410 415

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

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

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> Staphylococcus aureus

<400> 239

Ala Pro Thr Ala Arg Gly
1 5

<210> 240
<211> 17
<212> PRT
<213> Staphylococcus aureus

<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

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
 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
 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
 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
 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
 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
 180 185 190

Thr Leu Ser Ile Lys Gln Gly Leu Asp Arg Val Asn Pro
 195 200 205

<210> 242
 <211> 293
 <212> PRT
 <213> Staphylococcus aureus

<400> 242

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
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
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
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

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 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 Leu 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> 244
<211> 293
<212> PRT
<213> Staphylococcus aureus

<400> 244

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 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

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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> 245
<211> 293
<212> PRT
<213> Staphylococcus aureus

<400> 245

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

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Thr Leu Lys Tyr Val Gln Pro Leu 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> 246
<211> 285
<212> PRT
<213> Staphylococcus aureus

<400> 246

Cys Gly Asn Gln Gly Glu Lys Asn Asn Lys Ala Glu Thr Lys Ser Tyr
1                      5                      10                      15

Lys Met Asp Asp Gly Lys Thr Val Asp Ile Pro Lys Asp Pro Lys Arg
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
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
85                      90                      95

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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
 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
 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
 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
 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
 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
 275 280 285
 <210> 247
 <211> 233
 <212> PRT
 <213> Staphylococcus aureus
 <400> 247
 Gly Cys Gly Ile Gly Lys Glu Ala Glu Val Lys Lys Ser Phe Glu Lys
 1 5 10 15
 Thr Leu Ser Met Tyr Pro Ile Lys Asn Leu Glu Asp Leu Tyr Asp Lys
 20 25 30
 Glu Gly Tyr Arg Asp Asp Gln Phe Asp Lys Asn Asp Lys Gly Thr Trp
 35 40 45
 Ile Ile Asn Ser Glu Met Val Ile Gln Pro Asn Asn Glu Asp Met Val
 50 55 60

Ala Lys Gly Met Val Leu Tyr Met Asn Arg Asn Thr Lys Thr Thr Asn
65 70 75 80

Gly Tyr Tyr Tyr Val Asp Val Thr Lys Asp Glu Asp Glu Gly Lys Pro
85 90 95

His Asp Asn Glu Lys Arg Tyr Pro Val Lys Met Val Asp Asn Lys Ile
100 105 110

Ile Pro Thr Lys Glu Ile Lys Asp Glu Lys Ile Lys Lys Glu Ile Glu
115 120 125

Asn Phe Lys Phe Phe Val Gln Tyr Gly Asp Phe Lys Asn Leu Lys Asn
130 135 140

Tyr Lys Asp Gly Asp Ile Ser Tyr Asn Pro Glu Val Pro Ser Tyr Ser
145 150 155 160

Ala Lys Tyr Gln Leu Thr Asn Asp Asp Tyr Asn Val Lys Gln Leu Arg
165 170 175

Lys Arg Tyr Asp Ile Pro Thr Ser Lys Ala Pro Lys Leu Leu Leu Lys
180 185 190

Gly Ser Gly Asn Leu Lys Gly Ser Ser Val Gly Tyr Lys Asp Ile Glu
195 200 205

Phe Thr Phe Val Glu Lys Lys Glu Glu Asn Ile Tyr Phe Ser Asp Ser
210 215 220

Leu Asp Tyr Lys Lys Ser Gly Asp Val
225 230

<210> 248
<211> 288
<212> PRT
<213> Staphylococcus aureus

<400> 248

Met Ala Ser Cys Gly Asn Gln Gly Glu Lys Asn Asn Lys Ala Glu Thr
1 5 10 15

Lys Ser Tyr Lys Met Asp Asp Gly Lys Thr Val Asp Ile Pro Lys Asp
20 25 30

Pro Lys Arg Ile Ala Val Val Ala Pro Thr Tyr Ala Gly Gly Leu Lys
35 40 45

Lys Leu Gly Ala Asn Ile Val Ala Val Asn Gln Gln Val Asp Gln Ser
50 55 60

Lys Val Leu Lys Asp Lys Phe Lys Gly Val Thr Lys Ile Gly Asp Gly
65 70 75 80

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Asp Val Glu Lys Val Ala Lys Glu Lys Pro Asp Leu Ile Ile Val Tyr
      85                      90                      95

Ser Thr Asp Lys Asp Ile Lys Lys Tyr Gln Lys Val Ala Pro Thr Val
      100                    105                    110

Val Val Asp Tyr Asn Lys His Lys Tyr Leu Glu Gln Gln Glu Met Leu
      115                    120                    125

Gly Lys Ile Val Gly Lys Glu Asp Lys Val Lys Ala Trp Lys Lys Asp
      130                    135                    140

Trp Glu Glu Thr Thr Ala Lys Asp Gly Lys Glu Ile Lys Lys Ala Ile
      145                    150                    155                    160

Gly Gln Asp Ala Thr Val Ser Leu Phe Asp Glu Phe Asp Lys Lys Leu
      165                    170                    175

Tyr Thr Tyr Gly Asp Asn Trp Gly Arg Gly Gly Glu Val Leu Tyr Gln
      180                    185                    190

Ala Phe Gly Leu Lys Met Gln Pro Glu Gln Gln Lys Leu Thr Ala Lys
      195                    200                    205

Ala Gly Trp Ala Glu Val Lys Gln Glu Glu Ile Glu Lys Tyr Ala Gly
      210                    215                    220

Asp Tyr Ile Val Ser Thr Ser Glu Gly Lys Pro Thr Pro Gly Tyr Glu
      225                    230                    235                    240

Ser Thr Asn Met Trp Lys Asn Leu Lys Ala Thr Lys Glu Gly His Ile
      245                    250                    255

Val Lys Val Asp Ala Gly Thr Tyr Trp Tyr Asn Asp Pro Tyr Thr Leu
      260                    265                    270

Asp Phe Met Arg Lys Asp Leu Lys Glu Lys Leu Ile Lys Ala Ala Lys
      275                    280                    285

<210> 249
<211> 234
<212> PRT
<213> Staphylococcus aureus

<400> 249

Met Gly Cys Gly Ile Gly Lys Glu Ala Glu Val Lys Lys Ser Phe Glu
  1          5          10          15

Lys Thr Leu Ser Met Tyr Pro Ile Lys Asn Leu Glu Asp Leu Tyr Asp
      20          25          30

Lys Glu Gly Tyr Arg Asp Asp Gln Phe Asp Lys Asn Asp Lys Gly Thr
      35          40          45

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Trp Ile Ile Asn Ser Glu Met Val Ile Gln Pro Asn Asn Glu Asp Met
50 55 60

Val Ala Lys Gly Met Val Leu Tyr Met Asn Arg Asn Thr Lys Thr Thr
65 70 75 80

Asn Gly Tyr Tyr Tyr Val Asp Val Thr Lys Asp Glu Asp Glu Gly Lys
85 90 95

Pro His Asp Asn Glu Lys Arg Tyr Pro Val Lys Met Val Asp Asn Lys
100 105 110

Ile Ile Pro Thr Lys Glu Ile Lys Asp Glu Lys Ile Lys Lys Glu Ile
115 120 125

Glu Asn Phe Lys Phe Phe Val Gln Tyr Gly Asp Phe Lys Asn Leu Lys
130 135 140

Asn Tyr Lys Asp Gly Asp Ile Ser Tyr Asn Pro Glu Val Pro Ser Tyr
145 150 155 160

Ser Ala Lys Tyr Gln Leu Thr Asn Asp Asp Tyr Asn Val Lys Gln Leu
165 170 175

Arg Lys Arg Tyr Asp Ile Pro Thr Ser Lys Ala Pro Lys Leu Leu Leu
180 185 190

Lys Gly Ser Gly Asn Leu Lys Gly Ser Ser Val Gly Tyr Lys Asp Ile
195 200 205

Glu Phe Thr Phe Val Glu Lys Lys Glu Glu Asn Ile Tyr Phe Ser Asp
210 215 220

Ser Leu Asp Tyr Lys Lys Ser Gly Asp Val
225 230

<210> 250
<211> 206
<212> PRT
<213> Staphylococcus aureus

<400> 250

Met Ala Met Ile Lys Met Ser Pro Glu Glu Ile Arg Ala Lys Ser Gln
1 5 10 15

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

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
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	Gly	Gly	Tyr	Lys	Gly	Ile	Lys	Ala	Asp	100	105	110	
Gly	Gly	Lys	Val	Asp	Gln	Ala	Lys	Gln	Leu	Ala	Ala	Lys	Thr	Ala	Lys	115	120	125	
Asp	Ile	Glu	Ala	Cys	Gln	Lys	Gln	Thr	Gln	Gln	Leu	Ala	Glu	Tyr	Ile	130	135	140	
Glu	Gly	Ser	Asp	Trp	Glu	Gly	Gln	Phe	Ala	Asn	Lys	Val	Lys	Asp	Val	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			