

VACCINE CONSTRUCTS AND USES THEREOF AGAINST *STAPHYLOCOCCUS* INFECTIONS

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] N.A.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

[0002] N.A.

FIELD OF THE INVENTION

[0003] The present invention relates to vaccine constructs and uses thereof against *Staphylococcus* infections. More specifically, the present invention is concerned with vaccine constructs combining antigens and their uses against *Staphylococcus* infections such as bovine intramammary infections (IMI).

REFERENCE TO SEQUENCE LISTING

[0004] Pursuant to 37 C.F.R. 1.821(c), a sequence listing is submitted herewith as an ASCII compliant text file named SEQUENCE LISTING USP62411120_ST25, created on October 5, 2017 and having a size of 278 kilobytes. The content of the aforementioned file is hereby incorporated by reference in its entirety.

BACKGROUND OF THE INVENTION

[0005] Bovine mastitis is the most frequent and costly disease for dairy producers and *Staphylococcus aureus* is considered to be the transmittable bacterium that is the most often responsible for the development of the disease (Sears *et al.*, 2003). Staphylococcal IMIs, which may lead to mastitis, are difficult to treat and frequent relapses are common (Sandholm *et al.*, 1990).

[0006] The development of vaccines for the prevention and control of *S. aureus* IMIs has been extensively investigated although no formulation has demonstrated protective efficacy to date. This is probably because of inadequate vaccine targets (Middleton, 2008; Middleton 2009), high diversity among strains capable of provoking mastitis (Buzzola, 2007; Kerro-Dego, 2006; Middleton, 2008) or the failure to elicit an appropriate immune response (Bharathan, 2011; Ferens, 2000; Fowler, 2014; Proctor, 2012). It is increasingly understood that immunity solely based on vaccine-induced antibodies may be important but is however insufficient for inducing protection against *S. aureus* (Middleton 2008; Middleton 2009). It appears that cell mediated immunity (CMI) based on Th1 and Th17 type responses may be necessary to complete the protection (Fowler, 2014; Lin, 2009; Proctor, 2012; Spellberg, 2012).

[0007] Bacterial susceptibility to antibiotics *in vitro* is a poor predictor of therapeutic efficacy in chronically infected cows (Owens *et al.*, 1997). Although infections that follow treatment of mastitis can be due to newly acquired strains, they are often the result of the persistence of the original infective organism (Sandholm *et al.*, 1990; Myllys *et al.*, 1997). Existing therapies thus often fail to eliminate the infection and it would be highly desirable to find novel approaches to prevent or treat staphylococcal IMI.

[0008] A lack of vaccine efficacy and protective ability has been noted for commercially available *S. aureus* vaccines (Middleton, 2008). Thus, it would be highly desirable to use highly efficient *S. aureus* antigens that are

known to be expressed during IMI as vaccine components for protection against IMI and mastitis.

[0009] The present invention seeks to meet these and other needs.

[0010] The present description refers to a number of documents, the content of which is herein incorporated by reference in their entirety.

SUMMARY OF THE INVENTION

[0011] In a first aspect, the present invention provides fusion polypeptides displaying increased immunogenicity and their use as vaccine against staphylococcal IMI.

[0012] A characteristic of staphylococcal such as *S. aureus* IMI is the ability of *S. aureus* to persist within host cells. In particular, *S. aureus* small colony variants (SCVs) do not generally generate invasive infections and can be internalized in host cells. In a further aspect therefore, the present invention provides live-attenuated *S. aureus* strains for vaccine purposes based on the phenotypic aspects of SCVs to provide an immune response against such strains and increase the vaccine protective efficacy.

[0013] In an aspect, the present invention provides the following items:

[0014] Item 1: A fusion construct of formula (I): X-A-linker-B-Z (I) wherein: (1) A and B are identical or different and are independently: (a) a polypeptide comprising a SACOL0029 polypeptide as set forth in any one of the sequences depicted in FIG. 24 (SEQ ID NOs: 5 and 121 to 131), a SACOL0264 polypeptide (SEQ ID NO : 185), a SACOL0442 polypeptide as set forth in any one of the sequences depicted in FIG. 22D (SEQ ID NOs: 29 and 82 to 92), a SACOL0718 polypeptide (SEQ ID NO : 186), a SACOL0720 polypeptide as set forth in any one of the sequences depicted in FIGs. 23I-K (SEQ ID NOs: 11 and 109 to 120), a SACOL1353 polypeptide (SEQ ID NO : 187), a SACOL1416 polypeptide (SEQ ID NO : 188), a SACOL1611 polypeptide (SEQ ID NO : 189), a SACOL1867 polypeptide as set forth in any one of the sequences depicted in FIG. 25D (SEQ ID NOs: 152 to 164), a SACOL1912 polypeptide (SEQ ID NO : 43), a SACOL1944 polypeptide (SEQ ID NO : 190), a SACOL2144 polypeptide (SEQ ID NO : 191), a SACOL2365 polypeptide (SEQ ID NO : 192), a SACOL2385 polypeptide (SEQ ID NO : 50) or a SACOL2599 polypeptide (SEQ ID NO : 193), based on the gene nomenclature from the *Staphylococcus aureus* COL (SACOL) genome set forth in NCBI Reference Sequence NC_002951.2; (b) a polypeptide encoded by a gene from a same operon as a gene encoding the polypeptide of (a); (c) a polypeptide comprising an immunogenic fragment of at least 13 consecutive amino acids of (a) or (b); (d) a polypeptide comprising an amino acid sequence at least 60% identical overall to the sequence of the polypeptide of any one of (a) to (c); or (e) a polypeptide comprising an immunogenic variant comprising at least 13 consecutive amino acids of any one of (a) to (c); (2) the linker is an amino acid sequence of at least one amino acid or is absent; (3) X is absent or is an amino acid sequence of at least one amino acid; and (4) Z is absent or is an amino acid sequence of at least one amino acid.

[0015] Item 2: The construct of item 1, wherein (1) (a) is a polypeptide comprising a SACOL0029 polypeptide as set forth in any one of the sequences depicted in FIG. 24 (SEQ ID NOs: 5 and 121 to 131), a SACOL0442 polypeptide as set forth in any one of the sequences depicted in FIG. 22D (SEQ ID NOs: 29 and 82 to 92), a

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SACOL0720 polypeptide as set forth in any one of the sequences depicted in FIGs. 23I-K (SEQ ID NOs: 11 and 109 to 120), or a SACOL1867 polypeptide as set forth in any one of the sequences depicted in FIG. 25D (SEQ ID NOs: 152 to 164).

[0016] Item 3: The construct of item 2, wherein at least one of A and B is (a) a polypeptide comprising a SACOL0029 polypeptide as set forth in any one of the sequences depicted in FIG. 24 (SEQ ID NOs: 5 and 121 to 131); (b) a polypeptide encoded by a gene from a same operon as a gene encoding the polypeptide of (a); (c) a polypeptide comprising an immunogenic fragment of at least 13 consecutive amino acids of (a) or (b); (d) a polypeptide comprising an amino acid sequence at least 60% identical overall to the sequence of the polypeptide of any one of (a) to (c); or (e) a polypeptide comprising an immunogenic variant comprising at least 13 consecutive amino acids of any one of (a) to (d); and the other one of A and B is (a') a polypeptide comprising a SACOL1867 polypeptide as set forth in any one of the sequences depicted in FIG. 25D (SEQ ID NOs: 152 to 164); (b') a polypeptide encoded by a gene from a same operon as a gene encoding the polypeptide of (a'); (c') a polypeptide comprising an immunogenic fragment of at least 13 consecutive amino acids of (a') or (b'); (d') a polypeptide comprising an amino acid sequence at least 60% identical overall to the sequence of the polypeptide of any one of (a') to (c'); or (e') a polypeptide comprising an immunogenic variant comprising at least 12 consecutive amino acids of any one of (a') to (d').

[0017] Item 4: The construct of item 2, wherein at least one of A and B is (a) a polypeptide comprising a SACOL0442 polypeptide as set forth in any one of the sequences depicted in FIG. 22D (SEQ ID NOs: 29 and 82 to 92); (b) a polypeptide encoded by a gene from a same operon as a gene encoding the polypeptide of (a); (c) a polypeptide comprising an immunogenic fragment of at least 13 consecutive amino acids of (a) or (b); (d) a polypeptide comprising an amino acid sequence at least 60% identical overall to the sequence of the polypeptide of any one of (a) to (c); or (e) a polypeptide comprising an immunogenic variant comprising at least 13 consecutive amino acids of any one of (a) to (d); and the other one of A and B is (a') a polypeptide comprising a SACOL0720 polypeptide as set forth in any one of the sequences depicted in FIGs. 23I-K (SEQ ID NOs: 11 and 109 to 120); (b') a polypeptide encoded by a gene from a same operon as a gene encoding the polypeptide of (a'); (c') a polypeptide comprising an immunogenic fragment of at least 13 consecutive amino acids of (a') or (b'); (d') a polypeptide comprising an amino acid sequence at least 60% identical overall to the sequence of the polypeptide of any one of (a') to (c'); or (e') a polypeptide comprising an immunogenic variant comprising at least 12 consecutive amino acids of any one of (a') to (d').

[0018] Item 5: The construct of item 2, wherein A and B are identical or different and are (a) a polypeptide comprising a SACOL0720 polypeptide as set forth in any one of the sequences depicted in FIGs. 23I-K (SEQ ID NOs: 11 and 109 to 120); (b) a polypeptide encoded by a gene from a same operon as a gene encoding the polypeptide of (a); (c) a polypeptide comprising an immunogenic fragment of at least 13 consecutive amino acids of (a) or (b); (d) a polypeptide comprising an amino acid sequence at least 60% identical overall to the sequence of the polypeptide of any one of (a) to (c); or (e) a polypeptide comprising an immunogenic variant comprising at least 13 consecutive amino acids of any one of (a) to (d).

[0019] Item 6: The construct of any one of items 1-2 and 4, wherein said immunogenic fragment (d) comprises

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one or more of the following amino acid sequences: KDTINGKSNKSRNW (SEQ ID NO: 34); and KDGGKYTLESHKELQ (SEQ ID NO: 1).

[0020] Item 7: The construct of item 6, wherein said immunogenic fragment (d) comprises one or more of the following amino acid sequences : STQNSSSVQDKQLQKVEEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVAGRVYTPKRNITLNKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKDGGKYTLESHKELQKDRENVKINTADIKNVTFKLKSVNDIEQV (SEQ ID NO: 30); DKQLQKVEEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVAGRVYTPKRNITLNKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTK (SEQ ID NO :32); and DKQLQKVEEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVAGRVYTPKRNITLNKEVVTLKELDHIIIRFAHISYGLYMGEHLPKGNIVINTKDGGKYTLESHKELQKDRENVKINTADIKNVTFKLKSVNDIEQV (SEQ ID NO : 33).

[0021] Item 8: The construct of any one of items 1-2 and 4-5, wherein said immunogenic fragment (d) comprises one or more of the following amino acid sequences: QFGFDLKHKKDALA (SEQ ID NO: 21); TIKDQQKANQLAS (SEQ ID NO: 22); KDINKIYFMTDVDL (SEQ ID NO: 23); and DVDLGGPTFVLND (SEQ ID NO: 24).

[0022] Item 9: The construct of item 8, wherein said immunogenic fragment (d) comprises one or more of the following amino acid sequences: RASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNYKEVIHTKLYKDNLFDVKAKEPYNVTITSDKYIPNTDLKRGQADLFVAEGSIKDLVKHKKHGKAIIGTKKHHVNIKLKRDINKIYFMTDVDLGGPTFVLNDKDYQEIRKYTKAKHIVSQFGFDLKHKKDALALEKAKNKVDKSIETRSEAIISSISLTG (SEQ ID NO : 12); ASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNYKEVIHTKLYKDNLFDVKAKEPYNVTITSDKYIPNTDLKRGQADLFVAEGSIKDLVKHKKHGKAIIGTKKHHVNIKLKRDINKIYFMTDVDLGGPTFVLNDKDYQEIRKYTKAKHIVSQFGFDLKHKKDALALEKAKNKVDKSIETRSEAIISSISLTG (SEQ ID NO: 13); ASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNYKEVIHTKLYKDNLFDVKAKEPYNVTITSDKYIPNTDLKRGQADLFVAEGSIKDLVKHKKHGKAIIGTKKHHVNIKLKRDINKIYFMTDVDLGGPTFVLNDKDYQE (SEQ ID NO: 14); KDINKIYFMTDVDLGGPTFVLNDKDYQEIRKYTKAKHIVSQFGFDLKHKKDALA (SEQ ID NO : 15); KDINKIYFMTDVDLGGPTFVLNDK (SEQ ID NO : 16); KDINKIYFMTDVDLGGPTFVLNDKDY (SEQ ID NO : 17); KDINKIYFMTDVDLGGPTFVLND (SEQ ID NO : 19); SQFGFDLKHKKDALA (SEQ ID NO: 18); and KHIVSQFGFDLKHKKDALA (SEQ ID NO: 20).

[0023] Item 10: The construct of any one of items 1-3, wherein said immunogenic fragment (c') comprises one or more of the following amino acid sequences: PYNGVVSFKDATGF (SEQ ID NO: 165); AHPNGDKGNNGGIYK (SEQ ID NO: 167); SISDYPGEDISVM (SEQ ID NO: 169); RGPKGFNFNENVQA (SEQ ID NO: 172); QFESTGTIKRIKDN (SEQ ID NO: 175); and GNSGSPVLNSNNEV (SEQ ID NO: 178).

[0024] Item 11: The construct of item 10, wherein said immunogenic fragment (d) comprises the following amino acid sequence:

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TQVKDTNIFPYNGVVSFKDATGFVIGKNTIITNKHVSKDYKVGDRITAHPNGDKGNGGIYKIKSISDYPGDEDISVM
NIEEQAVVERGPKGFNFENVQAFNFAKDAKVDDKIKVIGYPLPAQNSFKQFESTGTIKRIKDNLNFDAYIEPGNSG
SPVLNSNNEVIGVVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ (SEQ ID NO: 39).

[0025] Item 12: The construct of any one of items 1 to 11, wherein the linker comprises at least four identical or different amino acids selected from the group consisting of glycine, serine, alanine, aspartate, glutamate and lysine.

[0026] Item 13: The construct of any one of items 1 to 12, wherein the linker comprises (GGGS)_n (SEQ ID NO: 67), (ERKYK)_n (SEQ ID NO: 61); or (EAAAK)_n (SEQ ID NO: 63), wherein n=1 to 5.

[0027] Item 14: The construct of any one of items 1 to 13, wherein said X comprises a polyhistidine of 6 to 10 amino acids.

[0028] Item 15: The construct of any one of items 1 to 13, wherein said X is absent.

[0029] Item 16: The construct of any one of items 1 to 15, wherein said Z is absent.

[0030] Item 17: An isolated nucleic acid molecule encoding the construct defined in any one of items 1 to 16.

[0031] Item 18: A vector comprising the isolated nucleic acid defined in item 17.

[0032] Item 19: A host cell comprising the vector defined in item 18.

[0033] Item 20: The cell of item 19, which is a live attenuated form of *Staphylococcus aureus*.

[0034] Item 21: The cell of item 20, wherein the live attenuated form of *Staphylococcus aureus* has a stabilized small colony variant (SCV) phenotype.

[0035] Item 22: The cell of item 21, wherein the live attenuated form of *Staphylococcus aureus* having a stabilized SCV phenotype is a $\Delta hemB\Delta 720$ *S. aureus*.

[0036] Item 23: A composition comprising: (A) at least one of the constructs defined in any one of items 1 to 16; at least one of the nucleic acid molecules defined in item 17; at least one of the vectors defined in item 18; or at least one of the cells defined in any one of items 19 to 22; and (B) (i) the polypeptide defined in any one of items 1 to 11; (ii) a live attenuated *Staphylococcus aureus*; (iii) a pharmaceutically acceptable excipient; (iv) an adjuvant; or (v) a combination of at least two of (i) to (iv).

[0037] Item 24: The composition of item 23, wherein the live attenuated form of *Staphylococcus aureus* expresses: (a) a polypeptide comprising a SACOL0029 polypeptide as set forth in any one of the sequences depicted in FIG. 24 (SEQ ID NOs: 5 and 121 to 131), a SACOL0264 polypeptide (SEQ ID NO: 185), a SACOL0442 polypeptide as set forth in any one of the sequences depicted in FIG. 22D (SEQ ID NOs: 29 and 82 to 92), a SACOL0718 polypeptide (SEQ ID NO: 186), a SACOL0720 polypeptide as set forth in any one of the sequences depicted in FIGs. 23I-K (SEQ ID NOs: 11 and 109 to 120), a SACOL1353 polypeptide (SEQ ID NO: 187), a SACOL1416 polypeptide (SEQ ID NO: 188), SACOL1611 (SEQ ID NO: 189), a SACOL1867 polypeptide as set forth in any one of the sequences depicted in FIG. 25D (SEQ ID NOs: 152 to 164), a SACOL1912 polypeptide (SEQ ID NO: 43), SACOL1944 (SEQ ID NO: 190), a SACOL2144 polypeptide (SEQ ID NO: 191), a

SACOL2365 polypeptide (SEQ ID NO : 192), a SACOL2385 polypeptide (SEQ ID NO : 50) or a SACOL2599 polypeptide (SEQ ID NO : 193) based on the gene nomenclature from the *Staphylococcus aureus* COL (SACOL) genome set forth in NCBI Reference Sequence NC_002951.2; (b) a polypeptide encoded by a gene from a same operon as a gene encoding the polypeptide of (a); (c) a polypeptide comprising an immunogenic fragment of at least 13 consecutive amino acids of (a) or (b); (d) a polypeptide comprising an amino acid sequence at least 60% identical overall to the sequence of the polypeptide of any one of (a) to (c); or (e) a polypeptide comprising an immunogenic variant comprising at least 13 consecutive amino acids of any one of (a) to (c).

[0038] Item 25: The composition of item 23 or 24, wherein the live attenuated form of *Staphylococcus aureus* has a stabilized small colony variant (SCV) phenotype.

[0039] Item 26: The composition of any one of items 23 to 25, wherein the adjuvant comprises alum, an oil (e.g., emulsified oil, mineral oil), saponin (e.g., Quil-A™), cyclic-diguanosine-5'-monophosphate (c-di-GMP), polyphosphasine, indolicidin, pathogen-associated molecular patterns (PAMPS) or a combination of at least two thereof.

[0040] Item 27: A method for preventing and/or treating a Staphylococcal intramammary infection (IMI) in a mammal, said method comprising administering to said mammal an effective amount of the construct defined in any one of items 1 to 16; of the nucleic acid molecule defined in item 17; of the vector defined in item 18; of the cell defined in any one of items 19 to 22; or of the composition defined in any one of items 23 to 26.

[0041] Item 28: The method of item 27, wherein said Staphylococcal IMI is caused by one or more *Staphylococcus aureus* strains.

[0042] Item 29: The method of item 27 or 28, wherein said mammal is a cow.

[0043] Item 30: A use of an effective amount of (i) the construct defined in any one of items 1 to 16; (ii) the nucleic acid molecule defined in item 17; (iii) the vector defined in item 18; of the cell defined in any one of items 19 to 22; (iv) the composition defined in any one of items 23 to 26; or (v) a combination of at least two of (i) to (iv), for preventing and/or treating a Staphylococcal intramammary infection (IMI) in a mammal.

[0044] Item 31: The use of item 30, wherein said Staphylococcal IMI is caused by one or more *Staphylococcus aureus* strains.

[0045] Item 32: The use of item 30 or 31, wherein said mammal is a cow.

[0046] Item 33: The construct defined in any one of items 1 to 16; the nucleic acid molecule defined in item 17; the vector defined in item 18; the cell defined in any one of items 19 to 22; the composition defined in any one of items 23 to 26 or a combination of at least two thereof, for use in the prevention and/or treatment of a Staphylococcal intramammary infection (IMI) in a mammal.

[0047] Item 34: The construct, nucleic acid molecule, vector, cell, composition or combination of item 33, wherein said Staphylococcal IMI is caused by one or more *Staphylococcus aureus* strains.

[0048] Item 35: The construct, nucleic acid molecule, vector, cell or composition of item 33 or 34, wherein said

mammal is a cow.

[0049] Item 36: A kit for preventing and/or treating a Staphylococcal intramammary infection (IMI) in a mammal comprising: (A) (i) at least one of the constructs defined in any one of items 1 to 16; (ii) at least one of the nucleic acid molecules defined in item 17; (iii) at least one of the vectors defined in items 18; (iv) at least one of the cells defined in any one of items 19 to 22; or (v) a combination of at least two of (i) to (iv), and (B) (i) the polypeptide defined in any one of items 1 to 11; (ii) a live attenuated *Staphylococcus aureus*; (iii) a pharmaceutically acceptable excipient; (iv) an adjuvant; (v) instructions for using the kit for preventing and/or treating a Staphylococcal intramammary infection (IMI) in a mammal; or (vi) a combination of at least two of (i) to (v).

BRIEF DESCRIPTION OF THE DRAWINGS

[0050] In the appended drawings :

[0051] **FIGs. 1A-D.** shows serum total IgG (FIG. 1A), IgG1 (FIG. 1B), and IgG2 (FIG. 1C) titers for the vaccinated (9) and placebo (10) cows for each antigen of the vaccine, namely SACOL0029, SACOL0442, SACOL0720, SACOL1867, SACOL1912, and SACOL2385, four weeks after the second immunization (just before the experimental infection). In FIG. 1D, the IgG2/IgG1 ratio is represented for the vaccinated cows. In FIGs. 1A, B and C, open circles (○) represent data for the vaccinated cows, black squares (■) represent data for the placebo cows. Each symbol represents the titer for one cow. Horizontal lines represent the medians: dashed lines represent the medians for the vaccinated cows while continuous lines represent the medians for the placebo cows. In FIGs. 1A, B and C, titers for the vaccinated cows are higher than the titers for the placebo cows ($P < 0.0001$). In FIG. 1D, symbols represent the ratio IgG2/IgG1 for each cow. Horizontal lines represent the medians. The different letters show statistical differences. ***, $P < 0.001$.

[0052] **FIG. 2.** shows antigen dependent proliferation of blood CD4⁺ cells from the vaccinated cows (9) and placebo cows (10) four weeks after the second immunization for each antigen. Each symbol represents the percentage of CD4⁺ cells that have proliferated for each cow after a week of incubation with the positive control (ConA) or each antigen, namely SACOL0029, SACOL0442, SACOL0720, SACOL1867, SACOL1912, and SACOL2385. Open circles (○) represent data for the vaccinated cows, black squares (■) represent data for the placebo cows. Horizontal lines represent the medians: dashed lines represent the medians for the vaccinated cows while continuous lines represent the medians for the placebo cows. Statistical analysis: Mixed procedure of SAS. The symbol * shows the statistical differences between the vaccinated and the placebo groups for antigens SACOL0029, SACOL0442, SACOL0720 and SACOL1912 (*, $P < 0.05$). In addition, the proliferation of CD8⁺ cells was similar for the vaccinated and placebo cows for all antigens with the exception of the antigen SACOL0720 for which higher proliferation of the CD8⁺ cells was observed for the vaccinated cows (data not shown).

[0053] **FIG. 3.** shows experimental *S. aureus* intramammary infections in dairy cows. Four weeks and 4 days after the second immunization, 63 Colony Forming Unit (CFU) of *S. aureus* were infused into 3 of the 4 quarters of the vaccinated (9) and placebo cows (10) at the evening milking (day 1, arrow in FIG. 3). Aseptic milk samples were taken at morning milking and Somatic Cell Counts (SCC) were determined by Valacta (Ste-Anne-

de-Bellevue, QC). Open circles (○) and the dashed line represent data for the vaccinated cows, while the black squares (■) and the continuous line represent data for the placebo cows. Each open circle represents the mean of SCC for all the infected quarters of the vaccinated cows (27) while each square represents the mean of SCC for all the infected quarters of the placebo cows (30 quarters). Over the challenge period, somatic cell counts in milk were found to be significantly lower for the vaccinated cows than for the placebo cows (***; $P < 0.001$).

[0054] FIGs. 4A-C. FIG. 4A shows the correlation between CFU and the SCC for each cow, and FIG. 4B shows the correlation between serum IgG1 titer against SACOL0442 and SCC for each cow. Each symbol represents data for one cow. In FIG. 4A, it represents the mean of SCC and CFU for the 3 infected quarters from the beginning to the end of the infection. In FIG. 4B, it represents the mean of SCC for the 3 infected quarters from the beginning to the end of the infection and the serum IgG1 titer against SACOL0442 four weeks after the second immunization and just before the experimental infection. Open circles represent data for the vaccinated cows and black squares represent data for the placebo cows. There is a strong correlation between the SCC/ml and the CFU/ml and a negative correlation between the SCC and the IgG1 titer against SACOL0442. In FIG. 4C, the correlation between SCC or CFU relative to milk IgG2 titer against SACOL0029 is shown for each cow ten days after experimental infection (6 weeks after the second immunization). Each symbol represents data for one cow ten days after the experimental infection. Aseptic milk samples were taken at morning milking and the viable counts of *S. aureus* were determined by 10-fold dilutions and plating on tryptic soy agar (TSA) plates while SCC were determined by Valacta (Ste-Anne-de-Bellevue, QC). SCC and CFU data for each cow is the mean of the data for the 3 infected quarters ten days after the experimental infection. Milk samples for the determination of milk IgG2 titers are the mix of an equivalent volume of milk from the 4 quarters of each cow 10 days after the experimental infection (6 weeks after the second immunization). Black squares (■) represent data for the placebo cows, open circles (○) represent data for the vaccinated cows.

[0055] FIG. 5. shows serum total IgG titers for the vaccinated cows for each antigen of a vaccine comprising the fused antigens SACOL0029 and SACOL1867 (shown as SACOL0029-1867) and the antigens SACOL0442 and SACOL0720. In the ELISA, the targeted antigens were SACOL0029-1867, SACOL0029, SACOL1867, SACOL0442 and SACOL0720. Each open circle represents the titer four weeks after the second immunization for each of the 11 cows whereas each black diamond represents the preimmune titer. Horizontal lines represent the medians: solid line for the preimmune sera, dotted line for the samples taken four weeks after immunization. Titers for the vaccinated cows are higher than the titers of the preimmune sera (**, $P < 0.01$; ***, $P < 0.001$ for the other antigens tested).

[0056] FIG. 6 shows serum total IgG titers against the SACOL1867 antigen of mice immunised with the fusion protein (SACOL0029-1867; fusion), a combination of the separate proteins (SACOL0029 + SACOL1867; combination), the SACOL0029 protein only (0029) or SACOL1867 protein only (1867), in equivalent molar quantities. Open circles (○) represent data for preimmune titers, black squares (■) represent data for the immune titers. For the preimmune titers, preimmune sera were mixed equally between the 5 mice of each immunization group to obtain a preimmune pool titer, represented by one open circle per group. For the immune titers, each

square symbol represents the titer for one mouse. Horizontal lines represent the medians: black lines represent the medians for the immune serums while dashed lines (and the open circle) represent the medians for the preimmune serums pool. Titers for the vaccinated mice in the fusion, combination and 1867 groups are higher than the titers for the preimmune mice ($P < 0.001$), and the titers of the mice that received SACOL0029 monovalent antigen only were not found to be significantly different from the titers of the preimmune pool against SACOL1867. Statistical significance between immune titers of fusion group versus the combination and the two monovalent vaccines groups is shown (***: $P < 0.001$).

[0057] **FIG. 7.** Serum total IgG (as measured by O.D. 450 nm in the ELISA assay) directed against a B-cell epitope sequence **KDGGKYTLESHKELQ** (SEQ ID NO: 1) contained in a fragment of the amino acid sequence of SACOL0442 (GEHLPKGNIVINTKDGGKYTLESHKELQKDRENVKINTAD, SEQ ID NO: 2), and obtained from mice immunized with either a fusion of peptides encoded from SACOL0442 and SACOL0720 **KDGGKYTLESHKELQEAAAKEAAAKDINKIYFMTDVLGGPTFVLND** (SEQ ID NO: 3) (Group 1) or the peptide **KDGGKYTLESHKELQ** (SEQ ID NO: 1) encoded from SACOL0442 (Group 2). Each group was composed of 4 animals ($n = 4$) that were injected two times with equimolar amounts of the sequence **KDGGKYTLESHKELQ** (SEQ ID NO: 1) (corresponding to 100 μg of **KDGGKYTLESHKELQEAAAKEAAAKDINKIYFMTDVLGGPTFVLND** (SEQ ID NO: 3) for Group 1 and 31.25 μg of **KDGGKYTLESHKELQ** (SEQ ID NO: 1) for Group 2) at a 2-week interval, and sera were prepared from blood harvested one week after the last injection. The ELISA assay was carried out with serum samples diluted 100 000 times and a fragment from SACOL0442 (GEHLPKGNIVINTKDGGKYTLESHKELQKDRENVKINTAD, (SEQ ID NO: 2)) was used as the target antigen containing the peptide epitope **KDGGKYTLESHKELQ** (SEQ ID NO: 1). Individual data are expressed as circles on the graph and the medians by bars. The difference between groups was found statistically significant ($P < 0.0286$, Kuskal-Wallis test, GraphPad Prism™ 7.00).

[0058] **FIGs. 8A-B.** Deletion of *hemB* in ATCC29213 and $\Delta 720$ strains of *Staphylococcus aureus*. (FIG. 8A) The *hemB* gene in the wild-type (WT) strain ATCC29213 and its isogenic mutant $\Delta 720$ was deleted by homologous recombination and replacement with an *ermA* cassette to create the mutant strains $\Delta hemB$ and $\Delta 720\Delta hemB$, respectively. Thick lines and numbers denote the PCR-amplified regions depicted in B for parental (1) and *hemB* deleted (2) strains. (FIG. 8B) PCR products of the WT strain and its isogenic $\Delta hemB$ mutant (similar results were obtained with $\Delta 720$ and $\Delta 720\Delta hemB$ strains).

[0059] **FIGs. 9A-C.** show influence of *S. aureus* $\Delta hemB$, $\Delta 720$, and $\Delta hemB\Delta 720$ mutations on MAC-T cell infectivity. MAC-T cells were infected with each of the four strains for 3h, then were incubated with lysostaphin an additional 30 min ($t = 3h$), 12h or 24h and lysed for measurement of viable intracellular bacteria (CFU). (FIG. 9A) Relative recovery of the initial inoculum found within cells at $t = 3h$ for $\Delta 720$, and (FIG. 9B) for $\Delta hemB\Delta 720$ mutants. Results are normalized according to that obtained for ATCC 29213 (WT) or $\Delta hemB$, respectively, and are expressed as means with SD (**, $P \leq 0.01$; ***, $P \leq 0.001$; unpaired t test). (FIG. 9C) Means and SD of intracellular CFUs for WT and mutants at 12h (left) and 24h (right). A two-way ANOVA and Tukey's multiple comparisons test was used (*: $P \leq 0.05$; ***, $P \leq 0.001$). All values indicate the mean of three independent experiments, each performed in triplicate.

[0060] FIG. 10. shows persistence of *S. aureus* ATCC 29213 (WT) and isogenic mutants within MAC-T cells over time. MAC-T cells were infected with each of the four strains for 3h, then were incubated with lysostaphin an additional 30 min, 12h or 24h and lysed for measurement of intracellular bacteria (CFU). Intracellular bacterial CFUs are expressed as the percentage of the initial inoculum after being transformed in base 10 logarithmic values (Log₁₀ CFU/ml). Values indicate the mean of three independent triplicate experiments with standard deviations.

[0061] FIGs. 11A-B. shows viability of MAC-T cells infected by *S. aureus* ATCC 29213 (WT) and isogenic mutants. MAC-T cells were infected with each of the four strains for 3h, then were incubated with lysostaphin for 12 h (FIG. 11A) or 24 h (FIG. 11B). MTT viability assays were then performed with a method described in Kubica et al., 2008. The results are reported as percent viability relative to uninfected cells and are expressed as the mean with SD of three independent experiments done in triplicate. Statistical significance with (Φ) symbol are compared to the WT (Two-way ANOVA and Tukey's multiple comparisons test: * or Φ: $P \leq 0.05$; **: $P \leq 0.01$; ***: $P \leq 0.001$; ΦΦΦΦ: $P \leq 0.0001$).

[0062] FIG. 12. Shows murine IMIs with the parental (WT) and $\Delta hemBA720$ ($\Delta\Delta$) strains. Mice were infected as previously described and glands harvested at the indicated hour (h) or day (D) after infection. Each column represents the median value of bacterial CFU counts for a group of glands, and ranges are indicated by bars. A minimum of six glands per group were used excepted for the WT strain at D7 (2 glands: only one mouse survived). Mortality of mice at specific time points is indicated by arrows. The asterisk indicates the clearance of $\Delta hemBA720$ from glands (below the detection limit of 10 CFU/gland).

[0063] FIG. 13. Double mutant ($\Delta 720\Delta hemB$) stimulates neutrophil influx in mammary glands to similar levels compared to WT in the first 24 hours following infection. Mice were infected as described in materials and methods, and a control group (PBS) of mice received a sterile PBS injection. Glands were harvested at indicated times, homogenized and kinetically assayed for MPO activity as described in materials and methods. Each dot represents MPO Units for one gland, which is shown as raw values adjusted by gram of gland. Means are represented by thick lines.

[0064] FIG. 14. Visual Inflammation of the large R4 and L4 mammary glands 24 h after mouse IMI with *S. aureus* ATCC 29213 (WT) and the double mutant $\Delta 720\Delta hemB$ ($\Delta\Delta$). Mice were infected as described in materials and methods, and control group (PBS) mice received a sterile PBS injection. Pictures show glands that were harvested after 24 h. In each panel, the R4 (left) and L4 (right) glands are shown.

[0065] FIG. 15A. Neutrophil infiltration goes back to normal levels after clearance of the double mutant $\Delta 720\Delta hemB$. Mice were infected as described in materials and methods, and a control group (PBS) of mice received a sterile PBS injection. Glands were harvested at the indicated times, homogenized and kinetically assayed for MPO activity as described in materials and methods. Columns represent means of MPO Units of a group of 6 glands (4 for the PBS control) adjusted by gram of gland, and error bars illustrate standard deviation. Statistical significance between the Day 4 and 12 groups post infection is shown by (Φ) symbol. One-Way ANOVA and Tukey's multiple comparison tests were used (ΦΦ: $P \leq 0.01$; NS: No significant difference between

groups).

[0066] FIGs. 15B-C. Immunization of mice with the live-attenuated double mutant ($\Delta 720\Delta hemB$) stimulates a strong humoral response against *S. aureus* bovine mastitis isolates of commonly found *spa* types. Mice were immunized as previously described: serums were collected before priming immunization (Preimmune) and ten days after the boost immunization (Immune). FIG. 15B. IgG titers rise with increasing doses of the live-attenuated strain $\Delta 720G\Delta hemB$: each dot represents the total IgG titer of one mouse against a $\Delta 720G\Delta hemB$ whole cell extract. Medians are represented by thick lines for Immune titers and dashed lines for Preimmune titers. Titers were compared to their corresponding preimmune titers (Two-way ANOVA and Tukey's multiple comparisons test: ****; $P \leq 0.0001$). FIG. 15C. Immunization with the live-attenuated mutant $\Delta 720G\Delta hemB$ confers IgG titers against components that are shared by mastitis strains of commonly found *spa* types. Each dot represents the total IgG titer of one mouse against the whole cell extract of the indicated strain. Medians are represented by thick lines for Immune titers and dashed lines for Preimmune titers. All immune titers were compared to their corresponding preimmune titer ($P \leq 0.0001$) and between clinical strains (Two-way ANOVA and Sidak's multiple comparisons test: NS: no significant difference).

[0067] FIG. 16. shows total serum IgG titers against SACOL0029-1867 fusion protein of mice immunised with the protein mix (composed of 5 μ g of the antigens SACOL0029, SACOL0442, SACOL0720, and the SACOL0029-1867 fusion), 10^5 CFU of the attenuated live strain $\Delta 720\Delta hemB$ alone or a combination of the protein mix and the $\Delta 720\Delta hemB$ strain. Open circles ($\circ$) represent data for preimmune titers, black squares ($\blacksquare$) represent data for the immune titers. Each symbol represents the titer for one mouse. Horizontal lines represent the medians: black lines represent the medians for the immune serums while dashed lines represent the medians for the preimmune serums. Titers for the vaccinated mice in the protein mix group and combination group are higher than the titers for the preimmune mice ($P < 0.001$). Statistical significance between immune titers of combination versus the two other vaccinated mice groups is shown (**; $P < 0.01$).

[0068] FIG. 17. shows total serum IgG titers against SACOL0029 of mice immunised with the protein mix (composed of 5 μ g of the antigens SACOL0029, SACOL0442, SACOL0720, and the SACOL0029-1867 fusion), 10^5 CFU of the attenuated live strain $\Delta 720\Delta hemB$ alone or a combination of the protein mix and the $\Delta 720\Delta hemB$ strain. Open circles ($\circ$) represent data for preimmune titers, black squares ($\blacksquare$) represent data for the immune titers. Each symbol represents the total IgG titer for one mouse. Horizontal lines represent the medians: black lines represent the medians for the immune serums while dashed lines represent the medians for the preimmune serums. Statistical significance between immune and preimmune titers of the three mice groups is shown (**; $P < 0.01$).

[0069] FIG. 18. shows total serum IgG titers against the staphylococcal surface protein ClfA for mice immunised with the SACOL0029, SACOL0442, SACOL0720, and SACOL0029-1867 protein mix, 10^5 CFU of the attenuated live strain $\Delta 720\Delta hemB$ alone or a combination of the protein mix and $\Delta 720\Delta hemB$. Open circles ($\circ$) represent data for preimmune titers, black squares ($\blacksquare$) represent data for the immune titers. Each symbol represents the titer for one mouse. Horizontal lines represent the medians: black lines represent the medians for the immune serums while dashed lines represent the medians for the preimmune serums. Statistical significance

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between preimmune titers and immune titers is shown (*: $P < 0.05$).

[0070] **FIG. 19.** below shows serum ratio of IgG2a/IgG1 titers against the SACOL0029-1867 fusion polypeptide for mice immunised with the protein mix, or the combination of the protein mix and the attenuated $\Delta 720\Delta hemB$ live strain.

[0071] **FIG. 20.** shows serum ratios against the SACOL0029 antigen. Open squares ($\square$) represent data for preimmune titers, black squares ($\blacksquare$) represent data for the immune titers. Each symbol represents the titer ratio for one mouse. Horizontal lines represent the medians. Statistical significance between the protein mix group versus combination group ratios is shown (*: $P < 0.05$; **: $P < 0.01$).

[0072] **FIGs. 21A-J.** I. SACOL0029 polynucleotides (full length sequence SEQ ID NO: 4) and polypeptides (full length, fragment(s) and variant(s) sequences SEQ ID NOs: 5 to 9). Selected epitopes are shown shaded and/or bolded; II. SACOL0720 polynucleotides (full length sequence SEQ ID NO: 10) and polypeptides (full length, fragments and variant(s) sequences SEQ ID NOs: 11 to 27). Selected epitopes are shown shaded; III. SACOL0442 polynucleotides (full length sequence SEQ ID NO: 28) and polypeptides (full length, fragments and variant(s) sequences SEQ ID NOs: 29 to 36 and 1). Selected epitopes are shown shaded; IV. SACOL1867 polynucleotides (full length sequence SEQ ID NO: 37) and polypeptides (full length, fragment(s) and variant(s) sequences SEQ ID NOs: 38 to 41). Selected epitopes are shown shaded. Predicted transmembrane (<http://www.enzim.hu/hmmtop/html/submit.html>) domain shown bolded; V. SACOL1912 polynucleotide (full length sequence SEQ ID NO: 42) and polypeptides (full length and variant(s) sequences SEQ ID NOs: 43 to 44). Selected epitopes are shown shaded (see e.g., SEQ ID NOs: 45-48); VI. SACOL2385 polynucleotide (full length SEQ ID NO: 49) and polypeptides (full length and variant(s) sequences SEQ ID NOs: 50 to 51). Selected epitopes are shown shaded (see e.g., SEQ ID NOs: 52-53); VII. Fusions: (i) SACOL0029-1867 fusion polynucleotide sequences (SEQ ID NOs: 54 and 56) and polypeptide sequences (SEQ ID NOs: 55, 57-58). In the polynucleotide and polypeptide sequences, the double underlined sequence, if any, is that of the polyhistidine, the italicized sequence is the sequence of the SACOL0029 fragment, the single underlined sequence is the sequence of the linker and the bolded sequence is the sequence of the SACOL1867 fragment; (ii) SACOL0720-720 fusion polypeptide sequence (SEQ ID NO: 27). In the polypeptide sequence, the double underlined sequence, if any, is that of the polyhistidine, the italicized sequences are the sequences of the SACOL0720 fragments and the single underlined sequence is the sequence of the linker; (iii) SACOL0442-720 fusion polypeptide sequence (SEQ ID NO: 3). In the polynucleotide and polypeptide sequences, the double underlined sequence, if any, is that of the polyhistidine, the italicized sequence is the sequence of the SACOL0442 fragment, the single underlined sequence is the sequence of the linker and the bolded sequence is the sequence of the SACOL0720 fragment; and VIII. Sequences of linkers (SEQ ID NOs: 59 to 70).

[0073] **FIGs. 22A-D.** I. Multiple polynucleotide sequences (SEQ ID NOs: 71-72, 28, 73 to 81) alignment for full length SACOL0442 and orthologues; II. Multiple polypeptide sequences (SEQ ID NOs: 29 and 82 to 92) alignment for full length SACOL0442, orthologues and consensus sequences derived therefrom are presented. In these sequences, "***" denotes that the residues in that column are identical in all sequences of the alignment, "*" denotes that conserved substitutions have been observed, and "." denotes that semi-conserved substitutions

have been observed. Consensus sequences derived from these alignments are also presented wherein X is any amino acid. In the polypeptide sequences, selected epitopes are shown shaded (see e.g., SEQ ID NOs: 1, 34, 93-97).

[0074] FIGs. 23A-K I. Multiple polynucleotide sequences (SEQ ID NOs: 98 to 104, 10, and 105 to 108) alignment for full length SACOL0720 and orthologues; II. Multiple polypeptide sequences (SEQ ID NOs: 11 and 109 to 120) alignment for full length SACOL0720, orthologues. and consensus sequences derived therefrom are presented. In these sequences, "*" denotes that the residues in that column are identical in all sequences of the alignment, ":" denotes that conserved substitutions have been observed, and "." denotes that semi-conserved substitutions have been observed. Consensus sequences derived from these alignments are also presented wherein X is any amino acid. In the polypeptide sequences, selected epitopes are shown shaded (see e.g., SEQ ID NOs: 22, 19 and 21).

[0075] FIG. 24 Multiple polypeptide sequences (SEQ ID NOs: 5 and 121 to 131) alignment for full length SACOL0029, orthologues. and consensus sequences derived therefrom are presented. In these sequences, "*" denotes that the residues in that column are identical in all sequences of the alignment, ":" denotes that conserved substitutions have been observed, and "." denotes that semi-conserved substitutions have been observed. Consensus sequences derived from these alignments are also presented wherein X is any amino acid. In the polypeptide sequences, selected epitopes are shown shaded (see e.g., SEQ ID NOs: 132-139). Bolded epitope identified by BCPred™. Shaded epitopes identified by AAp predictions.

[0076] FIGs. 25A-D. I-Multiple polynucleotide sequences (SEQ ID NOs: 140 to 151) alignment for full length SACOL1867 and orthologues; II- Multiple polypeptide sequences (SEQ ID NOs: 152 to 164) alignment for full length SACOL1867, orthologues. and consensus sequences derived therefrom are presented. In these sequences, "*" denotes that the residues in that column are identical in all sequences of the alignment, ":" denotes that conserved substitutions have been observed, and "." denotes that semi-conserved substitutions have been observed. Consensus sequences derived from these alignments are also presented wherein X is any amino acid. In the polypeptide sequences, selected epitopes are shown shaded (see e.g., SEQ ID NOs: 165-180) and the end of the signal peptide domain and/or transmembrane domain is marked with a line (separates signal peptide and/or transmembrane domain from secreted form).

[0077] FIG. 26. I - polynucleotide sequence (SEQ ID NO: 181) for full length SACOL1715 (*hemB*); and II-amino acid sequence (SEQ ID NO: 182) for full length SACOL1715 (*hemB*).

[0078] FIG. 27. I - polynucleotide sequence (SEQ ID NO: 183) for full length ClfA (NWMN_0756, newman); and II-amino acid sequence (SEQ ID NO: 184) for full length ClfA.

DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

[0079] The present invention showed that a fusion of two antigens created an unexpected synergy in the immune response.

[0080] In addition, the present invention also stabilized the SCV phenotype of a *Staphylococcus* via *hemB*

(complete deletion thus impairing the possibility of reversion to an invasive phenotype (Tuchscher, 2011)) enabling its use as a vaccine delivery system. HemB is coding for the HemB protein/monomer, which combines to create the porphobilinogen synthase or aminolevulinate dehydratase enzyme [EC 4.2.1.24]. In addition, further attenuation was brought about by inactivation of an antigen of the present invention, namely gene SACOL0720, which has been previously shown to be important for *S. aureus* in cationic peptide resistance (Falord, 2012; Kawada-Matsuo, 2011; Meehl, 2007) and *in vivo* during IMI (Allard, 2013). Hence, this attenuated double mutant strain expressing constructs of the present invention is usable for immunization and protection against IMIs.

General Definitions

[0081] Headings, and other identifiers, e.g., (a), (b), (i), (ii), etc., are presented merely for ease of reading the specification and claims. The use of headings or other identifiers in the specification or claims does not necessarily require the steps or elements be performed in alphabetical or numerical order or the order in which they are presented.

[0082] In the present description, a number of terms are extensively utilized. In order to provide a clear and consistent understanding of the specification and claims, including the scope to be given such terms, the following definitions are provided.

[0083] The use of the word "a" or "an" when used in conjunction with the term "comprising" in the claims and/or the specification may mean "one" but it is also consistent with the meaning of "one or more", "at least one", and "one or more than one".

[0084] Throughout this application, the term "about" is used to indicate that a value includes the standard deviation of error for the device or method being employed to determine the value. In general, the terminology "about" is meant to designate a possible variation of up to 10%. Therefore, a variation of 1, 2, 3, 4, 5, 6, 7, 8, 9 and 10% of a value is included in the term "about". Unless indicated otherwise, use of the term "about" before a range applies to both ends of the range.

[0085] As used in this specification and claim(s), the words "comprising" (and any form of comprising, such as "comprise" and "comprises"), "having" (and any form of having, such as "have" and "has"), "including" (and any form of including, such as "includes" and "include") or "containing" (and any form of containing, such as "contains" and "contain") are inclusive or open-ended and do not exclude additional, un-recited elements or method steps.

[0086] As used herein, the term "consists of" or "consisting of" means including only the elements, steps, or ingredients specifically recited in the particular claimed embodiment or claim.

Polypeptides, nucleic acids and delivery systems

[0087] As used herein, the term "vaccine" refers to any compound/agent ("vaccine component"), or combinations thereof, capable of inducing/eliciting an immune response in a host and which permits to treat and/or prevent an infection and/or a disease. Therefore, non-limiting examples of such agent include proteins, polypeptides, protein/polypeptide fragments, immunogens, antigens, peptide epitopes, epitopes, mixtures of proteins, peptides or epitopes as well as nucleic acids, genes or portions of genes (encoding a polypeptide or

protein of interest or a fragment thereof) added separately or in a contiguous sequence such as in nucleic acid vaccines, and the like.

[0088] In an aspect of the present invention, there is provided a fusion construct of formula I:

[0089] X-A-linker-B-Z (formula (I)),

[0090] Wherein A and B are identical or different and are each independently an antigenic polypeptide (i.e. native, fragment or variant thereof) of the present invention.

[0091] In a specific embodiment, A and/or B is (a) a polypeptide comprising a SACOL0029 polypeptide as set forth in any one of the sequences depicted in FIG. 24 (SEQ ID NOs: 5 and 121 to 131), a SACOL0264 polypeptide (SEQ ID NO : 185), a SACOL0442 polypeptide as set forth in any one of the sequences depicted in FIG. 22D (SEQ ID NOs: 29 and 82 to 92), a SACOL0718 polypeptide (SEQ ID NO : 186), a SACOL0720 polypeptide as set forth in any one of the sequences depicted in FIGs. 23I-J (SEQ ID NOs: 11 and 109 to 120), a SACOL1353 polypeptide (SEQ ID NO : 187), a SACOL1416 polypeptide (SEQ ID NO : 188), SACOL1611 (SEQ ID NO : 189), a SACOL1867 polypeptide as set forth in any one of the sequences depicted in FIG. 25D (SEQ ID NOs: 152 to 164), a SACOL1912 polypeptide as set forth in FIG. 21G-V (SEQ ID NO : 43), SACOL1944 (SEQ ID NO : 190), a SACOL2144 polypeptide (SEQ ID NO : 191), a SACOL2365 polypeptide (SEQ ID NO : 192), a SACOL2385 polypeptide as set forth in VI on FIG. 21H (SEQ ID NO : 50) or a SACOL2599 polypeptide (SEQ ID NO : 193). In a specific embodiment, the above polypeptide (a) is the secreted or extracellular fragment of the polypeptide defined above. Transmembrane domains can be predicted using, for example, the software TMpred™ (ExPASy) http://www.ch.embnet.org/software/TMPRED_form.html, <http://www.psort.org/psortb/index.html> <http://www.enzim.hu/hmmtop/html/submit.html> and/or SignalP 4.1 (<http://www.cbs.dtu.dk/services/SignalP>). TMpred™ and SignalP 4.1 predicted extracellular domain for: SACOL0720: AA 310-508; SACOL0442 AA 36 to 203. Enzim predicted a transmembrane domain SACOL1867 (1-40) so that extracellular domain was: AA 41-239 while <http://www.psort.org/psortb/index.html> predicted that SACOL1867 was an extracellular protein. Since the above-mentioned transmembrane and/or signal peptide domains are putative, the present invention encompasses cases where the antigens presented herein (e.g., SACOL1867) have or not a signal peptide and/or transmembrane domain and encompasses the corresponding extracellular fragments. In an embodiment, the above-mentioned polypeptide is a polypeptide normally secreted or expressed at the surface of the bacteria (e.g., *Staphylococcus aureus*).

[0092] The Genbank™ accession numbers for *S. aureus* genes listed herein and their encoded antigenic polypeptides encompassed by the present invention are depicted in Table I below:

Table I: Genbank™ accession numbers for the IMI-associated *S. aureus* genes and encoded polypeptides described herein

Gene name	GenBank™ Gene ID No.	GenBank™ protein No.
SACOL0029	3236748	YP_184940.1

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		(SEQ ID NO: 5)
SACOL0100	3236858	YP_185004.1
SACOL0101	3236840	YP_185005.1
SACOL0105	3236844	YP_185009.1
SACOL0148	3236734	YP_185048.1
SACOL0154	3238707	YP_185054.1
SACOL0204	3236774	YP_185103.1
SACOL0205	3236775	YP_185104.1
SACOL0264	3236683	YP_185159.1 WP_000570071 (SEQ ID NO: 185)
SACOL0442	3236485	YP_185332.1 (SEQ ID NO: 29)
SACOL0461	3236475	YP_185351.1
SACOL0608	3236353	YP_185493.1
SACOL0660	3238251	YP_185544.1
SACOL0688	3236721	YP_185570.1
SACOL0690	3236723	YP_185572.1
SACOL0704	3236241	YP_185586.1
SACOL0718	3236599	YP_185600.1 WP_000985996 (SEQ ID NO: 186)
SACOL0720	3236600	YP_185601.1 (SEQ ID NO: 11)
SACOL0829	3238649	YP_185703.1
SACOL1054	3236163	YP_185919.1
SACOL1142	3236098	YP_186005.1
SACOL1145	3237661	YP_186008.1

SACOL1320	3236394	YP_186175.1
SACOL1353	3236077	YP_186206.1 WP_000603968 (SEQ ID NO: 187)
SACOL1416	3236563	YP_186268.1 WP_000548932 (SEQ ID NO: 188)
SACOL1611	3236575	YP_186451.1 WP_001095260 (SEQ ID NO: 189)
SACOL1637	3238018	YP_186477.1
SACOL1680	3238476	YP_186520.1
SACOL1781	3236594	YP_186614.1
SACOL1812	3238705	YP_186645.1
SACOL1867	3236101	YP_186695.1 (SEQ ID NO: 38)
SACOL1912	3236086	YP_186737.1 (SEQ ID NO: 43)
SACOL1944	3237515	YP_186769.1 WP_000149064 (SEQ ID NO: 190)
SACOL2092	3238693	YP_186907.1
SACOL2144	3237436	YP_186957.1 WP_000908177 (SEQ ID NO: 191)
SACOL2169	3237416	YP_186981.1
SACOL2171	3237418	YP_186983.1
SACOL2321	3238070	YP_187128.1

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SACOL2325	3238483	YP_187132.1
SACOL2342	3235997	YP_187148.1
SACOL2365	3238203	YP_187170.1 WP_000827000 (SEQ ID NO: 192)
SACOL2379	3237628	YP_187183.1
SACOL2385	3238646	YP_187189.1 (SEQ ID NO: 50)
SACOL2599	3237186	YP_187390.1 AAW38600 (SEQ ID NO: 193)

[0093] Consensuses derived from the alignments of certain the above listed polypeptides are presented in FIGs. 21-25. In specific embodiment of these consensuses, each X in the consensus sequences (e.g., consensuses in FIGs. 21-25) is defined as being any amino acid, or absent when this position is absent in one or more of the orthologues presented in the alignment. In specific embodiment of these consensuses, each X in the consensus sequences is defined as being any amino acid that constitutes a conserved or semi-conserved substitution of any of the amino acid in the corresponding position in the orthologues presented in the alignment, or absent when this position is absent in one or more of the orthologues presented in the alignment. In FIGs. 21-25, conservative substitutions are denoted by the symbol “.” and semi-conservative substitutions are denoted by the symbol “.”. In another embodiment, each X refers to any amino acid belonging to the same class as any of the amino acid residues in the corresponding position in the orthologues presented in the alignment, or absent when this position is absent in one or more of the orthologues presented in the alignment. In another embodiment, each X refers to any amino acid in the corresponding position of the orthologues presented in the alignment, or absent when this position is absent in one or more of the orthologues presented in the alignment. In a specific embodiment, A and/or B is a polypeptide satisfying any one of these consensuses or a fragment thereof.

[0094] Conservative amino acid mutation may include addition, deletion, or substitution of an amino acid; a conservative amino acid substitution is defined herein as the substitution of an amino acid residue for another amino acid residue with similar chemical properties (e.g., size, charge, or polarity). Such a conservative amino acid substitution may be a basic, neutral, hydrophobic, or acidic amino acid for another of the same group (see e.g., Table II below). By the term “basic amino acid” it is meant hydrophilic amino acids having a side chain pK value of greater than 7, which are typically positively charged at physiological pH. Basic amino

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acids include histidine (His or H), arginine (Arg or R), and lysine (Lys or K). By the term "neutral amino acid" (also "polar amino acid"), it is meant hydrophilic amino acids having a side chain that is uncharged at physiological pH, but which has at least one bond in which the pair of electrons shared in common by two atoms is held more closely by one of the atoms. Polar amino acids include serine (Ser or S), threonine (Thr or T), cysteine (Cys or C), tyrosine (Tyr or Y), asparagine (Asn or N), and glutamine (Gln or Q). The term "hydrophobic amino acid" (also "non-polar amino acid") is meant to include amino acids exhibiting a hydrophobicity of greater than zero according to the normalized consensus hydrophobicity scale of Eisenberg (1984). Hydrophobic amino acids include proline (Pro or P), isoleucine (Ile or I), phenylalanine (Phe or F), valine (Val or V), leucine (Leu or L), tryptophan (Trp or W), methionine (Met or M), alanine (Ala or A), and glycine (Gly or G). "Acidic amino acid" refers to hydrophilic amino acids having a side chain pK value of less than 7, which are typically negatively charged at physiological pH. Acidic amino acids include glutamate (Glu or E), and aspartate (Asp or D).

[0095] A semi-conserved amino acid replaces one residue with another one that has similar steric conformation, but does not share chemical properties. Examples of semi-conservative substitutions would include substituting cysteine for alanine or leucine; substituting serine for asparagine; substituting valine for threonine; or substituting proline for alanine.

[0096] The Table II below indicates which amino acid belongs to each amino acid class.

Class	Name of the amino acids
Aliphatic	Glycine, Alanine, Valine, Leucine, Isoleucine
Hydroxyl or Sulfur/Selenium-containing	Serine, Cysteine, Selenocysteine, Threonine, Methionine
Cyclic	Proline
Aromatic	Phenylalanine, Tyrosine, Tryptophan
Basic	Histidine, Lysine, Arginine
Acidic and their Amide	Aspartate, Glutamate, Asparagine, Glutamine

[0097] The similarity and identity between amino acid or nucleotide sequences can be determined by comparing each position in the aligned sequences. Optimal alignment of sequences for comparisons of similarity and/or identity may be conducted using a variety of algorithms, for example using a multiple sequence alignment program/software well known in the art such as ClustalW™, SAGA™, UGENE™ or T-coffee™. Examples of multiple sequence alignments are described in the examples below and depicted in FIGs. 21A to 25.

Gene operon

[0098] In another embodiment, A and/or B is (b) a polypeptide encoded by a gene from a same operon as a gene encoding the polypeptide of (a) as defined above. For example, SACOL0718 is a gene from the same operon as SACOL0720.

Fragment

[0099] In another embodiment, A and/or B is (c) a polypeptide comprising an immunogenic fragment of at least 13 consecutive amino acids of (a) or (b) as defined above.

[00100] An immunogenic fragment of a protein/polypeptide is defined as a part of a protein/polypeptide which is capable of inducing/eliciting an immune response in a host. In an embodiment, the immunogenic fragment is capable of eliciting the same immune response in kind, albeit not necessarily in amount, as the protein/polypeptide. An immunogenic fragment of a protein/polypeptide preferably comprises one or more epitopes of said protein/polypeptide. An epitope of a protein/polypeptide is defined as a fragment of said protein/polypeptide of at least about 4 or 5 amino acids in length, capable of eliciting a specific antibody and/or an immune cell (e.g., a T cell or B cell) bearing a receptor capable of specifically binding said epitope. Two different kinds of epitopes exist: linear epitopes and conformational epitopes. A linear epitope comprises a stretch of consecutive amino acids. A conformational epitope is typically formed by several stretches of consecutive amino acids that are folded in position and together form an epitope in a properly folded protein. An immunogenic fragment as used herein refers to either one, or both, of said types of epitopes. In an embodiment where immunogenic fragments are used alone (i.e. not fused in a larger polypeptide construct (e.g., fusion with other antigenic fragment)), the immunogenic fragment of a protein/polypeptide comprises at least 16 amino acid residues. In a further embodiment, the immunogenic fragment comprises at least 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, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, or 160 consecutive amino acids of the native protein/polypeptide. In a specific embodiment, the fragment has at least 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, or 50 or more consecutive amino acids of the native protein/polypeptide. In an embodiment where the at least one immunogenic fragment forms part of a larger polypeptide construct (e.g., fusion with other antigenic polypeptide, fragment or variant thereof), the immunogenic fragment comprises at least 13 consecutive amino acid residues of the polypeptide. Without being so limited, fragments encompassed by the present invention comprise immunogenic fragments of at least 13 consecutive amino acids of SACOL029 as shown in FIG. 21 (and corresponding fragments in SACOL029 orthologues (e.g., depicted in FIG. 24); of SACOL0442 as shown in FIG. 21 (and corresponding fragments in SACOL0442 orthologues (e.g., depicted in FIG. 22); of SACOL0720 as shown in FIG. 21, (and corresponding fragments in SACOL0720 orthologues (e.g., depicted in FIG. 23); and of SACOL1867 as shown in FIG. 21 (and corresponding fragments in SACOL1867 orthologues (e.g., depicted in FIG. 25). In another embodiment, fragments encompassed by the present invention include immunogenic fragments comprising at least one epitope of antigenic proteins/polypeptides of the present invention (polypeptide (a) defined above). In another embodiment, fragments encompassed by the present invention include immunogenic fragments comprising at least one epitope as depicted (shaded) in any one of the antigenic proteins/polypeptides depicted in any one of FIGs. 21 to 25. Without being so limited, epitopes in a sequence may be predicted with softwares such as BCPred™, AAP™, FBCPred™ and ABCPred™.

[00101] In an embodiment, the above-mentioned immunogenic fragment comprises a sequence that is conserved (i.e. identical) in at least two different strains of *Staphylococcus aureus*. In further embodiments, the

above-mentioned immunogenic fragment comprises a sequence that is conserved (i.e. identical) in at least 3, 4, 5, 6, 7, 8, 9 or 10 different strains of *Staphylococcus aureus*. In another embodiment, the above-mentioned strains of *Staphylococcus aureus* are COL, RF122, NCTC 8325, JH1, JH9, Newman, Mu3, Mu50, USA300-FPR3757, N315, MW2 or MSSA476. In an embodiment, the above-mentioned strains of *Staphylococcus aureus* are associated with bovine mastitis (e.g., RF122).

Variants

[00102] In another embodiment, the above-mentioned polypeptide, or a polypeptide substantially identical to said polypeptide, is expressed in at least two different strains of *Staphylococcus aureus*. Substantially identical as used herein refers to polypeptides having at least 60% of identity, in embodiments at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% of identity in their amino acid sequences. In further embodiments, the polypeptides have at least 60%, 65%, 70%, 71%, 72%, 73%, 74%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% of identity in their amino acid sequences with other polypeptides to which they are compared.

[00103] In another embodiment, A and/or B is (d) a polypeptide comprising an amino acid sequence at least 60% identical overall to the sequence of the polypeptide of any one of (a) to (c) defined above. In other embodiments, the amino acid is at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to (a) (e.g., over their full length). In further embodiments, the amino acid is at least 60%, 65%, 70%, 71%, 72%, 73%, 74%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% to (a). For example, antigens orthologues presented in alignments of FIGs. 21-25 are not identical but present a certain identity with the antigens or fragments to which they are compared. Consensuses presented in these FIGs embody such percent identities.

[00104] In another embodiment, A and/or B is (e) a polypeptide comprising an immunogenic variant comprising at least 13 consecutive amino acids of any one of (a) to (d). An immunogenic variant of a protein/polypeptide is defined as a part of a protein/polypeptide which is capable of inducing/eliciting an immune response in a host. As will be understood by the person of ordinary skill, agents (proteins/polypeptides, fragments thereof) having non-naturally occurring modifications (e.g., immunogenic variants) and which are capable of inducing an immune response specific for the unmodified agent (e.g., capable of inducing the production of antibodies capable of recognizing the unmodified agent) are also within the scope of the term "vaccine component". For example, the vaccine components of the present invention can be modified to enhance their activity, stability, and/or bioavailability, and/or to reduce their toxicity. Conservative amino acid substitutions may be made, like for example replacement of an amino acid comprising an acidic side chain by another amino acid comprising an acidic side chain, replacement of a bulky amino acid by another bulky amino acid, replacement of an amino acid comprising a basic side chain by another amino acid comprising a basic side chain, and the like. A person skilled in the art is well able to generate variants of a protein/polypeptide. This is for instance done through screening of a peptide library or by peptide changing programs. An immunogenic variant according to the invention has essentially the same immunogenic properties of said protein in kind, not necessarily in amount. An immunogenic variant of a protein/polypeptide of the invention may for instance comprise a fusion protein and/or chimeric

protein. For example, the biological function of a protein identified herein predicted to be an exotoxin, enterotoxin or superantigen (e.g., SACOL0442) could potentially interfere with the mammalian immune system and antibody production, and/or show some toxicity in the host. Although such interference was not observed when the SACOL0442 polypeptide was used in combination with for example SACOL0720 during immunization, it may be useful to modify the protein or polypeptide used for vaccination so that the biological activity of the exotoxin is decreased. For such a purpose, it is possible to inactivate the exotoxin with chemicals (e.g., formaldehyde). It is also possible to use molecular biology techniques to delete or mutate the putative region(s) involved in exotoxin activity without losing immunogenicity (Chang *et al.*, 2008). Another example is the conjugation or mixture of amino acid-based components with nucleic acids (e.g., genes or portions of genes added separately or in a contiguous sequence) carbohydrates such as those found in microbial polysaccharide capsules or biofilms. Other examples of variants include antigens described herein or fragments thereof comprising at either of their N or C terminus or inserted within their antigen sequence, an oligopeptide useful for purification (e.g., affinity purification) or useful as a spacer or linker. Examples of oligopeptides useful for affinity purification include polyhistidine tags (e.g., 6-10 histidine residues including or not RGS tags (e.g. HHHHHH, RGSHHHHHH, or RGSHHHHHGS). The his-tag may also be followed by an amino acid sequence suitable to facilitate a removal of the polyhistidine-tag using endopeptidases. The "X" and/or "Z" segments as recited in formula (I) also may comprise such oligopeptide useful for purification and/or sequence suitable to facilitate removal of such oligopeptide useful for purification.

[00105] In specific embodiments, the immunogenic fragment comprises at least one epitope of the polypeptide (a). Without being so limited, in certain embodiments, the immunogenic fragment comprises at least one epitope of the polypeptide (a) as depicted (shaded) in the sequences presented in FIGs. 21-25. In other specific embodiments, the variants are as disclosed in FIGs. 21-25.

Linker

[00106] Insertion of linkers between fusion protein domains can increase bioactivity by augmenting distance between domains alleviating potential repulsive forces between different segments (e.g., antigenic fragments) of the construct resulting in improved and/or restored protein folding. Different sequences of polypeptide linkers can be used and are known to have distinct properties, such as flexible, rigid or cleavable linkers. The present invention encompasses the use of any such linkers including any one of those listed in Chen *et. al*, Adv Drug Deliv Rev. (2013), 65(10):1357-69 for example. Examples herein provide illustrations of specific linkers that were used (i.e. GGGGSGGGGSGGGGS (SEQ ID NO: 60), ERKYK (SEQ ID NO: 61), or and EAAAKEAAK (SEQ ID NO: 62)), i.e. flexible linker structures, rich in small hydrophilic amino acids that maintain distance between the two connected domains and improve their folding.

[00107] In another specific embodiment, the Fc comprises a CH2 domain, a CH3 domain and a hinge region. In another specific embodiment, the Fc is a constant domain of an immunoglobulin selected from the group consisting of IgG-1, IgG-2, IgG-3, IgG-3 and IgG-4. In another specific embodiment, the Fc is a constant domain of an immunoglobulin IgG-1.

[00108] Linkers may be included between contiguous antigens of the fusion (e.g., 1 linker in fusion comprising

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two antigens, 2 linkers in fusions comprising three antigens, three linkers in fusions comprising four antigens, etc.). In fusions where large protein domains are used, linker may be larger and may comprise a fragment crystallizable region (Fc).

[00109] In a specific embodiment, the linker is an amino acid sequence of at least one amino acid or is absent. In a specific embodiment, the linker comprises at least three (at least 4, 5, 6, 7, 8, 9 or 10) amino acids selected from the group consisting of glycine, serine, alanine, aspartate, glutamate and lysine. In a specific embodiment, the linker is (EAAAK)_n (SEQ ID NO: 63); (GGGGS)_n (SEQ ID NO: 67); or (XPXPXP)_n (SEQ ID NO: 69) wherein x is any amino acid; wherein n is any one of 1 to 5, more specifically 1, 2, 3, 4 or 5; EAAAKEAAAK (SEQ ID NO: 62); EAAAKEAAKEAAAK (SEQ ID NO: 64); GGGGS (SEQ ID NO: 67); GGGGSGGGGS (SEQ ID NO: 68); GGGGSGGGGSGGGGS (SEQ ID NO: 60); XPXPXP (SEQ ID NO: 69), wherein x is any amino acid; XPXPXPXPXPXP (SEQ ID NO: 70), wherein x is any amino acid; ERKYK (SEQ ID NO: 61); ERKYKERKYK (SEQ ID NO: 65); ERKYKERKYKERKYK (SEQ ID NO: 66). In a more specific embodiment, the linker is GGGGSGGGGSGGGGS (SEQ ID NO: 60), ERKYK (SEQ ID NO: 61), or EAAAKEAAAK (SEQ ID NO: 62).

N and C terminal of construct

[00110] X and Z are each independently absent or an amino acid sequence of at least one amino acid. Without being so limited, they may be one or more of amino acids resulting from cloning strategy, amino acids used to facilitate purification of the construct (e.g. polyhistidine), amino acids suitable to facilitate a removal of the purification-tag using endopeptidases. In specific embodiments, where the fusion construct comprises three or more antigen polypeptides, any one of X and/or Z may also include the sequence of a further antigen (antigen C, antigen D, etc.) and, optionally that of at least one further linker. Such embodiments wherein X and/or Z comprise one or more further antigen(s) and optionally linker(s), could be more specifically illustrated as e.g., formula (II) or (III) as follows X'-C-linker₁-A-linker₂-B-Z' (II) when the fusion comprises at least 3 antigens; or X'-C-linker₁-A-linker₂-B-linker₃-D-Z' (III) when the fusion comprises at least 4 antigens. In both formula (II) and (III) X', Z', linker₁, linker₂, and, the case being, linker₃, are identical or different and are independently defined as are X, Z and linker in formula (I) defined herein.

[00111] Hence, in specific embodiments, the fusion construct comprises 2, 3, 4 or more antigen polypeptides (and, the case being further linkers). In a more specific embodiment, and without being so limited the fusion construct may be SACOL0029_SACOL0442; SACOL0029_SACOL0720; SACOL0029_SACOL1867; SACOL0029_SACOL0720_SACOL1867; SACOL0029_SACOL0720_SACOL0442; SACOL0029_SACOL0720_SACOL1867; SACOL0442_SACOL0029_SACOL0720; SACOL0442_SACOL0029_SACOL1867; SACOL0442_SACOL1867_SACOL0720; SACOL0720_SACOL0442_SACOL1867; or SACOL0029_SACOL1867_SACOL0720_SACOL0442, or any of the foregoing constructs wherein the antigen polypeptides are in any other order.

Combination

[00112] The constructs of the present invention may be used as sole immunogenic component of a composition (e.g., vaccine) of the present invention or in combination with one or more further fusion construct(s),

immunogenic polypeptide(s), fragment(s) or variant(s) thereof and/or live attenuated bacteria (e.g., *S. aureus*) (expressing or not fusion constructs and/or polypeptide(s), fragment(s) or variant(s) thereof).

[00113] The one or more fusion constructs may be any immunogenic fusion construct including a further fusion construct as defined above (see e.g., Example 14).

[00114] The one or more immunogenic polypeptide(s), fragment(s) or variant(s) thereof for use in compositions of the present invention may be any polypeptide(s), fragment(s) or variant(s) that contribute to the immunogenicity of the compositions of the present invention as defined herein. Without being so limited, such polypeptide(s), fragment(s) or variant(s) includes (a) a polypeptide comprising a SACOL0029 polypeptide as set forth in any one of the sequences depicted in FIG. 24 (SEQ ID NOs: 5 and 121 to 131), a SACOL0264 polypeptide (SEQ ID NO : 185), a SACOL0442 polypeptide as set forth in any one of the sequences depicted in FIG. 22D (SEQ ID NOs: 29 and 82 to 92), a SACOL0718 polypeptide (SEQ ID NO : 186), a SACOL0720 polypeptide as set forth in any one of the sequences depicted in FIGs. 23I-K (SEQ ID NOs: 11 and 109 to 120), a SACOL1353 polypeptide (SEQ ID NO : 187), a SACOL1416 polypeptide (SEQ ID NO : 188), SACOL1611 (SEQ ID NO : 189), a SACOL1867 polypeptide as set forth in any one of the sequences depicted in FIG. 25D (SEQ ID NOs: 152 to 164), a SACOL1912 polypeptide (SEQ ID NO : 43), a SACOL1944 polypeptide (SEQ ID NO : 190), a SACOL2144 polypeptide (SEQ ID NO : 191), a SACOL2365 polypeptide (SEQ ID NO : 192), a SACOL2385 polypeptide (SEQ ID NO : 50) or a SACOL2599 polypeptide (SEQ ID NO : 193); (b) a polypeptide encoded by a gene from a same operon as a gene encoding the polypeptide of (a); (c) a polypeptide comprising an immunogenic fragment of at least 13 consecutive amino acids of (a) or (b); (d) a polypeptide comprising an amino acid sequence at least 60% identical overall to the sequence of the polypeptide of any one of (a) to (c); or (e) a polypeptide comprising an immunogenic variant comprising at least 13 consecutive amino acids of any one of (a) to (c), as defined above. Without being so limited, any such polypeptide(s), fragment(s) or variant(s) encompasses those included in compositions (e.g., vaccines #1 to # 8) exemplified in Examples 1 to 14 and 21-26.

Live attenuated bacteria

[00115] The live attenuated bacteria (e.g. *S. aureus*) for use in compositions of the present invention may be independent from the fusions constructs and/or polypeptide(s), fragment(s) or variant(s) thereof of the present invention, or be the vessel for (i.e. may express) such fusion constructs and/or polypeptide(s), fragment(s) or variant(s) thereof of the present invention.

[00116] Without being so limited, as illustrated herein, useful live attenuated bacteria in the context of combinations of the present invention include *Staphylococcus* (e.g., *aureus*) bacteria having at least one gene contributing to virulence (e.g., $\Delta 720$) or contributing to fitness in the host (e.g., a metabolic gene) mutated or deleted. Without being so limited, such gene may be any one of the genes identified in Novick 2003, Novick 2008, or Maresso and Schneewind 2008.

[00117] In a further embodiment, the live attenuated bacteria may be further attenuated by having a stabilized SCV phenotype. As used herein the terms "SCV phenotype" refers to bacteria having a dysfunctional oxidative

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metabolism causing a slow growth, an alteration in the expression of virulence factors, and an ability to be internalized in host cells. As used herein the term « stabilized SCV phenotype» is used to denote an SCV strain retaining the SCV phenotype i.e. unable to produce invasive revertants (*i.e.*, a reversion to the normal growth phenotype). Such stabilized SCV *S. aureus* may be produced by mutating or deleting any one of the genes (*e.g.*, $\Delta hemB$) listed in Table III below. Without being limited, the present invention encompasses the use of the stabilized SCV *S. aureus* exemplified in Examples 15 to 25. Mutation as used herein includes a substitution, a deletion and/or an insertion of one or more nucleotides that prevents expression of the polypeptide encoded by a gene of the present invention or that prevents expression of a functional polypeptide. In a preferred embodiment, the mutation prevents expression of the polypeptide. In another specific embodiment, the two mutations in the same attenuated live or inactivated strain of *S. aureus* are a deletion or an insertion. It is expected that a mutated strain of *S. aureus* having a mutation at any position of one of the genes of the present invention that prevents expression of the polypeptide can be used as an attenuated live vaccine in accordance with the present invention. Attenuated live vaccines, *i.e.* vaccines comprising the bacterium according to the invention in a live attenuated form, have the advantage over inactivated vaccines that they best mimic the natural way of infection. In addition, their replicating abilities allow vaccination with low amounts of bacteria; their number will automatically increase until it reaches the trigger level of the immune system. From that moment on, the immune system will be triggered and will finally eliminate the bacteria. A minor disadvantage of the use of live attenuated bacteria however might be that inherently there is a certain level of virulence left. This need not be a real disadvantage as long as the level of virulence is acceptable, *i.e.* as long as the vaccine at least decreases the bacterial infection (*e.g.*, IMI) symptoms. Of course, the lower the remaining virulence of the live attenuated vaccine is, the less influence the vaccination has on weight gain during/after vaccination.

Table III: Genbank™ accession numbers for *S. aureus* genes associated with SCV phenotype (Kahl, 2014)

Gene Name	GenBank™ Gene ID No.	GenBank™ Protein No.
hemB	3238571 (SACOL1715)	AAW36820.1 WP_000667126.1 GI:446589780 EC:4.2.1.24
menB	3236546 (SACOL1052)	AAW36517.1 WP_000526687.1 GI:446448832 EC:2.2.1.9
thyA	3238178 (SACOL1462)	AAW36663.1 WP_000667126.1

		GI:446589780 EC:2.1.1.45
fusA	3236183 (SACOL0593)	AAW37703.1 GI:57285609
FusE (gene: rplF)	3238328 (SACOL2224)	AAW37099.1 GI:57285005
relA (relA2)	3238211 (SACOL1689)	AAW36795.1 GI:57284701 EC:2.7.6.5
cspB	3238398 (SACOL2731)	AAW37379.1 GI:57285285
hemH	3236274 (SACOL1888)	AAW36901.1 GI:57284807 EC:4.99.1.1
ctaA	3237823 (SACOL1124)	AAW38004.1 GI:57285910

Nucleic acids

[00118] The nucleic acid of the present invention preferably comprises a nucleotide sequence that encodes one or more proteins/polypeptides noted above (or fragments thereof) operably linked to regulatory elements needed for gene expression, such as a promoter, an initiation codon, a stop codon, enhancers, and a polyadenylation signal. Regulatory elements are preferably selected that are operable in the species to which they are to be administered. In specific embodiments, the nucleic acid is as depicted in FIGs. 21 to 25.

[00119] Within the context of the present invention is the *in vivo* administration of a nucleic acid of the invention to a mammal so that one or more proteins/polypeptides (or a fragment thereof) of interest is/are expressed in the mammal (e.g., nucleic acid vaccine, DNA or RNA vaccine).

Delivery systems

[00120] The nucleic acid of the present vaccine can be "naked" DNA or can be operably incorporated in a vector. Nucleic acids may be delivered to cells *in vivo* using methods well known in the art such as direct injection of DNA, receptor-mediated DNA uptake, viral-mediated transfection or non-viral transfection and lipid-based transfection, all of which may involve the use of vectors. Direct injection has been used to introduce naked DNA

into cells *in vivo* (see *e.g.*, Acsadi *et al.* (1991) *Nature* **332**:815-818; Wolff *et al.* (1990) *Science* **247**:1465-1468). A delivery apparatus (*e.g.*, a "gene gun") for injecting DNA into cells *in vivo* may be used. Such an apparatus may be commercially available (*e.g.*, from BioRad). Naked DNA may also be introduced into cells by complexing the DNA to a cation, such as polylysine, which is coupled to a ligand for a cell-surface receptor (see for example Wu, G. and Wu, C. H. (1988) *J. Biol. Chem.* **263**: 14621; Wilson *et al.* (1992) *J. Biol. Chem.* **267**: 963-967; and U.S. Pat. No. 5,166,320). Binding of the DNA-ligand complex to the receptor may facilitate uptake of the DNA by receptor-mediated endocytosis. A DNA-ligand complex linked to adenovirus capsids which disrupt endosomes, thereby releasing material into the cytoplasm, may be used to avoid degradation of the complex by intracellular lysosomes (see for example Curiel *et al.* (1991) *Proc. Natl. Acad. Sci. USA* **88**: 8850; Cristiano *et al.* (1993) *Proc. Natl. Acad. Sci. USA* **90**:2122-2126).

[00121] Useful delivery vectors include biodegradable microcapsules, immuno-stimulating complexes (ISCOMs) or liposomes, and genetically engineered attenuated live vectors such as cells, viruses or bacteria.

[00122] Liposome vectors are unilamellar or multilamellar vesicles, having a membrane portion formed of lipophilic material and an interior aqueous portion. The aqueous portion is used in the present invention to contain the polynucleotide material to be delivered to the target cell. It is generally preferred that the liposome forming materials have a cationic group, such as a quaternary ammonium group, and one or more lipophilic groups, such as saturated or unsaturated alkyl groups having about 6 to about 30 carbon atoms. One group of suitable materials is described in European Patent Publication No. 0187702, and further discussed in U.S. Pat. No. 6,228,844 to Wolff *et al.*, the pertinent disclosures of which are incorporated by reference. Many other suitable liposome-forming cationic lipid compounds are described in the literature. See, *e.g.*, L. Stamatatos, *et al.*, *Biochemistry* **27**:3917-3925 (1988); and H. Eibl, *et al.*, *Biophysical Chemistry* **10**:261-271 (1979). Alternatively, a microsphere such as a polylactide-coglycolide biodegradable microsphere can be utilized. A nucleic acid construct is encapsulated or otherwise complexed with the liposome or microsphere for delivery of the nucleic acid to a tissue, as is known in the art.

[00123] Preferred viral vectors include Bacteriophages, Herpes virus, Adenovirus, Polio virus, Vaccinia virus, defective retroviruses, adeno-associated virus (AAV) and Avipox. Methods of transforming viral vector with an exogenous DNA construct are also well described in the art. See Sambrook and Russell, above.

[00124] As indicated above, the nucleic acid (*e.g.*, DNA or RNA) may be incorporated in a host such as a host cell *in vitro* or *ex vivo* (*e.g.*, an immune cell such as a dendritic cell) or, as indicated above, in an attenuated microbial host (*e.g.*, attenuated *S. aureus*, SCV, *etc.*, see *e.g.*, Examples 25-26 for instance) by transfection or transformation, and the transfected or transformed cell or microorganism, which expresses the polypeptide (*e.g.* fusion of multiple antigens or fragments therefor and/or single antigens or fragments thereof) of interest, may be administered to the subject. Following administration, the cell will express the protein or polypeptide of interest (or a variant or fragment thereof) in the subject, which will in turn lead to the induction of an immune response directed against the protein, polypeptide or fragment thereof.

[00125] The use of attenuated live bacteria to immunize and/or to deliver specific constructs or antigen mixture

of the present invention represents an interesting approach to improve immune responses (Griffiths and Khader, 2014). Live attenuated organisms that mimic natural infection stimulate the immune system in a powerful manner, eliciting broad and robust immune responses that produce both serum and mucosal antibodies, and effector and memory T cells which act synergistically to protect against disease (Detmer and Glenting, 2006; Kollaritsch et al, 2000; Pasetti et al., 2011). Examples of suitable attenuated live bacterial vectors include *S. aureus*, *Salmonella typhimurium*, *Salmonella typhi*, *Shigella*, *Bacillus*, *Lactobacillus*, Bacille Calmette-Guerin (BCG), *Escherichia coli*, *Vibrio cholerae*, *Campylobacter*, or any other suitable bacterial vector, as is known in the art. Methods of transforming live bacterial vectors with an exogenous DNA construct are well described in the art. See, for example, Joseph Sambrook and David W. Russell, Molecular Cloning, A Laboratory Manual, 3rd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (2001). The present invention encompasses the use of a composition comprising an attenuated live bacterium (e.g., Δ hemB Δ 720 *S. aureus* expressing the construct of the present invention as sole immunogenic component or in combination with other attenuated live bacteria each expressing another polypeptide, fragment or variant of the present invention (e.g., SACOL0442, SACOL0720 or fragments or variants thereof).

Compositions

[00126] The polypeptides, nucleic acids and delivery systems (e.g., host cells comprising said nucleic acids or vectors) described herein can be formulated into compositions. As used herein, the term "pharmaceutically acceptable" refers to vaccine components (e.g., excipients, carriers, adjuvants) and compositions that are physiologically tolerable and do not typically produce an allergic or similar untoward reaction, such as gastric upset, dizziness and the like, when administered to a subject. Preferably, as used herein, the term "pharmaceutically acceptable" means approved by regulatory agency of the federal or state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and in humans. The term "excipient" refers to a diluent, carrier, or vehicle with which the vaccine components of the present invention may be administered. Sterile water or aqueous saline solutions and aqueous dextrose and glycerol solutions may be employed as carriers, particularly for injectable solutions.

[00127] In an embodiment, the agent of the present invention is administered in combination with an adjuvant or immunostimulant. Suitable adjuvant or immunostimulant that may improve the efficacy of components to raise an immune response include but is not limited to oils (e.g., mineral oils, emulsified oil such as MONTANIDE™ or EMULSIGEN™-D), metallic salts (e.g., alum, aluminum hydroxide or aluminum phosphate), cationic peptides (Bowdish et al., 2005; Hancock, et al., 2000) such as indolicidin, a cationic peptide produced by the cow's immune cells (Falla et al., 1996), natural and artificial microbial components (e.g., bacterial liposaccharides, Freund's adjuvants, muramyl dipeptide (MDP), cyclic-diguanosine-5'-monophosphate (c-di-GMP), pathogen-associated molecular patterns (PAMPS) such as surface polysaccharides, lipopolysaccharides, glycans, peptidoglycan or microbial DNA (e.g., CpG), plant components such as saponins (e.g., Quil-A™), and/or one or more substances that have a carrier effect (e.g., bentonite, latex particles, liposomes, ISCOM™, DNA and polyphosphazine (PCPP) copolymers). Immunization with synthetic nanoparticles (such as those made from a biodegradable synthetic polymer like poly(D,L-lactico-glycolic acid)) containing antigens plus ligands that signal

through TLR to stimulate proinflammatory cytokines is also possible (Kasturi et al, 2011).

[00128] Vaccine components of the invention may be administered in a pharmaceutical composition. Pharmaceutical compositions may be administered in unit dosage form. Any appropriate route of administration may be employed, for example, parenteral, subcutaneous, intramuscular, intramammary, intracranial, intraorbital, ophthalmic, intraventricular, intracapsular, intraarticular, intraspinal, intracisternal, intraperitoneal, intranasal, aerosol, or oral administration. Examples of specific routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, intramammary; oral (*e.g.*, inhalation); transdermal (topical); transmucosal, and rectal administration.

[00129] Conventional pharmaceutical practice may be employed to provide suitable formulations or compositions to administer such vaccine components with or without adjuvants to subjects. Methods well known in the art for making pharmaceutical compositions and formulations are found in, for example, Remington: The Science and Practice of Pharmacy, (20th ed.) ed. A. R. Gennaro A R., 2000, Lippincott: Philadelphia. Formulations for parenteral administration may, for example, contain excipients, sterile water, or saline, polyalkylene glycols such as polyethylene glycol, miglyol, oils of vegetable origin, or hydrogenated naphthalenes. Biocompatible, biodegradable lactide polymer, lactide/glycolide copolymer, or polyoxyethylene-polyoxypropylene copolymers may be used to control the release of the compounds. Other potentially useful parenteral delivery systems for compounds of the invention include ethylenevinyl acetate copolymer particles, osmotic pumps, implantable infusion systems, and liposomes. Formulations for inhalation or intramammary injection may contain excipients, for example, lactose, or may be aqueous solutions containing, for example, polyoxyethylene-9-lauryl ether, miglyol, glycocholate and deoxycholate, or may be oily solutions (*e.g.*, paraffin oil) for administration in the form of nasal drops, or as a gel.

[00130] Therapeutic formulations may be in the form of liquid solutions or suspension; for oral administration, formulations may be in the form of tablets or capsules; and for intranasal formulations, in the form of powders, nasal drops, or aerosols. Solutions or suspensions used for parenteral, intradermal, intramammary or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils (*e.g.*, paraffin oil), polyethylene glycols, glycerin, propylene glycol, miglyol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; reducing agents such as dithiothreitol, buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

[00131] Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous or intramammary administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor™ ELTM (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS).

[00132] Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets or feed. For the purpose of oral vaccine administration, the active components can be incorporated with excipients and used in the form of tablets, troches, capsules or in feed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel™, or com starch; a lubricant such as magnesium stearate or sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

[00133] For administration by inhalation, the vaccine components are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, e.g., a gas such as carbon dioxide, or a nebulizer.

[00134] Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

[00135] Liposomal suspensions (including liposomes targeted to specific cell types) can also be used as pharmaceutically acceptable carriers.

[00136] The pharmaceutical compositions may also contain preserving agents, solubilizing agents, stabilizing agents, wetting agents, emulsifiers, sweeteners, colorants, odorants, salts for the variation of osmotic pressure, buffers, coating agents or antioxidants. They may also contain other therapeutically valuable agents.

[00137] Intravenous, intramuscular, subcutaneous, intramammary or oral administration is a preferred form of use. The dosages in which the components of the present invention are administered in effective amounts depend on the nature of the specific active ingredient, the host and the requirements of the subject and the mode of application.

Microbial Targets

[00138] Polypeptides, nucleic acids and delivery systems of the present invention may be used as antimicrobial agents against Staphylococcal infections including those causing intramammary infection (IMI). In a preferred embodiment, the Staphylococcal infections are caused by *Staphylococcus aureus*.

Methods of immunizing with polypeptides, nucleic acids, vectors, cells, compositions and delivery systems

[00139] Encompassed by the methods, uses, pharmaceutical compositions and kits of the present invention is passive and active immunization.

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[00140] Passive immunization is the injection of antibodies or antiserum, previously generated against the pathogen (or antigens described herein), in order to protect or cure a recipient animal of an infection or future infection. Protection fades over the course of a few weeks during which time the active immunization with polypeptides, nucleic acids or delivery systems (e.g., as described above) will have time to generate a lasting protective response. Serum for passive immunization can be generated by immunization of donor animals using the polypeptides, nucleic acids or delivery systems, as described herein. This serum, which contains antibodies against the antigens, can be used immediately or stored under appropriate conditions. It can be used to combat acute infections (e.g., IMI) or as a prophylactic (Tuchscherer *et al.*, 2008). Use of antibodies or serums in a passive immunization can be combined with other agents such as an antibiotic to increase the cure rate of an infection currently in progress or to increase protection against an imminent infection.

[00141] Active immunization is administration of the polypeptides, nucleic acids or delivery systems as described herein to a subject.

[00142] The components identified in accordance with the teachings of the present invention have a prophylactic and/or therapeutic value such as they can be used to raise an immune response to prevent and/or combat diseases or conditions, and more particularly diseases or conditions related to microbial infections.

[00143] The terms "prevent/preventing/prevention" or "treat/treating/treatment" as used herein, refer to eliciting the desired biological response, *i.e.*, a prophylactic and therapeutic effect, respectively in a subject. In accordance with the present invention, the therapeutic effect comprises one or more of a decrease/reduction in the severity, intensity and/or duration of the microbial infection (e.g., staphylococcal infection) or any symptom thereof following administration of the polypeptide, nucleic acid or delivery system (agent/composition of the present invention) of the present invention when compared to its severity, intensity and/or duration in the subject prior to treatment or as compared to that/those in a non-treated control subject having the infection or any symptom thereof. In accordance with the invention, a prophylactic effect may comprise a delay in the onset of the microbial infection (e.g., staphylococcal infection) or any symptom thereof in an asymptomatic subject at risk of experiencing the microbial infection (e.g., staphylococcal infection) or any symptom thereof at a future time; or a decrease/reduction in the severity, intensity and/or duration of a microbial infection (e.g., staphylococcal infection) or any symptom thereof occurring following administration of the agent/composition of the present invention, when compared to the timing of their onset or their severity, intensity and/or duration in a non-treated control subject (*i.e.* asymptomatic subject at risk of experiencing the microbial (e.g., bacterial) infection (e.g., staphylococcal infection) or any symptom thereof); and/or a decrease/reduction in the progression of any pre-existing microbial infection (e.g., staphylococcal infection) or any symptom thereof in a subject following administration of the agent/composition of the present invention when compared to the progression of microbial infection (e.g., staphylococcal infection) or any symptom thereof in a non-treated control subject having such pre-existing microbial infection (e.g., staphylococcal infection) or any symptom thereof. As used herein, in a therapeutic treatment, the agent/composition of the present invention is administered after the onset of the microbial infection (e.g., staphylococcal infection) or any symptom thereof. As used herein, in a prophylactic treatment, the agent/composition of the present invention is administered before the onset of the microbial

infection (e.g., staphylococcal infection) or any symptom thereof or after the onset thereof but before the progression thereof.

[00144] As used herein, "decrease" or "reduction" of microbial infection (e.g., staphylococcal infection) or any symptom thereof refers to a reduction in a symptom of at least 10% as compared to a control subject (a subject not treated with the agent/composition present invention), in an embodiment of at least 20% lower, in a further embodiment of at least 30% lower, in a further embodiment of at least 40% lower, in a further embodiment of at least 50% lower, in a further embodiment of at least 60% lower, in a further embodiment of at least 70% lower, in a further embodiment of at least 80% lower, in a further embodiment of at least 90% lower, in a further embodiment of 100% (complete inhibition).

[00145] As used herein, the term "symptom" in reference to a staphylococcal infection refers to any staphylococcal infection symptom such as pain, inflammation, fever, vomiting, diarrhea, fatigue muscle aches, anorexia, dehydration, low blood pressure, cellulitis, impetigo, boil and scalded skin syndrome. More particularly, in reference to a staphylococcal IMI, a staphylococcal IMI symptom refers for example to visual abnormalities in milk (e.g., such as a watery appearance, flakes, clots, malodorous, presence of blood), redness of the udder, swelling in the udder, tenderness in the udder, elevated rectal temperature ($>39.0^{\circ}\text{C}$), anorexia, decreased rumen motility and fatigue. An increase in milk somatic cell counts (SCC) is another staphylococcal IMI. Milk somatic cells include white blood cells such as leukocytes or neutrophils as well as epithelial cells. It is generally agreed that a SCC of $>200,000/\text{mL}$ may represent a staphylococcal IMI symptom or is indicative of a staphylococcal IMI.

Dosage

[00146] Toxicity or efficacy of vaccine components to elicit an immune response can be determined by standard procedures in cell cultures or experimental animals. The dose ratio between toxic and immune stimulatory effects can be measured. Components that exhibit large ratios are preferred. While components that exhibit toxic side effects may be used, care should be taken to design a delivery system in order to minimize potential damage to cells and, thereby, reduce side effects.

[00147] Data obtained from cell culture assays and laboratory animal studies can be used in formulating a range of dosage for use in large animals and humans. The dosage of such components lies preferably within a range of administered concentrations that include efficacy with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized.

[00148] Any suitable amount of the pharmaceutical composition may be administered to a subject. The dosages will depend on many factors. Typically, the amount of active ingredient contained within a single dose will be an amount that effectively prevents, or treats IMI without inducing significant toxicity. The skilled artisan will appreciate that certain factors may influence the dosage required to effectively raise an immune response in a subject. Moreover, the therapeutically effective amount of the antigens (e.g., fusion construct) of the present invention may require a series of doses. In general, an amount of about 0.01 mg - 500 mg of antigens including the fusion construct per dose, come into consideration. In a specific embodiment, an amount of about 0.1 mg - 1

mg of antigens including the fusion construct per dose, come into consideration. Generally, one, two or three doses of the vaccine may favor optimal development of immunity. The time between two doses may be as short as three or four weeks but it may be preferred to separate the priming dose (first dose) and the booster dose (second dose) by five, six, seven, eight, nine or ten weeks before stimulating the immune system with the booster shot. A subsequent booster shot (a recall shot) may also be optimal to provide a sustainable immunity. This recall could for example occur every half year (6 months), yearly, every two years, every three or every five years.

[00149] "Sample" or "biological sample" refers to any solid or liquid sample isolated from a live being. In a particular embodiment, it refers to any solid (e.g., tissue sample) or liquid sample isolated from a mammal, such as milk, a biopsy material (e.g., solid tissue sample), blood (e.g., plasma, serum or whole blood), saliva, synovial fluid, urine, amniotic fluid and cerebrospinal fluid. Such sample may be, for example, fresh, fixed (e.g., formalin-, alcohol- or acetone-fixed), paraffin-embedded or frozen prior to analysis of the infectious agent's expression level.

Patients

[00150] As used herein the term "subject" or "patient" refers to an animal, preferably a mammal such as but not limited to a human, cow (e.g., heifer, multiparous, primiparous, calf), goat, sheep, ewe, ass, horse, pig, chicken, cat, dog, etc. who is the object of treatment, observation or experiment. In a specific embodiment, it is a cow (e.g., at risk of experiencing staphylococcal (e.g., IMI) infection).

[00151] As used herein the terms "subject at risk of experiencing a staphylococcal infection (e.g., staphylococcal infection (e.g., IMI) or any symptom thereof at a future time" refers to a mammal (e.g., a cow (e.g., heifer, multiparous, primiparous, calf), goat, sheep) that is used for milk or meat production.

[00152] In an embodiment, the above-mentioned mammal is a cow.

Method of detection

[00153] Examples of methods to measure the amount/level of selected proteins/polypeptides include, but are not limited to: Western blot, immunoblot, enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), immunoprecipitation, surface plasmon resonance, chemiluminescence, fluorescent polarization, phosphorescence, immunohistochemical analysis, matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry, microcytometry, microarray, microscopy, flow cytometry, and assays based on a property of the protein including but not limited to DNA binding, ligand binding, interaction with other protein partners or enzymatic activity.

[00154] In an embodiment, the amount of the polypeptide/protein within the methods of the present invention is detected using antibodies that are directed specifically against the polypeptide/protein. The term "antibody" as used herein encompasses monoclonal antibodies, polyclonal antibodies, multispecific antibodies (e.g., bispecific antibodies), and antibody fragments, so long as they exhibit the desired biological activity or specificity. "Antibody fragments" comprise a portion of a full-length antibody, generally the antigen binding or variable region thereof. Interactions between antibodies and a target polypeptide are detected by radiometric, colorimetric, or fluorometric means. Detection of antigen-antibody complexes may be accomplished by addition of a secondary antibody that

is coupled to a detectable tag, such as for example, an enzyme, fluorophore, or chromophore.

[00155] Methods for making antibodies are well known in the art. Polyclonal antibodies can be prepared by immunizing a suitable subject (*e.g.*, rabbit, goat, mouse, or other mammal) with the polypeptide/protein of interest or a fragment thereof as an immunogen. A polypeptide/protein "fragment" "portion" or "segment" is a stretch of amino acid residues of at least about 5, 7, 10, 14, 15, 20, 21 or more amino acids of the polypeptide noted above. The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized exosomal marker polypeptide or a fragment thereof. At an appropriate time after immunization, *e.g.*, when the antibody titers are highest, antibody-producing cells can be obtained from the animal, usually a mouse, and can be used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein (1975) *Nature* 256: 495-497, the human B cell hybridoma technique (Kozbor et al. (1983) *Immunol. Today* 4: 72), the EBV-hybridoma technique (Cole et al. (1985) in *Monoclonal Antibodies and Cancer Therapy*, ed. Reisfeld and Sell (Alan R. Liss, Inc., New York, NY), pp. 77-96) or trioma techniques. The technology for producing hybridomas is well known (see generally Coligan et al., eds. (1994) *Current Protocols in Immunology*, John Wiley & Sons, Inc., New York, NY).

[00156] Alternatively, to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (*e.g.*, an antibody phage display library) with a polypeptide or a fragment thereof to thereby isolate immunoglobulin library members that bind the polypeptide. Kits for generating and screening phage display libraries are commercially available (*e.g.*, the Pharmacia Recombinant Phage Antibody System™, Catalog No. 27-9400-01; and the Stratagene SurfZAP™ Phage Display Kit, Catalog No. 240612).

[00157] Furthermore, antibodies directed against one or more of the polypeptides/proteins described herein may be obtained from commercial sources.

[00158] The use of immobilized antibodies specific for the polypeptides/proteins is also contemplated by the present invention and is well known by one of ordinary skill in the art. The antibodies could be immobilized onto a variety of solid supports, such as magnetic or chromatographic matrix particles, the surface of an assay plate (such as microtiter wells), pieces of a solid substrate material (such as plastic, nylon, paper), and the like. An assay strip could be prepared by coating the antibody or a plurality of antibodies in an array on solid support. This strip could then be dipped into the test sample and then processed quickly through washes and detection steps to generate a measurable signal, such as a colored spot.

[00159] The analysis of a plurality (2 or more) of polypeptides/proteins may be carried out separately or simultaneously with one test sample. Several polypeptides/proteins may be combined into one test for efficient processing of a multiple of samples.

[00160] The analysis of polypeptides/proteins could be carried out in a variety of physical formats as well. For example, the use of microtiter plates or automation could be used to facilitate the processing of large numbers of test samples. Alternatively, single sample formats could be developed to facilitate immediate treatment and

diagnosis in a timely fashion. Particularly useful physical formats comprise surfaces having a plurality of discrete, addressable locations for the detection of a plurality of different analytes. Such formats include protein microarrays, or "protein chips" (see, e.g., Ng and Ilag, J. Cell Mol. Med. 6: 329-340, 2002) and capillary devices.

[00161] In an embodiment, the above-mentioned level of expression is determined by measuring the level of expression of a mRNA transcribed from said one or more genes.

[00162] Methods to determine nucleic acid (mRNA) levels are known in the art, and include for example polymerase chain reaction (PCR), reverse transcriptase-PCR (RT-PCR), SAGE, quantitative PCR (q-PCR), Southern blot, Northern blot, sequence analysis, microarray analysis, detection of a reporter gene, or other DNA/RNA hybridization platforms. For RNA expression, preferred methods include, but are not limited to: extraction of cellular mRNA and Northern blotting using labeled probes that hybridize to transcripts encoding all or part of one or more of the nucleic acids encoding the protein/polypeptide of this invention; amplification of mRNA expressed from one or more of the nucleic acids encoding the proteins/polypeptides of this invention using specific primers, polymerase chain reaction (PCR), quantitative PCR (q-PCR), and reverse transcriptase-polymerase chain reaction (RT-PCR), followed by quantitative detection of the product by any of a variety of means; extraction of total RNA from the biological sample, which is then labeled and used to probe cDNAs or oligonucleotides encoding all or part of the nucleic acids encoding the proteins/polypeptides of this invention, arrayed on any of a variety of surfaces.

Kits

[00163] The present invention also encompasses kits comprising the components of the present invention. For example, the kit can comprise one or more components. The components can be packaged in a suitable container and device for administration. The kit can further comprise instructions for using the kit.

[00164] The present invention also provides a kit or package comprising reagents useful for administering one or more construct, polypeptide, nucleic acid, vector, host, compositions of the present invention, or a combination of at least two thereof, to a subject in need thereof for treating and/or preventing Staphylococcal IMI. Such kit may further comprise, for example, instructions for the prevention and/or treatment of Staphylococcal IMI, containers, reagents useful for performing the methods. The kit may further include where necessary agents for reducing background interference in a test, agents for increasing signal, software and algorithms for combining and interpolating marker values to produce a prediction of clinical outcome of interest, apparatus for conducting a test, calibration curves and charts, standardization curves and charts, and the like.

MODE(S) FOR CARRYING OUT THE INVENTION

[00165] The present invention is illustrated in further details by the following non-limiting examples.

EXAMPLE 1: Materials and Methods for Vaccine including SACOL0029, SACOL0442, SACOL0720, SACOL1867, SACOL1912 and SACOL2385 (Vaccine #1)

[00166] *Production of the antigens.* Six antigens that are highly expressed during *S. aureus* bovine intramammary infection were selected for inclusion in a first bovine vaccine (Vaccine #1). These antigens are:

SACOL0029 (GenBank™ accession No.: YP_184940.1) (SEQ ID NO: 5), SACOL0442 (YP_185332.1) (SEQ ID NO: 29), SACOL0720 (YP_185601.1) (SEQ ID NO: 11), SACOL1867 (GenBank™ accession No.: YP_186695.1) (SEQ ID NO: 38), SACOL1912 (GenBank™ accession No.: YP_186737.1) (SEQ ID NO: 43), and SACOL2385 (GenBank™ accession No.: YP_187189.1) (SEQ ID NO: 50). His-tagged recombinant proteins of SACOL0029, SACOL1867, SACOL1912, and SACOL2385 were engineered and produced by GenScript, Inc. (Piscataway, NJ). His-tagged recombinant proteins of SACOL0442 and SACOL0720 were engineered and produced using QIA expression technology (pQE30 plasmid) from Qiagen Inc. (Mississauga, ON, Canada), according to the manufacturers' recommendations. See, FIG. 21 I to VI for the his-tagged sequences of the antigens. Examples 2-5 and FIGs. 1-4 relate to this vaccine #1.

[00167] *Immunization of dairy cows.* Nineteen healthy multiparous Holstein cows in mid-lactation were housed in a level II biosafety barn at the Dairy and Swine Research and Development Centre of Agriculture and Agri-Food Canada (Sherbrooke, QC). Cows were randomly divided into 2 groups: one group (10 cows) received saline (placebo group); the other group (9 cows) received the vaccine #1 (vaccinated group). The vaccine was composed of 300 µg of each of six antigens (SACOL0029, SACOL0720, SACOL1867, SACOL1912, and SACOL2385) combined with Emulsigen™-D (MVP Technologies, Omaha, NE), CpG ODN 2007 (TCGTCGTTGTCGTTTGTGCGTT (SEQ ID NO: 194), a pathogen-associated molecular pattern (PAMP), VIDO, Saskatoon, SW) and the cationic peptide indolicidin (ILPWKWPWWPWRR (SEQ ID NO: 195), used to induce the cow's immune response, (Chemprep Inc., Miami, FL). Two immunizations were performed 10 weeks apart, subcutaneously in the neck. No adverse side effects were observed. Blood from the caudal vein and milk samples were taken before the first immunization (preimmune serums) and then every two weeks for the detection of total IgG, IgG1 and IgG2. Larger volumes of blood from the jugular vein (150 mL was taken before the first immunization and 14 weeks after the first immunization (i.e., 4 weeks after the second immunization) for peripheral blood mononuclear cells (PBMCs) isolation and analysis of the cellular immune responses.

[00168] *Detection of total IgG, IgG1 and IgG2 by ELISA.* Detection of total IgG, IgG1 and IgG2 against each of the antigens in serum and milk was performed as previously described with some modifications (Ster et al., *Vet. Immunol. Immunopathol.* (2010), 136: 311-318). Nunc MaxiSorp™ 96-well plates (Thermo Fisher Scientific Inc., Rochester, NY) were coated with the test antigen (5 µg/mL diluted in carbonate/bicarbonate buffer, Sigma Aldrich, Oakville, ON) and incubated overnight at 37°C. The plates were then saturated with the PBS containing 0.5% gelatin (BD, Franklin Lakes, NJ) for 1 h at 37°C. One hundred microliters of two-fold serial dilutions of the sera in PBS containing 0.5% gelatin and 0.1% Tween™ 20 were loaded into the plates and incubated for 1 h at 37°C. The plates were washed three times with PBS containing 0.1% Tween™ 20. One hundred microliters of horseradish peroxidase (HRP)-conjugated secondary antibody were added to the plate. The secondary antibodies used were a goat anti-bovine IgG (Jackson ImmunoResearch Laboratories Inc., West Grove, PA), a sheep anti-bovine IgG1 (AbD Serotec, Raleigh, NC) or a sheep anti-bovine IgG2 (AbD Serotec), diluted 1/50,000 1/20,000 and 1/20,000 respectively in PBS containing 0.5% gelatin and 0.1% Tween™ 20. After 1 h of incubation at 37°C followed by 3 washes, peroxidase activity was detected with 3,3',5,5'-tetramethylbenzidine (TMB) reagent (KPL Inc., Gaithersburg, MD) according to the manufacturer's

recommendations.

[00169] Detection of total IgG, IgG1 and IgG2 in milk was carried out using the same procedure with few modifications. Milk samples were diluted into PBS containing 0.5% gelatin. The sheep anti-bovine IgG2 was diluted 1/10,000 into PBS containing 0.5% gelatin and 0.1% TweenTM 20.

[00170] *Evaluation of the cellular immune response.* PBMCs were isolated from jugular vein blood and labelled with carboxyfluorescein diacetate, succinimidyl ester (CFDA-SE; Molecular Probes Inc., Eugene, OR) as previously described (Loiselle et al., *J. Dairy. Sci.* (2009), 92:1900-1912). At the end of the CFDA-SE labelling procedure, the PBMCs were suspended in RPMI medium containing 5% FBS and 1X antibiotic/antimycotic (A5955, Sigma Chemical Aldrich). The PBMCs (5×10^6 cells per well) were stimulated with the mitogen concanavalin A (ConA; positive control; Sigma Aldrich) at a final concentration of 1 $\mu\text{g/mL}$, or each antigen (5 μg per well) and incubated for 7 days at 37°C. As a negative control, the PBMCs were incubated without any mitogen. Stimulations were performed in duplicate (Ster et al., 2010).

[00171] The proliferation of CD4⁺ and CD8⁺ cells was evaluated after incubation with the different mitogens. The cells were centrifuged at 300 $\times$ g for 5 min, suspended in PBS containing 0.5% BSA. The mouse anti-bovine CD8 coupled with Alexa FluorTM 647 (diluted 1/20, AbD Serotec) and the mouse anti-bovine CD4 coupled with rPE (diluted 1/20, AbD Serotec) were then added. After 20 min of incubation on ice, the cells were washed three times with PBS containing 0.5% BSA. The cells were then suspended in PBS with 0.5% formaldehyde. The percentages of the proliferative populations were determined by flow cytometry on a BD FACS Canto II flow cytometer using the BD FACS Diva software.

[00172] *Experimental S. aureus in IMI in dairy cows.* Before their use in experimental IMI, the relationship between the absorbance of the bacterial cultures (A600 nm) and CFU was determined. The day of the challenge, a volume of the overnight culture of *S. aureus* in Mueller Hinton broth (MHB; BD) was transferred to 200 mL of fresh MHB to obtain an A600 nm of 0.1 and subsequently grown at 35°C until the A600 nm reached a value corresponding to 10^8 CFU/mL in the exponential phase of growth. The strain to be used in this experimental infection (CLJ08-3) had previously been characterized in the co-inventor's lab (Allard et al., *Vet. Microbiol.* (2013) 162: 761- 770). For intramammary infusions, bacteria were routinely diluted in sterile PBS (Sigma Aldrich) to obtain approximately 50 CFU in 3 mL. In this experiment, the inoculum was plated on TSA and found to contain 63 cfu in 3 mL.

[00173] Somatic cell count (SCC) determinations and bacterial analysis of aseptic quarter milk samples were carried out prior to experimental IMI to ensure that all cows were free of IMI. Experimental infusion of mammary quarters with bacteria was performed in three (randomly chosen) of the four quarters of each cow after the evening milking according to a procedure previously described (Petitclerc et al., *J. Dairy. Sci.* (2007), 90: 2778-2787) with few modifications. Briefly, before inoculation, teats were scrubbed with gauze soaked in 70% ethanol. Teats were allowed to air-dry before intramammary infusion of 3 mL of bacterial suspension (containing 63 CFU) into three of the four quarters. Immediately after infusion, all quarters were thoroughly massaged and teats were dipped in an iodophore-based teat sanitizer. Disposable gloves were worn throughout the procedure and

disinfected before proceeding to the next animal. All quarters infused with *S. aureus* became infected and all cows showed clinical signs (inflammation, and/or poor milk appearance) of mastitis at some time during the first few days after infusion of *S. aureus*.

[00174] *Evaluation of the S. aureus viable counts after experimental infections.* Aseptic milk samples were taken before the morning milking three times a week during the 3 first weeks following the experimental infection and then twice a week for the 2 remaining weeks. After foremilk was discarded and the teats were disinfected with 70% ethanol, a 10-mL milk sample was aseptically collected in a 50-mL sterile vial for each individual quarter. Milk samples were serially diluted and 100 μ L of each dilution were plated on both tryptic soy agar (Becton Dickinson) and mannitol salt agar plates (Becton Dickinson) for CFU determinations and *S. aureus* identification. Plates were then incubated for 24h at 35°C before the colonies were counted. The dilutions that showed between 30 and 300 colonies were used to calculate the bacterial concentration. Each dilution was plated in duplicate.

[00175] *Evaluation of the somatic cell counts.* At the same frequency as for aseptic milk samples, milk was harvested using individual quarter milking units at morning milking and weighed for the determination of quarter milk production. A non-aseptic 50-mL sample was also taken from each quarter milking units for the determination of the SCC by a commercial laboratory (Valacta Inc., Ste-Anne-de-Bellevue, QC, Canada). The milking units were thoroughly washed and disinfected with an iodine-based germicide detergent (K.O. Dyne®, GEA Farm Technologies, Westmoreland, NY) between their uses on each cow. All other materials in contact with milk were disinfected with 70% ethanol.

[00176] *Statistical analysis.* Statistical analyses of the experimental infection data were performed using the MIXED procedure of SAS (SAS Institute Inc., Cary, NC) as repeated measurements. For the analysis of SCC and CFU, data were log10 transformed prior to analysis. Statistical analysis of the antibody titers and of the correlation between CFU and SCC was performed using GraphPad Prism™ v6.05.

[00177] *Ethics statement.* All animal experiments were approved by the Agriculture and Agri-Food Canada local institutional animal care committee and conducted in accordance with the guidelines of the Canadian Council on Animal Care.

EXAMPLE 2: Serum total IgG1 titers following vaccination - vaccine #1

[00178] Recombinant His-tagged antigens for SACOL0029 (GenBank™ accession No.: YP_184940.1) (SEQ ID NO: 5), SACOL0442 (SEQ ID NO: 29), SACOL0720 (SEQ ID NO: 11), SACOL1867 (GenBank™ accession No.: YP_186695.1) (SEQ ID NO: 38), SACOL1912 (GenBank™ accession No.: YP_186737.1) (SEQ ID NO: 43), and SACOL2385 (GenBank™ accession No.: YP_187189.1) (SEQ ID NO: 50), were prepared and administered to healthy cows as described in Example 1 (*Production of the antigens and Immunization of dairy cows*). Nine dairy cows received the vaccine and 10 cows received saline (placebo). Total serum IgG, IgG1 and IgG2 titers were detected as described in Example 1 (*Detection of total IgG, IgG1 and IgG2 by ELISA*).

[00179] As expected, and as shown in FIGs 1B-C, immunization induced an increased production of antigen-specific serum IgG1 and IgG2 for the vaccinated group in comparison to the placebo group. Interestingly, the

IgG2/IgG1 ratio was 1 for SACOL0442 (see FIG. 1D), which is an indication of a balanced Th1/Th2 immune response to this antigen. For the antigens SACOL0029, SACOL0720, SACOL1912 and SACOL2385, the IgG2/IgG1 ratio is significantly lower than the ratio for SACOL0442 which indicated that these antigens induced mostly an IgG1 antibody response via the Th2 pathway.

EXAMPLE 3: Antigen dependent proliferation of blood CD4+ and CD8+ cells following vaccination-vaccine #1

[00180] Antigen dependent proliferation of blood CD4+ and CD8+ cells from the vaccinated cows (9) and placebo cows (10) was evaluated as described in Example 1 (*Evaluation of the cellular immune response*) four weeks after the second immunization (just before the experimental infection) for each antigen. The results for CD4+ cells are shown in FIG. 2, in which each symbol represents the percentage of CD4+ cells that have proliferated for each cow after a week of incubation with the positive control (ConA) or each antigen. Open circles (○) represent data for the vaccinated cows, black squares (■) represent data for the placebo cows. Horizontal lines represent the medians: dashed lines represent the medians for the vaccinated cows while continuous lines represent the medians for the placebo cows.

[00181] The symbol * shows the statistical differences between the vaccinated and the placebo groups for antigens SACOL0029, SACOL0442, SACOL0720 and SACOL1912 (*, $P < 0.05$).

[00182] In addition, the proliferation of CD8+ cells was similar for the vaccinated and placebo cows for all antigens with the exception of the antigen SACOL0720 for with higher proliferation of the CD8+ cells was observed for the vaccinated cows (data not shown). Induction of CD8+ cells also seemed to be important for the resolution of the infection (Riollet et al., 2001; Burton and Erskine, 2003). The vaccine was able to stimulate both cellular (CD8+) and humoral (CD4+) immune response. The vaccine #1 with its different antigens leads to a balanced immune response.

EXAMPLE 4: Protection effect of the vaccine as evaluated by following the evolution of somatic cell counts (SCC) - vaccine #1

[00183] Experimental *S. aureus* IMI infection in dairy cows were carried out and evaluated as described in Example 1 (*Experimental S. aureus IMI in dairy cows, Evaluation of the S. aureus viable counts after experimental infections, Evaluation of the somatic cell counts and Statistical analysis*). Four weeks and 4 days after the second immunization, 63 CFU of *S. aureus* were infused into 3 of the 4 quarters of the vaccinated (9) and placebo cows (10) at the evening milking (day 1, arrow in FIG. 3). Aseptic milk samples were taken at morning milking and SCC was determined by Valacta (Ste-Anne-de-Bellevue, QC). The results are shown FIG. 3, in which open circles (○) and the dashed line represent data for the vaccinated cows, while the black squares (■) and the continuous line represent data for the placebo cows. Each open circle represents the mean of SCC for all the infected quarters of the vaccinated cows (27) while each square represents the mean of SCC for all the infected quarters of the placebo cows (30 quarters).

[00184] Over the challenge period, SCC in milk were found to be significantly lower for the vaccinated cows than for the placebo cows (***; $P < 0.001$), indicating less inflammation and a better control of the

infection in the vaccinated cows.

EXAMPLE 5: Correlation between SCC or the viable counts of *S. aureus* (CFU) relative to serum or milk IgG titers against specific antigens - vaccine #1

[00185] As shown in FIGs. 4A-B, SCC were positively correlated to *S. aureus* CFU of the challenge period (FIG. 4A, $r=0.82$, $P<0.0001$) and negatively correlated to the serum IgG1 titer against SACOL0442 measured prior to the infection (FIG. 4B, $r=-0.49$, $P<0.05$). Vaccination thus had reduced this criterium of inflammation induced by the challenge. A similar analysis was performed with the samples collected at day 10. The same correlations were observed as previously obtained but at this particular time point SCC and *S. aureus* CFU also correlated to the milk IgG2 titer against SACOL0029 (Fig 4C, $r=-0.48$, $P<0.05$ and $r=-0.58$, $P<0.05$, respectively). These results show that more than one antigen is involved in the immune response against the infection.

EXAMPLE 6: Materials and methods for vaccine including SACOL0442, SACOL0720, and a fusion between SACOL1867 and SACOL0029 - vaccine #2

[00186] *Production of the antigens.* Four antigens that are highly expressed during *S. aureus* bovine intramammary infection were selected for inclusion in vaccine #2. The antigens are polypeptides encoded by: SACOL0029 (GenBank™ accession No.: YP_184940.1) (SEQ ID NO: 5), SACOL1867 (GenBank™ accession No.: YP_186695.1) (SEQ ID NO: 38), SACOL0442 (SEQ ID NO: 29), and SACOL0720 (SEQ ID NO: 11). The SACOL0029 and SACOL1867 antigens were included in the form of a fusion. His-tagged recombinant proteins of SACOL0720 and SACOL0029-1867 were engineered and produced by GenScript, Inc. (Piscataway, NJ). A his-tagged recombinant protein of SACOL0442 was engineered and produced using QIA expression technology (pQE30 plasmid) from Qiagen Inc. (Mississauga, ON, Canada), according to the manufacturers' recommendations. (see FIGs. 21D-E and I, and items II, III and VII for SACOL0720, SACOL0442, and SACOL0029-1867 his-tagged sequences). The surface protein ClfA (SEQ ID NO: 184), was also additionally produced by using the QIA expression vector by cloning the *clfA* gene from *S. aureus* ATCC 25904. The latter recombinant protein was not part of the vaccine composition but was used in ELISA assays to determine IgG titers of sera against other *S. aureus* proteins such as ClfA.

[00187] The vaccine was composed of 300 µg of each of 3 antigens (SACOL0442 and SACOL0720 as defined in Example 1 and the fusion SACOL0029-1867) and with Emulsigen™-D (MVP Technologies, Omaha, NE), CpG ODN 2007 (i.e. TCGTCGTTGTCGTTTGTGCGTT (SEQ ID NO: 194) (IDT, Coralville, IA)), and indolicidin (ILPWKWPWWPWR (SEQ ID NO: 195, GenScript, Piscataway, NJ, Chemprep Inc., Miami, FL) (vaccine #2).

[00188] *Immunization of dairy cows.* Eleven healthy multiparous Holstein cows in mid-lactation were housed in a level II biosafety barn at the Dairy and Swine Research and Development Centre of Agriculture and Agri-Food Canada (Sherbrooke, QC). Cows received the vaccine #2 (vaccinated group). Two immunizations were performed 10 weeks apart, subcutaneously in the neck. No adverse side effects were observed. Blood from the caudal vein and milk samples were taken before the first immunization (preimmune serums) and then every week for the detection of total IgG.

[00189] *Detection of total IgG by ELISA.* Detection of total IgG against each of the antigens in serum was

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performed as previously described with some modifications (Ster et al., *Vet. Immunol. Immunopathol.* (2010), 136: 311-318). Nunc MaxiSorp™ 96-well plates (Thermo Fisher Scientific Inc., Rochester, NY) were coated with the test antigen (5 µg/mL diluted in carbonate/bicarbonate buffer, Sigma Aldrich, Oakville, ON) and incubated overnight at 37°C. The plates were then saturated with the PBS containing 0.5% gelatin (BD, Franklin Lakes, NJ) for 1 h at 37°C. One hundred microliters of two-fold serial dilutions of the sera in PBS containing 0.5% gelatin and 0.1% Tween™ 20 were loaded into the plates and incubated for 1 h at 37°C. The plates were washed three times with PBS containing 0.1% Tween™ 20. One hundred microliters of horseradish peroxidase (HRP)-conjugated secondary antibody were added to the plate. The secondary antibodies used were a goat anti-bovine IgG (Jackson ImmunoResearch Laboratories Inc., West Grove, PA) diluted 1/1000,000 in PBS containing 0.5% gelatin and 0.1% Tween™ 20. After 1 h of incubation at 37°C followed by 3 washes, peroxidase activity was detected with 3,3',5,5'-tetramethylbenzidine (TMB) reagent (KPL Inc., Gaithersburg, MD) according to the manufacturer's recommendations.

EXAMPLE 7: The fusion of antigens induces high antibody titers - vaccine #2

[00190] FIG. 5 shows serum total IgG titers for the vaccinated cows for each antigen of the vaccine (including the fused antigens SACOL0029 and SACOL1867 (labeled SACOL0029-1867 on FIG. 5). Each open circle represents the titer four weeks after the second immunization for each cow (just before the experimental infection) whereas each black diamond represents the preimmune titer. Horizontal lines represent the medians: solid line for the preimmune serums, dotted line for the samples taken four weeks after immunization. Titers for the vaccinated cows are higher than the titers of the preimmune serums (**, $P < 0.01$; ***, $P < 0.001$ for the other antigens tested).

[00191] FIG. 5 thus shows that the vaccine composed of three separate antigens, including a fusion peptide, induces a strong immune response in the cows. Furthermore, FIG. 5 surprisingly shows that the fused antigens SACOL0029 and SACOL1867 (fusion SACOL0029-SACOL1867) raised antibody titers that were above those raised by each of the antigen alone (Compare FIG. 1A vs. FIG. 5) and that such fused antigens provide an additional benefit to the vaccine.

[00192] More particularly, when administered individually in a vaccine, the titers of immune cows against SACOL0029 and SACOL1867 reached 3200 and 51200, respectively (FIG. 1A), whereas when these antigens were administered as a fusion, the titers of immune cows reached 12800 and 409600, respectively (FIG. 5), showing that the fusion create an unexpected synergy in the immune response.

EXAMPLE 8: Materials and methods for vaccine comprising SACOL0029, SACOL1867, and a fusion between SACOL1867 and SACOL0029 - vaccine #3

[00193] *Production of the antigens.* Three antigens derived from two genes that are highly expressed during *S. aureus* bovine intramammary infection were selected for inclusion in a vaccine. These antigens are: SACOL0029 (GenBank™ accession No.: YP_184940.1) (SEQ ID NO: 5), SACOL1867 (GenBank™ accession No.: YP_186695.1) (SEQ ID NO: 38) and a fusion between SACOL1867 and SACOL0029 (GenBank™ accession

No.: YP_184940.1) (SEQ ID NO: 5). His-tagged recombinant proteins of SACOL0029, SACOL1867 and SACOL0029-1867 were engineered and produced by GenScript, Inc. (Piscataway, NJ). (see FIGs. 21A, F and I, items I, IV and VII for SACOL0029, SACOL1867, and SACOL0029-1867 his-tagged sequences).

[00194] *Immunization of mice.* The immunogenic properties of recombinant *S. aureus* proteins encoded by the SACOL0029, SACOL1867 genes and a fusion of SACOL0029 and SACOL1867 were evaluated in mice. Four groups of mice received the exact equimolar quantity of proteins, either in a monovalent form (SACOL0029 or SACOL1867) or in a multivalent form (the fusion SACOL0029-1867 or SACOL0029 together with SACOL1867 in combination), were compared.

[00195] In brief, the theoretical molecular weight of each amino acid sequence corresponding to the entire fusion or to the SACOL0029 or SACOL1867 portion of the fusion were calculated using the ExPASy™ Bioinformatic resource portal (http://web.expasy.org/cgi-bin/compute_pi/pi_tool).

[00196] Five micrograms of the fusion were administered to one group of mice. The corresponding molar quantity of 5 µg of the SACOL0029-1867 fusion was determined to be 168.55 pmol, in regard to its theoretical molecular weight. An amount of 1.15 µg and 3.69 µg of SACOL0029 and SACOL1867, respectively was administered in two other groups of mice in order to provide 168.55 pmol of each antigen, respectively. The last group of mice received the combination of the two individual antigens (168.55 pmol of each).

[00197] For the preparation of the immunization doses, SACOL0029, SACOL1867 and the SACOL0029-1867 fusion polypeptides were individually mixed and suspended in PBS to obtain the final equimolar quantity of each antigenic dose in a volume of 100 µl. Twenty CD-1 female mice were randomly divided into 4 groups: group A (5 mice) received 5 µg of the SACOL0029-1867 fusion protein (**Fusion**); group B (5 mice) received 1.15 µg of SACOL0029 and 3.69 µg of SACOL1867 (**Combination**); group C (5 mice) received 1.15 µg of SACOL0029 (**0029**) and group D received 3.69 µg of SACOL1867 (**1867**). The CD-1 mice were immunized by two subcutaneous injections in the neck two weeks apart. No adverse side effects were observed during the totality of the experimental immunization period. Blood samples were taken just before the first priming injection (preimmune serums) and ten days after the boost immunization (immune serums). The blood aliquots were allowed to clot at room temperature for an hour, centrifuged at 10,000 g for 10 min at 4°C. The sera were harvested and kept at -20°C until subsequent analysis.

[00198] *Detection of total IgG by ELISA.* Detection of serum total IgG against SACOL0029 and SACOL1867 recombinant proteins was performed as previously described with some modifications (Ster et al., *Vet. Immunol. Immunopathol.* (2010), 136: 311-318). Nunc MaxiSorp™ 96-well plates (Thermo Fisher Scientific Inc., Rochester, NY) were coated with 75 µl of each of the test antigen (6.67 µg/mL diluted in carbonate/bicarbonate buffer, Sigma Aldrich, Oakville, ON) and incubated overnight at room temperature. The plates were then saturated with PBS containing 5% skim milk powder for 1 h at 37°C. One hundred microliters of four-fold serial dilutions of the sera in PBS containing 3% milk and 0.025% Tween™ 20 were loaded into the plates and incubated for 1 h at 37°C. The plates were washed three times with PBS containing 0.05% Tween™ 20. One hundred microliters of horseradish peroxidase (HRP)-conjugated secondary antibody were then added to the plate. The secondary

antibody used was a commercial goat anti-mouse IgG (Jackson ImmunoResearch Laboratories Inc., West Grove, PA), diluted 1/5000 in PBS containing 3% milk and 0.025% Tween™ 20. After 1 h of incubation at 37°C followed by 3 washes, peroxidase activity was detected with the addition of one hundred microliters of 3,3',5,5'-tetramethylbenzidine (TMB) reagent (KPL Inc., Gaithersburg, MD, according to the manufacturer's recommendations.

[00199] *Statistical analysis* Statistical analysis of the antibody titers and of the correlation was performed using GraphPad Prism™ v6.05.

EXAMPLE 9: The fusion of antigens induces significantly higher antibody titers compared to monovalent antigens or a combination of antigens - vaccine #3

[00200] FIG. 6 shows that an antigen (SACOL1867) included in a fusion polypeptide (i.e., the SACOL0029-1867 fusion protein) can induce a strong and specific antibody immune response against that specific antigen (SACOL1867), and, more importantly, that this response can be significantly higher than that obtained with a monovalent form of this antigen (SACOL1867 administered alone) or a multivalent combination of individual polypeptides that are part of the fusion (combination of SACOL1867 plus SACOL0029). Thus, in addition to the advantage of generating an immune response against multiple polypeptidic targets, such fused antigens also provide the additional benefit of greatly improving the antibody titers against those targets.

EXAMPLE 10: Materials and methods for vaccines including SACOL0720 fragment(s) and/or SACOL442 fragment(s) – vaccines #4-6

[00201] *Production of the antigens.* Peptides and amino acid fragments of 15 to 50 amino acids in length and derived from sequences SACOL0442 and/or SACOL0720 were selected based on the presence of B-cell epitopes. Fusions of peptide epitopes were also designed in which an amino acid linker (for example, EAAAKEAAK (SEQ ID NO: 62), or ERKYK (SEQ ID NO: 61) or KDYERKYKKHIVS (SEQ ID NO: 196)) joined the various epitopes. Peptides and amino acid fragments were synthesized by Biomatik, Inc. (Cambridge, ON). Upon receipt, lyophilised peptides and amino acid fragments were suspended in sterile water at a concentration of 5 mg/mL and stored at -80 °C until day of use.

[00202] *Immunization of mice.* Peptides and amino acid fragments were used as antigens for immunization of mice. For the preparation of the immunization doses, each peptide and amino acid fragment or a combination of such were mixed and suspended in PBS containing 20 % of the EMULSIGEN®-D oil-in-water emulsion adjuvant to obtain a final dose of 100 µg of polypeptide per dose, unless otherwise specified. CD-1 female mice were randomly divided into different groups of 3 to 4 animals. Mice were immunized by two subcutaneous injections in the neck two weeks apart. No adverse side effects were observed during the totality of the experimental period. Blood samples were taken just before the first priming injection (preimmune serums) and ten days after the boost immunization (immune serums). The blood aliquots were allowed to clot at room temperature for an hour, and then centrifuged at 10,000 g for 10 min at 4°C. The sera were harvested and kept at -20°C until subsequent analysis.

[00203] *Detection of total IgG by ELISA.* Detection of serum total IgG, against specific amino acid sequences

found in the antigens used for the immunization of mice, was performed as previously described with some modifications (Ster et al., *Vet. Immunol. Immunopathol.* (2010), 136: 311-318). Nunc MaxiSorp™ 96-well plates (Thermo Fisher Scientific Inc., Rochester, NY) were coated with 100 µl of each of the target amino acid sequences diluted at a final concentration of 5 µg/mL in carbonate/bicarbonate buffer (Sigma Aldrich, Oakville, ON) and incubated overnight at room temperature. The plates were then saturated with PBS containing 5% skim milk powder for 1 h at 37°C. One hundred microliters of four-fold or two-fold serial dilutions of the sera in PBS containing 1% milk and 0.025% Tween™ 20 were loaded into the plates and incubated for 1 h at 37°C. The plates were then washed three times with PBS containing 0.05% Tween™ 20. One hundred microliters of horseradish peroxidase (HRP)-conjugated secondary antibody were then added to the plate. The secondary antibody used was a goat anti-mouse IgG (Jackson ImmunoResearch Laboratories Inc., West Grove, PA), diluted 1/5000 in PBS containing 1% milk and 0.025% Tween™ 20. After 1 h of incubation at 37°C followed by 3 washes with PBS Tween™ 20 and a final wash with PBS, peroxidase activity was detected with 3,3',5,5'-tetramethylbenzidine (TMB) reagent (KPL Inc., Gaithersburg, MD) according to the manufacturer's recommendations.

[00204] *Statistical analysis.* Statistical analysis of the antibody titers and optical densities was performed using GraphPad Prism™ v6.05.

EXAMPLE 11: Immune response against a fusion of peptides that includes epitopes encoded from sequences SACOL0442 and SACOL0720 - vaccine #4

[00205] A fusion of peptide epitopes encoded from SACOL0442 and SACOL0720 was used to vaccinate mice (n = 4). The sequence of the fusion of peptides was **KDGGKYTLESHKELQ***EAAAKEAAAK***DKINKIYFMTD****VDLGGPTFVLND** (SEQ ID NO: 3) (vaccine #4), where the linker is italicized and the different epitopes are identified in bold characters. The epitopes were **KDGGKYTLESHKELQ** (SEQ ID NO: 1) encoded from SACOL0442, **DKINKIYFMTD****VDL** (SEQ ID NO: 23) encoded from SACOL0720, and **VDLGGPTFVLND** (SEQ ID NO: 24) also encoded from SACOL0720. The IgG antibodies from the sera harvested from the animals were able to bind amino acid fragments comprising B-cell epitopes from either SACOL0442 (i.e. **KDGGKYTLESHKELQ** (SEQ ID NO: 1)) and/or SACOL0720 (i.e. **QFGFDLKHKKDALA** (SEQ ID NO: 21); **DKINKIYFMTD****VDL** (SEQ ID NO: 23), **VDLGGPTFVLND** (SEQ ID NO: 24)) in ELISA assays with antibody titers of 1/6400 or higher. The fusion of peptides used for immunization and the amino acid fragments or polypeptides used as antibody targets in ELISA assays are shown in Table III below. In this table, the epitopes are in bold and the linker sequence is italicized.

Table III- Polypeptide vaccine and antibody response targets

Fusion of peptides used for vaccination

KDGGKYTLESHKELQ*EAAAKEAAAK***DKINKIYFMTD****VDLGGPTFVLND** (SEQ ID NO: 3)

Peptides and polypeptides targets bound by IgG from vaccinated mice in an ELISA assay

KDGGKYTLESHKELQ*EAAAKEAAAK***DKINKIYFMTD****VDLGGPTFVLND** (SEQ ID NO: 3) (fusion of

peptides);

GEHLPKGNIVINTKDGGKYTLESHKELQKDRENVKINTAD (SEQ ID NO: 2) (fragment encoded by SACOL0442);

KDINKIYFMTDVLGGPTFVLNDKDYERKYKKHIVSQFGFDLKHKKDALA (SEQ ID NO: 27) (variant comprising fragments encoded by SACOL0720)

SACOL0442 (SEQ ID NO: 55) (i.e. polyhistidine version shown in FIG. 21E, item II);

SACOL0720 (SEQ ID NO: 25) (i.e. polyhistidine version shown in FIG. 21D, item III);

[00206] All antibody targets shown above were bound in an ELISA assay by IgG from mice vaccinated with the fusion antigen above.

[00207] This demonstrates that a fusion of peptide epitopes encoded by both SACOL0442 and SACOL0720 can be used to immunize and elicit an immune response in a mammal. The obtained immune response includes the production of antibodies that recognize SACOL0442 or SACOL0720, amino acid fragments or variants encoded from either SACOL0442 or SACOL0720.

EXAMPLE 12: A fusion of multiple epitopes used as an antigen in immunizations significantly enhances the immune response against a single epitope – vaccine #4

[00208] A fusion of peptide epitopes encoded from SACOL0442 and SACOL0720 was used to vaccinate mice (n = 4). The sequence of the fusion of peptides was **KDGGKYTLESHKELQ***EAAAKEAAAK***KDINKIYFMTDVLGGPTFVLND** (SEQ ID NO: 3), where the linker is italicized and the different epitopes are identified in bold characters. The epitopes were KDGGKYTLESHKELQ (SEQ ID NO: 1) encoded from SACOL0442, KDINKIYFMTDVL (SEQ ID NO: 23) encoded from SACOL0720, and DVDLGGPTFVLND (SEQ ID NO: 24) also encoded from SACOL0720. Another group of mice (n = 4) was immunized with the single peptide epitope KDGGKYTLESHKELQ (SEQ ID NO: 1), encoded from SACOL0442.

[00209] Sera were collected from animals and tested for the presence of IgG antibodies directed toward an amino acid fragment encoded from SACOL0442 (GEHLPKGNIVINTKDGGKYTLESHKELQKDRENVKINTAD) (SEQ ID NO: 2), which contains the peptide epitope KDGGKYTLESHKELQ (SEQ ID NO: 1).

[00210] As shown on FIG. 7, immunization with the fusion of three peptide epitopes (one encoded from SACOL0442 and two encoded from SACOL0720) significantly increased the antibody production against an amino acid fragment encoded from SACOL0442 (GEHLPKGNIVINTKDGGKYTLESHKELQKDRENVKINTAD) (SEQ ID NO: 2), which contains the peptide epitope KDGGKYTLESHKELQ (SEQ ID NO: 1), compared to the antibody level obtained when only using the peptide epitope KDGGKYTLESHKELQ (SEQ ID NO: 1) as antigen for immunization.

EXAMPLE 13: Immune response against a polypeptide fragment of 50 amino acids encoded a variant of SACOL0720 -vaccine #5

[00211] A group of mice (n = 3) was vaccinated with a 50-amino acid peptide fragment

(**KDINKIYFMTDVLGGPTFVLNDKDYERKYKKHIVSQFGFDLKHKKDALA** (SEQ ID NO: 27)) (vaccine #5) containing B-cell epitopes (bold characters) encoded from the sequence SACOL0720, more specifically epitopes KDINKIYFMTDVL (SEQ ID NO: 23), DVDLGGPTFVLND (SEQ ID NO: 24) and QFGFDLKHKKDALA (SEQ ID NO: 21). The overall sequence of **KDINKIYFMTDVLGGPTFVLNDKDYERKYKKHIVSQFGFDLKHKKDALA** (SEQ ID NO: 27) vary from the native sequence of SACOL0720 by four amino acids in the region linking the epitopes DVDLGGPTFVLND (SEQ ID NO: 24) and QFGFDLKHKKDALA (SEQ ID NO: 21). Vaccine #5 can thus be considered being a variant fragment of SACOL0720 or a fusion of epitopes from SACOL0720, which are spaced by linker ERKYK (SEQ ID NO: 61).

[00212] Sera were tested for the presence of IgG antibodies directed toward a fragment of the native protein encoded by SACOL0720 (SEQ ID NO: 25) (i.e. polyhistidine version shown in FIG. 21D, item II). Both mice vaccinated with the peptide fragment corresponding to the variant sequence of amino acids (or fusion SACOL0720-720) produced antibodies that recognized epitopes in the original sequence of amino acids in an ELISA assay with titers of 1/6400 or higher.

[00213] This demonstrates that an amino acid fragment that comprises epitopes encoded from sequence SACOL0720 can elicit an immune response in a mammal. This also further demonstrates that a variant of the native sequence has the capacity to stimulate the immune system against the original fragment sequence containing B-cell epitopes.

EXAMPLE 14 : Immune response against a combination of fusions (peptide fusion 0442-0720 and polypeptide fusion 0029-1867) - vaccine #6

[00214] A fusion of peptide epitopes encoded from SACOL0442 and SACOL0720 (see sequence in FIG. 21I, Item VII- fusions) was combined to a polypeptide fusion containing sequences of SACOL0029 and SACOL1867 (see sequence in FIG. 21I, Item VII fusions) and was used to vaccinate mice (vaccine #6).

[00215] For the preparation of the immunization doses, the peptide fusion 0442-0720 and the polypeptide fusion 1867-0029 were mixed and suspended in PBS containing 20 % of the EMULSIGEN®-D oil-in-water emulsion adjuvant to obtain a final dose of 100 µg and 5 µg per dose of the peptide fusion (0442-0720) and the polypeptide fusion (0029-1867), respectively. CD-1 female mice (n = 3) were immunized by three subcutaneous injections in the neck. The first two injections were made one week apart and the third injection 3 weeks after the second one. No adverse side effects were observed during the totality of the experimental period. Blood samples were taken just before the first priming injection (preimmune serums) and fourteen days after the last boost immunization (immune serums). The blood aliquots were allowed to clot at room temperature for an hour, and then centrifuged at 10,000 g for 10 min at 4°C. The sera were harvested and kept at -20°C until subsequent analysis.

[00216] The IgG antibodies from the sera harvested from the animals were able to bind amino acid fragments comprising epitopes from either SACOL0442 or SACOL0720 or to polypeptide SACOL0029 or SACOL1867 in ELISA assays with antibody titers of 1/6400 or higher. The fusion of peptides and polypeptides used for immunization and the polypeptides or amino acid fragments used as antibody targets in ELISA assays are shown

in the Table IV below.

Table IV- Mixed polypeptide fusion vaccine and antibody response targets

A mixture of the fusion of peptides 0442-0720 and polypeptide fusion 0029-1867 was used for vaccination (vaccine #6)

The epitopes are in bold and the linker sequence is italicized

0442-0720: **KDGGKYTLESHKELQ***EAAAKEAAAK***KDINKIYFMTD****VDLGGPTFVLND** (SEQ ID NO: 3)

0029-1867: SACOL0029-**GGGSGGGSGGGGS**-SACOL1867 (SEQ ID NO: 55)

Peptides and polypeptides bound by IgG from vaccinated mice in an ELISA assay

GEHLPKGNIVINTKDGGKYTLESHKELQKDRENVKINTAD (fragment encoded by SACOL0442) (SEQ ID NO: 2) (see sequence in FIG. 21I, Item VII- fusions);

KDINKIYFMTD**VDLGGPTFVLND****KDYERKYKKHIVSQFGDLKHKDALA** (fragment encoded by SACOL0720) (SEQ ID NO: 27) (see sequence in FIG. 21I, Item VII- fusions);

SACOL1867 (SEQ ID NO: 40) (see his-tagged sequence in FIG. 21F, Item IV);

SACOL0029 (SEQ ID NO: 8) (see his-tagged sequence in FIG. 21A, Item I);

[00217] This demonstrates that a combination of fusions (e.g., peptide fusion 0442-0720 mixed with the polypeptide fusion 0029-1867) can be used to immunize and elicit an immune response in a mammal. The obtained immune response includes the production of antibodies that recognize amino acid sequences encoded from either SACOL0442 or SACOL0720 or SACOL0029 or SACOL1867.

EXAMPLE 15: Materials and methods for attenuated live mutant

[00218] *Bacterial strains and growth conditions.* Strains used in Examples 15-25 are listed in Table V. *S. aureus* ATCC 29213 and its isogenic mutant $\Delta 720$ were previously described (Allard *et al.* 2013). Except otherwise stated, *S. aureus* strains were grown in tryptic soy broth (TSB) and agar (TSA) (BD, ON, Canada), and *Escherichia coli* DH5 α were grown in LB and LBA medium (BD). Whenever required, ampicillin (100 μ g/ml) (Sigma, Oakville, Ontario, Canada), chloramphenicol (20 μ g/ml) (ICN Biomedicals, Irvine, CA), and erythromycin (10 μ g/ml) (Sigma) were added to agar plates. For the immunological tests, four different bovine mastitis isolates were selected corresponding to some of the predominant *S. aureus spa* types found in Canadian dairy herds and elsewhere in the world (Veh *et al.*, 2015; Mitra *et al.*, 2013). Strain SHY97-3906 (*spa* t529) was isolated from a case of clinical bovine mastitis that occurred during the lactation period, and CLJ08-3 (*spa* t359) was originally isolated from a cow with persistent mastitis at dry-off (Allard *et al.*, 2013). Strains Sa3151 (*spa* t13401) and Sa3181 (*spa* t267) were obtained from the Canadian Bovine Mastitis and Milk Quality Research Network (CBMMQRN) Mastitis Pathogen Culture Collection (Université de Montréal, Faculté de médecine vétérinaire, St-Hyacinthe, QC, Canada), and were isolated from cases of subclinical intramammary infections.

Table V- Strains and plasmids used in Examples 15-25

Strain or plasmid	Relevant details	Source or reference
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Strains		
<i>S. aureus</i>		
RN4220	Derivative of 8325-4, acceptor of foreign DNA, r-	Kreiswirth <i>et al.</i> (1983)
ATCC29213	Wild Type, SACOL0720 (<i>vraG</i>) positive, normal phenotype	American Type Culture Collection
Δ720	SACOL0720 (<i>vraG</i>) transposon insertion isogenic mutant of ATCC29213	Allard <i>et al.</i> (2013)
Δ <i>hemB</i>	<i>hemB::Emr</i> ; isogenic mutant of ATCC29213, SCV phenotype	As described herein
Δ720Δ <i>hemB</i>	<i>hemB::Emr</i> ; isogenic mutant of Δ720, SCV phenotype	As described herein
<i>E. coli</i>		
SHY97-3906 (<i>spa</i> t529)		isolated from a case of clinical bovine mastitis
CLJ08-3 (<i>spa</i> t359)		isolated from a cow with persistent mastitis at dry-off
Sa3151 (<i>spa</i> t13401)		CBMMQRN) Mastitis Pathogen Culture Collection
Sa3181 (<i>spa</i> t267)		CBMMQRN) Mastitis Pathogen Culture Collection
DH5α	<i>lacZDM15) hsdR17 recA1 endA1 gyrA96 thi-1 relA1</i>	Invitrogen (ON, Canada)
Plasmids		
pBT2	Shuttle vector, temperature-sensitive, AprCmr	Brückner (1997)
PBT-E	pBT2 derivative, inserted <i>ErmA</i> cassette	As described herein
pBT-E <i>hemB</i>	pBT2 derivative, for <i>hemB</i> deletion; Ap ^r Cm ^r Em ^r	As described herein

[00219] *Cell culture conditions.* An established bovine mammary epithelial cell (BMEC) line, MAC-T (Huynh *et al.*, 1991), was used as a cell culture model of infection. The MAC-T cells were routinely cultured and maintained in Dulbecco's modified Eagle's medium (DMEM) containing 10% heat-inactivated fetal bovine serum (FBS), supplemented with 5μg/ml insulin (Roche Diagnostics Inc., Laval, Canada) and 1μg/ml hydrocortisone (Sigma), and incubated at 37°C in a humidified incubator with 5% CO₂. Cell culture reagents were purchased from Wisent

(St-Bruno, QC, Canada).

[00220] *DNA manipulations.* Recommendations from the manufacturers of kits were followed for genomic DNA isolation (Sigma), plasmid DNA isolation (Qiagen, ON, Canada), extraction of DNA fragments from agarose gels (Qiagen) and purification of PCR products and of digested DNA fragments (Qiagen). An additional treatment of 1h with lysostaphin (Sigma) at 200 µg/ml was used to achieve efficient lysis of *S. aureus* cells in genomic and plasmid DNA isolations. Primers (IDT® Integrated DNA Technologies; Coraville, Iowa, USA) were designed to add restriction sites upstream and downstream of the amplified products. PCRs were performed using the Taq DNA Polymerase (NEB, Pickering, ON, Canada) for routine PCR or the Q5 high fidelity DNA Polymerase (NEB) for cloning, and cycling times and temperatures were optimized for each primer pair. Plasmid constructs were generated using *E. coli* DH5α (Invitrogen, Burlington, ON, Canada), restriction enzymes (NEB), and the T4 DNA ligase (NEB). Plasmid constructs were validated by restriction digestion patterns and DNA sequencing before electroporation in *S. aureus* RN4220 (Kreiswirth *et al.*, 1983) and in final host strains. Plasmids used in Examples 15-25 are listed in Table V above.

[00221] *Generation of live attenuated *S. aureus* strain Δ720 and ΔhemB.* An isogenic *hemB* mutant of the ATCC 29213 strain was constructed, in which the *hemB* gene was deleted and replaced by the insertion of an *emrA* cassette by homologous recombination. *S. aureus* ATCC 29213 mutant for gene SACOL0720 (Δ720) was generated using the TargeTron™ Gene Knockout System (with the TargeTron™ Vector pNL9164 (Sigma-Aldrich Canada Ltd.) (Chen *et al.*, 2007) for disruption of bacterial genes by insertion of group II introns (fragment size of approx. 2Kb as previously described (Allard *et al.*, 2013) between nucleotide 803 and 804 in *S. aureus* ATCC29213. The manufacturer protocols and recommendations were followed.

[00222] *Generation of ΔhemBΔ720.* To achieve a second mutation in gene *hemB* in order to obtain a SCV phenotype in the Δ720 mutant genetic background, another strategy was used: the temperature-sensitive pBT2-*hemB:emrA* (pBT-E:*hemB*) was used in a strategy previously described (Mitchell *et al.*, 2008), with some modifications. Briefly, the pBT-E plasmid was constructed by the insertion of an *emrA* cassette between XbaI and SalI sites of temperature-sensitive shuttle vector pBT2 (Brückner, 1997). The flanking regions of gene *hemB* (SACOL1715) DNA fragments were amplified from *S. aureus* ATCC 29213 and were cloned on both sides of the *emrA* cassette into the plasmid pBT-E. The plasmid was then transferred for propagation into *S. aureus* RN4220 (res-). After bacterial lysis with lysostaphin (200 µg/ml for 1 h at room temperature), plasmid DNA was isolated and used to transform ATCC 29213 and Δ720 by electroporation. For plasmid integration and mutant generation, bacteria were first grown overnight at 30°C with 10 µg/ml of erythromycin and a 1 µg/ml hemin supplementation (Sigma-Aldrich, ON, Canada). Bacteria were then diluted 1:1000 and grown overnight at 42°C with 2.5 µg/ml of erythromycin and 1 µg/ml hemin. This step was repeated twice. Finally, bacteria were diluted 1:1000 and grown overnight at 42°C without antibiotics. Mutants with the inactivated *hemB* gene were selected as resistant to erythromycin and sensitive to chloramphenicol, together with an SCV phenotype that can be complemented (i.e., reversion to the normal growth phenotype) by a 5 µg/ml hemin supplementation on agar plates. The deletion of *hemB* in the ATCC 29213 (i.e., Δ*hemB*) and Δ720 (i.e., Δ*hemB*Δ720) strains was confirmed by PCR (see FIGs. 8A and B).

[00223] *Hemin supplementation in broth culture.* To evaluate the capacity of hemin to restore optimal growth kinetics of *S. aureus* $\Delta hemB$ and the double mutant $\Delta 720\Delta hemB$, overnight bacterial cultures were diluted to an $A_{600\text{ nm}}$ of approximately 0.1 in culture tubes containing fresh BHI supplemented with hemin (Sigma) added at various concentrations. The $A_{600\text{ nm}}$ of cultures was monitored at different points in time during the incubation period at 35°C (225 rpm).

[00224] *S. aureus infection of bovine mammary epithelial cells (BMECs).* MAC-T BMECs were used for the characterization of intracellular infectivity and persistence of ATCC 29213 (WT) and its isogenic mutants. Forty-eight hours before infection, $1 \times 10^5/\text{ml}$ MAC-T cells were seeded on treated 24-well plates (Corning) to obtain 30 % confluence. Monolayers were grown to confluence under 10% CO_2 at 37°C. Six hours prior to infection, monolayers were washed with DMEM and incubated with invasion medium (IM) (growth medium without antibiotics containing 1% heat-inactivated FBS). Overnight bacterial cultures were diluted 1:20 in fresh TSB and grown to mid-logarithmic growth phase, then washed with PBS and diluted in IM to a multiplicity of infection of 10. Invasion was achieved by incubating monolayers with bacteria for 3 h. Monolayers were then washed with DMEM and incubated with IM containing 20 $\mu\text{g}/\text{ml}$ lysostaphin to kill extracellular bacteria. The use of lysostaphin to kill extracellular normal and SCV *S. aureus* was previously validated in cell invasion assays (Moisan *et al.*, 2006 and Tuchscher *et al.*, 2011). The treatment was allowed for 30 min to determine CFUs at 3h of infection, or for an additional 12 or 24 h. Then, following extensive washing with Dulbecco's Phosphate-Buffered Saline (DPBS), monolayers were detached with trypsinization and lysed with 0.05% Triton X-100 and PBS was added to obtain a final 1X concentration. The lysate was serially diluted and plated on TSA for CFUs determination.

[00225] *BMECs viability and metabolic activity assay.* To determine the cytotoxic damage inflicted by *S. aureus* ATCC 29213 (WT) and its isogenic mutants on MAC-T cells, the MTT cell metabolic activity assay that measures the reduction of 3-[4,5-dimethylthiazol-2-yl]-2,5 diphenyl tetrazolium bromide (MTT) into an insoluble formazan product in viable cells, was performed. The assay followed the method of Kubica *et al.* (Kubica *et al.*, 2008) with some modifications. Briefly, *S. aureus* infection of cells was achieved as described in the persistence assay, but instead of lysis after 12 h or 24 h, cells were incubated with 100 μl of MTT reagent (5 mg/ml) (Sigma) in DPBS for 2 h at 37 °C. Following this, an acidic solvent solution of 16 % SDS and 40 % PMF, pH 4.7, was added to lyse the cells and solubilize the crystals of formazan overnight. The samples were read using an Epoch microplate reader (Biotek Instruments Inc.) at a wavelength of 570 nm. All assays were performed in triplicate, and control wells with uninfected cells (high viability control) or lysed WT infected cells (bacteria background control; treated with 0.05 % triton X-100 for 10 min before MTT addition) were included to each plate. The level of metabolic activity was calculated using the following formula:

[00226] $(\text{absorbance of the sample} - \text{background control}) / \text{high control} \times 100.$

[00227] *Virulence in the mouse mastitis model.* The mouse mastitis model of infection is based on that previously described (Brouillette, 2005; Brouillette, 2004). All the experiments performed with mice were approved by the ethics committee on animal experimentation of the Faculté des sciences of the Université de Sherbrooke and were conducted in accordance with the guidelines of the Canadian Council on Animal Care.

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Briefly, one hour following removal of 12-14 day-old offspring, lactating CD-1 mice (Charles River Laboratories) were anesthetized with ketamine and xylazine at 87 and 13 mg/kg of body weight, respectively, and mammary glands were inoculated under a binocular. Mammary ducts were exposed by a small cut at the near ends of teats and a 100 μ l-bacterial suspension containing 10^2 CFUs in endotoxin-free phosphate-buffered saline (PBS, Sigma) was injected through the teat canal using a 32-gauge blunt needle. Two glands (fourth on the right [R4] and fourth on the left [L4] from head to tail) were inoculated for each animal. Mammary glands were aseptically harvested at the indicated times, weighed and visually evaluated for inflammation. Bacterial burden was evaluated after mechanical tissue homogenization in PBS, serial dilutions, and plating on agar for CFU determination. In a second experiment, homogenized glands were conserved for protein extraction for myeloperoxidase (MPO) activity enzymatic assays.

[00228] *Mammary gland protein extraction.* Total protein extraction from mammary glands was performed by an optimized method previously described (Pulli *et al.*, 2013), with some modifications. Mammary tissues were homogenized in a buffer containing a final concentration of potassium phosphate of 50 mM, pH 6.0, and hexadecyltrimethylammonium bromide (CTAB) 50 mM (Sigma). The samples were then sonicated, freeze-thawed in liquid nitrogen, and centrifuged at 2000 g for 15 min at 4°C. Finally, the fat layer was removed by aspiration, and supernatants were saved for a final centrifugation of 15 min at 15 000 g, to discard every cellular debris. Supernatants were distributed in aliquots and kept at -80 °C until use for the enzymatic assays or protein concentration determination as measured by the bicinchoninic acid method (BCA) Protein Assay Kit (Thermo-Scientific).

[00229] *MPO activity assay.* Neutrophil recruitment in mammary tissues was measured by quantification of MPO enzyme activity by the *o*-dianisidine- H_2O_2 method, modified for microplates (Bradley, RD. and Rothstein, GPPC., 1982). In a 96-well microplate, 10 μ l of tissue extraction supernatants were incubated with a solution of *o*-dianisidine hydrochloride (0.167 mg/mL) (Sigma) and 0.0005% H_2O_2 (Sigma) in 50 mM CTAB phosphate buffer 50 mM, pH 6.0. The MPO activity was measured kinetically with intervals of 15 s over a period of 5 min in an Epoch microplate reader at 460 nm. A Unit of MPO was considered as the amount of enzyme that degrades 1 μ mol of H_2O_2 /min at 25°C, assuming an absorption coefficient of 11.3 mM⁻¹ cm⁻¹ at 460 nm for *o*-dianisidine (Zhang *et al.*, 2004). Results were expressed as units of MPO per g of gland.

[00230] *Mouse immunizations with the live attenuated mutant $\Delta 720\Delta hemB$.* The immunogenic properties of the attenuated strain $\Delta 720\Delta hemB$ administered as a live vaccine were evaluated in mice. In preliminary studies, the mice well tolerated intramuscular and subcutaneous (SC) injections of the attenuated strain. The doses of 10^6 , 10^7 and 10^8 CFUs and the SC route were selected for subsequent experiments. For the preparation of bacterial inoculum, *S. aureus* $\Delta 720\Delta hemB$ colonies previously grown on BHIA plates were washed twice in ice cold PBS and suspended in PBS containing 15% glycerol, then aliquoted and kept at -80 °C until subsequent use. The viable bacterial counts in the inoculum preparation was validated by serial dilution plating on BHIA. CD-1 mice were randomly divided into 3 groups: group 1 (n=3) received a dose of 10^6 CFUs; group 2 (n=3), 10^7 CFUs, and group 3 (n=3), 10^8 CFUs. Mice were immunized by two subcutaneous injections of bacteria in PBS (100 μ l), in the neck, two weeks apart. Blood samples were taken just before the priming injection (preimmune serums) and

ten days after the boost immunization (immune serums). Blood aliquots were allowed to clot at room temperature for an hour and then centrifuged at 10,000 g for 10 min at 4 °C. The serums were collected and kept at -20 °C until subsequent analysis.

[00231] Preparation of *S. aureus* cell extracts. Preparation of *S. aureus* whole cell extracts was done as previously described with some modifications (Asli *et al.*, 2016). Briefly, overnight bacterial cultures were diluted 1/1000 in fresh BHI broth, and then incubated at 35 °C (225 rpm) until an A600nm of ~ 0.8 was reached. Bacterial cells were centrifuged and pellets were washed in ice-cold PBS twice and suspended with the addition of 5 ml of PBS per ml of pellet. Bacterial suspensions were first treated with lysostaphin (Sigma) (100 µg/ml of pellet) for 1 h at 37°C, and then 3 µg of protease inhibitor cocktail (Sigma), 8 µg of RNase A (Sigma) and 8 µg of DNase (Qiagen) per ml of pellet were added to the suspension. After 30 min at room temperature, cells were mechanically disrupted by 3 to 4 passages in a SLM Aminco™ French Pressure cell disrupter, and then centrifuged at 12,000 × g and 4 °C for 10 min to remove unbroken cells. Supernatant was collected and total protein concentration was determined as previously described with the BCA Protein Assay Kit.

[00232] Detection of mouse total IgG by ELISA. Detection of serum total IgG against the $\Delta 720\Delta hemB$ vaccination strain and each of the bovine IMI isolates was performed to demonstrate and measure the systemic humoral response generated by the immunization of mice. For target antigens, Nunc MaxiSorp™ 96-well plates (Thermo Fisher Scientific Inc., Rochester, NY) were coated with 100 µl of each of the whole *S. aureus* cell extracts (10 µg/ml diluted in carbonate/bicarbonate buffer, Sigma), and incubated overnight at room temperature. The plates were then saturated with PBS containing 5% skim milk powder for 1 h at 37°C, followed by a second blocking step with an addition of 5% porcine serum to prevent unspecific *S. aureus* protein A interactions. One hundred microliters of two-fold serial dilutions of the sera in the dilution buffer (PBS with 2% milk, 5% porcine serum and 0.025% Tween™ 20) were loaded into the plates and incubated for 1 h at 37°C. Plates were then washed three times with PBS containing 0.05% Tween™ 20, and loaded with 100 µl of horseradish peroxidase (HRP)-conjugated goat anti-mouse IgG (Jackson ImmunoResearch Laboratories Inc., West Grove, PA) diluted 1/5000 in the dilution buffer. After 1 h of incubation at 37°C followed by 3 washes, peroxidase activity was detected with 3,3',5,5'-tetramethylbenzidine (TMB) reagent (KPL Inc., Gaithersburg, MD) according to the manufacturer's recommendations.

[00233] Statistical analysis. Statistical analyses were carried out with the GraphPad Prism™ software (v.6.02). Intracellular bacterial CFUs and bacterial CFUs/g of gland (IMI in mice) were transformed in base 10 logarithm values before being used for statistical analyses. Statistical tests used for the analysis of each experiment and significance are specified in the figure legends.

EXAMPLE 16: Construction of strain *S. aureus* ATCC 29213 $\Delta 720$, $\Delta hemB$ and $\Delta 720\Delta hemB$

[00234] Live attenuated organisms that mimic natural infection stimulate the immune system in a powerful manner, eliciting broad and robust immune responses that produce both serum and mucosal antibodies, and effector and memory T cells which act synergistically to protect against disease (Detmer, 2006; Kollaritsch, 2000; Pasetti, 2011).

[00235] A mutation in gene SACOL0720 was shown to alter the virulence of *S. aureus* in experimental IMI infections in the cow (Allard et al., 2013).

[00236] Further live-attenuated strains were prepared for vaccine purposes based on the phenotypic aspects of *S. aureus* SCVs. SCVs do not generally generate invasive infections (i.e. additional attenuation) and can be internalized in host cells and therefore will stimulate the cell-mediated immune response in addition to the humoral immune response.

[00237] A stable *S. aureus* SCV was first created through the deletion of the *hemB* gene ($\Delta hemB$) (see Example 15, *Generation of live attenuated S. aureus strain $\Delta 720$ and $\Delta hemB$*). Further attenuation of this SCV was then achieved by inactivation of gene SACOL0720 ($\Delta 720$) (see Example 15, *Generation of $\Delta hemB\Delta 720$*).

[00238] After infection of MAC-T bovine mammary epithelial cells, the double mutant ($\Delta 720\Delta hemB$) significantly showed lower internalization and cell destruction compared to that seen with $\Delta hemB$ and $\Delta 720$, respectively.

EXAMPLE 17: Strain *S. aureus* $\Delta hemB\Delta 720$ is attenuated in MAC-T cells

[00239] The infectivity of ATCC 29213 (WT), $\Delta 720$, $\Delta hemB$ and $\Delta hemB\Delta 720$ strains were then compared in intracellular persistence assays using MAC-T cells. By comparing the three mutant strains to their isogenic WT parent, distinct effects of mutations in genes *hemB* and SACOL0720 were observed. A short 3-h incubation of bacteria with cell monolayers followed by the addition of lysostaphin to eliminate extracellular bacteria demonstrated high levels of internalization into MAC-T cells for both WT and $\Delta hemB$ strains, based on the recovery of viable intracellular bacteria (CFUs) (FIGs. 9A and B). The single $\Delta 720$ mutant however showed significantly less ($P \leq 0.01$) internalization compared to its parental WT strain (FIG. 9A). The reduction in internalization seen in $\Delta 720$ was even more pronounced when comparing the double mutant $\Delta hemB\Delta 720$ to $\Delta hemB$, with a 10-fold reduction of inoculum recovery in this 3-h internalization assay ($P \leq 0.001$, FIG. 9B). This initial reduction of internalized bacterial load was still apparent 12 and 24 h post invasion (PI) for the double mutant strain $\Delta hemB\Delta 720$ (FIG. 9C), as illustrated by the 1-log¹⁰ reduction of CFU/ml at both time points compared to that observed for $\Delta hemB$ ($P \leq 0.001$). The difference in initial intracellular bacterial loads between the single $\Delta 720$ mutant and WT strains (FIG. 9A) gradually vanished with longer incubation times (FIG. 9C), as both strains did not well persist in MAC-T cells (FIG. 10). On the opposite, intracellular CFUs recovered for the single $\Delta hemB$ strain was significantly higher compared to that recovered for the three other strains at 24 h PI (FIG. 9C, $P \leq 0.001$ against all). Overall and as expected for the SCV phenotype, the $\Delta hemB$ strain showed a higher intracellular persistence than any other strain over time (FIG. 10). These results suggest that the $\Delta 720$ mutation mainly reduces the internalization process into MAC-T cells. Results further demonstrate that the $\Delta hemB\Delta 720$ mutant is still capable of internalization and persistence into BMECs but at a much lower degree than that seen with the single $\Delta hemB$ mutant.

[00240] The $\Delta hemB\Delta 720$ and $\Delta hemB$ SCVs cause low BMEC disruption. As reported above, $\Delta hemB$ and $\Delta hemB\Delta 720$ SCV strains showed a greater persistence over time in MAC-T cells, as illustrated by their sustained viability at 12 and 24 h PI in comparison with WT and $\Delta 720$ strains (FIGs. 9C and 10). The percentage of the

inoculum recovered from cells stayed nearly the same from 0 to 24 h after lysostaphin addition, both for the double and single *hemB* mutants, with a slight increase at 12 h, indicating intracellular growth (FIG. 10). Both strains started to decrease at a slow rate after this time of infection. However, the apparent reduction of intracellular CFUs for the WT and $\Delta 720$ strains was concomitant with the visual observation of increasing damage to cell monolayers over time, in comparison to that observed with strains of the SCV phenotypes.

[00241] *MAC-T cells viability was also evaluated following infection by each of the four strains studied.* MAC-T cell viability was evaluated by the MTT method (Kubica et al., 2008). Results show that both SCV strains ($\Delta hemB$ and $\Delta hemB\Delta 720$) caused significantly less MAC-T killing in this assay in contrast to the WT and $\Delta 720$ strains. When compared to $\Delta hemB$, the WT strain nearly reduced by half the viability of cells at 12 h (FIG. 11A: WT: 25.4 %; $\Delta hemB$: 48.4%). This difference was still apparent at 24 h (FIG. 11B: 16.3% vs. 34.5 %, respectively), even if the bacterial load was 10 times higher for the $\Delta hemB$ mutant (FIG. 9C). The MAC-T cells were more damaged by $\Delta hemB$ than by the double mutant $\Delta 720\Delta hemB$ but the difference was only significant at 24 h ($P \leq 0.01$). When compared directly to the WT strain, the double mutant $\Delta 720\Delta hemB$ sustained epithelial cells viability 2.3 times more at 12 h (FIG. 11A) and 2.7 times more at 24 h (FIG. 11B) (12 and 24 h: $P \leq 0.0001$). Therefore, the greater intracellular persistence of both SCVs strains compared to the WT and $\Delta 720$ strains over time (FIG. 10) was likely to be attributed to a lower toxicity of the SCVs to MAC-T cells (FIG. 11). Taken together, results from the BMEC infection assays provided evidence of an additive effect of both $\Delta hemB$ and $\Delta 720$ mutations for the attenuation of the WT strain.

EXAMPLE 18: Strain *S. aureus* $\Delta hemB\Delta 720$ is attenuated in a mouse IMI model

[00242] To attest attenuation of $\Delta hemB\Delta 720$ in an *in vivo* model of infection, the virulence of the double mutant was evaluated and compared to the WT strain in a murine IMI model (Brouillette and Malouin, 2005). For both strains, the exponential phase of infection took place mainly within the first 12 h post-infection, while the maximal bacterial burden was reached at 24 h for the double mutant and 48 h (day 2 [D2]) for the WT strain (FIG. 12). At 24 h, the double mutant showed a reduction of $1.9 \log^{10}$ in mean CFU/g of gland compared to WT ($P \leq 0.05$). Also after 24 h, the mutant bacterial burden showed a constant decline until complete bacterial clearance was reached at day 12 (shown by the asterisk on FIG. 12). In contrast, the parental WT strain provoked severe invasive infections compared to the mutant, killing 3 of 9 remaining mice at day 2 and 2 of 3 mice at day 7 (FIG. 12; arrows) before glands could be harvested for those groups. Mice surviving the WT infection maintained high viable counts ($9 \log^{10}$ CFU/g of gland) at day 7, an approximate $5 \log^{10}$ difference in bacterial burden compared to the double mutant. These results clearly demonstrate a markedly reduced capacity of strain $\Delta hemB\Delta 720$ to multiply and survive in the mammary gland. The $\Delta hemB\Delta 720$ double mutant is therefore strongly attenuated in a mouse intramammary infection (IMI) model and is efficiently cleared from mammary glands.

[00243] The attenuated strain $\Delta hemB\Delta 720$ appears ideal for vaccination purposes and for intracellular delivery of antigens. Indeed, the low and temporary internalization of $\Delta hemB\Delta 720$ should help stimulation of cell-mediated immunity, a component of the immune response that is important for defense against *S. aureus* (Fowler and Proctor, 2014).

EXAMPLE 19: Inflammatory response to $\Delta 720\Delta hemB$ and WT strains following IMI

[00244] To monitor the inflammatory response (immune response) of the mice to infections with WT and mutant strains, neutrophil infiltration in glands was evaluated by the MPO enzymatic activity of total protein extracts of gland homogenates. MPO activity in biological samples has previously been strongly correlated with absolute number of neutrophils (Xia, 1997), and is hence an adequate marker. During the first hours after infection, neutrophil recruitment followed similar profiles for the double mutant and WT infected glands (FIG. 13), with exponential intensification of apparent neutrophil infiltration from 12 h to 24 h post infection coinciding with bacterial growth albeit with a certain delay. The absolute numbers of polymorphonuclear cells in relation with the bacterial load in mammary glands was previously shown to not always peak at the same time (Brouillette, 2005). No significant difference in MPO activity could be observed at 6, 12 and 24 h between glands infected by mutant and WT strains (FIG. 13). This equivalence in apparent neutrophil infiltration did not however correlate with the visual observation of inflammation at 24 h, at which point the WT infection generated extensive redness of infected glands in comparison to the double mutant (photographs of FIG. 14). On the contrary, mutant infected glands were not visually altered on the macroscopic level compared to PBS controls. The disparity between visual assessment of inflammation and neutrophil infiltration results could be attributed to the differences in bacterial loads (FIGs. 9A-C) and the cytotoxic activity of the WT strain (FIG. 11), and could be coherent with the highly invasive and disseminative capacity of the strain via toxins and enzymes expression. Hence, these results indicate that neutrophil recruitment in the glands infected by the mutant strain was equivalent to that seen with the WT strain and that this was sufficient to allow a subsequent decline and clearance of the mutant bacterial loads.

[00245] Lastly, to confirm strain safety, and to assess that this inflammatory response was not consequent to an inadmissible reactogenic strain, MPO activity was monitored in $\Delta 720\Delta hemB$ infected glands 4 and 12 days after infection. The level of activity was then compared to levels obtained with PBS injected mice. As illustrated in FIG. 15, the apparent neutrophil presence in mutant infected glands was still high 4 days after infection, with MPO activity ranging from 8 to 21 Units/g of gland. Besides, gland involution, the process by which the lactating gland returns to a morphologically near pre-pregnant state, is ordinarily associated with neutrophilic recruitment that allows phagocytosis of apoptotic cells during the remodelling of tissue (Stein, 2007). In the days following infection in this model, mice glands are already in that normal state of modification, as indicated by their rapid shrinking. However, the MPO levels in mutant infected glands went through a substantial decline between day 4 and 12, ($P \leq 0.01$). MPO levels were then considered to be back to a normal level at day 12 showing no significant difference from that obtained with the PBS-injected mice. The inflammatory response of $\Delta 720\Delta hemB$ infected glands goes back to normal levels with bacterial clearance (FIG. 15).

EXAMPLE 20: Immunization with $\Delta 720G\Delta hemB$ generates a strong humoral response against several *S. aureus* bovine intramammary infection isolates.

[00246] To confirm that immunization with the live $\Delta 720\Delta hemB$ can indeed generate a strong immune response suitable for its use as a putative live vaccine against *S. aureus* intramammary infections, mice were immunized with different doses of the live vaccine and serum total IgGs were assayed for binding to whole cell extracts of a variety of *S. aureus* bovine isolates. First, doses of 10^6 , 10^7 and 10^8 CFUs, administered subcutaneously in the

neck, triggered no adverse effect such as modification of mice behavior or signs of inflammation or necrosis at the immunization site throughout the immunization period. Furthermore, immunization using increasing amounts of the live double mutant ATCC 29213 $\Delta 720\Delta hemB$ yielded increasing titers of systemic IgG antibodies against a whole cell extract of its own antigens (FIG. 15B). The titers of the immune sera were significantly higher than those of the preimmune sera, demonstrating specificity of antibody production against *S. aureus* antigens present in the live vaccine. Most importantly, immunization using increasing amounts of $\Delta 720\Delta hemB$ also yielded a consequential rise of antibody titers against a variety *S. aureus* strains isolated from bovine mastitis, including strains from the major *spa* types found in Canada and elsewhere in the world (FIG. 15C). These results clearly show that (i) immunization with the double mutant can raise an immune response, and that (ii) the strain background (ATCC 29213) share sufficient common features with bovine mastitis strains so that the antibody response also strongly recognizes strains of major *spa* types.

[00247] Immunization of mice using subcutaneous injections of live $\Delta 720\Delta hemB$ raised a strong humoral response as judged by the high titers of total IgG measured against a whole bacterial cell extract. Also, the vaccine strain $\Delta 720\Delta hemB$ had sufficient common features with bovine mastitis strains so that the antibody response also strongly recognized strains from a variety of common mastitis associated *spa* types.

[00248] Although this demonstrated that the double mutant background (ATCC 29213) share many common features with bovine mastitis strains, such a double mutant can be created in any desired genetic background if one wishes, notably in any strain that was isolated from bovine mastitis, such as but not limited to *S. aureus* strain RF122.

[00249] These results show that a SCV strain having some residual intracellular capabilities can allow immune cells recruitment without establishing a severe infection. Such an SCV strain may act as a live-attenuated vaccine that adequately stimulates the immune response to combat pathogens with intracellular abilities.

EXAMPLE 21: Material and methods - SACOL0442, SACOL0720, SACOL0029 and a fusion between SACOL1867 and SACOL0029 + attenuated live bacteria (vaccine #7)

[00250] *Production of the antigens.* The production of antigens was performed as described in Example 6, in the section *production of the antigens* except for the additional presence of the antigen SACOL0029. His-tagged recombinant proteins of SACOL0029 were engineered and produced by GenScript, Inc. (Piscataway, NJ). (see FIGs. 21A, item I, his-tagged sequence).

[00251] *Generation of live attenuated *S. aureus* strain $\Delta 720\Delta hemB$.* The generation of live attenuated *S. aureus* strain was performed as described in Example 15 (*Generation of $\Delta hemB\Delta 720$*).

[00252] *Immunization of mice.* The immunogenic properties of recombinant *S. aureus* proteins encoded by the SACOL0442, SACOL0720, SACOL0029 genes and a fusion of SACOL0029 and SACOL1867 genes in combination, or not, with the live attenuated bacterial strain *S. aureus* $\Delta 720\Delta hemB$ were evaluated in mice. The mice well tolerated a dose of 10^3 , 10^5 , 10^6 , 10^7 and 10^8 CFU by subcutaneous injections in the neck and intramuscular injections in the thigh. The dose of 10^5 and the subcutaneous route were selected for the following

experiments.

[00253] For the preparation of bacterial inoculum, *S. aureus* $\Delta 720\Delta hemB$ colonies previously grown on BHIA plates were washed twice in ice cold PBS and resuspended in PBS containing 15% glycerol, then aliquoted and kept at -80°C until subsequent use. To obtain the final mice immunization dose, corresponding to 10^5 CFU of attenuated bacteria, the frozen inoculum bacterial concentration was evaluated by serial dilution plating on BHIA and then was diluted to a final concentration of 10^5 CFU/ml in PBS on the day of immunization.

[00254] For the preparation of protein doses, SACOL0029, SACOL0442, SACOL0720, and the SACOL0029-1867 fusion polypeptide were mixed and suspended in PBS to obtain a final dose of 5 μg each. CD-1 female mice were randomly divided into 3 groups: group 1 (5 mice) received a mixed protein dose (protein Mix); group 2 (5 mice) received an attenuated bacteria ($\Delta 720\Delta hemB$) dose ($\Delta 720\Delta hemB$); group 3 (6 mice) received a combination of mixed proteins and attenuated bacteria (combination). CD-1 female mice were immunized by two subcutaneous injections in the neck two weeks apart. The proteins and bacterial strains doses were diluted in PBS as previously described and administered in a final volume of 100 μl for each group of mice. No adverse side effects were observed during the totality of the experimental immunization period. Blood samples were taken just before the first priming injection (preimmune serums) and ten days after the boost immunization (immune serums). The blood aliquots were allowed to clot at room temperature for an hour, centrifuged at 10,000 g for 10 min at 4°C . The sera were harvested and kept at -20°C until subsequent analysis.

[00255] *Detection of total IgG, IgG1 and IgG2 by ELISA.* Detection of serum total IgG, IgG1 and IgG2 against each of the antigens previously used for immunization was performed as previously described with some modifications (Ster et al., *Vet. Immunol. Immunopathol.* (2010), 136: 311-318). In addition, detection of IgG against staphylococcal surface protein ClfA was performed to demonstrate the supplementary advantages of using a live strain to enhance and balance the immune response against *S. aureus*. Nunc MaxiSorp™ 96-well plates (Thermo Fisher Scientific Inc., Rochester, NY) were coated with 75 μl of each of the test antigen (6.67 $\mu\text{g/mL}$ diluted in carbonate/bicarbonate buffer, Sigma Aldrich, Oakville, ON) and incubated overnight at room temperature. The plates were then saturated with PBS containing 5% skim milk powder for 1 h at 37°C . One hundred microliters of four-fold serial dilutions of the sera in PBS containing 3% milk and 0.025% Tween™ 20 were loaded into the plates and incubated for 1 h at 37°C . The plates were washed three times with PBS containing 0.05% Tween™ 20. One hundred microliters of horseradish peroxidase (HRP)-conjugated secondary antibody were then added to the plate. The secondary antibodies used were a goat anti-mouse IgG, IgG2a and IgG1 (Jackson ImmunoResearch Laboratories Inc., West Grove, PA), diluted 1/5000 respectively in PBS containing 3% milk and 0.025% Tween™ 20. After 1 h of incubation at 37°C followed by 3 washes, peroxidase activity was detected with 3,3',5,5'-tetramethylbenzidine (TMB) reagent (KPL Inc., Gaithersburg, MD) according to the manufacturer's recommendations.

[00256] *Statistical analysis.* Statistical analysis of the antibody titers and of the correlation was performed using GraphPad Prism™ v6.05.

EXAMPLE 22: The fusion of antigens and the combination with a live attenuated *S. aureus* strain induces

high antibody titers in mice – vaccine #7

[00257] The antigens and live attenuated *S. aureus* strain $\Delta 720\Delta hemB$ are produced as described in Example 21. Mice are immunized and IgGs detected as described in Example 21.

[00258] The results in FIG. 16 show that immunization with the SACOL0029-1867 fusion (either when co-administered with other antigens or with a live attenuated strain) induces high and specific antibody responses in mice.

EXAMPLE 23: The live attenuated *S. aureus* strain significantly improves antibody immune response against some specific antigens – vaccine #7

[00259] The antigens and live attenuated *S. aureus* strain $\Delta 720\Delta hemB$ are produced as described in Example 21. Mice are immunized and IgGs detected as described in Example 21.

[00260] The results in FIG. 17 show that immunization with the attenuated live strain $\Delta 720\Delta hemB$ significantly increases the production of specific IgG antibodies against the SACOL0029 antigen, in comparison to that obtained with IgG antibodies from mice immunized with the protein mix alone.

EXAMPLE 24: The live attenuated *S. aureus* strain induces significant antibody titers against additional surface proteins of *S. aureus* – vaccine #7

[00261] The antigens and live attenuated *S. aureus* strain $\Delta 720\Delta hemB$ are produced as described in Example 21. Mice are immunized and IgGs detected as described in Example 21.

[00262] The results in FIG. 18 show that immunization with the attenuated live strain $\Delta 720\Delta hemB$ (alone or when co-administered with polypeptide antigens) significantly increases the production of specific antibodies against the staphylococcal surface protein ClfA, compared to that achieved with the protein mix alone composed of SACOL0029, SACOL0442, SACOL0720, and SACOL0029-1867.

EXAMPLE 25: The live attenuated *S. aureus* strain significantly balances the Th1/Th2 immune response – vaccine #7

[00263] The antigens and live attenuated *S. aureus* strain $\Delta 720\Delta hemB$ are produced as described in Example 21.

[00264] Serum IgG2a and IgG1 isotypes against the SACOL0029-1867 fusion protein were detected in serums of vaccinated mice as previously described and the ratio of IgG2a to IgG1 titers of each mouse was determined. IgG2a isotype is associated with the Th1 immune response in mice, whereas IgG1 is a marker for the Th2 response. As described in Example 5, the induction of IgG2 production in cows and the extent of the IgG2 titers in milk significantly correlates with protection of the cows against a challenge with *S. aureus*, as judged by the levels of the corresponding somatic cells (SCC) or bacterial counts (CFU) in milk of the cows (FIG. 4C).

[00265] The results shown in FIGs. 19 and 20 demonstrate that the attenuated live strain $\Delta 720\Delta hemB$ included in the combination immunization vaccine ($\Delta 720\Delta hemB$ *S. aureus* administered with SACOL0029, SACOL0442, SACOL0720, and SACOL0029-1867) induces a significantly higher IgG2a/IgG1 antibody ratio against the

SACOL0029-1867 fusion and SACOL0029 proteins than that seen with the protein mix immunization (SACOL0029, SACOL0442, SACOL0720, and SACOL0029-1867), resulting in a significantly more balanced Th1/Th2 response.

[00266] Examples 21 to 25 above show that even if a strong antibody response was obtained by the immunization with different antigens (including e.g., SACOL0029-1867 fusion) in a protein mix composition, the immunization of mice with a combination of these antigens with a live attenuated strain significantly improved immune responses against *S. aureus*, by inducing higher antibody titers against some specific antigens (e.g., SACOL0029), by the production of antibodies against other staphylococcal proteins (e.g., ClfA), and by achieving a more balanced IgG2a/IgG1 ratio, a good marker of a stronger Th1 type response, against the antigens co-administered with the live strain.

EXAMPLE 26: Expression of recombinant proteins in strain *S. aureus* Δ hemBA720 – Vaccines #8, 9, 10 etc.

[00267] Genes SACOL0442, SACOL0720, SACOL0029, and/or SACOL1867 as well as the fusion (e.g., size of 50 AA or more) of the genes (or of fragments thereof) SACOL0029 and SACOL1867 (SACOL0029-SACOL1867), fusions of fragments (e.g., epitopes) of SACOL720 and/or of SACOL0442 (fusion 720-720) (fusion 442-720) or any other fusion of genes or fragments thereof e.g., SACOL0029-SACOL0442, SACOL0029-SACOL0720, SACOL0029-SACOL0720-SACOL0442, SACOL0029-SACOL0720-SACOL1867, SACOL0029-SACOL1867-SACOL0442, SACOL0442-SACOL0029-SACOL0720, SACOL0442-SACOL0029-SACOL0720, SACOL0442-SACOL1867-SACOL0720, SACOL0720-SACOL0442-SACOL1867, SACOL04029-SACOL1867-SACOL0720-SACOL0442, are cloned in plasmid pCN36 (Charpentier *et al.*, 2004) under a constitutive promoter (*PblaZ* from plasmid pCN40) (Charpentier *et al.*, 2004) and expressed in the *S. aureus* Δ hemBA720 strain. Certain protein antigens proposed herein are predicted to be an exotoxin, enterotoxin or superantigen (e.g., SACOL0442) or proteins useful for protection against host defenses (e.g., SACOL0720) and could potentially interfere with the mammalian immune system and antibody production, and/or show some toxicity in the host. Although such interference was not observed with the vaccine composition and formulations described here, it may be useful to modify the protein or polypeptide expressed in the *S. aureus* Δ hemBA720 strain so that the cloned genes do not complement its virulence. For such a purpose, it is possible to use molecular biology techniques to delete or mutate the putative region(s) involved in such protein activity without losing immunogenicity (Chang *et al.*, 2008). This is the approach the applicants used to prepare the antigens of vaccine compositions of the present invention.

[00268] Expression of individual recombinant protein products by each of the *S. aureus* Δ hemBA720 strains carrying one of the constructed expression vectors is validated by LC-MS/MS analyses. Briefly, strains grown in BHI with 15 μ g/ml tetracycline to mid-logarithmic phase were centrifuged and pellets were inactivated with ethanol. Samples were kept at -20°C until cell lysis and trypsin digestion procedures. Samples are incubated with lysostaphin and trypsin at 37°C, followed by cell disruption by mechanical homogenization using glass beads and a beadbeater. Lysates are then centrifuged for 25 min at 13 000 rpm at 4 °C in order to remove cell debris, before

following with protein digestion with trypsin, reduction and alkylation were done by standard procedures before sample injection for protein detection using the MRM method of LC-MS/MS.

[00269] Alternatively, recombinant protein expression is also confirmed by Western blots of bacterial lysates.

EXAMPLE 27: Mouse immunization with attenuated strains expressing antigens – Vaccines #8, etc.

[00270] CD-1 female mice are vaccinated by two subcutaneous injections two weeks apart. Each of the *S. aureus* Δ hemBA720 strains carrying or not one of the constructed expression vectors, are diluted in saline and administered in a final volume of 100 μ l per dose. Group 1 receives a double-mutant strain alone; group 2 receives a double-mutant strain expressing fusion SACOL0029-1867; group 3 receives a double-mutant strain expressing fusion SACOL0029-0442; group 4 receives a double-mutant strain expressing fusion SACOL0029-0720; group 5 receives a mixture of double-mutant strains, one expressing fusion SACOL0029-1867 and the other expressing fusion SACOL0029-0442; group 6 receives a mixture of double-mutant strains, one expressing fusion SACOL0029-1867 and the other expressing fusion SACOL0029-0720; and group 7 receives a mixture of double-mutant strains. Blood samples are taken just before the first injection and twelve days after the second one. The samples are allowed to clot at room temperature for an hour, then centrifuged at 2 000 g for 10 min at 4°C. The supernatants (sera) are harvested and kept at -20°C until subsequent analysis. Mice are euthanized at day 27 and blood is collected by cardiac puncture. The immune sera are recovered, aliquoted and stored as for the pre-immune sera.

[00271] The immune response to vaccination is evaluated by enzyme-linked immunosorbent assay (ELISA) for the presence of serum polyclonal IgG antibodies directed towards *S. aureus* whole cells (Wood strain) or specific recombinant proteins. Anti-mouse IgG-HRP (HRP: horseradish peroxidase) is used as a secondary antibody to detect the colorimetric production of 3,3',5,5'-tetramethylbenzidine (TMB) substrate oxidation by peroxidase activity using a spectrophotometer.

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Phe	Ser	Phe	Val	Ala	Leu	Lys	Tyr	Ala	His	Lys	Leu	Asn	Met	Thr	Glu
	35					40					45				

Ser	Tyr	Pro	Ile	Ile	Lys	Glu	Gly	Ser	Gln	Val	Gly	Ser	Tyr	Phe	Leu
50					55				60						

Phe	Phe	Ile	Ile	Ile	Ala	Phe	Leu	Leu	Tyr	Ala	Asn	Val	Leu	Phe	Ile
65					70				75					80	

Lys	Arg	Arg	Ser	Tyr	Glu	Leu	Ala	Leu	Tyr	Gln	Thr	Leu	Gly	Leu	Ser
			85					90						95	

Lys	Phe	Asn	Ile	Ile	Tyr	Ile	Leu	Met	Leu	Glu	Gln	Leu	Leu	Ile	Phe
		100					105					110			

Ile	Ile	Thr	Ala	Ile	Leu	Gly	Ile	Ile	Ile	Gly	Ile	Phe	Gly	Ser	Lys
		115				120					125				

Leu Leu Leu Met Ile Val Phe Thr Leu Leu Gly Ile Lys Glu Lys Val
130 135 140

Pro Ile Ile Phe Ser Leu Arg Ala Val Phe Glu Thr Leu Met Leu Ile
145 150 155 160

Gly Val Ala Tyr Phe Leu Thr Ser Ala Gln Asn Phe Ile Leu Val Phe
165 170 175

Lys Gln Ser Ile Ser Gln Met Ser Lys Asn Asn Gln Val Lys Glu Thr
180 185 190

Asn His Asn Lys Ile Thr Phe Glu Glu Val Val Leu Gly Ile Leu Gly
195 200 205

Ile Val Leu Ile Thr Thr Gly Tyr Tyr Leu Ser Leu Asn Ile Val Gln
210 215 220

Tyr Tyr Asp Ser Ile Gly Thr Leu Met Phe Ile Leu Leu Ser Thr Val
225 230 235 240

Ile Gly Ala Tyr Leu Phe Phe Lys Ser Ser Val Ser Leu Val Phe Lys
245 250 255

Met Val Lys Lys Phe Arg Lys Gly Val Ile Ser Val Asn Asp Val Met
260 265 270

Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys Asn Ala Phe Ser Leu
275 280 285

Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val Ser Val Leu Cys Phe
290 295 300

Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu Ile Lys Tyr Thr Ala
305 310 315 320

Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys Ala Asn Gln Leu Ala
325 330 335

Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe Tyr Asn Tyr Lys Glu
340 345 350

Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu Phe Asp Val Lys Ala
355 360 365

Lys Glu Pro Tyr Asn Val Thr Ile Thr Ser Asp Lys Tyr Ile Pro Asn
370 375 380

Thr Asp Leu Lys Arg Gly Gln Ala Asp Leu Phe Val Ala Glu Gly Ser
385 390 395 400

Ile Lys Asp Leu Val Lys His Lys Lys His Gly Lys Ala Ile Ile Gly
405 410 415

Thr Lys Lys His His Val Asn Ile Lys Leu Arg Lys Asp Ile Asn Lys
420 425 430

Ile Tyr Phe Met Thr Asp Val Asp Leu Gly Gly Pro Thr Phe Val Leu
435 440 445

Asn Asp Lys Asp Tyr Gln Glu Ile Arg Lys Tyr Thr Lys Ala Lys His
450 455 460

Ile Val Ser Gln Phe Gly Phe Asp Leu Lys His Lys Lys Asp Ala Leu
465 470 475 480

Ala Leu Glu Lys Ala Lys Asn Lys Val Asp Lys Ser Ile Glu Thr Arg
485 490 495

Ser Glu Ala Ile Ser Ser Ile Ser Ser Leu Thr Gly Ile Leu Leu Phe
500 505 510

Val Thr Ser Phe Leu Gly Ile Thr Phe Leu Ile Ala Val Cys Cys Ile
515 520 525

Ile Tyr Ile Lys Gln Ile Asp Glu Thr Glu Asp Glu Leu Glu Asn Tyr
530 535 540

Ser Ile Leu Arg Lys Leu Gly Phe Thr Gln Lys Asp Met Ala Arg Gly
 545 550 555 560

Leu Lys Phe Lys Ile Met Phe Asn Phe Gly Leu Pro Leu Val Ile Ala
 565 570 575

Leu Ser His Ala Tyr Phe Thr Ser Leu Ala Tyr Met Lys Leu Met Gly
 580 585 590

Thr Thr Asn Gln Ile Pro Val Phe Ile Val Met Gly Leu Tyr Ile Cys
 595 600 605

Met Tyr Ala Val Phe Ala Val Thr Ala Tyr Asn His Ser Lys Arg Thr
 610 615 620

Ile Arg His Ser Ile
 625

<210> 12
 <211> 200
 <212> PRT
 <213> Staphylococcus aureus

<400> 12

Arg Ala Ser Leu Ser Ser Glu Ile Lys Tyr Thr Ala Pro His Asp Val
 1 5 10 15

Thr Ile Lys Asp Gln Gln Lys Ala Asn Gln Leu Ala Ser Glu Leu Asn
 20 25 30

Asn Gln Lys Ile Pro His Phe Tyr Asn Tyr Lys Glu Val Ile His Thr
 35 40 45

Lys Leu Tyr Lys Asp Asn Leu Phe Asp Val Lys Ala Lys Glu Pro Tyr
 50 55 60

Asn Val Thr Ile Thr Ser Asp Lys Tyr Ile Pro Asn Thr Asp Leu Lys
 65 70 75 80

Arg Gly Gln Ala Asp Leu Phe Val Ala Glu Gly Ser Ile Lys Asp Leu
85 90 95

Val Lys His Lys Lys His Gly Lys Ala Ile Ile Gly Thr Lys Lys His
100 105 110

His Val Asn Ile Lys Leu Arg Lys Asp Ile Asn Lys Ile Tyr Phe Met
115 120 125

Thr Asp Val Asp Leu Gly Gly Pro Thr Phe Val Leu Asn Asp Lys Asp
130 135 140

Tyr Gln Glu Ile Arg Lys Tyr Thr Lys Ala Lys His Ile Val Ser Gln
145 150 155 160

Phe Gly Phe Asp Leu Lys His Lys Lys Asp Ala Leu Ala Leu Glu Lys
165 170 175

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

Ser Ser Ile Ser Ser Leu Thr Gly
195 200

<210> 13
<211> 199
<212> PRT
<213> Staphylococcus aureus

<400> 13

Ala Ser Leu Ser Ser Glu Ile Lys Tyr Thr Ala Pro His Asp Val Thr
1 5 10 15

Ile Lys Asp Gln Gln Lys Ala Asn Gln Leu Ala Ser Glu Leu Asn Asn
20 25 30

Gln Lys Ile Pro His Phe Tyr Asn Tyr Lys Glu Val Ile His Thr Lys
35 40 45

Leu Tyr Lys Asp Asn Leu Phe Asp Val Lys Ala Lys Glu Pro Tyr Asn

50	55	60
Val Thr Ile Thr Ser Asp Lys Tyr Ile Pro Asn Thr Asp Leu Lys Arg		
65	70	75 80
Gly Gln Ala Asp Leu Phe Val Ala Glu Gly Ser Ile Lys Asp Leu Val		
	85	90 95
Lys His Lys Lys His Gly Lys Ala Ile Ile Gly Thr Lys Lys His His		
	100	105 110
Val Asn Ile Lys Leu Arg Lys Asp Ile Asn Lys Ile Tyr Phe Met Thr		
	115	120 125
Asp Val Asp Leu Gly Gly Pro Thr Phe Val Leu Asn Asp Lys Asp Tyr		
	130	135 140
Gln Glu Ile Arg Lys Tyr Thr Lys Ala Lys His Ile Val Ser Gln Phe		
145	150	155 160
Gly Phe Asp Leu Lys His Lys Lys Asp Ala Leu Ala Leu Glu Lys Ala		
	165	170 175
Lys Asn Lys Val Asp Lys Ser Ile Glu Thr Arg Ser Glu Ala Ile Ser		
	180	185 190
Ser Ile Ser Ser Leu Thr Gly		
	195	

<210> 14
 <211> 146
 <212> PRT
 <213> Staphylococcus aureus

<400> 14

Ala Ser Leu Ser Ser Glu Ile Lys Tyr Thr Ala Pro His Asp Val Thr
1 5 10 15

Ile Lys Asp Gln Gln Lys Ala Asn Gln Leu Ala Ser Glu Leu Asn Asn
20 25 30

Gln Lys Ile Pro His Phe Tyr Asn Tyr Lys Glu Val Ile His Thr Lys
 35 40 45

Leu Tyr Lys Asp Asn Leu Phe Asp Val Lys Ala Lys Glu Pro Tyr Asn
 50 55 60

Val Thr Ile Thr Ser Asp Lys Tyr Ile Pro Asn Thr Asp Leu Lys Arg
 65 70 75 80

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

Lys His Lys Lys His Gly Lys Ala Ile Ile Gly Thr Lys Lys His His
 100 105 110

Val Asn Ile Lys Leu Arg Lys Asp Ile Asn Lys Ile Tyr Phe Met Thr
 115 120 125

Asp Val Asp Leu Gly Gly Pro Thr Phe Val Leu Asn Asp Lys Asp Tyr
 130 135 140

Gln Glu
 145

<210> 15
 <211> 54
 <212> PRT
 <213> Staphylococcus aureus

<400> 15

Lys Asp Ile Asn Lys Ile Tyr Phe Met Thr Asp Val Asp Leu Gly Gly
 1 5 10 15

Pro Thr Phe Val Leu Asn Asp Lys Asp Tyr Gln Glu Ile Arg Lys Tyr
 20 25 30

Thr Lys Ala Lys His Ile Val Ser Gln Phe Gly Phe Asp Leu Lys His
 35 40 45

Lys Lys Asp Ala Leu Ala
50

<210> 16
<211> 25
<212> PRT
<213> Staphylococcus aureus

<400> 16

Lys Asp Ile Asn Lys Ile Tyr Phe Met Thr Asp Val Asp Leu Gly Gly
1 5 10 15

Pro Thr Phe Val Leu Asn Asp Lys Asp
20 25

<210> 17
<211> 26
<212> PRT
<213> Staphylococcus aureus

<400> 17

Lys Asp Ile Asn Lys Ile Tyr Phe Met Thr Asp Val Asp Leu Gly Gly
1 5 10 15

Pro Thr Phe Val Leu Asn Asp Lys Asp Tyr
20 25

<210> 18
<211> 15
<212> PRT
<213> Staphylococcus aureus

<400> 18

Ser Gln Phe Gly Phe Asp Leu Lys His Lys Lys Asp Ala Leu Ala
1 5 10 15

<210> 19
<211> 23
<212> PRT
<213> Staphylococcus aureus

<400> 19

Lys Asp Ile Asn Lys Ile Tyr Phe Met Thr Asp Val Asp Leu Gly Gly
1 5 10 15

Pro Thr Phe Val Leu Asn Asp
20

<210> 20
<211> 19
<212> PRT
<213> Staphylococcus aureus

<400> 20

Lys His Ile Val Ser Gln Phe Gly Phe Asp Leu Lys His Lys Lys Asp
1 5 10 15

Ala Leu Ala

<210> 21
<211> 14
<212> PRT
<213> Staphylococcus aureus

<400> 21

Gln Phe Gly Phe Asp Leu Lys His Lys Lys Asp Ala Leu Ala
1 5 10

<210> 22
<211> 13
<212> PRT
<213> Staphylococcus aureus

<400> 22

Thr Ile Lys Asp Gln Gln Lys Ala Asn Gln Leu Ala Ser
1 5 10

<210> 23
<211> 14
<212> PRT
<213> Staphylococcus aureus

<400> 23

Lys Asp Ile Asn Lys Ile Tyr Phe Met Thr Asp Val Asp Leu
1 5 10

<210> 24
<211> 13
<212> PRT
<213> Staphylococcus aureus

<400> 24

Asp Val Asp Leu Gly Gly Pro Thr Phe Val Leu Asn Asp
1 5 10

<210> 25
<211> 153
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 25

Met His His His His His His Ala Ser Leu Ser Ser Glu Ile Lys Tyr
1 5 10 15

Thr Ala Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys Ala Asn Gln
20 25 30

Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe Tyr Asn Tyr
35 40 45

Lys Glu Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu Phe Asp Val
50 55 60

Lys Ala Lys Glu Pro Tyr Asn Val Thr Ile Thr Ser Asp Lys Tyr Ile
65 70 75 80

Pro Asn Thr Asp Leu Lys Arg Gly Gln Ala Asp Leu Phe Val Ala Glu
85 90 95

Gly Ser Ile Lys Asp Leu Val Lys His Lys Lys His Gly Lys Ala Ile
100 105 110

Ile Gly Thr Lys Lys His His Val Asn Ile Lys Leu Arg Lys Asp Ile
115 120 125

Asn Lys Ile Tyr Phe Met Thr Asp Val Asp Leu Gly Gly Pro Thr Phe
130 135 140

Val Leu Asn Asp Lys Asp Tyr Gln Glu
145 150

<210> 26
<211> 158
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 26

Met Arg Gly Ser His His His His His His Gly Ser Ala Ser Leu Ser
1 5 10 15

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

Gln Lys Ala Asn Gln Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile Pro
35 40 45

His Phe Tyr Asn Tyr Lys Glu Val Ile His Thr Lys Leu Tyr Lys Asp
50 55 60

Asn Leu Phe Asp Val Lys Ala Lys Glu Pro Tyr Asn Val Thr Ile Thr
65 70 75 80

Ser Asp Lys Tyr Ile Pro Asn Thr Asp Leu Lys Arg Gly Gln Ala Asp
85 90 95

Leu Phe Val Ala Glu Gly Ser Ile Lys Asp Leu Val Lys His Lys Lys
100 105 110

His Gly Lys Ala Ile Ile Gly Thr Lys Lys His His Val Asn Ile Lys
115 120 125

Leu Arg Lys Asp Ile Asn Lys Ile Tyr Phe Met Thr Asp Val Asp Leu
130 135 140

Gly Gly Pro Thr Phe Val Leu Asn Asp Lys Asp Tyr Gln Glu
145 150 155

<210> 27
<211> 50
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 27

Lys Asp Ile Asn Lys Ile Tyr Phe Met Thr Asp Val Asp Leu Gly Gly
1 5 10 15

Pro Thr Phe Val Leu Asn Asp Lys Asp Tyr Glu Arg Lys Tyr Lys Lys
20 25 30

His Ile Val Ser Gln Phe Gly Phe Asp Leu Lys His Lys Lys Asp Ala
35 40 45

Leu Ala
50

<210> 28
<211> 612
<212> DNA
<213> Staphylococcus aureus

<400> 28
atgttcaaaa aatatgactc aaaaaattca atcgtattaa aatctattct atcgctaggt 60
atcatctatg ggggaacatt tggaatatat ccaaaagcag acgcgtcaac acaaaattcc 120
tcaagtgtac aagataaaca attacaaaaa gttgaagaag taccaaataa ttcagaaaaa 180
gctttgggta aaaaacttta cgatagatac agcaaggata caataaatgg aaaatcta 240

aaatctagga attgggttta ttcagagaga cctttaaatg aaaaccaagt tcgtatacat 300
 ttagaaggaa catacacagt tgctggcaga gtgtatacac ctaagaggaa tattactctt 360
 aataaagaag ttgtcacttt aaaagaattg gatcatatca taagatttgc tcatatttcc 420
 tatggcttgt atatgggaga acatttgcct aaaggtaaca tcgtcataaa tacaaaagat 480
 ggtggtaaat atacattaga gtcgcataaa gagctacaaa aagataggga aaatgtaaaa 540
 attaatacag ccgatataaa aaatgtaact ttcaaacttg tgaaaagtgt taatgacatt 600
 gaacaagttt ga 612

<210> 29
 <211> 203
 <212> PRT
 <213> Staphylococcus aureus

<400> 29

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> 30
<211> 168
<212> PRT
<213> Staphylococcus aureus

<400> 30

Ser Thr Gln Asn Ser Ser Ser Val Gln Asp Lys Gln Leu Gln Lys Val
1 5 10 15

Glu Glu Val Pro Asn Asn Ser Glu Lys Ala Leu Val Lys Lys Leu Tyr
20 25 30

Asp Arg Tyr Ser Lys Asp Thr Ile Asn Gly Lys Ser Asn Lys Ser Arg
35 40 45

Asn Trp Val Tyr Ser Glu Arg Pro Leu Asn Glu Asn Gln Val Arg Ile
50 55 60

His Leu Glu Gly Thr Tyr Thr Val Ala Gly Arg Val Tyr Thr Pro Lys
65 70 75 80

Arg Asn Ile Thr Leu Asn Lys Glu Val Val Thr Leu Lys Glu Leu Asp
85 90 95

His Ile Ile Arg Phe Ala His Ile Ser Tyr Gly Leu Tyr Met Gly Glu
100 105 110

His Leu Pro Lys Gly Asn Ile Val Ile Asn Thr Lys Asp Gly Gly Lys
115 120 125

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

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

Ser Val Asn Asp Ile Glu Gln Val
165

<210> 31
<211> 116
<212> PRT
<213> Staphylococcus aureus

<400> 31

Gln Asp Lys Gln Leu Gln Lys Val Glu Glu Val Pro Asn Asn Ser Glu
1 5 10 15

Lys Ala Leu Val Lys Lys Leu Tyr Asp Arg Tyr Ser Lys Asp Thr Ile
20 25 30

Asn Gly Lys Ser Asn Lys Ser Arg Asn Trp Val Tyr Ser Glu Arg Pro
35 40 45

Leu Asn Glu Asn Gln Val Arg Ile His Leu Glu Gly Thr Tyr Thr Val
50 55 60

Ala Gly Arg Val Tyr Thr Pro Lys Arg Asn Ile Thr Leu Asn Lys Glu
65 70 75 80

Val Val Thr Leu Lys Glu Leu Asp His Ile Ile Arg Phe Ala His Ile
85 90 95

Ser Tyr Gly Leu Tyr Met Gly Glu His Leu Pro Lys Gly Asn Ile Val
100 105 110

Ile Asn Thr Lys
115

<210> 32
<211> 115
<212> PRT
<213> Staphylococcus aureus

<400> 32

Asp Lys Gln Leu Gln Lys Val Glu Glu Val Pro Asn Asn Ser Glu Lys
1 5 10 15

Ala Leu Val Lys Lys Leu Tyr Asp Arg Tyr Ser Lys Asp Thr Ile Asn
20 25 30

Gly Lys Ser Asn Lys Ser Arg Asn Trp Val Tyr Ser Glu Arg Pro Leu
35 40 45

Asn Glu Asn Gln Val Arg Ile His Leu Glu Gly Thr Tyr Thr Val Ala
50 55 60

Gly Arg Val Tyr Thr Pro Lys Arg Asn Ile Thr Leu Asn Lys Glu Val
65 70 75 80

Val Thr Leu Lys Glu Leu Asp His Ile Ile Arg Phe Ala His Ile Ser
85 90 95

Tyr Gly Leu Tyr Met Gly Glu His Leu Pro Lys Gly Asn Ile Val Ile
100 105 110

Asn Thr Lys
115

<210> 33
<211> 159
<212> PRT
<213> Staphylococcus aureus

<400> 33

Asp Lys Gln Leu Gln Lys Val Glu Glu Val Pro Asn Asn Ser Glu Lys
1 5 10 15

Ala Leu Val Lys Lys Leu Tyr Asp Arg Tyr Ser Lys Asp Thr Ile Asn
20 25 30

Gly Lys Ser Asn Lys Ser Arg Asn Trp Val Tyr Ser Glu Arg Pro Leu
35 40 45

Asn Glu Asn Gln Val Arg Ile His Leu Glu Gly Thr Tyr Thr Val Ala
50 55 60

Gly Arg Val Tyr Thr Pro Lys Arg Asn Ile Thr Leu Asn Lys Glu Val
65 70 75 80

Val Thr Leu Lys Glu Leu Asp His Ile Ile Arg Phe Ala His Ile Ser
85 90 95

Tyr Gly Leu Tyr Met Gly Glu His Leu Pro Lys Gly Asn Ile Val Ile
100 105 110

Asn Thr Lys Asp Gly Gly Lys Tyr Thr Leu Glu Ser His Lys Glu Leu
115 120 125

Gln Lys Asp Arg Glu Asn Val Lys Ile Asn Thr Ala Asp Ile Lys Asn
130 135 140

Val Thr Phe Lys Leu Val Lys Ser Val Asn Asp Ile Glu Gln Val
145 150 155

<210> 34

<211> 14

<212> PRT

<213> Staphylococcus aureus

<400> 34

Lys Asp Thr Ile Asn Gly Lys Ser Asn Lys Ser Arg Asn Trp
1 5 10

<210> 35
 <211> 166
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic sequence

<400> 35

Met His His His His His His Asp Lys Gln Leu Gln Lys Val Glu Glu
 1 5 10 15

Val Pro Asn Asn Ser Glu Lys Ala Leu Val Lys Lys Leu Tyr Asp Arg
 20 25 30

Tyr Ser Lys Asp Thr Ile Asn Gly Lys Ser Asn Lys Ser Arg Asn Trp
 35 40 45

Val Tyr Ser Glu Arg Pro Leu Asn Glu Asn Gln Val Arg Ile His Leu
 50 55 60

Glu Gly Thr Tyr Thr Val Ala Gly Arg Val Tyr Thr Pro Lys Arg Asn
 65 70 75 80

Ile Thr Leu Asn Lys Glu Val Val Thr Leu Lys Glu Leu Asp His Ile
 85 90 95

Ile Arg Phe Ala His Ile Ser Tyr Gly Leu Tyr Met Gly Glu His Leu
 100 105 110

Pro Lys Gly Asn Ile Val Ile Asn Thr Lys Asp Gly Gly Lys Tyr Thr
 115 120 125

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

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

Asn Asp Ile Glu Gln Val

165

<210> 36
<211> 171
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 36

Met Arg Gly Ser His His His His His His Gly Ser Asp Lys Gln Leu
1 5 10 15

Gln Lys Val Glu Glu Val Pro Asn Asn Ser Glu Lys Ala Leu Val Lys
20 25 30

Lys Leu Tyr Asp Arg Tyr Ser Lys Asp Thr Ile Asn Gly Lys Ser Asn
35 40 45

Lys Ser Arg Asn Trp Val Tyr Ser Glu Arg Pro Leu Asn Glu Asn Gln
50 55 60

Val Arg Ile His Leu Glu Gly Thr Tyr Thr Val Ala Gly Arg Val Tyr
65 70 75 80

Thr Pro Lys Arg Asn Ile Thr Leu Asn Lys Glu Val Val Thr Leu Lys
85 90 95

Glu Leu Asp His Ile Ile Arg Phe Ala His Ile Ser Tyr Gly Leu Tyr
100 105 110

Met Gly Glu His Leu Pro Lys Gly Asn Ile Val Ile Asn Thr Lys Asp
115 120 125

Gly Gly Lys Tyr Thr Leu Glu Ser His Lys Glu Leu Gln Lys Asp Arg
130 135 140

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

Leu Val Lys Ser Val Asn Asp Ile Glu Gln Val
 165 170

<210> 37
 <211> 720
 <212> DNA
 <213> Staphylococcus aureus

<400> 37
 atgaataaaa atatagtcac taaaagcatg gcagcattag ccattctaac ctacagtaact 60
 ggaataaatg ctgcagtcgt tgaagagaca caacaaatag caaatgcaga gaagaatggt 120
 acgcaagtta aagatacaaa tttttttcca tataatggcg tcgttttcatt taaagatgag 180
 acaggttttg taattggaaa aaatacaatt atcaccaata aacatgtatc aaaagattat 240
 aaagttggcg atagaattac tgcccatcca aacgggtgaca aaggaaatgg tggatatatat 300
 aaaattaaaa gcattttctga ttatccgggt gatgaagaca tctctgtcat gaatattgaa 360
 gaacaagcag tcgaacgtgg accaaaaggc ttttaatttta atgaaaatgt ccaagcattc 420
 aattttgcga aagatgctaa agttgatgac aaaattaaag ttattgggta cccattacct 480
 gctcaaaaata gtttttaaca gtttgaatct acaggaacta taaaaagaat caaagacaat 540
 atttttaaatt ttgatgcata cattgaaccg gggaattcag gatcaccagt tctaaattct 600
 aacaatgagg tcataggtgt ggtgtatggc ggtattggaa aaattgggtc tgaatataat 660
 ggtgccgtat actttacgcc tcaaatcaaa gattttattc aaaagcacat tgaacaataa 720

<210> 38
 <211> 239
 <212> PRT
 <213> Staphylococcus aureus

<400> 38

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> 39

<211> 199
 <212> PRT
 <213> Staphylococcus aureus

<400> 39

Thr Gln Val Lys Asp Thr Asn Ile Phe Pro Tyr Asn Gly Val Val Ser
 1 5 10 15

Phe Lys Asp Ala Thr Gly Phe Val Ile Gly Lys Asn Thr Ile Ile Thr
 20 25 30

Asn Lys His Val Ser Lys Asp Tyr Lys Val Gly Asp Arg Ile Thr Ala
 35 40 45

His Pro Asn Gly Asp Lys Gly Asn Gly Gly Ile Tyr Lys Ile Lys Ser
 50 55 60

Ile Ser Asp Tyr Pro Gly Asp Glu Asp Ile Ser Val Met Asn Ile Glu
 65 70 75 80

Glu Gln Ala Val Glu Arg Gly Pro Lys Gly Phe Asn Phe Asn Glu Asn
 85 90 95

Val Gln Ala Phe Asn Phe Ala Lys Asp Ala Lys Val Asp Asp Lys Ile
 100 105 110

Lys Val Ile Gly Tyr Pro Leu Pro Ala Gln Asn Ser Phe Lys Gln Phe
 115 120 125

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

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

Asn Asn Glu Val Ile Gly Val Val Tyr Gly Gly Ile Gly Lys Ile Gly
 165 170 175

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

Ile Gln Lys His Ile Glu Gln
195

<210> 40
<211> 206
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 40

Met His His His His His His Thr Gln Val Lys Asp Thr Asn Ile Phe
1 5 10 15

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

Gly Lys Asn Thr Ile Ile Thr Asn Lys His Val Ser Lys Asp Tyr Lys
35 40 45

Val Gly Asp Arg Ile Thr Ala His Pro Asn Gly Asp Lys Gly Asn Gly
50 55 60

Gly Ile Tyr Lys Ile Lys Ser Ile Ser Asp Tyr Pro Gly Asp Glu Asp
65 70 75 80

Ile Ser Val Met Asn Ile Glu Glu Gln Ala Val Glu Arg Gly Pro Lys
85 90 95

Gly Phe Asn Phe Asn Glu Asn Val Gln Ala Phe Asn Phe Ala Lys Asp
100 105 110

Ala Lys Val Asp Asp Lys Ile Lys Val Ile Gly Tyr Pro Leu Pro Ala
115 120 125

Gln Asn Ser Phe Lys Gln Phe Glu Ser Thr Gly Thr Ile Lys Arg Ile
130 135 140

Lys Asp Asn Ile Leu Asn Phe Asp Ala Tyr Ile Glu Pro Gly Asn Ser
 145 150 155 160

Gly Ser Pro Val Leu Asn Ser Asn Asn Glu Val Ile Gly Val Val Tyr
 165 170 175

Gly Gly Ile Gly Lys Ile Gly Ser Glu Tyr Asn Gly Ala Val Tyr Phe
 180 185 190

Thr Pro Gln Ile Lys Asp Phe Ile Gln Lys His Ile Glu Gln
 195 200 205

<210> 41
 <211> 211
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic sequence

<400> 41

Met Arg Gly Ser His His His His His His Gly Ser Thr Gln Val Lys
 1 5 10 15

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

Thr Gly Phe Val Ile Gly Lys Asn Thr Ile Ile Thr Asn Lys His Val
 35 40 45

Ser Lys Asp Tyr Lys Val Gly Asp Arg Ile Thr Ala His Pro Asn Gly
 50 55 60

Asp Lys Gly Asn Gly Gly Ile Tyr Lys Ile Lys Ser Ile Ser Asp Tyr
 65 70 75 80

Pro Gly Asp Glu Asp Ile Ser Val Met Asn Ile Glu Glu Gln Ala Val
 85 90 95

Glu Arg Gly Pro Lys Gly Phe Asn Phe Asn Glu Asn Val Gln Ala Phe
 100 105 110

Asn Phe Ala Lys Asp Ala Lys Val Asp Asp Lys Ile Lys Val Ile Gly
 115 120 125

Tyr Pro Leu Pro Ala Gln Asn Ser Phe Lys Gln Phe Glu Ser Thr Gly
 130 135 140

Thr Ile Lys Arg Ile Lys Asp Asn Ile Leu Asn Phe Asp Ala Tyr Ile
 145 150 155 160

Glu Pro Gly Asn Ser Gly Ser Pro Val Leu Asn Ser Asn Asn Glu Val
 165 170 175

Ile Gly Val Val Tyr Gly Gly Ile Gly Lys Ile Gly Ser Glu Tyr Asn
 180 185 190

Gly Ala Val Tyr Phe Thr Pro Gln Ile Lys Asp Phe Ile Gln Lys His
 195 200 205

Ile Glu Gln
 210

<210> 42
 <211> 600
 <212> DNA
 <213> Staphylococcus aureus

<400> 42
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 gatcaagcgc cagttctaga tgaattaaag aaaaatggtg aaaaacatgc tggtgatttt 180
 agccaaataa atattttaga ttatgacgat aaaaaatcat atttcgaagc gttagggtgta 240
 ccagcaggtc aagtttatcc aattgcttat gaaaaagatg caatcgaatt aatcgctgat 300
 aagattaaaa ctaaagaaaa taaagggaaa ttaacattac aagttgtttc tatcgatgag 360
 caaggtaagt taaatgtag tattcgtaa ggactaatgg aagcaagaga aattttctta 420
 gtagtgacag gtgctaataa acgagatgta gttgaaaaat tatatcaaga aaatggtaaa 480

acaagcttcg aaccagccga tttaaaagca catagaatgg taaatgttat tcttgataaa 540

gaagcggctg caggtttacc tgaagatggt aaagcttact ttacgtcacg ctttgcttaa 600

<210> 43

<211> 199

<212> PRT

<213> Staphylococcus aureus

<400> 43

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

Tyr Ala Ala Asp Ile Ile Arg Lys Gln Phe Asn Asn Asn Pro Thr Thr
20 25 30

Ile Ala Gly Phe His Leu Asp Thr Asp Gln Ala Pro Val Leu Asp Glu
35 40 45

Leu Lys Lys Asn Val Glu Lys His Ala Val Asp Phe Ser Gln Ile Asn
50 55 60

Ile Leu Asp Tyr Asp Asp Lys Lys Ser Tyr Phe Glu Ala Leu Gly Val
65 70 75 80

Pro Ala Gly Gln Val Tyr Pro Ile Ala Tyr Glu Lys Asp Ala Ile Glu
85 90 95

Leu Ile Ala Asp Lys Ile Lys Thr Lys Glu Asn Lys Gly Lys Leu Thr
100 105 110

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

Arg Gln Gly Leu Met Glu Ala Arg Glu Ile Phe Leu Val Val Thr Gly
130 135 140

Ala Asn Lys Arg Asp Val Val Glu Lys Leu Tyr Gln Glu Asn Gly Lys
145 150 155 160

Thr Ser Phe Glu Pro Ala Asp Leu Lys Ala His Arg Met Val Asn Val
165 170 175

Ile Leu Asp Lys Glu Ala Ala Ala Gly Leu Pro Glu Asp Val Lys Ala
180 185 190

Tyr Phe Thr Ser Arg Phe Ala
195

<210> 44
<211> 206
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 44

Met His His His His His His Met Ala Met Asn Phe Lys Val Phe Asp
1 5 10 15

Asn Ser Gln Leu Val Ala Glu Tyr Ala Ala Asp Ile Ile Arg Lys Gln
20 25 30

Phe Asn Asn Asn Pro Thr Thr Ile Ala Gly Phe His Leu Asp Thr Asp
35 40 45

Gln Ala Pro Val Leu Asp Glu Leu Lys Lys Asn Val Glu Lys His Ala
50 55 60

Val Asp Phe Ser Gln Ile Asn Ile Leu Asp Tyr Asp Asp Lys Lys Ser
65 70 75 80

Tyr Phe Glu Ala Leu Gly Val Pro Ala Gly Gln Val Tyr Pro Ile Ala
85 90 95

Tyr Glu Lys Asp Ala Ile Glu Leu Ile Ala Asp Lys Ile Lys Thr Lys
100 105 110

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

Gly Lys Leu Asn Val Ser Ile Arg Gln Gly Leu Met Glu Ala Arg Glu
130 135 140

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

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

Ala His Arg Met Val Asn Val Ile Leu Asp Lys Glu Ala Ala Ala Gly
180 185 190

Leu Pro Glu Asp Val Lys Ala Tyr Phe Thr Ser Arg Phe Ala
195 200 205

<210> 45
<211> 14
<212> PRT
<213> Staphylococcus aureus

<400> 45

Asp Ile Ile Arg Lys Gln Phe Asn Asn Asn Pro Thr Thr Ile
1 5 10

<210> 46
<211> 14
<212> PRT
<213> Staphylococcus aureus

<400> 46

Tyr Phe Glu Ala Leu Gly Val Pro Ala Gly Gln Val Tyr Pro
1 5 10

<210> 47
<211> 14
<212> PRT
<213> Staphylococcus aureus

<400> 47

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

1 5 10

<210> 48
 <211> 14
 <212> PRT
 <213> Staphylococcus aureus
 <400> 48

Gln Glu Asn Gly Lys Thr Ser Phe Glu Pro Ala Asp Leu Lys
 1 5 10

<210> 49
 <211> 429
 <212> DNA
 <213> Staphylococcus aureus

<400> 49
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 aatatatatg aaacagacga attatattac ttagaagctg aactagcagg tgtaaataaa 180
 gaagatatta gtatcgattt caataataat acgctcacta ttcaagctac tagaagcgca 240
 aaatacaaact ctgaacaact cattttagat gagcgtaact tcgaatcatt aatgcgtcaa 300
 tttgattttg aagctgttga taagcaacat attactgcta gttttgaaaa tgggttatta 360
 accattacct tgcctaaaat caaaccaagc aatgaaacta cttcatcaac atctattcca 420
 atttcatag 429

<210> 50
 <211> 93
 <212> PRT
 <213> Staphylococcus aureus
 <400> 50

Met Ile Leu Asn Phe Asn Gln Phe Glu Asn Gln Asn Phe Phe Asn Gly
 1 5 10 15

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

Phe Ser Thr Pro Ser Phe Val Thr Asn Ile Tyr Glu Thr Asp Glu Leu
35 40 45

Tyr Tyr Leu Glu Ala Glu Leu Ala Gly Val Asn Lys Glu Asp Ile Ser
50 55 60

Ile Asp Phe Asn Asn Asn Thr Leu Thr Ile Gln Ala Thr Arg Ser Ala
65 70 75 80

Lys Tyr Lys Ser Glu Gln Leu Ile Leu Asp Glu Arg Asn
85 90

<210> 51
<211> 100
<212> PRT
<213> Staphylococcus aureus

<400> 51

Met His His His His His His Met Ile Leu Asn Phe Asn Gln Phe Glu
1 5 10 15

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

Gly Lys Gln Val Phe Asn Tyr Phe Ser Thr Pro Ser Phe Val Thr Asn
35 40 45

Ile Tyr Glu Thr Asp Glu Leu Tyr Tyr Leu Glu Ala Glu Leu Ala Gly
50 55 60

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

Ile Gln Ala Thr Arg Ser Ala Lys Tyr Lys Ser Glu Gln Leu Ile Leu
85 90 95

Asp Glu Arg Asn
100

<210> 52

<211> 14
 <212> PRT
 <213> Staphylococcus aureus

<400> 52

Asn	Gly	Asn	Pro	Ser	Asp	Thr	Phe	Lys	Asp	Leu	Gly	Lys	Gln
1				5					10				

<210> 53
 <211> 14
 <212> PRT
 <213> Staphylococcus aureus

<400> 53

Glu	Asp	Ile	Ser	Ile	Asp	Phe	Asn	Asn	Asn	Thr	Leu	Thr	Ile
1				5					10				

<210> 54
 <211> 807
 <212> DNA
 <213> Artificial sequence

<220>
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<400> 54

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aatcaagaat ttgatttcga acgtgaattg acacaagatc catattcaaa agtataactta	120
tacagtatag aagaccatat cagaacatat aagatagaga aaggaggtgg cggttcagga	180
ggtggaggat ctggaggcgg tggatcaacg caagttaaag atacaaatat tttccatat	240
aatggcgtcg tttcatttaa agatgcgaca ggttttgtaa ttggaaaaaa tacaattatc	300
accaataaac atgtatcaaa agattataaa gttggcgata gaattactgc ccatccaaac	360
ggtgacaaag gaaatggtgg tatatataaa attaaaagca tttctgatta tccgggtgat	420
gaagacatct ctgtcatgaa tattgaagaa caagcagtcg aacgtggacc aaaaggcttt	480
aattttaatg aaaatgtcca agcattcaat ttgcgaaag atgctaaagt tgatgacaaa	540
attaaagtta ttggttaccc attacctgct caaaatagtt ttaaacagtt tgaatctaca	600
ggaactataa aaagaatcaa agacaatatt ttaaattttg atgcatacat tgaacccggg	660

aattcaggat caccagttct aaattctaac aatgagggtca taggtgtggt gtatggcggg	720
attggaaaaa ttggttctga atataatggt gccgtatact ttacgcctca aatcaaagat	780
tttattcaaa agcacattga acaataa	807

<210> 55
 <211> 268
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic sequence

<400> 55

Leu	Glu	Ser	Arg	Glu	Gln	Leu	Ser	Val	Glu	Glu	Tyr	Glu	Thr	Phe	Phe
1				5					10					15	

Asn	Arg	Phe	Asp	Asn	Gln	Glu	Phe	Asp	Phe	Glu	Arg	Glu	Leu	Thr	Gln
			20					25					30		

Asp	Pro	Tyr	Ser	Lys	Val	Tyr	Leu	Tyr	Ser	Ile	Glu	Asp	His	Ile	Arg
		35					40					45			

Thr	Tyr	Lys	Ile	Glu	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
	50					55					60				

Gly	Gly	Gly	Gly	Ser	Thr	Gln	Val	Lys	Asp	Thr	Asn	Ile	Phe	Pro	Tyr
65					70					75				80	

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

Asn	Thr	Ile	Ile	Thr	Asn	Lys	His	Val	Ser	Lys	Asp	Tyr	Lys	Val	Gly
		100						105					110		

Asp	Arg	Ile	Thr	Ala	His	Pro	Asn	Gly	Asp	Lys	Gly	Asn	Gly	Gly	Ile
		115					120					125			

Tyr	Lys	Ile	Lys	Ser	Ile	Ser	Asp	Tyr	Pro	Gly	Asp	Glu	Asp	Ile	Ser
	130					135					140				

Val Met Asn Ile Glu Glu Gln Ala Val Glu Arg Gly Pro Lys Gly Phe
145 150 155 160

Asn Phe Asn Glu Asn Val Gln Ala Phe Asn Phe Ala Lys Asp Ala Lys
165 170 175

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

Ser Phe Lys Gln Phe Glu Ser Thr Gly Thr Ile Lys Arg Ile Lys Asp
195 200 205

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

Pro Val Leu Asn Ser Asn Asn Glu Val Ile Gly Val Val Tyr Gly Gly
225 230 235 240

Ile Gly Lys Ile Gly Ser Glu Tyr Asn Gly Ala Val Tyr Phe Thr Pro
245 250 255

Gln Ile Lys Asp Phe Ile Gln Lys His Ile Glu Gln
260 265

<210> 56
<211> 825
<212> DNA
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 56
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accttcttta accgctttga taaccaagaa ttgatttcg aacgtgaact gaccaggat 120
ccgtattcta aagtgtatct gtacagtatc gaagatcata ttcgcacgta caaaatcgaa 180
aaaggcgggtg gcggttctgg cgggtggcgggt agtggcgggtg gcggtagcac ccagggtgaaa 240
gatacgaata tctttccgta taacggcgtg gtttctttta aagatgcgac cggcttcgtt 300

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atcggtaaaa acaccatcat cacgaacaaa catgtgagca aagattacaa agttggcgat      360
cgtattaccg cccacccgaa tggcgataag ggtaacggcg gtatctacaa aatcaaaagc      420
atctctgatt acccgggtga tgaagatatc agcgtgatga atattgaaga acaggcagtt      480
gaacgcggcc cgaaagggtt taacttcaat gaaaacgttc aggcgtttta tttcgcgaaa      540
gatgccaaag tggatgataa aatcaaagtt attggctatc cgctgccggc ccagaacagc      600
tttaaacagt tcgaatctac cggtacgata aaacgtatca aagataacat cctgaacttc      660
gatgcatata ttgaaccggg caatagtggg agcccgggtg tgaacagtaa caatgaagtt      720
attgggtgtg tttatggcgg tatcggcaaa attggtagcg aatacaacgg tgctgtgtat      780
tttacgccgc agatcaaaga cttcatccag aaacatatcg aacaa                        825

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<210> 57
<211> 275
<212> PRT
<213> Artificial sequence

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<220>
<223> synthetic sequence

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<400> 57

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Met His His His His His His Leu Glu Ser Arg Glu Gln Leu Ser Val
1           5           10           15

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Glu Glu Tyr Glu Thr Phe Phe Asn Arg Phe Asp Asn Gln Glu Phe Asp
          20           25           30

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Phe Glu Arg Glu Leu Thr Gln Asp Pro Tyr Ser Lys Val Tyr Leu Tyr
          35           40           45

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Ser Ile Glu Asp His Ile Arg Thr Tyr Lys Ile Glu Lys Gly Gly Gly
          50           55           60

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Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Thr Gln Val Lys
65           70           75           80

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

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Thr Gly Phe Val Ile Gly Lys Asn Thr Ile Ile Thr Asn Lys His Val
100 105 110

Ser Lys Asp Tyr Lys Val Gly Asp Arg Ile Thr Ala His Pro Asn Gly
115 120 125

Asp Lys Gly Asn Gly Gly Ile Tyr Lys Ile Lys Ser Ile Ser Asp Tyr
130 135 140

Pro Gly Asp Glu Asp Ile Ser Val Met Asn Ile Glu Glu Gln Ala Val
145 150 155 160

Glu Arg Gly Pro Lys Gly Phe Asn Phe Asn Glu Asn Val Gln Ala Phe
165 170 175

Asn Phe Ala Lys Asp Ala Lys Val Asp Asp Lys Ile Lys Val Ile Gly
180 185 190

Tyr Pro Leu Pro Ala Gln Asn Ser Phe Lys Gln Phe Glu Ser Thr Gly
195 200 205

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

Glu Pro Gly Asn Ser Gly Ser Pro Val Leu Asn Ser Asn Asn Glu Val
225 230 235 240

Ile Gly Val Val Tyr Gly Gly Ile Gly Lys Ile Gly Ser Glu Tyr Asn
245 250 255

Gly Ala Val Tyr Phe Thr Pro Gln Ile Lys Asp Phe Ile Gln Lys His
260 265 270

Ile Glu Gln
275

<210> 58
<211> 280
<212> PRT

<213> Artificial sequence

<220>

<223> synthetic sequence

<400> 58

Met Arg Gly Ser His His His His His His Gly Ser Leu Glu Ser Arg
1 5 10 15

Glu Gln Leu Ser Val Glu Glu Tyr Glu Thr Phe Phe Asn Arg Phe Asp
20 25 30

Asn Gln Glu Phe Asp Phe Glu Arg Glu Leu Thr Gln Asp Pro Tyr Ser
35 40 45

Lys Val Tyr Leu Tyr Ser Ile Glu Asp His Ile Arg Thr Tyr Lys Ile
50 55 60

Glu Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
65 70 75 80

Ser Thr Gln Val Lys Asp Thr Asn Ile Phe Pro Tyr Asn Gly Val Val
85 90 95

Ser Phe Lys Asp Ala Thr Gly Phe Val Ile Gly Lys Asn Thr Ile Ile
100 105 110

Thr Asn Lys His Val Ser Lys Asp Tyr Lys Val Gly Asp Arg Ile Thr
115 120 125

Ala His Pro Asn Gly Asp Lys Gly Asn Gly Gly Ile Tyr Lys Ile Lys
130 135 140

Ser Ile Ser Asp Tyr Pro Gly Asp Glu Asp Ile Ser Val Met Asn Ile
145 150 155 160

Glu Glu Gln Ala Val Glu Arg Gly Pro Lys Gly Phe Asn Phe Asn Glu
165 170 175

Asn Val Gln Ala Phe Asn Phe Ala Lys Asp Ala Lys Val Asp Asp Lys

	180		185		190										
Ile	Lys	Val	Ile	Gly	Tyr	Pro	Leu	Pro	Ala	Gln	Asn	Ser	Phe	Lys	Gln
	195						200					205			
Phe	Glu	Ser	Thr	Gly	Thr	Ile	Lys	Arg	Ile	Lys	Asp	Asn	Ile	Leu	Asn
	210					215					220				
Phe	Asp	Ala	Tyr	Ile	Glu	Pro	Gly	Asn	Ser	Gly	Ser	Pro	Val	Leu	Asn
225					230					235					240
Ser	Asn	Asn	Glu	Val	Ile	Gly	Val	Val	Tyr	Gly	Gly	Ile	Gly	Lys	Ile
			245						250					255	
Gly	Ser	Glu	Tyr	Asn	Gly	Ala	Val	Tyr	Phe	Thr	Pro	Gln	Ile	Lys	Asp
			260					265					270		
Phe	Ile	Gln	Lys	His	Ile	Glu	Gln								
	275						280								

<210> 59
 <211> 45
 <212> DNA
 <213> Artificial sequence

<220>
 <223> synthetic sequence

<400> 59
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45

<210> 60
 <211> 15
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic sequence

<400> 60

Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
1				5					10					15

<210> 61
<211> 5
<212> PRT
<213> Artificial sequence

<220>
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<400> 61

Glu Arg Lys Tyr Lys
1 5

<210> 62
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 62

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10

<210> 63
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 63

Glu Ala Ala Ala Lys
1 5

<210> 64
<211> 15
<212> PRT
<213> Artificial sequence

<220>
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<400> 64

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10 15

<210> 65
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 65

Glu Arg Lys Tyr Lys Glu Arg Lys Tyr Lys
1 5 10

<210> 66
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 66

Glu Arg Lys Tyr Lys Glu Arg Lys Tyr Lys Glu Arg Lys Tyr Lys
1 5 10 15

<210> 67
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 67

Gly Gly Gly Gly Ser
1 5

<210> 68
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 68

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 69
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic sequence

<220>
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<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (5)..(5)
<223> Xaa can be any naturally occurring amino acid

<400> 69

Xaa Pro Xaa Pro Xaa Pro
1 5

<210> 70
<211> 12
<212> PRT
<213> Artificial sequence

<220>
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<220>
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 <223> Xaa can be any naturally occurring amino acid

<220>
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 <222> (7)..(7)
 <223> Xaa can be any naturally occurring amino acid

<220>
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 <222> (9)..(9)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (11)..(11)
 <223> Xaa can be any naturally occurring amino acid

<400> 70

Xaa	Pro	Xaa	Pro	Xaa	Pro	Xaa	Pro	Xaa	Pro	Xaa	Pro
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<210> 71
 <211> 612
 <212> DNA
 <213> Staphylococcus aureus

<400> 71	
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ccaagtgtac aagataaaca attccaaaaa gttgaagaag taccaaataa ttcagaaaaa	180
gctttggtta aaaaacttta cgatagatac agccaaaata caataaacgg aaaatcta	240
aatctagga attgggttta ttcagagaga cttttaa	300
atg aaaaccaagt tcgtataaat	
ttagaaggaa catacagagt tgctgataga gtatatacac ctaagagaaa tattactctt	360
aataaagaag ttgtcacttt aaaggaattg gatcatatca taagatttgc tcatatttct	420

tatggccttat atatgggaga acatttgcct aaaggtaaca tcgtcataaa tacaaaagat	480
ggcggtaaat atacattaga gtcgcataaa gagctacaaa aagataggga aaatgtaaaa	540
attaatacag ccgatataaa aaatgtaact ttcaaacttg tgaaaagtgt taatgacatt	600
gaacaagttt ga	612

<210> 72
 <211> 612
 <212> DNA
 <213> Staphylococcus aureus

<400> 72	
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atcatctatg ggggaacatt tggaatatat ccaaaagcag acgcgtcaac acaaaattcc	120
ccaagtgtac aagataaaca attccaaaaa gttgaagaag taccaaataa ttcagaaaaa	180
gctttgggta aaaaacttta cgatagatac agccaaaata caataaacgg aaaatcta	240
aatctagga attgggttta ttcagagaga ctttaaatg aaaaccaagt tcgtataaat	300
ttagaaggaa catacagagt tgctgataga gtatatacac ctaagagaaa tattactctt	360
aataaagaag ttgtcacttt aaaggaattg gatcatatca taagatttgc tcatatttct	420
tatggccttat atatgggaga acatttgcct aaaggtaaca tcgtcataaa tacaaaagat	480
ggcggtaaat atacattaga gtcgcataaa gagctacaaa aagataggga aaatgtaaaa	540
attaatacag ccgatataaa aaatgtaact ttcaaacttg tgaaaagtgt taatgacatt	600
gaacaagttt ga	612

<210> 73
 <211> 612
 <212> DNA
 <213> Staphylococcus aureus

<400> 73	
atgttcaaaa aatatgactc aaaaaattca atcgtattaa aatctattct atcgctaggt	60
atcatctatg ggggaacatt tggaatatat ccaaaagcag acgcgtcaac acaaaattcc	120
tcaagtgtac aagataaaca attacaaaaa gttgaagaag taccaaataa ttcagaaaaa	180
gctttgggta aaaaacttta cgatagatac agcaaggata caataaatgg aaaatcta	240

aatctagga attgggttta ttcagagaga cctttaaatg aaaaccaagt tcgtatacat	300
ttagaaggaa catacacagt tgctggcaga gtgtatacac ctaagaggaa tattactctt	360
aataaagaag ttgtcacttt aaaagaattg gatcatatca taagatttgc tcatatttcc	420
tatggcttgt atatgggaga acatttgcct aaaggtaaca tcgtcataaa tacaaaagat	480
ggtggtaa atacattaga gtcgcataaa gagctacaaa aagataggga aaatgtaaaa	540
attaatacag ccgatataaa aaatgtaact ttcaaacttg tgaaaagtgt taatgacatt	600
gaacaagttt ga	612

<210> 74
 <211> 612
 <212> DNA
 <213> Staphylococcus aureus

<400> 74	
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tcaagtgtac aagataaaca attacaaaaa gttgaagaag taccaaataa ttcagaaaaa	180
gctttggtta aaaaacttta cgatagatac agcaaggata caataaatgg aaaatcta	240
aatctagga attgggttta ttcagagaga cctttaaatg aaaaccaagt tcgtatacat	300
ttagaaggaa catacacagt tgctggcaga gtgtatacac ctaagaggaa tattactctt	360
aataaagaag ttgtcacttt aaaagaattg gatcatatca taagatttgc tcatatttcc	420
tatggcttgt atatgggaga acatttgcct aaaggtaaca tcgtcataaa tacaaaagat	480
ggtggtaa atacattaga gtcgcataaa gagctacaaa aagataggga aaatgtaaaa	540
attaatacag ccgatataaa aaatgtaact ttcaaacttg tgaaaagtgt taatgacatt	600
gaacaagttt ga	612

<210> 75
 <211> 612
 <212> DNA
 <213> Staphylococcus aureus

<400> 75	
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tcaagtgtac aagataaaca attacaaaaa gttgaagaag taccaaataa ttcagaaaaa	180
gctttgggta aaaaacttta cgatagatac agcaaggata caataaatgg aaaatcta	240
aatctagga attgggttta ttcagagaga cctttaaatg aaaaccaagt tcgtatacat	300
ttagaaggaa catacacagt tgctggcaga gtgtatacac ctaagaggaa tattactctt	360
aataaagaag ttgtcacttt aaaagaattg gatcatatca taagatttgc tcatatttcc	420
tatggcttgt atatgggaga acatttgcct aaaggtaaca tcgtcataaa tacaaaagat	480
ggtggtaaat atacattaga gtcgcataaa gagctacaaa aagataggga aaatgtaaaa	540
attaatacag ccgatataaa aaatgtaact ttcaaacttg tgaaaagtgt taatgacatt	600
gaacaagttt ga	612

<210> 76
 <211> 612
 <212> DNA
 <213> Staphylococcus aureus

<400> 76	
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tcaagtgtac aagataaaca attacaaaaa gttgaagaag taccaaataa ttcagaaaaa	180
gctttgggta aaaaacttta cgatagatac agcaaggata caataaatgg aaaatcta	240
aatctagga attgggttta ttcagagaga cctttaaatg aaaaccaagt tcgtatacat	300
ttagaaggaa catacacagt tgctgataga gtatatacac ctaagagaaa tattactctt	360
aataaagaag ttgtcacttt aaaggaattg gatcatatca taagatttgc tcatatttct	420
tatggcttat atatgggaga acatttgcct aaaggtaaca tcgtcataaa tacaaaagat	480
ggcggtaaat atacattaga gtcgcataaa gagctacaaa aagataggga aaatgtaaaa	540
attaatacag ccgatataaa aaatgtaact ttcaaacttg tgaaaagtgt taatgacatt	600
gaacaagttt ga	612

<210> 77
 <211> 612

<212> DNA
<213> Staphylococcus aureus

<400> 77
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tcaagtgtac aagataaaca attacaaaaa gttgaagaag taccaaataa ttcagaaaaa 180
gctttgggta aaaaacttta cgatagatac agcaaggata caataaatgg aaaatctaata 240
aaatctagga attggggtta ttcagagaga cctttaaatg aaaaccaagt tcgtatacat 300
ttagaaggaa catacacagt tgctgataga gtatatacac ctaagagaaa tattactctt 360
aataaagaag ttgtcacttt aaaggaattg gatcatatca taagatttgc tcatatttct 420
tatggcttat atatgggaga acatttgcct aaaggtaaca tcgtcataaa taaaaagat 480
ggcggtaaat atacattaga gtcgcataaa gagctacaaa aagataggga aaatgtaaaa 540
attaatacag ccgatataaa aaatgtaact ttcaaacttg tgaaaagtgt taatgacatt 600
gaacaagttt ga 612

<210> 78
<211> 612
<212> DNA
<213> Staphylococcus aureus

<400> 78
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tcaagtgtac aagataaaca attacaaaaa gttgaagaag taccaaataa ttcagaaaaa 180
gctttgggta aaaaacttta cgatagatac agcaaggata caataaatgg aaaatctaata 240
aaatctagga attggggtta ttcagagaga cctttaaatg aaaaccaagt tcgtatacat 300
ttagaaggaa catacacagt tgctgataga gtatatacac ctaagagaaa tattactctt 360
aataaagaag ttgtcacttt aaaggaattg gatcatatca taagatttgc tcatatttct 420
tatggcttat atatgggaga acatttgcct aaaggtaaca tcgtcataaa taaaaagat 480
ggcggtaaat atacattaga gtcgcataaa gagctacaaa aagataggga aaatgtaaaa 540
attaatacag ccgatataaa aaatgtaact ttcaaacttg tgaaaagtgt taatgacatt 600

gaacaagttt ga 612

<210> 79
<211> 612
<212> DNA
<213> Staphylococcus aureus

<400> 79
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tcaagtgtac aagataaaca attacaaaaa gttgaagaag taccaaataa ttcagaaaaa 180
gctttgggta aaaaacttta cgatagatac agcaaggata caataaatgg aaaatctaata 240
aaatctagga attggggtta ttcagagaga cctttaaatg aaaaccaagt tcgtatacat 300
ttagaaggaa catacacagt tgctgataga gtatatacac ctaagagaaa tattactctt 360
aataaagaag ttgtcacttt aaaggaattg gatcatatca taagatttgc tcatatttct 420
tatggcttat atatgggaga acatttgcct aaaggtaaca tcgtcataaa tacaaaagat 480
ggcggtaaat atacattaga gtcgcataaa gagctacaaa aagataggga aaatgtaaaa 540
attaatacag ccgatataaa aaatgtaact ttcaaacttg tgaaaagtgt taatgacatt 600
gaacaagttt ga 612

<210> 80
<211> 612
<212> DNA
<213> Staphylococcus aureus

<400> 80
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atcatctatg ggggaacatt tggaatatat ccaaaagcag acgcgtcaac acaaaattcc 120
tcaagtgtac aagataaaca attacaaaaa gttgaagaag taccaaataa ttcagaaaaa 180
gctttgggta aaaaacttta cgatagatac agcaaggata caataaatgg aaaatctaata 240
aaatctagga attggggtta ttcagagaga cctttaaatg aaaaccaagt tcgtatacat 300
ttagaaggaa catacacagt tgctgataga gtatatacac ctaagagaaa tattactctt 360
aataaagaag ttgtcacttt aaaggaattg gatcatatca taagatttgc tcatatttct 420

tatggcttat atatgggaga acatttgcct aaaggttaaca tcgtcataaa tacaaaagat	480
ggcggtaaat atacattaga gtcgcataaa gagctacaaa aagataggga aaatgtaaaa	540
attaatacag cccgatataaa aaatgtaact ttcaaacttg tgaaaagtgt taatgacatt	600
gaacaagttt ga	612

<210> 81
 <211> 612
 <212> DNA
 <213> Staphylococcus aureus

<400> 81	
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atcatctatg ggggaacatt tggaatatat ccaaaagcag acgcgtcaac acaaaattcc	120
tcaagtgtac aagataaaca attccaaaaa gttgaagaag taccaaataa ttcagaaaaa	180
gctttggtta aaaaactgta cgatagatac agccaaaata caataaacgg aaaatcta	240
aaagctagga attgggttta ttcagagaga cttttaa	300
atg ctaagaggaa cattactctt	360
aataaagaag ttgtcacttt aaaagaattg gatcatatca taagatttgc tcatatttct	420
tatggcttat atatgggaga acatttgcct aaaggttaaca tcgtcataaa tacaaaagaat	480
ggcggtaaat atacattaga gtcgcacaaa gagttacaaa agaataggga aaatgtagaa	540
attaatactg atgatataaa aaatgtaact ttcgaacttg tgaaaagtgt taatgacatt	600
gaacaagttt ga	612

<210> 82
 <211> 203
 <212> PRT
 <213> Staphylococcus aureus

<400> 82

Met	Phe	Lys	Lys	Tyr	Asp	Ser	Lys	Asn	Ser	Ile	Val	Leu	Lys	Ser	Ile
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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> 83
 <211> 203
 <212> PRT
 <213> Staphylococcus aureus
 <400> 83

Met Phe Lys Lys Tyr Asp Ser Lys Asn Ser Ile Val Leu Lys Ser Ile
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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> 84
 <211> 203
 <212> PRT
 <213> Staphylococcus aureus

<400> 84

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 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> 85
<211> 203
<212> PRT
<213> Staphylococcus aureus

<400> 85

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 Asp 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

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

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<210> 86
<211> 203
<212> PRT
<213> Staphylococcus aureus
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<400> 86

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 Asp 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> 87
<211> 203
<212> PRT
<213> Staphylococcus aureus

<400> 87

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 Asp 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> 88
<211> 203
<212> PRT
<213> Staphylococcus aureus

<400> 88

Met Phe Lys Lys Tyr Asp Ser Lys Asn Ser Ile Val Leu Lys Ser Ile
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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 Asp 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> 89
<211> 203
<212> PRT
<213> Staphylococcus aureus

<400> 89

Met Phe Lys Lys Tyr Asp Ser Lys Asn Ser Ile Val Leu Lys Ser Ile
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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	Asp	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												
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<211>	203																		
<212>	PRT																		
<213>	Staphylococcus aureus																		
<400>	90																		
Met	Phe	Lys	Lys	Asn	Asp	Ser	Lys	Asn	Ser	Ile	Leu	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 Pro Ser Val Gln Asp Lys Gln Phe
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 Gln Asn 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 Asn Leu Glu Gly Thr Tyr Arg Val Ala Asp 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> 91
<211> 203

<212> PRT
<213> Staphylococcus aureus

<400> 91

Met Phe Lys Lys Tyr Asp Ser Lys Asn Ser Ile Val Leu Lys Ser Ile
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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 Phe
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 Gln Asn Thr Ile Asn Gly Lys Ser Asn
65 70 75 80

Lys Ala 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 Arg Val Ala Asp 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 Asn
145 150 155 160

Gly Gly Lys Tyr Thr Leu Glu Ser His Lys Glu Leu Gln Lys Asn Arg
165 170 175

Glu Asn Val Glu Ile Asn Thr Asp Asp Ile Lys Asn Val Thr Phe Glu
180 185 190

Leu Val Lys Ser Val Asn Asp Ile Glu Gln Val
195 200

<210> 92
<211> 203
<212> PRT
<213> Artificial sequence

<220>
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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

<220>
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<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (82)..(82)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (100)..(100)
<223> Xaa can be any naturally occurring amino acid

<220>
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<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (109)..(109)

<223> Xaa can be any naturally occurring amino acid

<220>

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<222> (160)..(160)

<223> Xaa can be any naturally occurring amino acid

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<222> (175)..(175)

<223> Xaa can be any naturally occurring amino acid

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<222> (180)..(180)

<223> Xaa can be any naturally occurring amino acid

<220>

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<222> (184)..(184)

<223> Xaa can be any naturally occurring amino acid

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<222> (192)..(192)

<223> Xaa can be any naturally occurring amino acid

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<222> (201)..(203)

<223> Xaa can be any naturally occurring amino acid

<400> 92

Met Phe Lys Lys Xaa Asp Ser Lys Asn Ser Ile Xaa Leu Lys Ser Ile
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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 Xaa Ser Val Gln Asp Lys Gln Xaa
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 Xaa Xaa Thr Ile Asn Gly Lys Ser Asn
65 70 75 80

Lys Xaa Arg Asn Trp Val Tyr Ser Glu Arg Pro Leu Asn Glu Asn Gln
85 90 95

Val Arg Ile Xaa Leu Glu Gly Thr Tyr Xaa Val Ala Xaa 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 Xaa
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Gly Gly Lys Tyr Thr Leu Glu Ser His Lys Glu Leu Gln Lys Xaa Arg
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<212> PRT

<213> Staphylococcus aureus

<400> 93

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catgttaata ttaagttgcg gaaagatatt aataaaatct attttatgac agatgttgat	1320
ttaggtggac caacgtttgt cttaaatgac aaagactatc aagaaataag aaagtataca	1380
aaagcaaagc atatcgtctc tcaatttgga ttcgatttga aacataaaaa agatgcttta	1440
gcattagaaa aagtgaaaaa taaagttgat aaatctatta aaacaagaag tgaagcgata	1500
agctcaatat caagtttaac cggaatatta ttatttgtaa catcattttt aggtattaca	1560
ttcttgattg ctgtatgttg cattatatac ataaagcaaa tagatgaaac cgaagatgag	1620
ttagagaatt atagtatttt gagaaagcct ggatttacac aaaaagatat ggcaagggga	1680
ctaaagttta aaattatgtt taattttggg ttacctttag ttattgcact atcacatgca	1740
tattttacat cattagcata tatgaaatta atgggtacaa cgaatcaa at accggttttc	1800
atagtaatgg gattatacat ttgtatgtat gctgtttttg cagtgcggc ttataatcat	1860
tccaagcgaa caattagaca ttccatataa	1890

<210> 105
 <211> 1890
 <212> DNA
 <213> Staphylococcus aureus

<400> 105	
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gctcataaac taaacatgac agagtcatat ccaattataa aggaaggctc acaagtcgga	180
agctactttc tatttttcat cataattgca tttttgttat atgccaatgt gttatttatt	240
aaacgacgaa gttatgagct tgcattatat caaacattag gtttatctaa attcaacatt	300
atttatatac taatgctcga acaattacta atatttataa ttacggcaat attaggtatt	360
attattggta tttttggttc gaaactgta ttaatgattg tctttacatt attaggaatt	420
aaagaaaagg ttccaattat ttttagtttg agggcggtat ttgaaacatt aatgttaatc	480
gggtgctgctt attttttaac atctgctcaa aattttatat tagtgttcaa acaatctatt	540

tcacagatgt caaagaataa ccagggttaaa gaaacaaatc ataataaaaat tacatttgaa	600
gagggttggtt taggcatctt aggtatagta ttgattacca caggatacta tctatctttg	660
aacattgttc aatattatga ttctatcggt acacttatgt ttatttttatt gtcaactgtg	720
attggggcat acttattttt taaaagctct gtttctctag tttttaaaat ggtgaagaag	780
tttagaaaag gtgttataag tgtaaatgat gtcattgttct catcatctat tatgtatcgt	840
attaagaaaa atgctttttc acttacgggc atggcaatca tttcagcgat tactgtttca	900
gttctttgct ttgctgctat aagtagagcg tccttatcaa gtgaaataaa atatactgca	960
ccacacgacg ttacaattaa agaccaacaa aaagctaatc aattagcaag tgaattaaac	1020
aatcaaaaaa ttcctcattt ttataattat aaagaagtaa ttcatacgaa attgtataaa	1080
gataatttat ttgatgtaaa agcgaaagaa ccatacaatg taacaattac tagtgataaa	1140
tacatcccta atactgattt gaaacgtggg caagctgatt tatttgtagc ggaaggttct	1200
atcaaagatt tagtgaaaca taagaagcat ggtaaggcaa ttataggaac gaaaaaacat	1260
catgttaata ttaagttacg taaagatatt aataaaatct attttatgac agatgttgat	1320
ttaggtggac caacgtttgt cttaaagac aaagactatc aagaaataag aaagtataca	1380
aaggcaaagc atacgtcttc tcaatttgga ttcgatttga aacataaaaa agatgcttta	1440
gcattagaaa aagcgaaaaa taaagttgat aaatctattg aaacaagaag tgaagcgata	1500
agctcaatat caagttaaac cggaatatta ttatttgtaa catcattttt aggtattaca	1560
ttcttgattg ctgtatgttg cattatatac ataaagcaaa tagatgaaac cgaagatgag	1620
ttagagaatt atagtatttt gagaaagctt ggatttacac aaaaagatat ggcaagggga	1680
ctaaagttta aaattatgtt taattttggg ttaccttag ttattgcact atcacatgca	1740
tattttacat cattagcata tatgaaatta atgggtacaa cgaatcaaatt accggttttc	1800
atagtaatgg gattatacat ttgtatgtat gctgtttttg cagtgcgggc ttataatcat	1860
tccaagcgaa caattagaca ttccatataa	1890

<210> 106
 <211> 1800
 <212> DNA
 <213> Staphylococcus aureus

<400> 106

ttgtatttta gctttgtagc attaaaatac gtcataaac taaacatgac agagtcatat	60
ccaattataa aggaaggctc acaagtcgga agctactttc tttttttcat cataattgca	120
tttttgttat atgccaatgt gttatttatt aaacgacgaa gttatgagct tgcattatat	180
caaacattag gtttatctaa attcaacatt atttatatac taatgctcga acaattacta	240
atatttataa ttacggcaat attaggtatt attattggta tttttggttc gaaactgtta	300
ttaatgattg tctttacatt attaggaatt aaagaaaagg ttccaattat ttttagtttg	360
agggcggtat ttgaaacatt aatgttaatc ggtgtcgctt attttttaac atctgctcaa	420
aattttatat tagtgttcaa acaatctatt tcacagatgt caaagaataa ccaggttaaa	480
gaaacaaatc ataataaaat tacatttgaa gaggttgttt taggcatctt aggtatagta	540
ttgattacca caggatacta tctatctttg aacattgttc aatattatga ttctatcggt	600
acacttatgt ttattttatt gtcaactgtg attggggcat acttattttt taaaagctct	660
gtttctctag tttttaaaat ggtgaagaag tttagaaaag gtgttataag tgtaaatgat	720
gtcatgttct catcatctat tatgtatcgt attaagaaaa atgctttttc acttacggtc	780
atggcaatca tttcagcgat tactgtttca gttctttgct ttgctgctat aagtagagcg	840
tccttatcaa gtgaaataaa atatactgca ccacacgacg ttacaattaa agaccaacaa	900
aaagctaatc aattagcaag tgaattaaac aatcaaaaaa ttcctcattt ttataattat	960
aaagaagtaa ttcatacgaa attgtataaa gataatttat ttgatgtaaa agcgaaagaa	1020
ccatacaatg taacaattac tagtgataaa tacatcccta atactgattt gaaacgtggg	1080
caagctgatt tatttgtagc ggaaggttct atcaaagatt tagtgaaaca taagaagcat	1140
ggtaaggcaa ttataggaac gaaaaaacat catgttaata ttaagttacg taaagatatt	1200
aataaaatct attttatgac agatgttgat ttaggtggac caacgtttgt cttaaatgac	1260
aaagactatc aagaaataag aaagtataca aaggcaaagc atatcgtctc tcaatttgga	1320
ttcgatttga aacataaaaa agatgcttta gcattagaaa aagcgaaaaa taaagttgat	1380
aatctattg aaacaagaag tgaagcgata agctcaatat caagttaaac cggaatatta	1440
ttatttgtaa catcatTTTT aggtattaca ttcttgattg ctgtatgttg cattatatac	1500
ataaagcaaa tagatgaaac cgaagatgag ttagagaatt atagtatttt gagaaagctt	1560

ggatttacac aaaaagatat ggcaagggga ctaaagttta aaattatggt taattttggg	1620
ttaccttttag ttattgcact atcacatgca tattttacat cattagcata tatgaaatta	1680
atgggtacaa cgaatcaa at accggttttc atagtaatgg gattatacat ttgtatgtat	1740
gctgtttttg cagtgcggc ttataatcat tccaagcgaa caattagaca ttccatataa	1800

<210> 107
 <211> 1755
 <212> DNA
 <213> Staphylococcus aureus

<400> 107	
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ttcatcataa ttgcatTTTT gttatatgcc aatgtgttat ttattaaacg acgaagttat	120
gagcttgcatt tatatcaaac attaggttta tctaaattca acattattta tataactaatg	180
ctcgaacaat tactaatatt tataattacg gcaatattag gtattattat tgggtattttt	240
ggttcgaaac tgttattaat gattgtcttt acattattag gaattaaaga aaagggtcca	300
attattttta gtttgagggc ggtatttgaa acattaatgt taatcgggtg cgcttatttt	360
ttaacatctg ctcaaaattt tatattagt ttcaaacaat ctatttcaca gatgtcaaag	420
aataaccagg ttaaagaaac aaatcataat aaaattacat ttgaagaggt tgttttaggc	480
atcttaggta tagtattgat taccacagga tactatctat ctttgaacat tgttcaatat	540
tatgattcta tcggtacact tatgtttatt ttattgtcaa ctgtgattgg ggcatactta	600
ttttttaaaa gctctgtttc tctagttttt aaaatgggtga agaagtttag aaaagggtgt	660
ataagtgtaa atgatgtcat gttctcatca tctattatgt atcgtattaa gaaaaatgct	720
ttttcactta cggatcatggc aatcatttca gcgattactg tttcagttct ttgctttgct	780
gctataagta gagcgtcctt atcaagtga ataaaaatata ctgcaccaca cgacgttaca	840
attaaagacc aacaaaaagc taatcaatta gcaagtgaat taaacaatca aaaaattcct	900
catttttata attataaaga agtaattcat acgaaattgt ataaagataa tttatttgat	960
gtaaaagcga aagaaccata caatgtaaca attactagt ataaatacat ccctaatact	1020
gatttgaaac gtgggcaagc tgatttattt gtagcggaag gttctatcaa agatttagtg	1080

aaacataaga agcatggtaa ggcaattata ggaacgaaaa aacatcatgt taatattaag	1140
ttacgtaaag atattaataa aatctatfff atgacagatg ttgatttagg tggaccaacg	1200
tttgtcttaa atgacaaaga ctatcaagaa ataagaaagt atacaaaggc aaagcatatc	1260
gtctctcaat ttggattcga ttgaaacat aaaaaagatg ctttagcatt agaaaaagcg	1320
aaaaataaag ttgataaatc tattgaaaca agaagtgaag cgataagctc aatatcaagt	1380
ttaaccggaa tattattatt tgtaacatca tttttaggta ttacattctt gattgctgta	1440
tgttgcatta tatacataaa gcaaatagat gaaaccgaag atgagttaga gaattatagt	1500
atfttgagaa agcttggatt tacacaaaaa gatatggcaa ggggactaaa gtttaaaatt	1560
atgtttaatt ttgggttacc tttagttatt gcactatcac atgcatatft tacatcatta	1620
gcatatatga aattaatggg tacaacgaat caaataccgg ttttcatagt aatgggatta	1680
tacatttgta tgtatgctgt ttttgcagtg acggcttata atcattccaa gcgaacaatt	1740
agacattcca tataa	1755

<210> 108
 <211> 1890
 <212> DNA
 <213> Staphylococcus aureus

<400> 108	
atgaccttta acgagataat atttaaaaat ttccgtcaaa atttatcaca ttatgccatc	60
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gctcataaac taaacatgac agagtcatat ccaattataa aggaaggctc acaagtcgga	180
agctactttc tatttttcat cataattgca tttttgttat atgccaatgt gttatttatt	240
aaacgacgaa gttatgagct tgcattatat caaacattag gtttatctaa attcaacatt	300
atttatatac taatgctcga acaattacta atatttataa ttacggcaat attaggtatt	360
attattggta tttttggttc gaaactgta ttaatgattg tctttacatt attaggaatt	420
aaagaaaagg ttccaattat ttttagtttg agggcggtat ttgaaacatt aatgttaatc	480
ggtgtcgctt attttttaac atctgctcaa aattttatat tagtgttcaa acaatctatt	540
tcacagatgt caaagaataa ccaggttaaa gaaacaaatc ataataaaat tacatttgaa	600
gaggttgttt taggcatctt aggtatagta ttgattacca caggatacta tctatctttg	660

aacattgttc aatattatga ttctatcggt acacttatgt ttattttatt gtcaactgtg	720
attggggcat acttattttt taaaagctct gtttctctag tttttaaaat ggtgaagaag	780
tttagaaaag gtgttataag tgtaaatgat gtcatgttct catcatctat tatgtatcgt	840
attaagaaaa atgctttttc acttacggtc atggcaatca tttcagcgat tactgtttca	900
gttctttgct ttgctgctat aagtagagcg tccttatcaa gtgaaataaa atatactgca	960
ccacacgacg ttacaattaa agaccaacaa aaagctaatc aattagcaag tgaattaaac	1020
aatcaaaaaa ttcctcattt ttataattat aaagaagtaa ttcatacgaa attgtataaa	1080
gataatttat ttgatgtaaa atcgaaacaa ccatacaatg taacaattac tagtgataaa	1140
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atcaaagatt tagtgaaaca taagaagcat ggtaaagcag ttataggaac gaaaaaacat	1260
catgttaata ttaagttacg taaagatatt aataaaatct attttatgac agatgttgat	1320
ttaggtggac caacgtttgt cttaaatgac aaagactatc aagaaataag aaagtataca	1380
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gcattagaaa aagcgaaaaa taaagttgat aaatctattg agacaagaag tgaagcgata	1500
agctcaatat caagtttaac cggaatatta ttatttgtaa catcatTTTT aggtattaca	1560
ttcttgattg ctgtatgttg cattatatac attaagcaaa tagatgaaac cgaagatgag	1620
ttagagaatt atagtatatt gagaaagctt ggatttacac aaaaagatat ggcaagggga	1680
ctaaagttta aaattatgtt taattttggg ttaccttag ttattgcact atcacatgca	1740
tattttacat cattagcata tatgaaatta atgggtacaa cgaatcaaat accggttttc	1800
atagtaatgg gattatacat ttgtatgtat gctgtttttg cagtgcggc ttataatcat	1860
tccaagcgaa caattagaca ttccatataa	1890

<210> 109
 <211> 629
 <212> PRT
 <213> Staphylococcus aureus

<400> 109

Met Thr Phe Asn Glu Ile Ile Phe Lys Asn Phe Arg Gln Asn Leu Ser

1	5	10	15
His Tyr Ala Ile Tyr Leu Phe Ser Leu Ile Thr Ser Val Val Leu Tyr	20	25	30
Phe Ser Phe Val Ala Leu Lys Tyr Ala His Lys Leu Asn Met Thr Glu	35	40	45
Ser Tyr Pro Ile Ile Lys Glu Gly Ser Gln Val Gly Ser Tyr Phe Leu	50	55	60
Phe Phe Ile Ile Ile Ala Phe Leu Leu Tyr Ala Asn Val Leu Phe Ile	65	70	75
Lys Arg Arg Ser Tyr Glu Leu Ala Leu Tyr Gln Thr Leu Gly Leu Ser	85	90	95
Lys Phe Asn Ile Ile Tyr Ile Leu Met Leu Glu Gln Leu Leu Ile Phe	100	105	110
Ile Ile Thr Ala Ile Leu Gly Ile Ile Ile Gly Ile Phe Gly Ser Lys	115	120	125
Leu Leu Leu Met Ile Val Phe Thr Leu Leu Gly Ile Lys Glu Lys Val	130	135	140
Pro Ile Ile Phe Ser Leu Arg Ala Val Phe Glu Thr Leu Met Leu Ile	145	150	155
Gly Val Ala Tyr Phe Leu Thr Ser Ala Gln Asn Phe Ile Leu Val Phe	165	170	175
Lys Gln Ser Ile Ser Gln Met Ser Lys Asn Asn Gln Val Lys Glu Thr	180	185	190
Asn His Asn Lys Ile Thr Phe Glu Glu Val Val Leu Gly Ile Leu Gly	195	200	205
Ile Val Leu Ile Thr Thr Gly Tyr Tyr Leu Ser Leu Asn Ile Val Gln			

210		215		220
Tyr Tyr Asp Ser Ile Gly Thr Leu Met Phe Ile Leu Leu Ser Thr Val				
225		230		235 240
Ile Gly Ala Tyr Leu Phe Phe Lys Ser Ser Val Ser Leu Val Phe Lys				
	245		250	255
Met Val Lys Lys Phe Arg Lys Gly Val Ile Ser Val Asn Asp Val Met				
	260		265	270
Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys Asn Ala Phe Ser Leu				
	275		280	285
Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val Ser Val Leu Cys Phe				
	290		295	300
Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu Ile Lys Tyr Thr Ala				
305		310		315 320
Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys Ala Asn Gln Leu Ala				
	325		330	335
Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe Tyr Asn Tyr Lys Glu				
	340		345	350
Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu Phe Asp Val Lys Ala				
	355		360	365
Lys Glu Pro Tyr Asn Val Thr Ile Thr Ser Asp Lys Tyr Ile Pro Asn				
	370		375	380
Thr Asp Leu Lys Arg Gly Gln Ala Asp Leu Phe Val Ala Glu Gly Ser				
385		390		395 400
Ile Lys Asp Leu Val Lys His Lys Lys His Gly Lys Ala Ile Ile Gly				
	405		410	415
Thr Lys Lys His His Val Asn Ile Lys Leu Arg Lys Asp Ile Asn Lys				

420

425

430

Ile Tyr Phe Met Thr Asp Val Asp Leu Gly Gly Pro Thr Phe Val Leu
 435 440 445

Asn Asp Lys Asp Tyr Gln Glu Ile Arg Lys Tyr Thr Lys Ala Lys His
 450 455 460

Ile Val Ser Gln Phe Gly Phe Asp Leu Lys His Lys Lys Asp Ala Leu
 465 470 475 480

Ala Leu Glu Lys Ala Lys Asn Lys Val Asp Lys Ser Ile Glu Thr Arg
 485 490 495

Ser Glu Ala Ile Ser Ser Ile Ser Ser Leu Thr Gly Ile Leu Leu Phe
 500 505 510

Val Thr Ser Phe Leu Gly Ile Thr Phe Leu Ile Ala Val Cys Cys Ile
 515 520 525

Ile Tyr Ile Lys Gln Ile Asp Glu Thr Glu Asp Glu Leu Glu Asn Tyr
 530 535 540

Ser Ile Leu Arg Lys Leu Gly Phe Thr Gln Lys Asp Met Ala Arg Gly
 545 550 555 560

Leu Lys Phe Lys Ile Met Phe Asn Phe Gly Leu Pro Leu Val Ile Ala
 565 570 575

Leu Ser His Ala Tyr Phe Thr Ser Leu Ala Tyr Met Lys Leu Met Gly
 580 585 590

Thr Thr Asn Gln Ile Pro Val Phe Ile Val Met Gly Leu Tyr Ile Cys
 595 600 605

Met Tyr Ala Val Phe Ala Val Thr Ala Tyr Asn His Ser Lys Arg Thr
 610 615 620

Ile Arg His Ser Ile

625

<210> 110
<211> 599
<212> PRT
<213> Staphylococcus aureus

<400> 110

Met Tyr Phe Ser Phe Val Ala Leu Lys Tyr Ala His Lys Leu Asn Met
1 5 10 15

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

Phe Leu Phe Phe Ile Ile Ile Ala Phe Leu Leu Tyr Ala Asn Val Leu
35 40 45

Phe Ile Lys Arg Arg Ser Tyr Glu Leu Ala Leu Tyr Gln Thr Leu Gly
50 55 60

Leu Ser Lys Phe Asn Ile Ile Tyr Ile Leu Met Leu Glu Gln Leu Leu
65 70 75 80

Ile Phe Ile Ile Thr Ala Ile Leu Gly Ile Ile Ile Gly Ile Phe Gly
85 90 95

Ser Lys Leu Leu Leu Met Ile Val Phe Thr Leu Leu Gly Ile Lys Glu
100 105 110

Lys Val Pro Ile Ile Phe Ser Leu Arg Ala Val Phe Glu Thr Leu Met
115 120 125

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

Val Phe Lys Gln Ser Ile Ser Gln Met Ser Lys Asn Asn Gln Val Lys
145 150 155 160

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

Leu Gly Ile Val Leu Ile Thr Thr Gly Tyr Tyr Leu Ser Leu Asn Ile
180 185 190

Val Gln Tyr Tyr Asp Ser Ile Gly Thr Leu Met Phe Ile Leu Leu Ser
195 200 205

Thr Val Ile Gly Ala Tyr Leu Phe Phe Lys Ser Ser Val Ser Leu Val
210 215 220

Phe Lys Met Val Lys Lys Phe Arg Lys Gly Val Ile Ser Val Asn Asp
225 230 235 240

Val Met Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys Asn Ala Phe
245 250 255

Ser Leu Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val Ser Val Leu
260 265 270

Cys Phe Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu Ile Lys Tyr
275 280 285

Thr Ala Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys Ala Asn Gln
290 295 300

Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe Tyr Asn Tyr
305 310 315 320

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

Lys Ala Lys Glu Pro Tyr Asn Val Thr Ile Thr Ser Asp Lys Tyr Ile
340 345 350

Pro Asn Thr Asp Leu Lys Arg Gly Gln Ala Asp Leu Phe Val Ala Glu
355 360 365

Gly Ser Ile Lys Asp Leu Val Lys His Lys Lys His Gly Lys Ala Ile
370 375 380

Ile Gly Thr Lys Lys His His Val Asn Ile Lys Leu Arg Lys Asp Ile
385 390 395 400

Asn Lys Ile Tyr Phe Met Thr Asp Val Asp Leu Gly Gly Pro Thr Phe
405 410 415

Val Leu Asn Asp Lys Asp Tyr Gln Glu Ile Arg Lys Tyr Thr Lys Ala
420 425 430

Lys His Ile Val Ser Gln Phe Gly Phe Asp Leu Lys His Lys Lys Asp
435 440 445

Ala Leu Ala Leu Glu Lys Ala Lys Asn Lys Val Asp Lys Ser Ile Glu
450 455 460

Thr Arg Ser Glu Ala Ile Ser Ser Ile Ser Ser Leu Thr Gly Ile Leu
465 470 475 480

Leu Phe Val Thr Ser Phe Leu Gly Ile Thr Phe Leu Ile Ala Val Cys
485 490 495

Cys Ile Ile Tyr Ile Lys Gln Ile Asp Glu Thr Glu Asp Glu Leu Glu
500 505 510

Asn Tyr Ser Ile Leu Arg Lys Leu Gly Phe Thr Gln Lys Asp Met Ala
515 520 525

Arg Gly Leu Lys Phe Lys Ile Met Phe Asn Phe Gly Leu Pro Leu Val
530 535 540

Ile Ala Leu Ser His Ala Tyr Phe Thr Ser Leu Ala Tyr Met Lys Leu
545 550 555 560

Met Gly Thr Thr Asn Gln Ile Pro Val Phe Ile Val Met Gly Leu Tyr
565 570 575

Ile Cys Met Tyr Ala Val Phe Ala Val Thr Ala Tyr Asn His Ser Lys
580 585 590

Arg Thr Ile Arg His Ser Ile
595

<210> 111
<211> 584
<212> PRT
<213> Staphylococcus aureus

<400> 111

Met Thr Glu Ser Tyr Pro Ile Ile Lys Glu Gly Ser Gln Val Gly Ser
1 5 10 15

Tyr Phe Leu Phe Phe Ile Ile Ile Ala Phe Leu Leu Tyr Ala Asn Val
20 25 30

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

Gly Leu Ser Lys Phe Asn Ile Ile Tyr Ile Leu Met Leu Glu Gln Leu
50 55 60

Leu Ile Phe Ile Ile Thr Ala Ile Leu Gly Ile Ile Ile Gly Ile Phe
65 70 75 80

Gly Ser Lys Leu Leu Leu Met Ile Val Phe Thr Leu Leu Gly Ile Lys
85 90 95

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

Met Leu Ile Gly Val Ala Tyr Phe Leu Thr Ser Ala Gln Asn Phe Ile
115 120 125

Leu Val Phe Lys Gln Ser Ile Ser Gln Met Ser Lys Asn Asn Gln Val
130 135 140

Lys Glu Thr Asn His Asn Lys Ile Thr Phe Glu Glu Val Val Leu Gly
145 150 155 160

Ile Leu Gly Ile Val Leu Ile Thr Thr Gly Tyr Tyr Leu Ser Leu Asn
165 170 175

Ile Val Gln Tyr Tyr Asp Ser Ile Gly Thr Leu Met Phe Ile Leu Leu
180 185 190

Ser Thr Val Ile Gly Ala Tyr Leu Phe Phe Lys Ser Ser Val Ser Leu
195 200 205

Val Phe Lys Met Val Lys Lys Phe Arg Lys Gly Val Ile Ser Val Asn
210 215 220

Asp Val Met Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys Asn Ala
225 230 235 240

Phe Ser Leu Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val Ser Val
245 250 255

Leu Cys Phe Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu Ile Lys
260 265 270

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

Gln Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe Tyr Asn
290 295 300

Tyr Lys Glu Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu Phe Asp
305 310 315 320

Val Lys Ala Lys Glu Pro Tyr Asn Val Thr Ile Thr Ser Asp Lys Tyr
325 330 335

Ile Pro Asn Thr Asp Leu Lys Arg Gly Gln Ala Asp Leu Phe Val Ala
340 345 350

Glu Gly Ser Ile Lys Asp Leu Val Lys His Lys Lys His Gly Lys Ala
355 360 365

Ile Ile Gly Thr Lys Lys His His Val Asn Ile Lys Leu Arg Lys Asp
370 375 380

Ile Asn Lys Ile Tyr Phe Met Thr Asp Val Asp Leu Gly Gly Pro Thr
385 390 395 400

Phe Val Leu Asn Asp Lys Asp Tyr Gln Glu Ile Arg Lys Tyr Thr Lys
405 410 415

Ala Lys His Ile Val Ser Gln Phe Gly Phe Asp Leu Lys His Lys Lys
420 425 430

Asp Ala Leu Ala Leu Glu Lys Ala Lys Asn Lys Val Asp Lys Ser Ile
435 440 445

Glu Thr Arg Ser Glu Ala Ile Ser Ser Ile Ser Ser Leu Thr Gly Ile
450 455 460

Leu Leu Phe Val Thr Ser Phe Leu Gly Ile Thr Phe Leu Ile Ala Val
465 470 475 480

Cys Cys Ile Ile Tyr Ile Lys Gln Ile Asp Glu Thr Glu Asp Glu Leu
485 490 495

Glu Asn Tyr Ser Ile Leu Arg Lys Leu Gly Phe Thr Gln Lys Asp Met
500 505 510

Ala Arg Gly Leu Lys Phe Lys Ile Met Phe Asn Phe Gly Leu Pro Leu
515 520 525

Val Ile Ala Leu Ser His Ala Tyr Phe Thr Ser Leu Ala Tyr Met Lys
530 535 540

Leu Met Gly Thr Thr Asn Gln Ile Pro Val Phe Ile Val Met Gly Leu
545 550 555 560

Tyr Ile Cys Met Tyr Ala Val Phe Ala Val Thr Ala Tyr Asn His Ser
565 570 575

Lys Arg Thr Ile Arg His Ser Ile
580

<210> 112
<211> 584
<212> PRT
<213> Staphylococcus aureus

<400> 112

Met Thr Glu Ser Tyr Pro Ile Ile Lys Glu Gly Ser Gln Val Gly Ser
1 5 10 15

Tyr Phe Leu Phe Phe Ile Ile Ile Ala Phe Leu Leu Tyr Ala Asn Val
20 25 30

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

Gly Leu Ser Lys Phe Asn Ile Ile Tyr Ile Leu Met Leu Glu Gln Leu
50 55 60

Leu Ile Phe Ile Ile Thr Ala Ile Leu Gly Ile Ile Ile Gly Ile Phe
65 70 75 80

Gly Ser Lys Leu Leu Leu Met Ile Val Phe Thr Leu Leu Gly Ile Lys
85 90 95

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

Met Leu Ile Gly Val Ala Tyr Phe Leu Thr Ser Ala Gln Asn Phe Ile
115 120 125

Leu Val Phe Lys Gln Ser Ile Ser Gln Met Ser Lys Asn Asn Gln Val
130 135 140

Lys Glu Thr Asn His Asn Lys Ile Thr Phe Glu Glu Val Val Leu Gly
145 150 155 160

Ile Leu Gly Ile Val Leu Ile Ile Thr Gly Tyr Tyr Leu Ser Leu Asn
 165 170 175

Ile Val Gln Tyr Tyr Asp Ser Ile Gly Ile Leu Met Phe Ile Leu Leu
 180 185 190

Ser Thr Val Ile Gly Ala Tyr Leu Phe Phe Lys Ser Ser Val Ser Leu
 195 200 205

Val Phe Lys Met Val Lys Lys Phe Arg Lys Gly Val Ile Ser Val Asn
 210 215 220

Asp Val Met Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys Asn Ala
 225 230 235 240

Phe Ser Leu Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val Ser Val
 245 250 255

Leu Cys Phe Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu Ile Lys
 260 265 270

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

Gln Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe Tyr Asn
 290 295 300

Tyr Lys Glu Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu Phe Asp
 305 310 315 320

Val Lys Ala Lys Glu Pro Tyr Asn Val Thr Ile Thr Ser Asp Lys Tyr
 325 330 335

Ile Pro Asn Thr Asp Leu Lys Arg Gly Gln Ala Asp Leu Phe Val Ala
 340 345 350

Glu Gly Ser Ile Lys Asp Leu Val Lys His Lys Lys His Gly Lys Ala
 355 360 365

Ile Ile Gly Thr Lys Lys His His Val Asn Ile Lys Leu Arg Lys Asp
370 375 380

Ile Asn Lys Ile Tyr Phe Met Thr Asp Val Asp Leu Gly Gly Pro Thr
385 390 395 400

Phe Val Leu Asn Asp Lys Asp Tyr Gln Glu Ile Arg Lys Tyr Thr Lys
405 410 415

Ala Lys His Ile Val Ser Gln Phe Gly Phe Asp Leu Lys His Lys Lys
420 425 430

Asp Ala Leu Ala Leu Glu Lys Val Lys Asn Lys Val Asp Lys Ser Ile
435 440 445

Lys Thr Arg Ser Glu Ala Ile Ser Ser Ile Ser Ser Leu Thr Gly Ile
450 455 460

Leu Leu Phe Val Thr Ser Phe Leu Gly Ile Thr Phe Leu Ile Ala Val
465 470 475 480

Cys Cys Ile Ile Tyr Ile Lys Gln Ile Asp Glu Thr Glu Asp Glu Leu
485 490 495

Glu Asn Tyr Ser Ile Leu Arg Lys Leu Gly Phe Thr Gln Lys Asp Met
500 505 510

Ala Arg Gly Leu Lys Phe Lys Ile Met Phe Asn Phe Gly Leu Pro Leu
515 520 525

Val Ile Ala Leu Ser His Ala Tyr Phe Thr Ser Leu Ala Tyr Met Lys
530 535 540

Leu Met Gly Thr Thr Asn Gln Ile Pro Val Phe Ile Val Met Gly Leu
545 550 555 560

Tyr Ile Cys Met Tyr Ala Val Phe Ala Val Thr Ala Tyr Asn His Ser
565 570 575

Lys Arg Thr Ile Arg His Ser Ile
580

<210> 113
<211> 584
<212> PRT
<213> Staphylococcus aureus

<400> 113

Met Thr Glu Ser Tyr Pro Ile Ile Lys Glu Gly Ser Gln Val Gly Ser
1 5 10 15

Tyr Phe Leu Phe Phe Ile Ile Ile Ala Phe Leu Leu Tyr Ala Asn Val
20 25 30

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

Gly Leu Ser Lys Phe Asn Ile Ile Tyr Ile Leu Met Leu Glu Gln Leu
50 55 60

Leu Ile Phe Ile Ile Thr Ala Ile Leu Gly Ile Ile Ile Gly Ile Phe
65 70 75 80

Gly Ser Lys Leu Leu Leu Met Ile Val Phe Thr Leu Leu Gly Ile Lys
85 90 95

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

Met Leu Ile Gly Val Ala Tyr Phe Leu Thr Ser Ala Gln Asn Phe Ile
115 120 125

Leu Val Phe Lys Gln Ser Ile Ser Gln Met Ser Lys Asn Asn Gln Val
130 135 140

Lys Glu Thr Asn His Asn Lys Ile Thr Phe Glu Glu Val Val Leu Gly
145 150 155 160

Ile Leu Gly Ile Val Leu Ile Ile Thr Gly Tyr Tyr Leu Ser Leu Asn

165	170	175
Ile Val Gln Tyr Tyr Asp Ser Ile Gly Ile Leu Met Phe Ile Leu Leu 180 185 190		
Ser Thr Val Ile Gly Ala Tyr Leu Phe Phe Lys Ser Ser Val Ser Leu 195 200 205		
Val Phe Lys Met Val Lys Lys Phe Arg Lys Gly Val Ile Ser Val Asn 210 215 220		
Asp Val Met Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys Asn Ala 225 230 235 240		
Phe Ser Leu Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val Ser Val 245 250 255		
Leu Cys Phe Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu Ile Lys 260 265 270		
Tyr Thr Ala Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys Ala Asn 275 280 285		
Gln Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe Tyr Asn 290 295 300		
Tyr Lys Glu Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu Phe Asp 305 310 315 320		
Val Lys Ala Lys Glu Pro Tyr Asn Val Thr Ile Thr Ser Asp Lys Tyr 325 330 335		
Ile Pro Asn Thr Asp Leu Lys Arg Gly Gln Ala Asp Leu Phe Val Ala 340 345 350		
Glu Gly Ser Ile Lys Asp Leu Val Lys His Lys Lys His Gly Lys Ala 355 360 365		
Ile Ile Gly Thr Lys Lys His His Val Asn Ile Lys Leu Arg Lys Asp		

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

580

<210> 114
<211> 584
<212> PRT
<213> Staphylococcus aureus

<400> 114

Met Thr Glu Ser Tyr Pro Ile Ile Lys Glu Gly Ser Gln Val Gly Ser
1 5 10 15

Tyr Phe Leu Phe Phe Ile Ile Ile Ala Phe Leu Leu Tyr Ala Asn Val
20 25 30

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

Gly Leu Ser Lys Phe Asn Ile Ile Tyr Ile Leu Met Leu Glu Gln Leu
50 55 60

Leu Ile Phe Ile Ile Thr Ala Ile Leu Gly Ile Ile Ile Gly Ile Phe
65 70 75 80

Gly Ser Lys Leu Leu Leu Met Ile Val Phe Thr Leu Leu Gly Ile Lys
85 90 95

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

Met Leu Ile Gly Val Ala Tyr Phe Leu Thr Ser Ala Gln Asn Phe Ile
115 120 125

Leu Val Phe Lys Gln Ser Ile Ser Gln Met Ser Lys Asn Asn Gln Val
130 135 140

Lys Glu Thr Asn His Asn Lys Ile Thr Phe Glu Glu Val Val Leu Gly
145 150 155 160

Ile Leu Gly Ile Val Leu Ile Thr Thr Gly Tyr Tyr Leu Ser Leu Asn
165 170 175

Ile Val Gln Tyr Tyr Asp Ser Ile Gly Ile Leu Met Phe Ile Leu Leu
180 185 190

Ser Thr Val Ile Gly Ala Tyr Leu Phe Phe Lys Ser Ser Val Ser Leu
195 200 205

Val Phe Lys Met Val Lys Lys Phe Arg Lys Gly Val Ile Ser Val Asn
210 215 220

Asp Val Met Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys Asn Ala
225 230 235 240

Phe Ser Leu Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val Ser Val
245 250 255

Leu Cys Phe Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu Ile Lys
260 265 270

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

Gln Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe Tyr Asn
290 295 300

Tyr Lys Glu Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu Phe Asp
305 310 315 320

Val Lys Ala Lys Glu Pro Tyr Asn Val Thr Ile Thr Ser Asp Lys Tyr
325 330 335

Ile Pro Asn Thr Asp Leu Lys Arg Gly Gln Ala Asp Leu Phe Val Ala
340 345 350

Glu Gly Ser Ile Lys Asp Leu Val Lys His Lys Lys His Gly Lys Ala
355 360 365

Ile Ile Gly Thr Lys Lys His His Val Asn Ile Lys Leu Arg Lys Asp
370 375 380

Ile Asn Lys Ile Tyr Phe Met Thr Asp Val Asp Leu Gly Gly Pro Thr
385 390 395 400

Phe Val Leu Asn Asp Lys Asp Tyr Gln Glu Ile Arg Lys Tyr Thr Lys
405 410 415

Ala Lys His Ile Val Ser Gln Phe Gly Phe Asp Leu Lys His Lys Lys
420 425 430

Asp Ala Leu Ala Leu Glu Lys Val Lys Asn Lys Val Asp Lys Ser Ile
435 440 445

Lys Thr Arg Ser Glu Ala Ile Ser Ser Ile Ser Ser Leu Thr Gly Ile
450 455 460

Leu Leu Phe Val Thr Ser Phe Leu Gly Ile Thr Phe Leu Ile Ala Val
465 470 475 480

Cys Cys Ile Ile Tyr Ile Lys Gln Ile Asp Glu Thr Glu Asp Glu Leu
485 490 495

Glu Asn Tyr Ser Ile Leu Arg Lys Leu Gly Phe Thr Gln Lys Asp Met
500 505 510

Ala Arg Gly Leu Lys Phe Lys Ile Met Phe Asn Phe Gly Leu Pro Leu
515 520 525

Val Ile Ala Leu Ser His Ala Tyr Phe Thr Ser Leu Ala Tyr Met Lys
530 535 540

Leu Met Gly Thr Thr Asn Gln Ile Pro Val Phe Ile Val Met Gly Leu
545 550 555 560

Tyr Ile Cys Met Tyr Ala Val Phe Ala Val Thr Ala Tyr Asn His Ser
565 570 575

Lys Arg Thr Ile Arg His Ser Ile
580

<210> 115
 <211> 629
 <212> PRT
 <213> Staphylococcus aureus

<400> 115

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

His Tyr Ala Ile Tyr Leu Phe Ser Leu Ile Thr Ser Val Val Leu Tyr
 20 25 30

Phe Ser Phe Val Ala Leu Lys Tyr Ala His Lys Leu Asn Met Thr Glu
 35 40 45

Ser Tyr Pro Ile Ile Lys Glu Gly Ser Gln Val Gly Ser Tyr Phe Leu
 50 55 60

Phe Phe Ile Ile Ile Ala Phe Leu Leu Tyr Ala Asn Val Leu Phe Ile
 65 70 75 80

Lys Arg Arg Ser Tyr Glu Leu Ala Leu Tyr Gln Thr Leu Gly Leu Ser
 85 90 95

Lys Phe Asn Ile Ile Tyr Ile Leu Met Leu Glu Gln Leu Leu Ile Phe
 100 105 110

Ile Ile Thr Ala Ile Leu Gly Ile Ile Ile Gly Ile Phe Gly Ser Lys
 115 120 125

Leu Leu Leu Met Ile Val Phe Thr Leu Leu Gly Ile Lys Glu Lys Val
 130 135 140

Pro Ile Ile Phe Ser Leu Arg Ala Val Phe Glu Thr Leu Met Leu Ile
 145 150 155 160

Gly Val Ala Tyr Phe Leu Thr Ser Ala Gln Asn Phe Ile Leu Val Phe
 165 170 175

Lys Gln Ser Ile Ser Gln Met Ser Lys Asn Asn Gln Val Lys Glu Thr
180 185 190

Asn His Asn Lys Ile Thr Phe Glu Glu Val Val Leu Gly Ile Leu Gly
195 200 205

Ile Val Leu Ile Thr Thr Gly Tyr Tyr Leu Ser Leu Asn Ile Val Gln
210 215 220

Tyr Tyr Asp Ser Ile Gly Ile Leu Met Phe Ile Leu Leu Ser Thr Val
225 230 235 240

Ile Gly Ala Tyr Leu Phe Phe Lys Ser Ser Val Ser Leu Val Phe Lys
245 250 255

Met Val Lys Lys Phe Arg Lys Gly Val Ile Ser Val Asn Asp Val Met
260 265 270

Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys Asn Ala Phe Ser Leu
275 280 285

Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val Ser Val Leu Cys Phe
290 295 300

Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu Ile Lys Tyr Thr Ala
305 310 315 320

Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys Ala Asn Gln Leu Ala
325 330 335

Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe Tyr Asn Tyr Lys Glu
340 345 350

Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu Phe Asp Val Lys Ala
355 360 365

Lys Glu Pro Tyr Asn Val Thr Ile Thr Ser Asp Lys Tyr Ile Pro Asn
370 375 380

Thr Asp Leu Lys Arg Gly Gln Ala Asp Leu Phe Val Ala Glu Gly Ser
385 390 395 400

Ile Lys Asp Leu Val Lys His Lys Lys His Gly Lys Ala Ile Ile Gly
405 410 415

Thr Lys Lys His His Val Asn Ile Lys Leu Arg Lys Asp Ile Asn Lys
420 425 430

Ile Tyr Phe Met Thr Asp Val Asp Leu Gly Gly Pro Thr Phe Val Leu
435 440 445

Asn Asp Lys Asp Tyr Gln Glu Ile Arg Lys Tyr Thr Lys Ala Lys His
450 455 460

Ile Val Ser Gln Phe Gly Phe Asp Leu Lys His Lys Lys Asp Ala Leu
465 470 475 480

Ala Leu Glu Lys Val Lys Asn Lys Val Asp Lys Ser Ile Lys Thr Arg
485 490 495

Ser Glu Ala Ile Ser Ser Ile Ser Ser Leu Thr Gly Ile Leu Leu Phe
500 505 510

Val Thr Ser Phe Leu Gly Ile Thr Phe Leu Ile Ala Val Cys Cys Ile
515 520 525

Ile Tyr Ile Lys Gln Ile Asp Glu Thr Glu Asp Glu Leu Glu Asn Tyr
530 535 540

Ser Ile Leu Arg Lys Leu Gly Phe Thr Gln Lys Asp Met Ala Arg Gly
545 550 555 560

Leu Lys Phe Lys Ile Met Phe Asn Phe Gly Leu Pro Leu Val Ile Ala
565 570 575

Leu Ser His Ala Tyr Phe Thr Ser Leu Ala Tyr Met Lys Leu Met Gly
580 585 590

Thr Thr Asn Gln Ile Pro Val Phe Ile Val Met Gly Leu Tyr Ile Cys
595 600 605

Met Tyr Ala Val Phe Ala Val Thr Ala Tyr Asn His Ser Lys Arg Thr
610 615 620

Ile Arg His Ser Ile
625

<210> 116
<211> 629
<212> PRT
<213> Staphylococcus aureus

<400> 116

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

His Tyr Ala Ile Tyr Leu Phe Ser Leu Ile Thr Ser Val Val Leu Tyr
20 25 30

Phe Ser Phe Val Ala Leu Lys Tyr Ala His Lys Leu Asn Met Thr Glu
35 40 45

Ser Tyr Pro Ile Ile Lys Glu Gly Ser Gln Val Gly Ser Tyr Phe Leu
50 55 60

Phe Phe Ile Ile Ile Ala Phe Leu Leu Tyr Ala Asn Val Leu Phe Ile
65 70 75 80

Lys Arg Arg Ser Tyr Glu Leu Ala Leu Tyr Gln Thr Leu Gly Leu Ser
85 90 95

Lys Phe Asn Ile Ile Tyr Ile Leu Met Leu Glu Gln Leu Leu Ile Phe
100 105 110

Ile Ile Thr Ala Ile Leu Gly Ile Ile Ile Gly Ile Phe Gly Ser Lys
115 120 125

Leu Leu Leu Met Ile Val Phe Thr Leu Leu Gly Ile Lys Glu Lys Val
 130 135 140

Pro Ile Ile Phe Ser Leu Arg Ala Val Phe Glu Thr Leu Met Leu Ile
 145 150 155 160

Gly Val Ala Tyr Phe Leu Thr Ser Ala Gln Asn Phe Ile Leu Val Phe
 165 170 175

Lys Gln Ser Ile Ser Gln Met Ser Lys Asn Asn Gln Val Lys Glu Thr
 180 185 190

Asn His Asn Lys Ile Thr Phe Glu Glu Val Val Leu Gly Ile Leu Gly
 195 200 205

Ile Val Leu Ile Thr Thr Gly Tyr Tyr Leu Ser Leu Asn Ile Val Gln
 210 215 220

Tyr Tyr Asp Ser Ile Gly Ile Leu Met Phe Ile Leu Leu Ser Thr Val
 225 230 235 240

Ile Gly Ala Tyr Leu Phe Phe Lys Ser Ser Val Ser Leu Val Phe Lys
 245 250 255

Met Val Lys Lys Phe Arg Lys Gly Val Ile Ser Val Asn Asp Val Met
 260 265 270

Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys Asn Ala Phe Ser Leu
 275 280 285

Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val Ser Val Leu Cys Phe
 290 295 300

Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu Ile Lys Tyr Thr Ala
 305 310 315 320

Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys Ala Asn Gln Leu Ala
 325 330 335

Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe Tyr Asn Tyr Lys Glu
340 345 350

Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu Phe Asp Val Lys Ala
355 360 365

Lys Glu Pro Tyr Asn Val Thr Ile Thr Ser Asp Lys Tyr Ile Pro Asn
370 375 380

Thr Asp Leu Lys Arg Gly Gln Ala Asp Leu Phe Val Ala Glu Gly Ser
385 390 395 400

Ile Lys Asp Leu Val Lys His Lys Lys His Gly Lys Ala Ile Ile Gly
405 410 415

Thr Lys Lys His His Val Asn Ile Lys Leu Arg Lys Asp Ile Asn Lys
420 425 430

Ile Tyr Phe Met Thr Asp Val Asp Leu Gly Gly Pro Thr Phe Val Leu
435 440 445

Asn Asp Lys Asp Tyr Gln Glu Ile Arg Lys Tyr Thr Lys Ala Lys His
450 455 460

Ile Val Ser Gln Phe Gly Phe Asp Leu Lys His Lys Lys Asp Ala Leu
465 470 475 480

Ala Leu Glu Lys Val Lys Asn Lys Val Asp Lys Ser Ile Lys Thr Arg
485 490 495

Ser Glu Ala Ile Ser Ser Ile Ser Ser Leu Thr Gly Ile Leu Leu Phe
500 505 510

Val Thr Ser Phe Leu Gly Ile Thr Phe Leu Ile Ala Val Cys Cys Ile
515 520 525

Ile Tyr Ile Lys Gln Ile Asp Glu Thr Glu Asp Glu Leu Glu Asn Tyr
530 535 540

Ser Ile Leu Arg Lys Leu Gly Phe Thr Gln Lys Asp Met Ala Arg Gly
545 550 555 560

Leu Lys Phe Lys Ile Met Phe Asn Phe Gly Leu Pro Leu Val Ile Ala
565 570 575

Leu Ser His Ala Tyr Phe Thr Ser Leu Ala Tyr Met Lys Leu Met Gly
580 585 590

Thr Thr Asn Gln Ile Pro Val Phe Ile Val Met Gly Leu Tyr Ile Cys
595 600 605

Met Tyr Ala Val Phe Ala Val Thr Ala Tyr Asn His Ser Lys Arg Thr
610 615 620

Ile Arg His Ser Ile
625

<210> 117
<211> 629
<212> PRT
<213> Staphylococcus aureus

<400> 117

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

His Tyr Ala Ile Tyr Leu Phe Ser Leu Ile Thr Ser Val Val Leu Tyr
20 25 30

Phe Ser Phe Val Ala Leu Lys Tyr Ala His Lys Leu Asn Met Thr Glu
35 40 45

Ser Tyr Pro Ile Ile Lys Glu Gly Ser Gln Val Gly Ser Tyr Phe Leu
50 55 60

Phe Phe Ile Ile Ile Ala Phe Leu Leu Tyr Ala Asn Val Leu Phe Ile
65 70 75 80

Lys Arg Arg Ser Tyr Glu Leu Ala Leu Tyr Gln Thr Leu Gly Leu Ser

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

500

505

510

Val Thr Ser Phe Leu Gly Ile Thr Phe Leu Ile Ala Val Cys Cys Ile
 515 520 525

Ile Tyr Ile Lys Gln Ile Asp Glu Thr Glu Asp Glu Leu Glu Asn Tyr
 530 535 540

Ser Ile Leu Arg Lys Leu Gly Phe Thr Gln Lys Asp Met Ala Arg Gly
 545 550 555 560

Leu Lys Phe Lys Ile Met Phe Asn Phe Gly Leu Pro Leu Val Ile Ala
 565 570 575

Leu Ser His Ala Tyr Phe Thr Ser Leu Ala Tyr Met Lys Leu Met Gly
 580 585 590

Thr Thr Asn Gln Ile Pro Val Phe Ile Val Met Gly Leu Tyr Ile Cys
 595 600 605

Met Tyr Ala Val Phe Ala Val Thr Ala Tyr Asn His Ser Lys Arg Thr
 610 615 620

Ile Arg His Ser Ile
 625

<210> 118
 <211> 629
 <212> PRT
 <213> Staphylococcus aureus

<400> 118

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

His Tyr Ala Ile Tyr Leu Phe Ser Leu Ile Thr Ser Val Val Leu Tyr
 20 25 30

Phe Ser Phe Val Ala Leu Lys Tyr Ala His Lys Leu Asn Met Thr Glu
 35 40 45

Ser Tyr Pro Ile Ile Lys Glu Gly Ser Gln Val Gly Ser Tyr Phe Leu
50 55 60

Phe Phe Ile Ile Ile Ala Phe Leu Leu Tyr Ala Asn Val Leu Phe Ile
65 70 75 80

Lys Arg Arg Ser Tyr Glu Leu Ala Leu Tyr Gln Thr Leu Gly Leu Ser
85 90 95

Lys Phe Asn Ile Ile Tyr Ile Leu Met Leu Glu Gln Leu Leu Ile Phe
100 105 110

Ile Ile Thr Ala Ile Leu Gly Ile Ile Ile Gly Ile Phe Gly Ser Lys
115 120 125

Leu Leu Leu Met Ile Val Phe Thr Leu Leu Gly Ile Lys Glu Lys Val
130 135 140

Pro Ile Ile Phe Ser Leu Arg Ala Val Phe Glu Thr Leu Met Leu Ile
145 150 155 160

Gly Val Ala Tyr Phe Leu Thr Ser Ala Gln Asn Phe Ile Leu Val Phe
165 170 175

Lys Gln Ser Ile Ser Gln Met Ser Lys Asn Asn Gln Val Lys Glu Thr
180 185 190

Asn His Asn Lys Ile Thr Phe Glu Glu Val Val Leu Gly Ile Leu Gly
195 200 205

Ile Val Leu Ile Thr Thr Gly Tyr Tyr Leu Ser Leu Asn Ile Val Gln
210 215 220

Tyr Tyr Asp Ser Ile Gly Ile Leu Met Phe Ile Leu Leu Ser Thr Val
225 230 235 240

Ile Gly Ala Tyr Leu Phe Phe Lys Ser Ser Val Ser Leu Val Phe Lys
245 250 255

Met Val Lys Lys Phe Arg Lys Gly Val Ile Ser Val Asn Asp Val Met
260 265 270

Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys Asn Ala Phe Ser Leu
275 280 285

Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val Ser Val Leu Cys Phe
290 295 300

Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu Ile Lys Tyr Thr Ala
305 310 315 320

Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys Ala Asn Gln Leu Ala
325 330 335

Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe Tyr Asn Tyr Lys Glu
340 345 350

Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu Phe Asp Val Lys Ala
355 360 365

Lys Glu Pro Tyr Asn Val Thr Ile Thr Ser Asp Lys Tyr Ile Pro Asn
370 375 380

Thr Asp Leu Lys Arg Gly Gln Ala Asp Leu Phe Val Ala Glu Gly Ser
385 390 395 400

Ile Lys Asp Leu Val Lys His Lys Lys His Gly Lys Ala Val Ile Gly
405 410 415

Thr Lys Lys His His Val Asn Ile Lys Leu Arg Lys Asp Ile Asn Lys
420 425 430

Ile Tyr Phe Met Thr Asp Val Asp Leu Gly Gly Pro Thr Phe Val Leu
435 440 445

Asn Asp Lys Asp Tyr Gln Glu Ile Arg Lys Tyr Thr Lys Ala Lys His
450 455 460

Ile Val Ser Gln Phe Gly Phe Asp Leu Lys His Lys Lys Asp Ala Leu
465 470 475 480

Ala Leu Glu Lys Val Lys Asn Lys Val Asp Lys Ser Ile Lys Thr Arg
485 490 495

Ser Glu Ala Ile Ser Ser Ile Ser Ser Leu Thr Gly Ile Leu Leu Phe
500 505 510

Val Thr Ser Phe Leu Gly Ile Thr Phe Leu Ile Ala Val Cys Cys Ile
515 520 525

Ile Tyr Ile Lys Gln Ile Asp Glu Thr Glu Asp Glu Leu Glu Asn Tyr
530 535 540

Ser Ile Leu Arg Lys Leu Gly Phe Thr Gln Lys Asp Met Ala Arg Gly
545 550 555 560

Leu Lys Phe Lys Ile Met Phe Asn Phe Gly Leu Pro Leu Val Ile Ala
565 570 575

Leu Ser His Ala Tyr Phe Thr Ser Leu Ala Tyr Met Lys Leu Met Gly
580 585 590

Thr Thr Asn Gln Ile Pro Val Phe Ile Val Met Gly Leu Tyr Ile Cys
595 600 605

Met Tyr Ala Val Phe Ala Val Thr Ala Tyr Asn His Ser Lys Arg Thr
610 615 620

Ile Arg His Ser Ile
625

<210> 119
<211> 629
<212> PRT
<213> Staphylococcus aureus

<400> 119

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

His Tyr Ala Ile Tyr Leu Phe Ser Leu Ile Thr Ser Val Val Leu Tyr
20 25 30

Phe Ser Phe Val Ala Leu Lys Tyr Ala His Lys Leu Asn Met Thr Glu
35 40 45

Ser Tyr Pro Ile Ile Lys Glu Gly Ser Gln Val Gly Ser Tyr Phe Leu
50 55 60

Phe Phe Ile Ile Ile Ala Phe Leu Leu Tyr Ala Asn Val Leu Phe Ile
65 70 75 80

Lys Arg Arg Ser Tyr Glu Leu Ala Leu Tyr Gln Thr Leu Gly Leu Ser
85 90 95

Lys Phe Asn Ile Ile Tyr Ile Leu Met Leu Glu Gln Leu Leu Ile Phe
100 105 110

Ile Ile Thr Ala Ile Leu Gly Ile Ile Ile Gly Ile Phe Gly Ser Lys
115 120 125

Leu Leu Leu Met Ile Val Phe Thr Leu Leu Gly Ile Lys Glu Lys Val
130 135 140

Pro Ile Ile Phe Ser Leu Arg Ala Val Phe Glu Thr Leu Met Leu Ile
145 150 155 160

Gly Val Ala Tyr Phe Leu Thr Ser Ala Gln Asn Phe Ile Leu Val Phe
165 170 175

Lys Gln Ser Ile Ser Gln Met Ser Lys Asn Asn Gln Val Lys Glu Thr
180 185 190

Asn His Asn Lys Ile Thr Phe Glu Glu Val Val Leu Gly Ile Leu Gly
195 200 205

Ile Val Leu Ile Thr Thr Gly Tyr Tyr Leu Ser Leu Asn Ile Val Gln
210 215 220

Tyr Tyr Asp Ser Ile Gly Thr Leu Met Phe Ile Leu Leu Ser Thr Val
225 230 235 240

Ile Gly Ala Tyr Leu Phe Phe Lys Ser Ser Val Ser Leu Val Phe Lys
245 250 255

Met Val Lys Lys Phe Arg Lys Gly Val Ile Ser Val Asn Asp Val Met
260 265 270

Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys Asn Ala Phe Ser Leu
275 280 285

Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val Ser Val Leu Cys Phe
290 295 300

Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu Ile Lys Tyr Thr Ala
305 310 315 320

Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys Ala Asn Gln Leu Ala
325 330 335

Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe Tyr Asn Tyr Lys Glu
340 345 350

Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu Phe Asp Val Lys Ser
355 360 365

Lys Gln Pro Tyr Asn Val Thr Ile Thr Ser Asp Lys Tyr Ile Pro Ser
370 375 380

Thr Asp Leu Lys Arg Gly Gln Ala Asp Leu Phe Val Ala Glu Gly Ser
385 390 395 400

Ile Lys Asp Leu Val Lys His Lys Lys His Gly Lys Ala Val Ile Gly
405 410 415

Thr Lys Lys His His Val Asn Ile Lys Leu Arg Lys Asp Ile Asn Lys
420 425 430

Ile Tyr Phe Met Thr Asp Val Asp Leu Gly Gly Pro Thr Phe Val Leu
435 440 445

Asn Asp Lys Asp Tyr Gln Glu Ile Arg Lys Tyr Thr Lys Ala Lys His
450 455 460

Ile Val Ser Gln Phe Gly Phe Asp Leu Lys His Lys Lys Asp Ala Leu
465 470 475 480

Ala Leu Glu Lys Ala Lys Asn Lys Val Asp Lys Ser Ile Glu Thr Arg
485 490 495

Ser Glu Ala Ile Ser Ser Ile Ser Ser Leu Thr Gly Ile Leu Leu Phe
500 505 510

Val Thr Ser Phe Leu Gly Ile Thr Phe Leu Ile Ala Val Cys Cys Ile
515 520 525

Ile Tyr Ile Lys Gln Ile Asp Glu Thr Glu Asp Glu Leu Glu Asn Tyr
530 535 540

Ser Ile Leu Arg Lys Leu Gly Phe Thr Gln Lys Asp Met Ala Arg Gly
545 550 555 560

Leu Lys Phe Lys Ile Met Phe Asn Phe Gly Leu Pro Leu Val Ile Ala
565 570 575

Leu Ser His Ala Tyr Phe Thr Ser Leu Ala Tyr Met Lys Leu Met Gly
580 585 590

Thr Thr Asn Gln Ile Pro Val Phe Ile Val Met Gly Leu Tyr Ile Cys
595 600 605

Met Tyr Ala Val Phe Ala Val Thr Ala Tyr Asn His Ser Lys Arg Thr
610 615 620

Ile Arg His Ser Ile
625

<210> 120
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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Met Thr Glu
35 40 45

Ser Tyr Pro Ile Ile Lys Glu Gly Ser Gln Val Gly Ser Tyr Phe Leu
50 55 60

Phe Phe Ile Ile Ile Ala Phe Leu Leu Tyr Ala Asn Val Leu Phe Ile
65 70 75 80

Lys Arg Arg Ser Tyr Glu Leu Ala Leu Tyr Gln Thr Leu Gly Leu Ser
85 90 95

Lys Phe Asn Ile Ile Tyr Ile Leu Met Leu Glu Gln Leu Leu Ile Phe
100 105 110

Ile Ile Thr Ala Ile Leu Gly Ile Ile Ile Gly Ile Phe Gly Ser Lys
115 120 125

Leu Leu Leu Met Ile Val Phe Thr Leu Leu Gly Ile Lys Glu Lys Val
130 135 140

Pro Ile Ile Phe Ser Leu Arg Ala Val Phe Glu Thr Leu Met Leu Ile
145 150 155 160

Gly Val Ala Tyr Phe Leu Thr Ser Ala Gln Asn Phe Ile Leu Val Phe
165 170 175

Lys Gln Ser Ile Ser Gln Met Ser Lys Asn Asn Gln Val Lys Glu Thr
180 185 190

Asn His Asn Lys Ile Thr Phe Glu Glu Val Val Leu Gly Ile Leu Gly
195 200 205

Ile Val Leu Ile Xaa Thr Gly Tyr Tyr Leu Ser Leu Asn Ile Val Gln
210 215 220

Tyr Tyr Asp Ser Ile Gly Xaa Leu Met Phe Ile Leu Leu Ser Thr Val
225 230 235 240

Ile Gly Ala Tyr Leu Phe Phe Lys Ser Ser Val Ser Leu Val Phe Lys
245 250 255

Met Val Lys Lys Phe Arg Lys Gly Val Ile Ser Val Asn Asp Val Met
260 265 270

Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys Asn Ala Phe Ser Leu
275 280 285

Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val Ser Val Leu Cys Phe
290 295 300

Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu Ile Lys Tyr Thr Ala
305 310 315 320

Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys Ala Asn Gln Leu Ala
325 330 335

Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe Tyr Asn Tyr Lys Glu
340 345 350

Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu Phe Asp Val Lys Xaa
355 360 365

Lys Xaa Pro Tyr Asn Val Thr Ile Thr Ser Asp Lys Tyr Ile Pro Xaa
370 375 380

Thr Asp Leu Lys Arg Gly Gln Ala Asp Leu Phe Val Ala Glu Gly Ser
385 390 395 400

Ile Lys Asp Leu Val Lys His Lys Lys His Gly Lys Ala Xaa Ile Gly
405 410 415

Thr Lys Lys His His Val Asn Ile Lys Leu Arg Lys Asp Ile Asn Lys
420 425 430

Ile Tyr Phe Met Thr Asp Val Asp Leu Gly Gly Pro Thr Phe Val Leu
435 440 445

Asn Asp Lys Asp Tyr Gln Glu Ile Arg Lys Tyr Thr Lys Ala Lys His
450 455 460

Ile Val Ser Gln Phe Gly Phe Asp Leu Lys His Lys Lys Asp Ala Leu
465 470 475 480

Ala Leu Glu Lys Ala Xaa Asn Lys Val Asp Lys Ser Ile Xaa Thr Arg
485 490 495

Ser Glu Ala Ile Ser Ser Ile Ser Ser Leu Thr Gly Ile Leu Leu Phe
500 505 510

Val Thr Ser Phe Leu Gly Ile Thr Phe Leu Ile Ala Val Cys Cys Ile
515 520 525

Ile Tyr Ile Lys Gln Ile Asp Glu Thr Glu Asp Glu Leu Glu Asn Tyr
530 535 540

Ser Ile Leu Arg Lys Leu Gly Phe Thr Gln Lys Asp Met Ala Arg Gly
545 550 555 560

Leu Lys Phe Lys Ile Met Phe Asn Phe Gly Leu Pro Leu Val Ile Xaa
565 570 575

Leu Ser His Ala Tyr Phe Thr Ser Leu Ala Tyr Met Lys Leu Met Gly
580 585 590

Thr Thr Asn Gln Ile Pro Val Phe Ile Val Met Gly Leu Tyr Ile Cys
595 600 605

Met Tyr Ala Val Phe Ala Val Thr Ala Tyr Asn His Ser Lys Arg Thr
610 615 620

Ile Arg His Ser Ile
625

<210> 121
<211> 55
<212> PRT
<213> Staphylococcus aureus

<400> 121

Met Leu Glu Ser Arg Glu Gln Leu Ser Val Glu Glu Tyr Glu Thr Phe
1 5 10 15

Phe Asn Arg Phe Asp Asn Gln Glu Phe Asp Phe Glu Arg Glu Leu Thr
20 25 30

Gln Asp Pro Tyr Ser Lys Val Tyr Leu Tyr Ser Ile Glu Asp His Ile
35 40 45

Arg Thr Tyr Lys Ile Glu Lys
50 55

<210> 122
<211> 55
<212> PRT
<213> Staphylococcus aureus

<400> 122

Met Leu Glu Ser Arg Glu Gln Leu Ser Val Glu Glu Tyr Glu Thr Phe
1 5 10 15

Phe Asn Arg Phe Asp Asn Gln Glu Phe Asp Phe Glu Arg Glu Leu Thr
20 25 30

Gln Asp Pro Tyr Ser Lys Val Tyr Leu Tyr Ser Ile Glu Asp His Ile
35 40 45

Arg Thr Tyr Lys Ile Glu Lys
50 55

<210> 123
<211> 88
<212> PRT
<213> Staphylococcus aureus

<400> 123

Cys Leu Phe Ser Tyr Gly Ser Gly Ala Val Gly Glu Ile Phe Ser Gly
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Ser Ile Val Lys Gly Tyr Asp Lys Ala Leu Asp Lys Glu Lys His Leu
20 25 30

Asn Met Leu Glu Ser Arg Glu Gln Leu Ser Val Glu Glu Tyr Glu Thr
35 40 45

Phe Phe Asn Arg Phe Asp Asn Gln Glu Phe Asp Phe Glu Arg Glu Leu
50 55 60

Thr Gln Asp Pro Tyr Ser Lys Val Tyr Leu Tyr Ser Ile Glu Asp His
65 70 75 80

Ile Arg Thr Tyr Lys Ile Glu Lys
85

<210> 124
<211> 88
<212> PRT
<213> Staphylococcus aureus

<400> 124

Cys Leu Phe Ser Tyr Gly Ser Gly Ala Val Gly Glu Ile Phe Ser Gly
1 5 10 15

Ser Ile Val Lys Gly Tyr Asp Lys Ala Leu Asp Lys Glu Lys His Leu
20 25 30

Asn Met Leu Glu Ser Arg Glu Gln Leu Ser Val Glu Glu Tyr Glu Thr
35 40 45

Phe Phe Asn Arg Phe Asp Asn Gln Glu Phe Asp Phe Glu Arg Glu Leu
50 55 60

Thr Gln Asp Pro Tyr Ser Lys Val Tyr Leu Tyr Ser Ile Glu Asp His
65 70 75 80

Ile Arg Thr Tyr Lys Ile Glu Lys
85

<210> 125

<211> 88

<212> PRT

<213> Staphylococcus aureus

<400> 125

Cys Leu Phe Ser Tyr Gly Ser Gly Ala Val Gly Glu Ile Phe Ser Gly
1 5 10 15

Ser Ile Val Lys Gly Tyr Asp Lys Ala Leu Asp Lys Glu Lys His Leu
20 25 30

Asn Met Leu Glu Ser Arg Glu Gln Leu Ser Val Glu Glu Tyr Glu Thr
35 40 45

Phe Phe Asn Arg Phe Asp Asn Gln Glu Phe Asp Phe Glu Arg Glu Leu
50 55 60

Thr Gln Asp Pro Tyr Ser Lys Val Tyr Leu Tyr Ser Ile Glu Asp His
65 70 75 80

Ile Arg Thr Tyr Lys Ile Glu Lys
85

<210> 126
 <211> 78
 <212> PRT
 <213> Staphylococcus aureus

<400> 126

Gly Glu Phe Tyr Ser Ala Thr Leu Val Glu Gly Tyr Lys Asp His Leu
 1 5 10 15

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

Val Asp Ala Tyr Glu Thr Phe Phe Lys Arg Phe Asp Asp Val Asp Phe
 35 40 45

Asp Glu Gln Gln Asp Ala Val His Glu Asp Arg Arg Ile Phe Tyr Leu
 50 55 60

Ser Asn Ile Glu Asn Asn Val Arg Glu Tyr His Arg Pro Glu
 65 70 75

<210> 127
 <211> 88
 <212> PRT
 <213> Staphylococcus aureus

<400> 127

Gly Leu Phe Ser Tyr Gly Ser Gly Ser Val Gly Glu Phe Tyr Ser Ala
 1 5 10 15

Thr Leu Val Glu Gly Tyr Lys Asp His Leu Asp Gln Ala Ala His Lys
 20 25 30

Ala Leu Leu Asn Asn Arg Thr Glu Val Ser Val Asp Ala Tyr Glu Thr
 35 40 45

Phe Phe Lys Arg Phe Asp Asp Val Asp Phe Asp Glu Gln Gln Asp Ala
 50 55 60

Val His Glu Asp Arg Arg Ile Phe Tyr Leu Ser Asn Ile Glu Asn Asn

65

70

75

80

Val Arg Glu Tyr His Arg Pro Glu
85

<210> 128

<211> 78

<212> PRT

<213> Staphylococcus aureus

<400> 128

Gly Glu Phe Tyr Ser Ala Thr Leu Val Glu Gly Tyr Lys Asp His Leu
1 5 10 15

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

Val Asp Ala Tyr Glu Thr Phe Phe Lys Arg Phe Asp Asp Val Asp Phe
35 40 45

Asp Glu Glu Gln Asp Ala Val His Glu Asp Arg His Ile Phe Tyr Leu
50 55 60

Ser Asn Ile Glu Asn Asn Val Arg Glu Tyr His Arg Pro Glu
65 70 75

<210> 129

<211> 88

<212> PRT

<213> Staphylococcus aureus

<400> 129

Gly Leu Phe Ser Tyr Gly Ser Gly Ser Val Gly Glu Phe Tyr Ser Ala
1 5 10 15

Thr Leu Val Glu Gly Tyr Lys Asp His Leu Asp Gln Ala Ala His Lys
20 25 30

Ala Leu Leu Asn Asn Arg Thr Glu Val Ser Val Asp Ala Tyr Glu Thr
35 40 45

Phe Phe Lys Arg Phe Asp Asp Val Glu Phe Asp Glu Glu Gln Asp Ala
 50 55 60

Val His Glu Asp Arg His Ile Phe Tyr Leu Ser Asn Ile Glu Asn Asn
 65 70 75 80

Val Arg Glu Tyr His Arg Pro Glu
 85

<210> 130
 <211> 88
 <212> PRT
 <213> Staphylococcus aureus

<400> 130

Gly Leu Phe Ser Tyr Gly Ser Gly Ser Val Gly Glu Phe Tyr Ser Ala
 1 5 10 15

Thr Leu Val Glu Gly Tyr Lys Asp His Leu Asp Gln Ala Ala His Lys
 20 25 30

Ala Leu Leu Asn Asn Arg Thr Glu Val Ser Val Asp Ala Tyr Glu Thr
 35 40 45

Phe Phe Lys Arg Phe Asp Asp Val Glu Phe Asp Glu Glu Gln Asp Ala
 50 55 60

Val His Glu Asp Arg His Ile Phe Tyr Leu Ser Asn Ile Glu Asn Asn
 65 70 75 80

Val Arg Glu Tyr His Arg Pro Glu
 85

<210> 131
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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

<400> 131

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Leu Xaa Xaa Arg Xaa Xaa Xaa Ser Val Xaa Xaa Tyr Glu Thr
35 40 45

Phe Phe Xaa Arg Phe Asp Xaa Xaa Xaa Phe Asp Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Leu Xaa Xaa Ile Glu Xaa Xaa
65 70 75 80

Xaa Arg Xaa Tyr Xaa Xaa Xaa Xaa
85

<210> 132
<211> 14
<212> PRT
<213> Staphylococcus aureus

<400> 132

Glu Ser Arg Glu Gln Leu Ser Val Glu Glu Tyr Glu Thr Phe
1 5 10

<210> 133
<211> 14
<212> PRT
<213> Staphylococcus aureus

<400> 133

Asn Asn Arg Thr Glu Val Ser Val Asp Ala Tyr Glu Thr Phe
1 5 10

<210> 134
<211> 14
<212> PRT
<213> Staphylococcus aureus

<400> 134

Asn Gln Glu Phe Asp Phe Glu Arg Glu Leu Thr Gln Asp Pro
1 5 10

<210> 135
<211> 14
<212> PRT
<213> Staphylococcus aureus

<400> 135

Asp Val Asp Phe Asp Glu Gln Gln Asp Ala Val His Glu Asp
1 5 10

<210> 136
<211> 14
<212> PRT
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<400> 136

Asp Val Asp Phe Asp Glu Glu Gln Asp Ala Val His Glu Asp
1 5 10

<210> 137
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<212> PRT
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<400> 137

Asp Val Glu Phe Asp Glu Glu Gln Asp Ala Val His Glu Asp
1 5 10

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 <223> Xaa can be any naturally occurring amino acid

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 <222> (9)..(10)
 <223> Xaa can be any naturally occurring amino acid

<400> 138

Xaa Xaa Arg Xaa Xaa Xaa Ser Val Xaa Xaa Tyr Glu Thr Phe
 1 5 10

<210> 139
 <211> 14
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 <222> (6)..(14)
 <223> Xaa can be any naturally occurring amino acid

<400> 139

Xaa Xaa Xaa Phe Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10

<210> 140
 <211> 720
 <212> DNA
 <213> Staphylococcus aureus

<400> 140
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 attatattca gaaccaatth ttccaatacc gccatacacc acacctatga cctcattgtt 120
 agaatttaga actggtgatc ctgaattccc gggttcaatg tatgcatcaa aatttaaaat 180
 attgtctttg attcttttta tagttcctgt agattcaaac tgtttaaaac tattttgagc 240
 aggtaatggg taaccaataa ctttaatttt gtcatcaact ttagcatctt tcgcaaaatt 300
 taatgcttgg acattttcat taaaattaaa gccttttggt ccacgttcaa ctgcttgttc 360
 ttcaatattc atgacagaga tgtcttcata acccggataa tcagaaatgc ttttaatttt 420
 atatatacca ccatttcctt tgtcacgctc tggatgggca gtaattctat cgccaacttt 480
 ataatctttt gatacatgtt tattggtgat aattgtattt tttccaatta caaaacctgt 540
 cgcactttta aatgaaacga cgccattata tggaaaaata tttgtatctt taacttgcgt 600
 aacattcttc tctgcatttg ctatttggtg tgtctcttca acgactgcag catttattcc 660
 agttactgag gttagaatgg ctaatgctgc catgctttta atgactatat ttttattcat 720

<210> 141
 <211> 720
 <212> DNA
 <213> Staphylococcus aureus

<400> 141
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 agaatttaga actggtgatc ctgaattccc gggttcaatg tatgcatcaa aatttaaaat 180
 attgtctttg attcttttta tagttcctgt agattcaaac tgtttaaaac tattttgagc 240
 aggtaatggg taaccaataa ctttaatttt gtcatcaact ttagcatctt tcgcaaaatt 300
 taatgcttgg acattttcat taaaattaaa gccttttggt ccacgttcaa ctgcttgttc 360
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 atatatacca ccatttcctt tgtcacgctc tggatgggca gtaattctat cgccaacttt 480
 ataatctttt gatacatgtt tattggtgat aattgtattt tttccaatta caaaacctgt 540
 cgcactttta aatgaaacga cgccattata tggaaaaata tttgtatctt taacttgcgt 600

aacattcttc tctgcatttg ctatttggtg tgtctcttca acgactgcag cattttattcc	660
agttgctgag gttagaatgg ctaatgctgc catgctttta atgactatat ttttattcat	720

<210> 142
 <211> 740
 <212> DNA
 <213> Staphylococcus aureus

<400> 142	
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agaatttaga actggtgatc ctgaattccc gggttcaatg tatgcatcaa aattttaa	180
attgtctttg attcttttta tagttcctgt agattcaaac tgttttaa	240
aggtaatggg taaccaataa ctttaatttt gtcataact ttagcatctt tcgcaaaatt	300
gaatgcttgg acattttcat taaaattaaa gccttttggg ccacgttcga ctgcttgctt	360
ttcaatattc atgacagaga tgtcttcata acccgataa tcagaaatgc ttttaatttt	420
atatatacca ccatttcctt tgtcaccgtt tggatgggca gtaattctat cgccaacttt	480
ataatctttt gatacatgtt tattggtgat aattgtattt tttccaatta caaacctgt	540
cgcatcttta aatgaaacga cgccattata tggaaaaata tttgtatctt taacttgcgt	600
aacattcttc tctgcatttg ctatttggtg tgtctcttca acgactgcag cattttattcc	660
agttactgag gttagaatgg ctaatgctgc catgctttta atgactatat ttttattcat	720
aaaagcacat tgaacaataa	740

<210> 143
 <211> 720
 <212> DNA
 <213> Staphylococcus aureus

<400> 143	
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attatattca gaaccaatth ttccaatacc gccatacacc acacctatga cctcattgtt	120
agaatttaga actggtgatc ctgaattccc gggttcaatg tatgcatcaa aattttaa	180
attgtctttg attcttttta tagttcctgt agattcaaac tgttttaa	240

aggtaatggg taaccaataa ctttaatttt gtcacaaact ttagcatctt tcgcaaaatt	300
gaatgcttgg acattttcat taaaattaaa gccttttggg ccacgttcga ctgcttggtc	360
ttcaatattc atgacagaga tgtcttcac acccggataa tcagaaatgc ttttaatttt	420
atatatacca ccatttcctt tgtcacggtt tggatgggca gtaattctat cgccaacttt	480
ataatctttt gatacatggt tattggtgat aattgtatit tttccaatta caaaacctgt	540
cgcatcttta aatgaaacga cgccattata tggaaaaata tttgtatctt taacttgcgt	600
aacattcttc tctgcatttg ctatttggtg tgtctcttca acgactgcag catttattcc	660
agttactgag gttagaatgg ctaatgctgc catgctttta atgactatat ttttattcat	720

<210> 144
 <211> 720
 <212> DNA
 <213> Staphylococcus aureus

<400> 144	
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agaattttaga actggtgatc ctgaattccc gggttcaatg tatgcatcaa aatttaaaat	180
attgtctttg attcttttta tagttcctgt agattcaaac tgttttaaac tattttgagc	240
aggtaatggg taaccaataa ctttaatttt gtcacaaact ttagcatctt tcgcaaaatt	300
taatgcttgg acattttcat taaaattaaa gccttttggg ccacgttcga ctgcttggtc	360
ttcaatattc atgacagaga tgtcttcac acccggataa tcagaaatgc ttttaatttt	420
atatatacca ccatttcctt tgtcacggtt tggatgggca gtaattctat cgccaacttt	480
ataatctttt gatacatggt tattggtgat aattgtatit tttccaatta caaaacctgt	540
cgcatcttta aatgaaacga cgccattata tggaaaaata tttgtatctt taacttgcgt	600
aacattcttc tctgcatttg ctatttggtg tgtctcttca acgactgcag catttattcc	660
agttactgag gttagaatgg ctaatgctgc catgctttta atgactatat ttttattcat	720

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 <212> DNA
 <213> Staphylococcus aureus

<400> 145
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 attatattca gaaccaatth ttccaatacc gccatacacc acacctatga cctcattgtt 120
 agaatttaga actggatgat ctgaattccc gggttcaatg tatgcatcaa aatttaaaat 180
 attgtctttg attcttttta tagttcctgt agattcaaac tgtttaaaac tattttgagc 240
 aggtaatggg taaccaataa ctttaatttt gtcatcaact ttagcatctt tcgcaaaatt 300
 gaatgcttgg acattttcat taaaattaaa gccttttggg ccacgttcga ctgcttggtc 360
 ttcaatattc atgacagaga tgtcttcac acccgataa tcagaaatgc ttttaatttt 420
 atatatacca ccatttcctt tgtcacctgt tggatgggca gtaattctat cgccaacttt 480
 ataatctttt gatacatgtt tattggatgat aattgtattt tttccaatta caaacctgt 540
 cgcattctta aatgaaacga cgccattata tggaaaaata tttgtatctt taacttgcgt 600
 aacattcttc tctgattttg ctattttgtt tgtctcttca acgactgcag cttttattcc 660
 agttactgag gttagaatgg ctaatgctgc catgctttta atgactatat ttttattcat 720

<210> 146
 <211> 720
 <212> DNA
 <213> Staphylococcus aureus

<400> 146
 ttattgttca atgtgctttt gaataaaatc tttgatttga ggcgtaaagt atacggcacc 60
 attatattca gaaccaatth ttccaatacc gccatacacc acacctatga cctcattgtt 120
 agaatttaga actggatgat ctgaattccc gggttcaatg tatgcatcaa aatttaaaat 180
 attgtctttg attcttttta tagttcctgt agattcaaac tgtttaaaac tattttgagc 240
 aggtaatggg taaccaataa ctttaatttt gtcatcaact ttagcatctt tcgcaaaatt 300
 gaatgcttgg acattttcat taaaattaaa gccttttggg ccacgttcaa ctgcttggtc 360
 ttcaatattc atgacagaga tgtcttcac acccgataa tcagaaatgc ttttaatttt 420
 atatatacca ccatttcctt tgtcacctgt tggatgggca gtaattctat cgccaacttt 480
 ataatctttt gatacatgtt tattggatgat aattgtattt tttccaatta caaacctgt 540
 cgcattctta aatgaaacga cgccattata tggaaaaata tttgtatctt taacttgcgt 600

aacattcttc tctgcatttg ctatttggtg tgtctcttca acgactgcag catttattcc	660
agttactgag gttagaatgg ctaatgctgc catgctttta atgactatat ttttattcat	720

<210> 147
 <211> 720
 <212> DNA
 <213> Staphylococcus aureus

<400> 147	
ttattgttca atgtgctttt gaataaaatc tttgatttga ggcgtaaagt atacggcacc	60
attatattca gaaccaatth ttccaatacc gccatacacc acacctatga cctcattgtt	120
agaatttaga actggatgatc ctgaattccc gggttcaatg tatgcatcaa aatttaaaat	180
attgtctttg attcttttta tagttcctgt agattcaaac tgtttaaaac tattttgagc	240
aggtaatggg taaccaataa ctttaatttt gtcatcaact ttagcatctt tcgcaaaatt	300
gaatgcttgg acattttcat taaaattaaa gccttttggg ccacgttcaa ctgcttggtc	360
ttcaatattc atgacagaga tgtcttcac acccgataa tcagaaatgc ttttaatttt	420
atatatacca ccatttcctt tgtcaccgtt tggatgggca gtaattctat cgccaacttt	480
ataatctttt gatacatgtt tattgggtgat aattgtattt tttccaatta caaaacctgt	540
cgcacctta aatgaaacga cgccattata tggaaaatta tttgtatctt taacttgcgt	600
aacattcttc tctgcatttg ctatttggtg tgtctcttca acgactgcag catttattcc	660
agttactgag gttagaatgg ctaatgctgc catgctttta atgactatat ttttattcat	720

<210> 148
 <211> 720
 <212> DNA
 <213> Staphylococcus aureus

<400> 148	
ttattgttca atgtgctttt gaataaaatc tttgatttga ggcgtaaagt atacggcacc	60
attatattca gaaccaatth ttccaatacc gccatacacc acacctatga cctcattgtt	120
agaatttaga actggatgatc ctgaattccc gggttcaatg tatgcatcaa aatttaaaat	180
attgtctttg attcttttta tagttcctgt agattcaaac tgtttaaaac tattttgagc	240
aggtaatggg taaccaataa ctttaatttt gtcatcaact ttagcatctt tcgcaaaatt	300

gaatgcttgg acattttcat taaaattaaa gccttttggg ccacgttcaa ctgcttggtc	360
ttcaatattc atgacagaga tgtcttcac acccgataa tcagaaatgc ttttaatttt	420
atatatacca ccatttcctt tgtcaccgtt tggatgggca gtaattctat cgccaacttt	480
ataatctttt gatacatggt tattggtgat aattgtattt tttccaatta caaaacctgt	540
cgcacctta aatgaaacga cgccattata tggaaaatta tttgtatctt taacttgcgt	600
aacattcttc tctgcatttg ctatttggtg tgtctcttca acgactgcag catttattcc	660
agttactgag gttagaatgg ctaatgctgc catgctttta atgactatat ttttattcat	720

<210> 149
 <211> 720
 <212> DNA
 <213> *Staphylococcus aureus*

<400> 149	
ttattgttca atgtgctttt gaataaaatc tttgatttga ggcgtaaagt atacggcacc	60
attatattca gaaccaattt ttccaatacc gccatacacc acacctatga cctcattggt	120
agaatttaga actggtgatc ctgaattccc gggttcaatg tatgcatcaa aatttaaaat	180
attgtctttg attcttttta tagttcctgt agattcaaac tgtttaaaac tttttgagc	240
aggtaatggg taaccaataa ctttaatttt gtcacaaact ttagcatctt tcgcaaaatt	300
gaatgcttgg acattttcat taaaattaaa gccttttggg ccacgttcaa ctgcttggtc	360
ttcaatattc atgacagaga tgtcttcac acccgataa tcagaaatgc ttttaatttt	420
atatatacca ccatttcctt tgtcaccgtt tggatgggca gtaattctat cgccaacttt	480
ataatctttt gatacatggt tattggtgat aattgtattt tttccaatta caaaacctgt	540
cgcacctta aatgaaacga cgccattata tggaaaatta tttgtatctt taacttgcgt	600
aacattcttc tctgcatttg ctatttggtg tgtctcttca acgactgcag catttattcc	660
agttactgag gttagaatgg ctaatgctgc catgctttta atgactatat ttttattcat	720

<210> 150
 <211> 720
 <212> DNA
 <213> *Staphylococcus aureus*

<400> 150

ttattgttca atgtgctttt gaataaaatc tttgatttga ggcgtaaagt atacggcacc	60
attatattca gaaccaatth ttccaatacc gccatacacc acacctatga cctcattgtt	120
agaattttaga actggtgatc ctgaattccc gggttcaatg tatgcatcaa aattttaa	180
attgtctttg attcttttta tagttcctgt agattcaaac tgtttaaaac tattttgagc	240
aggtaatggg taaccaataa ctttaatttt gtcacaaact ttagcatctt tcgcaaaatt	300
gaatgcttgg acattttcat taaaattaaa gccttttggg ccacgttcaa ctgcttggtc	360
ttcaatattc atgacagaga tgtcttcac acccggataa tcagaaatgc ttttaatttt	420
atatatacca cattttcctt tgtcaccgtt tggatgggca gtaattctat cgccaacttt	480
ataatctttt gatacatgtt tattggtgat aattgtattt tttccaatta caaaacctgt	540
cgcaccttta aatgaaacga cgccattata tggaaaatta tttgtatctt taacttgcgt	600
aacattcttc tctgcatttg ctatttggtg tgtctcttca acgactgcag cattttattcc	660
agttactgag gttagaatgg ctaatgctgc catgctttta atgactatat ttttattcat	720

<210> 151

<211> 720

<212> DNA

<213> Staphylococcus aureus

<400> 151

ttattgttca atgtgctttt gaataaattc tttgatttga ggcgtaaaat aaactgcacc	60
attgtattct gatccgattt ttccaatacc tccatacaca actcctacga cttcattatt	120
taaattttaa actgggggatc ctgaatttcc aggctcgata tatgcatcaa aattttaa	180
attatcttta atacttttta cagttccagt tgattcaaat tgtttgaatg tattttgagc	240
tggtaaaggg tatccaataa ctttaatttt gtcgtcaact ttagcatctt tcgcaaaatt	300
gaatgcttgg acattttcat taaaattata accatttgct ccacgttcaa cagcattttc	360
ttcaacgttc attactgata taccctcatt acctggataa tcagaaatat ttttaatttt	420
ataaattcca ccgttgcctt tgtcaccatt tgggtgggca gtaattctat cgccaacttt	480
atagtccttt gatacatgtt tattggtgat aattgtattt ttttcaattg caaaacctgt	540
cgcaccttta aatgaaacga cgccattata tggaaaaaca tttgtatctt taacttgcgt	600

aacattcttc tctgcatttg ctatttggtg tgtctcatca acgactgcag catttattcc 660

agttactgag gttagaatgg ctaatgctgc catgctttta atgactatat ttttattcat 720

<210> 152

<211> 239

<212> PRT

<213> Staphylococcus aureus

<400> 152

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 Asp 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 Leu 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> 153
<211> 239
<212> PRT
<213> Staphylococcus aureus

<400> 153

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

Thr Ser Ala 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 Asp 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 Leu 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
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> 154		
<211> 239		
<212> PRT		
<213> Staphylococcus aureus		
<400> 154		
Met Asn Lys Asn Ile Val Ile Lys Ser Met Ala Ala Leu Ala Ile Leu		
1	5	10
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> 155

<211> 239

<212> PRT

<213> Staphylococcus aureus

<400> 155

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> 156
<211> 239
<212> PRT
<213> Staphylococcus aureus

<400> 156

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> 157

<211> 239

<212> PRT

<213> Staphylococcus aureus

<400> 157

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
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> 158						
<211> 239						
<212> PRT						
<213> Staphylococcus aureus						
<400> 158						
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 Asn
 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> 159
 <211> 239
 <212> PRT
 <213> Staphylococcus aureus

<400> 159

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 Asn
 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> 160
<211> 239
<212> PRT
<213> Staphylococcus aureus

<400> 160

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 Asn
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> 161
 <211> 239
 <212> PRT
 <213> Staphylococcus aureus

<400> 161

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 Asn

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> 162

<211> 239
 <212> PRT
 <213> Staphylococcus aureus

<400> 162

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 Asn
 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> 163
<211> 239
<212> PRT
<213> Staphylococcus aureus

<400> 163

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 Asp Glu Thr Gln Gln
20 25 30

Ile Ala Asn Ala Glu Lys Asn Val Thr Gln Val Lys Asp Thr Asn Val
35 40 45

Phe Pro Tyr Asn Gly Val Val Ser Phe Lys Asp Ala Thr Gly Phe Ala
50 55 60

Ile Glu 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 Asn Ile Ser Asp Tyr Pro Gly Asn Glu
100 105 110

Asp Ile Ser Val Met Asn Val Glu Glu Asn Ala Val Glu Arg Gly Ala
115 120 125

Asn Gly Tyr 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 Thr Phe Lys Gln Phe Glu Ser Thr Gly Thr Val Lys Ser
 165 170 175

Ile Lys Asp Asn Asn Leu Asn Phe Asp Ala Tyr Ile Glu Pro Gly Asn
 180 185 190

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

<210> 164
 <211> 239
 <212> PRT
 <213> Artificial sequence

<220>
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<220>
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 <223> Xaa can be any naturally occurring amino acid

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<220>
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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<220>
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 <223> Xaa can be any naturally occurring amino acid

<220>
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 <223> Xaa can be any naturally occurring amino acid

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 <223> Xaa can be any naturally occurring amino acid

<220>
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 <222> (231)..(231)
 <223> Xaa can be any naturally occurring amino acid

<400> 164

Met	Asn	Lys	Asn	Ile	Val	Ile	Lys	Ser	Met	Ala	Ala	Leu	Ala	Ile	Leu
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Thr	Ser	Xaa	Thr	Gly	Ile	Asn	Ala	Ala	Val	Val	Xaa	Glu	Thr	Gln	Gln
			20				25						30		

Ile	Ala	Asn	Ala	Glu	Lys	Asn	Val	Thr	Gln	Val	Lys	Asp	Thr	Asn	Xaa
	35						40					45			

Phe	Pro	Tyr	Asn	Gly	Val	Val	Ser	Phe	Lys	Asp	Ala	Thr	Gly	Phe	Xaa
	50					55					60				

Ile Xaa 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 Xaa Gly Asp Lys Gly Asn
85 90 95

Gly Gly Ile Tyr Lys Ile Lys Xaa Ile Ser Asp Tyr Pro Gly Xaa Glu
100 105 110

Asp Ile Ser Val Met Asn Xaa Glu Glu Xaa Ala Val Glu Arg Gly Xaa
115 120 125

Xaa Gly Xaa Asn Phe Asn Glu Asn Val Gln Ala Xaa 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 Xaa Phe Lys Gln Phe Glu Ser Thr Gly Thr Xaa Lys Xaa
165 170 175

Ile Lys Asp Asn Xaa Leu Asn Phe Asp Ala Tyr Ile Glu Pro Gly Asn
180 185 190

Ser Gly Ser Pro Val Leu Asn Xaa Asn Asn Glu Val Xaa 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 Xaa Phe Ile Gln Lys His Ile Glu Gln
225 230 235

<210> 165

<211> 14

<212> PRT

<213> Staphylococcus aureus

<400> 165

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

1 5 10

<210> 166
<211> 14
<212> PRT
<213> Staphylococcus aureus

<400> 166

Ala His Pro Asp Gly Asp Lys Gly Asn Gly Gly Ile Tyr Lys
1 5 10

<210> 167
<211> 14
<212> PRT
<213> Staphylococcus aureus

<400> 167

Ala His Pro Asn Gly Asp Lys Gly Asn Gly Gly Ile Tyr Lys
1 5 10

<210> 168
<211> 14
<212> PRT
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<220>
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<223> Xaa can be any naturally occurring amino acid

<400> 168

Ala His Pro Xaa Gly Asp Lys Gly Asn Gly Gly Ile Tyr Lys
1 5 10

<210> 169
<211> 14
<212> PRT
<213> Staphylococcus aureus

<400> 169

Ser Ile Ser Asp Tyr Pro Gly Asp Glu Asp Ile Ser Val Met
1 5 10

<210> 170
<211> 14
<212> PRT
<213> Staphylococcus aureus

<400> 170

Asn Ile Ser Asp Tyr Pro Gly Asn Glu Asp Ile Ser Val Met
1 5 10

<210> 171
<211> 14
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<220>
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<222> (8)..(8)
<223> Xaa can be any naturally occurring amino acid

<400> 171

Xaa Ile Ser Asp Tyr Pro Gly Xaa Glu Asp Ile Ser Val Met
1 5 10

<210> 172
<211> 14
<212> PRT
<213> Staphylococcus aureus

<400> 172

Arg Gly Pro Lys Gly Phe Asn Phe Asn Glu Asn Val Gln Ala
1 5 10

<210> 173

<211> 14
<212> PRT
<213> Staphylococcus aureus

<400> 173

Arg Gly Ala Asn Gly Tyr Asn Phe Asn Glu Asn Val Gln Ala
1 5 10

<210> 174
<211> 14
<212> PRT
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<223> Xaa can be any naturally occurring amino acid

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<221> misc_feature
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<223> Xaa can be any naturally occurring amino acid

<400> 174

Arg Gly Xaa Xaa Gly Xaa Asn Phe Asn Glu Asn Val Gln Ala
1 5 10

<210> 175
<211> 14
<212> PRT
<213> Staphylococcus aureus

<400> 175

Gln Phe Glu Ser Thr Gly Thr Ile Lys Arg Ile Lys Asp Asn
1 5 10

<210> 176
<211> 14
<212> PRT
<213> Staphylococcus aureus

<400> 176

Gln Phe Glu Ser Thr Gly Thr Val Lys Ser Ile Lys Asp Asn
 1 5 10

<210> 177
 <211> 14
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<220>
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<220>
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 <222> (8)..(8)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (10)..(10)
 <223> Xaa can be any naturally occurring amino acid

<400> 177

Gln Phe Glu Ser Thr Gly Thr Xaa Lys Xaa Ile Lys Asp Asn
 1 5 10

<210> 178
 <211> 14
 <212> PRT
 <213> Staphylococcus aureus

<400> 178

Gly Asn Ser Gly Ser Pro Val Leu Asn Ser Asn Asn Glu Val
 1 5 10

<210> 179
 <211> 14
 <212> PRT
 <213> Staphylococcus aureus

<400> 179

Gly Asn Ser Gly Ser Pro Val Leu Asn Leu Asn Asn Glu Val
 1 5 10

<210> 180
 <211> 14
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic sequence

<220>
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 <222> (10)..(10)
 <223> Xaa can be any naturally occurring amino acid

<400> 180

Gly Asn Ser Gly Ser Pro Val Leu Asn Xaa Asn Asn Glu Val
 1 5 10

<210> 181
 <211> 975
 <212> DNA
 <213> Staphylococcus aureus

<400> 181
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 gagaatcatg taagaaaaga agatttaata tatccaattt ttgtagttga aaaagacgat 120
 gtgaaaaaag aaattaagtc attgccaggt gtataccaaa tcagtttgaa tttacttgaa 180
 agtgaattaa aagaagctta tgacttaggc atacgtgccca ttatgttttt cgggtgttcca 240
 aactcaaaag atgatatagg tactgggtgca tacattcacg atgggtgttat tcaacaggca 300
 acacgtattg ctaaaaaaat gtatgatgac ttattaattg ttgcagacac ttgtttatgt 360
 gaatatactg atcatggtca ttgtggcgtg attgatgacc atacacatga cgttgacaat 420
 gataaatcat tgccactact tgttaaaaca gcaatttctc aagtggaagc tgggtgctgat 480
 attattgcgc caagtaatat gatggatggt tttgttgctg aaattcgtcg tggattagat 540
 gaagccggct attacaatat tcctataatg agttatgggtg tcaagtatgc atcaagtttc 600
 tttggacctt ttagagatgc agcagattca gcgccatcat ttggggatag aaaaacgtat 660
 cagatggacc ctgctaaccg tttggaagca cttcgtgaat tagaaagtga tcttaaagaa 720
 ggggtcgcaca tgatgattgt taaacctgct ctaagttatt tagatatagt tcgagatgtt 780

aaaaatcata cgaatgttcc agttgttgca tataatgtga gtggagaata tagtatgact 840
 aaagcagcgg cacaaaatgg ttggatagat gaagaacgtg tcgttatgga acaaatgggtt 900
 tcaatgaaac gtgcaggtgc tgatatgatt attacgtatt ttgcaaagga catttgtcgc 960
 tatttagata aataa 975

<210> 182
 <211> 324
 <212> PRT
 <213> Staphylococcus aureus

<400> 182

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

Asp Met Val Arg Glu Asn His Val Arg Lys Glu Asp Leu Ile Tyr Pro
 20 25 30

Ile Phe Val Val Glu Lys Asp Asp Val Lys Lys Glu Ile Lys Ser Leu
 35 40 45

Pro Gly Val Tyr Gln Ile Ser Leu Asn Leu Leu Glu Ser Glu Leu Lys
 50 55 60

Glu Ala Tyr Asp Leu Gly Ile Arg Ala Ile Met Phe Phe Gly Val Pro
 65 70 75 80

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

Ile Gln Gln Ala Thr Arg Ile Ala Lys Lys Met Tyr Asp Asp Leu Leu
 100 105 110

Ile Val Ala Asp Thr Cys Leu Cys Glu Tyr Thr Asp His Gly His Cys
 115 120 125

Gly Val Ile Asp Asp His Thr His Asp Val Asp Asn Asp Lys Ser Leu
 130 135 140

Pro Leu Leu Val Lys Thr Ala Ile Ser Gln Val Glu Ala Gly Ala Asp
 145 150 155 160

Ile Ile Ala Pro Ser Asn Met Met Asp Gly Phe Val Ala Glu Ile Arg
 165 170 175

Arg Gly Leu Asp Glu Ala Gly Tyr Tyr Asn Ile Pro Ile Met Ser Tyr
 180 185 190

Gly Val Lys Tyr Ala Ser Ser Phe Phe Gly Pro Phe Arg Asp Ala Ala
 195 200 205

Asp Ser Ala Pro Ser Phe Gly Asp Arg Lys Thr Tyr Gln Met Asp Pro
 210 215 220

Ala Asn Arg Leu Glu Ala Leu Arg Glu Leu Glu Ser Asp Leu Lys Glu
 225 230 235 240

Gly Cys Asp Met Met Ile Val Lys Pro Ala Leu Ser Tyr Leu Asp Ile
 245 250 255

Val Arg Asp Val Lys Asn His Thr Asn Val Pro Val Val Ala Tyr Asn
 260 265 270

Val Ser Gly Glu Tyr Ser Met Thr Lys Ala Ala Ala Gln Asn Gly Trp
 275 280 285

Ile Asp Glu Glu Arg Val Val Met Glu Gln Met Val Ser Met Lys Arg
 290 295 300

Ala Gly Ala Asp Met Ile Ile Thr Tyr Phe Ala Lys Asp Ile Cys Arg
 305 310 315 320

Tyr Leu Asp Lys

<210> 183
 <211> 2802
 <212> DNA
 <213> Staphylococcus aureus

<400> 183

atgaatatga agaaaaaaga aaaacacgca attcggaaaa aatcgattgg cgtggcttca	60
gtgctttag gtacgttaat cggtttttga ctactcagca gtaaagaagc agatgcaagt	120
gaaaaatagtg ttacgcaatc tgatagcgca agtaacgaaa gcaaaagtaa tgattcaagt	180
agcgtttagtg ctgcacctaa aacagacgac acaaactgta gtgatactaa aacatcgtca	240
aacactaata atggcgaaac gagtgtggcg caaaatccag cacaacagga aacgacacaa	300
tcatcatcaa caaatgcaac tacggaagaa acgccggtta ctggtgaagc tactactacg	360
acaacgaatc aagctaatac accggcaaca actcaatcaa gcaatacaaa tgcggaggaa	420
ttagtgaatc aaacaagtaa tgaaacgact tttaatgata ctaatacagt atcatctgta	480
aattcacctc aaaattctac aaatgcggaa aatgtttcaa caacgcaaga tacttcaact	540
gaagcaacac cttcaaaca tgaatcagct ccacagagta cagatgcaag taataaagat	600
gtagttaatc aagcggttaa tacaagtgcg cctagaatga gagcatttag tttagcggca	660
gtagctgcag atgcaccggc agctggcaca gatattacga atcagttgac gaatgtgaca	720
gttggtattg actctggtac gactgtgtat ccgcaccaag caggttatgt caaactgaat	780
tatgggtttt cagtgcctaa ttctgctgtt aaagggtgaca cattcaaaat aactgtacct	840
aaagaattaa acttaaatgg tgtaacttca actgctaaag tgccaccaat tatggctgga	900
gatcaagtat tggcaaatgg tgtaatcgat agtgatggta atgttattta tacatttaca	960
gactatgtaa atactaaaga tgatgtaaaa gcaactttga ccatgcccgc ttatattgac	1020
cctgaaaatg ttaaaaagac aggtaatgtg acattggcta ctggcatagg tagtacaaca	1080
gcaaacaaaa cagtattagt agattatgaa aaatatggta agttttataa cttatctatt	1140
aaagggtaca ttgaccaa atcgataaaaca aataatacgt atcgtcagac aatttatgtc	1200
aatccaagtg gagataacgt tattgcgccg gttttaacag gtaatttaaa accaaatacg	1260
gatagtaatg cattaataga tcagcaaaat acaagtatta aagtatataa agtagataat	1320
gcagctgatt tatctgaaag ttactttgtg aatccagaaa actttgagga tgtcactaat	1380
agtggaata ttacattccc aaatccaaat caatataaag tagagtttaa tacgcctgat	1440
gatcaaatta caacaccgta tatagtagtt gttaatggtc atattgatcc gaatagcaaa	1500

ggtgatttag ctttacgttc aactttatat ggggtataact cgaatataat ttggcgctct	1560
atgtcatggg acaacgaagt agcatttaat aacggatcag gttctgggtga cggtatcgat	1620
aaaccagttg ttcctgaaca acctgatgag cctgggtgaaa ttgaaccaat tccagaggat	1680
tcagattctg acccagggttc agattctggc agcgattcta attcagatag cggttcagat	1740
tcgggtagtg attctacatc agatagtggg tcagattcag cgagtgattc agattcagca	1800
agtgattcag actcagcgag tgattcagat tcagcaagcg attccgactc agcgagcgat	1860
tccgactcag acaatgactc ggattcagat agcgattctg actcagacag tgactcagat	1920
tccgacagtg actcagattc agatagcgat tctgactcag acagtgactc agattcagat	1980
agcgattcag attcagatag cgattcagat tccgacagtg attccgactc agacagcgat	2040
tctgactccg acagtgattc cgactcagac agcgattcag attccgacag tgattccgac	2100
tcagatagcg attccgactc agatagcgac tcagattcag acagcgattc agattcagac	2160
agcgattcag attcagatag cgattcagat tccgacagtg actcagattc cgacagtgac	2220
tcggattcag atagcgattc agattccgac agtgactcag attccgacag tgactcagac	2280
tcagacagtg attcggattc agcgagtgat tcggattcag atagtgattc cgactccgac	2340
agtgactcgg attcagatag cgactcagac tcggatagcg actcggattc agatagcgat	2400
tcggactcag atagcgattc agaatcagac agcgattcag aatcagacag cgattcagat	2460
tcagacagcg actcagacag tgactcagat tcagatagtg actcggattc agcgagtgat	2520
tcagactcag gtagtgactc cgattcatca agtgattccg actcagaaag tgattcaa	2580
agcgattccg agtcagggttc taacaataat gtagttccgc ctaattcacc taaaaatgg	2640
actaatgctt ctaataaaaa tgaggctaaa gatagttaaag aaccattacc agatacagg	2700
tctgaagatg aagcaaatac gtcactaatt tggggattat tagcatcaat aggttcatta	2760
ctacttttca gaagaaaaaa agaaaataaa gataagaaat aa	2802

<210> 184
 <211> 933
 <212> PRT
 <213> Staphylococcus aureus

 <400> 184

Met Asn Met Lys Lys Lys Glu Lys His Ala Ile Arg Lys Lys Ser Ile
 1 5 10 15

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

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

Ser Ala Ser Asn Glu Ser Lys Ser Asn Asp Ser Ser Ser Val Ser Ala
 50 55 60

Ala Pro Lys Thr Asp Asp Thr Asn Val Ser Asp Thr Lys Thr Ser Ser
 65 70 75 80

Asn Thr Asn Asn Gly Glu Thr Ser Val Ala Gln Asn Pro Ala Gln Gln
 85 90 95

Glu Thr Thr Gln Ser Ser Ser Thr Asn Ala Thr Thr Glu Glu Thr Pro
 100 105 110

Val Thr Gly Glu Ala Thr Thr Thr Thr Thr Asn Gln Ala Asn Thr Pro
 115 120 125

Ala Thr Thr Gln Ser Ser Asn Thr Asn Ala Glu Glu Leu Val Asn Gln
 130 135 140

Thr Ser Asn Glu Thr Thr Phe Asn Asp Thr Asn Thr Val Ser Ser Val
 145 150 155 160

Asn Ser Pro Gln Asn Ser Thr Asn Ala Glu Asn Val Ser Thr Thr Gln
 165 170 175

Asp Thr Ser Thr Glu Ala Thr Pro Ser Asn Asn Glu Ser Ala Pro Gln
 180 185 190

Ser Thr Asp Ala Ser Asn Lys Asp Val Val Asn Gln Ala Val Asn Thr
 195 200 205

Ser Ala Pro Arg Met Arg Ala Phe Ser Leu Ala Ala Val Ala Ala Asp
 210 215 220

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

Val Gly Ile Asp Ser Gly Thr Thr Val Tyr Pro His Gln Ala Gly Tyr
 245 250 255

Val Lys Leu Asn Tyr Gly Phe Ser Val Pro Asn Ser Ala Val Lys Gly
 260 265 270

Asp Thr Phe Lys Ile Thr Val Pro Lys Glu Leu Asn Leu Asn Gly Val
 275 280 285

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

Ala Asn Gly Val Ile Asp Ser Asp Gly Asn Val Ile Tyr Thr Phe Thr
 305 310 315 320

Asp Tyr Val Asn Thr Lys Asp Asp Val Lys Ala Thr Leu Thr Met Pro
 325 330 335

Ala Tyr Ile Asp Pro Glu Asn Val Lys Lys Thr Gly Asn Val Thr Leu
 340 345 350

Ala Thr Gly Ile Gly Ser Thr Thr Ala Asn Lys Thr Val Leu Val Asp
 355 360 365

Tyr Glu Lys Tyr Gly Lys Phe Tyr Asn Leu Ser Ile Lys Gly Thr Ile
 370 375 380

Asp Gln Ile Asp Lys Thr Asn Asn Thr Tyr Arg Gln Thr Ile Tyr Val
 385 390 395 400

Asn Pro Ser Gly Asp Asn Val Ile Ala Pro Val Leu Thr Gly Asn Leu
 405 410 415

Lys Pro Asn Thr Asp Ser Asn Ala Leu Ile Asp Gln Gln Asn Thr Ser
420 425 430

Ile Lys Val Tyr Lys Val Asp Asn Ala Ala Asp Leu Ser Glu Ser Tyr
435 440 445

Phe Val Asn Pro Glu Asn Phe Glu Asp Val Thr Asn Ser Val Asn Ile
450 455 460

Thr Phe Pro Asn Pro Asn Gln Tyr Lys Val Glu Phe Asn Thr Pro Asp
465 470 475 480

Asp Gln Ile Thr Thr Pro Tyr Ile Val Val Val Asn Gly His Ile Asp
485 490 495

Pro Asn Ser Lys Gly Asp Leu Ala Leu Arg Ser Thr Leu Tyr Gly Tyr
500 505 510

Asn Ser Asn Ile Ile Trp Arg Ser Met Ser Trp Asp Asn Glu Val Ala
515 520 525

Phe Asn Asn Gly Ser Gly Ser Gly Asp Gly Ile Asp Lys Pro Val Val
530 535 540

Pro Glu Gln Pro Asp Glu Pro Gly Glu Ile Glu Pro Ile Pro Glu Asp
545 550 555 560

Ser Asp Ser Asp Pro Gly Ser Asp Ser Gly Ser Asp Ser Asn Ser Asp
565 570 575

Ser Gly Ser Asp Ser Gly Ser Asp Ser Thr Ser Asp Ser Gly Ser Asp
580 585 590

Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp
595 600 605

Ser Asp Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Asp
610 615 620

Asn Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
625 630 635 640

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
645 650 655

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
660 665 670

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
675 680 685

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
690 695 700

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
705 710 715 720

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
725 730 735

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
740 745 750

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Ala
755 760 765

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
770 775 780

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
785 790 795 800

Ser Asp Ser Asp Ser Asp Ser Glu Ser Asp Ser Asp Ser Glu Ser Asp
805 810 815

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
820 825 830

Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Gly Ser Asp Ser Asp
835 840 845

Ser Ser Ser Asp Ser Asp Ser Glu Ser Asp Ser Asn Ser Asp Ser Glu
850 855 860

Ser Gly Ser Asn Asn Asn Val Val Pro Pro Asn Ser Pro Lys Asn Gly
865 870 875 880

Thr Asn Ala Ser Asn Lys Asn Glu Ala Lys Asp Ser Lys Glu Pro Leu
885 890 895

Pro Asp Thr Gly Ser Glu Asp Glu Ala Asn Thr Ser Leu Ile Trp Gly
900 905 910

Leu Leu Ala Ser Ile Gly Ser Leu Leu Leu Phe Arg Arg Lys Lys Glu
915 920 925

Asn Lys Asp Lys Lys
930

<210> 185
<211> 219
<212> PRT
<213> Staphylococcus aureus

<400> 185

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

Phe Asn His Leu Thr Met Ser Phe Asp Ser Asn Arg Leu Thr Val Leu
20 25 30

Leu Gly Asp Asn Gly Ala Gly Lys Ser Thr Leu Leu Arg Met Ile Ala
35 40 45

Gly Ile Glu Lys Ala Asn Asp Gly Thr Ile Asn Tyr Phe Gly Glu Lys
50 55 60

Trp Asn Gln Arg Gln Ile Gln Asn His Ile Gly Tyr Val Pro Gln Asp

65		70		75		80									
Ile	Ala	Leu	Phe	Glu	His	Met	Thr	Val	Ala	Glu	Asn	Ile	Lys	Phe	Phe
				85					90					95	
Lys	Ser	Leu	Cys	Lys	Asn	Pro	Ile	Asn	Asp	Thr	Thr	Ile	Asn	Glu	Tyr
			100					105					110		
Leu	Gln	Gln	Leu	Asn	Phe	Asp	Asp	Thr	Ser	Ala	Lys	Val	Ser	Thr	Leu
		115					120					125			
Ser	Gly	Gly	Asn	Lys	Arg	Lys	Ile	Asn	Ile	Leu	Val	Gly	Leu	Leu	Gly
	130					135					140				
Gln	Pro	Arg	Ile	Leu	Ile	Leu	Asp	Glu	Pro	Thr	Val	Gly	Ile	Asp	Leu
145					150					155					160
Lys	Ser	Arg	His	Asp	Ile	His	Gln	Leu	Leu	Asn	Ile	Met	Lys	Ser	Lys
				165					170					175	
Cys	Leu	Ile	Ile	Leu	Thr	Thr	His	His	Leu	Asp	Glu	Val	Glu	Ala	Leu
			180					185					190		
Ala	Asp	Asp	Ile	Lys	Leu	Ile	Gly	Gln	Asp	Pro	Phe	Tyr	Gln	His	Val
	195						200					205			
Leu	Glu	Asp	Lys	Gln	Trp	Thr	Tyr	Thr	Tyr	Tyr					
	210					215									
<210>	186														
<211>	253														
<212>	PRT														
<213>	Staphylococcus aureus														
<400>	186														
Met	Ala	Ile	Leu	Glu	Val	Lys	Gln	Leu	Thr	Lys	Ile	Tyr	Gly	Thr	Lys
1				5					10					15	
Lys	Met	Ala	Gln	Glu	Val	Leu	Arg	Asp	Ile	Asn	Met	Ser	Ile	Glu	Glu
			20					25					30		

Gly Glu Phe Ile Ala Ile Met Gly Pro Ser Gly Ser Gly Lys Thr Thr
35 40 45

Leu Leu Asn Val Leu Ser Ser Ile Asp Tyr Ile Ser Gln Gly Ser Ile
50 55 60

Thr Leu Lys Gly Lys Lys Leu Glu Lys Leu Ser Asn Lys Glu Leu Ser
65 70 75 80

Asp Ile Arg Lys His Asp Ile Gly Phe Ile Phe Gln Glu Tyr Asn Leu
85 90 95

Leu His Thr Leu Thr Val Lys Glu Asn Ile Met Leu Pro Leu Thr Val
100 105 110

Gln Lys Leu Asp Lys Glu His Met Leu Asn Arg Tyr Glu Lys Val Ala
115 120 125

Glu Ala Leu Asn Ile Leu Asp Ile Ser Asp Lys Tyr Pro Ser Glu Leu
130 135 140

Ser Gly Gly Gln Arg Gln Arg Thr Ser Ala Ala Arg Ala Phe Ile Thr
145 150 155 160

Leu Pro Ser Ile Ile Phe Ala Asp Glu Pro Thr Gly Ala Leu Asp Ser
165 170 175

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

Phe Lys Ser Thr Ile Ile Met Val Thr His Asp Pro Val Ala Ala Ser
195 200 205

Tyr Ala Asn Arg Val Val Met Leu Lys Asp Gly Gln Ile Phe Thr Glu
210 215 220

Leu Tyr Gln Gly Asp Asp Asp Lys His Thr Phe Phe Lys Glu Ile Ile
225 230 235 240

Arg Val Gln Ser Val Leu Gly Gly Val Asn Tyr Asp Leu
245 250

<210> 187
<211> 243
<212> PRT
<213> Staphylococcus aureus

<400> 187

Met Ile Leu Ser Tyr Leu Lys Ile Glu Phe Lys Val Ile Met Arg Lys
1 5 10 15

Lys Thr Thr Leu Ile Leu Ser Ile Leu Phe Pro Val Ile Phe Tyr Ile
20 25 30

Leu Phe Thr Ser Ile Leu Glu Leu Pro Glu Asp Val Lys Pro Lys Phe
35 40 45

Tyr Lys Glu Tyr Met Tyr Ser Met Thr Val Tyr Ser Leu Leu Ser Phe
50 55 60

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

Trp Arg Gln Arg Leu Met Val Thr Pro Phe Thr Phe Thr Ser Tyr Tyr
85 90 95

Ile Ser Lys Val Val Lys Thr Met Leu Gln Phe Ala Ile Ala Ile Leu
100 105 110

Val Ile Phe Met Val Gly His Phe Tyr Lys Gly Val Ala Met Ser Ala
115 120 125

Val Gln Trp Leu Glu Ser Gly Ile Phe Leu Trp Leu Gly Ala Ser Leu
130 135 140

Leu Ile Thr Phe Gly Ile Leu Phe Ser Leu Leu Asn Asp Ile Gln Lys
145 150 155 160

Thr Ser Ala Leu Ala Asn Ile Val Thr Ile Gly Leu Ala Val Leu Gly
165 170 175

Gly Leu Trp Phe Pro Ile Asn Thr Phe Pro Asn Trp Leu Gln His Val
180 185 190

Ala His Val Leu Pro Ser Tyr His Leu Arg Lys Leu Gly Val Asp Ile
195 200 205

Ala Ser Asn His His Ile Asn Leu Ile Ser Phe Ala Ile Ile Leu Leu
210 215 220

Tyr Ala Leu Gly Ser Ile Ile Ala Val Tyr Cys Ile Ser His Phe Lys
225 230 235 240

Arg Ala Glu

<210> 188
<211> 276
<212> PRT
<213> Staphylococcus aureus

<400> 188

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

Ala Phe Ile Phe Val Val Ile Val Leu Gln Phe Phe Val Ser Ser Glu
20 25 30

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

Leu His Leu Leu Gly Thr Asp Asp Tyr Gly Arg Asp Leu Phe Thr Arg
50 55 60

Ile Ile Ile Gly Ala Arg Ser Thr Leu Phe Val Thr Val Leu Thr Leu
65 70 75 80

Ile Ala Ile Val Val Ile Gly Val Thr Leu Gly Leu Phe Ala Gly Tyr
85 90 95

Lys Lys Gly Trp Ile Glu Arg Leu Val Leu Arg Phe Ile Asp Val Gly
100 105 110

Leu Ser Ile Pro Glu Phe Ile Ile Met Ile Ala Leu Ala Ser Phe Phe
115 120 125

Gln Pro Ser Leu Trp Asn Leu Val Ile Ser Ile Thr Leu Ile Lys Trp
130 135 140

Met Asn Tyr Thr Arg Leu Thr Arg Ser Ile Val Asn Ser Glu Met Asn
145 150 155 160

Lys Pro Tyr Ile Lys Met Ala Gln Leu Phe His Val Pro Thr Arg Thr
165 170 175

Ile Leu Ile Arg His Leu Thr Pro Lys Ile Ile Pro Ala Ile Ile Val
180 185 190

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

Ser Phe Ile Gly Leu Gly Ala Gln Pro Pro Thr Pro Glu Trp Gly Ala
210 215 220

Met Leu Gln Gln Gly Arg Asp Phe Ile Ser Ser His Pro Ile Met Leu
225 230 235 240

Ile Ala Pro Ala Ser Val Ile Ala Ile Thr Ile Leu Ile Phe Asn Leu
245 250 255

Thr Gly Asp Ala Leu Arg Asp Arg Leu Leu Lys Gln Arg Gly Glu Tyr
260 265 270

Asp Glu Ser His
275

<210> 189
 <211> 136
 <212> PRT
 <213> Staphylococcus aureus

<400> 189

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

Tyr Thr Asp Lys Arg Lys Asp Met Leu Asp Ile Phe Val Glu Glu Asp
 20 25 30

Lys Tyr Ile Asn Ala Lys Tyr Ile Gln Gln Val Met Asp Glu Asn Tyr
 35 40 45

Pro Gly Ile Ser Phe Asp Thr Ile Tyr Arg Asn Leu His Leu Phe Lys
 50 55 60

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

Arg Ile Ala Cys Thr Asn His His His His His Phe Ile Cys Glu Lys
 85 90 95

Cys Gly Asp Thr Lys Val Ile Asp Tyr Cys Pro Ile Asp Gln Ile Lys
 100 105 110

Leu Ser Leu Pro Gly Val Asn Ile His Lys His Lys Leu Glu Val Tyr
 115 120 125

Gly Val Cys Glu Ser Cys Gln Asp
 130 135

<210> 190
 <211> 233
 <212> PRT
 <213> Staphylococcus aureus

<400> 190

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

Leu Met Ile Ile Ala Asn Phe Tyr Tyr Ile Phe Phe Glu Lys Ile Gly
20 25 30

Phe Leu Leu Val Leu Leu Leu Gly Cys Val Leu Val Tyr Val Gly Tyr
35 40 45

Leu Tyr Phe His Lys Ile Arg Gly Leu Leu Ala Phe Trp Ile Gly Ala
50 55 60

Leu Leu Ile Ala Phe Thr Leu Leu Ser Asn Lys Tyr Thr Ile Ile Ile
65 70 75 80

Leu Phe Val Phe Leu Leu Leu Leu Ile Val Arg Tyr Leu Ile His Lys
85 90 95

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

Ser Phe Ile Lys Gln Lys Trp Phe Gly Glu Gln Arg Thr Pro Val Tyr
115 120 125

Val Tyr Lys Trp Glu Asp Val Gln Ile Gln His Gly Ile Gly Asp Leu
130 135 140

His Ile Asp Leu Thr Lys Ala Ala Asn Ile Lys Glu Asn Asn Thr Ile
145 150 155 160

Val Val Arg His Ile Leu Gly Lys Val Gln Val Ile Leu Pro Val Asn
165 170 175

Tyr Asn Ile Asn Leu His Val Ala Ala Phe Tyr Gly Ser Thr Tyr Val
180 185 190

Asn Glu Lys Ser Tyr Lys Val Glu Asn Asn Asn Ile His Ile Glu Glu
195 200 205

Met Met Lys Pro Asp Asn Tyr Thr Val Asn Ile Tyr Val Ser Thr Phe
210 215 220

Ile Gly Asp Val Glu Val Ile Tyr Arg
225 230

<210> 191
<211> 260
<212> PRT
<213> Staphylococcus aureus

<400> 191

Met Leu Ile Gln Leu Asp Gln Ile Gly Arg Met Lys Gln Gly Lys Thr
1 5 10 15

Ile Leu Lys Lys Ile Ser Trp Gln Ile Ala Lys Gly Asp Lys Trp Ile
20 25 30

Leu Tyr Gly Leu Asn Gly Ala Gly Lys Thr Thr Leu Leu Asn Ile Leu
35 40 45

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

Met Pro Gly Lys Val Gly Tyr Ser Ala Glu Thr Val Arg Gln His Ile
65 70 75 80

Gly Phe Val Ser His Ser Leu Leu Glu Lys Phe Gln Glu Gly Glu Arg
85 90 95

Val Ile Asp Val Val Ile Ser Gly Ala Phe Lys Ser Ile Gly Val Tyr
100 105 110

Gln Asp Ile Asp Asp Glu Ile Arg Asn Glu Ala His Gln Leu Leu Lys
115 120 125

Leu Val Gly Met Ser Ala Lys Ala Gln Gln Tyr Ile Gly Tyr Leu Ser
130 135 140

Thr Gly Glu Lys Gln Arg Val Met Ile Ala Arg Ala Leu Met Gly Gln
145 150 155 160

Pro Gln Val Leu Ile Leu Asp Glu Pro Ala Ala Gly Leu Asp Phe Ile
165 170 175

Ala Arg Glu Ser Leu Leu Ser Ile Leu Asp Ser Leu Ser Asp Ser Tyr
180 185 190

Pro Thr Leu Ala Met Ile Tyr Val Thr His Phe Ile Glu Glu Ile Thr
195 200 205

Ala Asn Phe Ser Lys Ile Leu Leu Leu Lys Asp Gly Gln Ser Ile Gln
210 215 220

Gln Gly Ala Val Glu Asp Ile Leu Thr Ser Glu Asn Met Ser Arg Phe
225 230 235 240

Phe Gln Lys Asn Val Ala Val Gln Arg Trp Asn Asn Arg Phe Ser Met
245 250 255

Ala Met Leu Glu
260

<210> 192
<211> 209
<212> PRT
<213> Staphylococcus aureus

<400> 192

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
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

<210> 193
<211> 439
<212> PRT
<213> Staphylococcus aureus

<400> 193

Met Arg Thr Gly His Tyr Thr Pro Ile Pro Asn Glu Pro His Tyr Leu
1 5 10 15

Val Ile Ser His Ala Asp Lys Leu Thr Ala Thr Glu Lys Ala Lys Leu

20					25					30					
Arg	Leu	Leu	Ile	Ile	Lys	Gln	Lys	Leu	Asp	Ile	Ser	Leu	Ala	Glu	Ser
	35					40					45				
Val	Val	Ser	Ser	Pro	Ile	Ala	Ser	Glu	His	Val	Ile	Glu	Gln	Leu	Thr
	50					55					60				
Leu	Phe	Gln	His	Glu	Arg	Arg	His	Leu	Arg	Pro	Lys	Ile	Ser	Ala	Thr
65					70					75					80
Phe	Leu	Ala	Trp	Leu	Leu	Ile	Phe	Leu	Met	Phe	Ala	Leu	Pro	Ile	Gly
			85						90					95	
Ile	Ala	Tyr	Gln	Phe	Ser	Asp	Trp	Phe	Gln	Asn	Gln	Tyr	Val	Ser	Ala
		100						105					110		
Trp	Ile	Glu	Tyr	Leu	Thr	Gln	Thr	Thr	Leu	Leu	Asn	His	Asp	Ile	Leu
	115						120					125			
Gln	His	Ile	Leu	Phe	Gly	Asp	Tyr	Gly	Val	Leu	Ser	Leu	Gly	Thr	Tyr
	130					135					140				
Ser	Leu	Val	Trp	Ala	Leu	Pro	Val	Val	Ile	Leu	Ile	Ser	Leu	Ser	Thr
145					150					155					160
Ala	Ile	Ile	Asp	Gln	Thr	Gly	Leu	Lys	Ser	Trp	Met	Ile	Trp	Ala	Ile
			165						170					175	
Glu	Pro	Ser	Met	Leu	Trp	Ile	Gly	Leu	Gln	Gly	Asn	Asp	Ile	Val	Pro
		180						185					190		
Leu	Leu	Glu	Gly	Phe	Gly	Cys	Asn	Ala	Ala	Ala	Ile	Ser	Gln	Ala	Ala
	195						200					205			
His	Gln	Cys	His	Thr	Cys	Thr	Lys	Thr	Gln	Cys	Met	Ser	Leu	Ile	Ser
	210					215					220				
Phe	Gly	Ser	Ser	Cys	Ser	Tyr	Gln	Ile	Gly	Ala	Thr	Leu	Ser	Ile	Phe

225		230		235		240
Ser Val Ala Gly Lys Ser Trp Leu Phe Met Pro Tyr Leu Ile Leu Val						
	245			250		255
Leu Leu Gly Gly Ile Leu His Asn Arg Ile Trp Leu Lys Lys Asn Asp						
	260		265			270
Gln Gln Leu Ser Val Pro Leu Pro Tyr Asp Arg Gln Leu His Met Pro						
	275		280			285
Asn Ile Arg Gln Met Leu Leu Gln Met Trp Gln Asn Ile Gln Met Phe						
	290		295			300
Ile Val Gln Ala Leu Pro Ile Phe Ile Thr Ile Cys Leu Ile Val Ser						
305		310		315		320
Ile Leu Ser Leu Thr Pro Ile Leu Asn Val Leu Ser Gln Ile Phe Thr						
	325		330			335
Pro Ile Leu Ser Leu Leu Gly Ile Ser Ser Glu Leu Ser Pro Gly Ile						
	340		345			350
Leu Phe Ser Met Ile Arg Lys Asp Gly Met Leu Leu Phe Asn Leu His						
	355		360			365
Gln Gly Ala Leu Leu Gln Gly Met Thr Ala Thr Gln Leu Leu Leu Leu						
	370		375			380
Val Phe Phe Ser Ser Thr Phe Thr Ala Cys Ser Val Thr Met Thr Met						
385		390		395		400
Leu Leu Lys His Leu Gly Gly Gln Ser Ala Leu Lys Leu Ile Gly Lys						
	405		410			415
Gln Met Val Thr Ser Leu Ser Leu Val Ile Gly Val Gly Ile Ile Val						
	420		425			430
Lys Ile Val Met Leu Ile Ile						

435

<210> 194
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 194
tcgtcgttgt cgttttgtcg tt

22

<210> 195
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 195

Ile Leu Pro Trp Lys Trp Pro Trp Trp Pro Trp Arg Arg
1 5 10

<210> 196
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic sequence

<400> 196

Lys Asp Tyr Glu Arg Lys Tyr Lys Lys His Ile Val Ser
1 5 10

CLAIMS**1. A fusion construct of formula (I):**

X-A-linker-B-Z (I)

wherein :

(1) A and B are identical or different and are independently:

- (a) a polypeptide comprising a SACOL0029 polypeptide as set forth in any one of the sequences depicted in FIG. 24 (SEQ ID NOs: 5 and 121 to 131), a SACOL0264 polypeptide (SEQ ID NO: 185), a SACOL0442 polypeptide as set forth in any one of the sequences depicted in FIG. 22D (SEQ ID NOs: 29 and 82 to 92), a SACOL0718 polypeptide (SEQ ID NO: 186), a SACOL0720 polypeptide as set forth in any one of the sequences depicted in FIGs. 23I-K (SEQ ID NOs: 11 and 109 to 120), a SACOL1353 polypeptide (SEQ ID NO: 187), a SACOL1416 polypeptide (SEQ ID NO: 188), a SACOL1611 polypeptide (SEQ ID NO: 189), a SACOL1867 polypeptide as set forth in any one of the sequences depicted in FIG. 25D (SEQ ID NOs: 152 to 164), a SACOL1912 polypeptide (SEQ ID NO: 43), a SACOL1944 polypeptide (SEQ ID NO: 190), a SACOL2144 polypeptide (SEQ ID NO: 191), a SACOL2365 polypeptide (SEQ ID NO: 192), a SACOL2385 polypeptide (SEQ ID NO: 50) or a SACOL2599 polypeptide (SEQ ID NO: 193), based on the gene nomenclature from the *Staphylococcus aureus* COL (SACOL) genome set forth in NCBI Reference Sequence NC_002951.2;
- (b) a polypeptide encoded by a gene from a same operon as a gene encoding the polypeptide of (a);
- (c) a polypeptide comprising an immunogenic fragment of at least 13 consecutive amino acids of (a) or (b);
- (d) a polypeptide comprising an amino acid sequence at least 60% identical overall to the sequence of the polypeptide of any one of (a) to (c); or
- (e) a polypeptide comprising an immunogenic variant comprising at least 13 consecutive amino acids of any one of (a) to (c);

(2) the linker is an amino acid sequence of at least one amino acid or is absent;

(3) X is absent or is an amino acid sequence of at least one amino acid; and

(4) Z is absent or is an amino acid sequence of at least one amino acid.

2. The construct of claim 1, wherein (1) (a) is a polypeptide comprising a SACOL0029 polypeptide as set forth in any one of the sequences depicted in FIG. 24 (SEQ ID NOs: 5 and 121 to 131), a SACOL0442 polypeptide as set forth in any one of the sequences depicted in FIG. 22D (SEQ ID NOs: 29 and 82 to 92), a SACOL0720 polypeptide as set forth in any one of the sequences depicted in FIGs. 23I-K (SEQ ID NOs: 11 and 109 to

120), or a SACOL1867 polypeptide as set forth in any one of the sequences depicted in FIG. 25D (SEQ ID NOs: 152 to 164).

3. The construct of claim 2, wherein at least one of A and B is (a) a polypeptide comprising a SACOL0029 polypeptide as set forth in any one of the sequences depicted in FIG. 24 (SEQ ID NOs: 5 and 121 to 131); (b) a polypeptide encoded by a gene from a same operon as a gene encoding the polypeptide of (a); (c) a polypeptide comprising an immunogenic fragment of at least 13 consecutive amino acids of (a) or (b); (d) a polypeptide comprising an amino acid sequence at least 60% identical overall to the sequence of the polypeptide of any one of (a) to (c); or (e) a polypeptide comprising an immunogenic variant comprising at least 13 consecutive amino acids of any one of (a) to (c); and the other one of A and B is (a') a polypeptide comprising a SACOL1867 polypeptide as set forth in any one of the sequences depicted in FIG. 25D (SEQ ID NOs: 152 to 164); (b') a polypeptide encoded by a gene from a same operon as a gene encoding the polypeptide of (a'); (c') a polypeptide comprising an immunogenic fragment of at least 13 consecutive amino acids of (a') or (b'); (d') a polypeptide comprising an amino acid sequence at least 60% identical overall to the sequence of the polypeptide of any one of (a') to (c'); or (e') a polypeptide comprising an immunogenic variant comprising at least 12 consecutive amino acids of any one of (a') to (c').
4. The construct of claim 2, wherein at least one of A and B is (a) a polypeptide comprising a SACOL0442 polypeptide as set forth in any one of the sequences depicted in FIG. 22D (SEQ ID NOs: 29 and 82 to 92); (b) a polypeptide encoded by a gene from a same operon as a gene encoding the polypeptide of (a); (c) a polypeptide comprising an immunogenic fragment of at least 13 consecutive amino acids of (a) or (b); (d) a polypeptide comprising an amino acid sequence at least 60% identical overall to the sequence of the polypeptide of any one of (a) to (c); or (e) a polypeptide comprising an immunogenic variant comprising at least 13 consecutive amino acids of any one of (a) to (d); and the other one of A and B is (a') a polypeptide comprising a SACOL0720 polypeptide as set forth in any one of the sequences depicted in FIGs. 23I-K (SEQ ID NOs: 11 and 109 to 120); (b') a polypeptide encoded by a gene from a same operon as a gene encoding the polypeptide of (a'); (c') a polypeptide comprising an immunogenic fragment of at least 13 consecutive amino acids of (a') or (b'); (d') a polypeptide comprising an amino acid sequence at least 60% identical overall to the sequence of the polypeptide of any one of (a') to (c'); or (e') a polypeptide comprising an immunogenic variant comprising at least 12 consecutive amino acids of any one of (a') to (d').
5. The construct of claim 2, wherein A and B are identical or different and are (a) a polypeptide comprising a SACOL0720 polypeptide as set forth in any one of the sequences depicted in FIGs. 23I-K (SEQ ID NOs: 11 and 109 to 120); (b) a polypeptide encoded by a gene from a same operon as a gene encoding the polypeptide of (a); (c) a polypeptide comprising an immunogenic fragment of at least 13 consecutive amino acids of (a) or (b); (d) a polypeptide comprising an amino acid sequence at least 60% identical overall to the sequence of the polypeptide of any one of (a) to (c); or (e) a polypeptide comprising an immunogenic variant comprising at least 13 consecutive amino acids of any one of (a) to (d).
6. The construct of any one of claims 1-2 and 4, wherein said immunogenic fragment (d) comprises one or more of the following amino acid sequences: KDTINGKSNKSRNW (SEQ ID NO: 34); and KDGGKYTLESHKELQ

(SEQ ID NO: 1).

7. The construct of claim 6, wherein said immunogenic fragment (d) comprises one or more of the following amino acid sequences :
 STQNSSSVQDKQLQKVVEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTV
 AGRVYTPKRNITLNKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKDGGKYTLESHKELQKDRENVKINT
 ADIKNVTFKLKSVNDIEQV (SEQ ID NO: 30);
 DKQLQKVVEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVAGRVYTPKR
 NITLNKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTK (SEQ ID NO :32); and
 DKQLQKVVEVPNNSEKALVKKLYDRYSKDTINGKSNKSRNWVYSERPLNENQVRIHLEGTYTVAGRVYTPKR
 NITLNKEVVTLKELDHIIRFAHISYGLYMGEHLPKGNIVINTKDGGKYTLESHKELQKDRENVKINTADIKNVTFKL
 VKSVNDIEQV (SEQ ID NO : 33).
8. The construct of any one of claims 1-2 and 4-5, wherein said immunogenic fragment (d) comprises one or more of the following amino acid sequences: QFGFDLKHKKDALA (SEQ ID NO: 21); TIKDQQKANQLAS (SEQ ID NO: 22); KDINKIYFMTDVL (SEQ ID NO: 23); and DVDLGGPTFVLND (SEQ ID NO: 24).
9. The construct of claim 8, wherein said immunogenic fragment (d) comprises one or more of the following amino acid sequences:
 RASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNYKEVIHTKLYKDNLFDVKAKEPYNVTITSDKYIP
 NTDLKRQADLFVAEGSIKDLVKHKKHGKAIIGTKKHVNIKLKRDINKIYFMTDVLGGPTFVLNDKDYQEIRK
 YTKAHIVSQFGFDLKHKKDALALEKAKNKVDKSIETRSEAISSISLTG (SEQ ID NO : 12);
 ASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNYKEVIHTKLYKDNLFDVKAKEPYNVTITSDKYIPNT
 DLKRQADLFVAEGSIKDLVKHKKHGKAIIGTKKHVNIKLKRDINKIYFMTDVLGGPTFVLNDKDYQEIRKYT
 KAHIVSQFGFDLKHKKDALALEKAKNKVDKSIETRSEAISSISLTG (SEQ ID NO: 13);
 ASLSSEIKYTAPHDVTIKDQQKANQLASELNNQKIPHFYNYKEVIHTKLYKDNLFDVKAKEPYNVTITSDKYIPNT
 DLKRQADLFVAEGSIKDLVKHKKHGKAIIGTKKHVNIKLKRDINKIYFMTDVLGGPTFVLNDKDYQE (SEQ
 ID NO: 14); KDINKIYFMTDVLGGPTFVLNDKDYQEIRKYTKAHIVSQFGFDLKHKKDALA (SEQ ID NO : 15);
 KDINKIYFMTDVLGGPTFVLNDKDY (SEQ ID NO : 17); KDINKIYFMTDVLGGPTFVLNDKD (SEQ ID NO :
 16); KDINKIYFMTDVLGGPTFVLND (SEQ ID NO : 19); KHIVSQFGFDLKHKKDALA (SEQ ID NO: 20) and
 SQFGFDLKHKKDALA (SEQ ID NO: 18).
10. The construct of any one of claims 1-3, wherein said immunogenic fragment (c') comprises one or more of the following amino acid sequences: PYNGVVSFKDATGF (SEQ ID NO: 165); AHPNGDKGNGGIYK (SEQ ID NO: 167); SISDYPGDEDISVM (SEQ ID NO: 169); RGPKGFNFNENVQA (SEQ ID NO: 172); QFESTGTIKRIKDN (SEQ ID NO: 175); and GNSGSPVLNSNNEV (SEQ ID NO: 178).
11. The construct of claim 10, wherein said immunogenic fragment (d) comprises the following amino acid sequence:
 TQVKDTNIFPYNGVVSFKDATGFVIGKNTIITNKHVSKDYKVGDRITAHPNGDKGNGGIYKISISDYPGDEDIS
 VMNIEQAVERGPKGFNFNENVQAFNFAKDAKVDDKIKVIGYPLPAQNSFKQFESTGTIKRIKDNILNFDAYIEP

GNSGSPVLNSNNEVIGVYGGIGKIGSEYNGAVYFTPQIKDFIQKHIEQ (SEQ ID NO: 39).

12. The construct of any one of claims 1 to 11, wherein the linker comprises at least four identical or different amino acids selected from the group consisting of glycine, serine, alanine, aspartate, glutamate and lysine.
13. The construct of any one of claims 1 to 12, wherein the linker comprises (GGGGS)_n (SEQ ID NO: 67), (ERKYK)_n (SEQ ID NO: 61); or (EAAAK)_n (SEQ ID NO: 63), wherein n=1 to 5.
14. The construct of any one of claims 1 to 13, wherein said X comprises a polyhistidine of 6 to 10 amino acids.
15. The construct of any one of claims 1 to 13, wherein said X is absent.
16. The construct of any one of claims 1 to 15, wherein said Z is absent.
17. An isolated nucleic acid molecule encoding the construct defined in any one of claims 1 to 16.
18. A vector comprising the isolated nucleic acid defined in claim 17.
19. A host cell comprising the vector defined in claim 18.
20. The cell of claim 19, which is a live attenuated form of *Staphylococcus aureus*.
21. The cell of claim 20, wherein the live attenuated form of *Staphylococcus aureus* has a stabilized small colony variant (SCV) phenotype.
22. The cell of claim 21, wherein the live attenuated form of *Staphylococcus aureus* having a stabilized SCV phenotype is a Δ hemB Δ 720 *S. aureus*.
23. A composition comprising:
 - (A) at least one of the constructs defined in any one of claims 1 to 16; at least one of the nucleic acid molecules defined in claim 17; at least one of the vectors defined in claims 18; or at least one of the cells defined in any one of claims 19 to 22; and
 - (B) (i) a polypeptide defined in any one of claims 1 to 11;
 - (ii) a live attenuated *Staphylococcus aureus*;
 - (iii) a pharmaceutically acceptable excipient;
 - (iv) an adjuvant; or
 - (v) a combination of at least two of (i) to (iv).
24. The composition of claim 23, wherein the live attenuated form of *Staphylococcus aureus* expresses:
 - (a) a polypeptide comprising a SACOL0029 polypeptide as set forth in any one of the sequences depicted in FIG. 24 (SEQ ID NOs: 5 and 121 to 131), a SACOL0264 polypeptide (SEQ ID NO: 185), a SACOL0442 polypeptide as set forth in any one of the sequences depicted in FIG. 22D (SEQ ID NOs: 29 and 82 to 92), a SACOL0718 polypeptide (SEQ ID NO: 186), a SACOL0720 polypeptide as set forth in any one of the sequences depicted in FIGs. 23I-J (SEQ ID NOs: 11 and 109 to 120), a

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SACOL1353 polypeptide (SEQ ID NO : 187), a SACOL1416 polypeptide (SEQ ID NO : 188), SACOL1611 (SEQ ID NO : 189), a SACOL1867 polypeptide as set forth in any one of the sequences depicted in FIG. 25D (SEQ ID NOs: 152 to 164), a SACOL1912 polypeptide (SEQ ID NO : 43), SACOL1944 (SEQ ID NO : 190), a SACOL2144 polypeptide (SEQ ID NO : 191), a SACOL2365 polypeptide (SEQ ID NO : 192), a SACOL2385 polypeptide (SEQ ID NO : 50) or a SACOL2599 polypeptide (SEQ ID NO : 193) based on the gene nomenclature from the *Staphylococcus aureus* COL (SACOL) genome set forth in NCBI Reference Sequence NC_002951.2;

- (b) a polypeptide encoded by a gene from a same operon as a gene encoding the polypeptide of (a);
 - (c) a polypeptide comprising an immunogenic fragment of at least 13 consecutive amino acids of (a) or (b);
 - (d) a polypeptide comprising an amino acid sequence at least 60% identical overall to the sequence of the polypeptide of any one of (a) to (c); or
 - (e) a polypeptide comprising an immunogenic variant comprising at least 13 consecutive amino acids of any one of (a) to (c).
25. The composition of claim 23 or 24, wherein the live attenuated form of *Staphylococcus aureus* has a stabilized small colony variant (SCV) phenotype.
26. The composition of any one of claims 23 to 25, wherein the adjuvant comprises alum, an oil, saponin, cyclic-diguanosine-5'-monophosphate (c-di-GMP), polyphosphasine, indolicidin, pathogen-associated molecular patterns (PAMPS), liposome or a combination of at least two thereof.
27. A method for preventing and/or treating a Staphylococcal intramammary infection (IMI) in a mammal, said method comprising administering to said mammal an effective amount of the construct defined in any one of claims 1 to 16; of the nucleic acid molecule defined in claim 17; of the vector defined in claim 18; of the cell defined in any one of claims 19 to 22; or of the composition defined in any one of claims 23 to 26.
28. The method of claim 27, wherein said Staphylococcal IMI is caused by one or more *Staphylococcus aureus* strains.
29. The method of claim 27 or 28, wherein said mammal is a cow.
30. A use of an effective amount of (i) the construct defined in any one of claims 1 to 16; (ii) the nucleic acid molecule defined in claim 17; (iii) the vector defined in claim 18; of the cell defined in any one of claims 19 to 22; (iv) the composition defined in any one of claims 23 to 26; or (v) a combination of at least two of (i) to (iv), for preventing and/or treating a Staphylococcal intramammary infection (IMI) in a mammal.
31. The use of claim 30, wherein said Staphylococcal IMI is caused by one or more *Staphylococcus aureus* strains.
32. The use of claim 30 or 31, wherein said mammal is a cow.
33. The construct defined in any one of claims 1 to 16; the nucleic acid molecule defined in claim 17; the vector

defined in claim 18; the cell defined in any one of claims 19 to 22; the composition defined in any one of claims 23 to 26 or a combination of at least two thereof, for use in the prevention and/or treatment of a Staphylococcal intramammary infection (IMI) in a mammal.

34. The construct, nucleic acid molecule, vector, cell, composition or combination of claim 33, wherein said Staphylococcal IMI is caused by one or more *Staphylococcus aureus* strains.

35. The construct, nucleic acid molecule, vector, cell or composition of claim 33 or 34, wherein said mammal is a cow.

36. A kit for preventing and/or treating a Staphylococcal intramammary infection (IMI) in a mammal comprising:

(A) (i) at least one of the constructs defined in any one of claims 1 to 16; (ii) at least one of the nucleic acid molecules defined in claim 17; (iii) at least one of the vectors defined in claim 18; (iv) at least one of the cells defined in any one of claims 19 to 22; or (v) a combination of at least two of (i) to (iv), and

(B) (i) the polypeptide defined in any one of claims 1 to 11;

(ii) a live attenuated *Staphylococcus aureus*;

(iii) a pharmaceutically acceptable excipient;

(iv) an adjuvant;

(v) instructions for using the kit for preventing and/or treating a Staphylococcal intramammary infection (IMI) in a mammal; or

(vi) a combination of at least two of (i) to (v).