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(54) **COMPOSITIONS AND METHODS RELATED TO PROTEIN A (SPA) ANTIBODIES AS AN ENHANCER OF IMMUNE RESPONSE**

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See application file for complete search history.

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ABSTRACT

The present invention concerns methods and compositions for treating or preventing a bacterial infection, particularly infection by a *Staphylococcus* bacterium. The invention provides methods and compositions for stimulating an immune response against the bacteria. In certain embodiments, the methods and compositions involve a non-toxicogenic Protein A (SpA) variant or an antibody directed thereto.

9 Claims, 1 Drawing Sheet

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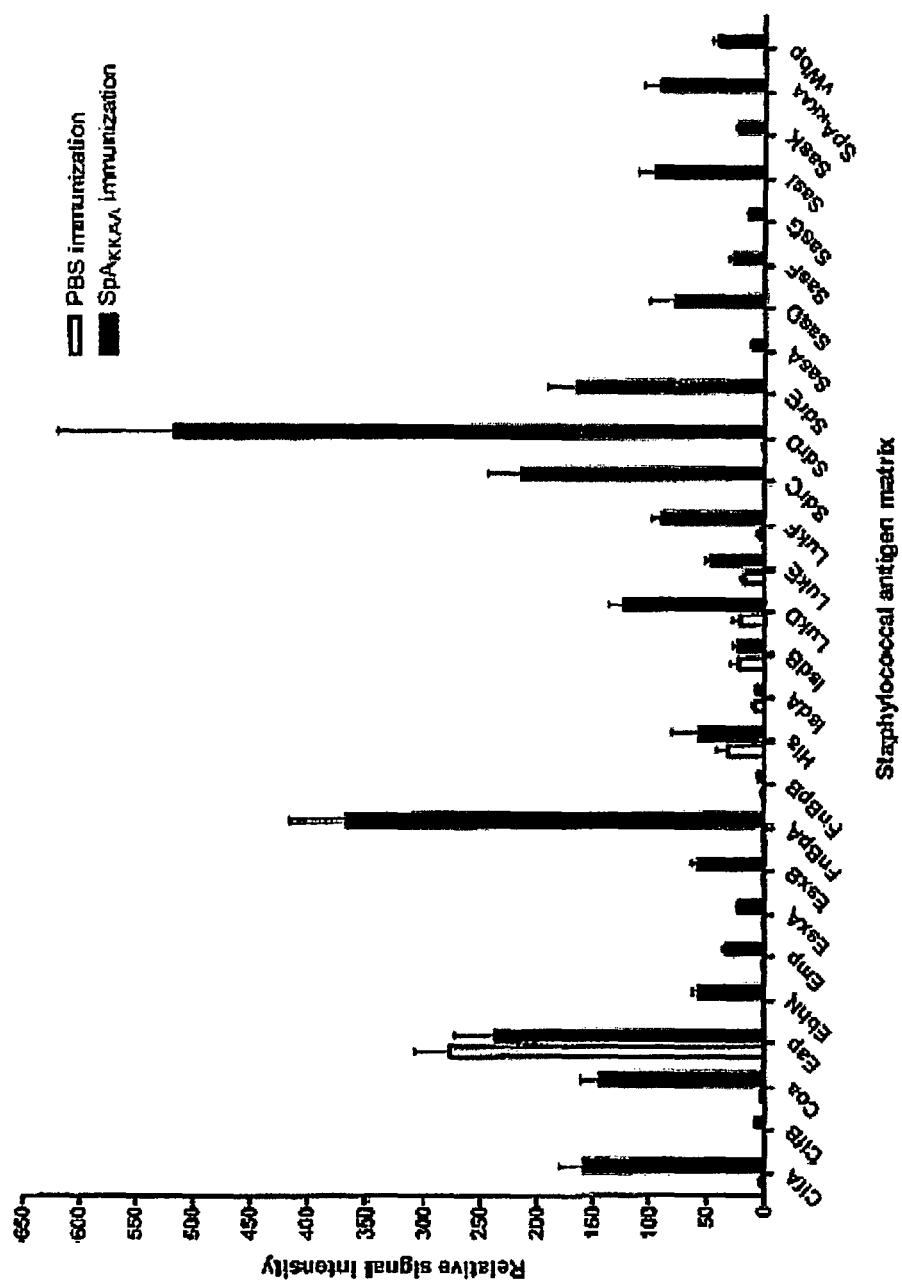
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COMPOSITIONS AND METHODS RELATED TO PROTEIN A (SPA) ANTIBODIES AS AN ENHANCER OF IMMUNE RESPONSE

This application is a continuation of U.S. patent application Ser. No. 14/335,411 filed Jul. 18, 2014 (now issued as U.S. Pat. No. 9,212,219), which is a continuation of U.S. patent application Ser. No. 13/639,465 filed Jan. 18, 2013 (now issued as U.S. Pat. No. 8,808,699), which is a national stage application under 35 U.S.C. 371 of International Application No. PCT/US2011/031213 filed Apr. 5, 2011, which claims priority to U.S. Provisional Patent Application Ser. No. 61/321,050 filed Apr. 5, 2010. U.S. patent application Ser. No. 14/335,411 is also a continuation-in-part of U.S. patent application Ser. No. 13/260,878 (now issued as U.S. Pat. No. 9,567,379), which is a national stage application under 35 U.S.C. 371 of International Application No. PCT/US2010/029959 filed Apr. 5, 2010, which claims priority to U.S. Provisional Patent Application Ser. No. 61/287,996 filed Dec. 8, 2009, U.S. Provisional Patent Application Ser. No. 61/237,956 filed Aug. 28, 2009, and U.S. Provisional Patent Application Ser. No. 61/166,432 filed Apr. 3, 2009. The entire contents of each of the above-referenced disclosures are specifically incorporated herein by reference without disclaimer.

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BACKGROUND OF THE INVENTION

I. Field of the Invention

The present invention relates generally to the fields of immunology, microbiology, and pathology. More particularly, it concerns methods and compositions for enhancing an immune response against a bacterial antigen.

II. Background

The number of both community acquired and hospital acquired infections have increased over recent years with the increased use of intravascular devices. Hospital acquired (nosocomial) infections are a major cause of morbidity and mortality, more particularly in the United States, where it affects more than 2 million patients annually. The most frequent infections are urinary tract infections (33% of the infections), followed by pneumonia (15.5%), surgical site infections (14.8%) and primary bloodstream infections (13%) (Emori and Gaynes, 1993).

The major nosocomial pathogens include *Staphylococcus aureus*, coagulase-negative Staphylococci (mostly *Staphylococcus epidermidis*), *enterococcus* spp., *Escherichia coli* and *Pseudomonas aeruginosa*. Although these pathogens cause approximately the same number of infections, the severity of the disorders they can produce combined with the frequency of antibiotic resistant isolates balance this ranking towards *S. aureus* and *S. epidermidis* as being the most significant nosocomial pathogens.

Staphylococci can cause a wide variety of diseases in humans and other animals through either toxin production or invasion. Staphylococcal toxins are also a common cause of food poisoning, as the bacteria can grow in improperly-stored food.

Staphylococcus epidermidis is a normal skin commensal, which is also an important opportunistic pathogen responsible for infections of impaired medical devices and infections at sites of surgery. Medical devices infected by *S. epidermidis* include cardiac pacemakers, cerebrospinal fluid

shunts, continuous ambulatory peritoneal dialysis catheters, orthopedic devices and prosthetic heart valves.

Staphylococcus aureus is the most common cause of nosocomial infections with a significant morbidity and mortality. It is the cause of some cases of osteomyelitis, endocarditis, septic arthritis, pneumonia, abscesses, and toxic shock syndrome. *S. aureus* can survive on dry surfaces, increasing the chance of transmission. Any *S. aureus* infection can cause the staphylococcal scalded skin syndrome, a cutaneous reaction to exotoxin absorbed into the bloodstream. It can also cause a type of septicemia called pyaemia that can be life-threatening. Problematically, Methicillin-resistant *Staphylococcus aureus* (MRSA) has become a major cause of hospital-acquired infections.

S. aureus and *S. epidermidis* infections are typically treated with antibiotics, with penicillin being the drug of choice, whereas vancomycin is used for methicillin resistant isolates. The percentage of staphylococcal strains exhibiting wide-spectrum resistance to antibiotics has become increasingly prevalent, posing a threat for effective antimicrobial therapy. In addition, the recent emergence of vancomycin resistant *S. aureus* strain has aroused fear that MRSA strains are emerging and spreading for which no effective therapy is available.

An alternative to antibiotic treatment for staphylococcal infections is under investigation that uses antibodies directed against staphylococcal antigens. This therapy involves administration of polyclonal antisera (WO00/15238, WO00/12132) or treatment with monoclonal antibodies against lipoteichoic acid (WO98/57994).

An alternative approach would be the use of active vaccination to generate an immune response against staphylococci. The *S. aureus* genome has been sequenced and many of the coding sequences have been identified (WO02/094868, EP0786519), which can lead to the identification of potential antigens. The same is true for *S. epidermidis* (WO01/34809). As a refinement of this approach, others have identified proteins that are recognized by hyperimmune sera from patients who have suffered staphylococcal infection (WO01/98499, WO02/059148).

S. aureus secretes a plethora of virulence factors into the extracellular milieu (Archer, 1998; Dinges et al., 2000; Foster, 2005; Shaw et al., 2004; Sibbald et al., 2006). Like most secreted proteins, these virulence factors are translocated by the Sec machinery across the plasma membrane. Proteins secreted by the Sec machinery bear an N-terminal leader peptide that is removed by leader peptidase once the pre-protein is engaged in the Sec translocon (Dalbey and Wickner, 1985; van Wely et al., 2001). Recent genome analysis suggests that Actinobacteria and members of the Firmicutes encode an additional secretion system that recognizes a subset of proteins in a Sec-independent manner (Pallen, 2002). ESAT-6 (early secreted antigen target 6 kDa) and CFP-10 (culture filtrate antigen 10 kDa) of *Mycobacterium tuberculosis* represent the first substrates of this novel secretion system termed ESX-1 or Ssm in *M. tuberculosis* (Andersen et al., 1995; Hsu et al., 2003; Pym et al., 2003; Stanley et al., 2003). In *S. aureus*, two ESAT-6 like factors designated EsxA and EsxB are secreted by the Ess pathway (ESAT-6 secretion system) (Burts et al., 2005).

The first generation of vaccines targeted against *S. aureus* or against the exoproteins it produces have met with limited success (Lee, 1996). There remains a need to develop effective vaccines against staphylococcal infections. Additional compositions for treating staphylococcal infections are also needed.

SUMMARY OF THE INVENTION

Protein A (SpA) (SEQ ID NO:33), a cell wall anchored surface protein of *Staphylococcus aureus*, provides for bacterial evasion from innate and adaptive immune responses. Protein A binds immunoglobulins at their Fc portion, interacts with the VH3 domain of B cell receptors inappropriately stimulating B cell proliferation and apoptosis, binds to von Willebrand factor A1 domains to activate intracellular clotting, and also binds to the TNF Receptor-1 to contribute to the pathogenesis of staphylococcal pneumonia. Due to the fact that Protein A captures immunoglobulin and displays toxic attributes, the possibility that this surface molecule may function as a vaccine in humans has not been rigorously pursued. Here the inventors demonstrate that antibodies specific for Protein A stimulate or enhance an immune response to other bacterial antigens.

Embodiments include the use of antibodies that specifically bind Protein A and peptides that elicit such antibodies in methods and compositions for the treatment, attenuation, or prevention of bacterial and/or staphylococcal infection and/or pathological conditions resulting from such an infection. Furthermore, the present invention provides methods and compositions that can be used to treat (e.g., limiting staphylococcal abscess formation and/or persistence in a subject), attenuate, or prevent bacterial infection or pathological conditions resulting from such infection.

In certain aspects, methods for stimulating or enhancing an immune response involve administering to the subject an effective amount of an isolated protein A (SpA) specific antibody and a bacterial antigen. The bacterial antigen or immunogenic fragment can be administered before, after, and/or concurrently with the protein A specific antibody. The bacterial antigen or immunogenic fragment and the Protein A specific antibody can be administered in the same or a separate composition.

In a further aspect, the methods include stimulating or enhancing an immune response involving administering an SpA polypeptide variant prior to or after the administration of one or more bacterial antigens. The SpA polypeptide variant can be administered 12, 24, 48, 72 hours, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 days before or after administration of one or more bacterial antigen. In certain aspects, a subject administered a SpA polypeptide variant can be evaluated for production of SpA specific antibodies prior to administration of one or more bacterial antigens or bacteria. In certain embodiments a SpA polypeptide variant can be administered 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more times prior to or after administration of one or more bacterial antigen or bacteria. In certain embodiments the SpA variant is a full length SpA variant comprising a variant A, B, C, D, and/or E domain. In certain aspects, the SpA variant comprises or consists of the amino acid sequence that is 80, 90, 95, 98, 99, or 100% identical to the amino acid sequence of SEQ ID NO:34. In other embodiments the SpA variant comprises a segment of SpA. The SpA segment can comprise at least or at most 1, 2, 3, 4, 5 or more IgG binding domains. The IgG domains can be at least or at most 1, 2, 3, 4, 5 or more variant A, B, C, D, or E domains. In certain aspects the SpA variant comprises at least or at most 1, 2, 3, 4, 5, or more variant A domains. In a further aspect the SpA variant comprises at least or at most 1, 2, 3, 4, 5, or more variant B domains. In still a further aspect the SpA variant comprises at least or at most 1, 2, 3, 4, 5, or more variant C domains. In yet a further aspect the SpA variant comprises at least or at most 1, 2, 3, 4, 5, or more variant D domains. In certain aspects the SpA variant comprises at least or at most 1, 2, 3, 4, 5, or more

variant E domains. In a further aspect the SpA variant comprises a combination of A, B, C, D, and E domains in various combinations and permutations. The combinations can include all or part of a SpA signal peptide segment, a SpA region X segment, and/or a SpA sorting signal segment. In other aspects the SpA variant does not include a SpA signal peptide segment, a SpA region X segment, and/or a SpA sorting signal segment. In certain aspects a variant A domain comprises a substitution at position(s) 7, 8, 34, and/or 35 of SEQ ID NO:4. In another aspect a variant B domain comprises a substitution at position(s) 7, 8, 34, and/or 35 of SEQ ID NO:6. In still another aspect a variant C domain comprises a substitution at position(s) 7, 8, 34, and/or 35 of SEQ ID NO:5. In certain aspects a variant D domain comprises a substitution at position(s) 9, 10, 36, and/or 37 of SEQ ID NO:2. In a further aspect a variant E domain comprises a substitution at position(s) 6, 7, 33, and/or 34 of SEQ ID NO:3. In certain aspects, an SpA domain D variant or its equivalent can comprise a mutation at position 9 and 36; 9 and 37; 9 and 10; 36 and 37; 10 and 36; 10 and 37; 9, 36, and 37; 10, 36, and 37, 9, 10 and 36; or 9, 10 and 37 of SEQ ID NO:2. In a further aspect, analogous mutations can be included in one or more of domains A, B, C, or E. In further aspects, the amino acid glutamine (Q) at position 9 of SEQ ID NO:2 (or its analogous amino acid in other SpA domains) can be replaced with an alanine (A), an asparagine (N), an aspartic acid (D), a cysteine (C), a glutamic acid (E), a phenylalanine (F), a glycine (G), a histidine (H), an isoleucine (I), a lysine (K), a leucine (L), a methionine (M), a proline (P), a serine (S), a threonine (T), a valine (V), a tryptophane (W), or a tyrosine (Y). In some aspects the glutamine at position 9 can be substituted with an arginine (R). In a further aspect, the glutamine at position 9 of SEQ ID NO:2, or its equivalent, can be substituted with a lysine or a glycine. Any 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more of the substitutions can be explicitly excluded. In another aspect, the amino acid glutamine (Q) at position 10 of SEQ ID NO:2 (or its analogous amino acid in other SpA domains) can be replaced with an alanine (A), an asparagine (N), an aspartic acid (D), a cysteine (C), a glutamic acid (E), a phenylalanine (F), a glycine (G), a histidine (H), an isoleucine (I), a lysine (K), a leucine (L), a methionine (M), a proline (P), a serine (S), a threonine (T), a valine (V), a tryptophane (W), or a tyrosine (Y). In some aspects the glutamine at position 10 can be substituted with an arginine (R). In a further aspect, the glutamine at position 10 of SEQ ID NO:2, or its equivalent, can be substituted with a lysine or a glycine. Any 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more of the substitutions can be explicitly excluded. In certain aspects, the aspartic acid (D) at position 36 of SEQ ID NO:2 (or its analogous amino acid in other SpA domains) can be replaced with an alanine (A), an asparagine (N), an arginine (R), a cysteine (C), a phenylalanine (F), a glycine (G), a histidine (H), an isoleucine (I), a lysine (K), a leucine (L), a methionine (M), a proline (P), a glutamine (Q), a serine (S), a threonine (T), a valine (V), a tryptophane (W), or a tyrosine (Y). In some aspects the aspartic acid at position 36 can be substituted with a glutamic acid (E). In certain aspects, an aspartic acid at position 36 of SEQ ID NO:2, or its equivalent, can be substituted with an alanine or a serine. Any 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more of the substitutions can be explicitly excluded. In another aspect, the aspartic acid (D) at position 37 of SEQ ID NO:2 (or its analogous amino acid in other SpA domains) can be replaced with an alanine (A), an asparagine (N), an arginine (R), a cysteine (C), a phenylalanine (F), a glycine (G), a histidine (H), an isoleucine (I), a lysine (K), a leucine (L), a

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methionine (M), a proline (P), a glutamine (Q), a serine (S), a threonine (T), a valine (V), a tryptophane (W), or a tyrosine (Y). In some aspects the aspartic acid at position 37 can be substituted with a glutamic acid (E). In certain aspects, an aspartic acid at position 37 of SEQ ID NO:2, or its equivalent, can be substituted with an alanine or a serine. Any 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more of the substitutions can be explicitly excluded. In a particular embodiment the amino at position 9 of SEQ ID NO:2 (or an analogous amino acid in another SpA domain) is replaced by an alanine (A), a glycine (G), an isoleucine (I), a leucine (L), a proline (P), a serine (S), or a valine (V). In certain aspects the amino acid at position 9 of SEQ ID NO:2 is replaced by a glycine. In a further aspect the amino acid at position 9 of SEQ ID NO:2 is replaced by a lysine. In a particular embodiment the amino at position 10 of SEQ ID NO:2 (or an analogous amino acid in another SpA domain) is replaced by an alanine (A), a glycine (G), an isoleucine (I), a leucine (L), a proline (P), a serine (S), or a valine (V). In certain aspects the amino acid at position 10 of SEQ ID NO:2 is replaced by a glycine. In a further aspect the amino acid at position 10 of SEQ ID NO:2 is replaced by a lysine. In a particular embodiment the amino at position 36 of SEQ ID NO:2 (or an analogous amino acid in another SpA domain) is replaced by an alanine (A), a glycine (G), an isoleucine (I), a leucine (L), a proline (P), a serine (S), or a valine (V). In certain aspects the amino acid at position 36 of SEQ ID NO:2 is replaced by a serine. In a further aspect the amino acid at position 36 of SEQ ID NO:2 is replaced by an alanine. In a particular embodiment the amino at position 37 of SEQ ID NO:2 (or an analogous amino acid in another SpA domain) is replaced by an alanine (A), a glycine (G), an isoleucine (I), a leucine (L), a proline (P), a serine (S), or a valine (V). In certain aspects the amino acid at position 37 of SEQ ID NO:2 is replaced by a serine. In a further aspect the amino acid at position 37 of SEQ ID NO:2 is replaced by an alanine. In certain aspects the SpA variant includes a substitution of (a) one or more amino acid substitution in an IgG Fc binding sub-domain of SpA domain A, B, C, D, and/or E that disrupts or decreases binding to IgG Fc, and (b) one or more amino acid substitution in a V_H3 binding sub-domain of SpA domain A, B, C, D, and/or E that disrupts or decreases binding to V_H3 . In still further aspects the amino acid sequence of a SpA variant comprises an amino acid sequence that is at least 50%, 60%, 70%, 80%, 90%, 95%, or 100% identical, including all values and ranges there between, to the amino acid sequence of SEQ ID NOs:2-6. In a further aspect the SpA variant includes (a) one or more amino acid substitution in an IgG Fc binding sub-domain of SpA domain D, or at a corresponding amino acid position in other IgG domains, that disrupts or decreases binding to IgG Fc, and (b) one or more amino acid substitution in a V_H3 binding sub-domain of SpA domain D, or at a corresponding amino acid position in other IgG domains, that disrupts or decreases binding to V_H3 . In certain aspects amino acid residue F5, Q9, Q10, S11, F13, Y14, L17, N28, I31, and/or K35 (SEQ ID NO:2, QQNNFNKDDQQSAFYEILNMPNLNEAQRNGFIQS-LKDDPSQSTNNVLGEAKKLNES) of the IgG Fc binding sub-domain of domain D are modified or substituted. In certain aspects amino acid residue Q26, G29, F30, S33, D36, D37, Q40, N43, and/or E47 (SEQ ID NO:2) of the V_H3 binding sub-domain of domain D are modified or substituted such that binding to Fc or V_H3 is attenuated. In further aspects corresponding modifications or substitutions can be engineered in corresponding positions of the domain A, B, C, and/or E. Corresponding positions are defined by alignment of the domain D amino acid sequence with one or more

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of the amino acid sequences from other IgG binding domains of SpA. In certain aspects the amino acid substitution can be any of the other 20 amino acids. In a further aspect conservative amino acid substitutions can be specifically excluded from possible amino acid substitutions. In other aspects only non-conservative substitutions are included. In any event, any substitution or combination of substitutions that reduces the binding of the domain such that SpA toxicity is significantly reduced is contemplated. The significance of the reduction in binding refers to a variant that produces minimal to no toxicity when introduced into a subject and can be assessed using in vitro methods described herein. In certain embodiments, a variant SpA comprises at least or at most 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more variant SpA domain D peptides. In certain aspects 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19 or more amino acid residues of the variant SpA are substituted or modified—including but not limited to amino acids F5, Q9, Q10, S11, F13, Y14, L17, N28, I31, and/or K35 (SEQ ID NO:2) of the IgG Fc binding sub-domain of domain D and amino acid residue Q26, G29, F30, S33, D36, D37, Q40, N43, and/or E47 (SEQ ID NO:2) of the V_H3 binding sub-domain of domain D. In one aspect of the invention glutamine residues at position 9 and/or 10 of SEQ ID NO:2 (or corresponding positions in other domains) are mutated. In another aspect, aspartic acid residues 36 and/or 37 of SEQ ID NO:2 (or corresponding positions in other domains) are mutated. In a further aspect, glutamine 9 and 10, and aspartic acid residues 36 and 37 are mutated. Purified non-toxigenic SpA or SpA-D mutants/variants described herein are no longer able to significantly bind (i.e., demonstrate attenuated or disrupted binding affinity) Fcγ or F(ab)₂ V_H3 and also do not stimulate B cell apoptosis. These non-toxigenic Protein A variants can be used to enhance or stimulate an immune response against a bacterial antigen, thereby raising humoral immune responses that confer protective immunity against *S. aureus* challenge. Compared to wild-type full-length Protein A or the wild-type SpA-domain D, immunization with SpA-D variants resulted in an increase in Protein A specific antibody. Using a mouse model of staphylococcal challenge and abscess formation, it was observed that immunization with the non-toxigenic Protein A variants generated significant protection from staphylococcal infection and abscess formation. As virtually all *S. aureus* strains express Protein A, immunization of humans with the non-toxigenic Protein A variants can neutralize this virulence factor and thereby establish protective immunity. In certain aspects the protective immunity protects or ameliorates infection by drug resistant strains of *Staphylococcus*, such as USA300 and other MRSA strains. In certain embodiments 1, 2, 3, 4, 5, 6, 7, 8, 9 10 or more SpA variants can be specifically excluded from the claimed invention.

Bacterial antigens include, but are not limited to (i) a secreted virulence factor, and/or a cell surface protein or peptide, or (ii) a recombinant nucleic acid molecule encoding a secreted virulence factor, and/or a cell surface protein or peptide. The bacterial antigen can include one or more of at least or at most 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19 additional staphylococcal antigen or immunogenic fragment thereof, including, but not limited to FnBpA, FnBpB, LukD (GI:2765304), Luke (GI:2765303), LukF (GI:12231006), SasA, SasD, SasG, SasI, SasK, SpA (and variants thereof), Eap, Ebh, Emp, EsaB, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, Coa, Hla (e.g., H35 mutants), IsdC, SasF, vWbp, vWh, 52 kDa vitronectin binding protein (WO 01/60852), Aaa (GenBank

CAC80837), Aap (GenBank accession AJ249487), Ant (GenBank accession NP_372518), autolysin glucosaminidase, autolysin amidase, Cna, collagen binding protein (U.S. Pat. No. 6,288,214), EFB (FIB), Elastin binding protein (EbpS), EPB, FbpA, fibrinogen binding protein (U.S. Pat. No. 6,008,341), Fibronectin binding protein (U.S. Pat. No. 5,840,846), FnbA, FnbB, GehD (US 2002/0169288), HarA, HBP, Immunodominant ABC transporter, IsaA/PisA, laminin receptor, Lipase GehD, MAP, Mg²⁺ transporter, MHC II analogue (U.S. Pat. No. 5,648,240), MRPII, Npase, RNA III activating protein (RAP), SasA, SasB, SasC, SasD, SasK, SBI, SdrF (WO 00/12689), SdrG/Fig (WO 00/12689), SdrH (WO 00/12689), SEA exotoxins (WO 00/02523), SEB exotoxins (WO 00/02523), SitC and Ni ABC transporter, SitC/MntC/saliva binding protein (U.S. Pat. No. 5,801,234), SsaA, SSP-1, SSP-2, and/or Vitronectin binding protein (see PCT publications WO2007/113222, WO2007/113223, WO2006/032472, WO2006/032475, WO2006/032500, each of which is incorporated herein by reference in their entirety). In certain aspects, the bacterial antigen is a staphylococcal antigen. The staphylococcal antigen can be selected from the group consisting of: FnBpA, FnBpB, LukD, LukE, LukF, SasA, SasD, SasG, SasI, SasK, SpA (and variants thereof), Eap, Ebh, Emp, EsaB, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, Coa, Hla (e.g., H35 mutants), IsdC, SasF, vWbp, vWh and immunogenic fragments thereof. In certain aspects the bacterial antigens include one or more of sta001, sta002, sta003, sta004, sta005, sta006, sta007, sta008, sta009, sta010, sta011, sta012, sta013, sta014, sta015, sta016, sta017, sta018, sta019, sta020, sta021, sta022, sta023, sta024, sta025, sta026, sta027, sta028, sta029, sta030, sta031, sta032, sta033, sta034, sta035, sta036, sta037, sta038, sta039, sta040, sta041, sta042, sta043, sta044, sta045, sta046, sta047, sta048, sta049, sta050, sta051, sta052, sta053, sta054, sta055, sta056, sta057, sta058, sta059, sta060, sta061, sta062, sta063, sta064, sta065, sta066, sta067, sta068, sta069, sta070, sta071, sta072, sta073, sta074, sta075, sta076, sta077, sta078, sta079, sta080, sta081, sta082, sta083, sta084, sta085, sta086, sta087, sta088, sta089, sta090, sta091, sta092, sta093, sta094, sta095, sta096, sta097, sta098, sta099, sta100, sta101, sta102, sta103, sta104, sta105, sta106, sta107, sta108, sta109, sta110, sta111, sta112, sta113, sta114, sta115, sta116, sta117, sta118, sta119, sta120, or EsxAB hybrid (SEQ ID NO:155) polypeptide or immunogenic fragment thereof (see PCT publication WO/2010/119343, which is incorporated herein by reference in its entirety).

In certain embodiments, the claimed invention specifically excludes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more of FnBpA, FnBpB, LukD (GI:2765304), LukE (GI:2765303), LukF (GI:12231006), SasA, SasD, SasG, SasI, SasK, SpA (and variants thereof), Eap, Ebh, Emp, EsaB, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, Coa, Hla (e.g., H35 mutants), IsdC, SasF, vWbp, vWh, 52 kDa vitronectin binding protein (WO 01/60852), Aaa (GenBank CAC80837), Aap (GenBank accession AJ249487), Ant (GenBank accession NP_372518), autolysin glucosaminidase, autolysin amidase, Cna, collagen binding protein (U.S. Pat. No. 6,288,214), EFB (FIB), Elastin binding protein (EbpS), EPB, FbpA, fibrinogen binding protein (U.S. Pat. No. 6,008,341), Fibronectin binding protein (U.S. Pat. No. 5,840,846), FnbA, FnbB, GehD (US 2002/0169288), HarA, HBP, Immunodominant ABC transporter, IsaA/PisA, laminin receptor, Lipase GehD, MAP, Mg²⁺ transporter, MHC II analogue (U.S. Pat. No. 5,648,240), MRPII, Npase, RNA III activating protein (RAP), SasA, SasB, SasC, SasD, SasK,

SBI, SdrF (WO 00/12689), SdrG/Fig (WO 00/12689), SdrH (WO 00/12689), SEA exotoxins (WO 00/02523), SEB exotoxins (WO 00/02523), SitC and Ni ABC transporter, SitC/MntC/saliva binding protein (U.S. Pat. No. 5,801,234), SsaA, SSP-1, SSP-2, and/or Vitronectin binding protein (see PCT publications WO2007/113222, WO2007/113223, WO2006/032472, WO2006/032475, WO2006/032500, each of which is incorporated herein by reference in their entirety). In certain aspects, the bacterial antigen is a staphylococcal antigen. The staphylococcal antigen can be selected from the group consisting of: FnBpA, FnBpB, LukD, LukE, LukF, SasA, SasD, SasG, SasI, SasK, SpA (and variants thereof), Eap, Ebh, Emp, EsaB, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, Coa, Hla (e.g., H35 mutants), IsdC, SasF, vWbp, vWh and immunogenic fragments thereof. In certain aspects the bacterial antigens include one or more of sta001, sta002, sta003, sta004, sta005, sta006, sta007, sta008, sta009, sta010, sta011, sta012, sta013, sta014, sta015, sta016, sta017, sta018, sta019, sta020, sta021, sta022, sta023, sta024, sta025, sta026, sta027, sta028, sta029, sta030, sta031, sta032, sta033, sta034, sta035, sta036, sta037, sta038, sta039, sta040, sta041, sta042, sta043, sta044, sta045, sta046, sta047, sta048, sta049, sta050, sta051, sta052, sta053, sta054, sta055, sta056, sta057, sta058, sta059, sta060, sta061, sta062, sta063, sta064, sta065, sta066, sta067, sta068, sta069, sta070, sta071, sta072, sta073, sta074, sta075, sta076, sta077, sta078, sta079, sta080, sta081, sta082, sta083, sta084, sta085, sta086, sta087, sta088, sta089, sta090, sta091, sta092, sta093, sta094, sta095, sta096, sta097, sta098, sta099, sta100, sta101, sta102, sta103, sta104, sta105, sta106, sta107, sta108, sta109, sta110, sta111, sta112, sta113, sta114, sta115, sta116, sta117, sta118, sta119, sta120, or EsxAB hybrid polypeptide or immunogenic fragment thereof

Certain embodiments are directed to an immunogenic composition comprising an isolated Protein A (SpA) specific antibody and a bacterial antigen, wherein the Protein A specific antibody enhances an immune response to the bacterial antigen. In certain aspects, the antibody is a polyclonal antibody, a monoclonal antibody, or an antibody fragment. In still further aspects, the bacterial antigen is comprised in or on a bacteria. The bacteria can be an attenuated bacteria, in particular an attenuated staphylococcal bacteria.

In certain embodiments a subject is administered an SpA polypeptide variant (before or after administering one or more bacterial antigens) or administered a protein A specific antibody in combination with one or more bacterial antigens selected from: FnBpA antigen or immunogenic fragment thereof, FnBpB antigen or immunogenic fragment thereof, LukD antigen or immunogenic fragment thereof, LukE antigen or immunogenic fragment thereof, LukF antigen or immunogenic fragment thereof, SasA antigen or immunogenic fragment thereof, SasD antigen or immunogenic fragment thereof, SasG antigen or immunogenic fragment thereof, SasI antigen or immunogenic fragment thereof, SasK antigen or immunogenic fragment thereof, SpA (and variants thereof) antigen or immunogenic fragment thereof, Eap antigen or immunogenic fragment thereof, Ebh antigen or immunogenic fragment thereof, Emp antigen or immunogenic fragment thereof, EsaB antigen or immunogenic fragment thereof, EsaC antigen or immunogenic fragment thereof, EsxA antigen or immunogenic fragment thereof, EsxB antigen or immunogenic fragment thereof, SdrC antigen or immunogenic fragment thereof, SdrD antigen or immunogenic fragment thereof, SdrE antigen or immuno-

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In other aspects, a subject is administered an SpA polypeptide variant (before or after one or more bacterial antigens) or administered a protein A antibody (before, concurrently or after one or more bacterial antigens) in combination with FnBpA and 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more bacterial antigens selected from FnBpB, LukD, LukE, LukF, SasA, SasD, SasG, SasI, SasK, SpA (and variants thereof), Eap, Ebh, Emp, EsaB, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, Coa, Hla (e.g., H35 mutants), IsdC, SasF, vWbp, vWh, sta001, sta002, sta003, sta004, sta005, sta006, sta007, sta008, sta009, sta010, sta011, sta012, sta013, sta014, sta015, sta016, sta017, sta018, sta019, sta020, sta021, sta022, sta023, sta024, sta025, sta026, sta027, sta028, sta029, sta030, sta031, sta032, sta033, sta034, sta035, sta036, sta037, sta038, sta039, sta040, sta041, sta042, sta043, sta044, sta045, sta046, sta047, sta048, sta049, sta050, sta051, sta052, sta053, sta054, sta055, sta056, sta057, sta058, sta059, sta060, sta061, sta062, sta063, sta064, sta065, sta066, sta067, sta068, sta069.

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sta006, sta007, sta008, sta009, sta010, sta011, sta012, sta013, sta014, sta015, sta016, sta017, sta018, sta019, sta020, sta021, sta022, sta023, sta024, sta025, sta026, sta027, sta028, sta029, sta030, sta031, sta032, sta033, sta034, sta035, sta036, sta037, sta038, sta039, sta040, sta041, sta042, sta043, sta044, sta045, sta046, sta047, sta048, sta049, sta050, sta051, sta052, sta053, sta054, sta055, sta056, sta057, sta058, sta059, sta060, sta061, sta062, sta063, sta064, sta065, sta066, sta067, sta068, sta069, sta070, sta071, sta072, sta073, sta074, sta075, sta076, sta077, sta078, sta079, sta080, sta081, sta082, sta083, sta084, sta085, sta086, sta087, sta088, sta089, sta090, sta091, sta092, sta093, sta094, sta095, sta096, sta097, sta098, sta099, sta100, sta101, sta102, sta103, sta104, sta105, sta106, sta107, sta108, sta109, sta110, sta111, sta112, sta113, sta114, sta115, sta116, sta117, sta118, sta119, sta120, or EsxAB hybrid polypeptide or immunogenic fragment thereof.

In other aspects, a subject is administered an SpA polypeptide variant (before or after one or more bacterial antigens) or administered a protein A antibody (before, concurrently or after one or more bacterial antigens) in combination with vWbp and 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more bacterial antigens selected from FnBpA, FnBpB, LukD, LukE, LukF, SasA, SasD, SasG, SasI, SasK, SpA (and variants thereof), Eap, Ebh, Emp, EsaB, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, Coa, Hla (e.g., H35 mutants), IsdC, SasF, vWh, sta001, sta002, sta003, sta004, sta005, sta006, sta007, sta008, sta009, sta010, sta011, sta012, sta013, sta014, sta015, sta016, sta017, sta018, sta019, sta020, sta021, sta022, sta023, sta024, sta025, sta026, sta027, sta028, sta029, sta030, sta031, sta032, sta033, sta034, sta035, sta036, sta037, sta038, sta039, sta040, sta041, sta042, sta043, sta044, sta045, sta046, sta047, sta048, sta049, sta050, sta051, sta052, sta053, sta054, sta055, sta056, sta057, sta058, sta059, sta060, sta061, sta062, sta063, sta064, sta065, sta066, sta067, sta068, sta069, sta070, sta071, sta072, sta073, sta074, sta075, sta076, sta077, sta078, sta079, sta080, sta081, sta082, sta083, sta084, sta085, sta086, sta087, sta088, sta089, sta090, sta091, sta092, sta093, sta094, sta095, sta096, sta097, sta098, sta099, sta100, sta101, sta102, sta103, sta104, sta105, sta106, sta107, sta108, sta109, sta110, sta111, sta112, sta113, sta114, sta115, sta116, sta117, sta118, sta119, sta120, or EsxAB hybrid polypeptide or immunogenic fragment thereof.

In other aspects, a subject is administered an SpA polypeptide variant (before or after one or more bacterial antigens) or administered a protein A antibody (before, concurrently or after one or more bacterial antigens) in combination with vWh and 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more bacterial antigens selected from FnBpA, FnBpB, LukD, LukE, LukF, SasA, SasD, SasG, SasI, SasK, SpA (and variants thereof), Eap, Ebh, Emp, EsaB, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, Coa, Hla (e.g., H35 mutants), IsdC, SasF, vWbp, sta001, sta002, sta003, sta004, sta005, sta006, sta007, sta008, sta009, sta010, sta011, sta012, sta013, sta014, sta015, sta016, sta017, sta018, sta019, sta020, sta021, sta022, sta023, sta024, sta025, sta026, sta027, sta028, sta029, sta030, sta031, sta032, sta033, sta034, sta035, sta036, sta037, sta038, sta039, sta040, sta041, sta042, sta043, sta044, sta045, sta046, sta047, sta048, sta049, sta050, sta051, sta052, sta053, sta054, sta055, sta056, sta057, sta058, sta059, sta060, sta061, sta062, sta063, sta064, sta065, sta066, sta067, sta068, sta069,

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sta070, sta071, sta072, sta073, sta074, sta075, sta076, sta077, sta078, sta079, sta080, sta081, sta082, sta083, sta084, sta085, sta086, sta087, sta088, sta089, sta090, sta091, sta092, sta093, sta094, sta095, sta096, sta097, sta098, sta099, sta100, sta101, sta102, sta103, sta104, sta105, sta106, sta107, sta108, sta109, sta110, sta111, sta112, sta113, sta114, sta115, sta116, sta117, sta118, sta119, sta120, or EsxAB hybrid polypeptide or immunogenic fragment thereof.

Certain embodiments are directed to the above listed antibody and bacterial antigen combinations comprised in a vaccine composition having a pharmaceutically acceptable excipient.

Further embodiments include methods of making a vaccine comprising the steps of mixing antibody and antigens to make the compositions described herein.

Still further embodiments include methods of preventing or treating staphylococcal infection comprising the step of administering the vaccine as described herein to a patient in need thereof.

Certain embodiments are directed to use of the compositions described herein in the treatment or prevention of bacterial or staphylococcal infection. Certain embodiments are directed to use of the compositions described herein in the treatment or prevention of pathological conditions resulting from bacterial or staphylococcal infection.

A further embodiment includes methods for treating a bacterial infection in a subject comprising providing to a subject having, suspected of having or at risk of developing a bacterial infection effective amounts of an isolated Protein A (SpA) specific antibody and one or more bacterial antigens. In certain aspects, the one or more bacterial antigens are comprised in or on a bacteria, or are isolated recombinant polypeptides or peptides. In a further aspect the bacteria comprising the antigens is an attenuated bacteria, in a particular aspect the attenuated bacteria is a staphylococcal bacteria. In certain aspects the subject is diagnosed with a staphylococcal infection. In various aspects described above, the bacterial antigen is a staphylococcal antigen. The staphylococcal antigen can be selected from the group consisting of: FnBpA, FnBpB, LukD, LukE, LukF, SasA, SasD, SasG, SasI, SasK, SpA (and variants thereof), Eap, Ebh, Emp, EsaB, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, Coa, Hla (e.g., H35 mutants), IsdC, SasF, vWbp, vWh and immunogenic fragments thereof.

The methods further include steps wherein two or more bacterial antigens are provided to the subject. In certain aspects the Protein A (SpA) specific antibody is provided before, after, and/or concurrently with the bacterial antigen. In certain aspects, the Protein A (SpA) specific antibody and the one or more bacterial antigens are provided in the same composition. In a further aspect, the subject is a mammal, particularly human.

Embodiments include methods for enhancing an immune response against a bacterium in a subject. In certain aspects the methods include providing to the subject effective amounts of an isolated Protein A (SpA) specific antibody and one or more antigens from the bacterium. In a further aspect the methods include pre-immunization with an SpA polypeptide variant followed by administration of one or more antigens from the bacterium. Still further aspects include administration of an SpA polypeptide variant after administration of one or more antigens from the bacterium. In certain aspects, one or more bacterial antigens are comprised in or on or produced by a bacteria, or are isolated recombinant polypeptides or peptides. In a further aspect the bacteria comprising the antigens is an attenuated bacteria, in

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a particular aspect the attenuated bacteria is a staphylococcal bacteria. In certain aspects the subject is diagnosed with a staphylococcal infection. In various aspects described above, the bacterial antigen is a staphylococcal antigen. The staphylococcal antigen can be selected from the group consisting of: FnBpA, FnBpB, LukD, LukE, LukF, SasA, SasD, SasG, SasI, SasK, SpA (and variants thereof), Eap, Ebh, Emp, EsaB, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, Coa, Hla (e.g., H35 mutants), IsdC, SasF, vWbp, vWh and immunogenic fragments thereof. In certain aspects the *staphylococcus* bacterium is a *S. aureus* bacterium. In a further aspect, the *staphylococcus* bacterium is resistant to one or more treatments, such as methicillin resistant. In certain aspects the composition is administered more than one time to the subject.

In certain aspects, a bacterium delivering a composition of the invention will be limited or attenuated with respect to prolonged or persistent growth or abscess formation. In yet a further aspect, bacterial antigens can be overexpressed in an attenuated bacterium to further enhance or supplement an immune response or vaccine formulation.

The term "FnBpA protein" refers to a protein that includes isolated wild-type FnBpA polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria FnBpA proteins.

The term "FnBpB protein" refers to a protein that includes isolated wild-type FnBpB polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria FnBpB proteins.

The term "LukD protein" refers to a protein that includes isolated wild-type LukD polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria LukD proteins.

The term "LukE protein" refers to a protein that includes isolated wild-type LukE polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria LukE proteins.

The term "LukF protein" refers to a protein that includes isolated wild-type LukF polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria LukF proteins.

The term "SasA protein" refers to a protein that includes isolated wild-type SasA polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria SasA proteins.

The term "SasD protein" refers to a protein that includes isolated wild-type SasD polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria SasD proteins.

The term "SasG protein" refers to a protein that includes isolated wild-type SasG polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria SasG proteins.

The term "SasI protein" refers to a protein that includes isolated wild-type SasI polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria SasI proteins.

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The term "SasK protein" refers to a protein that includes isolated wild-type SasK polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria SasK proteins.

The term "EsxA protein" refers to a protein that includes isolated wild-type EsxA polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria EsxA proteins.

The term "EsxB protein" refers to a protein that includes isolated wild-type EsxB polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria EsxB proteins.

The term "SdrD protein" refers to a protein that includes isolated wild-type SdrD polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria SdrD proteins.

The term "SdrE protein" refers to a protein that includes isolated wild-type SdrE polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria SdrE proteins.

The term "IsdA protein" refers to a protein that includes isolated wild-type IsdA polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria IsdA proteins.

The term "IsdB protein" refers to a protein that includes isolated wild-type IsdB polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria IsdB proteins.

The term "Eap protein" refers to a protein that includes isolated wild-type Eap polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria Eap proteins.

The term "Ebh protein" refers to a protein that includes isolated wild-type Ebh polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria Ebh proteins.

The term "Emp protein" refers to a protein that includes isolated wild-type Emp polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria Emp proteins.

The term "EsaB protein" refers to a protein that includes isolated wild-type EsaB polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria EsaB proteins.

The term "EsaC protein" refers to a protein that includes isolated wild-type EsaC polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria EsaC proteins.

The term "SdrC protein" refers to a protein that includes isolated wild-type SdrC polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria SdrC proteins.

The term "ClfA protein" refers to a protein that includes isolated wild-type ClfA polypeptides from *staphylococcus*

bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria ClfA proteins.

The term "ClfB protein" refers to a protein that includes isolated wild-type ClfB polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria ClfB proteins.

The term "Coa protein" refers to a protein that includes isolated wild-type Coa polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria Coa proteins.

The term "Hla protein" refers to a protein that includes isolated wild-type Hla polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria Hla proteins.

The term "IsdC protein" refers to a protein that includes isolated wild-type IsdC polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria IsdC proteins.

The term "SasF protein" refers to a protein that includes isolated wild-type SasF polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria SasF proteins.

The term "vWbp protein" refers to a protein that includes isolated wild-type vWbp (von Willebrand factor binding protein) polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria vWbp proteins.

The term "vWh protein" refers to a protein that includes isolated wild-type vWh (von Willebrand factor binding protein homolog) polypeptides from *staphylococcus* bacteria and segments thereof, as well as variants that stimulate an immune response against *staphylococcus* bacteria vWh proteins.

An immune response refers to a humoral response, a cellular response, or both a humoral and cellular response in an organism. An immune response can be measured by assays that include, but are not limited to, assays measuring the presence or amount of antibodies that specifically recognize a protein or cell surface protein, assays measuring T-cell activation or proliferation, and/or assays that measure modulation in terms of activity or expression of one or more cytokines.

In still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to a FnBpA protein. In certain aspects the FnBpA protein will have all or part of the amino acid sequence of accession number A32192/GI: 97812.

In still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an FnBpB protein. In certain aspects the FnBpB protein will have all or part of the amino acid sequence of accession number A32192/GI: 97812.

In still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an LukD protein. In

certain aspects the LukD protein will have all or part of the amino acid sequence of accession number CAA73668/GI: 2765304.

In still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an LukE protein. In certain aspects the LukE protein will have all or part of the amino acid sequence of accession number CAA73667.1/GI: 2765303.

In still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an LukF protein. In certain aspects the LukF protein will have all or part of the amino acid sequence of accession number AAC60446.1/GI: 410007.

In still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an SasA protein. In certain aspects the SasA protein will have all or part of the amino acid sequence of accession number Q06904.2/GI: 93141309.

In still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an SasD protein. In certain aspects the SasD protein will have all or part of the amino acid sequence of accession number AAR15215.1/GI: 38259745.

In still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an SasG protein. In certain aspects the SasG protein will have all or part of the amino acid sequence of accession number Q2G2B2.1/GI: 122540575.

In still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an SasI protein. In certain aspects the SasI protein will have all or part of the amino acid sequence of accession number AAR15295.1/GI: 38259905.

In still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an SasK protein. In certain aspects the SasK protein will have all or part of the amino acid sequence of accession number ZP_06340589.1/GI: 283767674.

In still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an EsxA protein. In certain aspects the EsxA protein will have all or part of the amino acid sequence of SEQ ID NO:11.

In still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an EsxB protein. In certain aspects the EsxB protein will have all or part of the amino acid sequence of SEQ ID NO:12.

In yet still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%,

98%, or 99% identical or similar to an SdrD protein. In certain aspects the SdrD protein will have all or part of the amino acid sequence of SEQ ID NO:13.

In further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an SdrE protein. In certain aspects the SdrE protein will have all or part of the amino acid sequence of SEQ ID NO:14.

In still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an IsdA protein. In certain aspects the IsdA protein will have all or part of the amino acid sequence of SEQ ID NO:15.

In yet still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an IsdB protein. In certain aspects the IsdB protein will have all or part of the amino acid sequence of SEQ ID NO:16.

Embodiments of the invention include compositions that include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to a EsaB protein. In certain aspects the EsaB protein will have all or part of the amino acid sequence of SEQ ID NO:17.

In a further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to a ClfB protein. In certain aspects the ClfB protein will have all or part of the amino acid sequence of SEQ ID NO:18.

In still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an IsdC protein. In certain aspects the IsdC protein will have all or part of the amino acid sequence of SEQ ID NO:19.

In yet further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to a SasF protein. In certain aspects the SasF protein will have all or part of the amino acid sequence of SEQ ID NO:20.

In yet still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to a SdrC protein. In certain aspects the SdrC protein will have all or part of the amino acid sequence of SEQ ID NO:21.

In yet still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to a ClfA protein. In certain aspects the ClfA protein will have all or part of the amino acid sequence of SEQ ID NO:22.

In yet still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an Eap protein. In certain aspects the Eap protein will have all or part of the amino acid sequence of SEQ ID NO:23.

In yet still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%,

98%, or 99% identical or similar to an Ebh protein. In certain aspects the Ebh protein will have all or part of the amino acid sequence of SEQ ID NO:24.

In yet still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an Emp protein. In certain aspects the Emp protein will have all or part of the amino acid sequence of SEQ ID NO:25.

In yet still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an EsaC protein. In certain aspects the EsaC protein will have all or part of the amino acid sequence of SEQ ID NO:26. Sequence of EsaC polypeptides can be found in the protein databases and include, but are not limited to accession numbers ZP_02760162 (GI:168727885), NP_645081.1 (GI:21281993), and NP_370813.1 (GI:15923279), each of which is incorporated herein by reference as of the priority date of this application.

In yet still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to a Coa protein. In certain aspects the Coa protein will have all or part of the amino acid sequence of SEQ ID NO:27.

In yet still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to a Hla protein. In certain aspects the Hla protein will have all or part of the amino acid sequence of SEQ ID NO:28.

In yet still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to a vWa protein. In certain aspects the vWa protein will have all or part of the amino acid sequence of SEQ ID NO:29.

In yet still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to a vWbp protein. In certain aspects the vWbp protein will have all or part of the amino acid sequence of SEQ ID NO:32.

In certain aspects, a polypeptide or segment/fragment can have a sequence that is at least 85%, at least 90%, at least 95%, at least 98%, or at least 99% or more identical to the amino acid sequence of the reference polypeptide. The term "similarity" refers to a polypeptide that has a sequence that has a certain percentage of amino acids that are either identical with the reference polypeptide or constitute conservative substitutions with the reference polypeptides.

The 'sta001' antigen is annotated as '5'-nucleotidase family protein'. In the NCTC 8325 strain sta001 is SAOUHSC_00025 and has amino acid sequence SEQ ID NO:35 (GI:88193846). In the Newman strain it is nwmn_0022 (GI:151220234). It has also been referred to as AdsA and SasH and SA0024.

Useful sta001 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:35 and/or may comprise an amino acid sequence: (a) having 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identity to SEQ ID NO: 35; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO: 35, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20,

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25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta001 proteins include variants of SEQ ID NO: 35. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 35. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 35 while retaining at least one epitope of SEQ ID NO: 35. The final 34 C-terminal amino acids of SEQ ID NO: 35 can usefully be omitted. The first 38 N-terminal amino acids of SEQ ID NO: 35 can usefully be omitted. Other fragments omit one or more protein domains.

The sta002 antigen is annotated as 'lipoprotein'. In the NCTC*8325 strain sta002 is SAOUHSC 00356 and has amino acid sequence SEQ ID NO:36 (GI:88194155). In the Newman strain it is nwmn_0364 (GI:151220576).

Useful sta002 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:36 and/or may comprise an amino acid sequence: (a) having 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identity to SEQ ID NO:36; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:36, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150 or more). These sta002 proteins include variants of SEQ ID NO:36. Preferred 5 fragments of (b) comprise an epitope from SEQ ID NO:36. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:36 while retaining at least one epitope of SEQ ID NO:36. The first 18 N-terminal amino acids of SEQ ID NO:36 can usefully be omitted. Other fragments omit one or more protein domains. sta002₁₉₋₁₈₇ and sta002₁₉₋₁₂₄ are two useful fragments of SEQ ID NO:36 which reduce the antigen's similarity with human proteins.

The 'sta003' antigen is annotated as 'surface protein'. In the NCTC 8325 strain sta003 is SAOUHSC_00400 and has amino acid sequence SEQ ID NO:37 (GI:88194195). In the Newman strain it is nwmn_0401 (GI:151220613).

Useful sta003 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:37 and/or may comprise an amino acid sequence: (a) having 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identity to SEQ ID NO:37; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:37, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta003 proteins include variants of SEQ ID NO:37. Preferred fragments of (b) comprise an epitope from SEQ ID NO:37. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:37 while retaining at least one epitope of SEQ ID NO:37. The first 32 N-terminal amino acids of SEQ ID NO:37 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta004' antigen is annotated as 'Siderophore binding protein FatB'. In the NCTC 8325 strain sta004 is SAOUHSC_00749 and has amino acid sequence SEQ ID NO:38 (GI:88194514). In the Newman strain it is nwmn_0705 (GI:151220917).

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Useful sta004 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:38 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:38; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:38, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta004 proteins include variants of SEQ ID NO:38. Preferred fragments of (b) comprise an epitope from SEQ ID NO:38. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:38 while retaining at least one epitope of SEQ ID NO:38. The first 18 N-terminal amino acids of SEQ ID NO:38 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta005' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta005 is 10 SAOUHSC_01127 and has amino acid sequence SEQ ID NO:39 (GI:88194870). In the Newman strain it is nwmn_1077 (GI:151221289).

Useful sta005 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:39 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:39; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:39, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta005 proteins include variants of SEQ ID NO:39. Preferred fragments of (b) comprise an epitope from SEQ ID NO:39. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:39 while retaining at least one epitope of SEQ ID NO:39. The first 18 N-terminal amino acids of SEQ ID NO:39 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta006' antigen is annotated as 'ferrichrome-binding protein', and has also been referred to as 25 'FhuD2' in the literature. In the NCTC 8325 strain sta006 is SAOUHSC_02554 and has amino acid sequence SEQ ID NO:40 (GI:88196199). In the Newman strain it is nwmn_2185 (GI:151222397).

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

Other fragments omit one or more protein domains. A sta006 antigen may be lipidated e.g. with an acylated N-terminus cysteine. One useful sta006 sequence has a Met-Ala-Ser-sequence at the N-terminus.

The 'sta007' antigen is annotated as 'secretory antigen precursor'. In the NCTC 8325 strain sta007 is SAOUHSC_02571 and has amino acid sequence SEQ ID NO:41 (GI:88196215). In the Newman strain it is nwmn_2199 (GI:151222411). Proteomic analysis has revealed that this protein is secreted or surface-exposed.

Useful sta007 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:41 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:41; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:41, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta007 proteins include variants of SEQ ID NO:41. Preferred fragments of (b) comprise an epitope from SEQ ID NO:41. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:41 while retaining at least one epitope of SEQ ID NO:41. The first 27 N-terminal amino acids of SEQ ID NO:41 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta008' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta008 is SAOUHSC_02650 and has amino acid sequence SEQ ID NO:42 (GI:88196290). In the Newman strain it is nwmn_2270 (GI:151222482).

Useful sta008 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:42 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:42; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:42, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta008 proteins include variants of SEQ ID NO:42. Preferred fragments of (b) comprise an epitope from SEQ ID NO:42. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:42 while retaining at least one epitope of SEQ ID NO:42. The first 17 N-terminal amino acids of SEQ ID NO:42 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta009' antigen is annotated as 'immunoglobulin G-binding protein Sbi'. In the NCTC 8325 strain sta009 is SAOUHSC_02706 and has amino acid sequence SEQ ID NO:43 (GI:88196346). In the Newman strain it is nwmn_2317 (GI:151222529).

Useful sta009 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:43 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:43; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:43, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta009 proteins include variants of SEQ

ID NO:43. Preferred fragments of (b) comprise an epitope from SEQ ID NO:43. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:43 while retaining at least one epitope of SEQ ID NO:43. The first 29 N-terminal amino acids of SEQ ID NO:43 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta010' antigen is annotated as 'immunodominant antigen A'. In the NCTC 8325 strain sta010 is SAOUHSC_02887 and has amino acid sequence SEQ ID NO:44 (GI:88196515). In the Newman strain it is nwmn_2469 (GI:151222681). Proteomic analysis has revealed that this protein is secreted or surface-exposed.

Useful sta010 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:44 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:44; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:44, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta010 proteins include variants of SEQ ID NO:44. Preferred fragments of (b) comprise an epitope from SEQ ID NO:44. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:44 while retaining at least one epitope of SEQ ID NO:44. The first 29 N-terminal amino acids of SEQ ID NO:44 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta011' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta011 is SAOUHSC_00052 and has amino acid sequence SEQ ID NO:45 (GI:88193872).

Useful sta011 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:45 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:45; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:45, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta011 proteins include variants of SEQ ID NO:45. Preferred fragments of (b) comprise an epitope from SEQ ID NO:45. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:45 while retaining at least one epitope of SEQ ID NO:45. The first 23 N-terminal amino acids of SEQ ID NO:45 can usefully be omitted. Other fragments omit one or more protein domains. A sta011 antigen may be lipidated e.g. with an acylated N-terminus cysteine.

The 'sta012' antigen is annotated as 'protein with leader'. In the NCTC 8325 strain sta012 is SAOUHSC_00106 and has amino acid sequence SEQ ID NO:46 (GI:88193919).

Useful sta012 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:46 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:46; and/or (b) com-

prising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:46, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta012 proteins include variants of SEQ ID NO:46. Preferred fragments of (b) comprise an epitope from SEQ ID NO:46. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:46 while retaining at least one epitope of SEQ ID NO:46. The first 21 N-terminal amino acids of SEQ ID NO:46 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta013' antigen is annotated as 'poly-gamma-glutamate capsule biosynthesis protein'. In the NCTC 8325 strain staOB is SAOUHSC_00107 and has amino acid sequence SEQ ID NO:47 (GI:88193920).

Useful sta013 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:47 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:47; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:47, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta013 proteins include variants of SEQ ID NO:47. Preferred fragments of (b) comprise an epitope from SEQ ID NO:47. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:47 while retaining at least one epitope of SEQ ID NO:47. Other fragments omit one or more protein domains.

The 'sta014' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta014 is SAOUHSC_00137 and has amino acid sequence SEQ ID NO:48 (GI:88193950).

Useful sta014 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:48 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:48; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:48, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta014 proteins include variants of SEQ ID NO:48. Preferred fragments of (b) comprise an epitope from SEQ ID NO:48. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:48 while retaining at least one epitope of SEQ ID NO:48. The first 17 N-terminal amino acids of SEQ ID NO:48 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta015' antigen is annotated as 'extracellular solute-binding protein; ROD containing lipoprotein'. In the NCTC 8325 strain sta015 is SAOUHSC_00170 and has amino acid sequence SEQ ID NO:49 (GI:88193980).

Useful sta015 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:49 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:49; and/or (b) com-

prising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:49, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta015 proteins include variants of SEQ ID NO:49. Preferred fragments of (b) comprise an epitope from SEQ ID NO:49. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:49 while retaining at least one epitope of SEQ ID NO:49. The first 18 N-terminal amino acids of SEQ ID NO:49 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta016' antigen is annotated as 'gamma-glutamyl-transpeptidase'. In the NCTC 8325 strain sta016 is SAOUHSC_00171 and has amino acid sequence SEQ ID NO:50 (GI:88193981).

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

The 'sta017' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta017 is SAOUHSC_00186 and has amino acid sequence SEQ ID NO:51 (GI:88193996).

Useful sta017 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:51 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:51; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:51, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta017 proteins include variants of SEQ ID NO:51. Preferred fragments of (b) comprise an epitope from SEQ ID NO:51. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:51 while retaining at least one epitope of SEQ ID NO:51. The first 17 N-terminal amino acids of SEQ ID NO:51 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta018' antigen is annotated as 'extracellular solute-binding protein'. In the NCTC 8325 strain sta018 is SAOUHSC_00201 and has amino acid sequence SEQ ID NO:52 (GI:88194011).

Useful sta018 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:52 and/or may comprise an amino acid sequence: (a) having 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identity to SEQ ID NO:52; and/or (b) comprising a fragment

of at least 'n' consecutive amino acids of SEQ ID NO:52, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta018 proteins include variants of SEQ ID NO:52. Preferred fragments of (b) comprise an epitope from SEQ ID NO:52. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:52 while retaining at least one epitope of SEQ ID NO:52. Other fragments omit one or more protein domains.

The 'sta019' antigen is annotated as 'peptidoglycan hydrolase'. In the NCTC 8325 strain sta019 is SAOUHSC_00248 and has amino acid sequence SEQ ID NO:53 (GI:88194055). In the Newman strain it is nwmm_0210 (GI:151220422).

Useful sta019 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:53 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:53; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:53, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta019 proteins include variants of SEQ ID NO:53. Preferred fragments of (b) comprise an epitope from SEQ ID NO:53. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:53 while retaining at least one epitope of SEQ ID NO:53. The first 25 N-terminal amino acids of SEQ ID NO:53 can usefully be omitted. Other fragments omit one or more protein domains.

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

The 'sta020' antigen is annotated as 'exported protein'. In the NCTC 8325 strain sta020 is SAOUHSC_00253 and has amino acid sequence SEQ ID NO:54 (GI:88 194059).

Useful sta020 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:54 and/or may comprise an amino acid sequence: (a) having 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identity to SEQ ID NO:54; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:54, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta020 proteins include variants of SEQ ID NO:54. Preferred fragments of (b) comprise an epitope from SEQ ID NO:54. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:54 while retaining at least one epitope of SEQ ID NO:54. The first 30 N-terminal amino acids of SEQ ID NO:54 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta021' antigen is annotated as 'secretory antigen SsaA-like protein'. In the NCTC 8325 strain sta021 is SAOUHSC_00256 and has amino acid sequence SEQ ID NO:55 (GI:88194062).

Useful sta021 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:55 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:55; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:55, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta021 proteins include variants of SEQ ID NO:55. Preferred fragments of (b) comprise an epitope from SEQ ID NO:55. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:55 while retaining at least one epitope of SEQ ID NO:55. The first 24 N-terminal amino acids of SEQ ID NO:55 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta022' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta022 is SAOUHSC_00279 and has amino acid sequence SEQ ID NO:56 (GI:88194083).

Useful sta022 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:56 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:56; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:56, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These sta022 proteins include variants of SEQ ID NO:56. Preferred fragments of (b) comprise an epitope from SEQ ID NO:56. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:56 while retaining at least one epitope of SEQ ID NO:56. The first 17 N-terminal amino acids of SEQ ID NO:56 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta023' antigen is annotated as '5'-nucleotidase; lipoprotein e(P4) family'. In the NCTC 8325 strain sta023 is SAOUHSC_00284 and has amino acid sequence SEQ ID NO:57 (GI:88194087).

Useful sta023 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:57 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:57; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:57, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta023 proteins include variants of SEQ ID NO:57. Preferred fragments of (b) comprise an epitope from SEQ ID NO:57. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:57 while retaining at least one epitope of SEQ ID NO:57. The first 31 N-terminal amino acids of SEQ ID NO:57 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta024' antigen is annotated as 'lipase precursor'. In the NCTC 8325 strain sta024 is SAOUHSC_00300 and has amino acid sequence SEQ ID NO:58 (GI:88194101).

Useful sta024 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:58 and/or may comprise an amino acid sequence: (a) having 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identity to SEQ ID NO:58; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:58, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta024 proteins include variants of SEQ ID NO:58. Preferred fragments of (b) comprise an epitope from SEQ ID NO:58. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:58 while retaining at least one epitope of SEQ ID NO:58. The first 37 N-terminal amino acids of SEQ ID NO:58 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta025' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta025 is SAOUHSC_00362 and has amino acid sequence SEQ ID NO:59 (GI:88194160).

Useful sta025 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:59 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:59; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:59, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta025 proteins include variants of SEQ ID NO:59. Preferred fragments of (b) comprise an epitope from SEQ ID NO:59. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:59 while retaining at least one epitope of SEQ ID NO:59. The first 19 N-terminal amino acids of SEQ ID NO:59 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta026' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta026 is SAOUHSC_00404 and has amino acid sequence SEQ ID NO:60 (GI:88194198).

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

The 'sta027' antigen is annotated as 'probable lipase'. In the NCTC 8325 strain sta027 is SAOUHSC_00661 and has amino acid sequence SEQ ID NO:61 (GI:88194426).

Useful sta027 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:61 and/or may comprise an amino acid sequence: (a) having 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identity to SEQ ID NO:61; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:61, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta027 proteins include variants of SEQ ID NO:61. Preferred fragments of (b) comprise an epitope from SEQ ID NO:61. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:61 while retaining at least one epitope of SEQ ID NO:61. The first 23 N-terminal amino acids of SEQ ID NO:61 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta028' antigen is annotated as 'secretory antigen SsaA-like protein'. In the NCTC 8325 strain sta028 is SAOUHSC_00671 and has amino acid sequence SEQ ID NO:62 (GI:88194436). In the Newman strain it is nwmn_0634 (GI:151220846).

Useful sta028 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:62 and/or may comprise an amino acid sequence: (a) having 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identity to SEQ ID NO:62; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:62, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta028 proteins include variants of SEQ ID NO:62. Preferred fragments of (b) comprise an epitope from SEQ ID NO:62. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:62 while retaining at least one epitope of SEQ ID NO:62. The first 25 N-terminal amino acids of SEQ ID NO:62 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta029' antigen is annotated as 'ferrichrome binding protein'. In the NCTC 8325 strain sta029 is SAOUHSC_00754 and has amino acid sequence SEQ ID NO:63 (GI:88194518).

Useful sta029 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:63 and/or may comprise an amino acid sequence: (a) having 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identity to SEQ ID NO:63; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:63, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta029 proteins include variants of SEQ ID NO:63. Preferred fragments of (b) comprise an epitope from SEQ ID NO:63. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:63 while retaining at least one epitope of SEQ ID NO:63. The final 25 C-terminal amino acids of SEQ ID NO:63 can usefully be omitted. The first 19 N-terminal amino acids of SEQ ID NO:63 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta030' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta030 is SAOUHSC_00808 and has amino acid sequence SEQ ID NO:64 (GI:88194568).

Useful sta030 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:64 and/or may comprise an amino acid sequence: (a) having 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identity to SEQ ID NO:64; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:64, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta030 proteins include variants of SEQ ID NO:64. Preferred fragments of (b) comprise an epitope from SEQ ID NO:64. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:64 while retaining at least one epitope of SEQ ID NO:64. The first 17 N-terminal amino acids of SEQ ID NO:64 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta031' antigen is annotated as '5-nucleotidase family protein'. In the NCTC 8325 strain sta031 is SAOUHSC_00860 and has amino acid sequence SEQ ID NO:65 (GI:88194617).

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

The 'sta032' antigen is annotated as 'serine protease HtrA'. In the NCTC 8325 strain sta032 is SAOUHSC_00958 and has amino acid sequence SEQ ID NO:66 (GI:88194715).

Useful sta032 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:66 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:66; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:66, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta032 proteins include variants of SEQ ID NO:66. Preferred fragments of (b) comprise an epitope from SEQ ID NO:66. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:66 while retaining at least one epitope of SEQ ID NO:66. Other fragments omit one or more protein domains.

The 'sta033' antigen is annotated as 'cysteine protease precursor'. In the NCTC 8325 strain sta033 is SAOUHSC_00987 and has amino acid sequence SEQ ID NO:67 (GI:88194744).

Useful sta033 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:67 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:67; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:67, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta033 proteins include variants of SEQ ID NO:67. Preferred fragments of (b) comprise an epitope from SEQ ID NO:67. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:67 while retaining at least one epitope of SEQ ID NO:67. The first 29 N-terminal amino acids of SEQ ID NO:67 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta034' antigen is annotated as 'glutamyl endopeptidase precursor'. In the NCTC 8325 strain sta034 is SAOUHSC_00988 and has amino acid sequence SEQ ID NO:68 (GI:88194745).

Useful sta034 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:68 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:68; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:68, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta034 proteins include variants of SEQ ID NO:68. Preferred fragments of (b) comprise an epitope from SEQ ID NO:68. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:68 while retaining at least one epitope of SEQ ID NO:68. The first 29 N-terminal amino acids of SEQ ID NO:68 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta035' antigen is annotated as 'fnt protein'. In the NCTC 8325 strain sta035 is SAOUHSC_00998 and has amino acid sequence SEQ ID NO:69 (GI:88194754).

Useful sta035 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:69 and/or may comprise an amino acid sequence: (a) having 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identity to SEQ ID NO:69; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:69, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta035 proteins include variants of SEQ ID NO:69. Preferred fragments of (b) comprise an epitope from SEQ ID NO:69. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:69 while retaining at least one epitope of

SEQ ID NO:69. The first 25 N-terminal amino acids of SEQ ID NO:69 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta036' antigen is annotated as 'iron-regulated protein with leader'. In the NCTC 8325 strain sta036 is SAOUHSC_01084 and has amino acid sequence SEQ ID NO:70 (GI:88194831).

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

The 'sta037' antigen is annotated as 'iron ABC transporter; iron-binding protein IsdE'. In the NCTC 8325 strain sta037 is SAOUHSC 01085 and has amino acid sequence SEQ ID NO:71 (GI:88194832).

Useful sta037 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:71 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:71; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:71, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta037 proteins include variants of SEQ ID NO:71. Preferred fragments of (b) comprise an epitope from SEQ ID NO:71. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:71 while retaining at least one epitope of SEQ ID NO:71. The first 9 N-terminal amino acids of SEQ ID NO:71 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta038' antigen is annotated as 'NPQTN specific sortase B'. In the NCTC 8325 strain sta038 is SAOUHSC_01088 and has amino acid sequence SEQ ID NO:72 (GI:88194835).

Useful sta038 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:72 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:72; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:72, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta038 proteins include variants of SEQ ID NO:72. Preferred fragments of (b) comprise an epitope from SEQ ID NO:72. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or

more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:72 while retaining at least one epitope of SEQ ID NO:72. The first 21 N-terminal amino acids of SEQ ID NO:72 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta039' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta039 is SAOUHSC_01124 and has amino acid sequence SEQ ID NO:73 (GI:88194868).

Useful sta039 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:73 and/or may comprise an amino acid sequence: (a) having 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identity to SEQ ID NO:73; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:73, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta039 proteins include variants of SEQ ID NO:73. Preferred fragments of (b) comprise an epitope from SEQ ID NO:73. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:73 while retaining at least one epitope of SEQ ID NO:73. The first 22 N-terminal amino acids of SEQ ID NO:73 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta040' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta040 is SAOUHSC_011125 and has amino acid sequence SEQ ID NO:74 (GI:88194869). In the Newman strain it is nwmn_1076 (GI:151221288).

Useful sta040 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:74 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:74; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:74, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta040 proteins include variants of SEQ ID NO:74. Preferred fragments of (b) comprise an epitope from SEQ ID NO:74. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:74 while retaining at least one epitope of SEQ ID NO:74. The first 21 N-terminal amino acids of SEQ ID NO:74 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta041' antigen is annotated as 'fibronectin-binding protein A-related'. In the NCTC 8325 strain sta041 is SAOUHSC_01175 and has amino acid sequence SEQ ID NO:75 (GI:88194914).

Useful sta041 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:75 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:75; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:75, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta041 proteins include variants of SEQ

ID NO:75. Preferred fragments of (b) comprise an epitope from SEQ ID NO:75. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:75 while retaining at least one epitope of SEQ ID NO:75. Other fragments omit one or more protein domains.

The 'sta042' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta042 is SAOUHSC_01180 and has amino acid sequence SEQ ID NO:76 (GI:88194919).

Useful sta042 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:76 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:76; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:76, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta042 proteins include variants of SEQ ID NO:76. Preferred fragments of (b) comprise an epitope from SEQ ID NO:76. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:76 while retaining at least one epitope of SEQ ID NO:76. The first 18 N-terminal amino acids of SEQ ID NO:76 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta043', antigen is annotated as 'cell wall hydrolase'. In the NCTC 8325 strain sta043 is SAOUHSC_01219 and has amino acid sequence SEQ ID NO:77 (GI:88194955).

Useful sta043 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:77 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:77; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:77, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta043 proteins include variants of SEQ ID NO:77. Preferred fragments of (b) comprise an epitope from SEQ ID NO:77. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:77 while retaining at least one epitope of SEQ ID NO:77. The first 38 N-terminal amino acids of SEQ ID NO:77 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta044' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta044 is SAOUHSC_01508 and has amino acid sequence SEQ ID NO:78 (GI:88195223).

Useful sta044 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:78 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:78; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:78, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta044 proteins include variants of SEQ ID NO:78. Preferred fragments of (b) comprise an epitope from SEQ ID NO:78. Other preferred fragments lack one or

more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:78 while retaining at least one epitope of SEQ ID NO:78. The first 17 N-terminal amino acids of SEQ ID NO:78 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta045' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta045 is SAOUHSC_01627 and has amino acid sequence SEQ ID NO:79 (GI:88195337).

Useful sta045 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:79 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:79; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:79, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150 or more). These sta045 proteins include variants of SEQ ID NO:79. Preferred fragments of (b) comprise an epitope from SEQ ID NO:79. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:79 while retaining at least one epitope of SEQ ID NO:79. The first 16 N-terminal amino acids of SEQ ID NO:79 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta046' antigen is annotated as 'Excalibur protein'. In the NCTC 8325 strain sta046 is SAOUHSC_01918 and has amino acid sequence SEQ ID NO:80 (GI:88195613).

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

The 'sta047' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta047 is SAOUHSC_01920 and has amino acid sequence SEQ ID NO:81 (GI:88195615).

Useful sta047 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:81 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:81; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:81, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta047 proteins include variants of SEQ ID NO:81. Preferred fragments of (b) comprise an epitope from SEQ ID NO:81. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or

more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:81 while retaining at least one epitope of SEQ ID NO:81. The first 18 N-terminal amino acids of SEQ ID NO:81 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta048' antigen is annotated as 'intracellular serine protease'. In the NCTC 8325 strain sta048 is SAOUHSC_01949 and has amino acid sequence SEQ ID NO:82 (GI:88195642).

Useful sta048 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:82 and/or may comprise an amino acid sequence: (a) having 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identity to SEQ ID NO:82; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:82, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta048 proteins include variants of SEQ ID NO:82. Preferred fragments of (b) comprise an epitope from SEQ ID NO:82. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:82 while retaining at least one epitope of SEQ ID NO:82. The first 27 N-terminal amino acids of SEQ ID NO:82 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta049' antigen is annotated as 'protein export protein PrsA'. In the NCTC 8325 strain sta049 is SAOUHSC_01972 and has amino acid sequence SEQ ID NO:83 (GI:88195663). In the Newman strain it is nwmm_I733 (GI:151221945).

Useful sta049 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:83 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:83; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:83, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta049 proteins include variants of SEQ ID NO:83. Preferred fragments of (b) comprise an epitope from SEQ ID NO:83. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:83 while retaining at least one epitope of SEQ ID NO:83. The first 25 N-terminal amino acids of SEQ ID NO:83 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta050' antigen is annotated as 'staphopain thiol proteinase'. In the NCTC 8325 strain sta050 is SAOUHSC_02127 and has amino acid sequence SEQ ID NO:84 (GI:88195808).

Useful sta050 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:84 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:84; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:84, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta050 proteins include variants of SEQ

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

The 'sta051' antigen is annotated as 'protein with leader'. In the NCTC 8325 strain sta051 is SAOUHSC_02147 and has amino acid sequence SEQ ID NO:85 (GI:88195827).

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

The 'sta052' antigen is annotated as 'ferric hydroxamate receptor I'. In the NCTC 8325 strain sta052 is SAOUHSC_02246 and has amino acid sequence SEQ ID NO:86 (GI:88195918).

Useful sta052 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:86 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:86; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:86, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta052 proteins include variants of SEQ ID NO:86. Preferred fragments of (b) comprise an epitope from SEQ ID NO:86. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:86 while retaining at least one epitope of SEQ ID NO:86. The first 17 N-terminal amino acids of SEQ ID NO:86 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta053' antigen is annotated as 'srdH family protein'. In the NCTC 8325 strain sta053 is SAOUHSC_02257 and has amino acid sequence SEQ ID NO:87 (GI:88195928).

Useful sta053 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:87 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:87; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:87, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta053 proteins include variants of SEQ

ID NO:87. Preferred fragments of (b) comprise an epitope from SEQ ID NO:87. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:87 while retaining at least one epitope of SEQ ID NO:87. The first 26 N-terminal amino acids of SEQ ID NO:87 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta054' antigen is annotated as 'Probable transglycosylase isaA precursor'. In the NCTC 8325 strain sta054 is SAOUHSC_02333 and has amino acid sequence SEQ ID NO:88 (GI:88195999).

Useful sta054 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:88 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:88; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:88, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta054 proteins include variants of SEQ ID NO:88. Preferred fragments of (b) comprise an epitope from SEQ ID NO:88. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:88 while retaining at least one epitope of SEQ ID NO:88. The first 27 N-terminal amino acids of SEQ ID NO:88 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta055' antigen is annotated as 'surface hydrolase'. In the NCTC 8325 strain sta055 is SAOUHSC_02448 and has amino acid sequence SEQ ID NO:89 (GI:88196100).

Useful sta055 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:89 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:89; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:89, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta055 proteins include variants of SEQ ID NO:89. Preferred fragments of (b) comprise an epitope from SEQ ID NO:89. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:89 while retaining at least one epitope of SEQ ID NO:89. The first 31 N-terminal amino acids of SEQ ID NO:89 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta056' antigen is annotated as 'hyaluronate lyase'. In the NCTC 8325 strain sta056 is SAOUHSC_02463 and has amino acid sequence SEQ ID NO:90 (GI:88196115).

Useful sta056 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:90 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:90; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:90, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta056 proteins include variants of SEQ

ID NO:90. Preferred fragments of (b) comprise an epitope from SEQ ID NO:90. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:90 while retaining at least one epitope of SEQ ID NO:90. The first 24 N-terminal amino acids of SEQ ID NO:90 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta057' antigen is annotated as 'secretory antigen precursor SsaA'. In the NCTC 8325 strain sta057 is SAOUHSC_02576 and has amino acid sequence SEQ ID NO:91 (GI:88 196220). In the Newman strain it is nwmn_2203 (GI:151222415).

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

The 'sta058' antigen is annotated as 'Zn-binding lipoprotein adcA-like'. In the NCTC 8325 strain sta058 is SAOUHSC_02690 and has amino acid sequence SEQ ID NO:92 (GI:88196330).

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

The 'sta059' antigen is annotated as 'gamma-hemolysin h-gamma-ii subunit'. In the NCTC 8325 strain sta059 is SAOUHSC_02708 and has amino acid sequence SEQ ID NO:93 (GI:88196348).

Useful sta059 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:93 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:93; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of

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SEQ In NO:93, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta059 proteins include variants of SEQ ID NO:93. Preferred fragments of (b) comprise an epitope from SEQ ID NO:93. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ In NO:93 while retaining at least one epitope of SEQ ID NO:93. The first 20 N-terminal amino acids of SEQ In NO:93 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta060' antigen is annotated as 'peptide ABC transporter; peptide-binding protein'. In the NCTC 8325 strain sta060 IS SAOUHSC 02767 and has amino acid sequence SEQ ID NO:94 (GI:88196403).

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

The 'sta061' antigen is annotated as 'protein with leader'. In the NCTC 8325 strain sta061 is SAOUHSC_02783 and has amino acid sequence SEQ ID NO:95 (GI:88196419).

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

The 'sta062' antigen is annotated as 'protein with leader'. In the NCTC 8325 strain sta062 is SAOUHSC_02788 and has amino acid sequence SEQ ID NO:96 (GI:88 196424).

Useful sta062 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:96 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:96; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of

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SEQ ID NO:96, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta062 proteins include variants of SEQ ID NO:96. Preferred fragments of (b) comprise an epitope from SEQ ID NO:96. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:96 while retaining at least one epitope of SEQ ID NO:96. The first 22 N-terminal amino acids of SEQ ID NO:96 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta063' antigen is annotated as 'auricolysin'. In the NCTC 8325 strain sta063 is SAOUHSC_02971 and has amino acid sequence SEQ ID NO:97 (GI:88196592).

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

The 'sta064' antigen is annotated as 'lipase'. In the NCTC 8325 strain sta064 is SAOUHSC_03006 and has amino acid sequence SEQ ID NO:98 (GI:88 196625). In the Newman strain it is nwmn 2569 (GI:151222781).

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

The 'sta065' antigen is annotated as '1-phosphatidylinositol phosphodiesterase precursor'. In the NCTC 8325 strain sta065 is SAOUHSC 00051 and has amino acid sequence SEQ ID NO:99 (GI:88193871).

Useful sta065 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:99 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:99; and/or (b) com-

prising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:99, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta065 proteins include variants of SEQ ID NO:99. Preferred fragments of (b) comprise an epitope from SEQ ID NO:99. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:99 while retaining at least one epitope of SEQ ID NO:99. The first 26 N-terminal amino acids of SEQ ID NO:99 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta066' antigen is annotated as 'protein'. In the NCTC 8325 strain sta066 is SAOUHSC_00172 and has amino acid sequence SEQ ID NO:100 (GI:88193982).

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

The 'sta067' antigen is annotated as 'bacterial extracellular solute-binding protein'. In the NCTC 8325 strain sta067 is SAOUHSC_00176 and has amino acid sequence SEQ ID NO:101 (GI:88 193986).

Useful sta067 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:101 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:101; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:101, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta067 proteins include variants of SEQ ID NO:101. Preferred fragments of (b) comprise an epitope from SEQ ID NO:101. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:101 while retaining at least one epitope of SEQ ID NO:101. The first 20 N-terminal amino acids of SEQ ID NO:101 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta068' antigen is annotated as 'iron permease FTR1'. In the NCTC 8325 strain sta068 is SAOUHSC_00327 and has amino acid sequence SEQ ID NO:102 (GI:88194127).

Useful sta068 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:102 and/or may comprise an amino acid sequence: (a) having

50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:102; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:102, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta068 proteins include variants of SEQ ID NO:102. Preferred fragments of (b) comprise an epitope from SEQ ID NO:102. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:102 while retaining at least one epitope of SEQ ID NO:102. The final 20 C-terminal amino acids of SEQ ID NO:102 can usefully be omitted. The first 14 N-terminal amino acids of SEQ ID NO:102 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta069' antigen is annotated as 'autolysin precursor'. In the NCTC 8325 strain sta069 is SAOUHSC_00427 and has amino acid sequence SEQ ID NO:103 (GI:88194219).

Useful sta069 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:103 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:103; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:103, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta069 proteins include variants of SEQ ID NO:103. Preferred fragments of (b) comprise an epitope from SEQ ID NO:103. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:103 while retaining at least one epitope of SEQ ID NO:103. The first 25 N-terminal amino acids of SEQ ID NO:103 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta070' antigen is annotated as 'immunogenic secreted precursor-like protein (truncated)'. In the NCTC 8325 strain sta070 is SAOUHSC_00773 and has amino acid sequence SEQ ID NO:104 (GI:88194535).

Useful sta070 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:104 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:104; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:104, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta070 proteins include variants of SEQ ID NO:104. Preferred fragments of (b) comprise an epitope from SEQ ID NO:104. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:104 while retaining at least one epitope of SEQ ID NO:104. The first 24 N-terminal amino acids of SEQ ID NO:104 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta071' antigen is annotated as 'hemolysin'. In the NCTC 8325 strain sta071 is SAOUHSC_00854 and has amino acid sequence SEQ ID NO:105 (GI:88194612).

Useful sta071 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:105 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:105; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:105, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta071 proteins include variants of SEQ ID NO:105. Preferred fragments of (b) comprise an epitope from SEQ ID NO:105. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:105 while retaining at least one epitope of SEQ ID NO:105. The first 24 N-terminal amino acids of SEQ ID NO:105 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta072' antigen is annotated as 'extramembranal protein'. In the NCTC 8325 strain sta072 is SAOUHSC_00872 and has amino acid sequence SEQ ID NO:106 (GI:88194629).

Useful sta072 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:106 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:106; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:106, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta072 proteins include variants of SEQ ID NO:106. Preferred fragments of (b) comprise an epitope from SEQ ID NO:106. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:106 while retaining at least one epitope of SEQ ID NO:106. The first 24 N-terminal amino acids of SEQ ID NO:106 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta073' antigen is annotated as 'bifunctional autolysin precursor'. In the NCTC 8325 strain sta073 is SAOUHSC_00994 and has amino acid sequence SEQ ID NO:107 (GI:88194750). In the Newman strain it is nwmn_0922 (GI:151221134). Proteomic analysis has revealed that this protein is secreted or surface-exposed.

Useful sta073 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:107 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:107; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:107, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta073 proteins include variants of SEQ ID NO:107. Preferred fragments of (b) comprise an epitope from SEQ ID NO:107. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or

one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:107 while retaining at least one epitope of SEQ ID NO:107. The first 24 N-terminal amino acids of SEQ ID NO:107 can usefully be omitted. Other fragments omit one or more protein domains.

A Sta073 antigen can usefully be included in a composition in combination with a Sta112. Sta073 does not adsorb well to aluminium hydroxide adjuvants, so Sta073 present in a composition may be unadsorbed or may be adsorbed to an alternative adjuvant e.g. to an aluminium phosphate.

The 'sta074' antigen is annotated as 'factor essential for methicillin resistance'. In the NCTC 8325 strain sta074 is SAOUHSC_01220 and has amino acid sequence SEQ ID NO:108 (GI:88194956).

Useful sta074 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:108 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:108; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:108, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta074 proteins include variants of SEQ ID NO:108. Preferred fragments of (b) comprise an epitope from SEQ ID NO:108. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:108 while retaining at least one epitope of SEQ ID NO:108. Other fragments omit one or more protein domains.

The 'sta075' antigen is annotated as 'insulysin; peptidase family M16'. In the NCTC 8325 strain sta075 is SAOUHSC_01256 and has amino acid sequence SEQ ID NO:109 (GI:88194989).

Useful sta075 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:109 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:109; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:109, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta075 proteins include variants of SEQ ID NO:109. Preferred fragments of (b) comprise an epitope from SEQ ID NO:109. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:109 while retaining at least one epitope of SEQ ID NO:109. Other fragments omit one or more protein domains.

The 'sta076' antigen is annotated as 'hydrolase'. In the NCTC 8325 strain sta076 is SAOUHSC_01263 and has amino acid sequence SEQ ID NO:110 (GI:88194996).

Useful sta076 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:110 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:110; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:110, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100,

150, 200, 250 or more). These sta076 proteins include variants of SEQ ID NO:110. Preferred fragments of (b) comprise an epitope from SEQ ID NO:110. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:110 while retaining at least one epitope of SEQ ID NO:110. The first 24 N-terminal amino acids of SEQ ID NO:110 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta077' antigen is annotated as 'protein'. In the NCTC 8325 strain sta077 is SAOUHSC_01317 and has amino acid sequence SEQ ID NO:111 (GI:88195047). Pro-

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tomic analysis has revealed that this protein is secreted or surface-exposed.

Useful sta077 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:111 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:111; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:111, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta077 proteins include variants of SEQ ID NO:111. Preferred fragments of (b) comprise an epitope from SEQ ID NO:111. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:111 while retaining at least one epitope of SEQ ID NO:111. The first 20 N-terminal amino acids of SEQ ID NO:111 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta078' antigen is annotated as 'FtsK/SpoIIIE family protein'. In the NCTC 8325 strain sta078 is SAOUHSC_01857 and has amino acid sequence SEQ ID NO:112 (GI:88195555).

Useful sta078 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:112 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:112; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:112, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta078 proteins include variants of SEQ ID NO:112. Preferred fragments of (b) comprise an epitope from SEQ ID NO:112. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:112 while retaining at least one epitope of SEQ ID NO:112. Other fragments omit one or more protein domains.

The 'sta079' antigen is annotated as 'serine protease SpIF'. In the NCTC 8325 strain sta079 is SAOUHSC_01935 and has amino acid sequence SEQ ID NO:113 (GI:88195630).

Useful sta079 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:113 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%,

99%, 30 99.5% or more) to SEQ ID NO:113; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:113, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta079 proteins include variants of SEQ ID NO:113. Preferred fragments of (b) comprise an epitope from SEQ ID NO:113. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the 35 C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:113 while retaining at least one epitope of SEQ ID NO:113. The first 36 N-terminal amino acids of SEQ ID NO:113 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta080' antigen is annotated as 'serine protease SpIE'. In the NCTC 8325 strain sta080 is SAOUHSC_01936 and has amino acid sequence SEQ ID NO:114 (GI:88195631).

Useful sta080 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:114 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:114; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:114, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta080 proteins include variants of SEQ ID NO:114. Preferred fragments of (b) comprise an epitope from SEQ ID NO:114. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:114 while retaining at least one epitope of SEQ ID NO:114. The first 36 N-terminal amino acids of SEQ ID NO:114 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta081' antigen is annotated as 'serine protease SpID (EC:3.4.21.19)'. In the NCTC 8325 strain sta081 is SAOUHSC_01938 and has amino acid sequence SEQ ID NO:154 (GI:88195633).

Useful sta081 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:154 and/or may comprise an amino acid sequence: (a) having 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more identity to SEQ ID NO:154; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:154, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta081 proteins include variants of SEQ ID NO:154. Preferred fragments of (b) comprise an epitope from SEQ ID NO:154. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from 30 the N-terminus of SEQ ID NO:154 while retaining at least one epitope of SEQ ID NO:154. The first 36 N-terminal amino acids of SEQ ID NO:154 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta082' antigen is annotated as 'serine protease SpIC'. In the NCTC 8325 strain sta082 is SAOUHSC_01939 and has amino acid sequence SEQ ID NO:115 (GI:88195634).

Useful sta082 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:115 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:115; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:115, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta082 proteins include variants of SEQ ID NO:115. Preferred fragments of (b) comprise an epitope from SEQ ID NO:115. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:115 while retaining at least one epitope of SEQ ID NO:115. The first 36 N-terminal amino acids of SEQ ID NO:115 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta083' antigen is annotated as 'serine protease SplB'. In the NCTC 8325 strain sta083 is SAOUHSC_01941 and has amino acid sequence SEQ ID NO:116 (GI:88195635).

Useful sta083 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:116 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:116; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:116, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta083 proteins include variants of SEQ ID NO:116. Preferred fragments of (b) comprise an epitope from SEQ ID NO:116. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:116 while retaining at least one epitope of SEQ ID NO:116. The first 36 N-terminal amino acids of SEQ ID NO:116 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta084' antigen is annotated as 'serine protease SplA'. In the NCTC 8325 strain sta084 is SAOUHSC_01942 and has amino acid sequence SEQ ID NO:117 (GI:88195636).

Useful sta084 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:117 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:117; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:117, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta084 proteins include variants of SEQ ID NO:117. Preferred fragments of (b) comprise an epitope from SEQ ID NO:117. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:117 while retaining at least one epitope of SEQ ID NO:117. The first 36 N-terminal amino acids of SEQ ID NO:117 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta085' antigen is annotated as 'staphylokinase precursor'. In the NCTC 8325 strain sta085 is SAOUHSC_02171 and has amino acid sequence SEQ ID NO:118 (GI:88195848).

Useful sta085 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:118 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:118; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:118, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150 or more). These sta085 proteins include variants of SEQ ID NO:118. Preferred fragments of (b) comprise an epitope from SEQ ID NO:118. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:118 while retaining at least one epitope of SEQ ID NO:118. The first 27 N-terminal amino acids of SEQ ID NO:118 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta086' antigen is annotated as 'OxaA-like protein'. In the NCTC 8325 strain sta086 is SAOUHSC_02327 and has amino acid sequence SEQ ID NO:119 (GI:88195993).

Useful sta086 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:119 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:119; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:119, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta086 proteins include variants of SEQ ID NO:119. Preferred fragments of (b) comprise an epitope from SEQ ID NO:119. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:119 while retaining at least one epitope of SEQ ID NO:119. The first 19 N-terminal amino acids of SEQ ID NO:119 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta087' antigen is annotated as 'teicoplanin resistance protein TcaA'. In the NCTC 8325 strain sta087 is SAOUHSC_02635 and has amino acid sequence SEQ ID NO:120 (GI:88196276).

Useful sta087 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:120 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:120; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:120, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta087 proteins include variants of SEQ ID NO:120. Preferred fragments of (b) comprise an epitope from SEQ ID NO:120. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:120.

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while retaining at least one epitope of SEQ ID NO:120. Other fragments omit one or more protein domains.

The 'sta088' antigen is annotated as 'esterase'. In the NCTC 8325 strain sta088 is SAOUHSC_02844 and has amino acid sequence SEQ ID NO:121 (GI:88196477).

Useful sta088 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:121 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:121; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:121, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta088 proteins include variants of SEQ ID NO:121. Preferred fragments of (b) comprise an epitope from SEQ ID NO:121. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:121 while retaining at least one epitope of SEQ ID NO:121. The first 18 N-terminal amino acids of SEQ ID NO:121 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta089' antigen is annotated as 'LysM domain protein'. In the NCTC 8325 strain sta089 is SAOUHSC_02855 and has amino acid sequence SEQ ID NO:122 (GI:88196486).

Useful sta089 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:122 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:122; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:122, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These sta089 proteins include variants of SEQ ID NO:122. Preferred fragments of (b) comprise an epitope from SEQ ID NO:122. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:122 while retaining at least one epitope of SEQ ID NO:122. The first 20 N-terminal amino acids of SEQ ID NO:122 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta090' antigen is annotated as 'LysM domain protein'. In the NCTC 8325 strain sta090 is SAOUHSC_02883 and has amino acid sequence SEQ ID NO:123 (GI:88196512).

Useful sta090 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:123 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:123; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:123, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta090 proteins include variants of SEQ ID NO:123. Preferred fragments of (b) comprise an epitope from SEQ ID NO:123. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15,

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20, 25 or more) from the N-terminus of SEQ ID NO:123 while retaining at least one epitope of SEQ ID NO:123. The first 26 N-terminal amino acids of SEQ ID NO:123 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta091' antigen is annotated as 'lipoprotein'. In the NCTC 8325 strain sta091 is SAOUHSC_00685 and has amino acid sequence SEQ ID NO:124 (GI:88194450).

Useful sta091 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:124 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:124; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:124, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These sta091 proteins include variants of SEQ ID NO:124. Preferred fragments of (b) comprise an epitope from SEQ ID NO:124. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:124 while retaining at least one epitope of SEQ ID NO:124. The first 15 N-terminal amino acids of SEQ ID NO:124 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta092' antigen is annotated as 'M23/M37 peptidase domain protein'. In the NCTC 8325 strain sta092 is SAOUHSC_00174 and has amino acid sequence SEQ ID NO:125 (GI:88193984).

Useful sta092 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:125 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:125; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:125, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150 or more). These sta092 proteins include variants of SEQ ID NO:125. Preferred fragments of (b) comprise an epitope from SEQ ID NO:125. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:125 while retaining at least one epitope of SEQ ID NO:125. The first 25 N-terminal amino acids of SEQ ID NO:125 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta093' antigen is annotated as 'protein'. In the NCTC 8325 strain sta093 is SAOUHSC_01854 and has amino acid sequence SEQ ID NO:126 (GI:88195552).

Useful sta093 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:126 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:126; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:126, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta093 proteins include variants of SEQ ID NO:126. Preferred fragments of (b) comprise an epitope from SEQ ID NO:126. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or

one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:126 while retaining at least one epitope of SEQ ID NO:126. Other fragments omit one or more protein domains.

The 'sta094' antigen is annotated as 'protein'. In the NCTC 8325 strain sta094 is SAOUHSC_01512 and has amino acid sequence SEQ ID NO:127 (GI:88195226).

Useful sta094 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:127 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:127; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:127, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta094 proteins include variants of SEQ ID NO:127. Preferred fragments of (b) comprise an epitope from SEQ ID NO:127. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:127 while retaining at least one epitope of SEQ ID NO:127. The first 17 N-terminal amino acids of SEQ ID NO:127 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta095' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta095 is SAOUHSC_00383 and has amino acid sequence SEQ ID NO:128 (GI:88194180). In the Newman strain it is nwmn_0388 (GI:151220600).

Useful sta095 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:128 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:128; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:128, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta095 proteins include variants of SEQ ID NO:128. Preferred fragments of (b) comprise an epitope from SEQ ID NO:128. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:128 while retaining at least one epitope of SEQ ID NO:128. The first 32 N-terminal amino acids of SEQ ID NO:128 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta096' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta096 is SAOUHSC_00384 and has amino acid sequence SEQ ID NO:129 (GI:88194181). Useful sta096 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:129 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:129; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:129, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta096 proteins include variants of SEQ ID NO:129. Preferred fragments of (b) comprise an epitope from SEQ ID NO:129. Other

preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:129 while retaining at least one epitope of SEQ ID NO:129. The first 30 N-terminal amino acids of SEQ ID NO:129 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta097' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta097 is SAOUHSC_00386 and has amino acid sequence SEQ ID NO:130 (GI:88194182).

Useful sta097 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:130 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:130; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:130, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta097 proteins include variants of SEQ ID NO:130. Preferred fragments of (b) comprise an epitope from SEQ ID NO:130. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:130 while retaining at least one epitope of SEQ ID NO:130. The first 30 N-terminal amino acids of SEQ ID NO:130 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta098' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta098 is SAOUHSC_00389 and has amino acid sequence SEQ ID NO:131 (GI:88194184). In the Newman strain it is nwmn_0391 (GI:151220603).

Useful sta098 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:131 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:131; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:131, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta098 proteins include variants of SEQ ID NO:131. Preferred fragments of (b) comprise an epitope from SEQ ID NO:131. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:131 while retaining at least one epitope of SEQ ID NO:131. The first 30 N-terminal amino acids of SEQ ID NO:131 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta099' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta099 is SAOUHSC_00390 and has amino acid sequence SEQ ID NO:132 (GI:88194185).

Useful sta099 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:132 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:132; and/or (b)

comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:132, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta099 proteins include variants of SEQ ID NO:132. Preferred fragments of (b) comprise an epitope from SEQ ID NO:132. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:132 while retaining at least one epitope of SEQ ID NO:132. The first 30 N-terminal amino acids of SEQ ID NO:132 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta100' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta100 is SAOUHSC_00391 and has amino acid sequence SEQ ID NO:133 (GI:88194186).

Useful sta100 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:133 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:133; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:133, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta100 proteins include variants of SEQ ID NO:133. Preferred fragments of (b) comprise an epitope from SEQ ID NO:133. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:133 while retaining at least one epitope of SEQ ID NO:133. The first 30 N-terminal amino acids of SEQ ID NO:133 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta101' antigen is annotated as 'superantigen-like protein 7'. In the NCTC 8325 strain sta101 is SAOUHSC_00392 and has amino acid sequence SEQ ID NO:134 (GI:88194187). In the Newman strain it is nwrrn_0394 (GI:151220606).

Useful sta101 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:134 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:134; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:134, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta101 proteins include variants of SEQ ID NO:134. Preferred fragments of (b) comprise an epitope from SEQ ID NO:134. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:134 while retaining at least one epitope of SEQ ID NO:134. The first 30 N-terminal amino acids of SEQ ID NO:134 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta102' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta102 is SAOUHSC_00393 and has amino acid sequence SEQ ID NO:135 (GI:88194188).

Useful sta102 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:135 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:135; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:135, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta102 proteins include variants of SEQ ID NO:135. Preferred fragments of (b) comprise an epitope from SEQ ID NO:135. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:135 while retaining at least one epitope of SEQ ID NO:135. The first 17 N-terminal amino acids of SEQ ID NO:135 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta103' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta103 is SAOUHSC_00394 and has amino acid sequence SEQ ID NO:136 (GI:88194189).

Useful sta103 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:136 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:136; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:136, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta103 proteins include variants of SEQ ID NO:136. Preferred fragments of (b) comprise an epitope from SEQ ID NO:136. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:136 while retaining at least one epitope of SEQ ID NO:136. The first 23 N-terminal amino acids of SEQ ID NO:136 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta104' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta104 is SAOUHSC_00395 and has amino acid sequence SEQ ID NO:137 (GI:88194190).

Useful sta104 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:137 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:137; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:137, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta104 proteins include variants of SEQ ID NO:137. Preferred fragments of (b) comprise an epitope from SEQ ID NO:137. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:137 while retaining at least one epitope of SEQ ID NO:137. Other fragments omit one or more protein domains.

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The 'sta105' antigen is annotated as 'superantigen-like protein'. In the NCTC 8325 strain sta105 is 20 SAOUHSC_00399 and has amino acid sequence SEQ ID NO:138 (GI:88194194). In the Newman strain it is nwmn_0400 (GI:151220612).

Useful sta105 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:138 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:138; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:138, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta105 proteins include variants of SEQ ID NO:138. Preferred fragments of (b) comprise an epitope from SEQ ID NO:138. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:138 while retaining at least one epitope of SEQ ID NO:138. The first 30 N-terminal amino acids of SEQ ID NO:138 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta106' antigen is annotated as 'hypothetical protein'. In the NCTC 8325 strain sta106 is SAOUHSC_01115 and has amino acid sequence SEQ ID NO:139 (GI:88194861).

Useful sta106 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:139 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:139; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:139, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These sta106 proteins include variants of SEQ ID NO:139. Preferred fragments of (b) comprise an epitope from SEQ ID NO:139. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:139 while retaining at least one epitope of SEQ ID NO:139. The first 16 N-terminal amino acids of SEQ ID NO:139 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta107' antigen is annotated as 'hypothetical protein'. In the NCTC 8325 strain sta107 is SAOUHSC_00354 and has amino acid sequence SEQ ID NO:140 (GI:88194153).

Useful sta107 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:140 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:140; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:140, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta107 proteins include variants of SEQ ID NO:140. Preferred fragments of (b) comprise an epitope from SEQ ID NO:140. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25

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or more) from the N-terminus of SEQ ID NO:140 while retaining at least one epitope of SEQ ID NO:140. The first 35 N-terminal amino acids of SEQ ID NO:140 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta108' antigen is annotated as 'hypothetical protein'. In the NCTC 8325 strain sta108 is SAOUHSC_00717 and has amino acid sequence SEQ ID NO:141 (GI:88194482).

Useful sta108 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:141 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:141; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:141, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These sta108 proteins include variants of SEQ ID NO:141. Preferred fragments of (b) comprise an epitope from SEQ ID NO:141. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:141 while retaining at least one epitope of SEQ ID NO:141. The first 20 N-terminal amino acids of SEQ ID NO:141 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta109' antigen is annotated as 'N-acetylmuramoyl-L-alanine amidase'. In the NCTC 8325 strain sta109 is SAOUHSC_02979 and has amino acid sequence SEQ ID NO:142 (GI:88196599).

Useful sta109 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:142 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:142; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:142, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta109 proteins include variants of SEQ ID NO:142. Preferred fragments of (b) comprise an epitope from SEQ ID NO:142. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:142 while retaining at least one epitope of SEQ ID NO:142. The first 27 N-terminal amino acids of SEQ ID NO:142 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta110' antigen is annotated as 'hypothetical protein'. In the NCTC 8325 strain sta110 is SAOUHSC_01039 and has amino acid sequence SEQ ID NO:143 (GI:88194791).

Useful sta110 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:143 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:143; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:143, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). These sta110 proteins include variants of SEQ ID NO:143. Preferred fragments of (b) comprise an

epitope from SEQ ID NO:143. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:143 while retaining at least one epitope of SEQ ID NO:143. The first 19 N-terminal amino acids of SEQ ID NO:143 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta111' antigen is annotated as 'hypothetical protein'. In the NCTC 8325 strain sta111 is SAOUHSC_01005 and has amino acid sequence SEQ ID NO:144 (GI: 88194760).

Useful sta111 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:144 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:144; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:144, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These sta111 proteins include variants of SEQ ID NO:144. Preferred fragments of (b) comprise an epitope from SEQ ID NO:144. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:144 while retaining at least one epitope of SEQ ID NO:144. The first 20 N-terminal amino acids of SEQ ID NO:144 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta112' antigen is annotated as a putative 'ABC transporter, substrate-binding protein'. In the NCTC 8325 strain sta112 is SAOUHSC_00634 and has amino acid sequence SEQ ID NO:145 (GI:88194402).

Useful sta112 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:145 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:145; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:145, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta112 proteins include variants of SEQ ID NO:145. Preferred fragments of (b) comprise an epitope from SEQ ID NO:145. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:145 while retaining at least one epitope of SEQ ID NO:145. The first 17 N-terminal amino acids of SEQ ID NO:145 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta113' antigen is annotated as 'hypothetical protein'. In the NCTC 8325 strain sta113 is SAOUHSC_00728 and has amino acid sequence SEQ ID NO:146 (GI: 88194493).

Useful sta113 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:146 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:146; and/or (b) comprising a fragment of at least 'n' consecutive amino

acids of SEQ ID NO:146, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta113 proteins include variants of SEQ ID NO:146. Preferred fragments of (b) comprise an epitope from SEQ ID NO:146. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:146 while retaining at least one epitope of SEQ ID NO:146. The first 173 N-terminal amino acids of SEQ ID NO:146 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta114' antigen is annotated as 'hypothetical protein'. In the NCTC 8325 strain sta114 is SAOUHSC_00810 and has amino acid sequence SEQ ID NO:147 (GI: 88194570).

Useful sta114 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:147 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:147; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:147, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150 or more). These sta114 proteins include variants of SEQ ID NO:147. Preferred fragments of (b) comprise an epitope from SEQ ID NO:147. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:147 while retaining at least one epitope of SEQ ID NO:147. Other fragments omit one or more protein domains.

The 'sta115' antigen is annotated as 'hypothetical protein'. In the NCTC 8325 strain sta115 is SAOUHSC_00817 and has amino acid sequence SEQ ID NO:148 (GI: 88194576).

Useful sta115 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:148 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:148; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:148, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150 or more). These sta115 proteins include variants of SEQ ID NO:148. Preferred fragments of (b) comprise an epitope from SEQ ID NO:148. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:148 while retaining at least one epitope of SEQ ID NO:148. The first 18 N-terminal amino acids of SEQ ID NO:148 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta116' antigen is annotated as 'formyl peptide receptor-like 1 inhibitory protein'. In the NCTC 8325 strain sta116 is SAOUHSC_01112 and has amino acid sequence SEQ ID NO:149 (GI:88194858).

Useful sta116 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:149 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%,

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85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:149; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:149, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These sta116 proteins include variants of SEQ ID NO:149. Preferred fragments of (b) comprise an epitope from SEQ ID NO:149. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:149 while retaining at least one epitope of SEQ ID NO:149. The first 20 N-terminal amino acids of SEQ ID NO:149 can usefully be omitted. Other fragments omit one or more protein domains.

The 'sta117' antigen is annotated as 'truncated beta-hemolysin'. In the NCTC 8325 strain sta117 is SAOUHSC_02240 and has amino acid sequence SEQ ID NO:150 (GI:88195913).

Useful sta117 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:150 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:150; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:150, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta117 proteins include variants of SEQ ID NO:150. Preferred fragments of (b) comprise an epitope from SEQ ID NO:150. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:150 while retaining at least one epitope of SEQ ID NO:150. Other fragments omit one or more protein domains.

The 'sta118' antigen is annotated as 'cell division protein FtsZ'. In the NCTC 8325 strain sta118 is SAOUHSC_01150 and has amino acid sequence SEQ ID NO:151 (GI: 88194892).

Useful sta118 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:151 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:151; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:151, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These sta118 proteins include variants of SEQ ID NO:151. Preferred fragments of (b) comprise an epitope from SEQ ID NO:151. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:151 while retaining at least one epitope of SEQ ID NO:151. Other fragments omit one or more protein domains.

The 'sta119' antigen is annotated as 'thioredoxin'. In the NCTC 8325 strain sta119 is SAOUHSC_01100 and has amino acid sequence SEQ ID NO:152 (GI:88194846).

Useful sta119 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:152 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%,

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99%, 99.5% or more) to SEQ ID NO:152; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:152, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100 or more). These sta119 proteins include variants of SEQ ID NO:152. Preferred fragments of (b) comprise an epitope from SEQ ID NO:152. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:152 while retaining at least one epitope of SEQ ID NO:152. Other fragments omit one or more protein domains.

The 'sta120' antigen is annotated as 'alkyl hydroperoxide reductase subunit c'. In the NCTC 8325 strain sta120 is SAOUHSC_00365 and has amino acid sequence SEQ ID NO:153 (GI:88194163).

Useful sta120 antigens can elicit an antibody (e.g. when administered to a human) that recognizes SEQ ID NO:153 and/or may comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO:153; and/or (b) comprising a fragment of at least 'n' consecutive amino acids of SEQ ID NO:153, wherein 'n' is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150 or more). These sta120 proteins include variants of SEQ ID NO:153. Preferred fragments of (b) comprise an epitope from SEQ ID NO:153. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO:153 while retaining at least one epitope of SEQ ID NO:153. Other fragments omit one or more protein domains.

The polypeptides described herein may include 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more variant amino acids within at least, or at most 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 300, 400, 500, 550, 1000 or more contiguous amino acids, or any range derivable therein, of SEQ ID NO:2-30, or SEQ ID NO:32-155.

A polypeptide segment or immunogenic fragment as described herein may include 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106,

107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 300, 400, 500, 550, 1000 or more contiguous amino acids, or any range derivable therein, of SEQ ID NO:2-30, or SEQ ID NO:33-155.

The immunogenic compositions of the invention may further comprise capsular polysaccharides including one or more of PIA (also known as PNAG) and/or *S. aureus* Type V and/or type VIII capsular polysaccharide and/or *S. epidermidis* Type I, and/or Type II and/or Type III capsular polysaccharide.

The compositions may be formulated in a pharmaceutically acceptable composition. In certain aspects of the invention the *staphylococcus* bacterium is an *S. aureus* bacterium.

In further aspects, a composition may be administered more than one time to the subject, and may be administered 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20 or more times. The administration of the compositions include, but is not limited to oral, parenteral, subcutaneous, intramuscular, intravenous, or various combinations thereof, including inhalation or aspiration.

In still further embodiments, a composition comprises a recombinant nucleic acid molecule encoding a polypeptide described herein or segments/fragments thereof. Typically a recombinant nucleic acid molecule encoding a polypeptide described herein contains a heterologous promoter. In certain aspects, a recombinant nucleic acid molecule of the invention is a vector, in still other aspects the vector is a plasmid. In certain embodiments the vector is a viral vector. In certain aspects a composition includes a recombinant, non-*staphylococcus* bacterium containing or expressing a polypeptide described herein. In particular aspects the recombinant non-*staphylococcus* bacteria is *Salmonella* or another gram-positive bacteria. A composition is typically administered to mammals, such as human subjects, but administration to other animals that are capable of eliciting an immune response is contemplated. In further aspects the *staphylococcus* bacterium containing or expressing the polypeptide is *Staphylococcus aureus*. In further embodiments the immune response is a protective immune response.

In further embodiments a composition comprises a recombinant nucleic acid molecule encoding all or part of one or more of a SpA, SpA polypeptide variant, Eap, Ebh, Emp, EsaB, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, Coa, Hla, IsdC, SasF, SpA, vWbp, or vWh protein or peptide or variant thereof. Additional staphylococcal antigens that can be used in combination with the polypeptides described herein include, but are not limited to 52 kDa vitronectin binding protein (WO 01/60852), Aaa, Aap, Ant, autolysin glucosaminidase, autolysin amidase, Cna, collagen binding protein (U.S. Pat. No. 6,288,214), EFB (FIB), Elastin binding protein (EbpS), EPB, FbpA, fibrinogen binding protein (U.S. Pat. No. 6,008,341), Fibronectin binding protein (U.S. Pat. No. 5,840,846), FnbA, FnbB, GehD (US 2002/0169288), HarA, HBP, Immunodominant ABC transporter, IsaA/PisA, laminin

receptor, Lipase GehD, MAP, Mg2+ transporter, MHC II analogue (U.S. Pat. No. 5,648,240), MRPII, Npase, RNA III activating protein (RAP), SasA, SasB, SasC, SasD, SasK, SBI, SdrF (WO 00/12689), SdrG/Fig (WO 00/12689), SdrH (WO 00/12689), SEA exotoxins (WO 00/02523), SEB exotoxins (WO 00/02523), SitC and Ni ABC transporter, SitC/MntC/saliva binding protein (U.S. Pat. No. 5,801,234), SsaA, SSP-1, SSP-2, and/or Vitronectin binding protein. In particular aspects, a bacteria is a recombinant non-*staphylococcus* bacteria, such as a *Salmonella* or other gram-positive bacteria. Certain embodiments include compositions comprising recombinant nucleic acid molecules encoding all or part of one or more of, sta001, sta002, sta003, sta004, sta005, sta006, sta007, sta008, sta009, sta010, sta011, sta012, sta013, sta014, sta015, sta016, sta017, sta018, sta019, sta020, sta021, sta022, sta023, sta024, sta025, sta026, sta027, sta028, sta029, sta030, sta031, sta032, sta033, sta034, sta035, sta036, sta037, sta038, sta039, sta040, sta041, sta042, sta043, sta044, sta045, sta046, sta047, sta048, sta049, sta050, sta051, sta052, sta053, sta054, sta055, sta056, sta057, sta058, sta059, sta060, sta061, sta062, sta063, sta064, sta065, sta066, sta067, sta068, sta069, sta070, sta071, sta072, sta073, sta074, sta075, sta076, sta077, sta078, sta079, sta080, sta081, sta082, sta083, sta084, sta085, sta086, sta087, sta088, sta089, sta090, sta091, sta092, sta093, sta094, sta095, sta096, sta097, sta098, sta099, sta100, sta101, sta102, sta103, sta104, sta105, sta106, sta107, sta108, sta109, sta110, sta111, sta112, sta113, sta114, sta115, sta116, sta117, sta118, sta119, sta120, or EsxAB hybrid polypeptide or immunogenic fragment thereof.

Compositions of the invention are typically administered to human subjects, but administration to other animals that are capable of eliciting an immune response to a bacterium, e.g., a *staphylococcus* bacterium, is contemplated, particularly cattle, horses, goats, sheep and other domestic animals, i.e., mammals.

In certain aspects the *staphylococcus* bacterium is a *Staphylococcus aureus*. In further embodiments the immune response is a protective immune response. In still further aspects, the methods and compositions of the invention can be used to prevent, ameliorate, reduce, or treat infection of tissues or glands, e.g., mammary glands, particularly mastitis and other infections. Other methods include, but are not limited to prophylactically reducing bacterial burden in a subject not exhibiting signs of infection, particularly those subjects suspected of or at risk of being colonized by a target bacteria, e.g., patients that are or will be at risk or susceptible to infection during a hospital stay, treatment, and/or recovery.

Any embodiment discussed with respect to one aspect of the invention applies to other aspects of the invention as well. In particular, any embodiment discussed in the context of a SpA variant polypeptide, peptide, nucleic acid, or antibody may specifically exclude one or more of Eap, Ebh, Emp, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, Coa, Hla, IsdC, SasF, vWbp, vWh, 52 kDa vitronectin binding protein (WO 01/60852), Aaa, Aap, Ant, autolysin glucosaminidase, autolysin amidase, Cna, collagen binding protein (U.S. Pat. No. 6,288,214), EFB (FIB), Elastin binding protein (EbpS), EPB, FbpA, fibrinogen binding protein (U.S. Pat. No. 6,008,341), Fibronectin binding protein (U.S. Pat. No. 5,840,846), FnbA, FnbB, GehD (US 2002/0169288), HarA, HBP, Immunodominant ABC transporter, IsaA/PisA, laminin receptor, Lipase GchD, MAP, Mg2+ transporter, MHC II analogue (U.S. Pat. No. 5,648,240), MRPII, Npase, RNA III activating protein

(RAP), SasA, SasB, SasC, SasD, SasK, SBI, SdrF (WO 00/12689), SdrG/Fig (WO 00/12689), SdrH (WO 00/12689), SEA exotoxins (WO 00/02523), SEB exotoxins (WO 00/02523), SitC and Ni ABC transporter, SitC/MntC/saliva binding protein (U.S. Pat. No. 5,801,234), SsaA, SSP-1, SSP-2, and/or Vitronectin binding protein (or nucleic acids), sta001, sta002, sta003, sta004, sta005, sta006, sta007, sta008, sta009, sta010, sta011, sta012, sta013, sta014, sta015, sta016, sta017, sta018, sta019, sta020, sta021, sta022, sta023, sta024, sta025, sta026, sta027, sta028, sta029, sta030, sta031, sta032, sta033, sta034, sta035, sta036, sta037, sta038, sta039, sta040, sta041, sta042, sta043, sta044, sta045, sta046, sta047, sta048, sta049, sta050, sta051, sta052, sta053, sta054, sta055, sta056, sta057, sta058, sta059, sta060, sta061, sta062, sta063, sta064, sta065, sta066, sta067, sta068, sta069, sta070, sta071, sta072, sta073, sta074, sta075, sta076, sta077, sta078, sta079, sta080, sta081, sta082, sta083, sta084, sta085, sta086, sta087, sta088, sta089, sta090, sta091, sta092, sta093, sta094, sta095, sta096, sta097, sta098, sta099, sta100, sta101, sta102, sta103, sta104, sta105, sta106, sta107, sta108, sta109, sta110, sta111, sta112, sta113, sta114, sta115, sta116, sta117, sta118, sta119, sta120, or EsxAB hybrid polypeptide or immunogenic fragment thereof and vice versa.

Embodiments of the invention include compositions that contain or do not contain a bacterium. A composition may or may not include an attenuated or viable or intact staphylococcal bacterium. In certain aspects, the composition comprises a bacterium that is not a staphylococcal bacterium or does not contain staphylococcal bacteria. In certain embodiments a bacterial composition comprises an isolated or recombinantly expressed staphylococcal Protein A variant or a nucleotide encoding the same. The composition may be or include a recombinantly engineered *staphylococcus* bacterium that has been altered in a way that comprises specifically altering the bacterium with respect to a secreted virulence factor or cell surface protein. For example, the bacteria may be recombinantly modified to express more of the virulence factor or cell surface protein than it would express if unmodified.

The term "isolated" can refer to a nucleic acid or polypeptide that is substantially free of cellular material, bacterial material, viral material, or culture medium (when produced by recombinant DNA techniques) of their source of origin, or chemical precursors or other chemicals (when chemically synthesized). Moreover, an isolated compound refers to one that can be administered to a subject as an isolated compound; in other words, the compound may not simply be considered "isolated" if it is adhered to a column or embedded in an agarose gel. Moreover, an "isolated nucleic acid fragment" or "isolated peptide" is a nucleic acid or protein fragment that is not naturally occurring as a fragment and/or is not typically in the functional state.

Moieties of the invention, such as polypeptides, peptides, antigens, or immunogens, may be conjugated or linked covalently or noncovalently to other moieties such as adjuvants, proteins, peptides, supports, fluorescence moieties, or labels. The term "conjugate" or "immunoconjugate" is broadly used to define the operative association of one moiety with another agent and is not intended to refer solely to any type of operative association, and is particularly not limited to chemical "conjugation." Recombinant fusion proteins are particularly contemplated. Compositions of the invention may further comprise an adjuvant or a pharmaceutically acceptable excipient. An adjuvant may be covalently or non-covalently coupled to a polypeptide or peptide

of the invention. In certain aspects, the adjuvant is chemically conjugated to a protein, polypeptide, or peptide.

The term "providing" is used according to its ordinary meaning to indicate "to supply or furnish for use." In some embodiments, the protein is provided directly by administering the protein, while in other embodiments, the protein is effectively provided by administering a nucleic acid that encodes the protein. In certain aspects the invention contemplates compositions comprising various combinations of nucleic acid, antigens, peptides, and/or epitopes.

The subject will have (e.g., are diagnosed with a staphylococcal infection), will be suspected of having, or will be determined to be at risk of developing a staphylococcal infection. Compositions of the present invention include immunogenic compositions wherein the antigen(s) or epitope(s) are contained in an amount effective to achieve the intended purpose. More specifically, an effective amount means an amount of active ingredients necessary to stimulate or elicit an immune response, or provide resistance to, amelioration of, or mitigation of infection. In more specific aspects, an effective amount prevents, alleviates or ameliorates symptoms of disease or infection, or prolongs the survival of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any preparation used in the methods of the invention, an effective amount or dose can be estimated initially from in vitro studies, cell culture, and/or animal model assays. For example, a dose can be formulated in animal models to achieve a desired immune response or circulating antibody concentration or titer. Such information can be used to more accurately determine useful doses in humans.

The use of the term "or" in the claims is used to mean "and/or" unless explicitly indicated to refer to alternatives only or the alternatives are mutually exclusive, although the disclosure supports a definition that refers to only alternatives and "and/or." It is also contemplated that anything listed using the term "or" may also be specifically excluded.

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.

Following long-standing patent law, the words "a" and "an," when used in conjunction with the word "comprising" in the claims or specification, denotes one or more, unless specifically noted.

Other objects, features and advantages of the present invention will become apparent from the following detailed description. It should be understood, however, that the detailed description and the specific examples, while indicating specific embodiments of the invention, are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description.

DESCRIPTION OF THE DRAWINGS

So that the matter in which the above-recited features, advantages and objects of the invention as well as others which will become clear are attained and can be understood in detail, more particular descriptions and certain embodiments of the invention briefly summarized above are illustrated in the appended drawings. These drawings form a part of the specification. It is to be noted, however, that the

appended drawings illustrate certain embodiments of the invention and therefore are not to be considered limiting in their scope.

FIG. 1 Immunization with SpA_{KKAA} modifies host immune responses to staphylococcal infection. Cohorts of BALB/c mice (n=15) were immunized with SpA_{KKAA} or with PBS/adjuvant control (mock) and then challenged by intravenous inoculation with 5×10⁶ CFU *S. aureus* USA300 LAC. Thirty days after infection, animals were bled and serum samples were analyzed for antibody responses to staphylococcal antigens. Twenty-seven recombinant, six-histidyl tagged staphylococcal proteins (ClfA, ClfB, Coa, Eap, Ebh, Emp, EsxA, EsxB, FnbpA, FnbpB, Hla, IsdA, IsdB, LukD, LukE, LukF, SdrC, SdrD, SdrE, SasA, SasD, SasF, SasG, SasI, SasK, SpA_{KKAA} and vWbp) were purified by Ni-NTA affinity chromatography and immobilized on nitrocellulose membrane at 2 µg. Signal intensities in sera from mice were quantified and normalized by infrared imaging. Data are the means, and error bars represent SEM (±).

DETAILED DESCRIPTION

Staphylococcus aureus is a commensal of the human skin and nares, and the leading cause of bloodstream, skin and soft tissue infections (Klebens et al., 2007). Recent dramatic increases in the mortality of staphylococcal diseases are attributed to the spread of methicillin-resistant *S. aureus* (MRSA) strains often not susceptible to antibiotics (Kennedy et al., 2008). In a large retrospective study, the incidence of MRSA infections was 4.6% of all hospital admissions in the United States (Klebens et al., 2007). The annual health care costs for 94,300 MRSA infected individuals in the United States exceed \$2.4 billion (Klebens et al., 2007). The current MRSA epidemic has precipitated a public health crisis that needs to be addressed by development of a preventive vaccine (Boucher and Corey, 2008). To date, an FDA licensed vaccine that prevents *S. aureus* diseases is not available.

The inventors describe here the use of Protein A, a cell wall anchored surface protein of staphylococci, for the generation of variants that can serve as subunit vaccines. The pathogenesis of staphylococcal infections is initiated as bacteria invade the skin or blood stream via trauma, surgical wounds, or medical devices (Lowy, 1998). Although the invading pathogen may be phagocytosed and killed, staphylococci can also escape innate immune defenses and seed infections in organ tissues, inducing inflammatory responses that attract macrophages, neutrophils, and other phagocytes (Lowy, 1998). The responsive invasion of immune cells to the site of infection is accompanied by liquefaction necrosis as the host seeks to prevent staphylococcal spread and allow for removal of necrotic tissue debris (Lam et al., 1963). Such lesions can be observed by microscopy as hypercellular areas containing necrotic tissue, leukocytes, and a central nidus of bacteria (Lam et al., 1963). Unless staphylococcal abscesses are surgically drained and treated with antibiotics, disseminated infection and septicemia produce a lethal outcome (Sheagren, 1984).

I. STAPHYLOCOCCAL ANTIGENS

A. Staphylococcal Protein A (SpA)

All *Staphylococcus aureus* strains express the structural gene for Protein A (spa) (Jensen, 1958; Said-Salim et al., 2003), a well characterized virulence factor whose cell wall anchored surface protein product (SpA) encompasses five

highly homologous immunoglobulin binding domains designated E, D, A, B, and C (Sjodahl, 1977). These domains display ~80% identity at the amino acid level, are 56 to 61 residues in length, and are organized as tandem repeats (Uhlen et al., 1984). SpA is synthesized as a precursor protein with an N-terminal YSIRK/GS signal peptide and a C-terminal LPXTG motif sorting signal (DeDent et al., 2008; Schneewind et al., 1992). Cell wall anchored Protein A is displayed in great abundance on the staphylococcal surface (DeDent et al., 2007; Sjoquist et al., 1972). Each of its immunoglobulin binding domains is composed of anti-parallel α-helices that assemble into a three helix bundle and bind the Fc domain of immunoglobulin G (IgG) (Deisenhofer, 1981; Deisenhofer et al., 1978), the VH3 heavy chain (Fab) of IgM (i.e., the B cell receptor) (Graille et al., 2000), the von Willebrand factor at its A1 domain [vWF A1 is a ligand for platelets] (O'Seaghdha et al., 2006) and the tumor necrosis factor α (TNF-α) receptor I (TNFRI) (Gomez et al., 2006), which is displayed on surfaces of airway epithelia (Gomez et al., 2004; Gomez et al., 2007).

SpA impedes neutrophil phagocytosis of staphylococci through its attribute of binding the Fc component of IgG (Jensen, 1958; Uhlen et al., 1984). Moreover, SpA is able to activate intravascular clotting via its binding to von Willebrand factor A1 domains (Hartleib et al., 2000). Plasma proteins such as fibrinogen and fibronectin act as bridges between staphylococci (ClfA and ClfB) and the platelet integrin GPIIb/IIIa (O'Brien et al., 2002), an activity that is supplemented through Protein A association with vWF A1, which allows staphylococci to capture platelets via the GPIb-α platelet receptor (Foster, 2005; O'Seaghdha et al., 2006). SpA also binds TNFRI and this interaction contributes to the pathogenesis of staphylococcal pneumonia (Gomez et al., 2004). SpA activates proinflammatory signaling through TNFR1 mediated activation of TRAF2, the p38/c-Jun kinase, mitogen activate protein kinase (MAPK) and the Rel-transcription factor NF-κB. SpA binding further induces TNFR1 shedding, an activity that appears to require the TNF-converting enzyme (TACE) (Gomez et al., 2007). All of the aforementioned SpA activities are mediated through its five IgG binding domains and can be perturbed by the same amino acid substitutions, initially defined by their requirement for the interaction between Protein A and human IgG1 (Cedergren et al., 1993).

SpA also functions as a B cell superantigen by capturing the Fab region of VH3 bearing IgM, the B cell receptor (Gomez et al., 2007; Goodyear et al., 2003; Goodyear and Silverman, 2004; Roben et al., 1995). Following intravenous challenge, staphylococcal Protein A (SpA) mutations show a reduction in staphylococcal load in organ tissues and dramatically diminished ability to form abscesses (described herein). During infection with wildtype *S. aureus*, abscesses are formed within forty-eight hours and are detectable by light microscopy of hematoxylin-eosin stained, thin-sectioned kidney tissue, initially marked by an influx of polymorphonuclear leukocytes (PMNs). On day 5 of infection, abscesses increase in size and enclosed a central population of staphylococci, surrounded by a layer of eosinophilic, amorphous material and a large cuff of PMNs. Histopathology revealed massive necrosis of PMNs in proximity to the staphylococcal nidus at the center of abscess lesions as well as a mantle of healthy phagocytes. The inventors also observed a rim of necrotic PMNs at the periphery of abscess lesions, bordering the eosinophilic pseudocapsule that separated healthy renal tissue from the infectious lesion. Staphy-

lococcal variants lacking Protein A are unable to establish the histopathology features of abscesses and are cleared during infection.

In previous studies, Cedergren et al. (1993) engineered five individual substitutions in the Fc fragment binding sub-domain of the B domain of SpA, L17D, N28A, I31A and K35A. These authors created these proteins to test data gathered from a three dimensional structure of a complex between one domain of SpA and Fc₁. Cedergren et al. determined the effects of these mutations on stability and binding, but did not contemplate use of such substitutions for the production of a vaccine antigen.

Brown et al. (1998) describe studies designed to engineer new proteins based on SpA that allow the use of more favorable elution conditions when used as affinity ligands. The mutations studied included single mutations of Q13A, Q14H, N15A, N15H, F17H, Y18F, L21H, N32H, or K39H. Brown et al. report that Q13A, N15A, N15H, and N32H substitutions made little difference to the dissociation constant values and that the Y18F substitution resulted in a 2 fold decrease in binding affinity as compared to wild type SpA. Brown et al. also report that L21H and F17H substitutions decrease the binding affinity by five-fold and a hundred-fold respectively. The authors also studied analogous substitutions in two tandem domains. Thus, the Brown et al. studies were directed to generating a SpA with a more favorable elution profile, hence the use of His substitutions to provide a pH sensitive alteration in the binding affinity. Brown et al. is silent on the use of SpA as a vaccine antigen.

Graille et al. (2000) describe a crystal structure of domain D of SpA and the Fab fragment of a human IgM antibody. Graille et al. define by analysis of a crystal structure the D domain amino acid residues that interact with the Fab fragment as residues Q26, G29, F30, Q32, S33, D36, D37, Q40, N43, E47, or L51, as well as the amino acid residues that form the interface between the domain D sub-domains. Graille et al. define the molecular interactions of these two proteins, but is silent in regard to any use of substitutions in the interacting residues in producing a vaccine antigen.

O'Seaghdha et al. (2006) describe studies directed at elucidating which sub-domain of domain D binds vWF. The authors generated single mutations in either the Fc or VH3 binding sub-domains, i.e., amino acid residues F5A, Q9A, Q10A, F13A, Y14A, L17A, N28A, I31A, K35A, G29A, F30A, S33A, D36A, D37A, Q40A, E47A, or Q32A. The authors discovered that vWF binds the same sub-domain that binds Fc. O'Seaghdha et al. define the sub-domain of domain D responsible for binding vWF, but is silent in regard to any use of substitutions in the interacting residues in producing a vaccine antigen.

Gomez et al. (2006) describe the identification of residues responsible for activation of the TNFR1 by using single mutations of F5A, F13A, Y14A, L17A, N21A, I31A, Q32A, and K35A. Gomez et al. is silent in regard to any use of substitutions in the interacting residues in producing a vaccine antigen.

Recombinant affinity tagged Protein A, a polypeptide encompassing the five IgG domains (EDCAB) (Sjodahl, 1977) but lacking the C-terminal Region X (Guss et al., 1984), was purified from recombinant *E. coli* and used as a vaccine antigen (Stranger-Jones et al., 2006). Because of the attributes of SpA in binding the Fc portion of IgG, a specific humoral immune response to Protein A could not be measured (Stranger-Jones et al., 2006). The inventors have overcome this obstacle through the generation of SpA-DQ9, 10K; D36,37A. BALB/c mice immunized with recombinant Protein A (SpA) displayed significant protection against

intravenous challenge with *S. aureus* strains: a 2.951 log reduction in staphylococcal load as compared to the wild-type ($P>0.005$; Student's t-test) (Stranger-Jones et al., 2006). SpA specific antibodies may cause phagocytic clearance prior to abscess formation and/or impact the formation of the aforementioned eosinophilic barrier in abscesses that separate staphylococcal communities from immune cells since these do not form during infection with Protein A mutant strains. Each of the five SpA domains (i.e., domains formed from three helix bundles designated E, D, A, B, and C) exerts similar binding properties (Jansson et al., 1998). The solution and crystal structure of the domain D has been solved both with and without the Fc and VH3 (Fab) ligands, which bind Protein A in a non-competitive manner at distinct sites (Graille et al., 2000). Mutations in residues known to be involved in IgG binding (F5, Q9, Q10, S11, F13, Y14, L17, N28, I31 and K35) are also required for vWF A1 and TNFR1 binding (Cedergren et al., 1993; Gomez et al., 2006; O'Seaghdha et al., 2006), whereas residues important for the VH3 interaction (Q26, G29, F30, S33, D36, D37, Q40, N43, E47) appear to have no impact on the other binding activities (Graille et al., 2000; Jansson et al., 1998). SpA specifically targets a subset of B cells that express VH3 family related IgM on their surface, i.e., VH3 type B cell receptors (Roben et al., 1995). Upon interaction with SpA, these B cells proliferate and commit to apoptosis, leading to preferential and prolonged deletion of innate-like B lymphocytes (i.e., marginal zone B cells and follicular B2 cells) (Goodyear et al., 2003; Goodyear et al., 2004).

Molecular Basis of Protein A Surface Display and Function.

Protein A is synthesized as a precursor in the bacterial cytoplasm and secreted via its YSIRK signal peptide at the cross wall, i.e. the cell division septum of staphylococci (FIG. 1) (DeDent et al., 2007; DeDent et al., 2008). Following cleavage of the C-terminal LPXTG sorting signal, Protein A is anchored to bacterial peptidoglycan cross-bridges by sortase A (Mazmanian et al., 1999; Schneewind et al., 1995; Mazmanian et al., 2000). Protein A is the most abundant surface protein of staphylococci; the molecule is expressed by virtually all *S. aureus* strains (Cespedes et al., 2005; Kennedy et al., 2008; Said-Salim et al., 2003). Staphylococci turn over 15-20% of their cell wall per division cycle (Navarre and Schneewind, 1999). Murine hydrolases cleave the glycan strands and wall peptides of peptidoglycan, thereby releasing Protein A with its attached C-terminal cell wall disaccharide tetrapeptide into the extracellular medium (Ton-That et al., 1999). Thus, by physiological design, Protein A is both anchored to the cell wall and displayed on the bacterial surface but also released into surrounding tissues during host infection (Marraffini et al., 2006).

Protein A captures immunoglobulins on the bacterial surface and this biochemical activity enables staphylococcal escape from host innate and acquired immune responses (Jensen, 1958; Goodyear et al., 2004). Interestingly, region X of Protein A (Guss et al., 1984), a repeat domain that tethers the IgG binding domains to the LPXTG sorting signal/cell wall anchor, is perhaps the most variable portion of the staphylococcal genome (Said-Salim, 2003; Schneewind et al., 1992). Each of the five immunoglobulin binding domains of Protein A (SpA), formed from three helix bundles and designated E, D, A, B, and C, exerts similar structural and functional properties (Sjodahl, 1977; Jansson et al., 1998). The solution and crystal structure of the domain D has been solved both with and without the Fc and V_H3 (Fab) ligands, which bind Protein A in a non-competitive manner at distinct sites (Graille 2000).

In the crystal structure complex, the Fab interacts with helix II and helix III of domain D via a surface composed of four VH region β -strands (Graille 2000). The major axis of helix II of domain D is approximately 50° to the orientation of the strands, and the interhelical portion of domain D is most proximal to the CO strand. The site of interaction on Fab is remote from the Ig light chain and the heavy chain constant region. The interaction involves the following domain D residues: Asp-36 of helix II, Asp-37 and Gln-40 in the loop between helix II and helix III and several other residues (Graille 2000). Both interacting surfaces are composed predominantly of polar side chains, with three negatively charged residues on domain D and two positively charged residues on the 2A2 Fab buried by the interaction, providing an overall electrostatic attraction between the two molecules. Of the five polar interactions identified between Fab and domain D, three are between side chains. A salt bridge is formed between Arg-H19 and Asp-36 and two hydrogen bonds are made between Tyr-H59 and Asp-37 and between Asn-H82a and Ser-33. Because of the conservation of Asp-36 and Asp-37 in all five IgG binding domains of Protein A, the inventors mutated these residues.

The SpA-D sites responsible for Fab binding are structurally separate from the domain surface that mediates Fc γ binding. The interaction of Fc γ with domain D primarily involves residues in helix I with lesser involvement of helix II (Gouda et al., 1992; Deisenhofer, 1981). With the exception of the Gln-32, a minor contact in both complexes, none of the residues that mediate the Fc γ interaction are involved in Fab binding. To examine the spatial relationship between these different Ig-binding sites, the SpA domains in these complexes have been superimposed to construct a model of a complex between Fab, the SpA-domain D, and the Fc γ molecule. In this ternary model, Fab and Fc γ form a sandwich about opposite faces of the helix II without evidence of steric hindrance of either interaction. These findings illustrate how, despite its small size (i.e., 56-61 aa), an SpA domain can simultaneously display both activities, explaining experimental evidence that the interactions of Fab with an individual domain are noncompetitive. Residues for the interaction between SpA-D and Fc γ are Gln-9 and Gln-10.

In contrast, occupancy of the Fc portion of IgG on the domain D blocks its interaction with vWF A1 and probably also TNFR1 (O'Seaghdha et al., 2006). Mutations in residues essential for IgG Fc binding (F5, Q9, Q10, S11, F13, Y14, L17, N28, I131 and K35) are also required for vWF A1 and TNFR1 binding (O'Seaghdha et al., 2006; Cedergren et al., 1993; Gomez et al., 2006), whereas residues critical for the VH3 interaction (Q26, G29, F30, S33, D36, D37, Q40, N43, E47) have no impact on the binding activities of IgG Fc, vWF A1 or TNFR1 (Jansson et al., 1998; Graille et al., 2000). The Protein A immunoglobulin Fab binding activity targets a subset of B cells that express V_H3 family related IgM on their surface, i.e., these molecules function as VH3type B cell receptors (Roben et al., 1995). Upon interaction with SpA, these B cells rapidly proliferate and then commit to apoptosis, leading to preferential and prolonged deletion of innate-like B lymphocytes (i.e., marginal zone B cells and follicular B2 cells) (Goodyear and Silverman, 2004; Goodyear and Silverman, 2003). More than 40% of circulating B cells are targeted by the Protein A interaction and the V_H3 family represents the largest family of human B cell receptors to impart protective humoral responses against pathogens (Goodyear and Silverman, 2004; Goodyear and Silverman, 2003). Thus, Protein A functions analogously to staphylococcal superantigens (Roben et al., 1995), albeit that the latter class of molecules, for example SEB,

TSST-1, TSST-2, form complexes with the T cell receptor to inappropriately stimulate host immune responses and thereby precipitating characteristic disease features of staphylococcal infections (Roben et al., 1995; Tiedemann et al., 1995). Together these findings document the contributions of Protein A in establishing staphylococcal infections and in modulating host immune responses.

In sum, Protein A domains can be viewed as displaying two different interfaces for binding with host molecules and any development of Protein A based vaccines must consider the generation of variants that do not perturb host cell signaling, platelet aggregation, sequestration of immunoglobulins or the induction of B cell proliferation and apoptosis. Such Protein A variants should also be useful in analyzing vaccines for the ability of raising antibodies that block the aforementioned SpA activities and occupy the five repeat domains at their dual binding interfaces. This goal is articulated and pursued here for the first time and methods are described in detail for the generation of Protein A variants that can be used as a safe vaccine for humans. To perturb IgG Fc γ , vWF A1 and TNFR1 binding, glutamine (Q) 9 and 10 [numbering derived from the SpA domain D as described in Uhlen et al., 1984] were mutated, and generated lysine substitutions for both glutamines with the expectation that these abolish the ligand attributes at the first binding interface. To perturb IgM Fab VH3 binding, aspartate (D) 36 and 37 were mutated, each of which is required for the association with the B cell receptor. D36 and D37 were both substituted with alanine Q9,10K and D36,37A mutations are here combined in the recombinant molecule SpA-DQ9,10K; D36,37A and tested for the binding attributes of Protein A. Further, SpA-D and SpA-DQ9,10K; D36,37A are subjected to immunization studies in mice and rabbits and analyzed for [1] the production of specific antibodies (SpA-D Ab); [2] the ability of SpA-D Ab to block the association between Protein A and its four different ligands; and, [3] the attributes of SpA-D Ab to generate protective immunity against staphylococcal infections.

In certain embodiments the SpA variant is a full length SpA variant comprising a variant A, B, C, D, and E domain. In certain aspects, the SpA variant comprises or consists of the amino acid sequence that is 80, 90, 95, 98, 99, or 100% identical to the amino acid sequence of SEQ ID NO:34. In other embodiments the SpA variant comprises a segment of SpA. The SpA segment can comprise at least or at most 1, 2, 3, 4, 5 or more IgG binding domains. The IgG domains can be at least or at most 1, 2, 3, 4, 5 or more variant A, B, C, D, or E domains. In certain aspects the SpA variant comprises at least or at most 1, 2, 3, 4, 5, or more variant A domains. In a further aspect the SpA variant comprises at least or at most 1, 2, 3, 4, 5, or more variant B domains. In still a further aspect the SpA variant comprises at least or at most 1, 2, 3, 4, 5, or more variant C domains. In yet a further aspect the SpA variant comprises at least or at most 1, 2, 3, 4, 5, or more variant D domains. In certain aspects the SpA variant comprises at least or at most 1, 2, 3, 4, 5, or more variant E domains. In a further aspect the SpA variant comprises a combination of A, B, C, D, and E domains in various combinations and permutations. The combinations can include all or part of a SpA signal peptide segment, a SpA region X segment, and/or a SpA sorting signal segment. In other aspects the SpA variant does not include a SpA signal peptide segment, a SpA region X segment, and/or a SpA sorting signal segment. In certain aspects a variant A domain comprises a substitution at position(s) 7, 8, 34, and/or 35 of SEQ ID NO:4. In another aspect a variant B domain comprises a substitution at position(s) 7, 8, 34,

and/or 35 of SEQ ID NO:6. In still another aspect a variant C domain comprises a substitution at position(s) 7, 8, 34, and/or 35 of SEQ ID NO:5. In certain aspects a variant D domain comprises a substitution at position(s) 9, 10, 37, and/or 38 of SEQ ID NO:2. In a further aspect a variant E domain comprises a substitution at position(s) 6, 7, 33, and/or 34 of SEQ ID NO:3.

In certain aspects the SpA variant includes a substitution of (a) one or more amino acid substitution in an IgG Fc binding sub-domain of SpA domain A, B, C, D, and/or E that disrupts or decreases binding to IgG Fc, and (b) one or more amino acid substitution in a V_H3 binding sub-domain of SpA domain A, B, C, D, and/or E that disrupts or decreases binding to V_H3 . In still further aspects the amino acid sequence of a SpA variant comprises an amino acid sequence that is at least 50%, 60%, 70%, 80%, 90%, 95%, or 100% identical, including all values and ranges there between, to the amino acid sequence of SEQ ID NOs:2-6.

In a further aspect the SpA variant includes (a) one or more amino acid substitution in an IgG Fc binding sub-domain of SpA domain D, or at a corresponding amino acid position in other IgG domains, that disrupts or decreases binding to IgG Fc, and (b) one or more amino acid substitution in a V_H3 binding sub-domain of SpA domain D, or at a corresponding amino acid position in other IgG domains, that disrupts or decreases binding to V_H3 . In certain aspects amino acid residue F5, Q9, Q10, S11, F13, Y14, L17, N28, I31, and/or K35 (SEQ ID NO:2, QQNNFNKDDQSSA-FYEILNMPNLNEAQRNGFIQSLKDDPSQSTNV-LGEAKKLNES) of the IgG Fc binding sub-domain of domain D are modified or substituted. In certain aspects amino acid residue Q26, G29, F30, S33, D36, D37, Q40, N43, and/or E47 (SEQ ID NO:2) of the V_H3 binding sub-domain of domain D are modified or substituted such that binding to Fc or V_H3 is attenuated. In further aspects corresponding modifications or substitutions can be engineered in corresponding positions of the domain A, B, C, and/or E. Corresponding positions are defined by alignment of the domain D amino acid sequence with one or more of the amino acid sequences from other IgG binding domains of SpA. In certain aspects the amino acid substitution can be any of the other 20 amino acids. In a further aspect conservative amino acid substitutions can be specifically excluded from possible amino acid substitutions. In other aspects only non-conservative substitutions are included. In any event, any substitution or combination of substitutions that reduces the binding of the domain such that SpA toxicity is significantly reduced is contemplated. The significance of the reduction in binding refers to a variant that produces minimal to no toxicity when introduced into a subject and can be assessed using in vitro methods described herein.

In certain embodiments, a variant SpA comprises at least or at most 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more variant SpA domain D peptides. In certain aspects 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19 or more amino acid residues of the variant SpA are substituted or modified—including but not limited to amino acids F5, Q9, Q10, S11, F13, Y14, L17, N28, I31, and/or K35 (SEQ ID NO:2) of the IgG Fc binding sub-domain of domain D and amino acid residue Q26, G29, F30, S33, D36, D37, Q40, N43, and/or E47 (SEQ ID NO:2) of the V_H3 binding sub-domain of domain D. In one aspect of the invention glutamine residues at position 9 and/or 10 of SEQ ID NO:2 (or corresponding positions in other domains) are mutated. In another aspect, aspartic acid residues 36 and/or 37 of SEQ ID NO:2 (or corresponding positions in other domains) are mutated. In a further aspect, glutamine 9 and 10, and aspartic acid residues

36 and 37 are mutated. Purified non-toxicogenic SpA or SpA-D mutants/variants described herein are no longer able to significantly bind (i.e., demonstrate attenuated or disrupted binding affinity) Fcγ or F(ab)₂ V_H3 and also do not stimulate B cell apoptosis. These non-toxicogenic Protein A variants can be used as subunit vaccines and raise humoral immune responses and confer protective immunity against *S. aureus* challenge. Compared to wild-type full-length Protein A or the wild-type SpA-domain D, immunization with SpA-D variants resulted in an increase in Protein A specific antibody. Using a mouse model of staphylococcal challenge and abscess formation, it was observed that immunization with the non-toxicogenic Protein A variants generated significant protection from staphylococcal infection and abscess formation. As virtually all *S. aureus* strains express Protein A, immunization of humans with the non-toxicogenic Protein A variants can neutralize this virulence factor and thereby establish protective immunity. In certain aspects the protective immunity protects or ameliorates infection by drug resistant strains of *Staphylococcus*, such as USA300 and other MRSA strains.

In still further aspects, the bacterial antigen is multimerized, e.g., dimerized or a linear fusion of two or more polypeptides or peptide segments. In certain aspects of the invention, a composition comprises multimers or concatamers of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more isolated cell surface proteins or segments thereof. Concatamers are linear polypeptides having one or more repeating peptide units. Bacterial antigens or fragments can be consecutive or separated by a spacer or other peptide sequences, e.g., one or more additional bacterial peptide. In a further aspect, the other polypeptides or peptides contained in the multimer or concatamer can include, but are not limited to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 of FnBpA, FnBpB, LukD, LukE, LukF, SasA, SasD, SasG, SasI, SasK, SpA (and variants thereof), Eap, Ehb, Emp, EsaB, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, Coa, Hla (e.g., H35 mutants), IsdC, SasF, vWbp, or vWh or immunogenic fragments thereof. Additional staphylococcal antigens that can be used including, but are not limited to 52 kDa vitronectin binding protein (WO 01/60852), Aaa, Aap, Ant, autolysin glucosaminidase, autolysin amidase, Cna, collagen binding protein (U.S. Pat. No. 6,288,214), EFB (FIB), Elastin binding protein (EbpS), EPB, FbpA, fibrinogen binding protein (U.S. Pat. No. 6,008,341), Fibronectin binding protein (U.S. Pat. No. 5,840,846), FnbA, FnbB, GchD (US 2002/0169288), HarA, HBP, Immunodominant ABC transporter, IsaA/PisA, laminin receptor, Lipase GehD, MAP, Mg2+ transporter, MHC II analogue (U.S. Pat. No. 5,648,240), MRPII, Npase, RNA III activating protein (RAP), SasA, SasB, SasC, SasD, SasK, SBI, SdrF (WO 00/12689), SdrG/Fig (WO 00/12689), SdrH (WO 00/12689), SEA exotoxins (WO 00/02523), SEB exotoxins (WO 00/02523), SitC and Ni ABC transporter, SitC/MntC/saliva binding protein (U.S. Pat. No. 5,801,234), SsaA, SSP-1, SSP-2, and/or Vitronectin binding protein.

Yet still further embodiments include vaccines comprising a pharmaceutically acceptable composition having a combination or permutation of protein(s) or peptide(s) described herein, wherein the composition is capable of stimulating and/or enhancing an immune response against a *staphylococcus* bacterium. The vaccine may comprise an isolated protein(s) or peptide(s) described. In certain aspects of the invention the bacterial antigen, or any other combination or permutation of protein(s) or peptide(s) described are multimerized, e.g., dimerized or concatamerized. In a

further aspect, the vaccine composition is contaminated by less than about 10, 9, 8, 7, 6, 5, 4, 3, 2, 1, 0.5, 0.25, 0.05% (or any range derivable therein) of other Staphylococcal proteins. A composition may further comprise an isolated protein A specific antibody or fragment thereof.

B. Staphylococcal Coagulases

Coagulases are enzymes produced by *Staphylococcus* bacteria that convert fibrinogen to fibrin. Coa and vW_h activate prothrombin without proteolysis (Friedrich et al., 2003). The coagulase•prothrombin complex recognizes fibrinogen as a specific substrate, converting it directly into fibrin. The crystal structure of the active complex revealed binding of the D1 and D2 domains to prothrombin and insertion of its Ile1-Val² N-terminus into the Ile¹⁶ pocket, inducing a functional active site in the zymogen through conformational change (Friedrich et al., 2003). Exosite I of α-thrombin, the fibrinogen recognition site, and proexosite I on prothrombin are blocked by the D2 of Coa (Friedrich et al., 2003). Nevertheless, association of the tetrameric (Coa•prothrombin)₂ complex binds fibrinogen at a new site with high affinity (Panizzi et al., 2006). This model explains the coagulant properties and efficient fibrinogen conversion by coagulase (Panizzi et al., 2006).

Fibrinogen is a large glycoprotein (Mr ~340,000), formed by three pairs of Aα-, Bβ-, and γ-chains covalently linked to form a “dimer of trimers,” where A and B designate the fibrinopeptides released by thrombin cleavage (Panizzi et al., 2006). The elongated molecule folds into three separate domains, a central fragment E that contains the N-termini of all six chains and two flanking fragments D formed mainly by the C-termini of the Bβ- and γ-chains. These globular domains are connected by long triple-helical structures. Coagulase-prothrombin complexes, which convert human fibrinogen to the self-polymerizing fibrin, are not targeted by circulating thrombin inhibitors (Panizzi et al., 2006). Thus, staphylococcal coagulases bypass the physiological blood coagulation pathway.

All *S. aureus* strains secrete coagulase and vWbp (Bjerketorp et al., 2004; Field and Smith, 1945). Although early work reported important contributions of coagulase to the pathogenesis of staphylococcal infections (Ekstedt and Yotis, 1960; Smith et al., 1947), more recent investigations with molecular genetics tools challenged this view by observing no virulence phenotypes with endocarditis, skin abscess and mastitis models in mice (Moreillon et al., 1995; Phonimdaeng et al., 1990). Generating isogenic variants of *S. aureus* Newman, a fully virulent clinical isolate (Duthie et al., 1952), it is described herein that coa mutants indeed display virulence defects in a lethal bacteremia and renal abscess model in mice. In the inventors experience, *S. aureus* 8325-4 is not fully virulent and it is presumed that mutational lesions in this strain may not be able to reveal virulence defects in vivo. Moreover, antibodies raised against Coa or vWbp perturb the pathogenesis of *S. aureus* Newman infections to a degree mirroring the impact of gene deletions. Coa and vWbp contribute to staphylococcal abscess formation and lethal bacteremia and may also function as protective antigens in subunit vaccines.

Biochemical studies document the biological value of antibodies against Coa and vWbp. By binding to antigen and blocking its association with clotting factors, the antibodies prevent the formation of Coa•prothrombin and vWbp•prothrombin complexes. Passive transfer studies revealed protection of experimental animals against staphylococcal abscess formation and lethal challenge by Coa and

vWbp antibodies. Thus, Coa and vWbp neutralizing antibodies generate immune protection against staphylococcal disease.

Earlier studies revealed a requirement of coagulase for resisting phagocytosis in blood (Smith et al., 1947) and the inventors observed a similar phenotype for Δcoa mutants in lepirudin-treated mouse blood (see Example 3 below). As vWbp displays higher affinity for human prothrombin than the mouse counterpart, it is suspected the same may be true for ΔvWbp variants in human blood. Further, expression of Coa and vWbp in abscess lesions as well as their striking distribution in the eosinophilic pseudocapsule surrounding (staphylococcal abscess communities (SACs) or the peripheral fibrin wall, suggest that secreted coagulases contribute to the establishment of these lesions. This hypothesis was tested and, indeed, Δcoa mutants were defective in the establishment of abscesses. A corresponding test, blocking Coa function with specific antibodies, produced the same effect. Consequently, it is proposed that the clotting of fibrin is a critical event in the establishment of staphylococcal abscesses that can be targeted for the development of protective vaccines. Due to their overlapping function on human prothrombin, both Coa and vWbp are considered excellent candidates for vaccine development.

C. Other Staphylococcal Antigens

Research over the past several decades identified *S. aureus* exotoxins, surface proteins and regulatory molecules as important virulence factors (Foster, 2005; Mazmanian et al., 2001; Novick, 2003). Much progress has been achieved regarding the regulation of these genes. For example, staphylococci perform a bacterial census via the secretion of auto-inducing peptides that bind to a cognate receptor at threshold concentration, thereby activating phospho-relay reactions and transcriptional activation of many of the exotoxin genes (Novick, 2003). The pathogenesis of staphylococcal infections relies on these virulence factors (secreted exotoxins, exopolysaccharides, and surface adhesins). The development of staphylococcal vaccines is hindered by the multifaceted nature of staphylococcal invasion mechanisms. It is well established that live attenuated microorganisms are highly effective vaccines; immune responses elicited by such vaccines are often of greater magnitude and of longer duration than those produced by non-replicating immunogens. One explanation for this may be that live attenuated strains establish limited infections in the host and mimic the early stages of natural infection. Embodiments of the invention are directed to compositions and methods including variant SpA polypeptides and peptides, as well as other immunogenic extracellular proteins, polypeptides, and peptides (including both secreted and cell surface proteins or peptides) of gram positive bacteria for the use in mitigating or immunizing against infection. In particular embodiments the bacteria is a *staphylococcus* bacteria. Extracellular proteins, polypeptides, or peptides include, but are not limited to secreted and cell surface proteins of the targeted bacteria.

The human pathogen *S. aureus* secretes EsxA and EsxB, two ESAT-6 like proteins, across the bacterial envelope (Burts et al., 2005, which is incorporated herein by reference). Staphylococcal esxA and esxB are clustered with six other genes in the order of transcription: esxA esaA essA esaB essB essC esaC esxB. The acronyms esa, ess, and esx stand for ESAT-6 secretion accessory, system, and extracellular, respectively, depending whether the encoded proteins play an accessory (esa) or direct (ess) role for secretion, or are secreted (esx) in the extracellular milieu. The entire cluster of eight genes is herein referred to as the Ess cluster. EsxA, esxB, essA, essB, and essC are all required for

synthesis or secretion of EsxA and EsxB. Mutants that fail to produce EsxA, EsxB, and EssC display defects in the pathogenesis of *S. aureus* murine abscesses, suggesting that this specialized secretion system may be a general strategy of human bacterial pathogenesis. Secretion of non-WXG100 substrates by the ESX-1 pathway has been reported for several antigens including EspA, EspB, Rv3483c, and Rv3615c (Fortune et al., 2005; MacGurn et al., 2005; McLaughlin et al., 2007; Xu et al., 2007). The alternate ESX-5 pathway has also been shown to secrete both WXG100 and non-WXG100 proteins in pathogenic mycobacteria (Abdallah et al., 2007; Abdallah et al., 2006).

The *Staphylococcus aureus* Ess pathway can be viewed as a secretion module equipped with specialized transport components (Ess), accessory factors (Esa) and cognate secretion substrates (Esx). EssA, EssB and EssC are required for EsxA and EsxB secretion. Because EssA, EssB and EssC are predicted to be transmembrane proteins, it is contemplated that these proteins form a secretion apparatus. Some of the proteins in the ess gene cluster may actively transport secreted substrates (acting as motor) while others may regulate transport (regulator). Regulation may be achieved, but need not be limited to, transcriptional or post-translational mechanisms for secreted polypeptides, sorting of specific substrates to defined locations (e.g., extracellular medium or host cells), or timing of secretion events during infection. At this point, it is unclear whether all secreted Esx proteins function as toxins or contribute indirectly to pathogenesis.

Staphylococci rely on surface protein mediated-adhesion to host cells or invasion of tissues as a strategy for escape from immune defenses. Furthermore, *S. aureus* utilize surface proteins to sequester iron from the host during infection. The majority of surface proteins involved in staphylococcal pathogenesis carry C-terminal sorting signals, i.e., they are covalently linked to the cell wall envelope by sortase. Further, staphylococcal strains lacking the genes required for surface protein anchoring, i.e., sortase A and B, display a dramatic defect in the virulence in several different mouse models of disease. Thus, surface protein antigens represent a validated vaccine target as the corresponding genes are essential for the development of staphylococcal disease and can be exploited in various embodiments of the invention. The sortase enzyme superfamily are Gram-positive transpeptidases responsible for anchoring surface protein virulence factors to the peptidoglycan cell wall layer. Two sortase isoforms have been identified in *Staphylococcus aureus*, SrtA and SrtB. These enzymes have been shown to recognize a LPXTG motif in substrate proteins. The SrtB isoform appears to be important in heme iron acquisition and iron homeostasis, whereas the SrtA isoform plays a critical role in the pathogenesis of Gram-positive bacteria by modulating the ability of the bacterium to adhere to host tissue via the covalent anchoring of adhesins and other proteins to the cell wall peptidoglycan. In certain embodiments the SpA variants described herein can be used in combination with other staphylococcal proteins such as Coa, Eap, Ebh, Emp, EsaC, EsaB, EsxA, EsxB, Hla, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, IsdC, SasF, vWbp, and/or vWh proteins.

Certain aspects of the invention include methods and compositions concerning proteinaceous compositions including polypeptides, peptides, or nucleic acid encoding SpA variant(s) and other staphylococcal antigens such as other proteins transported by the Ess pathway, or sortase substrates. These proteins may be modified by deletion, insertion, and/or substitution.

The Esx polypeptides include the amino acid sequence of Esx proteins from bacteria in the *Staphylococcus* genus. The Esx sequence may be from a particular *staphylococcus* species, such as *Staphylococcus aureus*, and may be from a particular strain, such as Newman. In certain embodiments, the EsxA sequence is SAV0282 from strain Mu50 (which is the same amino acid sequence for Newman) and can be accessed using Genbank Accession Number Q99WU4 (gil68565539), which is hereby incorporated by reference. In other embodiments, the EsxB sequence is SAV0290 from strain Mu50 (which is the same amino acid sequence for Newman) and can be accessed using Genbank Accession Number Q99WT7 (gil68565532), which is hereby incorporated by reference. In further embodiments, other polypeptides transported by the Ess pathway may be used, the sequences of which may be identified by one of skill in the art using databases and internet accessible resources.

The sortase substrate polypeptides include, but are not limited to the amino acid sequence of SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, IsdC or SasF proteins from bacteria in the *Staphylococcus* genus. The sortase substrate polypeptide sequence may be from a particular *staphylococcus* species, such as *Staphylococcus aureus*, and may be from a particular strain, such as Newman. In certain embodiments, the SdrD sequence is from strain N315 and can be accessed using Genbank Accession Number NP_373773.1 (gil15926240), which is incorporated by reference. In other embodiments, the SdrE sequence is from strain N315 and can be accessed using Genbank Accession Number NP_373774.1 (gil15926241), which is incorporated by reference. In other embodiments, the IsdA sequence is SAV1130 from strain Mu50 (which is the same amino acid sequence for Newman) and can be accessed using Genbank Accession Number NP_371654.1 (gil15924120), which is incorporated by reference. In other embodiments, the IsdB sequence is SAV1129 from strain Mu50 (which is the same amino acid sequence for Newman) and can be accessed using Genbank Accession Number NP_371653.1 (gil15924119), which is incorporated by reference. In further embodiments, other polypeptides transported by the Ess pathway or processed by sortase may be used, the sequences of which may be identified by one of skill in the art using databases and internet accessible resources.

Examples of various proteins that can be used in the context of the present invention can be identified by analysis of database submissions of bacterial genomes, including but not limited to accession numbers NC_002951 (GI:57650036 and GenBank CP000046), NC_002758 (GI:57634611 and GenBank BA000017), NC_002745 (GI:29165615 and GenBank BA000018), NC_003923 (GI:21281729 and GenBank BA000033), NC_002952 (GI:49482253 and GenBank BX571856), NC_002953 (GI:49484912 and GenBank BX571857), NC_007793 (GI:87125858 and GenBank CP000255), NC_007795 (GI:87201381 and GenBank CP000253) each of which are incorporated by reference.

As used herein, a "protein" or "polypeptide" refers to a molecule comprising at least ten amino acid residues. In some embodiments, a wild-type version of a protein or polypeptide are employed, however, in many embodiments of the invention, a modified protein or polypeptide is employed to generate an immune response. The terms described above may be used interchangeably. A "modified protein" or "modified polypeptide" or a "variant" refers to a protein or polypeptide whose chemical structure, particularly its amino acid sequence, is altered with respect to the wild-type protein or polypeptide. In some embodiments, a modified/variant protein or polypeptide has at least one

modified activity or function (recognizing that proteins or polypeptides may have multiple activities or functions). It is specifically contemplated that a modified/variant protein or polypeptide may be altered with respect to one activity or function yet retain a wild-type activity or function in other respects, such as immunogenicity.

In certain embodiments the size of a protein or polypeptide (wild-type or modified) may comprise, but is not limited to, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600, 625, 650, 675, 700, 725, 750, 775, 800, 825, 850, 875, 900, 925, 950, 975, 1000, 1100, 1200, 1300, 1400, 1500, 1750, 2000, 2250, 2500 amino molecules or greater, and any range derivable therein, or derivative of a corresponding amino sequence described or referenced herein. It is contemplated that polypeptides may be mutated by truncation, rendering them shorter than their corresponding wild-type form, but also they might be altered by fusing or conjugating a heterologous protein sequence with a particular function (e.g., for targeting or localization, for enhanced immunogenicity, for purification purposes, etc.).

As used herein, an "amino molecule" refers to any amino acid, amino acid derivative, or amino acid mimic known in the art. In certain embodiments, the residues of the proteinaceous molecule are sequential, without any non-amino molecule interrupting the sequence of amino molecule residues. In other embodiments, the sequence may comprise one or more non-amino molecule moieties. In particular embodiments, the sequence of residues of the proteinaceous molecule may be interrupted by one or more non-amino molecule moieties.

Accordingly, the term "proteinaceous composition" encompasses amino molecule sequences comprising at least one of the 20 common amino acids in naturally synthesized proteins, or at least one modified or unusual amino acid.

Proteinaceous compositions may be made by any technique known to those of skill in the art, including (i) the expression of proteins, polypeptides, or peptides through standard molecular biological techniques, (ii) the isolation of proteinaceous compounds from natural sources, or (iii) the chemical synthesis of proteinaceous materials. The nucleotide as well as the protein, polypeptide, and peptide sequences for various genes have been previously disclosed, and may be found in the recognized computerized databases. One such database is the National Center for Biotechnology Information's Genbank and GenPept databases (on the World Wide Web at ncbi.nlm.nih.gov/). The coding regions for these genes may be amplified and/or expressed using the techniques disclosed herein or as would be known to those of ordinary skill in the art.

Amino acid sequence variants of SpA, coagulases and other polypeptides of the invention can be substitutional, insertional, or deletion variants. A variation in a polypeptide of the invention may affect 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, or more non-contiguous or contiguous amino acids of the polypeptide, as compared to wild-type. A variant can comprise an amino acid sequence that is at least 50%, 60%, 70%, 80%, or 90%, including all values and ranges there between, identical to any sequence provided or referenced herein, e.g., SEQ ID NO:2-8 or SEQ ID NO:11-30. A variant can include 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more substitute amino acids. A polypeptide processed or secreted by the Ess pathway or other surface proteins (see Table 1) or sortase substrates from any *staphylococcus* species and strain are contemplated for use in compositions and methods described herein.

Deletion variants typically lack one or more residues of the native or wild-type protein. Individual residues can be deleted or a number of contiguous amino acids can be deleted. A stop codon may be introduced (by substitution or insertion) into an encoding nucleic acid sequence to generate a truncated protein. Insertional mutants typically involve the addition of material at a non-terminal point in the polypeptide. This may include the insertion of one or more residues. Terminal additions, called fusion proteins, may also be generated. These fusion proteins include multimers or concatamers of one or more peptide or polypeptide described or referenced herein.

Substitutional variants typically contain the exchange of one amino acid for another at one or more sites within the protein, and may be designed to modulate one or more properties of the polypeptide, with or without the loss of other functions or properties. Substitutions may be conservative, that is, one amino acid is replaced with one of similar shape and charge. Conservative substitutions are well known in the art and include, for example, the changes of: alanine to serine; arginine to lysine; asparagine to glutamine or histidine; aspartate to glutamate; cysteine to serine; glutamine to asparagine; glutamate to aspartate; glycine to proline; histidine to asparagine or glutamine; isoleucine to leucine or valine; leucine to valine or isoleucine; lysine to arginine; methionine to leucine or isoleucine; phenylalanine to tyrosine, leucine or methionine; serine to threonine; threonine to serine; tryptophan to tyrosine; tyrosine to tryptophan or phenylalanine; and valine to isoleucine or leucine. Alternatively, substitutions may be non-conservative such that a function or activity of the polypeptide is affected. Non-conservative changes typically involve substituting a residue with one that is chemically dissimilar, such as a polar or charged amino acid for a nonpolar or uncharged amino acid, and vice versa.

TABLE 1

Exemplary surface proteins of <i>S. aureus</i> strains.								
SAV #	SA#	Surface	MW2	Mu50	N315	Newman	MRSA252*	MSSA476*
SAV0111	SA0107	Spa	492	450	450	520	516	492
SAV2503	SA2291	FnBPA	1015	1038	1038	741	—	1015
SAV2502	SA2290	FnBPB	943	961	961	677	965	957
SAV0811	SA0742	ClfA	946	935	989	933	1029	928
SAV2630	SA2423	ClfB	907	877	877	913	873	905

TABLE 1-continued

Exemplary surface proteins of <i>S. aureus</i> strains.								
SAV #	SA#	Surface	MW2	Mu50	N315	Newman	MRSA252*	MSSA476*
Np	Np	Cna	1183	—	—	—	1183	1183
SAV0561	SA0519	SdrC	955	953	953	947	906	957
SAV0562	SA0520	SdrD	1347	1385	1385	1315	—	1365
SAV0563	SA0521	SdrE	1141	1141	1141	1166	1137	1141
Np	Np	Pls	—	—	—	—	—	—
SAV2654	SA2447	SasA	2275	2271	2271	2271	1351	2275
SAV2160	SA1964	SasB	686	2481	2481	2481	2222	685
	SA1577	SasC	2186	213	2186	2186	2189	2186
SAV0134	SA0129	SasD	241	241	241	241	221	241
SAV1130	SA0977	SasE/IsdA	350	350	350	350	354	350
SAV2646	SA2439	SasF	635	635	635	635	627	635
SAV2496		SasG	1371	525	927	—	—	1371
SAV0023	SA0022	SasH	772	—	772	772	786	786
SAV1731	SA1552	SasI	895	891	891	891	534	895
SAV1129	SA0976	SasJ/IsdB	645	645	645	645	652	645
	SA2381	SasK	198	211	211	—	—	197
	Np	SasL	—	232	—	—	—	—
SAV1131	SA0978	IsdC	227	227	227	227	227	227

Proteins of the invention may be recombinant, or synthesized in vitro. Alternatively, a non-recombinant or recombinant protein may be isolated from bacteria. It is also contemplated that a bacteria containing such a variant may be implemented in compositions and methods of the invention. Consequently, a protein need not be isolated.

The term “functionally equivalent codon” is used herein to refer to codons that encode the same amino acid, such as the six codons for arginine or serine, and also refers to codons that encode biologically equivalent amino acids (see Table 2, below).

TABLE 2

Codon Table			
Amino Acids		Codons	
Alanine	Ala	A	GCA GCC GCG GCU
Cysteine	Cys	C	UGC UGU
Aspartic acid	Asp	D	GAC GAU
Glutamic acid	Glu	E	GAA GAG
Phenylalanine	Phe	F	UUC UUU
Glycine	Gly	G	GGA GGC GGG GGU
Histidine	His	H	CAC CAU
Isoleucine	Ile	I	AUA AUC AUU
Lysine	Lys	K	AAA AAG
Leucine	Leu	L	UUA UUG CUA CUC CUG CUU
Methionine	Met	M	AUG
Asparagine	Asn	N	AAC AAU
Proline	Pro	P	CCA CCC CCG CCU
Glutamine	Gln	Q	CAA CAG
Arginine	Arg	R	AGA AGG CGA CGC CGG CGU
Serine	Ser	S	AGC AGU UCA UCC UCG UCU
Threonine	Thr	T	ACA ACC ACG ACU
Valine	Val	V	GUA GUC GUG GUU
Tryptophan	Trp	W	UGG
Tyrosine	Tyr	Y	UAC UAU

It also will be understood that amino acid and nucleic acid sequences may include additional residues, such as additional N- or C-terminal amino acids, or 5' or 3' sequences, respectively, and yet still be essentially as set forth in one of the sequences disclosed herein, so long as the sequence meets the criteria set forth above, including the maintenance of biological protein activity (e.g., immunogenicity) where protein expression is concerned. The addition of terminal sequences particularly applies to nucleic acid sequences that may, for example, include various non-coding sequences flanking either of the 5' or 3' portions of the coding region.

The following is a discussion based upon changing of the amino acids of a protein to create a variant polypeptide or peptide. For example, certain amino acids may be substituted for other amino acids in a protein structure with or without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's functional activity, certain amino acid substitutions can be made in a protein sequence, and in its underlying DNA coding sequence, and nevertheless produce a protein with a desirable property. It is thus contemplated by the inventors that various changes may be made in the DNA sequences of genes.

It is contemplated that in compositions of the invention, there is between about 0.001 mg and about 10 mg of total polypeptide, peptide, and/or protein per ml. The concentration of protein in a composition can be about, at least about or at most about 0.001, 0.010, 0.050, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.5, 2.0, 2.5, 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5, 8.0, 8.5, 9.0, 9.5, 10.0 mg/ml or more (or any range derivable therein). Of this, about, at least about, or at most about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% may be an SpA variant or a coagulase, and may be used in combination with other peptides or polypeptides, such as other bacterial peptides and/or antigens.

The present invention contemplates the administration of variant SpA polypeptides or peptides to effect a preventative therapy or therapeutic effect against the development of a disease or condition associated with infection by a *staphylococcus* pathogen.

In certain aspects, combinations of staphylococcal antigens are used in the production of an immunogenic composition that is effective at treating or preventing staphylococcal infection. Staphylococcal infections progress through several different stages. For example, the staphylococcal life cycle involves commensal colonization, initiation of infection by accessing adjoining tissues or the bloodstream, and/or anaerobic multiplication in the blood. The interplay

between *S. aureus* virulence determinants and the host defense mechanisms can induce complications such as endocarditis, metastatic abscess formation, and sepsis syndrome. Different molecules on the surface of the bacterium are involved in different steps of the infection cycle. Combinations of certain antigens can elicit an immune response which protects against multiple stages of staphylococcal infection. The effectiveness of the immune response can be measured either in animal model assays and/or using an opsonophagocytic assay.

D. Polypeptides and Polypeptide Production

The present invention describes polypeptides, peptides, and proteins and immunogenic fragments thereof for use in various embodiments of the present invention. For example, specific polypeptides are assayed for or used to elicit an immune response. In specific embodiments, all or part of the proteins of the invention can also be synthesized in solution or on a solid support in accordance with conventional techniques. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. See, for example, Stewart and Young, (1984); Tam et al., (1983); Merrifield, (1986); and Barany and Merrifield (1979), each incorporated herein by reference.

Alternatively, recombinant DNA technology may be employed wherein a nucleotide sequence which encodes a peptide of the invention is inserted into an expression vector, transformed or transfected into an appropriate host cell and cultivated under conditions suitable for expression.

One embodiment of the invention includes the use of gene transfer to cells, including microorganisms, for the production and/or presentation of polypeptides or peptides. The gene for the polypeptide or peptide of interest may be transferred into appropriate host cells followed by culture of cells under the appropriate conditions. The generation of recombinant expression vectors, and the elements included therein, are well known in the art and briefly discussed herein. Alternatively, the protein to be produced may be an endogenous protein normally synthesized by the cell that is isolated and purified.

Another embodiment of the present invention uses autologous B lymphocyte cell lines, which are transfected with a viral vector that expresses an immunogen product, and more specifically, a protein having immunogenic activity. Other examples of mammalian host cell lines include, but are not limited to Vero and HeLa cells, other B- and T-cell lines, such as CEM, 721.221, H9, Jurkat, Raji, as well as cell lines of Chinese hamster ovary, W138, BHK, COS-7, 293, HepG2, 3T3, RIN and MDCK cells. In addition, a host cell strain may be chosen that modulates the expression of the inserted sequences, or that modifies and processes the gene product in the manner desired. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed.

A number of selection systems may be used including, but not limited to HSV thymidine kinase, hypoxanthine-guanine phosphoribosyltransferase, and adenine phosphoribosyltransferase genes, in tk-, hgprt- or aprt-cells, respectively. Also, anti-metabolite resistance can be used as the basis of selection: for dhfr, which confers resistance to trimethoprim and methotrexate; gpt, which confers resistance to myco-

phenolic acid; neo, which confers resistance to the aminoglycoside G418; and hygromycin, which confers resistance to hygromycin.

Animal cells can be propagated in vitro in two modes: as non-anchorage-dependent cells growing in suspension throughout the bulk of the culture or as anchorage-dependent cells requiring attachment to a solid substrate for their propagation (i.e., a monolayer type of cell growth).

Non-anchorage dependent or suspension cultures from continuous established cell lines are the most widely used means of large scale production of cells and cell products. However, suspension cultured cells have limitations, such as tumorigenic potential and lower protein production than adherent cells.

Where a protein is specifically mentioned herein, it is preferably a reference to a native or recombinant protein or optionally a protein in which any signal sequence has been removed. The protein may be isolated directly from the staphylococcal strain or produced by recombinant DNA techniques. Immunogenic fragments of the protein may be incorporated into the immunogenic composition of the invention. These are fragments comprising at least 10 amino acids, 20 amino acids, 30 amino acids, 40 amino acids, 50 amino acids, or 100 amino acids, including all values and ranges there between, taken contiguously from the amino acid sequence of the protein. In addition, such immunogenic fragments are immunologically reactive with antibodies generated against the Staphylococcal proteins or with antibodies generated by infection of a mammalian host with Staphylococci. Immunogenic fragments also include fragments that when administered at an effective dose, (either alone or as a hapten bound to a carrier), elicit a protective or therapeutic immune response against Staphylococcal infection, in certain aspects it is protective against *S. aureus* and/or *S. epidermidis* infection. Such an immunogenic fragment may include, for example, the protein lacking an N-terminal leader sequence, and/or a transmembrane domain and/or a C-terminal anchor domain. In a preferred aspect the immunogenic fragment according to the invention comprises substantially all of the extracellular domain of a protein which has at least 80% identity, at least 85% identity, at least 90% identity, at least 95% identity, or at least 97-99% identity, including all values and ranges there between, to a sequence selected segment of a polypeptide described or referenced herein.

Also included in immunogenic compositions of the invention are fusion proteins composed of one or more Staphylococcal proteins, or immunogenic fragments of staphylococcal proteins. Such fusion proteins may be made recombinantly and may comprise one portion of at least 1, 2, 3, 4, 5, or 6 staphylococcal proteins or segments. Alternatively, a fusion protein may comprise multiple portions of at least 1, 2, 3, 4 or 5 staphylococcal proteins. These may combine different Staphylococcal proteins and/or multiples of the same protein or protein fragment, or immunogenic fragments in the same protein (forming a multimer or a concatamer). Alternatively, the invention also includes individual fusion proteins of Staphylococcal proteins or immunogenic fragments thereof, as a fusion protein with heterologous sequences such as a provider of T-cell epitopes or purification tags, for example: β -galactosidase, glutathione-S-transferase, green fluorescent proteins (GFP), epitope tags such as FLAG, myc tag, poly histidine, or viral surface proteins such as influenza virus haemagglutinin, or bacterial proteins such as tetanus toxoid, diphtheria toxoid, or CRM197.

II. NUCLEIC ACIDS

In certain embodiments, the present invention concerns recombinant polynucleotides encoding the proteins, polypeptides, peptides of the invention. The nucleic acid sequences for SpA, coagulases and other bacterial proteins are included, all of which are incorporated by reference, and can be used to prepare peptides or polypeptides.

As used in this application, the term "polynucleotide" refers to a nucleic acid molecule that either is recombinant or has been isolated free of total genomic nucleic acid. Included within the term "polynucleotide" are oligonucleotides (nucleic acids of 100 residues or less in length), recombinant vectors, including, for example, plasmids, cosmids, phage, viruses, and the like. Polynucleotides include, in certain aspects, regulatory sequences, isolated substantially away from their naturally occurring genes or protein encoding sequences. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be RNA, DNA (genomic, cDNA or synthetic), analogs thereof, or a combination thereof. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide.

In this respect, the term "gene," "polynucleotide," or "nucleic acid" is used to refer to a nucleic acid that encodes a protein, polypeptide, or peptide (including any sequences required for proper transcription, post-translational modification, or localization). As will be understood by those in the art, this term encompasses genomic sequences, expression cassettes, cDNA sequences, and smaller engineered nucleic acid segments that express, or may be adapted to express, proteins, polypeptides, domains, peptides, fusion proteins, and mutants. A nucleic acid encoding all or part of a polypeptide may contain a contiguous nucleic acid sequence of: 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 441, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, 1000, 1010, 1020, 1030, 1040, 1050, 1060, 1070, 1080, 1090, 1095, 1100, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 9000, 10000, or more nucleotides, nucleosides, or base pairs, including all values and ranges therebetween, of a polynucleotide encoding one or more amino acid sequence described or referenced herein. It also is contemplated that a particular polypeptide may be encoded by nucleic acids containing variations having slightly different nucleic acid sequences but, nonetheless, encode the same or substantially similar protein (see Table 2 above).

In particular embodiments, the invention concerns isolated nucleic acid segments and recombinant vectors incorporating nucleic acid sequences that encode a variant SpA or coagulase. The term "recombinant" may be used in conjunction with a polynucleotide or polypeptide and generally refers to a polypeptide or polynucleotide produced and/or manipulated in vitro or that is a replication product of such a molecule.

In other embodiments, the invention concerns isolated nucleic acid segments and recombinant vectors incorporating nucleic acid sequences that encode a variant SpA or coagulase polypeptide or peptide to generate an immune response in a subject. In various embodiments the nucleic acids of the invention may be used in genetic vaccines.

The nucleic acid segments used in the present invention can be combined with other nucleic acid sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended recombinant nucleic acid protocol. In some cases, a nucleic acid sequence may encode a polypeptide sequence with additional heterologous coding sequences, for example to allow for purification of the polypeptide, transport, secretion, post-translational modification, or for therapeutic benefits such as targeting or efficacy. As discussed above, a tag or other heterologous polypeptide may be added to the modified polypeptide-encoding sequence, wherein "heterologous" refers to a polypeptide that is not the same as the modified polypeptide.

In certain other embodiments, the invention concerns isolated nucleic acid segments and recombinant vectors that include within their sequence a contiguous nucleic acid sequence from SEQ ID NO:1 (SpA domain D) or SEQ ID NO:3 (SpA) or any other nucleic acid sequences encoding coagulases or other secreted virulence factors and/or surface proteins including proteins transported by the Ess pathway, processed by sortase, or proteins incorporated herein by reference.

In certain embodiments, the present invention provides polynucleotide variants having substantial identity to the sequences disclosed herein; those comprising at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or higher sequence identity, including all values and ranges there between, compared to a polynucleotide sequence of this invention using the methods described herein (e.g., BLAST analysis using standard parameters).

The invention also contemplates the use of polynucleotides which are complementary to all the above described polynucleotides.

A. Vectors

Polypeptides of the invention may be encoded by a nucleic acid molecule comprised in a vector. The term "vector" is used to refer to a carrier nucleic acid molecule into which a heterologous nucleic acid sequence can be inserted for introduction into a cell where it can be replicated and expressed. A nucleic acid sequence can be "heterologous," which means that it is in a context foreign to the cell in which the vector is being introduced or to the nucleic acid in which is incorporated, which includes a sequence homologous to a sequence in the cell or nucleic acid but in a position within the host cell or nucleic acid where it is ordinarily not found. Vectors include DNAs, RNAs, plasmids, cosmids, viruses (bacteriophage, animal viruses, and plant viruses), and artificial chromosomes (e.g., YACs). One of skill in the art would be well equipped to construct a vector through standard recombinant techniques (for example Sambrook et al., 2001; Ausubel et al., 1996, both incorporated herein by reference). In addition to encoding a variant SpA polypeptide the vector can encode other polypeptide sequences such as a one or more other bacterial peptide, a tag, or an immunogenicity enhancing peptide. Useful vectors encoding such fusion proteins include pIN vectors (Inouye et al., 1985), vectors encoding a stretch of histidines, and pGEX vectors, for use in generating glutathione S-transferase (GST) soluble fusion proteins for later purification and separation or cleavage.

The term "expression vector" refers to a vector containing a nucleic acid sequence coding for at least part of a gene

product capable of being transcribed. In some cases, RNA molecules are then translated into a protein, polypeptide, or peptide. Expression vectors can contain a variety of "control sequences," which refer to nucleic acid sequences necessary for the transcription and possibly translation of an operably linked coding sequence in a particular host organism. In addition to control sequences that govern transcription and translation, vectors and expression vectors may contain nucleic acid sequences that serve other functions as well and are described herein.

1. Promoters and Enhancers

A "promoter" is a control sequence. The promoter is typically a region of a nucleic acid sequence at which initiation and rate of transcription are controlled. It may contain genetic elements at which regulatory proteins and molecules may bind such as RNA polymerase and other transcription factors. The phrases "operatively positioned," "operatively linked," "under control," and "under transcriptional control" mean that a promoter is in a correct functional location and/or orientation in relation to a nucleic acid sequence to control transcriptional initiation and expression of that sequence. A promoter may or may not be used in conjunction with an "enhancer," which refers to a cis-acting regulatory sequence involved in the transcriptional activation of a nucleic acid sequence.

Naturally, it may be important to employ a promoter and/or enhancer that effectively directs the expression of the DNA segment in the cell type or organism chosen for expression. Those of skill in the art of molecular biology generally know the use of promoters, enhancers, and cell type combinations for protein expression (see Sambrook et al., 2001, incorporated herein by reference). The promoters employed may be constitutive, tissue-specific, or inducible and in certain embodiments may direct high level expression of the introduced DNA segment under specified conditions, such as large-scale production of recombinant proteins or peptides.

Various elements/promoters may be employed in the context of the present invention to regulate the expression of a gene. Examples of such inducible elements, which are regions of a nucleic acid sequence that can be activated in response to a specific stimulus, include but are not limited to Immunoglobulin Heavy Chain (Banerji et al., 1983; Gilles et al., 1983; Grosschedl et al., 1985; Atchinson et al., 1986, 1987; Imler et al., 1987; Weinberger et al., 1984; Kiledjian et al., 1988; Porton et al., 1990), Immunoglobulin Light Chain (Queen et al., 1983; Picard et al., 1984), T Cell Receptor (Luria et al., 1987; Winoto et al., 1989; Redondo et al., 1990), HLA DQ α and/or DQ β (Sullivan et al., 1987), β Interferon (Goodbourn et al., 1986; Fujita et al., 1987; Goodbourn et al., 1988), Interleukin-2 (Greene et al., 1989), Interleukin-2 Receptor (Greene et al., 1989; Lin et al., 1990), MHC Class II 5 (Koch et al., 1989), MHC Class II HLA-DR α (Sherman et al., 1989), β -Actin (Kawamoto et al., 1988; Ng et al., 1989), Muscle Creatine Kinase (MCK) (Jaynes et al., 1988; Horlick et al., 1989; Johnson et al., 1989), Prealbumin (Transferrin) (Costa et al., 1988), Elastase I (Ornitz et al., 1987), Metallothionein (MTII) (Karin et al., 1987; Culotta et al., 1989), Collagenase (Pinkert et al., 1987; Angel et al., 1987), Albumin (Pinkert et al., 1987; Tronche et al., 1989, 1990), α -Fetoprotein (Godbout et al., 1988; Campere et al., 1989), γ -Globin (Bodine et al., 1987; Perez-Stable et al., 1990), β -Globin (Trudel et al., 1987), c-fos (Cohen et al., 1987), c-Ha-Ras (Triesman, 1986; Deschamps et al., 1985), Insulin (Edlund et al., 1985), Neural Cell Adhesion Molecule (NCAM) (Hirsh et al., 1990), α 1-Antitrypsin (Latimer et al., 1990),

H2B (TH2B) Histone (Hwang et al., 1990), Mouse and/or Type I Collagen (Ripe et al., 1989), Glucose-Regulated Proteins (GRP94 and GRP78) (Chang et al., 1989), Rat Growth Hormone (Larsen et al., 1986), Human Serum Amyloid A (SAA) (Edbrooke et al., 1989), Troponin I (TN I) (Yutzey et al., 1989), Platelet-Derived Growth Factor (PDGF) (Pech et al., 1989), Duchenne Muscular Dystrophy (Klamut et al., 1990), SV40 (Banerji et al., 1981; Moreau et al., 1981; Sleight et al., 1985; Firak et al., 1986; Herr et al., 1986; Imbra et al., 1986; Kadesch et al., 1986; Wang et al., 1986; Ondek et al., 1987; Kuhl et al., 1987; Schaffner et al., 1988), Polyoma (Swartzendruber et al., 1975; Vasseur et al., 1980; Katinka et al., 1980, 1981; Tyndell et al., 1981; Dandolo et al., 1983; de Villiers et al., 1984; Hen et al., 1986; Satake et al., 1988; Campbell et al., 1988), Retroviruses (Kriegler et al., 1982, 1983; Levinson et al., 1982; Kriegler et al., 1983, 1984a, b, 1988; Bosze et al., 1986; Miksieck et al., 1986; Celander et al., 1987; Thiesen et al., 1988; Celander et al., 1988; Choi et al., 1988; Reisman et al., 1989), Papilloma Virus (Campo et al., 1983; Lusky et al., 1983; Spandidos and Wilkie, 1983; Spalholz et al., 1985; Lusky et al., 1986; Cripe et al., 1987; Gloss et al., 1987; Hirochika et al., 1987; Stephens et al., 1987), Hepatitis B Virus (Bulla et al., 1986; Jameel et al., 1986; Shaul et al., 1987; Spandau et al., 1988; Vannice et al., 1988), Human Immunodeficiency Virus (Muesing et al., 1987; Hauber et al., 1988; Jakobovits et al., 1988; Feng et al., 1988; Takebe et al., 1988; Rosen et al., 1988; Berkhout et al., 1989; Laspias et al., 1989; Sharp et al., 1989; Braddock et al., 1989), Cytomegalovirus (CMV) IE (Weber et al., 1984; Boshart et al., 1985; Foecking et al., 1986), Gibbon Ape Leukemia Virus (Holbrook et al., 1987; Quinn et al., 1989).

Inducible elements include, but are not limited to MT II-Phorbol Ester (TFA)/Heavy metals (Palmiter et al., 1982; Haslinger et al., 1985; Searle et al., 1985; Stuart et al., 1985; Imagawa et al., 1987; Karin et al., 1987; Angel et al., 1987b; McNeall et al., 1989); MMTV (mouse mammary tumor virus)—Glucocorticoids (Huang et al., 1981; Lee et al., 1981; Majors et al., 1983; Chandler et al., 1983; Lee et al., 1984; Ponta et al., 1985; Sakai et al., 1988); β -Interferon-poly(rI)x/poly(rc) (Tavernier et al., 1983); Adenovirus 5 E2-E1A (Imperiale et al., 1984); Collagenase-Phorbol Ester (TPA) (Angel et al., 1987a); Stromelysin-Phorbol Ester (TPA) (Angel et al., 1987b); SV40-Phorbol Ester (TPA) (Angel et al., 1987b); Murine MX Gene-Interferon, Newcastle Disease Virus (Hug et al., 1988); GRP78 Gene-A23187 (Resendez et al., 1988); α -2-Macroglobulin-IL-6 (Kunz et al., 1989); Vimentin-Serum (Rittling et al., 1989); MHC Class I Gene H-2-kb-Interferon (Blonar et al., 1989); HSP70-E1A/SV40 Large T Antigen (Taylor et al., 1989, 1990a, 1990b); Proliferin-Phorbol Ester/TPA (Mordacq et al., 1989); Tumor Necrosis Factor-PMA (Hensel et al., 1989); and Thyroid Stimulating Hormone α Gene-Thyroid Hormone (Chatterjee et al., 1989).

The particular promoter that is employed to control the expression of peptide or protein encoding polynucleotide of the invention is not believed to be critical, so long as it is capable of expressing the polynucleotide in a targeted cell, preferably a bacterial cell. Where a human cell is targeted, it is preferable to position the polynucleotide coding region adjacent to and under the control of a promoter that is capable of being expressed in a human cell. Generally speaking, such a promoter might include either a bacterial, human or viral promoter.

In embodiments in which a vector is administered to a subject for expression of the protein, it is contemplated that a desirable promoter for use with the vector is one that is not

down-regulated by cytokines or one that is strong enough that even if down-regulated, it produces an effective amount of a variant SpA for eliciting an immune response. Non-limiting examples of these are CMV IE and RSV LTR. Tissue specific promoters can be used, particularly if expression is in cells in which expression of an antigen is desirable, such as dendritic cells or macrophages. The mammalian MHC I and MHC II promoters are examples of such tissue-specific promoters.

2. Initiation Signals and Internal Ribosome Binding Sites (IRES)

A specific initiation signal also may be required for efficient translation of coding sequences. These signals include the ATG initiation codon or adjacent sequences. Exogenous translational control signals, including the ATG initiation codon, may need to be provided. One of ordinary skill in the art would readily be capable of determining this and providing the necessary signals.

In certain embodiments of the invention, the use of internal ribosome entry sites (IRES) elements are used to create multigene, or polycistronic, messages. IRES elements are able to bypass the ribosome scanning model of 5' methylated Cap dependent translation and begin translation at internal sites (Pelletier and Sonenberg, 1988; Macejak and Samow, 1991). IRES elements can be linked to heterologous open reading frames. Multiple open reading frames can be transcribed together, each separated by an IRES, creating polycistronic messages. Multiple genes can be efficiently expressed using a single promoter/enhancer to transcribe a single message (see U.S. Pat. Nos. 5,925,565 and 5,935,819, herein incorporated by reference).

3. Selectable and Screenable Markers

In certain embodiments of the invention, cells containing a nucleic acid construct of the present invention may be identified in vitro or in vivo by encoding a screenable or selectable marker in the expression vector. When transcribed and translated, a marker confers an identifiable change to the cell permitting easy identification of cells containing the expression vector. Generally, a selectable marker is one that confers a property that allows for selection. A positive selectable marker is one in which the presence of the marker allows for its selection, while a negative selectable marker is one in which its presence prevents its selection. An example of a positive selectable marker is a drug resistance marker.

B. Host Cells

As used herein, the terms "cell," "cell line," and "cell culture" may be used interchangeably. All of these terms also include their progeny, which is any and all subsequent generations. It is understood that all progeny may not be identical due to deliberate or inadvertent mutations. In the context of expressing a heterologous nucleic acid sequence, "host cell" refers to a prokaryotic or eukaryotic cell, and it includes any transformable organism that is capable of replicating a vector or expressing a heterologous gene encoded by a vector. A host cell can, and has been, used as a recipient for vectors or viruses. A host cell may be "transfected" or "transformed," which refers to a process by which exogenous nucleic acid, such as a recombinant protein-encoding sequence, is transferred or introduced into the host cell. A transformed cell includes the primary subject cell and its progeny.

Host cells may be derived from prokaryotes or eukaryotes, including bacteria, yeast cells, insect cells, and mammalian cells for replication of the vector or expression of part or all of the nucleic acid sequence(s). Numerous cell lines and cultures are available for use as a host cell, and

they can be obtained through the American Type Culture Collection (ATCC), which is an organization that serves as an archive for living cultures and genetic materials (www.atcc.org).

C. Expression Systems

Numerous expression systems exist that comprise at least a part or all of the compositions discussed above. Prokaryote- and/or eukaryote-based systems can be employed for use with the present invention to produce nucleic acid sequences, or their cognate polypeptides, proteins and peptides. Many such systems are commercially and widely available.

The insect cell/baculovirus system can produce a high level of protein expression of a heterologous nucleic acid segment, such as described in U.S. Pat. Nos. 5,871,986, 4,879,236, both herein incorporated by reference, and which can be bought, for example, under the name MAXBAC® 2.0 from INVITROGEN® and BACPACK™ BACULOVIRUS EXPRESSION SYSTEM FROM CLONTECH®.

In addition to the disclosed expression systems of the invention, other examples of expression systems include STRATAGENE®'s COMPLETE CONTROL™ Inducible Mammalian Expression System, which involves a synthetic ecdysone-inducible receptor, or its pET Expression System, an *E. coli* expression system. Another example of an inducible expression system is available from INVITROGEN®, which carries the T-REX™ (tetracycline-regulated expression) System, an inducible mammalian expression system that uses the full-length CMV promoter. INVITROGEN® also provides a yeast expression system called the *Pichia methanolica* Expression System, which is designed for high-level production of recombinant proteins in the methylotrophic yeast *Pichia methanolica*. One of skill in the art would know how to express a vector, such as an expression construct, to produce a nucleic acid sequence or its cognate polypeptide, protein, or peptide.

III. POLYSACCHARIDES

The immunogenic compositions of the invention may further comprise capsular polysaccharides including one or more of PIA (also known as PNAG) and/or *S. aureus* Type V and/or type VIII capsular polysaccharide and/or *S. epidermidis* Type I, and/or Type II and/or Type III capsular polysaccharide.

A. PIA (PNAG)

It is now clear that the various forms of staphylococcal surface polysaccharides identified as PS/A, PIA and SAA are the same chemical entity—PNAG (Maira-Litran et al., 2004). Therefore the term PIA or PNAG encompasses all these polysaccharides or oligosaccharides derived from them.

PIA is a polysaccharide intercellular adhesin and is composed of a polymer of β -(1→6)-linked glucosamine substituted with N-acetyl and O-succinyl constituents. This polysaccharide is present in both *S. aureus* and *S. epidermidis* and can be isolated from either source (Joyce et al., 2003; Maira-Litran et al., 2002). For example, PNAG may be isolated from *S. aureus* strain MN8m (WO04/43407). PIA isolated from *S. epidermidis* is an integral constituent of biofilm. It is responsible for mediating cell-cell adhesion and probably also functions to shield the growing colony from the host's immune response. The polysaccharide previously known as poly-N-succinyl- β -(1→6)-glucosamine (PNSG) was recently shown not to have the expected structure since the identification of N-succinylation was incorrect (Maira-Litran et al., 2002). Therefore the polysaccharide formally

known as PNSG and now found to be PNAG is also encompassed by the term PIA.

PIA (or PNAG) may be of different sizes varying from over 400 kDa to between 75 and 400 kDa to between 10 and 75 kDa to oligosaccharides composed of up to 30 repeat units (of β -(1 $\rightarrow$ 6)-linked glucosamine substituted with N-acetyl and O-succinyl constituents). Any size of PIA polysaccharide or oligosaccharide may be used in an immunogenic composition of the invention, in one aspect the polysaccharide is over 40 kDa. Sizing may be achieved by any method known in the art, for instance by microfluidization, ultrasonic irradiation or by chemical cleavage (WO 03/53462, EP497524, EP497525). In certain aspects PIA (PNAG) is at least or at most 40-400 kDa, 40-300 kDa, 50-350 kDa, 60-300 kDa, 50-250 kDa and 60-200 kDa.

PIA (PNAG) can have different degree of acetylation due to substitution on the amino groups by acetate. PIA produced in vitro is almost fully substituted on amino groups (95-100%). Alternatively, a deacetylated PIA (PNAG) can be used having less than 60%, 50%, 40%, 30%, 20%, 10% acetylation. Use of a deacetylated PIA (PNAG) is preferred since non-acetylated epitopes of PNAG are efficient at mediating opsonic killing of Gram positive bacteria, preferably *S. aureus* and/or *S. epidermidis*. In certain aspects, the PIA (PNAG) has a size between 40 kDa and 300 kDa and is deacetylated so that less than 60%, 50%, 40%, 30% or 20% of amino groups are acetylated.

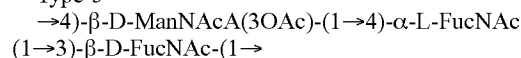
The term deacetylated PNAG (dPNAG) refers to a PNAG polysaccharide or oligosaccharide in which less than 60%, 50%, 40%, 30%, 20% or 10% of the amino groups are acetylated. In certain aspects, PNAG is deacetylated to form dPNAG by chemically treating the native polysaccharide. For example, the native PNAG is treated with a basic solution such that the pH rises to above 10. For instance the PNAG is treated with 0.1-5 M, 0.2-4 M, 0.3-3 M, 0.5-2 M, 0.75-1.5 M or 1 M NaOH, KOH or NH_4OH . Treatment is for at least 10 to 30 minutes, or 1, 2, 3, 4, 5, 10, 15 or 20 hours at a temperature of 20-100, 25-80, 30-60 or 30-50 or 35-45° C. dPNAG may be prepared as described in WO 04/43405.

The polysaccharide(s) can be conjugated or unconjugated to a carrier protein.

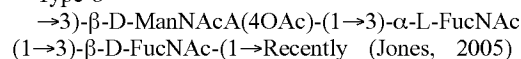
B. Type 5 and Type 8 Polysaccharides from *S. aureus*

Most strains of *S. aureus* that cause infection in man contain either Type 5 or Type 8 polysaccharides. Approximately 60% of human strains are Type 8 and approximately 30% are Type 5. The structures of Type 5 and Type 8 capsular polysaccharide antigens are described in Moreau et al., (1990) and Fournier et al., (1984). Both have FucNAc in their repeat unit as well as ManNAcA which can be used to introduce a sulfhydryl group. The structures are:

Type 5

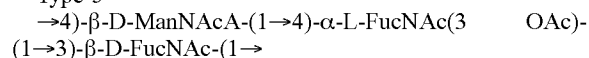


Type 8

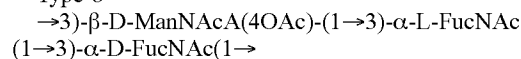


Recently (Jones, 2005) NMR spectroscopy revised the structures to:

Type 5



Type 8



Polysaccharides may be extracted from the appropriate strain of *S. aureus* using method well known to one of skill in the

art, See U.S. Pat. No. 6,294,177. For example, ATCC 12902 is a Type 5 *S. aureus* strain and ATCC 12605 is a Type 8 *S. aureus* strain.

Polysaccharides are of native size or alternatively may be sized, for instance by microfluidisation, ultrasonic irradiation, or by chemical treatment. The invention also covers oligosaccharides derived from the type 5 and 8 polysaccharides from *S. aureus*. The type 5 and 8 polysaccharides included in the immunogenic composition of the invention are preferably conjugated to a carrier protein as described below or are alternatively unconjugated. The immunogenic compositions of the invention alternatively contains either type 5 or type 8 polysaccharide.

C. *S. aureus* 336 Antigen

In an embodiment, the immunogenic composition of the invention comprises the *S. aureus* 336 antigen described in U.S. Pat. No. 6,294,177. The 336 antigen comprises β -linked hexosamine, contains no O-acetyl groups, and specifically binds to antibodies to *S. aureus* Type 336 deposited under ATCC 55804. In an embodiment, the 336 antigen is a polysaccharide which is of native size or alternatively may be sized, for instance by microfluidisation, ultrasonic irradiation, or by chemical treatment. The invention also covers oligosaccharides derived from the 336 antigen. The 336 antigen can be unconjugated or conjugated to a carrier protein.

D. Type I, II and III Polysaccharides from *S. epidermidis*

Amongst the problems associated with the use of polysaccharides in vaccination, is the fact that polysaccharides per se are poor immunogens. It is preferred that the polysaccharides utilized in the invention are linked to a protein carrier which provide bystander T-cell help to improve immunogenicity. Examples of such carriers which may be conjugated to polysaccharide immunogens include the Diphtheria and Tetanus toxoids (DT, DT CRM197 and TT respectively), Keyhole Limpet Haemocyanin (KLH), and the purified protein derivative of Tuberculin (PPD), *Pseudomonas aeruginosa* exoprotein A (rEPA), protein D from *Haemophilus influenzae*, pneumolysin or fragments of any of the above. Fragments suitable for use include fragments encompassing T-helper epitopes. In particular the protein D fragment from *H. influenza* will preferably contain the N-terminal 1/3 of the protein. Protein D is an IgD-binding protein from *Haemophilus influenzae* (EP 0 594 610 B1) and is a potential immunogen. In addition, staphylococcal proteins may be used as a carrier protein in the polysaccharide conjugates of the invention.

A carrier protein that would be particularly advantageous to use in the context of a staphylococcal vaccine is staphylococcal alpha toxoid. The native form may be conjugated to a polysaccharide since the process of conjugation reduces toxicity. Preferably genetically detoxified alpha toxins such as the His35Leu or His35Arg variants are used as carriers since residual toxicity is lower. Alternatively the alpha toxin is chemically detoxified by treatment with a cross-linking reagent, formaldehyde or glutaraldehyde. A genetically detoxified alpha toxin is optionally chemically detoxified, preferably by treatment with a cross-linking reagent, formaldehyde or glutaraldehyde to further reduce toxicity.

The polysaccharides may be linked to the carrier protein(s) by any known method (for example those methods described in U.S. Pat. Nos. 4,372,945, 4,474,757, and 4,356,170). Preferably, CDAP conjugation chemistry is carried out (see WO95/08348). In CDAP, the cyanating reagent 1-cyano-dimethylaminopyridinium tetrafluoroborate (CDAP) is preferably used for the synthesis of polysaccharide-protein conjugates. The cyanilation reaction can

be performed under relatively mild conditions, which avoids hydrolysis of the alkaline sensitive polysaccharides. This synthesis allows direct coupling to a carrier protein.

Conjugation preferably involves producing a direct linkage between the carrier protein and polysaccharide. Optionally a spacer (such as adipic dihydride (ADH)) may be introduced between the carrier protein and the polysaccharide.

IV. IMMUNE RESPONSE AND ASSAYS

As discussed above, the invention concerns evoking or inducing an immune response in a subject against a variant SpA or coagulase peptide. In one embodiment, the immune response can protect against or treat a subject having, suspected of having, or at risk of developing an infection or related disease, particularly those related to staphylococci. One use of the immunogenic compositions of the invention is to prevent nosocomial infections by inoculating a subject prior to undergoing procedures in a hospital or other environment having an increased risk of infection.

A. Immunoassays

The present invention includes the implementation of serological assays to evaluate whether and to what extent an immune response is induced or evoked by compositions of the invention. There are many types of immunoassays that can be implemented. Immunoassays encompassed by the present invention include, but are not limited to, those described in U.S. Pat. No. 4,367,110 (double monoclonal antibody sandwich assay) and U.S. Pat. No. 4,452,901 (western blot). Other assays include immunoprecipitation of labeled ligands and immunocytochemistry, both *in vitro* and *in vivo*.

Immunoassays generally are binding assays. Certain preferred immunoassays are the various types of enzyme linked immunosorbent assays (ELISAs) and radioimmunoassays (RIA) known in the art. Immunohistochemical detection using tissue sections is also particularly useful. In one example, antibodies or antigens are immobilized on a selected surface, such as a well in a polystyrene microtiter plate, dipstick, or column support. Then, a test composition suspected of containing the desired antigen or antibody, such as a clinical sample, is added to the wells. After binding and washing to remove non specifically bound immune complexes, the bound antigen or antibody may be detected. Detection is generally achieved by the addition of another antibody, specific for the desired antigen or antibody, that is linked to a detectable label. This type of ELISA is known as a "sandwich ELISA." Detection also may be achieved by the addition of a second antibody specific for the desired antigen, followed by the addition of a third antibody that has binding affinity for the second antibody, with the third antibody being linked to a detectable label.

Competition ELISAs are also possible implementations in which test samples compete for binding with known amounts of labeled antigens or antibodies. The amount of reactive species in the unknown sample is determined by mixing the sample with the known labeled species before or during incubation with coated wells. The presence of reactive species in the sample acts to reduce the amount of labeled species available for binding to the well and thus reduces the ultimate signal. Irrespective of the format employed, ELISAs have certain features in common, such as coating, incubating or binding, washing to remove non specifically bound species, and detecting the bound immune complexes.

Antigen or antibodies may also be linked to a solid support, such as in the form of plate, beads, dipstick, membrane, or column matrix, and the sample to be analyzed is applied to the immobilized antigen or antibody. In coating a plate with either antigen or antibody, one will generally incubate the wells of the plate with a solution of the antigen or antibody, either overnight or for a specified period. The wells of the plate will then be washed to remove incompletely-adsorbed material. Any remaining available surfaces of the wells are then "coated" with a nonspecific protein that is antigenically neutral with regard to the test antisera. These include bovine serum albumin (BSA), casein, and solutions of milk powder. The coating allows for blocking of nonspecific adsorption sites on the immobilizing surface and thus reduces the background caused by nonspecific binding of antisera onto the surface.

B. Diagnosis of Bacterial Infection

In addition to the use of proteins, polypeptides, and/or peptides, as well as antibodies binding these polypeptides, proteins, and/or peptides, to treat or prevent infection as described above, the present invention contemplates the use of these polypeptides, proteins, peptides, and/or antibodies in a variety of ways, including the detection of the presence of Staphylococci to diagnose an infection, whether in a patient or on medical equipment which may also become infected. In accordance with the invention, a preferred method of detecting the presence of infections involves the steps of obtaining a sample suspected of being infected by one or more staphylococcal bacteria species or strains, such as a sample taken from an individual, for example, from one's blood, saliva, tissues, bone, muscle, cartilage, or skin. Following isolation of the sample, diagnostic assays utilizing the polypeptides, proteins, peptides, and/or antibodies of the present invention may be carried out to detect the presence of staphylococci, and such assay techniques for determining such presence in a sample are well known to those skilled in the art and include methods such as radioimmunoassay, western blot analysis and ELISA assays. In general, in accordance with the invention, a method of diagnosing an infection is contemplated wherein a sample suspected of being infected with staphylococci has added to it the polypeptide, protein, peptide, antibody, or monoclonal antibody in accordance with the present invention, and staphylococci are indicated by antibody binding to the polypeptides, proteins, and/or peptides, or polypeptides, proteins, and/or peptides binding to the antibodies in the sample.

Accordingly, antibodies in accordance with the invention may be used for the prevention of infection from staphylococcal bacteria (i.e., passive immunization), for the treatment of an ongoing infection, or for use as research tools. The term "antibodies" as used herein includes monoclonal, polyclonal, chimeric, single chain, bispecific, simianized, and humanized or primatized antibodies as well as Fab fragments, such as those fragments which maintain the binding specificity of the antibodies, including the products of an Fab immunoglobulin expression library. Accordingly, the invention contemplates the use of single chains such as the variable heavy and light chains of the antibodies. Generation of any of these types of antibodies or antibody fragments is well known to those skilled in the art. Specific examples of the generation of an antibody to a bacterial protein can be found in U.S. Patent Application Pub. No. 20030153022, which is incorporated herein by reference in its entirety.

Any of the above described polypeptides, proteins, peptides, and/or antibodies may be labeled directly with a

detectable label for identification and quantification of staphylococcal bacteria. Labels for use in immunoassays are generally known to those skilled in the art and include enzymes, radioisotopes, and fluorescent, luminescent and chromogenic substances, including colored particles such as colloidal gold or latex beads. Suitable immunoassays include enzyme-linked immunosorbent assays (ELISA).

C. Protective Immunity

In some embodiments of the invention, proteinaceous compositions confer protective immunity to a subject. Protective immunity refers to a body's ability to mount a specific immune response that protects the subject from developing a particular disease or condition that involves the agent against which there is an immune response. An immunogenically effective amount is capable of conferring protective immunity to the subject.

As used herein in the specification and in the claims section that follows, the term polypeptide or peptide refer to a stretch of amino acids covalently linked there amongst via peptide bonds. Different polypeptides have different functionalities according to the present invention. While according to one aspect, a polypeptide is derived from an immunogen designed to induce an active immune response in a recipient, according to another aspect of the invention, a polypeptide is derived from an antibody which results following the elicitation of an active immune response in, for example, an animal, and which can serve to induce a passive immune response in the recipient. In both cases, however, the polypeptide is encoded by a polynucleotide according to any possible codon usage.

As used herein the phrase "immune response" or its equivalent "immunological response" refers to the development of a humoral (antibody mediated), cellular (mediated by antigen-specific T cells or their secretion products) or both humoral and cellular response directed against a protein, peptide, carbohydrate, or polypeptide of the invention in a recipient patient. Such a response can be an active response induced by administration of immunogen or a passive response induced by administration of antibody, antibody containing material, or primed T-cells. A cellular immune response is elicited by the presentation of polypeptide epitopes in association with Class I or Class II MHC molecules, to activate antigen-specific CD4 (+) T helper cells and/or CD8 (+) cytotoxic T cells. The response may also involve activation of monocytes, macrophages, NK cells, basophils, dendritic cells, astrocytes, microglia cells, eosinophils or other components of innate immunity. As used herein "active immunity" refers to any immunity conferred upon a subject by administration of an antigen.

As used herein "passive immunity" refers to any immunity conferred upon a subject without administration of an antigen to the subject. "Passive immunity" therefore includes, but is not limited to, administration of activated immune effectors including cellular mediators or protein mediators (e.g., monoclonal and/or polyclonal antibodies) of an immune response. A monoclonal or polyclonal antibody composition may be used in passive immunization for the prevention or treatment of infection by organisms that carry the antigen recognized by the antibody. An antibody composition may include antibodies that bind to a variety of antigens that may in turn be associated with various organisms. The antibody component can be a polyclonal antiserum. In certain aspects the antibody or antibodies are affinity purified from an animal or second subject that has been challenged with an antigen(s). Alternatively, an antibody mixture may be used, which is a mixture of monoclonal and/or polyclonal antibodies to antigens present in the same,

related, or different microbes or organisms, such as gram-positive bacteria, gram-negative bacteria, including but not limited to *staphylococcus* bacteria.

Passive immunity may be imparted to a patient or subject by administering to the patient immunoglobulins (Ig) and/or other immune factors obtained from a donor or other non-patient source having a known immunoreactivity. In other aspects, an antigenic composition of the present invention can be administered to a subject who then acts as a source or donor for globulin, produced in response to challenge with the antigenic composition ("hyperimmune globulin"), that contains antibodies directed against *Staphylococcus* or other organism. A subject thus treated would donate plasma from which hyperimmune globulin would then be obtained, via conventional plasma-fractionation methodology, and administered to another subject in order to impart resistance against or to treat *staphylococcus* infection. Hyperimmune globulins according to the invention are particularly useful for immune-compromised individuals, for individuals undergoing invasive procedures or where time does not permit the individual to produce their own antibodies in response to vaccination. See U.S. Pat. Nos. 6,936,258, 6,770,278, 6,756,361, 5,548,066, 5,512,282, 4,338,298, and 4,748,018, each of which is incorporated herein by reference in its entirety, for exemplary methods and compositions related to passive immunity.

For purposes of this specification and the accompanying claims the terms "epitope" and "antigenic determinant" are used interchangeably to refer to a site on an antigen to which B and/or T cells respond or recognize. B-cell epitopes can be formed both from contiguous amino acids or noncontiguous amino acids juxtaposed by tertiary folding of a protein. Epitopes formed from contiguous amino acids are typically retained on exposure to denaturing solvents whereas epitopes formed by tertiary folding are typically lost on treatment with denaturing solvents. An epitope typically includes at least 3, and more usually, at least 5 or 8-10 amino acids in a unique spatial conformation. Methods of determining spatial conformation of epitopes include, for example, x-ray crystallography and 2-dimensional nuclear magnetic resonance. See, e.g., Epitope Mapping Protocols (1996). Antibodies that recognize the same epitope can be identified in a simple immunoassay showing the ability of one antibody to block the binding of another antibody to a target antigen. T-cells recognize continuous epitopes of about nine amino acids for CD8 cells or about 13-15 amino acids for CD4 cells. T cells that recognize the epitope can be identified by in vitro assays that measure antigen-dependent proliferation, as determined by ³H-thymidine incorporation by primed T cells in response to an epitope (Burke et al., 1994), by antigen-dependent killing (cytotoxic T lymphocyte assay, Tigges et al., 1996) or by cytokine secretion.

The presence of a cell-mediated immunological response can be determined by proliferation assays (CD4 (+) T cells) or CTL (cytotoxic T lymphocyte) assays. The relative contributions of humoral and cellular responses to the protective or therapeutic effect of an immunogen can be distinguished by separately isolating IgG and T-cells from an immunized syngeneic animal and measuring protective or therapeutic effect in a second subject.

As used herein and in the claims, the terms "antibody" or "immunoglobulin" are used interchangeably and refer to any of several classes of structurally related proteins that function as part of the immune response of an animal or recipient, which proteins include IgG, IgD, IgE, IgA, IgM and related proteins.

Under normal physiological conditions antibodies are found in plasma and other body fluids and in the membrane of certain cells and are produced by lymphocytes of the type denoted B cells or their functional equivalent. Antibodies of the IgG class are made up of four polypeptide chains linked together by disulfide bonds. The four chains of intact IgG molecules are two identical heavy chains referred to as H-chains and two identical light chains referred to as L-chains.

In order to produce polyclonal antibodies, a host, such as a rabbit or goat, is immunized with the antigen or antigen fragment, generally with an adjuvant and, if necessary, coupled to a carrier. Antibodies to the antigen are subsequently collected from the sera of the host. The polyclonal antibody can be affinity purified against the antigen rendering it monospecific.

Monoclonal antibodies can be produced by hyperimmunization of an appropriate donor with the antigen or ex-vivo by use of primary cultures of splenic cells or cell lines derived from spleen (Anavi, 1998; Huston et al., 1991; Johnson et al., 1991; Mernaugh et al., 1995).

As used herein and in the claims, the phrase "an immunological portion of an antibody" includes a Fab fragment of an antibody, a Fv fragment of an antibody, a heavy chain of an antibody, a light chain of an antibody, a heterodimer consisting of a heavy chain and a light chain of an antibody, a variable fragment of a light chain of an antibody, a variable fragment of a heavy chain of an antibody, and a single chain variant of an antibody, which is also known as scFv. In addition, the term includes chimeric immunoglobulins which are the expression products of fused genes derived from different species, one of the species can be a human, in which case a chimeric immunoglobulin is said to be humanized. Typically, an immunological portion of an antibody competes with the intact antibody from which it was derived for specific binding to an antigen.

Optionally, an antibody or preferably an immunological portion of an antibody, can be chemically conjugated to, or expressed as, a fusion protein with other proteins. For purposes of this specification and the accompanying claims, all such fused proteins are included in the definition of antibodies or an immunological portion of an antibody.

As used herein the terms "immunogenic agent" or "immunogen" or "antigen" are used interchangeably to describe a molecule capable of inducing an immunological response against itself on administration to a recipient, either alone, in conjunction with an adjuvant, or presented on a display vehicle.

D. Treatment Methods

A method of the present invention includes treatment for a disease or condition caused by a *staphylococcus* pathogen. An immunogenic polypeptide of the invention can be given to induce an immune response in a person infected with *staphylococcus* or suspected of having been exposed to *staphylococcus*. Methods may be employed with respect to individuals who have tested positive for exposure to *staphylococcus* or who are deemed to be at risk for infection based on possible exposure.

In particular, the invention encompasses a method of treatment for staphylococcal infection, particularly hospital acquired nosocomial infections. The immunogenic compositions and vaccines of the invention are particularly advantageous to use in cases of elective surgery. Such patients will know the date of surgery in advance and could be inoculated in advance. The immunogenic compositions and vaccines of the invention are also advantageous to use to inoculate health care workers.

In some embodiments, the treatment is administered in the presence of adjuvants or carriers or other staphylococcal antigens. Furthermore, in some examples, treatment comprises administration of other agents commonly used against bacterial infection, such as one or more antibiotics.

The use of peptides for vaccination can require, but not necessarily, conjugation of the peptide to an immunogenic carrier protein, such as hepatitis B surface antigen, keyhole limpet hemocyanin, or bovine serum albumin. Methods for performing this conjugation are well known in the art.

V. VACCINE AND OTHER PHARMACEUTICAL COMPOSITIONS AND ADMINISTRATION

A. Vaccines

The present invention includes methods for preventing or ameliorating staphylococcal infections, particularly hospital acquired nosocomial infections. As such, the invention contemplates vaccines for use in both active and passive immunization embodiments. Immunogenic compositions, proposed to be suitable for use as a vaccine, may be prepared from immunogenic SpA polypeptide(s), such as a SpA domain D variant, or immunogenic coagulases. In other embodiments SpA or coagulases can be used in combination with other secreted virulence proteins, surface proteins or immunogenic fragments thereof. In certain aspects, antigenic material is extensively dialyzed to remove undesired small molecular weight molecules and/or lyophilized for more ready formulation into a desired vehicle.

Other options for a protein/peptide-based vaccine involve introducing nucleic acids encoding the antigen(s) as DNA vaccines. In this regard, recent reports described construction of recombinant vaccinia viruses expressing either 10 contiguous minimal CTL epitopes (Thomson, 1996) or a combination of B cell, cytotoxic T-lymphocyte (CTL), and T-helper (Th) epitopes from several microbes (An, 1997), and successful use of such constructs to immunize mice for priming protective immune responses. Thus, there is ample evidence in the literature for successful utilization of peptides, peptide-pulsed antigen presenting cells (APCs), and peptide-encoding constructs for efficient in vivo priming of protective immune responses. The use of nucleic acid sequences as vaccines is exemplified in U.S. Pat. Nos. 5,958,895 and 5,620,896.

The preparation of vaccines that contain polypeptide or peptide sequence(s) as active ingredients is generally well understood in the art, as exemplified by U.S. Pat. Nos. 4,608,251; 4,601,903; 4,599,231; 4,599,230; 4,596,792; and 4,578,770, all of which are incorporated herein by reference. Typically, such vaccines are prepared as injectables either as liquid solutions or suspensions: solid forms suitable for solution in or suspension in liquid prior to injection may also be prepared. The preparation may also be emulsified. The active immunogenic ingredient is often mixed with excipients that are pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like and combinations thereof. In addition, if desired, the vaccine may contain amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, or adjuvants that enhance the effectiveness of the vaccines. In specific embodiments, vaccines are formulated with a combination of substances, as described in U.S. Pat. Nos. 6,793,923 and 6,733,754, which are incorporated herein by reference.

Vaccines may be conventionally administered parenterally, by injection, for example, either subcutaneously or

intramuscularly. Additional formulations which are suitable for other modes of administration include suppositories and, in some cases, oral formulations. For suppositories, traditional binders and carriers may include, for example, polyalkylene glycols or triglycerides: such suppositories may be formed from mixtures containing the active ingredient in the range of about 0.5% to about 10%, preferably about 1% to about 2%. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate and the like. These compositions take the form of solutions, suspensions, tablets, pills, capsules, sustained release formulations or powders and contain about 10% to about 95% of active ingredient, preferably about 25% to about 70%.

The polypeptides and polypeptide-encoding DNA constructs may be formulated into a vaccine as neutral or salt forms. Pharmaceutically-acceptable salts include the acid addition salts (formed with the free amino groups of the peptide) and those that are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like.

Typically, vaccines are administered in a manner compatible with the dosage formulation, and in such amount as will be therapeutically effective and immunogenic. The quantity to be administered depends on the subject to be treated, including the capacity of the individual's immune system to synthesize antibodies and the degree of protection desired. Precise amounts of active ingredient required to be administered depend on the judgment of the practitioner. However, suitable dosage ranges are of the order of several hundred micrograms of active ingredient per vaccination. Suitable regimes for initial administration and booster shots are also variable, but are typified by an initial administration followed by subsequent inoculations or other administrations.

The manner of application may be varied widely. Any of the conventional methods for administration of a vaccine are applicable. These are believed to include oral application within a solid physiologically acceptable base or in a physiologically acceptable dispersion, parenterally, by injection and the like. The dosage of the vaccine will depend on the route of administration and will vary according to the size and health of the subject.

In certain instances, it will be desirable to have multiple administrations of the vaccine, e.g., 2, 3, 4, 5, 6 or more administrations. The vaccinations can be at 1, 2, 3, 4, 5, 6, 7, 8, to 5, 6, 7, 8, 9, 10, 11, 12 twelve week intervals, including all ranges there between. Periodic boosters at intervals of 1-5 years will be desirable to maintain protective levels of the antibodies. The course of the immunization may be followed by assays for antibodies against the antigens, as described in U.S. Pat. Nos. 3,791,932; 4,174,384 and 3,949,064.

1. Carriers

A given composition may vary in its immunogenicity. It is often necessary therefore to boost the host immune system, as may be achieved by coupling a peptide or polypeptide to a carrier. Exemplary and preferred carriers are keyhole limpet hemocyanin (KLH) and bovine serum albumin (BSA). Other albumins such as ovalbumin, mouse serum albumin, or rabbit serum albumin can also be used as carriers. Means for conjugating a polypeptide to a carrier protein are well known in the art and include glutaraldehyde, m-maleimidobenzoyl-N-hydroxysuccinimide ester, carbodiimide, and bis-biazotized benzidine.

2. Adjuvants

The immunogenicity of polypeptide or peptide compositions can be enhanced by the use of non-specific stimulators of the immune response, known as adjuvants. Suitable adjuvants include all acceptable immunostimulatory compounds, such as cytokines, toxins, or synthetic compositions. A number of adjuvants can be used to enhance an antibody response against a variant SpA polypeptide or coagulase, or any other bacterial protein or combination contemplated herein. Adjuvants can (1) trap the antigen in the body to cause a slow release; (2) attract cells involved in the immune response to the site of administration; (3) induce proliferation or activation of immune system cells; or (4) improve the spread of the antigen throughout the subject's body.

Adjuvants include, but are not limited to, oil-in-water emulsions, water-in-oil emulsions, mineral salts, polynucleotides, and natural substances. Specific adjuvants that may be used include IL-1, IL-2, IL-4, IL-7, IL-12, γ -interferon, GM-CSF, BCG, aluminum salts, such as aluminum hydroxide or other aluminum compound, MDP compounds, such as thur-MDP and nor-MDP, CGP (MTP-PE), lipid A, and monophosphoryl lipid A (MPL). RIBI, which contains three components extracted from bacteria, MPL, trehalose dimycolate (TDM), and cell wall skeleton (CWS) in a 2% squalene/Tween 80 emulsion. MHC antigens may even be used. Others adjuvants or methods are exemplified in U.S. Pat. Nos. 6,814,971, 5,084,269, 6,656,462, each of which is incorporated herein by reference).

Various methods of achieving adjuvant affect for the vaccine includes use of agents such as aluminum hydroxide or phosphate (alum), commonly used as about 0.05 to about 0.1% solution in phosphate buffered saline, admixture with synthetic polymers of sugars (Carbopol®) used as an about 0.25% solution, aggregation of the protein in the vaccine by heat treatment with temperatures ranging between about 70° to about 101° C. for a 30-second to 2-minute period, respectively. Aggregation by reactivating with pepsin-treated (Fab) antibodies to albumin; mixture with bacterial cells (e.g., *C. parvum*), endotoxins or lipopolysaccharide components of Gram-negative bacteria; emulsion in physiologically acceptable oil vehicles (e.g., mannide monooleate (Aracel A)); or emulsion with a 20% solution of a perfluorocarbon (Fluosol-DA®) used as a block substitute may also be employed to produce an adjuvant effect.

Examples of and often preferred adjuvants include complete Freund's adjuvant (a non-specific stimulator of the immune response containing killed *Mycobacterium tuberculosis*), incomplete Freund's adjuvants, and aluminum hydroxide.

In some aspects, it is preferred that the adjuvant be selected to be a preferential inducer of either a Th1 or a Th2 type of response. High levels of Th1-type cytokines tend to favor the induction of cell mediated immune responses to a given antigen, while high levels of Th2-type cytokines tend to favor the induction of humoral immune responses to the antigen.

The distinction of Th1 and Th2-type immune response is not absolute. In reality an individual will support an immune response which is described as being predominantly Th1 or predominantly Th2. However, it is often convenient to consider the families of cytokines in terms of that described in murine CD4+ T cell clones by Mosmann and Coffman (Mosmann, and Coffman, 1989). Traditionally, Th1-type responses are associated with the production of the INF- γ and IL-2 cytokines by T-lymphocytes. Other cytokines often directly associated with the induction of Th1-type immune responses are not produced by T-cells, such as IL-12. In

contrast, Th2-type responses are associated with the secretion of IL-4, IL-5, IL-6, IL-10.

In addition to adjuvants, it may be desirable to co-administer biologic response modifiers (BRM) to enhance immune responses. BRMs have been shown to upregulate T cell immunity or downregulate suppressor cell activity. Such BRMs include, but are not limited to, Cimetidine (CIM; 1200 mg/d) (Smith/Kline, PA); or low-dose Cyclophosphamide (CYP; 300 mg/m²) (Johnson/Mead, NJ) and cytokines such as γ -interferon, IL-2, or IL-12 or genes encoding proteins involved in immune helper functions, such as B-7.

B. Lipid Components and Moieties

In certain embodiments, the present invention concerns compositions comprising one or more lipids associated with a nucleic acid or a polypeptide/peptide. A lipid is a substance that is insoluble in water and extractable with an organic solvent. Compounds other than those specifically described herein are understood by one of skill in the art as lipids, and are encompassed by the compositions and methods of the present invention. A lipid component and a non-lipid may be attached to one another, either covalently or non-covalently.

A lipid may be a naturally occurring lipid or a synthetic lipid. However, a lipid is usually a biological substance. Biological lipids are well known in the art, and include for example, neutral fats, phospholipids, phosphoglycerides, steroids, terpenes, lysolipids, glycosphingolipids, glucolipids, sulphatides, lipids with ether and ester-linked fatty acids and polymerizable lipids, and combinations thereof.

A nucleic acid molecule or a polypeptide/peptide, associated with a lipid may be dispersed in a solution containing a lipid, dissolved with a lipid, emulsified with a lipid, mixed with a lipid, combined with a lipid, covalently bonded to a lipid, contained as a suspension in a lipid or otherwise associated with a lipid. A lipid or lipid-poxvirus-associated composition of the present invention is not limited to any particular structure. For example, they may also simply be interspersed in a solution, possibly forming aggregates which are not uniform in either size or shape. In another example, they may be present in a bilayer structure, as micelles, or with a "collapsed" structure. In another non-limiting example, a lipofectamine(Gibco BRL)-poxvirus or Superfect (Qiagen)-poxvirus complex is also contemplated.

In certain embodiments, a composition may comprise about 1%, about 2%, about 3%, about 4%, about 5%, about 6%, about 7%, about 8%, about 9%, about 10%, about 11%, about 12%, about 13%, about 14%, about 15%, about 16%, about 17%, about 18%, about 19%, about 20%, about 21%, about 22%, about 23%, about 24%, about 25%, about 26%, about 27%, about 28%, about 29%, about 30%, about 31%, about 32%, about 33%, about 34%, about 35%, about 36%, about 37%, about 38%, about 39%, about 40%, about 41%, about 42%, about 43%, about 44%, about 45%, about 46%, about 47%, about 48%, about 49%, about 50%, about 51%, about 52%, about 53%, about 54%, about 55%, about 56%, about 57%, about 58%, about 59%, about 60%, about 61%, about 62%, about 63%, about 64%, about 65%, about 66%, about 67%, about 68%, about 69%, about 70%, about 71%, about 72%, about 73%, about 74%, about 75%, about 76%, about 77%, about 78%, about 79%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or any range therebetween, of a particular lipid, lipid type, or non-lipid component such as an adjuvant, antigen, peptide, polypeptide, sugar, nucleic acid or other material disclosed herein or as would be known to one of skill in the art. In a non-limiting

example, a composition may comprise about 10% to about 20% neutral lipids, and about 33% to about 34% of a cerebroside, and about 1% cholesterol. In another non-limiting example, a liposome may comprise about 4% to about 12% terpenes, wherein about 1% of the micelle is specifically lycopene, leaving about 3% to about 11% of the liposome as comprising other terpenes; and about 10% to about 35% phosphatidyl choline, and about 1% of a non-lipid component. Thus, it is contemplated that compositions of the present invention may comprise any of the lipids, lipid types or other components in any combination or percentage range.

C. Combination Therapy

The compositions and related methods of the present invention, particularly administration of a secreted virulence factor or surface protein, including a variant SpA polypeptide or peptide, and/or other bacterial peptides or proteins to a patient/subject, may also be used in combination with the administration of traditional therapies. These include, but are not limited to, the administration of antibiotics such as streptomycin, ciprofloxacin, doxycycline, gentamycin, chloramphenicol, trimethoprim, sulfamethoxazole, ampicillin, tetracycline or various combinations of antibiotics.

In one aspect, it is contemplated that a polypeptide vaccine and/or therapy is used in conjunction with antibacterial treatment. Alternatively, the therapy may precede or follow the other agent treatment by intervals ranging from minutes to weeks. In embodiments where the other agents and/or a proteins or polynucleotides are administered separately, one would generally ensure that a significant period of time did not expire between the time of each delivery, such that the agent and antigenic composition would still be able to exert an advantageously combined effect on the subject. In such instances, it is contemplated that one may administer both modalities within about 12-24 h of each other or within about 6-12 h of each other. In some situations, it may be desirable to extend the time period for administration significantly, where several days (2, 3, 4, 5, 6 or 7) to several weeks (1, 2, 3, 4, 5, 6, 7 or 8) lapse between the respective administrations.

Various combinations may be employed, for example antibiotic therapy is "A" and the immunogenic molecule given as part of an immune therapy regime, such as an antigen, is "B":

A/B/A B/A/B B/B/A A/A/B A/B/B B/A/A A/B/B B/A/B/B

B/B/B/A B/B/A/B A/A/B/B A/B/A/B A/B/B/A B/B/A/A B/A/B/A B/A/A/B A/A/A/B B/A/A/A A/B/A/A A/A/B/A

Administration of the immunogenic compositions of the present invention to a patient/subject will follow general protocols for the administration of such compounds, taking into account the toxicity, if any, of the SpA composition, or other compositions described herein. It is expected that the treatment cycles would be repeated as necessary. It also is contemplated that various standard therapies, such as hydration, may be applied in combination with the described therapy.

D. General Pharmaceutical Compositions

In some embodiments, pharmaceutical compositions are administered to a subject. Different aspects of the present invention involve administering an effective amount of a composition to a subject. In some embodiments of the present invention, staphylococcal antigens, members of the Ess pathway, including polypeptides or peptides of the Esa or Esx class, and/or members of sortase substrates may be administered to the patient to protect against infection by one or more *staphylococcus* pathogens. Alternatively, an

expression vector encoding one or more such polypeptides or peptides may be given to a patient as a preventative treatment. Additionally, such compounds can be administered in combination with an antibiotic or an antibacterial. Such compositions will generally be dissolved or dispersed in a pharmaceutically acceptable carrier or aqueous medium.

In addition to the compounds formulated for parenteral administration, such as those for intravenous or intramuscular injection, other pharmaceutically acceptable forms include, e.g., tablets or other solids for oral administration; time release capsules; and any other form currently used, including creams, lotions, mouthwashes, inhalants and the like.

The active compounds of the present invention can be formulated for parenteral administration, e.g., formulated for injection via the intravenous, intramuscular, subcutaneous, or even intraperitoneal routes. The preparation of an aqueous composition that contains a compound or compounds that increase the expression of an MHC class I molecule will be known to those of skill in the art in light of the present disclosure. Typically, such compositions can be prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for use to prepare solutions or suspensions upon the addition of a liquid prior to injection can also be prepared; and, the preparations can also be emulsified.

Solutions of the active compounds as free base or pharmacologically acceptable salts can be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions can also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations contain a preservative to prevent the growth of microorganisms.

The pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions; formulations including sesame oil, peanut oil, or aqueous propylene glycol; and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. In all cases the form must be sterile and must be fluid to the extent that it may be easily injected. It also should be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi.

The proteinaceous compositions may be formulated into a neutral or salt form. Pharmaceutically acceptable salts, include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like.

The carrier also can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and vegetable oils. The proper fluidity can be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion, and by the use of surfactants. The prevention of the action of microorganisms can be brought about by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example,

sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions are prepared by incorporating the active compounds in the required amount in the appropriate solvent with various of the other ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the various sterilized active ingredients into a sterile vehicle which contains the basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum-drying and freeze-drying techniques, which yield a powder of the active ingredient, plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Administration of the compositions according to the present invention will typically be via any common route. This includes, but is not limited to oral, nasal, or buccal administration. Alternatively, administration may be by orthotic, intradermal, subcutaneous, intramuscular, intraperitoneal, intranasal, or intravenous injection. In certain embodiments, a vaccine composition may be inhaled (e.g., U.S. Pat. No. 6,651,655, which is specifically incorporated by reference). Such compositions would normally be administered as pharmaceutically acceptable compositions that include physiologically acceptable carriers, buffers or other excipients. As used herein, the term "pharmaceutically acceptable" refers to those compounds, materials, compositions, and/or dosage forms which are, within the scope of sound medical judgment, suitable for contact with the tissues of human beings and animals without excessive toxicity, irritation, allergic response, or other problem complications commensurate with a reasonable benefit/risk ratio. The term "pharmaceutically acceptable carrier," means a pharmaceutically acceptable material, composition or vehicle, such as a liquid or solid filler, diluent, excipient, solvent or encapsulating material, involved in carrying or transporting a chemical agent.

For parenteral administration in an aqueous solution, for example, the solution should be suitably buffered, if necessary, and the liquid diluent first rendered isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous, and intraperitoneal administration. In this connection, sterile aqueous media which can be employed will be known to those of skill in the art in light of the present disclosure. For example, one dosage could be dissolved in isotonic NaCl solution and either added to hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, Remington's Pharmaceutical Sciences, 1990). Some variation in dosage will necessarily occur depending on the condition of the subject. The person responsible for administration will, in any event, determine the appropriate dose for the individual subject.

An effective amount of therapeutic or prophylactic composition is determined based on the intended goal. The term "unit dose" or "dosage" refers to physically discrete units suitable for use in a subject, each unit containing a predetermined quantity of the composition calculated to produce the desired responses discussed above in association with its administration, i.e., the appropriate route and regimen. The quantity to be administered, both according to number of treatments and unit dose, depends on the protection desired. It is contemplated that in compositions of the invention, there is between about 0.001 mg and about 10 mg of total

antigen, antibody, polypeptide, peptide, and/or protein per ml. The concentration of protein in a composition can be about, at least about or at most about 0.001, 0.010, 0.050, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.5, 2.0, 2.5, 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5, 8.0, 8.5, 9.0, 9.5, 10.0 mg/ml or more (or any range derivable therein). Of this, about, at least about, or at most about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% may be an SpA variant or an antibody that specifically binds SpA. In certain embodiments a dose of about, at least about or at most about 0.001, 0.010, 0.050, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.5, 2.0, 2.5, 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5, 8.0, 8.5, 9.0, 9.5, 10.0 mg/kg or more, including all values and ranges there between are administered to a subject.

Precise amounts of the composition also depend on the judgment of the practitioner and are peculiar to each individual. Factors affecting dose include physical and clinical state of the subject, route of administration, intended goal of treatment (alleviation of symptoms versus cure), and potency, stability, and toxicity of the particular composition.

Upon formulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically or prophylactically effective. The formulations are easily administered in a variety of dosage forms, such as the type of injectable solutions described above.

E. In Vitro, Ex Vivo, or In Vivo Administration

As used herein, the term in vitro administration refers to manipulations performed on cells removed from or outside of a subject, including, but not limited to cells in culture. The term ex vivo administration refers to cells which have been manipulated in vitro, and are subsequently administered to a subject. The term in vivo administration includes all manipulations performed within a subject.

In certain aspects of the present invention, the compositions may be administered either in vitro, ex vivo, or in vivo. In certain in vitro embodiments, autologous B-lymphocyte cell lines are incubated with a virus vector of the instant invention for 24 to 48 hours or with a variant SpA and/or coagulase and/or any other composition described herein for two hours. The transduced cells can then be used for in vitro analysis, or alternatively for ex vivo administration. U.S. Pat. Nos. 4,690,915 and 5,199,942, both incorporated herein by reference, disclose methods for ex vivo manipulation of blood mononuclear cells and bone marrow cells for use in therapeutic applications.

F. Antibodies and Passive Immunization

Another aspect of the invention is a method of preparing an immunoglobulin for use in prevention or treatment of staphylococcal infection comprising the steps of immunizing a recipient or donor with the vaccine of the invention and isolating immunoglobulin from the recipient or donor. An immunoglobulin prepared by this method is a further aspect of the invention. A pharmaceutical composition comprising the immunoglobulin of the invention and a pharmaceutically acceptable carrier is a further aspect of the invention which could be used in the manufacture of a medicament for the treatment or prevention of staphylococcal disease. A method for treatment or prevention of staphylococcal infection comprising a step of administering to a patient an effective

amount of the pharmaceutical preparation of the invention is a further aspect of the invention.

Inocula for polyclonal antibody production are typically prepared by dispersing the antigenic composition in a physiologically tolerable diluent such as saline or other adjuvants suitable for human use to form an aqueous composition. An immunostimulatory amount of inoculum is administered to a mammal and the inoculated mammal is then maintained for a time sufficient for the antigenic composition to induce protective antibodies.

The antibodies can be isolated to the extent desired by well known techniques such as affinity chromatography (Harlow and Lane, 1988). Antibodies can include antiserum preparations from a variety of commonly used animals, e.g. goats, primates, donkeys, swine, horses, guinea pigs, rats or man.

An immunoglobulin produced in accordance with the present invention can include whole antibodies, antibody fragments or subfragments. Antibodies can be whole immunoglobulins of any class (e.g., IgG, IgM, IgA, IgD or IgE), chimeric antibodies or hybrid antibodies with dual specificity to two or more antigens of the invention. They may also be fragments (e.g., F(ab')₂, Fab', Fab, Fv and the like) including hybrid fragments. An immunoglobulin also includes natural, synthetic, or genetically engineered proteins that act like an antibody by binding to specific antigens to form a complex.

A vaccine of the present invention can be administered to a recipient who then acts as a source of immunoglobulin, produced in response to challenge from the specific vaccine. A subject thus treated would donate plasma from which hyperimmune globulin would be obtained via conventional plasma fractionation methodology. The hyperimmune globulin would be administered to another subject in order to impart resistance against or treat staphylococcal infection. Hyperimmune globulins of the invention are particularly useful for treatment or prevention of staphylococcal disease in infants, immune compromised individuals, or where treatment is required and there is no time for the individual to produce antibodies in response to vaccination.

An additional aspect of the invention is a pharmaceutical composition comprising two or more monoclonal antibodies (or fragments thereof; preferably human or humanised) reactive against at least two constituents of the immunogenic composition of the invention, which could be used to treat or prevent infection by Gram positive bacteria, preferably staphylococci, more preferably *S. aureus* or *S. epidermidis*. Such pharmaceutical compositions comprise monoclonal antibodies that can be whole immunoglobulins of any class, chimeric antibodies, or hybrid antibodies with specificity to two or more antigens of the invention. They may also be fragments (e.g., F(ab')₂, Fab', Fab, Fv and the like) including hybrid fragments.

Methods of making monoclonal antibodies are well known in the art and can include the fusion of splenocytes with myeloma cells (Kohler and Milstein, 1975; Harlow and Lane, 1988). Alternatively, monoclonal Fv fragments can be obtained by screening a suitable phage display library (Vaughan et al., 1998). Monoclonal antibodies may be humanized or part humanized by known methods.

VI. EXAMPLES

The following examples are given for the purpose of illustrating various embodiments of the invention and are not meant to limit the present invention in any fashion. One skilled in the art will appreciate readily that the present

invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those objects, ends and advantages inherent herein. The present examples, along with the methods described herein are presently representative of preferred embodiments, are exemplary, and are not intended as limitations on the scope of the invention. Changes therein and other uses which are encompassed within the spirit of the invention as defined by the scope of the claims will occur to those skilled in the art.

Example 1

Immunization with SpA_{KKAA} Modifies Host Immune Responses to Staphylococcal Infection

The model of immune evasion during *S. aureus* infections includes the initial activation of B cells via IgM receptor crosslinking by cell wall anchored or secreted protein A—up to 20% of peptidoglycan with attached surface protein is released during each bacterial division event (Ton-That et al., 1999). In the absence of specific antigen stimuli, activated B cells undergo apoptotic collapse, thereby diminishing host antibody production against antigens that are presented during staphylococcal infection. If so, neutralizing SpA-specific antibodies may enable animals to develop humoral immune responses against many different staphylococcal antigens. This possibility was investigated by immunizing BALB/c mice with SpA_{KKAA} or an adjuvant (aluminum hydroxide) control followed by intravenous challenge with a sublethal dose of MRSA strain USA300. Serum samples were withdrawn thirty days after MRSA challenge and then analyzed by immunoblotting with 27 staphylococcal antigens immobilized on a membrane filter (FIG. 1). Naïve mice, which had not been infected with the MRSA strain USA300 LAC, did not harbor antibodies against ClfA, ClfB, Coa, Eap, Ebh, Emp, EsxA, EsxB, FnbpA, FnbpB, Hla, IsdA, IsdB, LukD, LukE, LukF, SdrC, SdrD, SdrE, SasA, SasD, SasF, SasG, SasI, SasK, SpA_{KKAA} or vWbp (data not shown). Mock immunized mice that had been subjected to USA300 infection developed high-titer antibodies against the Eap protein as well as low-titer antibodies against IsdA, IsdB, Hla, LukD, LukE and LukF (FIG. 1). Animals that been immunized and that elaborated SpA_{KKAA}-specific antibodies [IgG titer 2,907 ($\pm$ 357); $P < 0.001$ SpA_{KKAA} vs. mock] mounted humoral immune responses against every one of the 27 antigens in response to a challenge with the MRSA strain USA300 (FIG. 1). With the exception of Eap, IsdA and IsdB antibodies, the serum of SpA_{KKAA}-immunized animals harbored higher antibody titers against each staphylococcal antigen when compared to mice that had been naïve at the time of challenge (FIG. 1).

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Leu Asn Met Pro Asn Leu Asn Glu Ala Gln Arg Asn Gly Phe Ile Gln
                20              25              30
Ser Leu Lys Asp Asp Pro Ser Gln Ser Thr Asn Val Leu Gly Glu Ala
35              40              45
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Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys
20              25              30
Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Gln Lys Leu
35              40              45
Asn Asp Ser
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1          5          10          15

Met Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu
          20          25          30

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

Leu Asn Glu Ser
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```

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1          5          10          15

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

Lys Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys
          35          40          45

Leu Asn Asp Ala
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```

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```

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1          5          10          15

Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu
          20          25          30

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

Leu Asn Asp Ala
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Asn Asn Phe Asn Lys Asp Xaa Xaa Ser Ala Phe Tyr Glu Ile Leu Asn
1          5          10          15

Met Pro Asn Leu Asn Glu Ala Gln Arg Asn Gly Phe Ile Gln Ser Leu
          20          25          30

Lys Xaa Xaa Pro Ser Gln Ser Thr Asn Val Leu Gly Glu Ala Lys Lys
          35          40          45

Leu Asn Glu Ser
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 1             5             10             15

Met Pro Asn Leu Asn Glu Ala Gln Arg Asn Gly Phe Ile Gln Ser Leu
          20             25             30

Lys Tyr Tyr Pro Ser Gln Ser Thr Asn Val Leu Gly Glu Ala Lys Lys
          35             40             45

Leu Asn Glu Ser
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<212> TYPE: PRT
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<400> SEQUENCE: 9

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Ala Ser Val Thr Leu Gly Thr Leu Leu Ile Ser Gly Gly Val Thr Pro
          20             25             30

Ala Ala Asn Ala Ala Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr
          35             40             45

Gln Val Leu Asn Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe
          50             55             60

Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly
          65             70             75             80

Glu Ala Gln Lys Leu Asn Asp Ser Gln Ala Pro Lys Ala Asp Ala Gln
          85             90             95

Gln Asn Asn Phe Asn Lys Asp Gln Gln Ser Ala Phe Tyr Glu Ile Leu
          100            105            110

Asn Met Pro Asn Leu Asn Glu Ala Gln Arg Asn Gly Phe Ile Gln Ser
          115            120            125

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

Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys
          145            150            155            160

Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn
          165            170            175

Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
          180            185            190

Gln Ser Ala Asn Leu Leu Ser Glu Ala Lys Lys Leu Asn Glu Ser Gln
          195            200            205

Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe
          210            215            220

Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly
          225            230            235            240

Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Val Ser Lys Glu Ile Leu

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245	250	255
Ala Glu Ala Lys Lys Leu Asn Asp	Ala Gln Ala Pro Lys Glu Glu Asp	
260	265	270
Asn Lys Lys Pro Gly Lys Glu Asp	Gly Asn Lys Pro Gly Lys Glu Asp	
275	280	285
Gly Asn Lys Pro Gly Lys Glu Asp	Asn Lys Lys Pro Gly Lys Glu Asp	
290	295	300
Gly Asn Lys Pro Gly Lys Glu Asp	Asn Asn Lys Pro Gly Lys Glu Asp	
305	310	315
Gly Asn Lys Pro Gly Lys Glu Asp	Asn Asn Lys Pro Gly Lys Glu Asp	
325	330	335
Gly Asn Lys Pro Gly Lys Glu Asp	Gly Asn Lys Pro Gly Lys Glu Asp	
340	345	350
Gly Asn Gly Val His Val Val Lys Pro	Gly Asp Thr Val Asn Asp Ile	
355	360	365
Ala Lys Ala Asn Gly Thr Thr Ala Asp	Lys Ile Ala Ala Asp Asn Lys	
370	375	380
Leu Ala Asp Lys Asn Met Ile Lys Pro	Gly Gln Glu Leu Val Val Asp	
385	390	395
Lys Lys Gln Pro Ala Asn His Ala Asp	Ala Asn Lys Ala Gln Ala Leu	
405	410	415
Pro Glu Thr Gly Glu Glu Asn Pro Phe	Ile Gly Thr Thr Val Phe Gly	
420	425	430
Gly Leu Ser Leu Ala Leu Gly Ala Ala	Leu Leu Ala Gly Arg Arg Arg	
435	440	445
Glu Leu		
450		
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20 25 30		
Ala Ala Asn Ala Ala Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr		
35 40 45		
Gln Val Leu Asn Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe		
50 55 60		
Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly		
65 70 75 80		
Glu Ala Gln Lys Leu Asn Asp Ser Gln Ala Pro Lys Ala Asp Ala Gln		
85 90 95		
Gln Asn Asn Phe Asn Lys Asp Gln Gln Ser Ala Phe Tyr Glu Ile Leu		
100 105 110		
Asn Met Pro Asn Leu Asn Glu Ala Gln Arg Asn Gly Phe Ile Gln Ser		
115 120 125		
Leu Lys Asp Asp Pro Ser Gln Ser Thr Asn Val Leu Gly Glu Ala Lys		
130 135 140		
Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys		
145 150 155 160		

[illegible]

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Ser	Tyr	Gly	Gln	Gly	Ser	Asp	Gln	Ile	Arg	Gln	Ile	Leu	Ser	Asp	Leu
			20					25					30		
Thr	Arg	Ala	Gln	Gly	Glu	Ile	Ala	Ala	Asn	Trp	Glu	Gly	Gln	Ala	Phe
		35					40					45			
Ser	Arg	Phe	Glu	Glu	Gln	Phe	Gln	Gln	Leu	Ser	Pro	Lys	Val	Glu	Lys
	50					55					60				
Phe	Ala	Gln	Leu	Leu	Glu	Ile	Lys	Gln	Gln	Leu	Asn	Ser	Thr	Ala	
65					70				75					80	

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

Gln

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<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 12

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Ala Lys Gln Leu Ala Ala Lys Ile Ala Lys Asp Ile Glu Ala Cys Gln
20 25 30
Lys Gln Thr Gln Gln Leu Ala Glu Tyr Ile Glu Gly Ser Asp Trp Glu
35 40 45
Gly Gln Phe Ala Asn Lys Val Lys Asp Val Leu Leu Ile Met Ala Lys
50 55 60
Phe Gln Glu Glu Leu Val Gln Pro Met Ala Asp His Gln Lys Ala Ile
65 70 75 80
Asp Asn Leu Ser Gln Asn Leu Ala Lys Tyr Asp Thr Leu Ser Ile Lys
85 90 95
Gln Gly Leu Asp Arg Val
100

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<213> ORGANISM: Staphylococcus sp

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20 25 30
Ala Ser Ile Leu Val Gly Thr Thr Leu Ile Phe Gly Leu Gly Asn Gln
35 40 45
Glu Ala Lys Ala Ala Glu Ser Thr Asn Lys Glu Leu Asn Glu Ala Thr
50 55 60
Thr Ser Ala Ser Asp Asn Gln Ser Ser Asp Lys Val Asp Met Gln Gln
65 70 75 80
Leu Asn Gln Glu Asp Asn Thr Lys Asn Asp Asn Gln Lys Glu Met Val
85 90 95
Ser Ser Gln Gly Asn Glu Thr Thr Ser Asn Gly Asn Lys Ser Ile Glu
100 105 110
Lys Glu Ser Val Gln Ser Thr Thr Gly Asn Lys Val Glu Val Ser Thr
115 120 125
Ala Lys Ser Asp Glu Gln Ala Ser Pro Lys Ser Thr Asn Glu Asp Leu
130 135 140
Asn Thr Lys Gln Thr Ile Ser Asn Gln Glu Gly Leu Gln Pro Asp Leu
145 150 155 160
Leu Glu Asn Lys Ser Val Val Asn Val Gln Pro Thr Asn Glu Glu Asn
165 170 175
Lys Lys Val Asp Ala Lys Thr Glu Ser Thr Thr Leu Asn Val Lys Ser
180 185 190

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Asp	Ala	Ile	Lys	Ser	Asn	Ala	Glu	Thr	Leu	Val	Asp	Asn	Asn	Ser	Asn
		195					200					205			
Ser	Asn	Asn	Glu	Asn	Asn	Ala	Asp	Ile	Ile	Leu	Pro	Lys	Ser	Thr	Ala
	210					215					220				
Pro	Lys	Ser	Leu	Asn	Thr	Arg	Met	Arg	Met	Ala	Ala	Ile	Gln	Pro	Asn
	225				230					235					240
Ser	Thr	Asp	Ser	Lys	Asn	Val	Asn	Asp	Leu	Ile	Thr	Ser	Asn	Thr	Thr
				245					250					255	
Leu	Thr	Val	Val	Asp	Ala	Asp	Asn	Ser	Lys	Thr	Ile	Val	Pro	Ala	Gln
			260					265					270		
Asp	Tyr	Leu	Ser	Leu	Lys	Ser	Gln	Ile	Thr	Val	Asp	Asp	Lys	Val	Lys
	275						280					285			
Ser	Gly	Asp	Tyr	Phe	Thr	Ile	Lys	Tyr	Ser	Asp	Thr	Val	Gln	Val	Tyr
	290					295					300				
Gly	Leu	Asn	Pro	Glu	Asp	Ile	Lys	Asn	Ile	Gly	Asp	Ile	Lys	Asp	Pro
	305				310					315					320
Asn	Asn	Gly	Glu	Thr	Ile	Ala	Thr	Ala	Lys	His	Asp	Thr	Ala	Asn	Asn
				325					330					335	
Leu	Ile	Thr	Tyr	Thr	Phe	Thr	Asp	Tyr	Val	Asp	Arg	Phe	Asn	Ser	Val
			340					345					350		
Lys	Met	Gly	Ile	Asn	Tyr	Ser	Ile	Tyr	Met	Asp	Ala	Asp	Thr	Ile	Pro
	355					360						365			
Val	Asp	Lys	Lys	Asp	Val	Pro	Phe	Ser	Val	Thr	Ile	Gly	Asn	Gln	Ile
	370					375					380				
Thr	Thr	Thr	Thr	Ala	Asp	Ile	Thr	Tyr	Pro	Ala	Tyr	Lys	Glu	Ala	Asp
	385				390					395					400
Asn	Asn	Ser	Ile	Gly	Ser	Ala	Phe	Thr	Glu	Thr	Val	Ser	His	Val	Gly
				405					410					415	
Asn	Val	Glu	Asp	Pro	Gly	Tyr	Tyr	Asn	Gln	Val	Val	Tyr	Val	Asn	Pro
			420					425					430		
Met	Asp	Lys	Asp	Leu	Lys	Gly	Ala	Lys	Leu	Lys	Val	Glu	Ala	Tyr	His
	435						440					445			
Pro	Lys	Tyr	Pro	Thr	Asn	Ile	Gly	Gln	Ile	Asn	Gln	Asn	Val	Thr	Asn
	450					455					460				
Ile	Lys	Ile	Tyr	Arg	Val	Pro	Glu	Gly	Tyr	Thr	Leu	Asn	Lys	Gly	Tyr
	465				470					475					480
Asp	Val	Asn	Thr	Asn	Asp	Leu	Val	Asp	Val	Thr	Asp	Glu	Phe	Lys	Asn
				485				490						495	
Lys	Met	Thr	Tyr	Gly	Ser	Asn	Gln	Ser	Val	Asn	Leu	Asp	Phe	Gly	Asp
			500					505					510		
Ile	Thr	Ser	Ala	Tyr	Val	Val	Met	Val	Asn	Thr	Lys	Phe	Gln	Tyr	Thr
			515					520				525			
Asn	Ser	Glu	Ser	Pro	Thr	Leu	Val	Gln	Met	Ala	Thr	Leu	Ser	Ser	Thr
	530					535						540			
Gly															

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Leu Pro Asn Gly Asp Tyr Arg Val Glu Phe Ser Asn Leu Pro Lys Gly		
625	630	635 640
Tyr Glu Val Thr Pro Ser Lys Gln Gly Asn Asn Glu Glu Leu Asp Ser		
	645	650 655
Asn Gly Leu Ser Ser Val Ile Thr Val Asn Gly Lys Asp Asn Leu Ser		
	660	665 670
Ala Asp Leu Gly Ile Tyr Lys Pro Lys Tyr Asn Leu Gly Asp Tyr Val		
	675	680 685
Trp Glu Asp Thr Asn Lys Asn Gly Ile Gln Asp Gln Asp Glu Lys Gly		
	690	695 700
Ile Ser Gly Val Thr Val Thr Leu Lys Asp Glu Asn Gly Asn Val Leu		
	705	710 715 720
Lys Thr Val Thr Thr Asp Ala Asp Gly Lys Tyr Lys Phe Thr Asp Leu		
	725	730 735
Asp Asn Gly Asn Tyr Lys Val Glu Phe Thr Thr Pro Glu Gly Tyr Thr		
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Pro Thr Thr Val Thr Ser Gly Ser Asp Ile Glu Lys Asp Ser Asn Gly		
	755	760 765
Leu Thr Thr Thr Gly Val Ile Asn Gly Ala Asp Asn Met Thr Leu Asp		
	770	775 780
Ser Gly Phe Tyr Lys Thr Pro Lys Tyr Asn Leu Gly Asn Tyr Val Trp		
	785	790 795 800
Glu Asp Thr Asn Lys Asp Gly Lys Gln Asp Ser Thr Glu Lys Gly Ile		
	805	810 815
Ser Gly Val Thr Val Thr Leu Lys Asn Glu Asn Gly Glu Val Leu Gln		
	820	825 830
Thr Thr Lys Thr Asp Lys Asp Gly Lys Tyr Gln Phe Thr Gly Leu Glu		
	835	840 845
Asn Gly Thr Tyr Lys Val Glu Phe Glu Thr Pro Ser Gly Tyr Thr Pro		
	850	855 860
Thr Gln Val Gly Ser Gly Thr Asp Glu Gly Ile Asp Ser Asn Gly Thr		
	865	870 875 880
Ser Thr Thr Gly Val Ile Lys Asp Lys Asp Asn Asp Thr Ile Asp Ser		
	885	890 895
Gly Phe Tyr Lys Pro Thr Tyr Asn Leu Gly Asp Tyr Val Trp Glu Asp		
	900	905 910
Thr Asn Lys Asn Gly Val Gln Asp Lys Asp Glu Lys Gly Ile Ser Gly		
	915	920 925
Val Thr Val Thr Leu Lys Asp Glu Asn Asp Lys Val Leu Lys Thr Val		
	930	935 940
Thr Thr Asp Glu Asn Gly Lys Tyr Gln Phe Thr Asp Leu Asn Asn Gly		
	945	950 955 960
Thr Tyr Lys Val Glu Phe Glu Thr Pro Ser Gly Tyr Thr Pro Thr Ser		
	965	970 975
Val Thr Ser Gly Asn Asp Thr Glu Lys Asp Ser Asn Gly Leu Thr Thr		
	980	985 990
Thr Gly Val Ile Lys Asp Ala Asp Asn Met Thr Leu Asp Ser Gly Phe		
	995	1000 1005
Tyr Lys Thr Pro Lys Tyr Ser Leu Gly Asp Tyr Val Trp Tyr Asp		
	1010	1015 1020
Ser Asn Lys Asp Gly Lys Gln Asp Ser Thr Glu Lys Gly Ile Lys		
	1025	1030 1035

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<210> SEQ ID NO 14
<211> LENGTH: 1141
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp
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<400> SEQUENCE: 14

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

Ser Asn Arg Leu Asn Lys Phe Ser Ile Arg Lys Tyr Thr Val Gly Thr
20      25      30

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

Glu Ala Lys Ala Ala Glu Asn Thr Ser Thr Glu Asn Ala Lys Gln Asp
50      55      60

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

Asn Ser Thr Thr Glu Asn Asp Ser Thr Asn Pro Ile Lys Lys Glu Thr
85      90      95

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

Thr Gln Gln Gln Gln Asn Asn Val Thr Ala Thr Thr Glu Thr Lys Pro
115     120     125

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

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

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

Lys Pro Thr Thr Pro Gln Glu Ser Thr Asn Ile Glu Asn Ser Gln Pro
180     185     190

Gln Pro Thr Pro Ser Lys Val Asp Asn Gln Val Thr Asp Ala Thr Asn
195     200     205

Pro Lys Glu Pro Val Asn Val Ser Lys Glu Glu Leu Lys Asn Asn Pro
210     215     220

Glu Lys Leu Lys Glu Leu Val Arg Asn Asp Asn Asn Thr Asp Arg Ser
225     230     235     240

Thr Lys Pro Val Ala Thr Ala Pro Thr Ser Val Ala Pro Lys Arg Leu
245     250     255

Asn Ala Lys Met Arg Phe Ala Val Ala Gln Pro Ala Ala Val Ala Ser
260     265     270

Asn Asn Val Asn Asp Leu Ile Thr Val Thr Lys Gln Thr Ile Lys Val
275     280     285

Gly Asp Gly Lys Asp Asn Val Ala Ala Ala His Asp Gly Lys Asp Ile
290     295     300

Glu Tyr Asp Thr Glu Phe Thr Ile Asp Asn Lys Val Lys Lys Gly Asp
305     310     315     320

Thr Met Thr Ile Asn Tyr Asp Lys Asn Val Ile Pro Ser Asp Leu Thr
325     330     335

Asp Lys Asn Asp Pro Ile Asp Ile Thr Asp Pro Ser Gly Glu Val Ile
340     345     350

Ala Lys Gly Thr Phe Asp Lys Ala Thr Lys Gln Ile Thr Tyr Thr Phe
355     360     365

Thr Asp Tyr Val Asp Lys Tyr Glu Asp Ile Lys Ala Arg Leu Thr Leu
370     375     380

Tyr Ser Tyr Ile Asp Lys Gln Ala Val Pro Asn Glu Thr Ser Leu Asn
385     390     395     400

Leu Thr Phe Ala Thr Ala Gly Lys Glu Thr Ser Gln Asn Val Ser Val
405     410     415

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Asp	Tyr	Gln	Asp	Pro	Met	Val	His	Gly	Asp	Ser	Asn	Ile	Gln	Ser	Ile
			420					425					430		
Phe	Thr	Lys	Leu	Asp	Glu	Asn	Lys	Gln	Thr	Ile	Glu	Gln	Gln	Ile	Tyr
		435					440					445			
Val	Asn	Pro	Leu	Lys	Lys	Thr	Ala	Thr	Asn	Thr	Lys	Val	Asp	Ile	Ala
	450					455					460				
Gly	Ser	Gln	Val	Asp	Asp	Tyr	Gly	Asn	Ile	Lys	Leu	Gly	Asn	Gly	Ser
465				470						475					480
Thr	Ile	Ile	Asp	Gln	Asn	Thr	Glu	Ile	Lys	Val	Tyr	Lys	Val	Asn	Pro
			485						490					495	
Asn	Gln	Gln	Leu	Pro	Gln	Ser	Asn	Arg	Ile	Tyr	Asp	Phe	Ser	Gln	Tyr
			500					505					510		
Glu	Asp	Val	Thr	Ser	Gln	Phe	Asp	Asn	Lys	Lys	Ser	Phe	Ser	Asn	Asn
	515						520					525			
Val	Ala	Thr	Leu	Asp	Phe	Gly	Asp	Ile	Asn	Ser	Ala	Tyr	Ile	Ile	Lys
	530					535					540				
Val	Val	Ser	Lys	Tyr	Thr	Pro	Thr	Ser	Asp	Gly	Glu	Leu	Asp	Ile	Ala
545					550					555					560
Gln	Gly	Thr	Ser	Met	Arg	Thr	Thr	Asp	Lys	Tyr	Gly	Tyr	Tyr	Asn	Tyr
				565					570					575	
Ala	Gly	Tyr	Ser	Asn	Phe	Ile	Val	Thr	Ser	Asn	Asp	Thr	Gly	Gly	Gly
			580					585					590		
Asp	Gly	Thr	Val	Lys	Pro	Glu	Glu	Lys	Leu	Tyr	Lys	Ile	Gly	Asp	Tyr
		595					600					605			
Val	Trp	Glu	Asp	Val	Asp	Lys	Asp	Gly	Val	Gln	Gly	Thr	Asp	Ser	Lys
	610					615					620				
Glu	Lys	Pro	Met	Ala	Asn	Val	Leu	Val	Thr	Leu	Thr	Tyr	Pro	Asp	Gly
625					630					635					640
Thr	Thr	Lys	Ser	Val	Arg	Thr	Asp	Ala	Asn	Gly	His	Tyr	Glu	Phe	Gly
				645				650						655	
Gly	Leu	Lys	Asp	Gly	Glu	Thr	Tyr	Thr	Val	Lys	Phe	Glu	Thr	Pro	Ala
			660					665					670		
Gly	Tyr	Leu	Pro	Thr	Lys	Val	Asn	Gly	Thr	Thr	Asp	Gly	Glu	Lys	Asp
		675					680					685			
Ser	Asn	Gly	Ser	Ser	Ile	Thr	Val	Lys	Ile	Asn	Gly	Lys	Asp	Asp	Met
	690					695					700				
Ser	Leu	Asp	Thr	Gly	Phe	Tyr	Lys	Glu	Pro	Lys	Tyr	Asn	Leu	Gly	Asp
705					710					715					720
Tyr	Val	Trp	Glu	Asp	Thr	Asn	Lys	Asp	Gly	Ile	Gln	Asp	Ala	Asn	Glu
			725						730					735	
Pro	Gly	Ile	Lys	Asp	Val	Lys	Val	Thr	Leu	Lys	Asp	Ser	Thr	Gly	Lys
			740					745					750		
Val	Ile	Gly	Thr	Thr	Thr	Thr	Asp	Ala	Ser	Gly	Lys	Tyr	Lys	Phe	Thr
		755					760					765			
Asp	Leu	Asp	Asn	Gly	Asn	Tyr	Thr	Val	Glu	Phe	Glu	Thr	Pro	Ala	Gly
	770					775					780				
Tyr	Thr	Pro	Thr	Val	Lys	Asn	Thr	Thr	Ala	Glu	Asp	Lys	Asp	Ser	Asn
785					790					795					800
Gly	Leu	Thr	Thr	Thr	Gly	Val	Ile	Lys	Asp	Ala	Asp	Asn	Met	Thr	Leu
				805					810					815	
Asp	Ser	Gly	Phe	Tyr	Lys	Thr	Pro	Lys	Tyr	Ser	Leu	Gly	Asp	Tyr	Val
			820					825					830		

Trp	Tyr	Asp	Ser	Asn	Lys	Asp	Gly	Lys	Gln	Asp	Ser	Thr	Glu	Lys	Gly
		835					840					845			
Ile	Lys	Asp	Val	Lys	Val	Thr	Leu	Leu	Asn	Glu	Lys	Gly	Glu	Val	Ile
	850					855				860					
Gly	Thr	Thr	Lys	Thr	Asp	Glu	Asn	Gly	Lys	Tyr	Arg	Phe	Asp	Asn	Leu
865					870					875					880
Asp	Ser	Gly	Lys	Tyr	Lys	Val	Ile	Phe	Glu	Lys	Pro	Ala	Gly	Leu	Thr
				885					890					895	
Gln	Thr	Val	Thr	Asn	Thr	Thr	Glu	Asp	Asp	Lys	Asp	Ala	Asp	Gly	Gly
			900					905					910		
Glu	Val	Asp	Val	Thr	Ile	Thr	Asp	His	Asp	Asp	Phe	Thr	Leu	Asp	Asn
	915						920					925			
Gly	Tyr	Phe	Glu	Glu	Asp	Thr	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
930						935					940				
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
945					950					955					960
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
				965					970					975	
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
				980				985					990		
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
	995						1000					1005			
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
1010						1015					1020				
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Ser
1025						1030					1035				
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
1040						1045					1050				
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Ser
1055						1060					1065				
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ala	Gly	
1070						1075					1080				
Lys	His	Thr	Pro	Val	Lys	Pro	Met	Ser	Thr	Thr	Lys	Asp	His	His	
1085						1090					1095				
Asn	Lys	Ala	Lys	Ala	Leu	Pro	Glu	Thr	Gly	Ser	Glu	Asn	Asn	Gly	
1100						1105					1110				
Ser	Asn	Asn	Ala	Thr	Leu	Phe	Gly	Gly	Leu	Phe	Ala	Ala	Leu	Gly	
1115						1120					1125				
Ser	Leu	Leu	Leu	Phe	Gly	Arg	Arg	Lys	Lys	Gln	Asn	Lys			
1130						1135					1140				

<400> SEQUENCE: 15

Met	Thr	Lys	His	Tyr	Leu	Asn	Ser	Lys	Tyr	Gln	Ser	Glu	Gln	Arg	Ser
1				5					10					15	
Ser	Ala	Met	Lys	Lys	Ile	Thr	Met	Gly	Thr	Ala	Ser	Ile	Ile	Leu	Gly
			20					25					30		
Ser	Leu	Val	Tyr	Ile	Gly	Ala	Asp	Ser	Gln	Gln	Val	Asn	Ala	Ala	Thr
		35					40					45			
Glu	Ala	Thr	Asn	Ala	Thr	Asn	Asn	Gln	Ser	Thr	Gln	Val	Ser	Gln	Ala
	50					55					60				

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Thr Ser Gln Pro Ile Asn Phe Gln Val Gln Lys Asp Gly Ser Ser Glu
 65 70 75 80
 Lys Ser His Met Asp Asp Tyr Met Gln His Pro Gly Lys Val Ile Lys
 85 90 95
 Gln Asn Asn Lys Tyr Tyr Phe Gln Thr Val Leu Asn Asn Ala Ser Phe
 100 105 110
 Trp Lys Glu Tyr Lys Phe Tyr Asn Ala Asn Asn Gln Glu Leu Ala Thr
 115 120 125
 Thr Val Val Asn Asp Asn Lys Lys Ala Asp Thr Arg Thr Ile Asn Val
 130 135 140
 Ala Val Glu Pro Gly Tyr Lys Ser Leu Thr Thr Lys Val His Ile Val
 145 150 155 160
 Val Pro Gln Ile Asn Tyr Asn His Arg Tyr Thr Thr His Leu Glu Phe
 165 170 175
 Glu Lys Ala Ile Pro Thr Leu Ala Asp Ala Ala Lys Pro Asn Asn Val
 180 185 190
 Lys Pro Val Gln Pro Lys Pro Ala Gln Pro Lys Thr Pro Thr Glu Gln
 195 200 205
 Thr Lys Pro Val Gln Pro Lys Val Glu Lys Val Lys Pro Thr Val Thr
 210 215 220
 Thr Thr Ser Lys Val Glu Asp Asn His Ser Thr Lys Val Val Ser Thr
 225 230 235 240
 Asp Thr Thr Lys Asp Gln Thr Lys Thr Gln Thr Ala His Thr Val Lys
 245 250 255
 Thr Ala Gln Thr Ala Gln Glu Gln Asn Lys Val Gln Thr Pro Val Lys
 260 265 270
 Asp Val Ala Thr Ala Lys Ser Glu Ser Asn Asn Gln Ala Val Ser Asp
 275 280 285
 Asn Lys Ser Gln Gln Thr Asn Lys Val Thr Lys His Asn Glu Thr Pro
 290 295 300
 Lys Gln Ala Ser Lys Ala Lys Glu Leu Pro Lys Thr Gly Leu Thr Ser
 305 310 315 320
 Val Asp Asn Phe Ile Ser Thr Val Ala Phe Ala Thr Leu Ala Leu Leu
 325 330 335
 Gly Ser Leu Ser Leu Leu Leu Phe Lys Arg Lys Glu Ser Lys
 340 345 350

<210> SEQ ID NO 16

<211> LENGTH: 645

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 16

Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
 1 5 10 15
 Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
 20 25 30
 Met Ser Asn Gly Glu Ala Gln Ala Ala Glu Glu Thr Gly Gly Thr
 35 40 45
 Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
 50 55 60
 Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
 65 70 75 80
 Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala

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85								90				95						
Lys	Glu	Val	Lys 100		Glu	Val	Lys	Ala	Pro 105		Lys	Glu	Thr	Lys	Ala 110		Val	Lys
Pro	Ala	Ala	Lys 115		Ala	Thr	Asn	Asn 120		Thr	Tyr	Pro	Ile	Leu 125		Asn	Gln	Glu
Leu	Arg	Glu	Ala	Ile	Lys	Asn 135		Pro	Ala	Ile	Lys	Asp 140		Lys	Asp	His	Ser	
Ala	Pro	Asn	Ser	Arg	Pro 150		Ile	Asp	Phe	Glu	Met	Lys	Lys	Glu	Asn	Gly	160	
Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser 170		Val	Lys	Pro	Ala	Arg	Val	175	
Ile	Phe	Thr	Asp 180		Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly	190	
Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys 205		Lys	Leu	Pro		
Ile	Lys	Leu	Val	Ser	Tyr	Asp 215		Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg		
Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr	240		
His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp 250		Tyr	Thr	Leu	Met	Glu	Phe	255	
Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp 265		Lys	Phe	Lys	Thr	Glu	Glu	Asp		
Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu			
Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp 300		Lys	Leu	Pro	Glu		
Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala	320		
Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln			
Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val			
Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys			
His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met			
Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln	400		
Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile			
Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys			
Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile			
Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys			
Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr	480		
Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln	495		
Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu			

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Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
  515                      520                      525

Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
  530                      535                      540

Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
  545                      550                      555                      560

Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
                      565                      570                      575

Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
                      580                      585                      590

His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
                      595                      600                      605

Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
  610                      615                      620

Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
  625                      630                      635                      640

Arg Lys Arg Lys Asn
                      645

```

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<210> SEQ ID NO 17
<211> LENGTH: 80
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

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<400> SEQUENCE: 17

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

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

Ile Ala Leu Val Leu Asp Ser Leu Asp Ile Ser Ile Phe Asp Val Asn
  35                      40                      45

Thr Gln Ile Lys Val Met Thr Lys Gly Gln Leu Leu Val Glu Asn Asp
  50                      55                      60

Arg Leu Ile Asp Tyr Gln Ile Ala Asp Gly Asp Ile Leu Lys Leu Leu
  65                      70                      75                      80

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<210> SEQ ID NO 18
<211> LENGTH: 877
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

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<400> SEQUENCE: 18

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```

Met Lys Lys Arg Ile Asp Tyr Leu Ser Asn Lys Gln Asn Lys Tyr Ser
  1                      5                      10                      15

Ile Arg Arg Phe Thr Val Gly Thr Thr Ser Val Ile Val Gly Ala Thr
  20                      25                      30

Ile Leu Phe Gly Ile Gly Asn His Gln Ala Gln Ala Ser Glu Gln Ser
  35                      40                      45

Asn Asp Thr Thr Gln Ser Ser Lys Asn Asn Ala Ser Ala Asp Ser Glu
  50                      55                      60

Lys Asn Asn Met Ile Glu Thr Pro Gln Leu Asn Thr Thr Ala Asn Asp
  65                      70                      75                      80

Thr Ser Asp Ile Ser Ala Asn Thr Asn Ser Ala Asn Val Asp Ser Thr
                      85                      90                      95

Thr Lys Pro Met Ser Thr Gln Thr Ser Asn Thr Thr Thr Thr Glu Pro
                      100                      105                      110

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Ala	Ser	Thr	Asn	Glu	Thr	Pro	Gln	Pro	Thr	Ala	Ile	Lys	Asn	Gln	Ala
		115					120					125			
Thr	Ala	Ala	Lys	Met	Gln	Asp	Gln	Thr	Val	Pro	Gln	Glu	Ala	Asn	Ser
	130					135					140				
Gln	Val	Asp	Asn	Lys	Thr	Thr	Asn	Asp	Ala	Asn	Ser	Ile	Ala	Thr	Asn
145					150					155					160
Ser	Glu	Leu	Lys	Asn	Ser	Gln	Thr	Leu	Asp	Leu	Pro	Gln	Ser	Ser	Pro
				165					170					175	
Gln	Thr	Ile	Ser	Asn	Ala	Gln	Gly	Thr	Ser	Lys	Pro	Ser	Val	Arg	Thr
		180						185					190		
Arg	Ala	Val	Arg	Ser	Leu	Ala	Val	Ala	Glu	Pro	Val	Val	Asn	Ala	Ala
		195					200					205			
Asp	Ala	Lys	Gly	Thr	Asn	Val	Asn	Asp	Lys	Val	Thr	Ala	Ser	Asn	Phe
	210					215					220				
Lys	Leu	Glu	Lys	Thr	Thr	Phe	Asp	Pro	Asn	Gln	Ser	Gly	Asn	Thr	Phe
225					230					235					240
Met	Ala	Ala	Asn	Phe	Thr	Val	Thr	Asp	Lys	Val	Lys	Ser	Gly	Asp	Tyr
				245					250					255	
Phe	Thr	Ala	Lys	Leu	Pro	Asp	Ser	Leu	Thr	Gly	Asn	Gly	Asp	Val	Asp
			260					265					270		
Tyr	Ser	Asn	Ser	Asn	Asn	Thr	Met	Pro	Ile	Ala	Asp	Ile	Lys	Ser	Thr
		275					280					285			
Asn	Gly	Asp	Val	Val	Ala	Lys	Ala	Thr	Tyr	Asp	Ile	Leu	Thr	Lys	Thr
	290					295					300				
Tyr	Thr	Phe	Val	Phe	Thr	Asp	Tyr	Val	Asn	Asn	Lys	Glu	Asn	Ile	Asn
305					310					315					320
Gly	Gln	Phe	Ser	Leu	Pro	Leu	Phe	Thr	Asp	Arg	Ala	Lys	Ala	Pro	Lys
				325					330					335	
Ser	Gly	Thr	Tyr	Asp	Ala	Asn	Ile	Asn	Ile	Ala	Asp	Glu	Met	Phe	Asn
			340					345					350		
Asn	Lys	Ile	Thr	Tyr	Asn	Tyr	Ser	Ser	Pro	Ile	Ala	Gly	Ile	Asp	Lys
		355					360					365			
Pro	Asn	Gly	Ala	Asn	Ile	Ser	Ser	Gln	Ile	Ile	Gly	Val	Asp	Thr	Ala
	370					375					380				
Ser	Gly	Gln	Asn	Thr	Tyr	Lys	Gln	Thr	Val	Phe	Val	Asn	Pro	Lys	Gln
385					390					395					400
Arg	Val	Leu	Gly	Asn	Thr	Trp	Val	Tyr	Ile	Lys	Gly	Tyr	Gln	Asp	Lys
				405					410					415	
Ile	Glu	Glu	Ser	Ser	Gly	Lys	Val	Ser	Ala	Thr	Asp	Thr	Lys	Leu	Arg
			420					425					430		
Ile	Phe	Glu	Val	Asn	Asp	Thr	Ser	Lys	Leu	Ser	Asp	Ser	Tyr	Tyr	Ala
		435					440					445			
Asp	Pro	Asn	Asp	Ser	Asn	Leu	Lys	Glu	Val	Thr	Asp	Gln	Phe	Lys	Asn
	450					455					460				
Arg															

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Arg	Tyr	Gly	Gly	Gly	Ser	Ala	Asp	Gly	Asp	Ser	Ala	Val	Asn	Pro	Lys
530						535					540				
Asp	Pro	Thr	Pro	Gly	Pro	Pro	Val	Asp	Pro	Glu	Pro	Ser	Pro	Asp	Pro
545					550					555					560
Glu	Pro	Glu	Pro	Thr	Pro	Asp	Pro	Glu	Pro	Ser	Pro	Asp	Pro	Glu	Pro
				565					570					575	
Glu	Pro	Ser	Pro	Asp	Pro	Asp	Pro	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
			580					585					590		
Gly	Ser	Asp	Ser	Asp	Ser	Gly	Ser	Asp	Ser	Asp	Ser	Glu	Ser	Asp	Ser
		595					600					605			
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Glu	Ser
	610					615					620				
Asp	Ser	Asp	Ser	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
625					630					635					640
Asp	Ser	Asp	Ser	Asp	Ser	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
				645					650					655	
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Glu	Ser	Asp	Ser	Asp	Ser	Glu	Ser
			660					665						670	
Asp	Ser	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
		675					680					685			
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
	690					695					700				
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Ser
705					710					715					720
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
				725					730					735	
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
			740					745					750		
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
			755				760					765			
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
	770					775					780				
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
785					790					795					800
Asp	Ser	Asp	Ser	Arg	Val	Thr	Pro	Pro	Asn	Asn	Glu	Gln	Lys	Ala	Pro
				805					810					815	
Ser	Asn	Pro	Lys	Gly	Glu	Val	Asn	His	Ser	Asn	Lys	Val	Ser	Lys	Gln
			820					825					830		
His	Lys	Thr	Asp	Ala	Leu	Pro	Glu	Thr	Gly	Asp	Lys	Ser	Glu	Asn	Thr
		835						840				845			
Asn	Ala	Thr	Leu	Phe	Gly	Ala	Met	Met	Ala	Leu	Leu	Gly	Ser	Leu	Leu
	850					855					860				
Leu	Phe	Arg	Lys	Arg	Lys	Gln	Asp	His	Lys	Glu	Lys	Ala			
865					870					875					

<210> SEQ ID NO 19

<211> LENGTH: 227

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 19

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

Ile	Ile	Ile	Ala	Thr	Phe	Ser	Asn	Ser	Ala	Asn	Ala	Ala	Asp	Ser	Gly
			20					25						30	

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Thr Leu Asn Tyr Glu Val Tyr Lys Tyr Asn Thr Asn Asp Thr Ser Ile
 35 40 45
 Ala Asn Asp Tyr Phe Asn Lys Pro Ala Lys Tyr Ile Lys Lys Asn Gly
 50 55 60
 Lys Leu Tyr Val Gln Ile Thr Val Asn His Ser His Trp Ile Thr Gly
 65 70 75 80
 Met Ser Ile Glu Gly His Lys Glu Asn Ile Ile Ser Lys Asn Thr Ala
 85 90 95
 Lys Asp Glu Arg Thr Ser Glu Phe Glu Val Ser Lys Leu Asn Gly Lys
 100 105 110
 Ile Asp Gly Lys Ile Asp Val Tyr Ile Asp Glu Lys Val Asn Gly Lys
 115 120 125
 Pro Phe Lys Tyr Asp His His Tyr Asn Ile Thr Tyr Lys Phe Asn Gly
 130 135 140
 Pro Thr Asp Val Ala Gly Ala Asn Ala Pro Gly Lys Asp Asp Lys Asn
 145 150 155 160
 Ser Ala Ser Gly Ser Asp Lys Gly Ser Asp Gly Thr Thr Thr Gly Gln
 165 170 175
 Ser Glu Ser Asn Ser Ser Asn Lys Asp Lys Val Glu Asn Pro Gln Thr
 180 185 190
 Asn Ala Gly Thr Pro Ala Tyr Ile Tyr Ala Ile Pro Val Ala Ser Leu
 195 200 205
 Ala Leu Leu Ile Ala Ile Thr Leu Phe Val Arg Lys Lys Ser Lys Gly
 210 215 220
 Asn Val Glu
 225

<210> SEQ ID NO 20
 <211> LENGTH: 635
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 20

Met Ala Lys Tyr Arg Gly Lys Pro Phe Gln Leu Tyr Val Lys Leu Ser
 1 5 10 15
 Cys Ser Thr Met Met Ala Ser Ser Ile Ile Leu Thr Asn Ile Leu Pro
 20 25 30
 Tyr Asp Ala Gln Ala Ala Ser Glu Lys Asp Thr Glu Ile Ser Lys Glu
 35 40 45
 Ile Leu Ser Lys Gln Asp Leu Leu Asp Lys Val Asp Lys Ala Ile Arg
 50 55 60
 Gln Ile Glu Gln Leu Lys Gln Leu Ser Ala Ser Ser Lys Ala His Tyr
 65 70 75 80
 Lys Ala Gln Leu Asn Glu Ala Lys Thr Ala Ser Gln Ile Asp Glu Ile
 85 90 95
 Ile Lys Arg Ala Asn Glu Leu Asp Ser Lys Glu Asn Lys Ser Ser His
 100 105 110
 Thr Glu Met Asn Gly Gln Ser Asp Ile Asp Ser Lys Leu Asp Gln Leu
 115 120 125
 Leu Lys Asp Leu Asn Glu Val Ser Ser Asn Val Asp Arg Gly Gln Gln
 130 135 140
 Ser Gly Glu Asp Asp Leu Asn Ala Met Lys Asn Asp Met Ser Gln Thr
 145 150 155 160
 Ala Thr Thr Lys Tyr Gly Glu Lys Asp Asp Lys Asn Asp Glu Ala Met

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165							170							175						
Val	Asn	Lys	Ala	Leu	Glu	Asp	Leu	Asp	His	Leu	Asn	Gln	Gln	Ile	His					
			180					185					190							
Lys	Ser	Lys	Asp	Ala	Leu	Lys	Asp	Ala	Ser	Lys	Asp	Pro	Ala	Val	Ser					
			195				200					205								
Thr	Thr	Asp	Ser	Asn	His	Glu	Val	Ala	Lys	Thr	Pro	Asn	Asn	Asp	Gly					
						215					220									
Ser	Gly	His	Val	Val	Leu	Asn	Lys	Phe	Leu	Ser	Asn	Glu	Glu	Asn	Gln					
					230					235					240					
Ser	His	Ser	Asn	Gln	Leu	Thr	Asp	Lys	Leu	Gln	Gly	Ser	Asp	Lys	Ile					
				245				250						255						
Asn	His	Ala	Met	Ile	Glu	Lys	Leu	Ala	Lys	Ser	Asn	Ala	Ser	Thr	Gln					
			260					265					270							
His	Tyr	Thr	Tyr	His	Lys	Leu	Asn	Thr	Leu	Gln	Ser	Leu	Asp	Gln	Arg					
			275				280					285								
Ile	Ala	Asn	Thr	Gln	Leu	Pro	Lys	Asn	Gln	Lys	Ser	Asp	Leu	Met	Ser					
						295					300									
Glu	Val	Asn	Lys	Thr	Lys	Glu	Arg	Ile	Lys	Ser	Gln	Arg	Asn	Ile	Ile					
					310					315					320					
Leu	Glu	Glu	Leu	Ala	Arg	Thr	Asp	Asp	Lys	Lys	Tyr	Ala	Thr	Gln	Ser					
				325					330					335						
Ile	Leu	Glu	Ser	Ile	Phe	Asn	Lys	Asp	Glu	Ala	Asp	Lys	Ile	Leu	Lys					
			340					345					350							
Asp	Ile	Arg	Val	Asp	Gly	Lys	Thr	Asp	Gln	Gln	Ile	Ala	Asp	Gln	Ile					
		355					360					365								
Thr	Arg	His	Ile	Asp	Gln	Leu	Ser	Leu	Thr	Thr	Ser	Asp	Asp	Leu	Leu					
						375					380									
Thr	Ser	Leu	Ile	Asp	Gln	Ser	Gln	Asp	Lys	Ser	Leu	Leu	Ile	Ser	Gln					
					390					395					400					
Ile	Leu	Gln	Thr	Lys	Leu	Gly	Lys	Ala	Glu	Ala	Asp	Lys	Leu	Ala	Lys					
				405				410						415						
Asp	Trp	Thr	Asn	Lys	Gly	Leu	Ser	Asn	Arg	Gln	Ile	Val	Asp	Gln	Leu					
			420					425					430							
Lys	Lys	His	Phe	Ala	Ser	Thr	Gly	Asp	Thr	Ser	Ser	Asp	Asp	Ile	Leu					
			435				440					445								
Lys	Ala	Ile	Leu	Asn	Asn	Ala	Lys	Asp	Lys	Lys	Gln	Ala	Ile	Glu	Thr					
						455					460									
Ile	Leu	Ala	Thr	Arg	Ile	Glu	Arg	Gln	Lys	Ala	Lys	Leu	Leu	Ala	Asp					
					470				475						480					
Leu	Ile	Thr	Lys	Ile	Glu	Thr	Asp	Gln	Asn	Lys	Ile	Phe	Asn	Leu	Val					
				485				490						495						
Lys	Ser	Ala	Leu	Asn	Gly	Lys	Ala	Asp	Asp	Leu	Leu	Asn	Leu	Gln	Lys					
				500				505					510							
Arg	Leu	Asn	Gln	Thr	Lys	Lys	Asp	Ile	Asp	Tyr	Ile	Leu	Ser	Pro	Ile					
				515			520					525								
Val	Asn	Arg	Pro	Ser	Leu	Leu	Asp	Arg	Leu	Asn	Lys	Asn	Gly	Lys	Thr					
						535					540									
Thr	Asp	Leu	Asn	Lys	Leu	Ala	Asn	Leu	Met	Asn	Gln	Gly	Ser	Asn	Leu					
					550					555				560						
Leu	Asp	Ser	Ile	Pro	Asp	Ile	Pro	Thr	Pro	Lys	Pro	Glu	Lys	Thr	Leu					
				565				570						575						
Thr	Leu	Gly	Lys	Gly	Asn	Gly	Leu	Leu	Ser	Gly	Leu	Leu	Asn	Ala	Asp					
			580				585						590							

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Gly Asn Val Ser Leu Pro Lys Ala Gly Glu Thr Ile Lys Glu His Trp
 595 600 605

Leu Pro Ile Ser Val Ile Val Gly Ala Met Gly Val Leu Met Ile Trp
 610 615 620

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

<210> SEQ ID NO 21
 <211> LENGTH: 953
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 21

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

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

Ile Leu Val Gly Thr Thr Leu Ile Phe Gly Leu Ser Gly His Glu Ala
 35 40 45

Lys Ala Ala Glu His Thr Asn Gly Glu Leu Asn Gln Ser Lys Asn Glu
 50 55 60

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

Gln Leu Lys Asp Asn Thr Gln Thr Ala Thr Ala Asp Gln Pro Lys Val
 85 90 95

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

Ser Pro Gln Asn Ala Thr Ala Ser Gln Ser Thr Thr Gln Thr Ser Asn
 115 120 125

Val Thr Thr Asn Asp Lys Ser Ser Thr Thr Tyr Ser Asn Glu Thr Asp
 130 135 140

Lys Ser Asn Leu Thr Gln Ala Lys Asn Val Ser Thr Thr Pro Lys Thr
 145 150 155 160

Thr Thr Ile Lys Gln Arg Ala Leu Asn Arg Met Ala Val Asn Thr Val
 165 170 175

Ala Ala Pro Gln Gln Gly Thr Asn Val Asn Asp Lys Val His Phe Thr
 180 185 190

Asn Ile Asp Ile Ala Ile Asp Lys Gly His Val Asn Lys Thr Thr Gly
 195 200 205

Asn Thr Glu Phe Trp Ala Thr Ser Ser Asp Val Leu Lys Leu Lys Ala
 210 215 220

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

Lys Tyr Gly Gln Tyr Phe Arg Pro Gly Ser Val Arg Leu Pro Ser Gln
 245 250 255

Thr Gln Asn Leu Tyr Asn Ala Gln Gly Asn Ile Ile Ala Lys Gly Ile
 260 265 270

Tyr Asp Ser Lys Thr Asn Thr Thr Thr Tyr Thr Phe Thr Asn Tyr Val
 275 280 285

Asp Gln Tyr Thr Asn Val Ser Gly Ser Phe Glu Gln Val Ala Phe Ala
 290 295 300

Lys Arg Glu Asn Ala Thr Thr Asp Lys Thr Ala Tyr Lys Met Glu Val
 305 310 315 320

Thr Leu Gly Asn Asp Thr Tyr Ser Lys Asp Val Ile Val Asp Tyr Gly

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325								330					335				
Asn	Gln	Lys	Gly 340		Gln	Gln	Leu	Ile	Ser 345	Ser	Thr	Asn	Tyr	Ile 350	Asn	Asn	
Glu	Asp	Leu	Ser	Arg	Asn	Met	Thr	Val	Tyr	Val	Asn	Gln	Pro	Lys	Lys		
Thr	Tyr	Thr	Lys	Glu	Thr	Phe	Val	Thr	Asn	Leu	Thr	Gly	Tyr	Lys	Phe		
Asn	Pro	Asp	Ala	Lys	Asn	Phe	Lys	Ile	Tyr	Glu	Val	Thr	Asp	Gln	Asn		
385					390					395					400		
Gln	Phe	Val	Asp	Ser	Phe	Thr	Pro	Asp	Thr	Ser	Lys	Leu	Lys	Asp	Val		
				405					410					415			
Thr	Gly	Gln	Phe	Asp	Val	Ile	Tyr	Ser	Asn	Asp	Asn	Lys	Thr	Ala	Thr		
			420					425					430				
Val	Asp	Leu	Leu	Asn	Gly	Gln	Ser	Ser	Ser	Asp	Lys	Gln	Tyr	Ile	Ile		
		435					440					445					
Gln	Gln	Val	Ala	Tyr	Pro	Asp	Asn	Ser	Ser	Thr	Asp	Asn	Gly	Lys	Ile		
		450				455					460						
Asp	Tyr	Thr	Leu	Glu	Thr	Gln	Asn	Gly	Lys	Ser	Ser	Trp	Ser	Asn	Ser		
465					470					475					480		
Tyr	Ser	Asn	Val	Asn	Gly	Ser	Ser	Thr	Ala	Asn	Gly	Asp	Gln	Lys	Lys		
				485					490					495			
Tyr	Asn	Leu	Gly	Asp	Tyr	Val	Trp	Glu	Asp	Thr	Asn	Lys	Asp	Gly	Lys		
			500					505					510				
Gln	Asp	Ala	Asn	Glu	Lys	Gly	Ile	Lys	Gly	Val	Tyr	Val	Ile	Leu	Lys		
		515					520					525					
Asp	Ser	Asn	Gly	Lys	Glu	Leu	Asp	Arg	Thr	Thr	Thr	Asp	Glu	Asn	Gly		
		530				535						540					
Lys	Tyr	Gln	Phe	Thr	Gly	Leu	Ser	Asn	Gly	Thr	Tyr	Ser	Val	Glu	Phe		
545					550					555					560		
Ser	Thr	Pro	Ala	Gly	Tyr	Thr	Pro	Thr	Thr	Ala	Asn	Ala	Gly	Thr	Asp		
				565					570					575			
Asp	Ala	Val	Asp	Ser	Asp	Gly	Leu	Thr	Thr	Thr	Gly	Val	Ile	Lys	Asp		
			580					585					590				
Ala	Asp	Asn	Met	Thr	Leu	Asp	Ser	Gly	Phe	Tyr	Lys	Thr	Pro	Lys	Tyr		
		595					600					605					
Ser	Leu	Gly	Asp	Tyr	Val	Trp	Tyr	Asp	Ser	Asn	Lys	Asp	Gly	Lys	Gln		
	610					615					620						
Asp	Ser	Thr	Glu	Lys	Gly	Ile	Lys	Gly	Val	Lys	Val	Thr	Leu	Gln	Asn		
625					630					635					640		
Glu	Lys	Gly	Glu	Val	Ile	Gly	Thr	Thr	Glu	Thr	Asp	Glu	Asn	Gly	Lys		
				645					650					655			
Tyr	Arg	Phe	Asp	Asn	Leu	Asp	Ser	Gly	Lys	Tyr	Lys	Val	Ile	Phe	Glu		
			660					665					670				
Lys	Pro	Ala	Gly	Leu	Thr	Gln	Thr	Gly	Thr	Asn	Thr	Thr	Glu	Asp	Asp		
		675					680					685					
Lys	Asp	Ala	Asp	Gly	Gly	Glu	Val	Asp	Val	Thr	Ile	Thr	Asp	His	Asp		
	690					695					700						
Asp	Phe	Thr	Leu	Asp	Asn	Gly	Tyr	Tyr	Glu	Glu	Glu	Thr	Ser	Asp	Ser		
705					710					715					720		
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser		
				725					730					735			
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser		
				740				745						750			

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Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
  755              760              765

Asp Ser Asp Ser Glu Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
  770              775              780

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
  785              790              795              800

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
      805              810              815

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
      820              825              830

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
      835              840              845

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
      850              855              860

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
      865              870              875              880

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Ala Gly Lys
      885              890              895

His Thr Pro Thr Lys Pro Met Ser Thr Val Lys Asp Gln His Lys Thr
      900              905              910

Ala Lys Ala Leu Pro Glu Thr Gly Ser Glu Asn Asn Asn Ser Asn Asn
      915              920              925

Gly Thr Leu Phe Gly Gly Leu Phe Ala Ala Leu Gly Ser Leu Leu Leu
      930              935              940

Phe Gly Arg Arg Lys Lys Gln Asn Lys
  945              950

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<210> SEQ ID NO 22

<211> LENGTH: 989

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 22

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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 Ser 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

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165								170					175				
Asp	Thr	Ser	Thr	Glu	Ala	Thr	Pro	Ser	Asn	Asn	Glu	Ser	Ala	Pro	Gln		
			180					185					190				
Asn	Thr	Asp	Ala	Ser	Asn	Lys	Asp	Val	Val	Ser	Gln	Ala	Val	Asn	Pro		
		195					200					205					
Ser	Thr	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	Asp	Val	Lys		
225					230					235					240		
Val	Thr	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	Asp	Asn	Lys	Glu	Asn	Val	Thr	Ala	Asn	Ile	Thr	Met	Pro		
			325						330					335			
Ala	Tyr	Ile	Asp	Pro	Glu	Asn	Val	Thr	Lys	Thr	Gly	Asn	Val	Thr	Leu		
		340						345					350				
Thr	Thr	Gly	Ile	Gly	Thr	Asn	Thr	Ala	Ser	Lys	Thr	Val	Leu	Ile	Asp		
		355					360					365					
Tyr	Glu	Lys	Tyr	Gly	Gln	Phe	His	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	Val	Leu	Pro	Ala	Leu	Thr	Gly	Asn	Leu		
			405						410					415			
Ile	Pro	Asn	Thr	Lys	Ser	Asn	Ala	Leu	Ile	Asp	Ala	Lys	Asn	Thr	Asp		
		420						425					430				
Ile	Lys	Val	Tyr	Arg	Val	Asp	Asn	Ala	Asn	Asp	Leu	Ser	Glu	Ser	Tyr		
		435					440					445					
Tyr	Val	Asn	Pro	Ser	Asp	Phe	Glu	Asp	Val	Thr	Asn	Gln	Val	Arg	Ile		
	450					455					460						
Ser	Phe	Pro	Asn	Ala	Asn	Gln	Tyr	Lys	Val	Glu	Phe	Pro	Thr	Asp	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	Ala	Ser	Thr	Gly	Asp	Leu	Ala	Leu	Arg	Ser	Thr	Phe	Tyr	Gly	Tyr		
		500						505					510				
Asp	Ser	Asn	Phe	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				

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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 Ala
  610                      615                      620

Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp
  625                      630                      635                      640

Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp
  645                      650                      655

Ser Asp Ser Ala Ser Asp Ser Asp Ser Ala 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 Asp
  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 Asp Ser Asp Ser Asp Ser Asp Ser Asp
  805                      810                      815

Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
  820                      825                      830

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
  835                      840                      845

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
  850                      855                      860

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
  865                      870                      875                      880

Ser Ala Ser Asp Ser Asp Ser Gly Ser Asp Ser Asp Ser Ser Ser Asp
  885                      890                      895

Ser Asp Ser Asp Ser Thr Ser Asp Thr Gly Ser Asp Asn Asp Ser Asp
  900                      905                      910

Ser Asp Ser Asn Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
  915                      920                      925

Pro Pro Asn Ser Pro Lys Asn Gly Thr Asn Ala Ser Asn Lys Asn Glu
  930                      935                      940

Ala Lys Asp Ser Lys Glu Pro Leu Pro Asp Thr Gly Ser Glu Asp Glu
  945                      950                      955                      960

Ala Asn Thr Ser Leu Ile Trp Gly Leu Leu Ala Ser Leu Gly Ser Leu
  965                      970                      975

Leu Leu Phe Arg Arg Lys Lys Glu Asn Lys Asp Lys Lys
  980                      985

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<210> SEQ ID NO 23

<211> LENGTH: 584

-continued

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 23

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

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

Lys Pro Leu Asp Lys Ser Ser Ser Ser Leu His His Gly Tyr Ser Lys
 35          40          45

Val His Val Pro Tyr Ala Ile Thr Val Asn Gly Thr Ser Gln Asn Ile
 50          55          60

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

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

Asp Ile Asp Leu Arg Leu Ser Lys Gln Ala Lys Tyr Thr Val Tyr Phe
100          105          110

Lys Asn Gly Thr Lys Lys Val Ile Asp Leu Lys Ala Gly Ile Tyr Thr
115          120          125

Ala Asp Leu Ile Asn Thr Ser Glu Ile Lys Ala Ile Asn Ile Asn Val
130          135          140

Asp Thr Lys Lys Gln Val Glu Asp Lys Lys Lys Asp Lys Ala Asn Tyr
145          150          155          160

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

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

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

Val Asp Leu Arg Leu Ser Lys Gln Ala Lys Tyr Thr Val Asn Phe Lys
210          215          220

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

Asn Leu Ile Asn Ser Ser Asp Ile Lys Ser Ile Asn Ile Asn Val Asp
245          250          255

Thr Lys Lys His Ile Glu Asn Lys Ala Lys Arg Asn Tyr Gln Val Pro
260          265          270

Tyr Ser Ile Asn Leu Asn Gly Thr Ser Thr Asn Ile Leu Ser Asn Leu
275          280          285

Ser Phe Ser Asn Lys Pro Trp Thr Asn Tyr Lys Asn Leu Thr Ser Gln
290          295          300

Ile Lys Ser Val Leu Lys His Asp Arg Gly Ile Ser Glu Gln Asp Leu
305          310          315          320

Lys Tyr Ala Lys Lys Ala Tyr Tyr Thr Val Tyr Phe Lys Asn Gly Gly
325          330          335

Lys Arg Ile Leu Gln Leu Asn Ser Lys Asn Tyr Thr Ala Asn Leu Val
340          345          350

His Ala Lys Asp Val Lys Arg Ile Glu Ile Thr Val Lys Thr Gly Thr
355          360          365

Lys Ala Lys Ala Asp Arg Tyr Val Pro Tyr Thr Ile Ala Val Asn Gly
370          375          380

Thr Ser Thr Pro Ile Leu Ser Asp Leu Lys Phe Thr Gly Asp Pro Arg
385          390          395          400

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Val Gly Tyr Lys Asp Ile Ser Lys Lys Val Lys Ser Val Leu Lys His
405 410 415

Asp Arg Gly Ile Gly Glu Arg Glu Leu Lys Tyr Ala Lys Lys Ala Thr
420 425 430

Tyr Thr Val His Phe Lys Asn Gly Thr Lys Lys Val Ile Asn Ile Asn
435 440 445

Ser Asn Ile Ser Gln Leu Asn Leu Leu Tyr Val Gln Asp Ile Lys Lys
450 455 460

Ile Asp Ile Asp Val Lys Thr Gly Thr Lys Ala Lys Ala Asp Ser Tyr
465 470 475 480

Val Pro Tyr Thr Ile Ala Val Asn Gly Thr Ser Thr Pro Ile Leu Ser
485 490 495

Lys Leu Lys Ile Ser Asn Lys Gln Leu Ile Ser Tyr Lys Tyr Leu Asn
500 505 510

Asp Lys Val Lys Ser Val Leu Lys Ser Glu Arg Gly Ile Ser Asp Leu
515 520 525

Asp Leu Lys Phe Ala Lys Gln Ala Lys Tyr Thr Val Tyr Phe Lys Asn
530 535 540

Gly Lys Lys Gln Val Val Asn Leu Lys Ser Asp Ile Phe Thr Pro Asn
545 550 555 560

Leu Phe Ser Ala Lys Asp Ile Lys Lys Ile Asp Ile Asp Val Lys Gln
565 570 575

Tyr Thr Lys Ser Lys Lys Asn Lys
580

<210> SEQ ID NO 24

<211> LENGTH: 10419

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

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

Asn Thr Ser Gln Ala His Ala Ala Glu Thr Asn Gln Pro Ala Ser Val
35 40 45

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

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

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

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

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

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

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

Glu Ala Asn Val Val Thr Ala Ser Asp Ser Ser Asp Asn Gly Asn Val
165 170 175

Gln His Asp Arg Asn Glu Leu Gln Ala Phe Phe Asp Ala Asn Tyr His

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180						185						190					
Asp	Tyr	Arg	Phe	Ile	Asp	Arg	Glu	Asn	Ala	Asp	Ser	Gly	Thr	Phe	Asn		
		195					200					205					
Tyr	Val	Lys	Gly	Ile	Phe	Asp	Lys	Ile	Asn	Thr	Leu	Leu	Gly	Ser	Asn		
		210				215					220						
Asp	Pro	Ile	Asn	Asn	Lys	Asp	Leu	Gln	Leu	Ala	Tyr	Lys	Glu	Leu	Glu		
		225			230					235					240		
Gln	Ala	Val	Ala	Leu	Ile	Arg	Thr	Met	Pro	Gln	Arg	Gln	Gln	Thr	Ser		
				245					250					255			
Arg	Arg	Ser	Asn	Arg	Ile	Gln	Thr	Arg	Ser	Val	Glu	Ser	Arg	Ala	Ala		
			260					265					270				
Glu	Pro	Arg	Ser	Val	Ser	Asp	Tyr	Gln	Asn	Ala	Asn	Ser	Ser	Tyr	Tyr		
		275					280					285					
Val	Glu	Asn	Ala	Asn	Asp	Gly	Ser	Gly	Tyr	Pro	Val	Gly	Thr	Tyr	Ile		
		290				295					300						
Asn	Ala	Ser	Ser	Lys	Gly	Ala	Pro	Tyr	Asn	Leu	Pro	Thr	Thr	Pro	Trp		
		305			310					315					320		
Asn	Thr	Leu	Lys	Ala	Ser	Asp	Ser	Lys	Glu	Ile	Ala	Leu	Met	Thr	Ala		
			325						330					335			
Lys	Gln	Thr	Gly	Asp	Gly	Tyr	Gln	Trp	Val	Ile	Lys	Phe	Asn	Lys	Gly		
			340					345					350				
His	Ala	Pro	His	Gln	Asn	Met	Ile	Phe	Trp	Phe	Ala	Leu	Pro	Ala	Asp		
		355					360					365					
Gln	Val	Pro	Val	Gly	Arg	Thr	Asp	Phe	Val	Thr	Val	Asn	Ser	Asp	Gly		
		370				375					380						
Thr	Asn	Val	Gln	Trp	Ser	His	Gly	Ala	Gly	Ala	Gly	Ala	Asn	Lys	Pro		
		385			390					395					400		
Leu	Gln	Gln	Met	Trp	Glu	Tyr	Gly	Val	Asn	Asp	Pro	His	Arg	Ser	His		
			405						410					415			
Asp	Phe	Lys	Ile	Arg	Asn	Arg	Ser	Gly	Gln	Val	Ile	Tyr	Asp	Trp	Pro		
			420					425					430				
Thr	Val	His	Ile	Tyr	Ser	Leu	Glu	Asp	Leu	Ser	Arg	Ala	Ser	Asp	Tyr		
		435					440					445					
Phe	Ser	Glu	Ala	Gly	Ala	Thr	Pro	Ala	Thr	Lys	Ala	Phe	Gly	Arg	Gln		
		450				455					460						
Asn	Phe	Glu	Tyr	Ile	Asn	Gly	Gln	Lys	Pro	Ala	Glu	Ser	Pro	Gly	Val		
		465			470					475					480		
Pro	Lys	Val	Tyr	Thr	Phe	Ile	Gly	Gln	Gly	Asp	Ala	Ser	Tyr	Thr	Ile		
			485						490					495			
Ser	Phe	Lys	Thr	Gln	Gly	Pro	Thr	Val	Asn	Lys	Leu	Tyr	Tyr	Ala	Ala		
			500					505					510				
Gly	Gly	Arg	Ala	Leu	Glu	Tyr	Asn	Gln	Leu	Phe	Met	Tyr	Ser	Gln	Leu		
		515					520					525					
Tyr	Val	Glu	Ser	Thr	Gln	Asp	His	Gln	Gln	Arg	Leu	Asn	Gly	Leu	Arg		
		530				535					540						
Gln	Val	Val	Asn	Arg	Thr	Tyr	Arg	Ile	Gly	Thr	Thr	Lys	Arg	Val	Glu		
					550					555					560		
Val	Ser	Gln	Gly	Asn	Val	Gln	Thr	Lys	Lys	Val	Leu	Glu	Ser	Thr	Asn		
				565					570					575			
Leu	Asn	Ile	Asp	Asp	Phe	Val	Asp	Asp	Pro	Leu	Ser	Tyr	Val	Lys	Thr		
			580					585					590				
Pro	Ser	Asn	Lys	Val	Leu	Gly	Phe	Tyr	Ser	Asn	Asn	Ala	Asn	Thr	Asn		
		595					600					605					

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Ala Phe Arg Pro Gly Gly Ala Gln Gln Leu Asn Glu Tyr Gln Leu Ser		
610	615	620
Gln Leu Phe Thr Asp Gln Lys Leu Gln Glu Ala Ala Arg Thr Arg Asn		
625	630	635 640
Pro Ile Arg Leu Met Ile Gly Phe Asp Tyr Pro Asp Ala Tyr Gly Asn		
	645	650 655
Ser Glu Thr Leu Val Pro Val Asn Leu Thr Val Leu Pro Glu Ile Gln		
	660	665 670
His Asn Ile Lys Phe Phe Lys Asn Asp Asp Thr Gln Asn Ile Ala Glu		
	675	680 685
Lys Pro Phe Ser Lys Gln Ala Gly His Pro Val Phe Tyr Val Tyr Ala		
	690	695 700
Gly Asn Gln Gly Asn Ala Ser Val Asn Leu Gly Gly Ser Val Thr Ser		
705	710	715 720
Ile Gln Pro Leu Arg Ile Asn Leu Thr Ser Asn Glu Asn Phe Thr Asp		
	725	730 735
Lys Asp Trp Gln Ile Thr Gly Ile Pro Arg Thr Leu His Ile Glu Asn		
	740	745 750
Ser Thr Asn Arg Pro Asn Asn Ala Arg Glu Arg Asn Ile Glu Leu Val		
	755	760 765
Gly Asn Leu Leu Pro Gly Asp Tyr Phe Gly Thr Ile Arg Phe Gly Arg		
	770	775 780
Lys Glu Gln Leu Phe Glu Ile Arg Val Lys Pro His Thr Pro Thr Ile		
785	790	795 800
Thr Thr Thr Ala Glu Gln Leu Arg Gly Thr Ala Leu Gln Lys Val Pro		
	805	810 815
Val Asn Ile Ser Gly Ile Pro Leu Asp Pro Ser Ala Leu Val Tyr Leu		
	820	825 830
Val Ala Pro Thr Asn Gln Thr Thr Asn Gly Gly Ser Glu Ala Asp Gln		
	835	840 845
Ile Pro Ser Gly Tyr Thr Ile Leu Ala Thr Gly Thr Pro Asp Gly Val		
	850	855 860
His Asn Thr Ile Thr Ile Arg Pro Gln Asp Tyr Val Val Phe Ile Pro		
865	870	875 880
Pro Val Gly Lys Gln Ile Arg Ala Val Val Tyr Tyr Asn Lys Val Val		
	885	890 895
Ala Ser Asn Met Ser Asn Ala Val Thr Ile Leu Pro Asp Asp Ile Pro		
	900	905 910
Pro Thr Ile Asn Asn Pro Val Gly Ile Asn Ala Lys Tyr Tyr Arg Gly		
	915	920 925
Asp Glu Val Asn Phe Thr Met Gly Val Ser Asp Arg His Ser Gly Ile		
	930	935 940
Lys Asn Thr Thr Ile Thr Thr Leu Pro Asn Gly Trp Thr Ser Asn Leu		
945	950	955 960
Thr Lys Ala Asp Lys Asn Asn Gly Ser Leu Ser Ile Thr Gly Arg Val		
	965	970 975
Ser Met Asn Gln Ala Phe Asn Ser Asp Ile Thr Phe Lys Val Ser Ala		
	980	985 990
Thr Asp Asn Val Asn Asn Thr Thr Asn Asp Ser Gln Ser Lys His Val		
	995	1000 1005
Ser Ile His Val Gly Lys Ile Ser Glu Asp Ala His Pro Ile Val		
1010	1015	1020

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Leu Gly	Asn Thr	Glu Lys	Val	Val Val Val	Asn Pro	Thr Ala Val
1025			1030		1035	
Ser Asn	Asp Glu	Lys Gln	Ser	Ile Ile Thr	Ala Phe	Met Asn Lys
1040			1045		1050	
Asn Gln	Asn Ile	Arg Gly	Tyr	Leu Ala Ser	Thr Asp	Pro Val Thr
1055			1060		1065	
Val Asp	Asn Asn	Gly Asn	Val	Thr Leu His	Tyr Arg	Asp Gly Ser
1070			1075		1080	
Ser Thr	Thr Leu	Asp Ala	Thr	Asn Val Met	Thr Tyr	Glu Pro Val
1085			1090		1095	
Val Lys	Pro Glu	Tyr Gln	Thr	Val Asn Ala	Ala Lys	Thr Ala Thr
1100			1105		1110	
Val Thr	Ile Ala	Lys Gly	Gln	Ser Phe Ser	Ile Gly	Asp Ile Lys
1115			1120		1125	
Gln Tyr	Phe Thr	Leu Ser	Asn	Gly Gln Pro	Ile Pro	Ser Gly Thr
1130			1135		1140	
Phe Thr	Asn Ile	Thr Ser	Asp	Arg Thr Ile	Pro Thr	Ala Gln Glu
1145			1150		1155	
Val Ser	Gln Met	Asn Ala	Gly	Thr Gln Leu	Tyr His	Ile Thr Ala
1160			1165		1170	
Thr Asn	Ala Tyr	His Lys	Asp	Ser Glu Asp	Phe Tyr	Ile Ser Leu
1175			1180		1185	
Lys Ile	Ile Asp	Val Lys	Gln	Pro Glu Gly	Asp Gln	Arg Val Tyr
1190			1195		1200	
Arg Thr	Ser Thr	Tyr Asp	Leu	Thr Thr Asp	Glu Ile	Ser Lys Val
1205			1210		1215	
Lys Gln	Ala Phe	Ile Asn	Ala	Asn Arg Asp	Val Ile	Thr Leu Ala
1220			1225		1230	
Glu Gly	Asp Ile	Ser Val	Thr	Asn Thr Pro	Asn Gly	Ala Asn Val
1235			1240		1245	
Ser Thr	Ile Thr	Val Asn	Ile	Asn Lys Gly	Arg Leu	Thr Lys Ser
1250			1255		1260	
Phe Ala	Ser Asn	Leu Ala	Asn	Met Asn Phe	Leu Arg	Trp Val Asn
1265			1270		1275	
Phe Pro	Gln Asp	Tyr Thr	Val	Thr Trp Thr	Asn Ala	Lys Ile Ala
1280			1285		1290	
Asn Arg	Pro Thr	Asp Gly	Gly	Leu Ser Trp	Ser Asp	Asp His Lys
1295			1300		1305	
Ser Leu	Ile Tyr	Arg Tyr	Asp	Ala Thr Leu	Gly Thr	Gln Ile Thr
1310			1315		1320	
Thr Asn	Asp Ile	Leu Thr	Met	Leu Lys Ala	Thr Thr	Thr Val Pro
1325			1330		1335	
Gly Leu	Arg Asn	Asn Ile	Thr	Gly Asn Glu	Lys Ser	Gln Ala Glu
1340			1345		1350	
Ala Gly	Gly Arg	Pro Asn	Phe	Arg Thr Thr	Gly Tyr	Ser Gln Ser
1355			1360		1365	
Asn Ala	Thr Thr	Asp Gly	Gln	Arg Gln Phe	Thr Leu	Asn Gly Gln
1370			1375		1380	
Val Ile	Gln Val	Leu Asp	Ile	Ile Asn Pro	Ser Asn	Gly Tyr Gly
1385			1390		1395	
Gly Gln	Pro Val	Thr Asn	Ser	Asn Thr Arg	Ala Asn	His Ser Asn
1400			1405		1410	
Ser Thr	Val Val	Asn Val	Asn	Glu Pro Ala	Ala Asn	Gly Ala Gly

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1415	1420	1425
Ala Phe Thr Ile Asp His Val	Val Lys Ser Asn Ser	Thr His Asn
1430	1435	1440
Ala Ser Asp Ala Val Tyr Lys	Ala Gln Leu Tyr Leu	Thr Pro Tyr
1445	1450	1455
Gly Pro Lys Gln Tyr Val Glu	His Leu Asn Gln Asn	Thr Gly Asn
1460	1465	1470
Thr Thr Asp Ala Ile Asn Ile	Tyr Phe Val Pro Ser	Asp Leu Val
1475	1480	1485
Asn Pro Thr Ile Ser Val Gly	Asn Tyr Thr Asn His	Gln Val Phe
1490	1495	1500
Ser Gly Glu Thr Phe Thr Asn	Thr Ile Thr Ala Asn	Asp Asn Phe
1505	1510	1515
Gly Val Gln Ser Val Thr Val	Pro Asn Thr Ser Gln	Ile Thr Gly
1520	1525	1530
Thr Val Asp Asn Asn His Gln	His Val Ser Ala Thr	Ala Pro Asn
1535	1540	1545
Val Thr Ser Ala Thr Asn Lys	Thr Ile Asn Leu Leu	Ala Thr Asp
1550	1555	1560
Thr Ser Gly Asn Thr Ala Thr	Thr Ser Phe Asn Val	Thr Val Lys
1565	1570	1575
Pro Leu Arg Asp Lys Tyr Arg	Val Gly Thr Ser Ser	Thr Ala Ala
1580	1585	1590
Asn Pro Val Arg Ile Ala Asn	Ile Ser Asn Asn Ala	Thr Val Ser
1595	1600	1605
Gln Ala Asp Gln Thr Thr Ile	Ile Asn Ser Leu Thr	Phe Thr Glu
1610	1615	1620
Thr Val Pro Asn Arg Ser Tyr	Ala Arg Ala Ser Ala	Asn Glu Ile
1625	1630	1635
Thr Ser Lys Thr Val Ser Asn	Val Ser Arg Thr Gly	Asn Asn Ala
1640	1645	1650
Asn Val Thr Val Thr Val Thr	Tyr Gln Asp Gly Thr	Thr Ser Thr
1655	1660	1665
Val Thr Val Pro Val Lys His	Val Ile Pro Glu Ile	Val Ala His
1670	1675	1680
Ser His Tyr Thr Val Gln Gly	Gln Asp Phe Pro Ala	Gly Asn Gly
1685	1690	1695
Ser Ser Ala Ser Asp Tyr Phe	Lys Leu Ser Asn Gly	Ser Asp Ile
1700	1705	1710
Ala Asp Ala Thr Ile Thr Trp	Val Ser Gly Gln Ala	Pro Asn Lys
1715	1720	1725
Asp Asn Thr Arg Ile Gly Glu	Asp Ile Thr Val Thr	Ala His Ile
1730	1735	1740
Leu Ile Asp Gly Glu Thr Thr	Pro Ile Thr Lys Thr	Ala Thr Tyr
1745	1750	1755
Lys Val Val Arg Thr Val Pro	Lys His Val Phe Glu	Thr Ala Arg
1760	1765	1770
Gly Val Leu Tyr Pro Gly Val	Ser Asp Met Tyr Asp	Ala Lys Gln
1775	1780	1785
Tyr Val Lys Pro Val Asn Asn	Ser Trp Ser Thr Asn	Ala Gln His
1790	1795	1800
Met Asn Phe Gln Phe Val Gly	Thr Tyr Gly Pro Asn	Lys Asp Val
1805	1810	1815

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Val Gly	Ile Ser Thr Arg	Leu	Ile Arg Val Thr	Tyr	Asp Asn Arg
1820		1825		1830	
Gln Thr	Glu Asp Leu Thr	Ile	Leu Ser Lys Val	Lys	Pro Asp Pro
1835		1840		1845	
Pro Arg	Ile Asp Ala Asn Ser	Val Thr Tyr Lys	Ala	Gly Leu Thr	
1850		1855		1860	
Asn Gln	Glu Ile Lys Val Asn	Asn Val Leu Asn	Asn	Ser Ser Val	
1865		1870		1875	
Lys Leu	Phe Lys Ala Asp Asn	Thr Pro Leu Asn	Val	Thr Asn Ile	
1880		1885		1890	
Thr His	Gly Ser Gly Phe Ser	Ser Val Val Thr	Val	Ser Asp Ala	
1895		1900		1905	
Leu Pro	Asn Gly Gly Ile Lys	Ala Lys Ser Ser	Ile	Ser Met Asn	
1910		1915		1920	
Asn Val	Thr Tyr Thr Thr Gln	Asp Glu His Gly	Gln	Val Val Thr	
1925		1930		1935	
Val Thr	Arg Asn Glu Ser Val	Asp Ser Asn Asp	Ser	Ala Thr Val	
1940		1945		1950	
Thr Val	Thr Pro Gln Leu Gln	Ala Thr Thr Glu	Gly	Ala Val Phe	
1955		1960		1965	
Ile Lys	Gly Gly Asp Gly Phe	Asp Phe Gly His	Val	Glu Arg Phe	
1970		1975		1980	
Ile Gln	Asn Pro Pro His Gly	Ala Thr Val Ala	Trp	His Asp Ser	
1985		1990		1995	
Pro Asp	Thr Trp Lys Asn Thr	Val Gly Asn Thr	His	Lys Thr Ala	
2000		2005		2010	
Val Val	Thr Leu Pro Asn Gly	Gln Gly Thr Arg	Asn	Val Glu Val	
2015		2020		2025	
Pro Val	Lys Val Tyr Pro Val	Ala Asn Ala Lys	Ala	Pro Ser Arg	
2030		2035		2040	
Asp Val	Lys Gly Gln Asn Leu	Thr Asn Gly Thr	Asp	Ala Met Asn	
2045		2050		2055	
Tyr Ile	Thr Phe Asp Pro Asn	Thr Asn Thr Asn	Gly	Ile Thr Ala	
2060		2065		2070	
Ala Trp	Ala Asn Arg Gln Gln	Pro Asn Asn Gln	Gln	Ala Gly Val	
2075		2080		2085	
Gln His	Leu Asn Val Asp Val	Thr Tyr Pro Gly	Ile	Ser Ala Ala	
2090		2095		2100	
Lys Arg	Val Pro Val Thr Val	Asn Val Tyr Gln	Phe	Glu Phe Pro	
2105		2110		2115	
Gln Thr	Thr Tyr Thr Thr Thr	Val Gly Gly Thr	Leu	Ala Ser Gly	
2120		2125		2130	
Thr Gln	Ala Ser Gly Tyr Ala	His Met Gln Asn	Ala	Thr Gly Leu	
2135		2140		2145	
Pro Thr	Asp Gly Phe Thr Tyr	Lys Trp Asn Arg	Asp	Thr Thr Gly	
2150		2155		2160	
Thr Asn	Asp Ala Asn Trp Ser	Ala Met Asn Lys	Pro	Asn Val Ala	
2165		2170		2175	
Lys Val	Val Asn Ala Lys Tyr	Asp Val Ile Tyr	Asn	Gly His Thr	
2180		2185		2190	
Phe Ala	Thr Ser Leu Pro Ala	Lys Phe Val Val	Lys	Asp Val Gln	
2195		2200		2205	

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Pro	Ala	Lys	Pro	Thr	Val	Thr	Glu	Thr	Ala	Ala	Gly	Ala	Ile	Thr
2210						2215					2220			
Ile	Ala	Pro	Gly	Ala	Asn	Gln	Thr	Val	Asn	Thr	His	Ala	Gly	Asn
2225						2230					2235			
Val	Thr	Thr	Tyr	Ala	Asp	Lys	Leu	Val	Ile	Lys	Arg	Asn	Gly	Asn
2240						2245					2250			
Val	Val	Thr	Thr	Phe	Thr	Arg	Arg	Asn	Asn	Thr	Ser	Pro	Trp	Val
2255						2260					2265			
Lys	Glu	Ala	Ser	Ala	Ala	Thr	Val	Ala	Gly	Ile	Ala	Gly	Thr	Asn
2270						2275					2280			
Asn	Gly	Ile	Thr	Val	Ala	Ala	Gly	Thr	Phe	Asn	Pro	Ala	Asp	Thr
2285						2290					2295			
Ile	Gln	Val	Val	Ala	Thr	Gln	Gly	Ser	Gly	Glu	Thr	Val	Ser	Asp
2300						2305					2310			
Glu	Gln	Arg	Ser	Asp	Asp	Phe	Thr	Val	Val	Ala	Pro	Gln	Pro	Asn
2315						2320					2325			
Gln	Ala	Thr	Thr	Lys	Ile	Trp	Gln	Asn	Gly	His	Ile	Asp	Ile	Thr
2330						2335					2340			
Pro	Asn	Asn	Pro	Ser	Gly	His	Leu	Ile	Asn	Pro	Thr	Gln	Ala	Met
2345						2350					2355			
Asp	Ile	Ala	Tyr	Thr	Glu	Lys	Val	Gly	Asn	Gly	Ala	Glu	His	Ser
2360						2365					2370			
Lys	Thr	Ile	Asn	Val	Val	Arg	Gly	Gln	Asn	Asn	Gln	Trp	Thr	Ile
2375						2380					2385			
Ala	Asn	Lys	Pro	Asp	Tyr	Val	Thr	Leu	Asp	Ala	Gln	Thr	Gly	Lys
2390						2395					2400			
Val	Thr	Phe	Asn	Ala	Asn	Thr	Ile	Lys	Pro	Asn	Ser	Ser	Ile	Thr
2405						2410					2415			
Ile	Thr	Pro	Lys	Ala	Gly	Thr	Gly	His	Ser	Val	Ser	Ser	Asn	Pro
2420						2425					2430			
Ser	Thr	Leu	Thr	Ala	Pro	Ala	Ala	His	Thr	Val	Asn	Thr	Thr	Glu
2435						2440					2445			
Ile	Val	Lys	Asp	Tyr	Gly	Ser	Asn	Val	Thr	Ala	Ala	Glu	Ile	Asn
2450						2455					2460			
Asn	Ala	Val	Gln	Val	Ala	Asn	Lys	Arg	Thr	Ala	Thr	Ile	Lys	Asn
2465						2470					2475			
Gly	Thr	Ala	Met	Pro	Thr	Asn	Leu	Ala	Gly	Gly	Ser	Thr	Thr	Thr
2480						2485					2490			
Ile	Pro	Val	Thr	Val	Thr	Tyr	Asn	Asp	Gly	Ser	Thr	Glu	Glu	Val
2495						2500					2505			
Gln	Glu	Ser	Ile	Phe	Thr	Lys	Ala	Asp	Lys	Arg	Glu	Leu	Ile	Thr
2510						2515					2520			
Ala	Lys	Asn	His	Leu	Asp	Asp	Pro	Val	Ser	Thr	Glu	Gly	Lys	Lys
2525						2530					2535			
Pro	Gly	Thr	Ile	Thr	Gln	Tyr	Asn	Asn	Ala	Met	His	Asn	Ala	Gln
2540						2545					2550			
Gln	Gln	Ile	Asn	Thr	Ala	Lys	Thr	Glu	Ala	Gln	Gln	Val	Ile	Asn
2555						2560					2565			
Asn	Glu	Arg	Ala	Thr	Pro	Gln	Gln	Val	Ser	Asp	Ala	Leu	Thr	Lys
2570						2575					2580			
Val	Arg	Ala	Ala	Gln	Thr	Lys	Ile	Asp	Gln	Ala	Lys	Ala	Leu	Leu
2585						2590					2595			
Gln	Asn	Lys	Glu	Asp	Asn	Ser	Gln	Leu	Val	Thr	Ser	Lys	Asn	Asn

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2600	2605	2610
Leu Gln Ser Ser Val Asn Gln Val Pro Ser Thr Ala Gly Met Thr		
2615	2620	2625
Gln Gln Ser Ile Asp Asn Tyr Asn Ala Lys Lys Arg Glu Ala Glu		
2630	2635	2640
Thr Glu Ile Thr Ala Ala Gln Arg Val Ile Asp Asn Gly Asp Ala		
2645	2650	2655
Thr Ala Gln Gln Ile Ser Asp Glu Lys His Arg Val Asp Asn Ala		
2660	2665	2670
Leu Thr Ala Leu Asn Gln Ala Lys His Asp Leu Thr Ala Asp Thr		
2675	2680	2685
His Ala Leu Glu Gln Ala Val Gln Gln Leu Asn Arg Thr Gly Thr		
2690	2695	2700
Thr Thr Gly Lys Lys Pro Ala Ser Ile Thr Ala Tyr Asn Asn Ser		
2705	2710	2715
Ile Arg Ala Leu Gln Ser Asp Leu Thr Ser Ala Lys Asn Ser Ala		
2720	2725	2730
Asn Ala Ile Ile Gln Lys Pro Ile Arg Thr Val Gln Glu Val Gln		
2735	2740	2745
Ser Ala Leu Thr Asn Val Asn Arg Val Asn Glu Arg Leu Thr Gln		
2750	2755	2760
Ala Ile Asn Gln Leu Val Pro Leu Ala Asp Asn Ser Ala Leu Lys		
2765	2770	2775
Thr Ala Lys Thr Lys Leu Asp Glu Glu Ile Asn Lys Ser Val Thr		
2780	2785	2790
Thr Asp Gly Met Thr Gln Ser Ser Ile Gln Ala Tyr Glu Asn Ala		
2795	2800	2805
Lys Arg Ala Gly Gln Thr Glu Ser Thr Asn Ala Gln Asn Val Ile		
2810	2815	2820
Asn Asn Gly Asp Ala Thr Asp Gln Gln Ile Ala Ala Glu Lys Thr		
2825	2830	2835
Lys Val Glu Glu Lys Tyr Asn Ser Leu Lys Gln Ala Ile Ala Gly		
2840	2845	2850
Leu Thr Pro Asp Leu Ala Pro Leu Gln Thr Ala Lys Thr Gln Leu		
2855	2860	2865
Gln Asn Asp Ile Asp Gln Pro Thr Ser Thr Thr Gly Met Thr Ser		
2870	2875	2880
Ala Ser Ile Ala Ala Phe Asn Glu Lys Leu Ser Ala Ala Arg Thr		
2885	2890	2895
Lys Ile Gln Glu Ile Asp Arg Val Leu Ala Ser His Pro Asp Val		
2900	2905	2910
Ala Thr Ile Arg Gln Asn Val Thr Ala Ala Asn Ala Ala Lys Ser		
2915	2920	2925
Ala Leu Asp Gln Ala Arg Asn Gly Leu Thr Val Asp Lys Ala Pro		
2930	2935	2940
Leu Glu Asn Ala Lys Asn Gln Leu Gln His Ser Ile Asp Thr Gln		
2945	2950	2955
Thr Ser Thr Thr Gly Met Thr Gln Asp Ser Ile Asn Ala Tyr Asn		
2960	2965	2970
Ala Lys Leu Thr Ala Ala Arg Asn Lys Ile Gln Gln Ile Asn Gln		
2975	2980	2985
Val Leu Ala Gly Ser Pro Thr Val Glu Gln Ile Asn Thr Asn Thr		
2990	2995	3000

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Ser Thr	Ala Asn Gln Ala Lys	Ser Asp Leu Asp His	Ala Arg Gln
3005	3010	3015	
Ala Leu	Thr Pro Asp Lys Ala	Pro Leu Gln Thr Ala	Lys Thr Gln
3020	3025	3030	
Leu Glu	Gln Ser Ile Asn Gln	Pro Thr Asp Thr Thr	Gly Met Thr
3035	3040	3045	
Thr Ala	Ser Leu Asn Ala Tyr	Asn Gln Lys Leu Gln	Ala Ala Arg
3050	3055	3060	
Gln Lys	Leu Thr Glu Ile Asn	Gln Val Leu Asn Gly	Asn Pro Thr
3065	3070	3075	
Val Gln	Asn Ile Asn Asp Lys	Val Thr Glu Ala Asn	Gln Ala Lys
3080	3085	3090	
Asp Gln	Leu Asn Thr Ala Arg	Gln Gly Leu Thr Leu	Asp Arg Gln
3095	3100	3105	
Pro Ala	Leu Thr Thr Leu His	Gly Ala Ser Asn Leu	Asn Gln Ala
3110	3115	3120	
Gln Gln	Asn Asn Phe Thr Gln	Gln Ile Asn Ala Ala	Gln Asn His
3125	3130	3135	
Ala Ala	Leu Glu Thr Ile Lys	Ser Asn Ile Thr Ala	Leu Asn Thr
3140	3145	3150	
Ala Met	Thr Lys Leu Lys Asp	Ser Val Ala Asp Asn	Asn Thr Ile
3155	3160	3165	
Lys Ser	Asp Gln Asn Tyr Thr	Asp Ala Thr Pro Ala	Asn Lys Gln
3170	3175	3180	
Ala Tyr	Asp Asn Ala Val Asn	Ala Ala Lys Gly Val	Ile Gly Glu
3185	3190	3195	
Thr Thr	Asn Pro Thr Met Asp	Val Asn Thr Val Asn	Gln Lys Ala
3200	3205	3210	
Ala Ser	Val Lys Ser Thr Lys	Asp Ala Leu Asp Gly	Gln Gln Asn
3215	3220	3225	
Leu Gln	Arg Ala Lys Thr Glu	Ala Thr Asn Ala Ile	Thr His Ala
3230	3235	3240	
Ser Asp	Leu Asn Gln Ala Gln	Lys Asn Ala Leu Thr	Gln Gln Val
3245	3250	3255	
Asn Ser	Ala Gln Asn Val Gln	Ala Val Asn Asp Ile	Lys Gln Thr
3260	3265	3270	
Thr Gln	Ser Leu Asn Thr Ala	Met Thr Gly Leu Lys	Arg Gly Val
3275	3280	3285	
Ala Asn	His Asn Gln Val Val	Gln Ser Asp Asn Tyr	Val Asn Ala
3290	3295	3300	
Asp Thr	Asn Lys Lys Asn Asp	Tyr Asn Asn Ala Tyr	Asn His Ala
3305	3310	3315	
Asn Asp	Ile Ile Asn Gly Asn	Ala Gln His Pro Val	Ile Thr Pro
3320	3325	3330	
Ser Asp	Val Asn Asn Ala Leu	Ser Asn Val Thr Ser	Lys Glu His
3335	3340	3345	
Ala Leu	Asn Gly Glu Ala Lys	Leu Asn Ala Ala Lys	Gln Glu Ala
3350	3355	3360	
Asn Thr	Ala Leu Gly His Leu	Asn Asn Leu Asn Asn	Ala Gln Arg
3365	3370	3375	
Gln Asn	Leu Gln Ser Gln Ile	Asn Gly Ala His Gln	Ile Asp Ala
3380	3385	3390	

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Val	Asn	Thr	Ile	Lys	Gln	Asn	Ala	Thr	Asn	Leu	Asn	Ser	Ala	Met
3395						3400					3405			
Gly	Asn	Leu	Arg	Gln	Ala	Val	Ala	Asp	Lys	Asp	Gln	Val	Lys	Arg
3410						3415					3420			
Thr	Glu	Asp	Tyr	Ala	Asp	Ala	Asp	Thr	Ala	Lys	Gln	Asn	Ala	Tyr
3425						3430					3435			
Asn	Ser	Ala	Val	Ser	Ser	Ala	Glu	Thr	Ile	Ile	Asn	Gln	Thr	Thr
3440						3445					3450			
Asn	Pro	Thr	Met	Ser	Val	Asp	Asp	Val	Asn	Arg	Ala	Thr	Ser	Ala
3455						3460					3465			
Val	Thr	Ser	Asn	Lys	Asn	Ala	Leu	Asn	Gly	Tyr	Glu	Lys	Leu	Ala
3470						3475					3480			
Gln	Ser	Lys	Thr	Asp	Ala	Ala	Arg	Ala	Ile	Asp	Ala	Leu	Pro	His
3485						3490					3495			
Leu	Asn	Asn	Ala	Gln	Lys	Ala	Asp	Val	Lys	Ser	Lys	Ile	Asn	Ala
3500						3505					3510			
Ala	Ser	Asn	Ile	Ala	Gly	Val	Asn	Thr	Val	Lys	Gln	Gln	Gly	Thr
3515						3520					3525			
Asp	Leu	Asn	Thr	Ala	Met	Gly	Asn	Leu	Gln	Gly	Ala	Ile	Asn	Asp
3530						3535					3540			
Glu	Gln	Thr	Thr	Leu	Asn	Ser	Gln	Asn	Tyr	Gln	Asp	Ala	Thr	Pro
3545						3550					3555			
Ser	Lys	Lys	Thr	Ala	Tyr	Thr	Asn	Ala	Val	Gln	Ala	Ala	Lys	Asp
3560						3565					3570			
Ile	Leu	Asn	Lys	Ser	Asn	Gly	Gln	Asn	Lys	Thr	Lys	Asp	Gln	Val
3575						3580					3585			
Thr	Glu	Ala	Met	Asn	Gln	Val	Asn	Ser	Ala	Lys	Asn	Asn	Leu	Asp
3590						3595					3600			
Gly	Thr	Arg	Leu	Leu	Asp	Gln	Ala	Lys	Gln	Thr	Ala	Lys	Gln	Gln
3605						3610					3615			
Leu	Asn	Asn	Met	Thr	His	Leu	Thr	Thr	Ala	Gln	Lys	Thr	Asn	Leu
3620						3625					3630			
Thr	Asn	Gln	Ile	Asn	Ser	Gly	Thr	Thr	Val	Ala	Gly	Val	Gln	Thr
3635						3640					3645			
Val	Gln	Ser	Asn	Ala	Asn	Thr	Leu	Asp	Gln	Ala	Met	Asn	Thr	Leu
3650						3655					3660			
Arg	Gln	Ser	Ile	Ala	Asn	Lys	Asp	Ala	Thr	Lys	Ala	Ser	Glu	Asp
3665						3670					3675			
Tyr	Val	Asp	Ala	Asn	Asn	Asp	Lys	Gln	Thr	Ala	Tyr	Asn	Asn	Ala
3680						3685					3690			
Val	Ala	Ala	Ala	Glu	Thr	Ile	Ile	Asn	Ala	Asn	Ser	Asn	Pro	Glu
3695						3700					3705			
Met	Asn	Pro	Ser	Thr	Ile	Thr	Gln	Lys	Ala	Glu	Gln	Val	Asn	Ser
3710						3715					3720			
Ser	Lys	Thr	Ala	Leu	Asn	Gly	Asp	Glu	Asn	Leu	Ala	Ala	Ala	Lys
3725						3730					3735			
Gln	Asn	Ala	Lys	Thr	Tyr	Leu	Asn	Thr	Leu	Thr	Ser	Ile	Thr	Asp
3740						3745					3750			
Ala	Gln	Lys	Asn	Asn	Leu	Ile	Ser	Gln	Ile	Thr	Ser	Ala	Thr	Arg
3755						3760					3765			
Val	Ser	Gly	Val	Asp	Thr	Val	Lys	Gln	Asn	Ala	Gln	His	Leu	Asp
3770						3775					3780			
Gln	Ala	Met	Ala	Ser	Leu	Gln	Asn	Gly	Ile	Asn	Asn	Glu	Ser	Gln

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3785	3790	3795
Val Lys Ser Ser Glu Lys Tyr Arg Asp Ala Asp Thr Asn Lys Gln 3800 3805 3810		
Gln Glu Tyr Asp Asn Ala Ile Thr Ala Ala Lys Ala Ile Leu Asn 3815 3820 3825		
Lys Ser Thr Gly Pro Asn Thr Ala Gln Asn Ala Val Glu Ala Ala 3830 3835 3840		
Leu Gln Arg Val Asn Asn Ala Lys Asp Ala Leu Asn Gly Asp Ala 3845 3850 3855		
Lys Leu Ile Ala Ala Gln Asn Ala Ala Lys Gln His Leu Gly Thr 3860 3865 3870		
Leu Thr His Ile Thr Thr Ala Gln Arg Asn Asp Leu Thr Asn Gln 3875 3880 3885		
Ile Ser Gln Ala Thr Asn Leu Ala Gly Val Glu Ser Val Lys Gln 3890 3895 3900		
Asn Ala Asn Ser Leu Asp Gly Ala Met Gly Asn Leu Gln Thr Ala 3905 3910 3915		
Ile Asn Asp Lys Ser Gly Thr Leu Ala Ser Gln Asn Phe Leu Asp 3920 3925 3930		
Ala Asp Glu Gln Lys Arg Asn Ala Tyr Asn Gln Ala Val Ser Ala 3935 3940 3945		
Ala Glu Thr Ile Leu Asn Lys Gln Thr Gly Pro Asn Thr Ala Lys 3950 3955 3960		
Thr Ala Val Glu Gln Ala Leu Asn Asn Val Asn Asn Ala Lys His 3965 3970 3975		
Ala Leu Asn Gly Thr Gln Asn Leu Asn Asn Ala Lys Gln Ala Ala 3980 3985 3990		
Ile Thr Ala Ile Asn Gly Ala Ser Asp Leu Asn Gln Lys Gln Lys 3995 4000 4005		
Asp Ala Leu Lys Ala Gln Ala Asn Gly Ala Gln Arg Val Ser Asn 4010 4015 4020		
Ala Gln Asp Val Gln His Asn Ala Thr Glu Leu Asn Thr Ala Met 4025 4030 4035		
Gly Thr Leu Lys His Ala Ile Ala Asp Lys Thr Asn Thr Leu Ala 4040 4045 4050		
Ser Ser Lys Tyr Val Asn Ala Asp Ser Thr Lys Gln Asn Ala Tyr 4055 4060 4065		
Thr Thr Lys Val Thr Asn Ala Glu His Ile Ile Ser Gly Thr Pro 4070 4075 4080		
Thr Val Val Thr Thr Pro Ser Glu Val Thr Ala Ala Ala Asn Gln 4085 4090 4095		
Val Asn Ser Ala Lys Gln Glu Leu Asn Gly Asp Glu Arg Leu Arg 4100 4105 4110		
Glu Ala Lys Gln Asn Ala Asn Thr Ala Ile Asp Ala Leu Thr Gln 4115 4120 4125		
Leu Asn Thr Pro Gln Lys Ala Lys Leu Lys Glu Gln Val Gly Gln 4130 4135 4140		
Ala Asn Arg Leu Glu Asp Val Gln Thr Val Gln Thr Asn Gly Gln 4145 4150 4155		
Ala Leu Asn Asn Ala Met Lys Gly Leu Arg Asp Ser Ile Ala Asn 4160 4165 4170		
Glu Thr Thr Val Lys Thr Ser Gln Asn Tyr Thr Asp Ala Ser Pro 4175 4180 4185		

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Asn	Asn	Gln	Ser	Thr	Tyr	Asn	Ser	Ala	Val	Ser	Asn	Ala	Lys	Gly
4190						4195					4200			
Ile	Ile	Asn	Gln	Thr	Asn	Asn	Pro	Thr	Met	Asp	Thr	Ser	Ala	Ile
4205						4210					4215			
Thr	Gln	Ala	Thr	Thr	Gln	Val	Asn	Asn	Ala	Lys	Asn	Gly	Leu	Asn
4220						4225					4230			
Gly	Ala	Glu	Asn	Leu	Arg	Asn	Ala	Gln	Asn	Thr	Ala	Lys	Gln	Asn
4235						4240					4245			
Leu	Asn	Thr	Leu	Ser	His	Leu	Thr	Asn	Asn	Gln	Lys	Ser	Ala	Ile
4250						4255					4260			
Ser	Ser	Gln	Ile	Asp	Arg	Ala	Gly	His	Val	Ser	Glu	Val	Thr	Ala
4265						4270					4275			
Thr	Lys	Asn	Ala	Ala	Thr	Glu	Leu	Asn	Thr	Gln	Met	Gly	Asn	Leu
4280						4285					4290			
Glu	Gln	Ala	Ile	His	Asp	Gln	Asn	Thr	Val	Lys	Gln	Ser	Val	Lys
4295						4300					4305			
Phe	Thr	Asp	Ala	Asp	Lys	Ala	Lys	Arg	Asp	Ala	Tyr	Thr	Asn	Ala
4310						4315					4320			
Val	Ser	Arg	Ala	Glu	Ala	Ile	Leu	Asn	Lys	Thr	Gln	Gly	Ala	Asn
4325						4330					4335			
Thr	Ser	Lys	Gln	Asp	Val	Glu	Ala	Ala	Ile	Gln	Asn	Val	Ser	Ser
4340						4345					4350			
Ala	Lys	Asn	Ala	Leu	Asn	Gly	Asp	Gln	Asn	Val	Thr	Asn	Ala	Lys
4355						4360					4365			
Asn	Ala	Ala	Lys	Asn	Ala	Leu	Asn	Asn	Leu	Thr	Ser	Ile	Asn	Asn
4370						4375					4380			
Ala	Gln	Lys	Arg	Asp	Leu	Thr	Thr	Lys	Ile	Asp	Gln	Ala	Thr	Thr
4385						4390					4395			
Val	Ala	Gly	Val	Glu	Ala	Val	Ser	Asn	Thr	Ser	Thr	Gln	Leu	Asn
4400						4405					4410			
Thr	Ala	Met	Ala	Asn	Leu	Gln	Asn	Gly	Ile	Asn	Asp	Lys	Thr	Asn
4415						4420					4425			
Thr	Leu	Ala	Ser	Glu	Asn	Tyr	His	Asp	Ala	Asp	Ser	Asp	Lys	Lys
4430						4435					4440			
Thr	Ala	Tyr	Thr	Gln	Ala	Val	Thr	Asn	Ala	Glu	Asn	Ile	Leu	Asn
4445						4450					4455			
Lys	Asn	Ser	Gly	Ser	Asn	Leu	Asp	Lys	Thr	Ala	Val	Glu	Asn	Ala
4460						4465					4470			
Leu	Ser	Gln	Val	Ala	Asn	Ala	Lys	Gly	Ala	Leu	Asn	Gly	Asn	His
4475						4480					4485			
Asn	Leu	Glu	Gln	Ala	Lys	Ser	Asn	Ala	Asn	Thr	Thr	Ile	Asn	Gly
4490						4495					4500			
Leu	Gln	His	Leu	Thr	Thr	Ala	Gln	Lys	Asp	Lys	Leu	Lys	Gln	Gln
4505						4510					4515			
Val	Gln	Gln	Ala	Gln	Asn	Val	Ala	Gly	Val	Asp	Thr	Val	Lys	Ser
4520						4525					4530			
Ser	Ala	Asn	Thr	Leu	Asn	Gly	Ala	Met	Gly	Thr	Leu	Arg	Asn	Ser
4535						4540					4545			
Ile	Gln	Asp	Asn	Thr	Ala	Thr	Lys	Asn	Gly	Gln	Asn	Tyr	Leu	Asp
4550						4555					4560			
Ala	Thr	Glu	Arg	Asn	Lys	Thr	Asn	Tyr	Asn	Asn	Ala	Val	Asp	Ser
4565						4570					4575			

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Ala	Asn	Gly	Val	Ile	Asn	Ala	Thr	Ser	Asn	Pro	Asn	Met	Asp	Ala
4580						4585					4590			
Asn	Ala	Ile	Asn	Gln	Ile	Ala	Thr	Gln	Val	Thr	Ser	Thr	Lys	Asn
4595						4600					4605			
Ala	Leu	Asp	Gly	Thr	His	Asn	Leu	Thr	Gln	Ala	Lys	Gln	Thr	Ala
4610						4615					4620			
Thr	Asn	Ala	Ile	Asp	Gly	Ala	Thr	Asn	Leu	Asn	Lys	Ala	Gln	Lys
4625						4630					4635			
Asp	Ala	Leu	Lys	Ala	Gln	Val	Thr	Ser	Ala	Gln	Arg	Val	Ala	Asn
4640						4645					4650			
Val	Thr	Ser	Ile	Gln	Gln	Thr	Ala	Asn	Glu	Leu	Asn	Thr	Ala	Met
4655						4660					4665			
Gly	Gln	Leu	Gln	His	Gly	Ile	Asp	Asp	Glu	Asn	Ala	Thr	Lys	Gln
4670						4675					4680			
Thr	Gln	Lys	Tyr	Arg	Asp	Ala	Glu	Gln	Ser	Lys	Lys	Thr	Ala	Tyr
4685						4690					4695			
Asp	Gln	Ala	Val	Ala	Ala	Ala	Lys	Ala	Ile	Leu	Asn	Lys	Gln	Thr
4700						4705					4710			
Gly	Ser	Asn	Ser	Asp	Lys	Ala	Ala	Val	Asp	Arg	Ala	Leu	Gln	Gln
4715						4720					4725			
Val	Thr	Ser	Thr	Lys	Asp	Ala	Leu	Asn	Gly	Asp	Ala	Lys	Leu	Ala
4730						4735					4740			
Glu	Ala	Lys	Ala	Ala	Ala	Lys	Gln	Asn	Leu	Gly	Thr	Leu	Asn	His
4745						4750					4755			
Ile	Thr	Asn	Ala	Gln	Arg	Thr	Asp	Leu	Glu	Gly	Gln	Ile	Asn	Gln
4760						4765					4770			
Ala	Thr	Thr	Val	Asp	Gly	Val	Asn	Thr	Val	Lys	Thr	Asn	Ala	Asn
4775						4780					4785			
Thr	Leu	Asp	Gly	Ala	Met	Asn	Ser	Leu	Gln	Gly	Ser	Ile	Asn	Asp
4790						4795					4800			
Lys	Asp	Ala	Thr	Leu	Arg	Asn	Gln	Asn	Tyr	Leu	Asp	Ala	Asp	Glu
4805						4810					4815			
Ser	Lys	Arg	Asn	Ala	Tyr	Thr	Gln	Ala	Val	Thr	Ala	Ala	Glu	Gly
4820						4825					4830			
Ile	Leu	Asn	Lys	Gln	Thr	Gly	Gly	Asn	Thr	Ser	Lys	Ala	Asp	Val
4835						4840					4845			
Asp	Asn	Ala	Leu	Asn	Ala	Val	Thr	Arg	Ala	Lys	Ala	Ala	Leu	Asn
4850						4855					4860			
Gly	Ala	Asp	Asn	Leu	Arg	Asn	Ala	Lys	Thr	Ser	Ala	Thr	Asn	Thr
4865						4870					4875			
Ile	Asp	Gly	Leu	Pro	Asn	Leu	Thr	Gln	Leu	Gln	Lys	Asp	Asn	Leu
4880						4885					4890			
Lys	His	Gln	Val	Glu	Gln	Ala	Gln	Asn	Val	Ala	Gly	Val	Asn	Gly
4895						4900					4905			
Val	Lys	Asp	Lys	Gly	Asn	Thr	Leu	Asn	Thr	Ala	Met	Gly	Ala	Leu
4910						4915					4920			
Arg	Thr	Ser	Ile	Gln	Asn	Asp	Asn	Thr	Thr	Lys	Thr	Ser	Gln	Asn
4925						4930					4935			
Tyr	Leu	Asp	Ala	Ser	Asp	Ser	Asn	Lys	Asn	Asn	Tyr	Asn	Thr	Ala
4940						4945					4950			
Val	Asn	Asn	Ala	Asn	Gly	Val	Ile	Asn	Ala	Thr	Asn	Asn	Pro	Asn
4955						4960					4965			
Met	Asp	Ala	Asn	Ala	Ile	Asn	Gly	Met	Ala	Asn	Gln	Val	Asn	Thr

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4970	4975	4980
Thr Lys Ala Ala Leu Asn Gly 4985	Ala Gln Asn Leu Ala Gln Ala Lys 4990	Ala Gln Ala Lys 4995
Thr Asn Ala Thr Asn Thr Ile 5000	Asn Asn Ala His Asp 5005	Leu Asn Gln 5010
Lys Gln Lys Asp Ala Leu Lys 5015	Thr Gln Val Asn Asn 5020	Ala Gln Arg 5025
Val Ser Asp Ala Asn Asn Val 5030	Gln His Thr Ala Thr 5035	Glu Leu Asn 5040
Ser Ala Met Thr Ala Leu Lys 5045	Ala Ala Ile Ala Asp 5050	Lys Glu Arg 5055
Thr Lys Ala Ser Gly Asn Tyr 5060	Val Asn Ala Asp Gln 5065	Glu Lys Arg 5070
Gln Ala Tyr Asp Ser Lys Val 5075	Thr Asn Ala Glu Asn 5080	Ile Ile Ser 5085
Gly Thr Pro Asn Ala Thr Leu 5090	Thr Val Asn Asp Val 5095	Asn Ser Ala 5100
Ala Ser Gln Val Asn Ala Ala 5105	Lys Thr Ala Leu Asn 5110	Gly Asp Asn 5115
Asn Leu Arg Val Ala Lys Glu 5120	His Ala Asn Asn Thr 5125	Ile Asp Gly 5130
Leu Ala Gln Leu Asn Asn Ala 5135	Gln Lys Ala Lys Leu 5140	Lys Glu Gln 5145
Val Gln Ser Ala Thr Thr Leu 5150	Asp Gly Val Gln Thr 5155	Val Lys Asn 5160
Ser Ser Gln Thr Leu Asn Thr 5165	Ala Met Lys Gly Leu 5170	Arg Asp Ser 5175
Ile Ala Asn Glu Ala Thr Ile 5180	Lys Ala Gly Gln Asn 5185	Tyr Thr Asp 5190
Ala Ser Pro Asn Asn Arg Asn 5195	Glu Tyr Asp Ser Ala 5200	Val Thr Ala 5205
Ala Lys Ala Ile Ile Asn Gln 5210	Thr Ser Asn Pro Thr 5215	Met Glu Pro 5220
Asn Thr Ile Thr Gln Val Thr 5225	Ser Gln Val Thr Thr 5230	Lys Glu Gln 5235
Ala Leu Asn Gly Ala Arg Asn 5240	Leu Ala Gln Ala Lys 5245	Thr Thr Ala 5250
Lys Asn Asn Leu Asn Asn Leu 5255	Thr Ser Ile Asn Asn 5260	Ala Gln Lys 5265
Asp Ala Leu Thr Arg Ser Ile 5270	Asp Gly Ala Thr Thr 5275	Val Ala Gly 5280
Val Asn Gln Glu Thr Ala Lys 5285	Ala Thr Glu Leu Asn 5290	Asn Ala Met 5295
His Ser Leu Gln Asn Gly Ile 5300	Asn Asp Glu Thr Gln 5305	Thr Lys Gln 5310
Thr Gln Lys Tyr Leu Asp Ala 5315	Glu Pro Ser Lys Lys 5320	Ser Ala Tyr 5325
Asp Gln Ala Val Asn Ala Ala 5330	Lys Ala Ile Leu Thr 5335	Lys Ala Ser 5340
Gly Gln Asn Val Asp Lys Ala 5345	Ala Val Glu Gln Ala 5350	Leu Gln Asn 5355
Val Asn Ser Thr Lys Thr Ala 5360	Leu Asn Gly Asp Ala 5365	Lys Leu Asn 5370

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Glu Ala	Lys Ala Ala Ala	Lys	Gln Thr Leu Gly	Thr	Leu Thr His
5375		5380		5385	
Ile Asn	Asn Ala Gln Arg	Thr	Ala Leu Asp Asn	Glu	Ile Thr Gln
5390		5395		5400	
Ala Thr	Asn Val Glu Gly	Val	Asn Thr Val Lys	Ala	Lys Ala Gln
5405		5410		5415	
Gln Leu	Asp Gly Ala Met	Gly	Gln Leu Glu Thr	Ser	Ile Arg Asp
5420		5425		5430	
Lys Asp	Thr Thr Leu Gln	Ser	Gln Asn Tyr Gln	Asp	Ala Asp Asp
5435		5440		5445	
Ala Lys	Arg Thr Ala Tyr	Ser	Gln Ala Val Asn	Ala	Ala Ala Thr
5450		5455		5460	
Ile Leu	Asn Lys Thr Ala	Gly	Gly Asn Thr Pro	Lys	Ala Asp Val
5465		5470		5475	
Glu Arg	Ala Met Gln Ala	Val	Thr Gln Ala Asn	Thr	Ala Leu Asn
5480		5485		5490	
Gly Ile	Gln Asn Leu Asp	Arg	Ala Lys Gln Ala	Ala	Asn Thr Ala
5495		5500		5505	
Ile Thr	Asn Ala Ser Asp	Leu	Asn Thr Lys Gln	Lys	Glu Ala Leu
5510		5515		5520	
Lys Ala	Gln Val Thr Ser	Ala	Gly Arg Val Ser	Ala	Ala Asn Gly
5525		5530		5535	
Val Glu	His Thr Ala Thr	Glu	Leu Asn Thr Ala	Met	Thr Ala Leu
5540		5545		5550	
Lys Arg	Ala Ile Ala Asp	Lys	Ala Glu Thr Lys	Ala	Ser Gly Asn
5555		5560		5565	
Tyr Val	Asn Ala Asp Ala	Asn	Lys Arg Gln Ala	Tyr	Asp Glu Lys
5570		5575		5580	
Val Thr	Ala Ala Glu Asn	Ile	Val Ser Gly Thr	Pro	Thr Pro Thr
5585		5590		5595	
Leu Thr	Pro Ala Asp Val	Thr	Asn Ala Ala Thr	Gln	Val Thr Asn
5600		5605		5610	
Ala Lys	Thr Gln Leu Asn	Gly	Asn His Asn Leu	Glu	Val Ala Lys
5615		5620		5625	
Gln Asn	Ala Asn Thr Ala	Ile	Asp Gly Leu Thr	Ser	Leu Asn Gly
5630		5635		5640	
Pro Gln	Lys Ala Lys Leu	Lys	Glu Gln Val Gly	Gln	Ala Thr Thr
5645		5650		5655	
Leu Pro	Asn Val Gln Thr	Val	Arg Asp Asn Ala	Gln	Thr Leu Asn
5660		5665		5670	
Thr Ala	Met Lys Gly Leu	Arg	Asp Ser Ile Ala	Asn	Glu Ala Thr
5675		5680		5685	
Ile Lys	Ala Gly Gln Asn	Tyr	Thr Asp Ala Ser	Gln	Asn Lys Gln
5690		5695		5700	
Thr Asp	Tyr Asn Ser Ala	Val	Thr Ala Ala Lys	Ala	Ile Ile Gly
5705		5710		5715	
Gln Thr	Thr Ser Pro Ser	Met	Asn Ala Gln Glu	Ile	Asn Gln Ala
5720		5725		5730	
Lys Asp	Gln Val Thr Ala	Lys	Gln Gln Ala Leu	Asn	Gly Gln Glu
5735		5740		5745	
Asn Leu	Arg Thr Ala Gln	Thr	Asn Ala Lys Gln	His	Leu Asn Gly
5750		5755		5760	

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Leu	Ser	Asp	Leu	Thr	Asp	Ala	Gln	Lys	Asp	Ala	Val	Lys	Arg	Gln
5765						5770					5775			
Ile	Glu	Gly	Ala	Thr	His	Val	Asn	Glu	Val	Thr	Gln	Ala	Gln	Asn
5780						5785					5790			
Asn	Ala	Asp	Ala	Leu	Asn	Thr	Ala	Met	Thr	Asn	Leu	Lys	Asn	Gly
5795						5800					5805			
Ile	Gln	Asp	Gln	Asn	Thr	Ile	Lys	Gln	Gly	Val	Asn	Phe	Thr	Asp
5810						5815					5820			
Ala	Asp	Glu	Ala	Lys	Arg	Asn	Ala	Tyr	Thr	Asn	Ala	Val	Thr	Gln
5825						5830					5835			
Ala	Glu	Gln	Ile	Leu	Asn	Lys	Ala	Gln	Gly	Pro	Asn	Thr	Ser	Lys
5840						5845					5850			
Asp	Gly	Val	Glu	Thr	Ala	Leu	Glu	Asn	Val	Gln	Arg	Ala	Lys	Asn
5855						5860					5865			
Glu	Leu	Asn	Gly	Asn	Gln	Asn	Val	Ala	Asn	Ala	Lys	Thr	Thr	Ala
5870						5875					5880			
Lys	Asn	Ala	Leu	Asn	Asn	Leu	Thr	Ser	Ile	Asn	Asn	Ala	Gln	Lys
5885						5890					5895			
Glu	Ala	Leu	Lys	Ser	Gln	Ile	Glu	Gly	Ala	Thr	Thr	Val	Ala	Gly
5900						5905					5910			
Val	Asn	Gln	Val	Ser	Thr	Thr	Ala	Ser	Glu	Leu	Asn	Thr	Ala	Met
5915						5920					5925			
Ser	Asn	Leu	Gln	Asn	Gly	Ile	Asn	Asp	Glu	Ala	Ala	Thr	Lys	Ala
5930						5935					5940			
Ala	Gln	Lys	Tyr	Thr	Asp	Ala	Asp	Arg	Glu	Lys	Gln	Thr	Ala	Tyr
5945						5950					5955			
Asn	Asp	Ala	Val	Thr	Ala	Ala	Lys	Thr	Leu	Leu	Asp	Lys	Thr	Ala
5960						5965					5970			
Gly	Ser	Asn	Asp	Asn	Lys	Ala	Ala	Val	Glu	Gln	Ala	Leu	Gln	Arg
5975						5980					5985			
Val	Asn	Thr	Ala	Lys	Thr	Ala	Leu	Asn	Gly	Asp	Glu	Arg	Leu	Asn
5990						5995					6000			
Glu	Ala	Lys	Asn	Thr	Ala	Lys	Gln	Gln	Val	Ala	Thr	Met	Ser	His
6005						6010					6015			
Leu	Thr	Asp	Ala	Gln	Lys	Ala	Asn	Leu	Thr	Ser	Gln	Ile	Glu	Ser
6020						6025					6030			
Gly	Thr	Thr	Val	Ala	Gly	Val	Gln	Gly	Ile	Gln	Ala	Asn	Ala	Gly
6035						6040					6045			
Thr	Leu	Asp	Gln	Ala	Met	Asn	Gln	Leu	Arg	Gln	Ser	Ile	Ala	Ser
6050						6055					6060			
Lys	Asp	Ala	Thr	Lys	Ser	Ser	Glu	Asp	Tyr	Gln	Asp	Ala	Asn	Ala
6065						6070					6075			
Asp	Leu	Gln	Asn	Ala	Tyr	Asn	Asp	Ala	Val	Thr	Asn	Ala	Glu	Gly
6080						6085					6090			
Ile	Ile	Ser	Ala	Thr	Asn	Asn	Pro	Glu	Met	Asn	Pro	Asp	Thr	Ile
6095						6100					6105			
Asn	Gln	Lys	Ala	Ser	Gln	Val	Asn	Ser	Ala	Lys	Ser	Ala	Leu	Asn
6110						6115					6120			
Gly	Asp	Glu	Lys	Leu	Ala	Ala	Ala	Lys	Gln	Thr	Ala	Lys	Ser	Asp
6125						6130					6135			
Ile	Gly	Arg	Leu	Thr	Asp	Leu	Asn	Asn	Ala	Gln	Arg	Thr	Ala	Ala
6140						6145					6150			
Asn	Ala	Glu	Val	Asp	Gln	Ala	Pro	Asn	Leu	Ala	Ala	Val	Thr	Ala

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6155	6160	6165
Ala Lys Asn Lys Ala Thr Ser Leu Asn Thr Ala Met Gly Asn Leu		
6170	6175	6180
Lys His Ala Leu Ala Glu Lys Asp Asn Thr Lys Arg Ser Val Asn		
6185	6190	6195
Tyr Thr Asp Ala Asp Gln Pro Lys Gln Gln Ala Tyr Asp Thr Ala		
6200	6205	6210
Val Thr Gln Ala Glu Ala Ile Thr Asn Ala Asn Gly Ser Asn Ala		
6215	6220	6225
Asn Glu Thr Gln Val Gln Ala Ala Leu Asn Gln Leu Asn Gln Ala		
6230	6235	6240
Lys Asn Asp Leu Asn Gly Asp Asn Lys Val Ala Gln Ala Lys Glu		
6245	6250	6255
Ser Ala Lys Arg Ala Leu Ala Ser Tyr Ser Asn Leu Asn Asn Ala		
6260	6265	6270
Gln Ser Thr Ala Ala Ile Ser Gln Ile Asp Asn Ala Thr Thr Val		
6275	6280	6285
Ala Gly Val Thr Ala Ala Gln Asn Thr Ala Asn Glu Leu Asn Thr		
6290	6295	6300
Ala Met Gly Gln Leu Gln Asn Gly Ile Asn Asp Gln Asn Thr Val		
6305	6310	6315
Lys Gln Gln Val Asn Phe Thr Asp Ala Asp Gln Gly Lys Lys Asp		
6320	6325	6330
Ala Tyr Thr Asn Ala Val Thr Asn Ala Gln Gly Ile Leu Asp Lys		
6335	6340	6345
Ala His Gly Gln Asn Met Thr Lys Ala Gln Val Glu Ala Ala Leu		
6350	6355	6360
Asn Gln Val Thr Thr Ala Lys Asn Ala Leu Asn Gly Asp Ala Asn		
6365	6370	6375
Val Arg Gln Ala Lys Ser Asp Ala Lys Ala Asn Leu Gly Thr Leu		
6380	6385	6390
Thr His Leu Asn Asn Ala Gln Lys Gln Asp Leu Thr Ser Gln Ile		
6395	6400	6405
Glu Gly Ala Thr Thr Val Asn Gly Val Asn Gly Val Lys Thr Lys		
6410	6415	6420
Ala Gln Asp Leu Asp Gly Ala Met Gln Arg Leu Gln Ser Ala Ile		
6425	6430	6435
Ala Asn Lys Asp Gln Thr Lys Ala Ser Glu Asn Tyr Ile Asp Ala		
6440	6445	6450
Asp Pro Thr Lys Lys Thr Ala Phe Asp Asn Ala Ile Thr Gln Ala		
6455	6460	6465
Glu Ser Tyr Leu Asn Lys Asp His Gly Ala Asn Lys Asp Lys Gln		
6470	6475	6480
Ala Val Glu Gln Ala Ile Gln Ser Val Thr Ser Thr Glu Asn Ala		
6485	6490	6495
Leu Asn Gly Asp Ala Asn Leu Gln Arg Ala Lys Thr Glu Ala Ile		
6500	6505	6510
Gln Ala Ile Asp Asn Leu Thr His Leu Asn Thr Pro Gln Lys Thr		
6515	6520	6525
Ala Leu Lys Gln Gln Val Asn Ala Ala Gln Arg Val Ser Gly Val		
6530	6535	6540
Thr Asp Leu Lys Asn Ser Ala Thr Ser Leu Asn Asn Ala Met Asp		
6545	6550	6555

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Gln Leu	Lys Gln Ala Ile Ala	Asp His Asp Thr Ile	Val Ala Ser
6560	6565	6570	
Gly Asn	Tyr Thr Asn Ala Ser	Pro Asp Lys Gln Gly	Ala Tyr Thr
6575	6580	6585	
Asp Ala	Tyr Asn Ala Ala Lys	Asn Ile Val Asn Gly	Ser Pro Asn
6590	6595	6600	
Val Ile	Thr Asn Ala Ala Asp	Val Thr Ala Ala Thr	Gln Arg Val
6605	6610	6615	
Asn Asn	Ala Glu Thr Gly Leu	Asn Gly Asp Thr Asn	Leu Ala Thr
6620	6625	6630	
Ala Lys	Gln Gln Ala Lys Asp	Ala Leu Arg Gln Met	Thr His Leu
6635	6640	6645	
Ser Asp	Ala Gln Lys Gln Ser	Ile Thr Gly Gln Ile	Asp Ser Ala
6650	6655	6660	
Thr Gln	Val Thr Gly Val Gln	Ser Val Lys Asp Asn	Ala Thr Asn
6665	6670	6675	
Leu Asp	Asn Ala Met Asn Gln	Leu Arg Asn Ser Ile	Ala Asn Lys
6680	6685	6690	
Asp Asp	Val Lys Ala Ser Gln	Pro Tyr Val Asp Ala	Asp Arg Asp
6695	6700	6705	
Lys Gln	Asn Ala Tyr Asn Thr	Ala Val Thr Asn Ala	Glu Asn Ile
6710	6715	6720	
Ile Asn	Ala Thr Ser Gln Pro	Thr Leu Asp Pro Ser	Ala Val Thr
6725	6730	6735	
Gln Ala	Ala Asn Gln Val Ser	Thr Asn Lys Thr Ala	Leu Asn Gly
6740	6745	6750	
Ala Gln	Asn Leu Ala Asn Lys	Lys Gln Glu Thr Thr	Ala Asn Ile
6755	6760	6765	
Asn Gln	Leu Ser His Leu Asn	Asn Ala Gln Lys Gln	Asp Leu Asn
6770	6775	6780	
Thr Gln	Val Thr Asn Ala Pro	Asn Ile Ser Thr Val	Asn Gln Val
6785	6790	6795	
Lys Thr	Lys Ala Glu Gln Leu	Asp Gln Ala Met Glu	Arg Leu Ile
6800	6805	6810	
Asn Gly	Ile Gln Asp Lys Asp	Gln Val Lys Gln Ser	Val Asn Phe
6815	6820	6825	
Thr Asp	Ala Asp Pro Glu Lys	Gln Thr Ala Tyr Asn	Asn Ala Val
6830	6835	6840	
Thr Ala	Ala Glu Asn Ile Ile	Asn Gln Ala Asn Gly	Thr Asn Ala
6845	6850	6855	
Asn Gln	Ser Gln Val Glu Ala	Ala Leu Ser Thr Val	Thr Thr Thr
6860	6865	6870	
Lys Gln	Ala Leu Asn Gly Asp	Arg Lys Val Thr Asp	Ala Lys Asn
6875	6880	6885	
Asn Ala	Asn Gln Thr Leu Ser	Thr Leu Asp Asn Leu	Asn Asn Ala
6890	6895	6900	
Gln Lys	Gly Ala Val Thr Gly	Asn Ile Asn Gln Ala	His Thr Val
6905	6910	6915	
Ala Glu	Val Thr Gln Ala Ile	Gln Thr Ala Gln Glu	Leu Asn Thr
6920	6925	6930	
Ala Met	Gly Asn Leu Lys Asn	Ser Leu Asn Asp Lys	Asp Thr Thr
6935	6940	6945	

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Leu Gly 6950	Ser Gln Asn Phe 6955	Ala Asp Ala Asp Pro 6960	Glu Lys Lys Asn 6965
Ala Tyr 6965	Asn Glu Ala Val 6970	His Asn Ala Glu Asn 6975	Ile Leu Asn Lys 6980
Ser Thr 6980	Gly Thr Asn Val 6985	Pro Lys Asp Gln Val 6990	Glu Ala Ala Met 6995
Asn Gln 6995	Val Asn Ala Thr 7000	Lys Ala Ala Leu Asn 7005	Gly Thr Gln Asn 7010
Leu Glu 7010	Lys Ala Lys Gln 7015	His Ala Asn Thr Ala 7020	Ile Asp Gly Leu 7025
Ser His 7025	Leu Thr Asn Ala 7030	Gln Lys Glu Ala Leu 7035	Lys Gln Leu Val 7040
Gln Gln 7040	Ser Thr Thr Val 7045	Ala Glu Ala Gln Gly 7050	Asn Glu Gln Lys 7055
Ala Asn 7055	Asn Val Asp Ala 7060	Ala Met Asp Lys Leu 7065	Arg Gln Ser Ile 7070
Ala Asp 7070	Asn Ala Thr Thr 7075	Lys Gln Asn Gln Asn 7080	Tyr Thr Asp Ala 7085
Ser Gln 7085	Asn Lys Lys Asp 7090	Ala Tyr Asn Asn Ala 7095	Val Thr Thr Ala 7100
Gln Gly 7100	Ile Ile Asp Gln 7105	Thr Thr Ser Pro Thr 7110	Leu Asp Pro Thr 7115
Val Ile 7115	Asn Gln Ala Ala 7120	Gly Gln Val Ser Thr 7125	Thr Lys Asn Ala 7130
Leu Asn 7130	Gly Asn Glu Asn 7135	Leu Glu Ala Ala Lys 7140	Gln Gln Ala Ser 7145
Gln Ser 7145	Leu Gly Ser Leu 7150	Asp Asn Leu Asn Asn 7155	Ala Gln Lys Gln 7160
Thr Val 7160	Thr Asp Gln Ile 7165	Asn Gly Ala His Thr 7170	Val Asp Glu Ala 7175
Asn Gln 7175	Ile Lys Gln Asn 7180	Ala Gln Asn Leu Asn 7185	Thr Ala Met Gly 7190
Asn Leu 7190	Lys Gln Ala Ile 7195	Ala Asp Lys Asp Ala 7200	Thr Lys Ala Thr 7205
Val Asn 7205	Phe Thr Asp Ala 7210	Asp Gln Ala Lys Gln 7215	Gln Ala Tyr Asn 7220
Thr Ala 7220	Val Thr Asn Ala 7225	Glu Asn Ile Ser Lys 7230	Ala Asn Gly Asn 7235
Ala Thr 7235	Gln Ala Glu Val 7240	Glu Gln Ala Ile Lys 7245	Gln Val Asn Ala 7250
Ala Lys 7250	Gln Ala Leu Asn 7255	Gly Asn Ala Asn Val 7260	Gln His Ala Lys 7265
Asp Glu 7265	Ala Thr Ala Leu 7270	Ile Asn Ser Ser Asn 7275	Asp Leu Asn Gln 7280
Ala Gln 7280	Lys Asp Ala Leu 7285	Lys Gln Gln Val Gln 7290	Asn Ala Thr Thr 7295
Val Ala 7295	Gly Val Asn Asn 7300	Val Lys Gln Thr Ala 7305	Gln Glu Leu Asn 7310
Asn Ala 7310	Met Thr Gln Leu 7315	Lys Gln Gly Ile Ala 7320	Asp Lys Glu Gln 7325
Thr Lys 7325	Ala Asp Gly Asn 7330	Phe Val Asn Ala Asp 7335	Pro Asp Lys Gln 7340
Asn Ala 7340	Tyr Asn Gln Ala 7345	Val Ala Lys Ala Glu 7350	Ala Leu Ile Ser 7355

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7340	7345	7350
Ala Thr Pro Asp Val Val Val Thr Pro Ser Glu Ile Thr Ala Ala		
7355	7360	7365
Leu Asn Lys Val Thr Gln Ala Lys Asn Asp Leu Asn Gly Asn Thr		
7370	7375	7380
Asn Leu Ala Thr Ala Lys Gln Asn Val Gln His Ala Ile Asp Gln		
7385	7390	7395
Leu Pro Asn Leu Asn Gln Ala Gln Arg Asp Glu Tyr Ser Lys Gln		
7400	7405	7410
Ile Thr Gln Ala Thr Leu Val Pro Asn Val Asn Ala Ile Gln Gln		
7415	7420	7425
Ala Ala Thr Thr Leu Asn Asp Ala Met Thr Gln Leu Lys Gln Gly		
7430	7435	7440
Ile Ala Asn Lys Ala Gln Ile Lys Gly Ser Glu Asn Tyr His Asp		
7445	7450	7455
Ala Asp Thr Asp Lys Gln Thr Ala Tyr Asp Asn Ala Val Thr Lys		
7460	7465	7470
Ala Glu Glu Leu Leu Lys Gln Thr Thr Asn Pro Thr Met Asp Pro		
7475	7480	7485
Asn Thr Ile Gln Gln Ala Leu Thr Lys Val Asn Asp Thr Asn Gln		
7490	7495	7500
Ala Leu Asn Gly Asn Gln Lys Leu Ala Asp Ala Lys Gln Asp Ala		
7505	7510	7515
Lys Thr Thr Leu Gly Thr Leu Asp His Leu Asn Asp Ala Gln Lys		
7520	7525	7530
Gln Ala Leu Thr Thr Gln Val Glu Gln Ala Pro Asp Ile Ala Thr		
7535	7540	7545
Val Asn Asn Val Lys Gln Asn Ala Gln Asn Leu Asn Asn Ala Met		
7550	7555	7560
Thr Asn Leu Asn Asn Ala Leu Gln Asp Lys Thr Glu Thr Leu Asn		
7565	7570	7575
Ser Ile Asn Phe Thr Asp Ala Asp Gln Ala Lys Lys Asp Ala Tyr		
7580	7585	7590
Thr Asn Ala Val Ser His Ala Glu Gly Ile Leu Ser Lys Ala Asn		
7595	7600	7605
Gly Ser Asn Ala Ser Gln Thr Glu Val Glu Gln Ala Met Gln Arg		
7610	7615	7620
Val Asn Glu Ala Lys Gln Ala Leu Asn Gly Asn Asp Asn Val Gln		
7625	7630	7635
Arg Ala Lys Asp Ala Ala Lys Gln Val Ile Thr Asn Ala Asn Asp		
7640	7645	7650
Leu Asn Gln Ala Gln Lys Asp Ala Leu Lys Gln Gln Val Asp Ala		
7655	7660	7665
Ala Gln Thr Val Ala Asn Val Asn Thr Ile Lys Gln Thr Ala Gln		
7670	7675	7680
Asp Leu Asn Gln Ala Met Thr Gln Leu Lys Gln Gly Ile Ala Asp		
7685	7690	7695
Lys Asp Gln Thr Lys Ala Asn Gly Asn Phe Val Asn Ala Asp Thr		
7700	7705	7710
Asp Lys Gln Asn Ala Tyr Asn Asn Ala Val Ala His Ala Glu Gln		
7715	7720	7725
Ile Ile Ser Gly Thr Pro Asn Ala Asn Val Asp Pro Gln Gln Val		
7730	7735	7740

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Ala Gln	Ala Leu Gln Gln Val	Asn Gln Ala Lys Gly	Asp Leu Asn
7745	7750	7755	
Gly Asn	His Asn Leu Gln Val	Ala Lys Asp Asn Ala	Asn Thr Ala
7760	7765	7770	
Ile Asp	Gln Leu Pro Asn Leu	Asn Gln Pro Gln Lys	Thr Ala Leu
7775	7780	7785	
Lys Asp	Gln Val Ser His Ala	Glu Leu Val Thr Gly	Val Asn Ala
7790	7795	7800	
Ile Lys	Gln Asn Ala Asp Ala	Leu Asn Asn Ala Met	Gly Thr Leu
7805	7810	7815	
Lys Gln	Gln Ile Gln Ala Asn	Ser Gln Val Pro Gln	Ser Val Asp
7820	7825	7830	
Phe Thr	Gln Ala Asp Gln Asp	Lys Gln Gln Ala Tyr	Asn Asn Ala
7835	7840	7845	
Ala Asn	Gln Ala Gln Gln Ile	Ala Asn Gly Ile Pro	Thr Pro Val
7850	7855	7860	
Leu Thr	Pro Asp Thr Val Thr	Gln Ala Val Thr Thr	Met Asn Gln
7865	7870	7875	
Ala Lys	Asp Ala Leu Asn Gly	Asp Glu Lys Leu Ala	Gln Ala Lys
7880	7885	7890	
Gln Glu	Ala Leu Ala Asn Leu	Asp Thr Leu Arg Asp	Leu Asn Gln
7895	7900	7905	
Pro Gln	Arg Asp Ala Leu Arg	Asn Gln Ile Asn Gln	Ala Gln Ala
7910	7915	7920	
Leu Ala	Thr Val Glu Gln Thr	Lys Gln Asn Ala Gln	Asn Val Asn
7925	7930	7935	
Thr Ala	Met Ser Asn Leu Lys	Gln Gly Ile Ala Asn	Lys Asp Thr
7940	7945	7950	
Val Lys	Ala Ser Glu Asn Tyr	His Asp Ala Asp Ala	Asp Lys Gln
7955	7960	7965	
Thr Ala	Tyr Thr Asn Ala Val	Ser Gln Ala Glu Gly	Ile Ile Asn
7970	7975	7980	
Gln Thr	Thr Asn Pro Thr Leu	Asn Pro Asp Glu Ile	Thr Arg Ala
7985	7990	7995	
Leu Thr	Gln Val Thr Asp Ala	Lys Asn Gly Leu Asn	Gly Glu Ala
8000	8005	8010	
Lys Leu	Ala Thr Glu Lys Gln	Asn Ala Lys Asp Ala	Val Ser Gly
8015	8020	8025	
Met Thr	His Leu Asn Asp Ala	Gln Lys Gln Ala Leu	Lys Gly Gln
8030	8035	8040	
Ile Asp	Gln Ser Pro Glu Ile	Ala Thr Val Asn Gln	Val Lys Gln
8045	8050	8055	
Thr Ala	Thr Ser Leu Asp Gln	Ala Met Asp Gln Leu	Ser Gln Ala
8060	8065	8070	
Ile Asn	Asp Lys Ala Gln Thr	Leu Ala Asp Gly Asn	Tyr Leu Asn
8075	8080	8085	
Ala Asp	Pro Asp Lys Gln Asn	Ala Tyr Lys Gln Ala	Val Ala Lys
8090	8095	8100	
Ala Glu	Ala Leu Leu Asn Lys	Gln Ser Gly Thr Asn	Glu Val Gln
8105	8110	8115	
Ala Gln	Val Glu Ser Ile Thr	Asn Glu Val Asn Ala	Ala Lys Gln
8120	8125	8130	

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Ala	Leu	Asn	Gly	Asn	Asp	Asn	Leu	Ala	Asn	Ala	Lys	Gln	Gln	Ala
8135						8140					8145			
Lys	Gln	Gln	Leu	Ala	Asn	Leu	Thr	His	Leu	Asn	Asp	Ala	Gln	Lys
8150						8155					8160			
Gln	Ser	Phe	Glu	Ser	Gln	Ile	Thr	Gln	Ala	Pro	Leu	Val	Thr	Asp
8165						8170					8175			
Val	Thr	Thr	Ile	Asn	Gln	Lys	Ala	Gln	Thr	Leu	Asp	His	Ala	Met
8180						8185					8190			
Glu	Leu	Leu	Arg	Asn	Ser	Val	Ala	Asp	Asn	Gln	Thr	Thr	Leu	Ala
8195						8200					8205			
Ser	Glu	Asp	Tyr	His	Asp	Ala	Thr	Ala	Gln	Arg	Gln	Asn	Asp	Tyr
8210						8215					8220			
Asn	Gln	Ala	Val	Thr	Ala	Ala	Asn	Asn	Ile	Ile	Asn	Gln	Thr	Thr
8225						8230					8235			
Ser	Pro	Thr	Met	Asn	Pro	Asp	Asp	Val	Asn	Gly	Ala	Thr	Thr	Gln
8240						8245					8250			
Val	Asn	Asn	Thr	Lys	Val	Ala	Leu	Asp	Gly	Asp	Glu	Asn	Leu	Ala
8255						8260					8265			
Ala	Ala	Lys	Gln	Gln	Ala	Asn	Asn	Arg	Leu	Asp	Gln	Leu	Asp	His
8270						8275					8280			
Leu	Asn	Asn	Ala	Gln	Lys	Gln	Gln	Leu	Gln	Ser	Gln	Ile	Thr	Gln
8285						8290					8295			
Ser	Ser	Asp	Ile	Ala	Ala	Val	Asn	Gly	His	Lys	Gln	Thr	Ala	Glu
8300						8305					8310			
Ser	Leu	Asn	Thr	Ala	Met	Gly	Asn	Leu	Ile	Asn	Ala	Ile	Ala	Asp
8315						8320					8325			
His	Gln	Ala	Val	Glu	Gln	Arg	Gly	Asn	Phe	Ile	Asn	Ala	Asp	Thr
8330						8335					8340			
Asp	Lys	Gln	Thr	Ala	Tyr	Asn	Thr	Ala	Val	Asn	Glu	Ala	Ala	Ala
8345						8350					8355			
Met	Ile	Asn	Lys	Gln	Thr	Gly	Gln	Asn	Ala	Asn	Gln	Thr	Glu	Val
8360						8365					8370			
Glu	Gln	Ala	Ile	Thr	Lys	Val	Gln	Thr	Thr	Leu	Gln	Ala	Leu	Asn
8375						8380					8385			
Gly	Asp	His	Asn	Leu	Gln	Val	Ala	Lys	Thr	Asn	Ala	Thr	Gln	Ala
8390						8395					8400			
Ile	Asp	Ala	Leu	Thr	Ser	Leu	Asn	Asp	Pro	Gln	Lys	Thr	Ala	Leu
8405						8410					8415			
Lys	Asp	Gln	Val	Thr	Ala	Ala	Thr	Leu	Val	Thr	Ala	Val	His	Gln
8420						8425					8430			
Ile	Glu	Gln	Asn	Ala	Asn	Thr	Leu	Asn	Gln	Ala	Met	His	Gly	Leu
8435						8440					8445			
Arg	Gln	Ser	Ile	Gln	Asp	Asn	Ala	Ala	Thr	Lys	Ala	Asn	Ser	Lys
8450						8455					8460			
Tyr	Ile	Asn	Glu	Asp	Gln	Pro	Glu	Gln	Gln	Asn	Tyr	Asp	Gln	Ala
8465						8470					8475			
Val	Gln	Ala	Ala	Asn	Asn	Ile	Ile	Asn	Glu	Gln	Thr	Ala	Thr	Leu
8480						8485					8490			
Asp	Asn	Asn	Ala	Ile	Asn	Gln	Ala	Ala	Thr	Thr	Val	Asn	Thr	Thr
8495						8500					8505			
Lys	Ala	Ala	Leu	His	Gly	Asp	Val	Lys	Leu	Gln	Asn	Asp	Lys	Asp
8510						8515					8520			
His	Ala	Lys	Gln	Thr	Val	Ser	Gln	Leu	Ala	His	Leu	Asn	Asn	Ala

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8525	8530	8535
Gln Lys His Met Glu Asp Thr	Leu Ile Asp Ser Glu Thr Thr Arg	
8540	8545	8550
Thr Ala Val Lys Gln Asp Leu	Thr Glu Ala Gln Ala Leu Asp Gln	
8555	8560	8565
Leu Met Asp Ala Leu Gln Gln	Ser Ile Ala Asp Lys Asp Ala Thr	
8570	8575	8580
Arg Ala Ser Ser Ala Tyr Val	Asn Ala Glu Pro Asn Lys Lys Gln	
8585	8590	8595
Ser Tyr Asp Glu Ala Val Gln	Asn Ala Glu Ser Ile Ile Ala Gly	
8600	8605	8610
Leu Asn Asn Pro Thr Ile Asn	Lys Gly Asn Val Ser Ser Ala Thr	
8615	8620	8625
Gln Ala Val Ile Ser Ser Lys	Asn Ala Leu Asp Gly Val Glu Arg	
8630	8635	8640
Leu Ala Gln Asp Lys Gln Thr	Ala Gly Asn Ser Leu Asn His Leu	
8645	8650	8655
Asp Gln Leu Thr Pro Ala Gln	Gln Gln Ala Leu Glu Asn Gln Ile	
8660	8665	8670
Asn Asn Ala Thr Thr Arg Gly	Glu Val Ala Gln Lys Leu Thr Glu	
8675	8680	8685
Ala Gln Ala Leu Asn Gln Ala	Met Glu Ala Leu Arg Asn Ser Ile	
8690	8695	8700
Gln Asp Gln Gln Gln Thr Glu	Ala Gly Ser Lys Phe Ile Asn Glu	
8705	8710	8715
Asp Lys Pro Gln Lys Asp Ala	Tyr Gln Ala Ala Val Gln Asn Ala	
8720	8725	8730
Lys Asp Leu Ile Asn Gln Thr	Asn Asn Pro Thr Leu Asp Lys Ala	
8735	8740	8745
Gln Val Glu Gln Leu Thr Gln	Ala Val Asn Gln Ala Lys Asp Asn	
8750	8755	8760
Leu His Gly Asp Gln Lys Leu	Ala Asp Asp Lys Gln His Ala Val	
8765	8770	8775
Thr Asp Leu Asn Gln Leu Asn	Gly Leu Asn Asn Pro Gln Arg Gln	
8780	8785	8790
Ala Leu Glu Ser Gln Ile Asn	Asn Ala Ala Thr Arg Gly Glu Val	
8795	8800	8805
Ala Gln Lys Leu Ala Glu Ala	Lys Ala Leu Asp Gln Ala Met Gln	
8810	8815	8820
Ala Leu Arg Asn Ser Ile Gln	Asp Gln Gln Gln Thr Glu Ser Gly	
8825	8830	8835
Ser Lys Phe Ile Asn Glu Asp	Lys Pro Gln Lys Asp Ala Tyr Gln	
8840	8845	8850
Ala Ala Val Gln Asn Ala Lys	Asp Leu Ile Asn Gln Thr Gly Asn	
8855	8860	8865
Pro Thr Leu Asp Lys Ser Gln	Val Glu Gln Leu Thr Gln Ala Val	
8870	8875	8880
Thr Thr Ala Lys Asp Asn Leu	His Gly Asp Gln Lys Leu Ala Arg	
8885	8890	8895
Asp Gln Gln Gln Ala Val Thr	Thr Val Asn Ala Leu Pro Asn Leu	
8900	8905	8910
Asn His Ala Gln Gln Gln Ala	Leu Thr Asp Ala Ile Asn Ala Ala	
8915	8920	8925

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Pro Thr	Arg Thr	Glu Val	Ala	Gln His	Val Gln	Thr	Ala Thr	Glu
8930			8935			8940		
Leu Asp	His Ala	Met Glu	Thr	Leu Lys	Asn Lys	Val	Asp Gln	Val
8945			8950			8955		
Asn Thr	Asp Lys	Ala Gln	Pro	Asn Tyr	Thr Glu	Ala	Ser Thr	Asp
8960			8965			8970		
Lys Lys	Glu Ala	Val Asp	Gln	Ala Leu	Gln Ala	Ala	Glu Ser	Ile
8975			8980			8985		
Thr Asp	Pro Thr	Asn Gly	Ser	Asn Ala	Asn Lys	Asp	Ala Val	Asp
8990			8995			9000		
Gln Val	Leu Thr	Lys Leu	Gln	Glu Lys	Glu Asn	Glu	Leu Asn	Gly
9005			9010			9015		
Asn Glu	Arg Val	Ala Glu	Ala	Lys Thr	Gln Ala	Lys	Gln Thr	Ile
9020			9025			9030		
Asp Gln	Leu Thr	His Leu	Asn	Ala Asp	Gln Ile	Ala	Thr Ala	Lys
9035			9040			9045		
Gln Asn	Ile Asp	Gln Ala	Thr	Lys Leu	Gln Pro	Ile	Ala Glu	Leu
9050			9055			9060		
Val Asp	Gln Ala	Thr Gln	Leu	Asn Gln	Ser Met	Asp	Gln Leu	Gln
9065			9070			9075		
Gln Ala	Val Asn	Glu His	Ala	Asn Val	Glu Gln	Thr	Val Asp	Tyr
9080			9085			9090		
Thr Gln	Ala Asp	Ser Asp	Lys	Gln Asn	Ala Tyr	Lys	Gln Ala	Ile
9095			9100			9105		
Ala Asp	Ala Glu	Asn Val	Leu	Lys Gln	Asn Ala	Asn	Lys Gln	Gln
9110			9115			9120		
Val Asp	Gln Ala	Leu Gln	Asn	Ile Leu	Asn Ala	Lys	Gln Ala	Leu
9125			9130			9135		
Asn Gly	Asp Glu	Arg Val	Ala	Leu Ala	Lys Thr	Asn	Gly Lys	His
9140			9145			9150		
Asp Ile	Asp Gln	Leu Asn	Ala	Leu Asn	Asn Ala	Gln	Gln Asp	Gly
9155			9160			9165		
Phe Lys	Gly Arg	Ile Asp	Gln	Ser Asn	Asp Leu	Asn	Gln Ile	Gln
9170			9175			9180		
Gln Ile	Val Asp	Glu Ala	Lys	Ala Leu	Asn Arg	Ala	Met Asp	Gln
9185			9190			9195		
Leu Ser	Gln Glu	Ile Thr	Asp	Asn Glu	Gly Arg	Thr	Lys Gly	Ser
9200			9205			9210		
Thr Asn	Tyr Val	Asn Ala	Asp	Thr Gln	Val Lys	Gln	Val Tyr	Asp
9215			9220			9225		
Glu Thr	Val Asp	Lys Ala	Lys	Gln Ala	Leu Asp	Lys	Ser Thr	Gly
9230			9235			9240		
Gln Asn	Leu Thr	Ala Lys	Gln	Val Ile	Lys Leu	Asn	Asp Ala	Val
9245			9250			9255		
Thr Ala	Ala Lys	Lys Ala	Leu	Asn Gly	Glu Glu	Arg	Leu Asn	Asn
9260			9265			9270		
Arg Lys	Ala Glu	Ala Leu	Gln	Arg Leu	Asp Gln	Leu	Thr His	Leu
9275			9280			9285		
Asn Asn	Ala Gln	Arg Gln	Leu	Ala Ile	Gln Gln	Ile	Asn Asn	Ala
9290			9295			9300		
Glu Thr	Leu Asn	Lys Ala	Ser	Arg Ala	Ile Asn	Arg	Ala Thr	Lys
9305			9310			9315		

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Leu Asp 9320	Asn Ala Met Gly 9325	Val Gln Gln Tyr 9330	Ile Asp Glu Gln 9330
His Leu 9335	Gly Val Ile Ser 9340	Thr Asn Tyr Ile 9345	Asn Ala Asp Asp 9345
Asn Leu 9350	Lys Ala Asn Tyr 9355	Asn Ala Ile Ala 9360	Asn Ala Ala His 9360
Glu Leu 9365	Asp Lys Val Gln 9370	Asn Ala Ile Ala 9375	Lys Ala Glu Ala 9375
Glu Gln 9380	Leu Lys Gln Asn 9385	Ile Asp Ala Gln 9390	Asn Ala Leu Asn 9390
Gly Asp 9395	Gln Asn Leu Ala 9400	Ala Lys Asp Lys 9405	Ala Asn Ala Phe 9405
Val Asn 9410	Ser Leu Asn Gly 9415	Asn Gln Gln Gln 9420	Asp Leu Ala 9420
His Lys 9425	Ala Ile Asn Asn 9430	Asp Thr Val Ser 9435	Val Thr Asp 9435
Ile Val 9440	Asn Asn Gln Ile 9445	Leu Asn Asp Ala 9450	Met Glu Thr Leu 9450
Lys His 9455	Leu Val Asp Asn 9460	Ile Pro Asn Ala 9465	Glu Gln Thr Val 9465
Asn Tyr 9470	Gln Asn Ala Asp 9475	Asn Ala Lys Thr 9480	Asn Phe Asp Asp 9480
Ala Lys 9485	Arg Leu Ala Asn 9490	Leu Leu Asn Ser 9495	Asp Asn Thr Asn 9495
Val Asn 9500	Asp Ile Asn Gly 9505	Ile Gln Ala Val 9510	Asn Asp Ala Ile 9510
His Asn 9515	Leu Asn Gly Asp 9520	Arg Leu Gln Asp 9525	Ala Lys Asp Lys 9525
Ala Ile 9530	Gln Ser Ile Asn 9535	Ala Leu Ala Asn 9540	Lys Leu Lys Glu 9540
Ile Glu 9545	Ala Ser Asn Ala 9550	Asp Gln Asp Lys 9555	Leu Ile Ala Lys 9555
Asn Lys 9560	Ala Glu Glu Leu 9565	Asn Ser Ile Ile 9570	Asn Asn Ile Asn 9570
Lys Ala 9575	Thr Ser Asn Gln 9580	Val Ser Gln Val 9585	Gln Thr Ala Gly 9585
Asn His 9590	Ala Ile Glu Gln 9595	His Ala Asn Glu 9600	Ile Pro Lys Ala 9600
Lys Ile 9605	Asp Ala Asn Lys 9610	Val Asp Lys Gln 9615	Val Gln Ala Leu 9615
Ile Asp 9620	Glu Ile Asp Arg 9625	Pro Asn Leu Thr 9630	Asp Lys Glu Lys 9630
Gln Ala 9635	Leu Lys Asp Arg 9640	Asn Gln Ile Leu 9645	Gln Gln Gly His 9645
Asn Gly 9650	Ile Asn Asn Ala 9655	Thr Lys Glu Glu 9660	Ile Glu Gln Ala 9660
Lys Ala 9665	Gln Leu Ala Gln 9670	Leu Gln Asp Ile 9675	Lys Asp Leu Val 9675
Lys Ala 9680	Lys Glu Asp Ala 9685	Gln Asp Val Asp 9690	Lys Gln Val Gln 9690
Ala Leu 9695	Ile Asp Glu Ile 9700	Gln Asn Pro Asn 9705	Leu Thr Asp Lys 9705
Glu Lys	Gln Ala Leu Lys Tyr	Arg Ile Asn Gln Ile	Leu Gln Gln

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9710	9715	9720
Gly His Asn Asp Ile Asn Asn Ala Leu Thr Lys Glu Glu Ile Glu 9725 9730 9735		
Gln Ala Lys Ala Gln Leu Ala Gln Ala Leu Gln Asp Ile Lys Asp 9740 9745 9750		
Leu Val Lys Ala Lys Glu Asp Ala Lys Asn Ala Ile Lys Ala Leu 9755 9760 9765		
Ala Asn Ala Lys Arg Asp Gln Ile Asn Ser Asn Pro Asp Leu Thr 9770 9775 9780		
Pro Glu Gln Lys Ala Lys Ala Leu Lys Glu Ile Asp Glu Ala Glu 9785 9790 9795		
Lys Arg Ala Leu Gln Asn Val Glu Asn Ala Gln Thr Ile Asp Gln 9800 9805 9810		
Leu Asn Arg Gly Leu Asn Leu Gly Leu Asp Asp Ile Arg Asn Thr 9815 9820 9825		
His Val Trp Glu Val Asp Glu Gln Pro Ala Val Asn Glu Ile Phe 9830 9835 9840		
Glu Ala Thr Pro Glu Gln Ile Leu Val Asn Gly Glu Leu Ile Val 9845 9850 9855		
His Arg Asp Asp Ile Ile Thr Glu Gln Asp Ile Leu Ala His Ile 9860 9865 9870		
Asn Leu Ile Asp Gln Leu Ser Ala Glu Val Ile Asp Thr Pro Ser 9875 9880 9885		
Thr Ala Thr Ile Ser Asp Ser Leu Thr Ala Lys Val Glu Val Thr 9890 9895 9900		
Leu Leu Asp Gly Ser Lys Val Ile Val Asn Val Pro Val Lys Val 9905 9910 9915		
Val Glu Lys Glu Leu Ser Val Val Lys Gln Gln Ala Ile Glu Ser 9920 9925 9930		
Ile Glu Asn Ala Ala Gln Gln Lys Ile Asn Glu Ile Asn Asn Ser 9935 9940 9945		
Val Thr Leu Thr Leu Glu Gln Lys Glu Ala Ala Ile Ala Glu Val 9950 9955 9960		
Asn Lys Leu Lys Gln Gln Ala Ile Asp His Val Asn Asn Ala Pro 9965 9970 9975		
Asp Val His Ser Val Glu Glu Ile Gln Gln Gln Glu Gln Ala His 9980 9985 9990		
Ile Glu Gln Phe Asn Pro Glu Gln Phe Thr Ile Glu Gln Ala Lys 9995 10000 10005		
Ser Asn Ala Ile Lys Ser Ile Glu Asp Ala Ile Gln His Met Ile 10010 10015 10020		
Asp Glu Ile Lys Ala Arg Thr Asp Leu Thr Asp Lys Glu Lys Gln 10025 10030 10035		
Glu Ala Ile Ala Lys Leu Asn Gln Leu Lys Glu Gln Ala Ile Gln 10040 10045 10050		
Ala Ile Gln Arg Ala Gln Ser Ile Asp Glu Ile Ser Glu Gln Leu 10055 10060 10065		
Glu Gln Phe Lys Ala Gln Met Lys Ala Ala Asn Pro Thr Ala Lys 10070 10075 10080		
Glu Leu Ala Lys Arg Lys Gln Glu Ala Ile Ser Arg Ile Lys Asp 10085 10090 10095		
Phe Ser Asn Glu Lys Ile Asn Ser Ile Arg Asn Ser Glu Ile Gly 10100 10105 10110		

Thr Ala 10115	Asp	Glu	Lys	Gln	Ala 10120	Ala	Met	Asn	Gln	Ile 10125	Asn	Glu	Ile
Val Leu 10130	Glu	Thr	Ile	Arg	Asp 10135	Ile	Asn	Asn	Ala	His 10140	Thr	Leu	Gln
Gln Val 10145	Glu	Ala	Ala	Leu	Asn 10150	Asn	Gly	Ile	Ala	Arg 10155	Ile	Ser	Ala
Val Gln 10160	Ile	Val	Thr	Ser	Asp 10165	Arg	Ala	Lys	Gln	Ser 10170	Ser	Ser	Thr
Gly Asn 10175	Glu	Ser	Asn	Ser	His 10180	Leu	Thr	Ile	Gly	Tyr 10185	Gly	Thr	Ala
Asn His 10190	Pro	Phe	Asn	Ser	Ser 10195	Thr	Ile	Gly	His	Lys 10200	Lys	Lys	Leu
Asp Glu 10205	Asp	Asp	Asp	Ile	Asp 10210	Pro	Leu	His	Met	Arg 10215	His	Phe	Ser
Asn Asn 10220	Phe	Gly	Asn	Val	Ile 10225	Lys	Asn	Ala	Ile	Gly 10230	Val	Val	Gly
Ile Ser 10235	Gly	Leu	Leu	Ala	Ser 10240	Phe	Trp	Phe	Phe	Ile 10245	Ala	Lys	Arg
Arg Arg 10250	Lys	Glu	Asp	Glu	Glu 10255	Glu	Glu	Leu	Glu	Ile 10260	Arg	Asp	Asn
Asn Lys 10265	Asp	Ser	Ile	Lys	Glu 10270	Thr	Leu	Asp	Asp	Thr 10275	Lys	His	Leu
Pro Leu 10280	Leu	Phe	Ala	Lys	Arg 10285	Arg	Arg	Lys	Glu	Asp 10290	Glu	Glu	Asp
Val Thr 10295	Val	Glu	Glu	Lys	Asp 10300	Ser	Leu	Asn	Asn	Gly 10305	Glu	Ser	Leu
Asp Lys 10310	Val	Lys	His	Thr	Pro 10315	Phe	Phe	Leu	Pro	Lys 10320	Arg	Arg	Arg
Lys Glu 10325	Asp	Glu	Glu	Asp	Val 10330	Glu	Val	Thr	Asn	Glu 10335	Asn	Thr	Asp
Glu Lys 10340	Val	Leu	Lys	Asp	Asn 10345	Glu	His	Ser	Pro	Leu 10350	Leu	Phe	Ala
Lys Arg 10355	Arg	Lys	Asp	Lys	Glu 10360	Glu	Asp	Val	Glu	Thr 10365	Thr	Thr	Ser
Ile Glu 10370	Ser	Lys	Asp	Glu	Asp 10375	Val	Pro	Leu	Leu	Leu 10380	Ala	Lys	Lys
Lys Asn 10385	Gln	Lys	Asp	Asn	Gln 10390	Ser	Lys	Asp	Lys	Lys 10395	Ser	Ala	Ser
Lys Asn 10400	Thr	Ser	Lys	Lys	Val 10405	Ala	Ala	Lys	Lys	Lys 10410	Lys	Lys	Lys
Ala Lys 10415	Lys	Asn	Lys	Lys									

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

Gln Ile Met Asn Ser Asn His Ala Lys Ala Ser Val Thr Glu Ser Val
20 25 30

Asp Lys Lys Phe Val Val Pro Glu Ser Gly Ile Asn Lys Ile Ile Pro

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35	40	45
Ala Tyr Asp Glu Phe Lys Asn Ser Pro Lys Val Asn Val Ser Asn Leu		
50	55	60
Thr Asp Asn Lys Asn Phe Val Ala Ser Glu Asp Lys Leu Asn Lys Ile		
65	70	80
Ala Asp Ser Ser Ala Ala Ser Lys Ile Val Asp Lys Asn Phe Val Val		
	85	90
Pro Glu Ser Lys Leu Gly Asn Ile Val Pro Glu Tyr Lys Glu Ile Asn		
	100	105
Asn Arg Val Asn Val Ala Thr Asn Asn Pro Ala Ser Gln Gln Val Asp		
	115	120
Lys His Phe Val Ala Lys Gly Pro Glu Val Asn Arg Phe Ile Thr Gln		
	130	135
Asn Lys Val Asn His His Phe Ile Thr Thr Gln Thr His Tyr Lys Lys		
	145	150
Val Ile Thr Ser Tyr Lys Ser Thr His Val His Lys His Val Asn His		
	165	170
Ala Lys Asp Ser Ile Asn Lys His Phe Ile Val Lys Pro Ser Glu Ser		
	180	185
Pro Arg Tyr Thr His Pro Ser Gln Ser Leu Ile Ile Lys His His Phe		
	195	200
Ala Val Pro Gly Tyr His Ala His Lys Phe Val Thr Pro Gly His Ala		
	210	215
Ser Ile Lys Ile Asn His Phe Cys Val Val Pro Gln Ile Asn Ser Phe		
	225	230
Lys Val Ile Pro Pro Tyr Gly His Asn Ser His Arg Met His Val Pro		
	245	250
Ser Phe Gln Asn Asn Thr Thr Ala Thr His Gln Asn Ala Lys Val Asn		
	260	265
Lys Ala Tyr Asp Tyr Lys Tyr Phe Tyr Ser Tyr Lys Val Val Lys Gly		
	275	280
Val Lys Lys Tyr Phe Ser Phe Ser Gln Ser Asn Gly Tyr Lys Ile Gly		
	290	295
Lys Pro Ser Leu Asn Ile Lys Asn Val Asn Tyr Gln Tyr Ala Val Pro		
	305	310
Ser Tyr Ser Pro Thr His Tyr Val Pro Glu Phe Lys Gly Ser Leu Pro		
	325	330
Ala Pro Arg Val		
340		

<210> SEQ ID NO 26

<211> LENGTH: 130

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 26

Met Asn Phe Asn Asp Ile Glu Thr Met Val Lys Ser Lys Phe Lys Asp		
1	5	10
Ile Lys Lys His Ala Glu Glu Ile Ala His Glu Ile Glu Val Arg Ser		
	20	25
Gly Tyr Leu Arg Lys Ala Glu Gln Tyr Lys Arg Leu Glu Phe Asn Leu		
	35	40
Ser Phe Ala Leu Asp Asp Ile Glu Ser Thr Ala Lys Asp Val Gln Thr		
	50	55
		60

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Ala Lys Ser Ser Ala Asn Lys Asp Ser Val Thr Val Lys Gly Lys Ala
65 70 75 80

Pro Asn Thr Leu Tyr Ile Glu Lys Arg Asn Leu Met Lys Gln Lys Leu
85 90 95

Glu Met Leu Gly Glu Asp Ile Asp Lys Asn Lys Glu Ser Leu Gln Lys
100 105 110

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

Met Asn
130

<210> SEQ ID NO 27
 <211> LENGTH: 636
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 27

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

Leu Phe Thr Trp Asp Asn Lys Ala Asp Ala Ile Val Thr Lys Asp Tyr
20 25 30

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

Asp Ser Arg Tyr Leu Asn Ser Ala Leu Tyr Tyr Leu Glu Asp Tyr Ile
50 55 60

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

Tyr Lys Glu Ala Lys Asp Arg Leu Leu Glu Lys Val Leu Arg Glu Asp
85 90 95

Gln Tyr Leu Leu Glu Arg Lys Lys Ser Gln Tyr Glu Asp Tyr Lys Gln
100 105 110

Trp Tyr Ala Asn Tyr Lys Lys Glu Asn Pro Arg Thr Asp Leu Lys Met
115 120 125

Ala Asn Phe His Lys Tyr Asn Leu Glu Glu Leu Ser Met Lys Glu Tyr
130 135 140

Asn Glu Leu Gln Asp Ala Leu Lys Arg Ala Leu Asp Asp Phe His Arg
145 150 155 160

Glu Val Lys Asp Ile Lys Asp Lys Asn Ser Asp Leu Lys Thr Phe Asn
165 170 175

Ala Ala Glu Glu Asp Lys Ala Thr Lys Glu Val Tyr Asp Leu Val Ser
180 185 190

Glu Ile Asp Thr Leu Val Val Ser Tyr Tyr Gly Asp Lys Asp Tyr Gly
195 200 205

Glu His Ala Lys Glu Leu Arg Ala Lys Leu Asp Leu Ile Leu Gly Asp
210 215 220

Thr Asp Asn Pro His Lys Ile Thr Asn Glu Arg Ile Lys Lys Glu Met
225 230 235 240

Ile Asp Asp Leu Asn Ser Ile Ile Asp Asp Phe Phe Met Glu Thr Lys
245 250 255

Gln Asn Arg Pro Lys Ser Ile Thr Lys Tyr Asn Pro Thr Thr His Asn
260 265 270

Tyr Lys Thr Asn Ser Asp Asn Lys Pro Asn Phe Asp Lys Leu Val Glu
275 280 285

Glu Thr Lys Lys Ala Val Lys Glu Ala Asp Asp Ser Trp Lys Lys Lys
290 295 300

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Thr Val Lys Lys Tyr Gly Glu Thr Glu Thr Lys Ser Pro Val Val Lys
 305 310 315 320
 Glu Glu Lys Lys Val Glu Glu Pro Gln Ala Pro Lys Val Asp Asn Gln
 325 330 335
 Gln Glu Val Lys Thr Thr Ala Gly Lys Ala Glu Glu Thr Thr Gln Pro
 340 345 350
 Val Ala Gln Pro Leu Val Lys Ile Pro Gln Gly Thr Ile Thr Gly Glu
 355 360 365
 Ile Val Lys Gly Pro Glu Tyr Pro Thr Met Glu Asn Lys Thr Val Gln
 370 375 380
 Gly Glu Ile Val Gln Gly Pro Asp Phe Leu Thr Met Glu Gln Ser Gly
 385 390 395 400
 Pro Ser Leu Ser Asn Asn Tyr Thr Asn Pro Pro Leu Thr Asn Pro Ile
 405 410 415
 Leu Glu Gly Leu Glu Gly Ser Ser Ser Lys Leu Glu Ile Lys Pro Gln
 420 425 430
 Gly Thr Glu Ser Thr Leu Lys Gly Thr Gln Gly Glu Ser Ser Asp Ile
 435 440 445
 Glu Val Lys Pro Gln Ala Thr Glu Thr Thr Glu Ala Ser Gln Tyr Gly
 450 455 460
 Pro Arg Pro Gln Phe Asn Lys Thr Pro Lys Tyr Val Lys Tyr Arg Asp
 465 470 475 480
 Ala Gly Thr Gly Ile Arg Glu Tyr Asn Asp Gly Thr Phe Gly Tyr Glu
 485 490 495
 Ala Arg Pro Arg Phe Asn Lys Pro Ser Glu Thr Asn Ala Tyr Asn Val
 500 505 510
 Thr Thr His Ala Asn Gly Gln Val Ser Tyr Gly Ala Arg Pro Thr Tyr
 515 520 525
 Lys Lys Pro Ser Glu Thr Asn Ala Tyr Asn Val Thr Thr His Ala Asn
 530 535 540
 Gly Gln Val Ser Tyr Gly Ala Arg Pro Thr Gln Asn Lys Pro Ser Lys
 545 550 555 560
 Thr Asn Ala Tyr Asn Val Thr Thr His Gly Asn Gly Gln Val Ser Tyr
 565 570 575
 Gly Ala Arg Pro Thr Gln Asn Lys Pro Ser Lys Thr Asn Ala Tyr Asn
 580 585 590
 Val Thr Thr His Ala Asn Gly Gln Val Ser Tyr Gly Ala Arg Pro Thr
 595 600 605
 Tyr Lys Lys Pro Ser Lys Thr Asn Ala Tyr Asn Val Thr Thr His Ala
 610 615 620
 Asp Gly Thr Ala Thr Tyr Gly Pro Arg Val Thr Lys
 625 630 635

<210> SEQ ID NO 28

<211> LENGTH: 745

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 28

Ala Glu Gln His Thr Pro Met Lys Ala His Ala Val Thr Thr Ile Asp
 1 5 10 15
 Lys Ala Thr Thr Asp Lys Gln Gln Val Pro Pro Thr Lys Glu Ala Ala
 20 25 30
 His His Ser Gly Lys Glu Ala Ala Thr Asn Val Ser Ala Ser Ala Gln

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35	40	45
Gly Thr Ala Asp Asp Thr Asn Ser Lys Val Thr Ser Asn Ala Pro Ser		
50	55	60
Asn Lys Pro Ser Thr Val Val Ser Thr Lys Val Asn Glu Thr Arg Asp		
65	70	75
Val Asp Thr Gln Gln Ala Ser Thr Gln Lys Pro Thr His Thr Ala Thr		
	85	90
Phe Lys Leu Ser Asn Ala Lys Thr Ala Ser Leu Ser Pro Arg Met Phe		
	100	105
Ala Ala Asn Ala Pro Gln Thr Thr Thr His Lys Ile Leu His Thr Asn		
	115	120
Asp Ile His Gly Arg Leu Ala Glu Glu Lys Gly Arg Val Ile Gly Met		
	130	135
Ala Lys Leu Lys Thr Val Lys Glu Gln Glu Lys Pro Asp Leu Met Leu		
	145	150
Asp Ala Gly Asp Ala Phe Gln Gly Leu Pro Leu Ser Asn Gln Ser Lys		
	165	170
Gly Glu Glu Met Ala Lys Ala Met Asn Ala Val Gly Tyr Asp Ala Met		
	180	185
Ala Val Gly Asn His Glu Phe Asp Phe Gly Tyr Asp Gln Leu Lys Lys		
	195	200
Leu Glu Gly Met Leu Asp Phe Pro Met Leu Ser Thr Asn Val Tyr Lys		
	210	215
Asp Gly Lys Arg Ala Phe Lys Pro Ser Thr Ile Val Thr Lys Asn Gly		
	225	230
Ile Arg Tyr Gly Ile Ile Gly Val Thr Thr Pro Glu Thr Lys Thr Lys		
	245	250
Thr Arg Pro Glu Gly Ile Lys Gly Val Glu Phe Arg Asp Pro Leu Gln		
	260	265
Ser Val Thr Ala Glu Met Met Arg Ile Tyr Lys Asp Val Asp Thr Phe		
	275	280
Val Val Ile Ser His Leu Gly Ile Asp Pro Ser Thr Gln Glu Thr Trp		
	290	295
Arg Gly Asp Tyr Leu Val Lys Gln Leu Ser Gln Asn Pro Gln Leu Lys		
	305	310
Lys Arg Ile Thr Val Ile Asp Gly His Ser His Thr Val Leu Gln Asn		
	325	330
Gly Gln Ile Tyr Asn Asn Asp Ala Leu Ala Gln Thr Gly Thr Ala Leu		
	340	345
Ala Asn Ile Gly Lys Ile Thr Phe Asn Tyr Arg Asn Gly Glu Val Ser		
	355	360
Asn Ile Lys Pro Ser Leu Ile Asn Val Lys Asp Val Glu Asn Val Thr		
	370	375
Pro Asn Lys Ala Leu Ala Glu Gln Ile Asn Gln Ala Asp Gln Thr Phe		
	385	390
Arg Ala Gln Thr Ala Glu Val Ile Ile Pro Asn Asn Thr Ile Asp Phe		
	405	410
Lys Gly Glu Arg Asp Asp Val Arg Thr Arg Glu Thr Asn Leu Gly Asn		
	420	425
Ala Ile Ala Asp Ala Met Glu Ala Tyr Gly Val Lys Asn Phe Ser Lys		
	435	440
Lys Thr Asp Phe Ala Val Thr Asn Gly Gly Gly Ile Arg Ala Ser Ile		
	450	455

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Ala Lys Gly Lys Val Thr Arg Tyr Asp Leu Ile Ser Val Leu Pro Phe
 465 470 475 480
 Gly Asn Thr Ile Ala Gln Ile Asp Val Lys Gly Ser Asp Val Trp Thr
 485 490 495
 Ala Phe Glu His Ser Leu Gly Ala Pro Thr Thr Gln Lys Asp Gly Lys
 500 505 510
 Thr Val Leu Thr Ala Asn Gly Gly Leu Leu His Ile Ser Asp Ser Ile
 515 520 525
 Arg Val Tyr Tyr Asp Ile Asn Lys Pro Ser Gly Lys Arg Ile Asn Ala
 530 535 540
 Ile Gln Ile Leu Asn Lys Glu Thr Gly Lys Phe Glu Asn Ile Asp Leu
 545 550 555 560
 Lys Arg Val Tyr His Val Thr Met Asn Asp Phe Thr Ala Ser Gly Gly
 565 570 575
 Asp Gly Tyr Ser Met Phe Gly Gly Pro Arg Glu Glu Gly Ile Ser Leu
 580 585 590
 Asp Gln Val Leu Ala Ser Tyr Leu Lys Thr Ala Asn Leu Ala Lys Tyr
 595 600 605
 Asp Thr Thr Glu Pro Gln Arg Met Leu Leu Gly Lys Pro Ala Val Ser
 610 615 620
 Glu Gln Pro Ala Lys Gly Gln Gln Gly Ser Lys Gly Ser Lys Ser Gly
 625 630 635 640
 Lys Asp Thr Gln Pro Ile Gly Asp Asp Lys Val Met Asp Pro Ala Lys
 645 650 655
 Lys Pro Ala Pro Gly Lys Val Val Leu Leu Leu Ala His Arg Gly Thr
 660 665 670
 Val Ser Ser Gly Thr Glu Gly Ser Gly Arg Thr Ile Glu Gly Ala Thr
 675 680 685
 Val Ser Ser Lys Ser Gly Lys Gln Leu Ala Arg Met Ser Val Pro Lys
 690 695 700
 Gly Ser Ala His Glu Lys Gln Leu Pro Lys Thr Gly Thr Asn Gln Ser
 705 710 715 720
 Ser Ser Pro Glu Ala Met Phe Val Leu Leu Ala Gly Ile Gly Leu Ile
 725 730 735
 Ala Thr Val Arg Arg Arg Lys Ala Ser
 740 745

<210> SEQ ID NO 29

<211> LENGTH: 628

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 29

Met Ser Asp Arg Phe Ile Lys Phe Asn Asp Glu Gln Leu Asp Ala Lys
 1 5 10 15
 Gln Val Met Met Leu Gln Asp Leu Ala Arg Leu Leu Leu Lys Asn Glu
 20 25 30
 Gln Thr Gln Val Lys Ile Gln Lys Phe Pro Tyr Tyr Asn Pro Val Gln
 35 40 45
 Asn Val Leu Ile Thr Ser Trp Phe Trp Ser His Arg Pro Ser His Ile
 50 55 60
 Glu Met Ala Gly Leu Lys Thr Asp Val Met Leu Ala Ala Tyr Gly Tyr
 65 70 75 80
 His Met Met Asp Val Gln Ile Val Asn Glu Val Val Gln Asp Lys Thr

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85								90				95			
Phe	Lys	His	Pro	Lys	Phe	Tyr	Gln	Gln	Leu	Phe	Lys	Leu	Leu	Glu	Asp
			100					105					110		
Met	Arg	Val	Leu	Asn	Ser	Ile	Lys	Val	Glu	Arg	Pro	Ser	Thr	Ala	Lys
		115					120					125			
Leu	Ile	Asp	Leu	Arg	Leu	Asp	Thr	Arg	Ile	Ser	Tyr	Thr	Glu	Ser	Gln
	130					135					140				
Ile	Lys	Val	Tyr	Arg	Thr	Lys	Thr	Gln	Tyr	Thr	Asp	Leu	Leu	Phe	Leu
145					150					155					160
Tyr	Leu	Glu	His	Ala	Phe	Leu	Ser	Gln	Asp	Phe	Phe	Asp	Ile	Pro	Ser
				165					170					175	
Ile	His	Ser	Asp	Leu	Asp	Asp	Ile	Leu	Val	Asn	Met	Phe	Leu	Tyr	Leu
			180					185					190		
Pro	Asn	Phe	Phe	Gln	Asn	Gln	Asn	Ser	Glu	Asp	Asn	Met	Tyr	Leu	Ala
		195					200					205			
Gln	Arg	Ile	Met	Tyr	Gln	Val	Asp	Asp	Ile	Leu	Lys	Glu	Asp	Met	Leu
	210					215					220				
Asn	Glu	Tyr	Tyr	Tyr	Leu	Pro	Lys	Thr	Leu	Tyr	Asn	Thr	Leu	Ala	Ser
225					230					235					240
Pro	Glu	Phe	Asp	Asp	Leu	Lys	Arg	Thr	Asp	Ala	Ser	Gln	Val	Asp	Gly
			245						250					255	
Gln	Asp	Asp	Thr	Ser	Glu	Asp	Asp	Asp	Asn	Glu	Ser	Glu	Lys	Ala	Asp
			260					265						270	
Ser	Lys	Ser	Ala	Asp	Ser	Glu	Ser	Lys	Gly	Gly	Ala	Tyr	Leu	Glu	Met
		275						280				285			
Glu	Leu	His	Glu	Gly	Gln	Asn	Ser	Glu	Thr	Leu	Gly	Asn	Asp	Glu	Ala
	290					295					300				
Arg	Glu	Gly	Asp	Ala	Thr	Asp	Asp	Met	Thr	Asp	Met	Met	Thr	Lys	Lys
305					310					315					320
Gly	Lys	Gly	Ser	Asn	Asp	Thr	Leu	Asn	Arg	Glu	Glu	Gly	Asp	Ala	Val
			325						330					335	
Gly	Gln	Ser	Gln	Ala	Phe	Gln	Leu	Asp	Gly	Val	Asn	Lys	Asn	Val	Glu
			340					345					350		
Ile	Lys	Trp	Gln	Ile	Pro	Glu	Ile	Glu	Pro	Gln	Tyr	Val	Leu	Glu	Tyr
		355					360					365			
Gln	Glu	Ser	Lys	Gln	Asp	Val	Gln	Tyr	Glu	Ile	Lys	Asp	Leu	Ile	Gln
	370					375					380				
Ile	Ile	Lys	Lys	Thr	Ile	Glu	Arg	Glu	Gln	Arg	Asp	Ala	Arg	Phe	Asn
385					390					395					400
Leu	Thr	Lys	Gly	Arg	Leu	Gln	Lys	Asp	Leu	Ile	Asn	Trp	Phe	Ile	Asp
			405						410					415	
Asp	Gln	Tyr	Lys	Leu	Phe	Tyr	Lys	Lys	Gln	Asp	Leu	Ser	Lys	Ser	Phe
			420					425					430		
Asp	Ala	Thr	Phe	Thr	Leu	Leu	Ile	Asp	Ala	Ser	Ala	Ser	Met	His	Asp
		435					440					445			
Lys	Met	Ala	Glu	Thr	Lys	Lys	Gly	Val	Val	Leu	Phe	His	Glu	Thr	Leu
	450						455					460			
Lys	Ala	Leu	Asn	Ile	Lys	His	Glu	Ile	Leu	Ser	Phe	Ser	Glu	Asp	Ala
465					470					475					480
Phe	Asp	Ser	Asp	Glu	His	Ala	Gln	Pro	Asn	Ile	Ile	Asn	Glu	Ile	Ile
				485					490					495	
Asn	Tyr	Asp	Tyr	Ser	Thr	Phe	Glu	Lys	Asp	Gly	Pro	Arg	Ile	Met	Ala
			500					505					510		

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Leu Glu Pro Gln Asp Asp Asn Arg Asp Gly Val Ala Ile Arg Val Ala
 515 520 525
 Ser Glu Arg Leu Met Arg Arg Asn Gln His Gln Arg Phe Leu Ile Val
 530 535 540
 Phe Ser Asp Gly Glu Pro Ser Ala Phe Asn Tyr Ser Gln Asp Gly Ile
 545 550 555 560
 Ile Asp Thr Tyr Glu Ala Val Glu Met Ser Arg Lys Phe Gly Ile Glu
 565 570 575
 Val Phe Asn Val Phe Leu Ser Gln Asp Pro Ile Thr Glu Asp Val Glu
 580 585 590
 Gln Thr Ile His Asn Ile Tyr Gly Gln Tyr Ala Ile Phe Val Glu Gly
 595 600 605
 Val Ala His Leu Pro Gly His Leu Ser Pro Leu Leu Lys Lys Leu Leu
 610 615 620
 Leu Lys Ser Leu
 625

<210> SEQ ID NO 30
 <211> LENGTH: 154
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 30

Ala Glu Ile Asn Lys Gln Thr Thr Ser Gln Gly Val Thr Thr Glu Lys
 1 5 10 15
 Asn Asn Gly Ile Ala Val Leu Glu Gln Asp Val Ile Thr Pro Thr Val
 20 25 30
 Lys Pro Gln Ala Lys Gln Asp Ile Ile Gln Ala Val Thr Thr Arg Lys
 35 40 45
 Gln Gln Ile Lys Lys Ser Asn Ala Ser Leu Gln Asp Glu Lys Asp Val
 50 55 60
 Ala Asn Asp Lys Ile Gly Lys Ile Glu Thr Lys Ala Ile Lys Asp Ile
 65 70 75 80
 Asp Ala Ala Thr Thr Asn Ala Gln Val Glu Ala Ile Lys Thr Lys Ala
 85 90 95
 Ile Asn Asp Ile Asn Gln Thr Thr Pro Ala Thr Thr Ala Lys Ala Ala
 100 105 110
 Ala Leu Glu Glu Phe Asp Glu Val Val Gln Ala Gln Ile Asp Gln Ala
 115 120 125
 Pro Leu Asn Pro Asp Thr Thr Asn Glu Glu Val Ala Glu Ala Ile Glu
 130 135 140
 Arg Ile Asn Ala Ala Lys Val Ser Gly Val
 145 150

<210> SEQ ID NO 31
 <211> LENGTH: 584
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 31

Met Lys Phe Lys Ser Leu Ile Thr Thr Thr Leu Ala Leu Gly Val Leu
 1 5 10 15
 Ala Ser Thr Gly Ala Asn Phe Asn Asn Asn Glu Ala Ser Ala Ala Ala
 20 25 30
 Lys Pro Leu Asp Lys Ser Ser Ser Ser Leu His His Gly Tyr Ser Lys
 35 40 45

Val 50	His	Val	Pro	Tyr	Ala	Ile 55	Thr	Val	Asn	Gly	Thr 60	Ser	Gln	Asn	Ile
Leu 65	Ser	Ser	Leu	Thr	Phe 70	Asn	Lys	Asn	Gln	Asn 75	Ile	Ser	Tyr	Lys	Asp 80
Leu	Glu	Asp	Arg	Val 85	Lys	Ser	Val	Leu	Lys 90	Ser	Asp	Arg	Gly	Ile 95	Ser
Asp	Ile	Asp	Leu	Arg 100	Leu	Ser	Lys	Gln	Ala 105	Lys	Tyr	Thr	Val 110	Tyr	Phe
Lys	Asn	Gly	Thr	Lys 115	Lys	Val	Ile	Asp	Leu 120	Lys	Ala	Gly 125	Ile	Tyr	Thr
Ala	Asp	Leu	Ile	Asn 130	Thr	Ser	Glu	Ile	Lys 135	Ala	Ile 140	Asn	Ile	Asn	Val
Asp 145	Thr	Lys	Lys	Gln 150	Val	Glu	Asp	Lys	Lys 155	Lys	Asp	Lys	Ala	Asn	Tyr 160
Gln	Val	Pro	Tyr	Thr 165	Ile	Thr	Val	Asn	Gly 170	Thr	Ser	Gln	Asn	Ile 175	Leu
Ser	Asn	Leu	Thr	Phe 180	Asn	Lys	Asn	Gln	Asn 185	Ile	Ser	Tyr	Lys 190	Asp	Leu
Glu	Asp	Lys	Val	Lys 195	Ser	Val	Leu	Glu	Ser 200	Asn	Arg	Gly 205	Ile	Thr	Asp
Val	Asp	Leu	Arg	Leu 210	Ser	Lys	Gln	Ala	Lys 215	Tyr	Thr 220	Val	Asn	Phe	Lys
Asn 225	Gly	Thr	Lys	Lys 230	Val	Ile	Asp	Leu	Lys 235	Ser	Gly 235	Ile	Tyr	Thr	Ala 240
Asn	Leu	Ile	Asn	Ser 245	Ser	Asp	Ile	Lys	Ser 250	Ile	Asn	Ile	Asn	Val 255	Asp
Thr	Lys	Lys	His 260	Ile	Glu	Asn	Lys	Ala 265	Lys	Arg	Asn	Tyr 270	Gln	Val	Pro
Tyr	Ser	Ile	Asn 275	Leu	Asn	Gly 280	Thr	Ser	Thr 285	Asn	Ile 285	Leu	Ser	Asn	Leu
Ser	Phe 290	Ser	Asn	Lys	Pro	Trp 295	Thr	Asn	Tyr 300	Lys	Asn 300	Leu	Thr	Ser	Gln
Ile 305	Lys	Ser	Val	Leu	Lys 310	His	Asp	Arg	Gly 315	Ile 315	Ser	Glu	Gln	Asp	Leu 320
Lys	Tyr	Ala	Lys	Lys 325	Ala	Tyr	Tyr	Thr	Val 330	Tyr	Phe	Lys	Asn	Gly 335	Gly
Lys	Arg	Ile	Leu 340	Gln	Leu	Asn	Ser	Lys 345	Asn	Tyr	Thr 350	Ala	Asn	Leu 350	Val
His	Ala 355	Lys	Asp	Val	Lys	Arg	Ile 360	Glu	Ile 365	Thr	Val 365	Lys	Thr	Gly	Thr
Lys	Ala 370	Lys	Ala	Asp	Arg	Tyr 375	Val	Pro	Tyr 380	Thr 380	Ile 380	Ala	Val	Asn	Gly
Thr 385	Ser	Thr	Pro	Ile 390	Leu	Ser	Asp	Leu	Lys 395	Phe 395	Thr 395	Gly	Asp	Pro	Arg 400
Val	Gly	Tyr	Lys	Asp 405	Ile	Ser	Lys	Lys	Val 410	Lys	Ser	Val	Leu	Lys 415	His
Asp	Arg	Gly	Ile 420	Gly	Glu	Arg	Glu	Leu 425	Lys	Tyr 425	Ala	Lys	Lys	Ala	Thr
Tyr	Thr 435	Val	His	Phe	Lys	Asn	Gly 440	Thr	Lys 445	Lys 445	Val 445	Ile 445	Asn	Ile	Asn
Ser	Asn 450	Ile	Ser	Gln	Leu	Asn 455	Leu	Leu	Tyr 460	Val 460	Gln 460	Asp	Ile	Lys	Lys

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Ile Asp Ile Asp Val Lys Thr Gly Thr Lys Ala Lys Ala Asp Ser Tyr
465                               470                               475                               480

Val Pro Tyr Thr Ile Ala Val Asn Gly Thr Ser Thr Pro Ile Leu Ser
                               485                               490                               495

Lys Leu Lys Ile Ser Asn Lys Gln Leu Ile Ser Tyr Lys Tyr Leu Asn
                               500                               505                               510

Asp Lys Val Lys Ser Val Leu Lys Ser Glu Arg Gly Ile Ser Asp Leu
                               515                               520                               525

Asp Leu Lys Phe Ala Lys Gln Ala Lys Tyr Thr Val Tyr Phe Lys Asn
                               530                               535                               540

Gly Lys Lys Gln Val Val Asn Leu Lys Ser Asp Ile Phe Thr Pro Asn
545                               550                               555                               560

Leu Phe Ser Ala Lys Asp Ile Lys Lys Ile Asp Ile Asp Val Lys Gln
                               565                               570                               575

Tyr Thr Lys Ser Lys Lys Asn Lys
                               580

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<210> SEQ ID NO 32
<211> LENGTH: 508
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

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<400> SEQUENCE: 32

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

Gln Ile Trp Glu Ser Asn Arg Ala Ser Ala Val Val Ser Gly Glu Lys
20          25          30

Asn Pro Tyr Val Ser Glu Ser Leu Lys Leu Thr Asn Asn Lys Asn Lys
35          40          45

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

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

Glu Ala Met Lys Lys Tyr Gln Gln Arg Phe Met Ala Glu Asp Glu Ala
85          90          95

Leu Lys Lys Phe Phe Ser Glu Glu Lys Lys Ile Lys Asn Gly Asn Thr
100         105         110

Asp Asn Leu Asp Tyr Leu Gly Leu Ser His Glu Arg Tyr Glu Ser Val
115         120         125

Phe Asn Thr Leu Lys Lys Gln Ser Glu Glu Phe Leu Lys Glu Ile Glu
130         135         140

Asp Ile Lys Lys Asp Asn Pro Glu Leu Lys Asp Phe Asn Glu Glu Glu
145         150         155         160

Gln Leu Lys Cys Asp Leu Glu Leu Asn Lys Leu Glu Asn Gln Ile Leu
165         170         175

Met Leu Gly Lys Thr Phe Tyr Gln Asn Tyr Arg Asp Asp Val Glu Ser
180         185         190

Leu Tyr Ser Lys Leu Asp Leu Ile Met Gly Tyr Lys Asp Glu Glu Arg
195         200         205

Ala Asn Lys Lys Ala Val Asn Lys Arg Met Leu Glu Asn Lys Lys Glu
210         215         220

Asp Leu Glu Thr Ile Ile Asp Glu Phe Phe Ser Asp Ile Asp Lys Thr
225         230         235         240

Arg Pro Asn Asn Ile Pro Val Leu Glu Asp Glu Lys Gln Glu Glu Lys
245         250         255

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Asn His Lys Asn Met Ala Gln Leu Lys Ser Asp Thr Glu Ala Ala Lys
 260 265 270
 Ser Asp Glu Ser Lys Arg Ser Lys Arg Ser Lys Arg Ser Leu Asn Thr
 275 280 285
 Gln Asn His Lys Pro Ala Ser Gln Glu Val Ser Glu Gln Gln Lys Ala
 290 295 300
 Glu Tyr Asp Lys Arg Ala Glu Glu Arg Lys Ala Arg Phe Leu Asp Asn
 305 310 315 320
 Gln Lys Ile Lys Lys Thr Pro Val Val Ser Leu Glu Tyr Asp Phe Glu
 325 330 335
 His Lys Gln Arg Ile Asp Asn Glu Asn Asp Lys Lys Leu Val Val Ser
 340 345 350
 Ala Pro Thr Lys Lys Pro Thr Ser Pro Thr Thr Tyr Thr Glu Thr Thr
 355 360 365
 Thr Gln Val Pro Met Pro Thr Val Glu Arg Gln Thr Gln Gln Gln Ile
 370 375 380
 Ile Tyr Asn Ala Pro Lys Gln Leu Ala Gly Leu Asn Gly Glu Ser His
 385 390 395 400
 Asp Phe Thr Thr Thr His Gln Ser Pro Thr Thr Ser Asn His Thr His
 405 410 415
 Asn Asn Val Val Glu Phe Glu Glu Thr Ser Ala Leu Pro Gly Arg Lys
 420 425 430
 Ser Gly Ser Leu Val Gly Ile Ser Gln Ile Asp Ser Ser His Leu Thr
 435 440 445
 Glu Arg Glu Lys Arg Val Ile Lys Arg Glu His Val Arg Glu Ala Gln
 450 455 460
 Lys Leu Val Asp Asn Tyr Lys Asp Thr His Ser Tyr Lys Asp Arg Ile
 465 470 475 480
 Asn Ala Gln Gln Lys Val Asn Thr Leu Ser Glu Gly His Gln Lys Arg
 485 490 495
 Phe Asn Lys Gln Ile Asn Lys Val Tyr Asn Gly Lys
 500 505

<210> SEQ ID NO 33

<211> LENGTH: 520

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 33

Met Leu Thr Leu Gln Ile His Thr Gly Gly Ile Asn Leu Lys Lys Lys
 1 5 10 15
 Asn Ile Tyr Ser Ile Arg Lys Leu Gly Val Gly Ile Ala Ser Val Thr
 20 25 30
 Leu Gly Thr Leu Leu Ile Ser Gly Gly Val Thr Pro Ala Ala Asn Ala
 35 40 45
 Ala Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr Gln Val Leu Asn
 50 55 60
 Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser Leu
 65 70 75 80
 Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Gln Lys
 85 90 95
 Leu Asn Asp Ser Gln Ala Pro Lys Ala Asp Ala Gln Gln Asn Asn Phe
 100 105 110
 Asn Lys Asp Gln Gln Ser Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn

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115					120					125					
Leu	Asn	Glu	Ala	Gln	Arg	Asn	Gly	Phe	Ile	Gln	Ser	Leu	Lys	Asp	Asp
130						135					140				
Pro	Ser	Gln	Ser	Thr	Asn	Val	Leu	Gly	Glu	Ala	Lys	Lys	Leu	Asn	Glu
145					150					155					160
Ser	Gln	Ala	Pro	Lys	Ala	Asp	Asn	Asn	Phe	Asn	Lys	Glu	Gln	Gln	Asn
				165					170					175	
Ala	Phe	Tyr	Glu	Ile	Leu	Asn	Met	Pro	Asn	Leu	Asn	Glu	Glu	Gln	Arg
			180					185						190	
Asn	Gly	Phe	Ile	Gln	Ser	Leu	Lys	Asp	Asp	Pro	Ser	Gln	Ser	Ala	Asn
		195					200					205			
Leu	Leu	Ser	Glu	Ala	Lys	Lys	Leu	Asn	Glu	Ser	Gln	Ala	Pro	Lys	Ala
210						215					220				
Asp	Asn	Lys	Phe	Asn	Lys	Glu	Gln	Gln	Asn	Ala	Phe	Tyr	Glu	Ile	Leu
225					230					235					240
His	Leu	Pro	Asn	Leu	Asn	Glu	Glu	Gln	Arg	Asn	Gly	Phe	Ile	Gln	Ser
			245						250					255	
Leu	Lys	Asp	Asp	Pro	Ser	Gln	Ser	Ala	Asn	Leu	Leu	Ala	Glu	Ala	Lys
		260						265					270		
Lys	Leu	Asn	Asp	Ala	Gln	Ala	Pro	Lys	Ala	Asp	Asn	Lys	Phe	Asn	Lys
		275					280					285			
Glu	Gln	Gln	Asn	Ala	Phe	Tyr	Glu	Ile	Leu	His	Leu	Pro	Asn	Leu	Thr
290						295					300				
Glu	Glu	Gln	Arg	Asn	Gly	Phe	Ile	Gln	Ser	Leu	Lys	Asp	Asp	Pro	Ser
305					310					315					320
Val	Ser	Lys	Glu	Ile	Leu	Ala	Glu	Ala	Lys	Lys	Leu	Asn	Asp	Ala	Gln
			325						330					335	
Ala	Pro	Lys	Glu	Glu	Asp	Asn	Asn	Lys	Pro	Gly	Lys	Glu	Asp	Gly	Asn
		340						345					350		
Lys	Pro	Gly	Lys	Glu	Asp	Asn	Asn	Lys	Pro	Gly	Lys	Glu	Asp	Asn	Lys
		355					360					365			
Lys	Pro	Gly	Lys	Glu	Asp	Asn	Asn	Lys	Pro	Gly	Lys	Glu	Asp	Asn	Asn
370						375					380				
Lys	Pro	Gly	Lys	Glu	Asp	Gly	Asn	Lys	Pro	Gly	Lys	Glu	Asp	Asn	Lys
385					390					395					400
Lys	Pro	Gly	Lys	Glu	Asp	Asn	Asn	Lys	Pro	Gly	Lys	Glu	Asp	Gly	Asn
			405						410					415	
Lys	Pro	Gly	Lys	Glu	Asp	Gly	Asn	Gly	Val	His	Val	Val	Lys	Pro	Gly
			420					425					430		
Asp	Thr	Val	Asn	Asp	Ile	Ala	Lys	Ala	Asn	Gly	Thr	Thr	Ala	Asp	Lys
		435						440					445		
Ile	Ala	Ala	Asp	Asn	Lys	Leu	Ala	Asp	Lys	Asn	Met	Ile	Lys	Pro	Gly
450						455					460				
Gln	Glu	Leu	Val	Val	Asp	Lys	Lys	Gln	Pro	Ala	Asn	His	Ala	Asp	Ala
465					470					475					480
Asn	Lys	Ala	Gln	Ala	Leu	Pro	Glu	Thr	Gly	Glu	Glu	Asn	Pro	Phe	Ile
			485						490					495	
Gly	Thr	Thr	Val	Phe	Gly	Gly	Leu	Ser	Leu	Ala	Leu	Gly	Ala	Ala	Leu
			500					505					510		
Leu	Ala	Gly	Arg	Arg	Arg	Glu	Leu								
		515					520								

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<211> LENGTH: 291
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 34
Ala Gln His Asp Glu Ala Lys Lys Asn Ala Phe Tyr Gln Val Leu Asn
1          5          10          15
Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser Leu
20          25          30
Lys Ala Ala Pro Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Gln Lys
35          40          45
Leu Asn Asp Ser Gln Ala Pro Lys Ala Asp Ala Gln Gln Asn Asn Phe
50          55          60
Asn Lys Asp Lys Lys Ser Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn
65          70          75          80
Leu Asn Glu Ala Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Ala Ala
85          90          95
Pro Ser Gln Ser Thr Asn Val Leu Gly Glu Ala Lys Lys Leu Asn Glu
100         105         110
Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys Glu Lys Lys Asn
115         120         125
Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg
130         135         140
Asn Gly Phe Ile Gln Ser Leu Lys Ala Ala Pro Ser Gln Ser Ala Asn
145         150         155         160
Leu Leu Ser Glu Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala
165         170         175
Asp Asn Lys Phe Asn Lys Glu Lys Lys Asn Ala Phe Tyr Glu Ile Leu
180         185         190
His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser
195         200         205
Leu Lys Ala Ala Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys
210         215         220
Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys
225         230         235         240
Glu Lys Lys Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Thr
245         250         255
Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Ala Ala Pro Ser
260         265         270
Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln
275         280         285
Ala Pro Lys
290

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<210> SEQ ID NO 35
<211> LENGTH: 772
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 35
Met Lys Ala Leu Leu Leu Lys Thr Ser Val Trp Leu Val Leu Leu Phe
1          5          10          15
Ser Val Met Gly Leu Trp Gln Val Ser Asn Ala Ala Glu Gln His Thr
20          25          30
Pro Met Lys Ala His Ala Val Thr Thr Ile Asp Lys Ala Thr Thr Asp
35          40          45

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Lys 50	Gln	Val	Pro	Thr	Lys	Glu	Ala	Ala	His	His	Ser	Gly	Lys		
Glu 65	Ala	Ala	Thr	Asn	Val 70	Ser	Ala	Ser	Ala	Gln 75	Gly	Thr	Ala	Asp	Asp 80
Thr	Asn	Ser	Lys	Val 85	Thr	Ser	Asn	Ala	Pro 90	Ser	Asn	Lys	Pro	Ser	Thr 95
Val	Val	Ser	Thr	Lys 100	Val	Asn	Glu	Thr 105	Arg	Asp	Val	Asp	Thr	Gln	Gln 110
Ala	Ser	Thr	Gln	Lys	Pro	Thr	His 120	Thr	Ala	Thr	Phe	Lys 125	Leu	Ser	Asn 130
Ala	Lys 130	Thr	Ala	Ser	Leu	Ser 135	Pro	Arg	Met	Phe	Ala 140	Ala	Asn	Ala	Pro 145
Gln 145	Thr	Thr	Thr	His 150	Lys	Ile	Leu	His	Thr	Asn 155	Asp	Ile	His	Gly	Arg 160
Leu	Ala	Glu	Glu	Lys 165	Gly	Arg	Val	Ile	Gly 170	Met	Ala	Lys	Leu	Lys	Thr 175
Val	Lys	Glu	Gln	Glu 180	Lys	Pro	Asp	Leu	Met 185	Leu	Asp	Ala	Gly 190	Asp	Ala 195
Phe	Gln	Gly	Leu	Pro	Leu	Ser	Asn 200	Gln	Ser	Lys	Gly 205	Glu	Glu	Met	Ala 210
Lys 210	Ala	Met	Asn	Ala	Val	Gly 215	Tyr	Asp	Ala	Met	Ala 220	Val	Gly	Asn	His 225
Glu 225	Phe	Asp	Phe	Gly	Tyr 230	Asp	Gln	Leu	Lys	Lys 235	Leu	Glu	Gly	Met	Leu 240
Asp	Phe	Pro	Met	Leu 245	Ser	Thr	Asn	Val	Tyr 250	Lys	Asp	Gly	Lys	Arg	Ala 255
Phe	Lys	Pro	Ser	Thr 260	Ile	Val	Thr	Lys 265	Asn	Gly	Ile	Arg 270	Tyr	Gly	Ile 275
Ile	Gly	Val	Thr	Thr 275	Pro	Glu	Thr 280	Lys	Thr	Lys	Thr	Arg 285	Pro	Glu	Gly 290
Ile 290	Lys	Gly	Val	Glu	Phe 295	Arg	Asp	Pro	Leu	Gln 300	Ser	Val	Thr	Ala	Glu 305
Met 305	Met	Arg	Ile	Tyr 310	Lys	Asp	Val	Asp	Thr	Phe 315	Val	Val	Ile	Ser	His 320
Leu	Gly	Ile	Asp	Pro 325	Ser	Thr	Gln	Glu	Thr 330	Trp	Arg	Gly	Asp	Tyr	Leu 335
Val	Lys	Gln	Leu	Ser 340	Gln	Asn	Pro	Gln 345	Leu	Lys	Lys	Arg 350	Ile	Thr	Val 355
Ile	Asp	Gly	His	Ser 355	His	Thr	Val 360	Leu	Gln	Asn	Gly 365	Gln	Ile	Tyr	Asn 370
Asn 370	Asp	Ala	Leu	Ala	Gln	Thr 375	Gly	Thr	Ala	Leu 380	Ala	Asn	Ile	Gly	Lys 385
Ile 385	Thr	Phe	Asn	Tyr 390	Arg	Asn	Gly	Glu	Val	Ser 395	Asn	Ile	Lys	Pro	Ser 400
Leu	Ile	Asn	Val	Lys 405	Asp	Val	Glu	Asn	Val 410	Thr	Pro	Asn	Lys	Ala	Leu 415
Ala	Glu	Gln	Ile	Asn 420	Gln	Ala	Asp	Gln	Thr	Phe	Arg	Ala 430	Gln	Thr	Ala 435
Glu	Val	Ile	Ile	Pro 435	Asn	Asn	Thr 440	Ile	Asp	Phe	Lys	Gly 445	Glu	Arg	Asp 450
Asp 450	Val	Arg	Thr	Arg 455	Glu	Thr	Asn	Leu	Gly	Asn 460	Ala	Ile	Ala	Asp	Ala 465

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Met	Glu	Ala	Tyr	Gly	Val	Lys	Asn	Phe	Ser	Lys	Lys	Thr	Asp	Phe	Ala	465	470	475	480
Val	Thr	Asn	Gly	Gly	Gly	Leu	Arg	Ala	Ser	Ile	Ala	Lys	Gly	Lys	Val	485	490	495	
Thr	Arg	Tyr	Asp	Leu	Ile	Ser	Val	Leu	Pro	Phe	Gly	Asn	Thr	Ile	Ala	500	505	510	
Gln	Ile	Asp	Val	Lys	Gly	Ser	Asp	Val	Trp	Thr	Ala	Phe	Glu	His	Ser	515	520	525	
Leu	Gly	Ala	Pro	Thr	Thr	Gln	Lys	Asp	Gly	Lys	Thr	Val	Leu	Thr	Ala	530	535	540	
Asn	Gly	Gly	Leu	Leu	His	Ile	Ser	Asp	Ser	Ile	Arg	Val	Tyr	Tyr	Asp	545	550	555	560
Ile	Asn	Lys	Pro	Ser	Gly	Lys	Arg	Ile	Asn	Ala	Ile	Gln	Ile	Leu	Asn	565	570	575	
Lys	Glu	Thr	Gly	Lys	Phe	Glu	Asn	Ile	Asp	Leu	Lys	Arg	Val	Tyr	His	580	585	590	
Val	Thr	Met	Asn	Asp	Phe	Thr	Ala	Ser	Gly	Gly	Asp	Gly	Tyr	Ser	Met	595	600	605	
Phe	Gly	Gly	Pro	Arg	Glu	Glu	Gly	Ile	Ser	Leu	Asp	Gln	Val	Leu	Ala	610	615	620	
Ser	Tyr	Leu	Lys	Thr	Ala	Asn	Leu	Ala	Lys	Tyr	Asp	Thr	Thr	Glu	Pro	625	630	635	640
Gln	Arg	Met	Leu	Leu	Gly	Lys	Pro	Ala	Val	Ser	Glu	Gln	Pro	Ala	Lys	645	650	655	
Gly	Gln	Gln	Gly	Ser	Lys	Gly	Ser	Lys	Ser	Gly	Lys	Asp	Thr	Gln	Pro	660	665	670	
Ile	Gly	Asp	Asp	Lys	Val	Met	Asp	Pro	Ala	Lys	Lys	Pro	Ala	Pro	Gly	675	680	685	
Lys	Val	Val	Leu	Leu	Leu	Ala	His	Arg	Gly	Thr	Val	Ser	Ser	Gly	Thr	690	695	700	
Glu	Gly	Ser	Gly	Arg	Thr	Ile	Glu	Gly	Ala	Thr	Val	Ser	Ser	Lys	Ser	705	710	715	720
Gly	Lys	Gln	Leu	Ala	Arg	Met	Ser	Val	Pro	Lys	Gly	Ser	Ala	His	Glu	725	730	735	
Lys	Gln	Leu	Pro	Lys	Thr	Gly	Thr	Asn	Gln	Ser	Ser	Ser	Pro	Glu	Ala	740	745	750	
Met	Phe	Val	Leu	Leu	Ala	Gly	Ile	Gly	Leu	Ile	Ala	Thr	Val	Arg	Arg	755	760	765	
Arg	Lys	Ala	Ser													770			

<210> SEQ ID NO 36
 <211> LENGTH: 190
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 36

Met	Lys	Leu	Lys	Ser	Leu	Ala	Val	Leu	Ser	Met	Ser	Ala	Val	Val	Leu	1	5	10	15
Thr	Ala	Cys	Gly	Asn	Asp	Thr	Pro	Lys	Asp	Glu	Thr	Lys	Ser	Thr	Glu	20	25	30	
Ser	Asn	Thr	Asn	Gln	Asp	Thr	Asn	Thr	Thr	Lys	Asp	Val	Ile	Ala	Leu	35	40	45	
Lys	Asp	Val	Lys	Thr	Ser	Pro	Glu	Asp	Ala	Val	Lys	Lys	Ala	Glu	Glu	50	55	60	

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

<210> SEQ ID NO 37
 <211> LENGTH: 502
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 37

Met Arg Glu Asn Phe Lys Leu Arg Lys Met Lys Val Gly Leu Val Ser
 1 5 10 15
 Val Ala Ile Thr Met Leu Tyr Ile Met Thr Asn Gly Gln Ala Glu Ala
 20 25 30
 Ser Glu Asn Gln Asn Ala Leu Ile Ser Asn Ile Asn Val Asp Asn Gln
 35 40 45
 Glu Lys Gln Asn Asn Val Asn Gln Ala Val Gln Pro Gln Asn Asn Thr
 50 55 60
 Asn Glu Thr Ser Lys Val Pro Ala Asn Phe Val Lys Leu Asn Asp Ile
 65 70 75 80
 Lys Pro Gly Asp Thr Ser Ile Gln Gly Thr Thr Leu Pro Asn Gln Phe
 85 90 95
 Ile Leu Leu Thr Ile Asp Lys Lys Asp Val Ser Ser Val Glu Asp Ser
 100 105 110
 Asp Ser Ser Phe Val Met Ser Asp Lys Asp Gly Asn Phe Lys Tyr Asp
 115 120 125
 Leu Asn Gly Arg Lys Ile Val His Asn Gln Glu Ile Glu Val Ser Ser
 130 135 140
 Ser Asp Pro Tyr Leu Gly Asp Asp Glu Glu Asp Glu Glu Val Glu Glu
 145 150 155 160
 Thr Ser Thr Glu Glu Val Gly Ala Glu Glu Glu Ser Thr Glu Ala Lys
 165 170 175
 Ala Thr Tyr Thr Thr Pro Arg Tyr Glu Lys Ala Tyr Glu Ile Pro Lys
 180 185 190
 Glu Gln Leu Lys Glu Lys Asp Gly His His Gln Val Phe Ile Glu Pro
 195 200 205
 Ile Thr Glu Gly Ser Gly Ile Ile Lys Gly His Thr Ser Val Lys Gly
 210 215 220
 Lys Val Ala Leu Ser Ile Asn Asn Lys Phe Ile Asn Phe Glu Thr Asn
 225 230 235 240
 Ala Asn Gly Gly Pro Asn Lys Glu Glu Ala Lys Ser Gly Ser Glu Gly

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245					250					255					
Ile	Trp	Met	Pro	Ile	Asp	Asp	Lys	Gly	Tyr	Phe	Asn	Phe	Asp	Phe	Lys
		260					265					270			
Thr	Lys	Arg	Phe	Asp	Asp	Leu	Glu	Leu	Lys	Lys	Asn	Asp	Glu	Ile	Ser
		275				280					285				
Leu	Thr	Phe	Ala	Pro	Asp	Asp	Glu	Asp	Glu	Ala	Leu	Lys	Ser	Leu	Ile
		290				295					300				
Phe	Lys	Thr	Lys	Val	Thr	Ser	Leu	Glu	Asp	Ile	Asp	Lys	Ala	Glu	Thr
		305				310					315				320
Lys	Tyr	Asp	His	Thr	Lys	Val	Glu	Lys	Val	Lys	Val	Leu	Lys	Asp	Val
			325						330					335	
Lys	Glu	Asp	Leu	His	Val	Asp	Glu	Ile	Tyr	Gly	Ser	Leu	Tyr	His	Thr
			340					345					350		
Glu	Lys	Gly	Lys	Gly	Ile	Leu	Asp	Lys	Glu	Gly	Thr	Lys	Val	Ile	Lys
		355					360					365			
Gly	Lys	Thr	Lys	Phe	Ala	Asn	Ala	Val	Val	Lys	Val	Asp	Ser	Glu	Leu
		370				375					380				
Gly	Glu	Gly	Gln	Glu	Phe	Pro	Asp	Leu	Gln	Val	Asp	Glu	Lys	Gly	Glu
		385				390					395				400
Phe	Ser	Phe	Asp	Val	Asp	His	Ala	Gly	Phe	Arg	Leu	Gln	Asn	Gly	Glu
			405						410					415	
Thr	Leu	Asn	Phe	Thr	Val	Val	Asp	Pro	Ile	Thr	Gly	Glu	Leu	Leu	Ser
			420					425					430		
Gly	Asn	Phe	Val	Ser	Lys	Asn	Ile	Asp	Ile	Tyr	Glu	Ser	Pro	Glu	Glu
		435					440					445			
Lys	Ala	Asp	Arg	Glu	Phe	Asp	Glu	Arg	Met	Glu	Asn	Thr	Pro	Ala	Tyr
		450				455					460				
His	Lys	Leu	His	Gly	Asp	Lys	Ile	Val	Gly	Tyr	Asp	Thr	Asn	Gly	Phe
		465				470					475				480
Pro	Ile	Thr	Trp	Phe	Tyr	Pro	Leu	Gly	Glu	Lys	Lys	Val	Glu	Arg	Lys
			485					490					495		
Ala	Pro	Lys	Leu	Glu	Lys										
			500												
<210> SEQ ID NO 38															
<211> LENGTH: 342															
<212> TYPE: PRT															
<213> ORGANISM: Staphylococcus sp															
<400> SEQUENCE: 38															
Met	Lys	Lys	Thr	Val	Leu	Tyr	Leu	Val	Leu	Ala	Val	Met	Phe	Leu	Leu
1			5						10					15	
Ala	Ala	Cys	Gly	Asn	Asn	Ser	Asp	Lys	Glu	Gln	Ser	Lys	Ser	Glu	Thr
		20						25					30		
Lys	Gly	Ser	Lys	Asp	Thr	Val	Lys	Ile	Glu	Asn	Asn	Tyr	Lys	Met	Arg
		35					40					45			
Gly	Glu	Lys	Lys	Asp	Gly	Ser	Asp	Ala	Lys	Lys	Val	Lys	Glu	Thr	Val
		50				55					60				
Glu	Val	Pro	Lys	Asn	Pro	Lys	Asn	Ala	Val	Val	Leu	Asp	Tyr	Gly	Ala
		65				70					75				80
Leu	Asp	Val	Met	Lys	Glu	Met	Gly	Leu	Ser	Asp	Lys	Val	Lys	Ala	Leu
			85					90						95	
Pro	Lys	Gly	Glu	Gly	Gly	Lys	Ser	Leu	Pro	Asn	Phe	Leu	Glu	Ser	Phe
			100					105					110		

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Lys Asp Asp Lys Tyr Thr Asn Val Gly Asn Leu Lys Glu Val Asn Phe
 115 120 125
 Asp Lys Leu Ala Ala Thr Lys Pro Glu Val Ile Phe Ile Ser Gly Arg
 130 135 140
 Thr Ala Asn Gln Lys Asn Leu Asp Glu Phe Lys Lys Ala Ala Pro Lys
 145 150 155 160
 Ala Lys Ile Val Tyr Val Gly Ala Asp Glu Lys Asn Leu Ile Gly Ser
 165 170 175
 Met Lys Gln Asn Thr Glu Asn Ile Gly Lys Ile Tyr Asp Lys Glu Asp
 180 185 190
 Lys Ala Lys Glu Leu Asn Lys Asp Leu Asp Asn Lys Ile Ala Ser Met
 195 200 205
 Lys Asp Lys Thr Lys Asn Phe Asn Lys Thr Val Met Tyr Leu Leu Val
 210 215 220
 Asn Glu Gly Glu Leu Ser Thr Phe Gly Pro Lys Gly Arg Phe Gly Gly
 225 230 235 240
 Leu Val Tyr Asp Thr Leu Gly Phe Asn Ala Val Asp Lys Lys Val Ser
 245 250 255
 Asn Ser Asn His Gly Gln Asn Val Ser Asn Glu Tyr Val Asn Lys Glu
 260 265 270
 Asn Pro Asp Val Ile Leu Ala Met Asp Arg Gly Gln Ala Ile Ser Gly
 275 280 285
 Lys Ser Thr Ala Lys Gln Ala Leu Asn Asn Pro Val Leu Lys Asn Val
 290 295 300
 Lys Ala Ile Lys Glu Asp Lys Val Tyr Asn Leu Asp Pro Lys Leu Trp
 305 310 315 320
 Tyr Phe Ala Ala Gly Ser Thr Thr Thr Thr Ile Lys Gln Ile Glu Glu
 325 330 335
 Leu Asp Lys Val Val Lys
 340

<210> SEQ ID NO 39

<211> LENGTH: 241

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 39

Met Lys Lys Asn Ile Met Asn Lys Leu Val Leu Ser Thr Ala Leu Leu
 1 5 10 15
 Leu Leu Glu Thr Thr Ser Thr Gln Leu Pro Lys Thr Pro Ile Ser Phe
 20 25 30
 Ser Ser Glu Ala Lys Ala Tyr Asn Ile Ser Glu Asn Glu Thr Asn Ile
 35 40 45
 Asn Glu Leu Ile Lys Tyr Tyr Thr Gln Pro His Phe Ser Leu Ser Gly
 50 55 60
 Lys Trp Leu Trp Gln Lys Pro Asn Gly Ser Ile His Ala Thr Leu Gln
 65 70 75 80
 Thr Trp Val Trp Tyr Ser His Ile Gln Val Phe Gly Ser Glu Ser Trp
 85 90 95
 Gly Asn Ile Asn Gln Leu Arg Asn Lys Tyr Val Asp Ile Phe Gly Thr
 100 105 110
 Lys Asp Glu Asp Thr Val Glu Gly Tyr Trp Thr Tyr Asp Glu Thr Phe
 115 120 125
 Thr Gly Gly Val Thr Pro Ala Ala Thr Ser Ser Asp Lys Pro Tyr Arg
 130 135 140

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Leu Phe Leu Lys Tyr Ser Asp Lys Gln Gln Thr Ile Ile Gly Gly His
 145 150 155 160
 Glu Phe Tyr Lys Gly Asn Lys Pro Val Leu Thr Leu Lys Glu Leu Asp
 165 170 175
 Phe Arg Ile Arg Gln Thr Leu Ile Lys Asn Lys Lys Leu Tyr Asn Gly
 180 185 190
 Glu Phe Asn Lys Gly Gln Ile Lys Ile Thr Ala Asp Gly Asn Asn Tyr
 195 200 205
 Thr Ile Asp Leu Ser Lys Lys Leu Lys Leu Thr Asp Thr Asn Arg Tyr
 210 215 220
 Val Lys Asn Pro Arg Asn Ala Glu Ile Glu Val Ile Leu Glu Lys Ser
 225 230 235 240

Asn

<210> SEQ ID NO 40
 <211> LENGTH: 302
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 40

Met Lys Lys Leu Leu Leu Pro Leu Ile Ile Met Leu Leu Val Leu Ala
 1 5 10 15
 Ala Cys Gly Asn Gln Gly Glu Lys Asn Asn Lys Ala Glu Thr Lys Ser
 20 25 30
 Tyr Lys Met Asp Asp Gly Lys Thr Val Asp Ile Pro Lys Asp Pro Lys
 35 40 45
 Arg Ile Ala Val Val Ala Pro Thr Tyr Ala Gly Gly Leu Lys Lys Leu
 50 55 60
 Gly Ala Asn Ile Val Ala Val Asn Gln Gln Val Asp Gln Ser Lys Val
 65 70 75 80
 Leu Lys Asp Lys Phe Lys Gly Val Thr Lys Ile Gly Asp Gly Asp Val
 85 90 95
 Glu Lys Val Ala Lys Glu Lys Pro Asp Leu Ile Ile Val Tyr Ser Thr
 100 105 110
 Asp Lys Asp Ile Lys Lys Tyr Gln Lys Val Ala Pro Thr Val Val Val
 115 120 125
 Asp Tyr Asn Lys His Lys Tyr Leu Glu Gln Gln Glu Met Leu Gly Lys
 130 135 140
 Ile Val Gly Lys Glu Asp Lys Val Lys Ala Trp Lys Lys Asp Trp Glu
 145 150 155 160
 Glu Thr Thr Ala Lys Asp Gly Lys Glu Ile Lys Lys Ala Ile Gly Gln
 165 170 175
 Asp Ala Thr Val Ser Leu Phe Asp Glu Phe Asp Lys Lys Leu Tyr Thr
 180 185 190
 Tyr Gly Asp Asn Trp Gly Arg Gly Gly Glu Val Leu Tyr Gln Ala Phe
 195 200 205
 Gly Leu Lys Met Gln Pro Glu Gln Gln Lys Leu Thr Ala Lys Ala Gly
 210 215 220
 Trp Ala Glu Val Lys Gln Glu Glu Ile Glu Lys Tyr Ala Gly Asp Tyr
 225 230 235 240
 Ile Val Ser Thr Ser Glu Gly Lys Pro Thr Pro Gly Tyr Glu Ser Thr
 245 250 255
 Asn Met Trp Lys Asn Leu Lys Ala Thr Lys Glu Gly His Ile Val Lys
 260 265 270

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Val Asp Ala Gly Thr Tyr Trp Tyr Asn Asp Pro Tyr Thr Leu Asp Phe
275 280 285

Met Arg Lys Asp Leu Lys Glu Lys Leu Leu Lys Ala Ala Lys
290 295 300

<210> SEQ ID NO 41

<211> LENGTH: 267

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 41

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> SEQ ID NO 42

<211> LENGTH: 209

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 42

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

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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

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Gln

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<210> SEQ ID NO 43
<211> LENGTH: 436
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

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<400> SEQUENCE: 43

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

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

Thr Gln Gln Thr Ser Thr Lys His Gln Thr Thr Gln Asn Asn Tyr Val
  35      40      45

Thr Asp Gln Gln Lys Ala Phe Tyr Gln Val Leu His Leu Lys Gly Ile
  50      55      60

Thr Glu Glu Gln Arg Asn Gln Tyr Ile Lys Thr Leu Arg Glu His Pro
  65      70      75      80

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

Pro Asp Arg Arg Val Ala Gln Gln Asn Ala Phe Tyr Asn Val Leu Lys
 100     105     110

Asn Asp Asn Leu Thr Glu Gln Glu Lys Asn Asn Tyr Ile Ala Gln Ile
 115     120     125

Lys Glu Asn Pro Asp Arg Ser Gln Gln Val Trp Val Glu Ser Val Gln
 130     135     140

Ser Ser Lys Ala Lys Glu Arg Gln Asn Ile Glu Asn Ala Asp Lys Ala
 145     150     155     160

Ile Lys Asp Phe Gln Asp Asn Lys Ala Pro His Asp Lys Ser Ala Ala
 165     170     175

Tyr Glu Ala Asn Ser Lys Leu Pro Lys Asp Leu Arg Asp Lys Asn Asn
 180     185     190

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

<210> SEQ ID NO 44

<211> LENGTH: 233

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 44

Met Lys Lys Thr Ile Met Ala Ser Ser Leu Ala Val Ala Leu Gly Val
 1 5 10 15
 Thr Gly Tyr Ala Ala Gly Thr Gly His Gln Ala His Ala Ala Glu Val
 20 25 30
 Asn Val Asp Gln Ala His Leu Val Asp Leu Ala His Asn His Gln Asp
 35 40 45
 Gln Leu Asn Ala Ala Pro Ile Lys Asp Gly Ala Tyr Asp Ile His Phe
 50 55 60
 Val Lys Asp Gly Phe Gln Tyr Asn Phe Thr Ser Asn Gly Thr Thr Trp
 65 70 75 80
 Ser Trp Ser Tyr Glu Ala Ala Asn Gly Gln Thr Ala Gly Phe Ser Asn
 85 90 95
 Val Ala Gly Ala Asp Tyr Thr Thr Ser Tyr Asn Gln Gly Ser Asn Val
 100 105 110
 Gln Ser Val Ser Tyr Asn Ala Gln Ser Ser Asn Ser Asn Val Glu Ala

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115					120					125					
Val	Ser	Ala	Pro	Thr	Tyr	His	Asn	Tyr	Ser	Thr	Ser	Thr	Thr	Ser	Ser
130						135					140				
Ser	Val	Arg	Leu	Ser	Asn	Gly	Asn	Thr	Ala	Gly	Ala	Thr	Gly	Ser	Ser
145					150					155					160
Ala	Ala	Gln	Leu	Met	Ala	Gln	Arg	Thr	Gly	Val	Ser	Ala	Ser	Thr	Trp
				165					170					175	
Ala	Ala	Ile	Ile	Ala	Arg	Glu	Ser	Asn	Gly	Gln	Val	Asn	Ala	Tyr	Asn
		180						185						190	
Pro	Ser	Gly	Ala	Ser	Gly	Leu	Phe	Gln	Thr	Met	Pro	Gly	Trp	Gly	Pro
		195				200						205			
Thr	Asn	Thr	Val	Asp	Gln	Gln	Ile	Asn	Ala	Ala	Val	Lys	Ala	Tyr	Lys
	210					215					220				
Ala	Gln	Gly	Leu	Gly	Ala	Trp	Gly	Phe							
225					230										

<210> SEQ ID NO 45
 <211> LENGTH: 256
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 45

Met	Met	Lys	Arg	Leu	Asn	Lys	Leu	Val	Leu	Gly	Ile	Ile	Phe	Leu	Phe
1				5					10					15	
Leu	Val	Ile	Ser	Ile	Thr	Ala	Gly	Cys	Gly	Ile	Gly	Lys	Glu	Ala	Glu
		20						25					30		
Val	Lys	Lys	Ser	Phe	Glu	Lys	Thr	Leu	Ser	Met	Tyr	Pro	Ile	Lys	Asn
	35						40					45			
Leu	Glu	Asp	Leu	Tyr	Asp	Lys	Glu	Gly	Tyr	Arg	Asp	Asp	Gln	Phe	Asp
	50				55					60					
Lys	Asn	Asp	Lys	Gly	Thr	Trp	Ile	Ile	Asn	Ser	Glu	Met	Val	Ile	Gln
	65				70				75						80
Pro	Asn	Asn	Glu	Asp	Met	Val	Ala	Lys	Gly	Met	Val	Leu	Tyr	Met	Asn
			85						90					95	
Arg	Asn	Thr	Lys	Thr	Thr	Asn	Gly	Tyr	Tyr	Tyr	Val	Asp	Val	Thr	Lys
		100						105					110		
Asp	Glu	Asp	Glu	Gly	Lys	Pro	His	Asp	Asn	Glu	Lys	Arg	Tyr	Pro	Val
	115						120					125			
Lys	Met	Val	Asp	Asn	Lys	Ile	Ile	Pro	Thr	Lys	Glu	Ile	Lys	Asp	Glu
	130					135					140				
Lys	Ile	Lys	Lys	Glu	Ile	Glu	Asn	Phe	Lys	Phe	Phe	Val	Gln	Tyr	Gly
	145				150					155					160
Asp	Phe	Lys	Asn	Leu	Lys	Asn	Tyr	Lys	Asp	Gly	Asp	Ile	Ser	Tyr	Asn
			165					170						175	
Pro	Glu	Val	Pro	Ser	Tyr	Ser	Ala	Lys	Tyr	Gln	Leu	Thr	Asn	Asp	Asp
		180						185					190		
Tyr	Asn	Val	Lys	Gln	Leu	Arg	Lys	Arg	Tyr	Asp	Ile	Pro	Thr	Ser	Lys
	195						200					205			
Ala	Pro	Lys	Leu	Leu	Leu	Lys	Gly	Ser	Gly	Asn	Leu	Lys	Gly	Ser	Ser
	210					215					220				
Val	Gly	Tyr	Lys	Asp	Ile	Glu	Phe	Thr	Phe	Val	Glu	Lys	Lys	Glu	Glu
	225				230					235					240
Asn	Ile	Tyr	Phe	Ser	Asp	Ser	Leu	Asp	Tyr	Lys	Lys	Ser	Gly	Asp	Val
				245				250						255	

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<210> SEQ ID NO 46
<211> LENGTH: 514
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 46

Met Lys Lys Ile Tyr Lys Ser Leu Thr Val Ser Ala Ile Val Ala Thr
1      5      10      15
Val Ser Leu Ser Ala Leu Pro Gln Ser Leu Ala Ile Thr His Glu Ser
20      25      30
Gln Pro Thr Lys Gln Gln Arg Thr Val Leu Phe Asp Arg Ser His Gly
35      40      45
Gln Thr Ala Gly Ala Ala Asp Trp Val Ser Asp Gly Ala Phe Ser Asp
50      55      60
Tyr Ala Asp Ser Ile Gln Lys Gln Gly Tyr Asp Val Lys Ala Ile Asp
65      70      75      80
Gly His Ser Asn Ile Thr Glu Ala Ser Leu Lys Ser Ser Lys Ile Phe
85      90      95
Val Ile Pro Glu Ala Asn Ile Pro Phe Lys Glu Ser Glu Gln Ala Ala
100     105     110
Ile Val Lys Tyr Val Lys Gln Gly Gly Asn Val Val Phe Ile Ser Asp
115     120     125
His Tyr Asn Ala Asp Arg Asn Leu Asn Arg Ile Asp Ser Ser Glu Ala
130     135     140
Met Asn Gly Tyr Arg Arg Gly Ala Tyr Glu Asp Met Ser Lys Gly Met
145     150     155     160
Asn Ala Glu Glu Lys Ser Ser Thr Ala Met Gln Gly Val Lys Ser Ser
165     170     175
Asp Trp Leu Ser Thr Asn Phe Gly Val Arg Phe Arg Tyr Asn Ala Leu
180     185     190
Gly Asp Leu Asn Thr Ser Asn Ile Val Ser Ser Lys Glu Ser Phe Gly
195     200     205
Ile Thr Glu Gly Val Lys Ser Val Ser Met His Ala Gly Ser Thr Leu
210     215     220
Ala Ile Thr Asn Pro Glu Lys Ala Lys Gly Ile Val Tyr Thr Pro Glu
225     230     235     240
Gln Leu Pro Ala Lys Ser Lys Trp Ser His Ala Val Asp Gln Gly Ile
245     250     255
Tyr Asn Gly Gly Gly Lys Ala Glu Gly Pro Tyr Val Ala Ile Ser Lys
260     265     270
Val Gly Lys Gly Lys Ala Ala Phe Ile Gly Asp Ser Ser Leu Val Glu
275     280     285
Asp Ser Ser Pro Lys Tyr Val Arg Glu Asp Asn Gly Glu Lys Lys Lys
290     295     300
Thr Tyr Asp Gly Phe Lys Glu Gln Asp Asn Gly Lys Leu Leu Asn Asn
305     310     315     320
Ile Thr Ala Trp Met Ser Lys Asp Asn Asp Gly Lys Ser Leu Lys Ala
325     330     335
Ser Ser Leu Thr Leu Asp Thr Lys Thr Lys Leu Leu Asp Phe Glu Arg
340     345     350
Pro Glu Arg Ser Thr Glu Pro Glu Lys Glu Pro Trp Ser Gln Pro Pro
355     360     365
Ser Gly Tyr Lys Trp Tyr Asp Pro Thr Thr Phe Lys Ala Gly Ser Tyr
370     375     380

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Gly Ser Glu Lys Gly Ala Asp Pro Gln Pro Asn Thr Pro Asp Asp His
 385 390 395 400
 Thr Pro Pro Asn Gln Asn Glu Lys Val Thr Phe Asp Ile Pro Gln Asn
 405 410 415
 Val Ser Val Asn Glu Pro Phe Glu Met Thr Ile His Leu Lys Gly Phe
 420 425 430
 Glu Ala Asn Gln Thr Leu Glu Asn Leu Arg Val Gly Ile Tyr Lys Glu
 435 440 445
 Gly Gly Arg Gln Ile Gly Gln Phe Ser Ser Lys Asp Asn Asp Tyr Asn
 450 455 460
 Pro Pro Gly Tyr Ser Thr Leu Pro Thr Val Lys Ala Asp Glu Asn Gly
 465 470 475 480
 Asn Val Thr Ile Lys Val Asn Ala Lys Val Leu Glu Ser Met Glu Gly
 485 490 495
 Ser Lys Ile Arg Leu Lys Leu Gly Asp Lys Thr Leu Ile Thr Thr Asp
 500 505 510
 Phe Lys

<210> SEQ ID NO 47
 <211> LENGTH: 511
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 47

Met Ser Asn Ile Ala Phe Tyr Val Val Ser Asp Val His Gly Tyr Ile
 1 5 10 15
 Phe Pro Thr Asp Phe Thr Ser Arg Asn Gln Tyr Gln Pro Met Gly Leu
 20 25 30
 Leu Leu Ala Asn His Val Ile Glu Gln Asp Arg Arg Gln Tyr Asp Gln
 35 40 45
 Ser Phe Lys Ile Asp Asn Gly Asp Phe Leu Gln Gly Ser Pro Phe Cys
 50 55 60
 Asn Tyr Leu Ile Ala His Ser Gly Ser Ser Gln Pro Leu Val Asp Phe
 65 70 75 80
 Tyr Asn Arg Met Ala Phe Asp Phe Gly Thr Leu Gly Asn His Glu Phe
 85 90 95
 Asn Tyr Gly Leu Pro Tyr Leu Lys Asp Thr Leu Arg Arg Leu Asn Tyr
 100 105 110
 Pro Val Leu Cys Ala Asn Ile Tyr Glu Asn Asp Ser Thr Leu Thr Asp
 115 120 125
 Asn Gly Val Lys Tyr Phe Gln Val Gly Asp Gln Thr Val Gly Val Ile
 130 135 140
 Gly Leu Thr Thr Gln Phe Ile Pro His Trp Glu Gln Pro Glu His Ile
 145 150 155 160
 Gln Ser Leu Thr Phe His Ser Ala Phe Glu Ile Leu Gln Gln Tyr Leu
 165 170 175
 Pro Glu Met Lys Arg His Ala Asp Ile Ile Val Val Cys Tyr His Gly
 180 185 190
 Gly Phe Glu Lys Asp Leu Glu Ser Gly Thr Pro Thr Glu Val Leu Thr
 195 200 205
 Gly Glu Asn Glu Gly Tyr Ala Met Leu Glu Ala Phe Ser Lys Asp Ile
 210 215 220
 Asp Ile Phe Ile Thr Gly His Gln His Arg Gln Ile Ala Glu Arg Phe
 225 230 235 240

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100					105					110					
Gly	His	His	Glu	Gly	Asn	Val	Ile	Met	Gly	Gln	Lys	Gly	Met	His	Leu
	115						120					125			
Asn	Glu	Phe	Asn	Asn	Asn	Gly	Asp	Asp	Tyr	His	Phe	Gly	Ile	Pro	His
	130					135					140				
Arg	Tyr	Ser	Thr	His	Tyr	Leu	Leu	Leu	Glu	Glu	Leu	Arg	Lys	Gln	Leu
	145					150					155				160
Lys	Ile	Lys	Pro	Gly	His	Phe	Ser	Tyr	His	Glu	Met	Ser	Pro	Ala	Glu
				165					170					175	
Met	Pro	Ala	Ala	Leu	Ser	Glu	His	Arg	Ile	Thr	Gly	Tyr	Ser	Val	Ala
			180					185					190		
Glu	Pro	Phe	Gly	Ala	Leu	Gly	Glu	Lys	Leu	Gly	Lys	Gly	Lys	Thr	Leu
		195					200					205			
Lys	His	Gly	Asp	Asp	Val	Ile	Pro	Asp	Ala	Tyr	Cys	Cys	Val	Leu	Val
	210					215					220				
Leu	Arg	Gly	Glu	Leu	Leu	Asp	Gln	His	Lys	Asp	Val	Ala	Gln	Ala	Phe
	225					230					235				240
Val	Gln	Asp	Tyr	Lys	Lys	Ser	Gly	Phe	Lys	Met	Asn	Asp	Arg	Lys	Gln
				245					250					255	
Ser	Val	Asp	Ile	Met	Thr	His	His	Phe	Lys	Gln	Ser	Arg	Asp	Val	Leu
			260					265					270		
Thr	Gln	Ser	Ala	Ala	Trp	Thr	Ser	Tyr	Gly	Asp	Leu	Thr	Ile	Lys	Pro
		275					280					285			
Ser	Gly	Tyr	Gln	Glu	Ile	Thr	Thr	Leu	Val	Lys	Gln	His	His	Leu	Phe
	290					295					300				
Asn	Pro	Pro	Ala	Tyr	Asp	Asp	Phe	Val	Glu	Pro	Ser	Leu	Tyr	Lys	Glu
	305					310					315				320
Ala	Ser	Arg	Ser												
<210> SEQ ID NO 49															
<211> LENGTH: 591															
<212> TYPE: PRT															
<213> ORGANISM: Staphylococcus sp															
<400> SEQUENCE: 49															
Met	Lys	Lys	Ile	Ile	Ser	Ile	Ala	Ile	Ile	Val	Leu	Ala	Leu	Val	Leu
1			5						10				15		
Ser	Gly	Cys	Gly	Val	Pro	Thr	Lys	Ser	Glu	Val	Ala	Gln	Lys	Ser	Ser
		20					25					30			
Lys	Val	Glu	Val	Lys	Gly	Glu	Arg	Pro	Thr	Ile	His	Phe	Leu	Gly	Gln
		35					40					45			
Ala	Ser	Tyr	Glu	Asn	Asp	Met	Asn	Ile	Val	Lys	Asp	Gln	Leu	Glu	Asn
	50					55					60				
Ala	Gly	Phe	Asn	Val	Lys	Met	Asn	Ile	Gln	Pro	Asp	Tyr	Gly	Ser	Tyr
	65					70					75				80
Arg	Thr	Gln	Arg	Gln	Ala	Gly	Asn	Tyr	Asp	Ile	Gln	Ile	Asp	Asp	Trp
			85				90						95		
Met	Thr	Val	Phe	Gly	Asp	Pro	Asn	Tyr	Ala	Met	Thr	Ala	Leu	Phe	Ser
		100					105					110			
Ser	Thr	Gly	Ser	Asn	Ser	Leu	Leu	Lys	Asp	Lys	His	Val	Asp	Gln	Leu
	115					120					125				
Leu	Asn	Lys	Ala	Ser	Thr	Gln	Asn	Glu	Ala	Asp	Val	Lys	Gln	Thr	Tyr
	130					135					140				
Lys	Gln	Ile	Glu	Asp	Glu	Val	Val	Phe	Asp	Lys	Gly	Tyr	Met	Ala	Pro

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145					150					155					160
Leu	Tyr	Gly	Ser	Lys	Lys	Asn	Leu	Val	Tyr	Asp	Asn	Lys	Val	Leu	Asp
				165					170					175	
Lys	Asn	Ser	Val	Gly	Leu	Pro	Asn	Ser	Arg	Ala	Leu	Ile	Trp	Gln	Gln
			180					185					190		
Phe	Asp	Tyr	Asn	Asn	Ser	Arg	Glu	Arg	Asp	Thr	Arg	Pro	Leu	Val	Met
	195						200					205			
Thr	Gln	Gln	Asp	Gly	Glu	Ile	Pro	Thr	Leu	Asp	Pro	Ile	Arg	Ser	Ile
210						215					220				
Ala	Pro	Ser	Val	Tyr	Ser	Ile	Asn	Met	Asn	Met	Tyr	Thr	Arg	Leu	Leu
225					230					235				240	
Leu	Leu	Asp	Glu	Asn	Asp	His	Leu	Thr	Thr	Lys	Gly	Ser	Leu	Ser	His
				245					250					255	
Asp	Tyr	Ala	Val	Asn	Lys	Asp	Asn	Lys	Ala	Phe	Tyr	Phe	Leu	Leu	Arg
		260						265					270		
Asp	Asp	Asp	Tyr	Phe	Ala	Lys	Val	Val	Asn	Gly	Gln	Ala	Arg	Asn	Thr
	275						280					285			
Gly	Glu	Arg	Val	Ser	Ala	Glu	Asp	Val	Lys	Phe	Ser	Leu	Asp	Arg	Ala
290						295					300				
Arg	Asp	Lys	Lys	Ser	Val	Pro	Asn	Asn	Asn	Thr	Tyr	Asn	Met	His	Lys
305					310					315				320	
His	Ile	Asn	Asp	Ile	Lys	Ile	Leu	Lys	Asp	Glu	Asp	Ile	Asp	Gln	Leu
				325					330					335	
Arg	Lys	Glu	Lys	Asp	Lys	Asp	Asp	Lys	Ser	Ile	Tyr	Asp	Lys	Leu	Leu
		340						345					350		
Lys	Ala	Tyr	Asn	Val	Lys	Ser	Leu	Thr	Thr	Asp	Gly	Gln	Lys	Val	Asn
	355						360					365			
Asn	Lys	Asp	Gly	Ile	Tyr	Gln	Ile	Val	Lys	Ile	Thr	Thr	Asp	Gln	Ser
370						375					380				
Met	Pro	Arg	Glu	Val	Asn	Tyr	Leu	Thr	His	Ser	Ser	Ala	Gly	Ile	Leu
385					390					395				400	
Ser	Lys	Lys	Phe	Val	Asn	Gln	Val	Asn	Gln	Glu	Tyr	Pro	Lys	Gly	Tyr
				405					410					415	
Gly	Asp	Ser	Ser	Thr	Ile	Pro	Ala	Asn	Ser	Asp	Gly	Lys	Asn	Ala	Leu
		420						425					430		
Tyr	Ala	Ser	Gly	Ala	Tyr	Ile	Met	Thr	Gln	Lys	Asn	Ala	Tyr	Gln	Ala
	435						440					445			
Thr	Phe	Gln	Arg	Asn	Pro	Gly	Phe	Asn	Glu	Thr	Glu	Lys	Gly	Ser	Tyr
	450					455					460				
Gly	Pro	Ala	Lys	Ile	Lys	Asn	Ile	Thr	Leu	Lys	Phe	Asn	Gly	Asp	Pro
465					470					475				480	
Asn	Asn	Ala	Leu	Ser	Glu	Leu	Arg	Asn	His	Ser	Ile	Asp	Met	Leu	Ala
				485					490					495	
Asp	Val	Asn	Gln	Lys	His	Phe	Asp	Leu	Ile	Lys	Ser	Asp	Lys	Asn	Leu
		500						505					510		
Ser	Ile	Ile	Arg	Lys	Asn	Gly	Arg	Lys	Ser	Val	Phe	Leu	Met	Leu	Asn
	515						520					525			
Ile	Lys	Lys	Gly	Ile	Phe	Lys	Thr	His	Pro	Asn	Leu	Arg	Gln	Ala	Val
	530					535					540				
Val	Asn	Ala	Ile	Asp	Gln	Asp	Gln	Phe	Ile	Lys	Phe	Tyr	Arg	Gly	Asp
545					550					555				560	
Lys	Phe	Lys	Ile	Ala	Ser	Pro	Ile	Thr	Pro	Leu	Val	Asp	Thr	Gly	Asn
				565					570					575	

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Glu Gln Arg Gln Asp Leu Glu Lys Val Glu Lys Ala Ile Asn Gln
 580 585 590

<210> SEQ ID NO 50
 <211> LENGTH: 668
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 50

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

Leu Ile Ser Val Ser His Pro Leu Ala Ala Lys Ile Gly Lys Asp Val
 20 25 30

Leu Asp Gln Gly Gly Asn Ala Met Asp Ala Val Ile Ala Ile Gln Leu
 35 40 45

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

Tyr Leu Leu Tyr Tyr Glu Gln Ser Thr Gly Ser Ile Thr Ala Phe Asp
 65 70 75 80

Ala Arg Glu Thr Ala Pro Glu His Val Asp Lys Gln Phe Tyr Leu Asp
 85 90 95

Asp Ser Gly Glu Tyr Lys Ser Phe Phe Asp Met Thr Thr His Gly Lys
 100 105 110

Thr Val Ala Val Pro Ala Ile Pro Lys Leu Phe Asp Tyr Ile His Lys
 115 120 125

Arg Tyr Ala Lys Leu Ser Leu Glu Asp Leu Ile Asn Pro Ala Ile Glu
 130 135 140

Leu Ala Ile Glu Gly His Ala Ala Asn Trp Ala Thr Glu Lys Tyr Ser
 145 150 155 160

Arg Gln Gln His Ala Arg Leu Thr Lys Tyr His Glu Thr Ala Gln Val
 165 170 175

Phe Thr His Glu Asn Gln Tyr Trp Arg Glu Gly Asp Trp Ile Val Gln
 180 185 190

Pro Glu Leu Gly Lys Thr Phe Gln Ile Leu Arg Glu Gln Gly Phe Asn
 195 200 205

Ala Phe Tyr Lys Gly Asp Ile Ala Lys Gln Leu Val Asn Val Val Lys
 210 215 220

Ala Cys Gly Gly Thr Ile Thr Leu Glu Asp Leu Ala Lys Tyr Asp Ile
 225 230 235 240

Gln Leu Lys Ala Pro Ile Ser Ala Thr Phe Lys Asp Tyr Asp Ile Tyr
 245 250 255

Ser Met Gly Pro Ser Ser Ser Gly Gly Ile Thr Val Ile Gln Ile Leu
 260 265 270

Lys Leu Leu Glu His Val Asp Leu Pro Ser Met Gly Pro Arg Ser Val
 275 280 285

Asp Tyr Leu His His Leu Ile Gln Ala Met His Leu Ala Tyr Ser Asp
 290 295 300

Arg Ala Gln Tyr Leu Ala Asp Asp Asn Phe His Glu Val Pro Val Gln
 305 310 315 320

Ser Leu Ile Asp Asp Asp Tyr Leu Lys Ala Arg Ser Thr Leu Ile Asp
 325 330 335

Ser Asn Lys Ala Asn Ile Asp Ile Glu His Gly Val Val Ser Asp Cys
 340 345 350

Ile Ser His Thr Asp Val Glu Glu Asn His Thr Glu Thr Thr His Phe

-continued

355	360	365
Cys Val Ile Asp Lys Glu Gly	Asn Ile Ala Ser Phe	Thr Thr Ser Ile
370	375	380
Gly Met Ile Tyr Gly Ser Gly	Ile Thr Ile Pro Gly	Tyr Gly Val Leu
385	390	395
Leu Asn Thr Thr Met Asp Gly	Phe Asp Val Val Asp	Gly Gly Ile Asn
	405	410
Glu Ile Ala Pro Tyr Lys Arg	Pro Leu Ser Asn Met	Ala Pro Thr Ile
	420	425
Val Met Tyr His Gly Lys Pro	Ile Leu Thr Val Gly	Ala Pro Gly Ala
	435	440
Ile Ser Ile Ile Ala Ser Val	Ala Gln Thr Leu Ile	Asn Val Leu Val
	450	455
Phe Gly Met Asp Ile Gln Gln	Ala Ile Asp Glu Pro	Arg Ile Tyr Ser
	465	470
Ser His Pro Asn Arg Ile Glu	Trp Glu Pro Gln Phe	Ser Gln Ser Thr
	485	490
Ile Leu Ala Leu Ile Ala His	Gly His Ala Met Glu	His Lys Pro Asp
	500	505
Ala Tyr Ile Gly Asp Val His	Gly Leu Gln Val Asp	Pro Thr Thr Tyr
	515	520
Glu Ala Ser Gly Gly Ser Asp	Asp Thr Arg Glu Gly	Thr Val Met Gly
	530	535
Gly Glu Val Leu Val Ile Arg	Lys Gln Pro Leu Pro	Tyr Arg Gln Met
	545	550
Tyr Asp Ser Asp Gly Phe Arg	Leu Tyr Phe Asn Asp	Val Gln Leu Pro
	565	570
Leu Leu Ala Asp Gln Val Arg	Trp Met His Asp Lys	Tyr Trp Val Asp
	580	585
Glu Ser Val Val Arg Ile Ile	Phe Pro Glu Val Ser	Ala His Ile Glu
	595	600
Asp Leu Arg Ser Tyr Glu Asn	Ala Gly Glu Asn Tyr	Ile Asp Ile Ala
	610	615
Trp Leu Ala Arg Lys Tyr Ala	Tyr Gln Val Thr Leu	Lys Asp Asp Gly
	625	630
Leu Tyr Leu Thr Asp Asp Thr	Tyr Thr Ser Val Lys	Arg Asn Thr Asn
	645	650
Ala Tyr Tyr Arg Tyr Asp Arg	Asp Ser Ile Thr Arg	
	660	665

<210> SEQ ID NO 51

<211> LENGTH: 322

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 51

Met Lys Ser Lys Ile Tyr Ile	Leu Leu Leu Phe Leu Ile	Phe Leu Ser
1	5	10
Ala Cys Ala Asn Thr Arg His	Ser Glu Ser Asp Lys Asn	Val Leu Thr
	20	25
Val Tyr Ser Pro Tyr Gln Ser	Asn Leu Ile Arg Pro	Ile Leu Asn Glu
	35	40
Phe Glu Lys Gln Glu His Val	Lys Ile Glu Ile Lys	His Gly Ser Thr
	50	55
		60

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Gln Val Leu Leu Ser Asn Leu His Asn Glu Asp Phe Ser Glu Arg Gly
 65 70 75 80
 Asp Val Phe Met Gly Gly Val Leu Ser Glu Thr Ile Asp His Pro Glu
 85 90 95
 Asp Phe Val Pro Tyr Gln Asp Thr Ser Val Thr Gln Gln Leu Glu Asp
 100 105 110
 Tyr Arg Ser Asn Asn Lys Tyr Val Thr Ser Phe Leu Leu Met Pro Thr
 115 120 125
 Val Ile Val Val Asn Ser Asp Leu Gln Gly Asp Ile Lys Ile Arg Gly
 130 135 140
 Tyr Gln Asp Leu Leu Gln Pro Ile Leu Lys Gly Lys Ile Ala Tyr Ser
 145 150 155 160
 Asn Pro Asn Thr Thr Thr Thr Gly Tyr Gln His Met Arg Ala Ile Tyr
 165 170 175
 Ser Met His His Arg Val Ser Asp Val His Gln Phe Gln Asn His Ala
 180 185 190
 Met Gln Leu Ser Lys Thr Ser Lys Val Ile Glu Asp Val Ala Lys Gly
 195 200 205
 Lys Tyr Tyr Ala Gly Leu Ser Tyr Glu Gln Asp Ala Arg Thr Trp Lys
 210 215 220
 Asn Lys Gly Tyr Pro Val Ser Ile Val Tyr Pro Ile Glu Gly Thr Met
 225 230 235 240
 Leu Asn Val Asp Gly Ile Ala Leu Val Lys Asn Ala His Pro His Pro
 245 250 255
 Lys Arg Lys Lys Leu Val Gln Tyr Leu Thr Ser Arg Ser Val Gln Gln
 260 265 270
 Arg Leu Val Ala Glu Phe Asp Ala Lys Ser Ile Arg Lys Asp Val Ser
 275 280 285
 Glu Gln Ser Asp Gln Ser Ile Glu Asn Leu Lys Asn Ile Pro Leu Ile
 290 295 300
 Pro Lys Ser Lys Leu Pro Asp Ile Pro His His Lys Phe Leu Glu Met
 305 310 315 320
 Ile Gln

<210> SEQ ID NO 52

<211> LENGTH: 470

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 52

Met His Ser Ser Gly Lys Asp Leu Asn Ile Ser Leu Pro Leu Lys Thr
 1 5 10 15
 Lys Ser Ile Ala Pro Tyr Glu Thr Asp Val Pro Val Lys Ile Gly Ala
 20 25 30
 Ala Glu Ser Leu Phe Lys Thr Asn Asp Gln Gly Lys Ile Glu Lys Ala
 35 40 45
 Leu Val Lys Ser Tyr His Gln Pro Asn Asp Thr Thr Leu Asp Ile Glu
 50 55 60
 Leu Lys Asp Asn Ile Lys Phe Gln Asn Gly Gln Lys Leu Thr Ala Glu
 65 70 75 80
 Lys Val Lys Ser Ser Leu Glu Asn Ser Met Lys Lys Ser Asp Leu Val
 85 90 95
 Lys Tyr Ser Leu Pro Ile Ser Ser Ile Thr Ala Lys Gly Gln Lys Leu
 100 105 110

Thr	Ile	Lys	Thr	Asn	Ser	Ala	Tyr	Pro	Glu	Leu	Val	Ser	Glu	Leu	Ala
115						120						125			
Asn	Pro	Phe	Met	Ala	Ile	Tyr	Asp	Thr	Asp	Ala	Lys	Ser	Asp	Val	Asn
130						135						140			
Gln	Thr	Pro	Val	Gly	Thr	Gly	Pro	Tyr	Gln	Ile	Lys	Asp	Tyr	Lys	Gln
145				150						155				160	
Ser	Arg	Lys	Ile	Ser	Leu	Ser	Asn	Phe	Lys	Asp	Tyr	Trp	Gln	Gly	Lys
				165				170						175	
Pro	Lys	Leu	Asp	His	Ile	Thr	Val	Thr	Tyr	Gln	Glu	Asp	Gly	Asn	Asn
		180						185				190			
Arg	Val	Arg	Asn	Leu	Glu	Ser	Gln	Lys	Asp	Asp	Leu	Ile	Thr	Asp	Val
		195				200						205			
Pro	Val	Asn	Lys	Val	Gln	Asp	Ile	Glu	Asn	Asn	Gln	Asn	Leu	Lys	Val
210						215				220					
Ser	Lys	Glu	Ser	Gly	Phe	Arg	Thr	Ser	Leu	Leu	Met	Tyr	Asn	His	Thr
225				230						235				240	
Asn	Lys	Lys	Met	Thr	Lys	Ser	Val	Arg	Glu	Ala	Leu	Asp	His	Ile	Ile
				245				250						255	
Asp	Arg	Gln	Gly	Ile	Ala	Asp	His	Ile	Tyr	Gln	Gly	Tyr	Ala	Lys	Pro
		260						265				270			
Ala	Thr	Ser	Pro	Phe	Asn	Asp	Lys	Ile	Pro	Tyr	Ile	Lys	Glu	Pro	Lys
		275				280						285			
Leu	Thr	Lys	Gln	Asn	Ile	Glu	Gln	Ala	Lys	Met	Leu	Leu	Ala	Lys	Asp
290						295				300					
Gly	Tyr	Thr	Lys	Glu	His	Pro	Leu	Lys	Ile	Lys	Leu	Ile	Thr	Tyr	Asp
305				310						315				320	
Gly	Arg	Pro	Glu	Leu	Ser	Lys	Ile	Ala	Gln	Val	Leu	Gln	Ser	Asp	Ala
				325				330						335	
Lys	Lys	Ala	Asn	Ile	Glu	Ile	Asp	Ile	Lys	Ser	Val	Asp	Asp	Ile	Glu
		340						345				350			
Gly	Tyr	Leu	Lys	Asp	Arg	Ser	Ala	Trp	Asp	Ala	Thr	Met	Tyr	Ser	Phe
355						360						365			
Gly	Thr	Ile	Pro	Arg	Gly	Asp	Thr	Gly	Tyr	Phe	Phe	Asn	Gln	Ala	Tyr
370						375				380					
Lys	Lys	Asp	Gly	Ala	Ile	Asn	Lys	Gly	Asp	Tyr	Asn	Asn	Ser	Asn	Val
385				390						395				400	
Asp	Asp	Leu	Ile	Asn	Gln	Leu	Asn	His	Thr	Val	Asp	Val	Lys	Glu	Arg
		405						410						415	
His	Asn	Ile	Ser	Asn	Asp	Ile	Ile	Lys	Leu	Ser	Ser	Arg	Asp	Val	Pro
		420						425				430			
Asn	Ser	Tyr	Ile	Ala	Tyr	Asn	Asp	Gln	Ile	Val	Ala	Ala	Asn	Ser	Lys
		435				440				445					
Val	Lys	Asn	Tyr	Lys	Val	Thr	Pro	Glu	Gly	Ile	Tyr	Leu	Ile	Asp	Tyr
450						455				460					
Arg	Thr	Thr	Ile	Glu	Arg										
465				470											

<400> SEQUENCE: 53

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

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Phe Thr Met Ala His Gln Ala Asp Ala Ala Glu Thr Thr Asn Thr Gln
 20 25 30
 Gln Ala His Thr Gln Met Ser Thr Gln Ser Gln Asp Val Ser Tyr Gly
 35 40 45
 Thr Tyr Tyr Thr Ile Asp Ser Asn Gly Asp Tyr His His Thr Pro Asp
 50 55 60
 Gly Asn Trp Asn Gln Ala Met Phe Asp Asn Lys Glu Tyr Ser Tyr Thr
 65 70 75 80
 Phe Val Asp Ala Gln Gly His Thr His Tyr Phe Tyr Asn Cys Tyr Pro
 85 90 95
 Lys Asn Ala Asn Ala Asn Gly Ser Gly Gln Thr Tyr Val Asn Pro Ala
 100 105 110
 Thr Ala Gly Asp Asn Asn Asp Tyr Thr Ala Ser Gln Ser Gln Gln His
 115 120 125
 Ile Asn Gln Tyr Gly Tyr Gln Ser Asn Val Gly Pro Asp Ala Ser Tyr
 130 135 140
 Tyr Ser His Ser Asn Asn Asn Gln Ala Tyr Asn Ser His Asp Gly Asn
 145 150 155 160
 Gly Lys Val Asn Tyr Pro Asn Gly Thr Ser Asn Gln Asn Gly Gly Ser
 165 170 175
 Ala Ser Lys Ala Thr Ala Ser Gly His Ala Lys Asp Ala Ser Trp Leu
 180 185 190
 Thr Ser Arg Lys Gln Leu Gln Pro Tyr Gly Gln Tyr His Gly Gly Gly
 195 200 205
 Ala His Tyr Gly Val Asp Tyr Ala Met Pro Glu Asn Ser Pro Val Tyr
 210 215 220
 Ser Leu Thr Asp Gly Thr Val Val Gln Ala Gly Trp Ser Asn Tyr Gly
 225 230 235 240
 Gly Gly Asn Gln Val Thr Ile Lys Glu Ala Asn Ser Asn Asn Tyr Gln
 245 250 255
 Trp Tyr Met His Asn Asn Arg Leu Thr Val Ser Ala Gly Asp Lys Val
 260 265 270
 Lys Ala Gly Asp Gln Ile Ala Tyr Ser Gly Ser Thr Gly Asn Ser Thr
 275 280 285
 Ala Pro His Val His Phe Gln Arg Met Ser Gly Gly Ile Gly Asn Gln
 290 295 300
 Tyr Ala Val Asp Pro Thr Ser Tyr Leu Gln Ser Arg
 305 310 315

<210> SEQ ID NO 54

<211> LENGTH: 507

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 54

Met Ser Lys Lys Leu Lys Ile Ile Ile Pro Ile Ile Ile Val Leu Leu
 1 5 10 15
 Leu Ile Gly Gly Ile Ala Trp Gly Val Tyr Ala Phe Phe Ala Asn Thr
 20 25 30
 Pro Lys Asn Thr Tyr Leu Lys Ser Glu Gln Gln Thr Ala Lys Met Tyr
 35 40 45
 Lys Asp Tyr Phe Asn Asp Arg Phe Glu Asn Glu Val Lys Phe Gln Glu
 50 55 60
 Lys Met Lys Asp Asn Ser Phe Leu Ser Ser Leu Glu Leu Ser Ala Asp

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65	70	75	80
Ala Ser Asp Glu Ile Val Lys Gly Leu Gly Ile Pro Lys Ser Val Val			
	85	90	95
Asn Ala Ser Lys Ile Lys Met Ser Tyr Gly His Asp Pro Lys Lys Glu			
	100	105	110
Lys Ser Met Ile Asn Leu Glu Pro Thr Ile Ala Asp Ser Ala Leu Gly			
	115	120	125
Lys Phe Gln Leu Ala Ala Asp Lys Asp Lys His Tyr Phe Glu Ser Pro			
	130	135	140
Leu Phe Lys Gly Lys Tyr Ser Val Asn Asn Ser Asp Leu Leu Ser Thr			
	145	150	155
Tyr Ser Lys Leu Thr Gly Glu Asp Glu Glu Thr Ala Lys Glu Asn Gly			
	165	170	175
Ile Thr Asn Gln Gln Leu Asn Leu Asn Thr Leu Phe Asn Asn Ala Gln			
	180	185	190
Ala Gln Gln Ser Asp Tyr Ser Lys Ile Ala Glu Lys Tyr Ser Glu Leu			
	195	200	205
Ile Val Asp Lys Leu Asp Asp Asp Asn Phe Asp Lys Gly Lys Lys Glu			
	210	215	220
Glu Ile Lys Val Asn Gly Glu Lys Tyr Lys Val Arg Pro Val Thr Leu			
	225	230	235
Thr Leu Ser Arg Ala Asp Thr Lys Lys Ile Thr Leu Ala Val Leu Glu			
	245	250	255
Glu Ala Lys Lys Asp Lys Asp Leu Lys Lys Leu Met Glu Glu Gln Gly			
	260	265	270
Ala Thr Lys Asp Phe Glu Lys Asp Ile Lys Lys Ala Ile Asp Asp Val			
	275	280	285
Lys Glu Thr Lys Lys Asp Glu Phe Ala Lys Ile Gln Ser Lys Ile Tyr			
	290	295	300
Thr Glu Lys His Thr Ile Val Lys Arg Glu Ile Thr Ile Thr Asp Lys			
	305	310	315
Glu Asn Asn Lys Thr Lys Ile Lys Gly Thr Asn Thr Leu Glu Asp Asp			
	325	330	335
Lys Leu Lys Leu Asp Tyr Ala Leu Asp Phe Asp Gln Asp Lys Tyr Thr			
	340	345	350
Tyr Ala Glu Ala Lys Tyr Thr Ile Lys Gly Val Ser Ser Lys Glu Lys			
	355	360	365
Asp Asn Lys Tyr Asn Asp Lys Tyr Glu Phe Gly Lys Lys Thr Glu Tyr			
	370	375	380
Asp Glu Ser Lys Ile Lys Leu Asp Asn Gln Glu Lys Val Asp Gly Thr			
	385	390	395
Lys Arg Gln Asp Lys Gly Lys Ile Thr Val Ala Leu Asp Lys Tyr Ser			
	405	410	415
Asp Glu Asn Glu Phe Thr Phe Glu Asn Asn Ile Asp Ser Asp Val Lys			
	420	425	430
Asn Asn Thr Gln Lys Ser Thr Leu Asn Ile Gly Ile Lys Tyr Ala Glu			
	435	440	445
Glu Pro Ile Asn Phe Ile Leu Lys Ser Ser Thr Lys Leu Lys Ala Asp			
	450	455	460
Ile Asp Phe Asp Asp Ser Gly Ala Lys Asp Phe Asn Ser Leu Ser Ser			
	465	470	475
Lys Asp Arg Glu Lys Leu Glu Lys Glu Ile Glu Lys Asn Gly Gly Lys			
	485	490	495

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

<210> SEQ ID NO 55
<211> LENGTH: 297
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 55

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Glu Val Ser Ser Tyr Asn Tyr Ile His
290 295

<210> SEQ ID NO 56
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 56

Met Lys Arg Ile Leu Val Val Phe Leu Met Leu Ala Ile Ile Leu Ala
1 5 10 15

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Gly Cys Ser Asn Lys Gly Glu Lys Tyr Gln Lys Asp Ile Asp Lys Val
 20 25 30
 Tyr Lys Glu Gln Asn Gln Met Asn Lys Ile Ala Ser Lys Val Gln Asn
 35 40 45
 Thr Ile Lys Thr Asp Ile Lys Gln Glu Asp Ser Asn Thr His Val Tyr
 50 55 60
 Lys Asp Gly Lys Val Ile Val Ile Gly Ile Gln Leu Tyr Lys Asp Arg
 65 70 75 80
 Glu Lys Met Tyr Tyr Phe Ala Tyr Glu Ile Lys Asp Gly Lys Ala Glu
 85 90 95
 Ile Asn Arg Glu Ile Asp Pro Ile Lys Tyr Met Lys Asp His Lys Ala
 100 105 110
 Asp Tyr Glu Asp Glu Asn Val Glu Val Glu Lys Asp
 115 120

<210> SEQ ID NO 57
 <211> LENGTH: 296
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 57

Met Asn Lys Ile Ser Lys Tyr Ile Ala Ile Ala Ser Leu Ser Val Ala
 1 5 10 15
 Val Thr Val Ser Ala Pro Gln Thr Thr Asn Ser Thr Ala Phe Ala Lys
 20 25 30
 Ser Ser Ala Glu Val Gln Gln Thr Gln Gln Ala Ser Ile Pro Ala Ser
 35 40 45
 Gln Lys Ala Asn Leu Gly Asn Gln Asn Leu Met Ala Val Ala Trp Tyr
 50 55 60
 Gln Asn Ser Ala Glu Ala Lys Ala Leu Tyr Leu Gln Gly Tyr Asn Ser
 65 70 75 80
 Ala Lys Thr Gln Leu Asp Lys Glu Ile Lys Lys Asn Lys Gly Lys His
 85 90 95
 Lys Leu Ala Ile Ala Leu Asp Leu Asp Glu Thr Val Leu Asp Asn Ser
 100 105 110
 Pro Tyr Gln Gly Tyr Ala Ser Ile His Asn Lys Pro Phe Pro Glu Gly
 115 120 125
 Trp His Glu Trp Val Gln Ala Ala Lys Ala Lys Pro Val Tyr Gly Ala
 130 135 140
 Lys Glu Phe Leu Lys Tyr Ala Asp Lys Lys Gly Val Asp Ile Tyr Tyr
 145 150 155 160
 Ile Ser Asp Arg Asp Lys Glu Lys Asp Leu Lys Ala Thr Gln Lys Asn
 165 170 175
 Leu Lys Gln Gln Gly Ile Pro Gln Ala Lys Lys Ser His Ile Leu Leu
 180 185 190
 Lys Gly Lys Asp Asp Lys Ser Lys Glu Ser Arg Arg Gln Met Val Gln
 195 200 205
 Lys Asp His Lys Leu Val Met Leu Phe Gly Asp Asn Leu Leu Asp Phe
 210 215 220
 Thr Asp Pro Lys Glu Ala Thr Ala Glu Ser Arg Glu Ala Leu Ile Glu
 225 230 235 240
 Lys His Lys Asp Asp Phe Gly Lys Lys Tyr Ile Ile Phe Pro Asn Pro
 245 250 255
 Met Tyr Gly Ser Trp Glu Ala Thr Ile Tyr Asn Asn Asn Tyr Lys Ala

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260	265	270
Ser Asp Lys Ala Lys Asp Lys Leu Arg Lys Asn Ala Ile Lys Gln Phe		
275	280	285
Asp Pro Lys Thr Gly Glu Val Lys		
290	295	

<210> SEQ ID NO 58
 <211> LENGTH: 690
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 58

Met Leu Arg Gly Gln Glu Glu Arg Lys Tyr Ser Ile Arg Lys Tyr Ser		
1	5	10
Ile Gly Val Val Ser Val Leu Ala Ala Thr Met Phe Val Val Ser Ser		
	20	25
His Glu Ala Gln Ala Ser Glu Lys Thr Ser Thr Asn Ala Ala Ala Gln		
	35	40
Lys Glu Thr Leu Asn Gln Pro Gly Glu Gln Gly Asn Ala Ile Thr Ser		
	50	55
His Gln Met Gln Ser Gly Lys Gln Leu Asp Asp Met His Lys Glu Asn		
65	70	75
Gly Lys Ser Gly Thr Val Thr Glu Gly Lys Asp Thr Leu Gln Ser Ser		
	85	90
Lys His Gln Ser Thr Gln Asn Ser Lys Thr Ile Arg Thr Gln Asn Asp		
	100	105
Asn Gln Val Lys Gln Asp Ser Glu Arg Gln Gly Ser Lys Gln Ser His		
	115	120
Gln Asn Asn Ala Thr Asn Asn Thr Glu Arg Gln Asn Asp Gln Val Gln		
	130	135
Asn Thr His His Ala Glu Arg Asn Gly Ser Gln Ser Thr Thr Ser Gln		
145	150	155
Ser Asn Asp Val Asp Lys Ser Gln Pro Ser Ile Pro Ala Gln Lys Val		
	165	170
Ile Pro Asn His Asp Lys Ala Ala Pro Thr Ser Thr Thr Pro Pro Ser		
	180	185
Asn Asp Lys Thr Ala Pro Lys Ser Thr Lys Ala Gln Asp Ala Thr Thr		
	195	200
Asp Lys His Pro Asn Gln Gln Asp Thr His Gln Pro Ala His Gln Ile		
	210	215
Ile Asp Ala Lys Gln Asp Asp Thr Val Arg Gln Ser Glu Gln Lys Pro		
225	230	235
Gln Val Gly Asp Leu Ser Lys His Ile Asp Gly Gln Asn Ser Pro Glu		
	245	250
Lys Pro Thr Asp Lys Asn Thr Asp Asn Lys Gln Leu Ile Lys Asp Ala		
	260	265
Leu Gln Ala Pro Lys Thr Arg Ser Thr Thr Asn Ala Ala Ala Asp Ala		
	275	280
Lys Lys Val Arg Pro Leu Lys Ala Asn Gln Val Gln Pro Leu Asn Lys		
	290	295
Tyr Pro Val Val Phe Val His Gly Phe Leu Gly Leu Val Gly Asp Asn		
305	310	315
Ala Pro Ala Leu Tyr Pro Asn Tyr Trp Gly Gly Asn Lys Phe Lys Val		
	325	330

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Ile Glu Glu Leu Arg Lys Gln Gly Tyr Asn Val His Gln Ala Ser Val
      340                      345                      350

Ser Ala Phe Gly Ser Asn Tyr Asp Arg Ala Val Glu Leu Tyr Tyr Tyr
      355                      360                      365

Ile Lys Gly Gly Arg Val Asp Tyr Gly Ala Ala His Ala Ala Lys Tyr
      370                      375                      380

Gly His Glu Arg Tyr Gly Lys Thr Tyr Lys Gly Ile Met Pro Asn Trp
      385                      390                      395                      400

Glu Pro Gly Lys Lys Val His Leu Val Gly His Ser Met Gly Gly Gln
      405                      410                      415

Thr Ile Arg Leu Met Glu Glu Phe Leu Arg Asn Gly Asn Lys Glu Glu
      420                      425                      430

Ile Ala Tyr His Lys Ala His Gly Gly Glu Ile Ser Pro Leu Phe Thr
      435                      440                      445

Gly Gly His Asn Asn Met Val Ala Ser Ile Thr Thr Leu Ala Thr Pro
      450                      455                      460

His Asn Gly Ser Gln Ala Ala Asp Lys Phe Gly Asn Thr Glu Ala Val
      465                      470                      475                      480

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

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

Glu Ser Tyr Ile Asp Tyr Ile Lys Arg Val Ser Lys Ser Lys Ile Trp
      515                      520                      525

Thr Ser Asp Asp Asn Ala Ala Tyr Asp Leu Thr Leu Asp Gly Ser Ala
      530                      535                      540

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

Tyr Thr Gly Val Ser Ser His Thr Gly Pro Leu Gly Tyr Glu Asn Pro
      565                      570                      575

Asp Leu Gly Thr Phe Phe Leu Met Ala Thr Thr Ser Arg Ile Ile Gly
      580                      585                      590

His Asp Ala Arg Glu Glu Trp Arg Lys Asn Asp Gly Val Val Pro Val
      595                      600                      605

Ile Ser Ser Leu His Pro Ser Asn Gln Pro Phe Val Asn Val Thr Asn
      610                      615                      620

Asp Glu Pro Ala Thr Arg Arg Gly Ile Trp Gln Val Lys Pro Ile Ile
      625                      630                      635                      640

Gln Gly Trp Asp His Val Asp Phe Ile Gly Val Asp Phe Leu Asp Phe
      645                      650                      655

Lys Arg Lys Gly Ala Glu Leu Ala Asn Phe Tyr Thr Gly Ile Ile Asn
      660                      665                      670

Asp Leu Leu Arg Val Glu Ala Thr Glu Ser Lys Gly Thr Gln Leu Lys
      675                      680                      685

Ala Ser
      690

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<210> SEQ ID NO 59

<211> LENGTH: 208

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 59

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

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Leu Thr Gly Cys Ala Ser Asp Gln Ser Asp Asn Glu Asp His His Thr
      20                      25                      30
Ser Thr Gly Ile His Ala Pro Lys Ser Ala Lys Lys Leu Glu Thr Lys
      35                      40                      45
Asp Ile Phe Asn Ser Asp Lys Lys Asn Ser Asp Ile Ser Asp Ala Glu
      50                      55                      60
Met Lys Gln Ala Ile Glu Lys Tyr Leu Ser Val Asn Ser Asp Ile Leu
      65                      70                      75                      80
Asp Asn Lys Tyr Ile Met Gln His Lys Leu Asp Lys Gln Ile Asp Ser
      85                      90                      95
Gln Thr Lys Val Thr Glu Lys Gln Ala Glu Thr Leu Ser His Leu Ser
      100                      105                      110
Asn Leu Ala Val Lys Asn Asp Leu His Phe Lys Lys Phe Val Thr Glu
      115                      120                      125
Asn Asn Ile Pro Lys Glu Tyr Lys Lys Pro Val Glu Leu Met Met Asn
      130                      135                      140
Tyr Phe Lys Ala Leu Asn Ser Thr Ile Ala Asn Val Asp Glu Asp Ile
      145                      150                      155                      160
Glu Lys Leu Ser Tyr Gln Pro Gln Asn Lys Ile Asn Val Val Asp Val
      165                      170                      175
Pro Thr Lys Tyr Ala Gly Asp Val Asn Lys Lys Gln Gln Asp Lys Ile
      180                      185                      190
Lys Asp Phe Leu Lys Ser Lys Gly Ile Lys Ser Asp Val Ile Asp Lys
      195                      200                      205

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<210> SEQ ID NO 60

<211> LENGTH: 261

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 60

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Met Lys Ser Ile Lys Arg Ile Gly Leu Cys Ile Ser Leu Leu Ile Leu
1      5      10      15
Ile Ile Phe Val Thr Ser Cys Asp Gly Asp Asn Lys Ile Ile Gly Asp
20     25     30
Ser Lys Glu Glu Gln Ile Lys Lys Ser Phe Ala Lys Thr Leu Asp Ile
35     40     45
Tyr Pro Ile Lys Asn Leu Glu Asp Leu Tyr Asp Lys Glu Gly Tyr Arg
50     55     60
Asp Gly Glu Phe Lys Lys Asp Asp Lys Gly Thr Trp Leu Ile Arg Ser
65     70     75     80
Glu Met Lys Ile Gln Leu Lys Gly Glu Asn Leu Glu Ser Arg Gly Ala
85     90     95
Val Leu Glu Ile Asn Arg Asn Thr Arg Thr Ala Lys Gly His Tyr Ile
100    105    110
Val Arg Glu Val Val Glu Asp Ser Asp Gly Met Thr His Asn His Thr
115    120    125
Lys Arg Tyr Pro Val Lys Met Glu Asn Asn Lys Met Ile Pro Leu Lys
130    135    140
Pro Ile Asp Asp Glu Lys Val Lys Lys Glu Ile Glu Glu Phe Asn Phe
145    150    155    160
Phe Val Gln Tyr Gly Asn Phe Lys Glu Leu Glu Asn Tyr Lys Glu Asp
165    170    175
Glu Val Ser Tyr Asn Pro Glu Val Pro Ile Tyr Ser Ala Lys Tyr Gln

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180	185	190
Leu Lys Asn Ser Asp Tyr Asn Val Glu Gln Leu Arg Lys Arg Tyr Asn		
195	200	205
Ile Pro Thr Gln Lys Ala Pro Lys Leu Leu Leu Lys Gly Ser Gly Asn		
210	215	220
Leu Lys Gly Ser Ser Val Gly Tyr Lys Asn Ile Glu Phe Thr Phe Ile		
225	230	235
Glu Asn Lys Glu Glu Asn Ile Tyr Phe Thr Asp Ser Ile Tyr Phe Asn		
245	250	255
Pro Ser Glu Asp Lys		
260		
<210> SEQ ID NO 61		
<211> LENGTH: 347		
<212> TYPE: PRT		
<213> ORGANISM: Staphylococcus sp		
<400> SEQUENCE: 61		
Met Asn Lys Asp Asn Lys Trp Thr Met Ile Thr Ala Leu Phe Ile Thr		
1	5	10
Val Ile Ser Val Leu Leu Ala Phe His Leu Lys Gln His Tyr Asp Gln		
20	25	30
Ile Thr Asn Glu Asn His Ala Asn Lys Asp Lys Ile Asn Ile Lys Asn		
35	40	45
Lys Asn Val Arg Ile Tyr Gln Asn Leu Thr Tyr Asn Arg Val Phe Pro		
50	55	60
Asn Ser Lys Leu Asp Ile Ile Thr Pro Val Asp Met Ser Ser Asn Ala		
65	70	75
Lys Leu Pro Val Ile Phe Trp Met His Gly Gly Gly Tyr Ile Ala Gly		
85	90	95
Asp Lys Gln Tyr Lys Asn Pro Leu Leu Ala Lys Ile Ala Glu Gln Gly		
100	105	110
Tyr Ile Val Val Asn Val Asn Tyr Ala Leu Ala Pro Gln Tyr Lys Tyr		
115	120	125
Pro Thr Pro Leu Ile Gln Met Asn Gln Ala Thr Gln Phe Ile Lys Glu		
130	135	140
Asn Lys Met Asn Leu Pro Ile Asp Phe Asn Gln Val Ile Ile Gly Gly		
145	150	155
Asp Ser Ala Gly Ala Gln Leu Ala Ser Gln Phe Thr Ala Ile Gln Thr		
165	170	175
Asn Asp Arg Leu Arg Glu Ala Met Lys Phe Asp Gln Ser Phe Lys Pro		
180	185	190
Ser Gln Ile Lys Gly Ala Ile Leu Phe Gly Gly Phe Tyr Asn Met Gln		
195	200	205
Thr Val Arg Glu Thr Glu Phe Pro Arg Ile Gln Leu Phe Met Lys Ser		
210	215	220
Tyr Thr Gly Glu Glu Asp Trp Glu Lys Ser Phe Lys Asn Ile Ser Gln		
225	230	235
Met Ser Thr Val Lys Gln Ser Thr Lys Asn Tyr Pro Pro Thr Phe Leu		
245	250	255
Ser Val Gly Asp Ser Asp Pro Phe Glu Ser Gln Asn Ile Glu Phe Ser		
260	265	270
Lys Lys Leu Gln Glu Leu Asn Val Pro Val Asp Thr Leu Phe Tyr Asp		
275	280	285

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Gly Thr His His Leu His His Gln Tyr Gln Phe His Leu Asn Lys Pro
 290 295 300

Glu Ser Ile Asp Asn Ile Lys Lys Val Leu Leu Phe Leu Ser Arg Asn
 305 310 315 320

Thr Ser Ser Ser Gly Ile Gln Thr Glu Glu Lys Pro Gln Ile Glu Asn
 325 330 335

Pro Ser Asn Glu Leu Pro Leu Asn Pro Leu Asn
 340 345

<210> SEQ ID NO 62
 <211> LENGTH: 265
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 62

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

Phe Leu Thr His His Asp Ala Gln Ala Ser Thr Gln His Thr Val Gln
 20 25 30

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

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

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

Thr Ser Pro Gln Ala Gly Ser Ala Ser Ser His Thr Val Gln Ala Gly
 85 90 95

Glu Ser Leu Asn Ile Ile Ala Ser Arg Tyr Gly Val Ser Val Asp Gln
 100 105 110

Leu Met Ala Ala Asn Asn Leu Arg Gly Tyr Leu Ile Met Pro Asn Gln
 115 120 125

Thr Leu Gln Ile Pro Asn Gly Gly Ser Gly Gly Thr Thr Pro Thr Ala
 130 135 140

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

Tyr Thr Ala Gly Gln Cys Thr Trp Tyr Val Phe Asp Arg Arg Ala Gln
 165 170 175

Ala Gly Ser Pro Ile Ser Thr Tyr Trp Ser Asp Ala Lys Tyr Trp Ala
 180 185 190

Gly Asn Ala Ala Asn Asp Gly Tyr Gln Val Asn Asn Thr Pro Ser Val
 195 200 205

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

Val Glu Arg Val Asn Gly Asp Gly Ser Ile Leu Ile Ser Glu Met Asn
 225 230 235 240

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

Glu Val Ser Ser Tyr Ala Phe Ile His
 260 265

<210> SEQ ID NO 63
 <211> LENGTH: 292
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 63

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

Ile Ser Ala Cys Gly Asn Lys Glu Lys Glu Ala Gln His Gln Phe Thr
      20      25      30

Lys Gln Phe Lys Asp Val Glu Gln Lys Gln Lys Glu Leu Gln His Val
      35      40      45

Met Asp Asn Ile His Leu Lys Glu Ile Asp His Leu Ser Lys Thr Asp
50      55      60

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

Lys Asn His Leu Ile Pro Lys Phe Glu Ala Tyr Tyr Lys Ser Ala Lys
      85      90      95

Asn Leu Pro Asp Asp Thr Met Lys Val Lys Lys Leu Lys Lys Glu Tyr
100      105      110

Met Thr Leu Ala Asn Glu Lys Lys Asp Ala Ile Tyr Gln Leu Lys Lys
115      120      125

Phe Ile Gly Leu Cys Asn Gln Ser Ile Lys Tyr Asn Glu Asp Ile Leu
130      135      140

Asp Tyr Thr Lys Gln Phe Glu Lys Asn Arg Tyr Lys Val Glu Ser Glu
145      150      155      160

Ile Lys Leu Ala Asp Asn Lys Ser Glu Ala Thr Asn Leu Thr Thr Lys
165      170      175

Leu Glu His Asn Asn Lys Ala Leu Arg Asp Thr Ala Lys Lys Asn Leu
180      185      190

Asp Asp Ser Lys Glu Asn Glu Val Lys Gly Ala Ile Lys Asn His Ile
195      200      205

Met Pro Met Ile Glu Lys Gln Ile Thr Asp Ile Asn Gln Thr Asn Ile
210      215      220

Ser Asp Lys His Val Asn Asn Ala Arg Lys Asn Ala Ile Glu Met Tyr
225      230      235      240

Tyr Ser Leu Gln Asn Tyr Tyr Asn Thr Arg Ile Glu Thr Ile Lys Val
245      250      255

Ser Glu Lys Leu Ser Lys Val Asp Val Asp Lys Leu Pro Lys Lys Gly
260      265      270

Ile Asp Ile Thr His Gly Asp Lys Ala Phe Glu Lys Lys Leu Glu Lys
275      280      285

Leu Glu Glu Lys
290

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<210> SEQ ID NO 64
<211> LENGTH: 242
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

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<400> SEQUENCE: 64

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

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

Lys Lys Lys Glu Asn Asp Asn Glu Glu Leu Asn Glu Glu Leu Lys Glu
35      40      45

Phe Lys Ser Lys Lys Asn Met Asp Ile Lys Ile Lys Gly Asp Thr Ile
50      55      60

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

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Met 1	Arg	Leu	Thr	Ile 5	Tyr	His	Thr	Asn	Asp 10	Ile	His	Ser	His	Leu 15	His
Glu	Tyr	Glu	Arg 20	Leu	Lys	Ala	Tyr	Met 25	Ala	Glu	His	Arg	Pro 30	Arg	Leu
Asn	His	Pro 35	Ser	Leu	Tyr	Val	Asp 40	Leu	Gly	Asp	His	Val 45	Asp	Leu	Ser
Ala	Pro 50	Ile	Thr	Glu	Ala	Thr 55	Leu	Gly	Lys	Lys	Asn 60	Val	Ala	Leu	Leu
Asn 65	Glu	Ala	Lys	Cys	Asp 70	Val	Ala	Thr	Ile	Gly 75	Asn	Asn	Glu	Gly	Met 80
Thr	Ile	Ser	Tyr 85	Ala	Leu	Asn	His	Leu	Tyr	Asp	Glu	Ala	Lys 95	Phe	
Ile	Val	Thr	Cys 100	Ser	Asn	Val	Ile	Asp 105	Glu	Ser	Gly	His 110	Leu	Pro	Asn
Asn	Ile 115	Val	Ser	Ser	Tyr	Ile	Lys 120	Asp	Ile	Asp	Gly	Val 125	Lys	Ile	Leu
Phe 130	Val	Ala	Ala	Thr	Ala	Pro 135	Phe	Thr	Pro	Phe	Tyr	Arg 140	Ala	Leu	Asn
Trp 145	Ile	Val	Thr	Asp 150	Pro	Leu	Glu	Ser	Ile	Lys 155	Glu	Glu	Ile	Glu	Leu 160
Gln	Arg	Gly	Lys 165	Phe	Asp	Val	Leu	Ile	Val 170	Leu	Ser	His	Cys	Gly 175	Ile
Phe	Phe	Asp 180	Glu	Thr	Leu	Cys	Gln	Glu 185	Leu	Pro	Glu	Ile	Asp 190	Val	Ile
Phe	Gly 195	Ser	His	Thr	His	His	Tyr 200	Phe	Glu	His	Gly	Glu 205	Ile	Asn	Asn

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

<210> SEQ ID NO 66

<211> LENGTH: 774

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 66

Met Glu Trp Thr Leu Val Asp Ile Gly Lys Lys His Val Ile Pro Lys
 1 5 10 15
 Ser Gln Tyr Arg Arg Lys Arg Arg Glu Phe Phe His Asn Glu Asp Arg
 20 25 30
 Glu Glu Asn Leu Asn Gln His Gln Asp Lys Gln Asn Ile Asp Asn Thr
 35 40 45
 Thr Ser Lys Lys Ala Asp Lys Gln Ile His Lys Asp Ser Ile Asp Lys
 50 55 60
 His Glu Arg Phe Lys Asn Ser Leu Ser Ser His Leu Glu Gln Arg Asn
 65 70 75 80
 Arg Asp Val Asn Glu Asn Lys Ala Glu Glu Ser Lys Ser Asn Gln Asp
 85 90 95
 Ser Lys Ser Ala Tyr Asn Arg Asp His Tyr Leu Thr Asp Asp Val Ser
 100 105 110
 Lys Lys Gln Asn Ser Leu Asp Ser Val Asp Gln Asp Thr Glu Lys Ser
 115 120 125
 Lys Tyr Tyr Glu Gln Asn Ser Glu Ala Thr Leu Ser Thr Lys Ser Thr

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130					135					140					
Asp 145	Lys	Val	Glu	Ser	Thr 150	Glu	Met	Arg	Lys	Leu 155	Ser	Ser	Asp	Lys	Asn 160
Lys	Val	Gly	His	Glu 165	Glu	Gln	His	Val	Leu 170	Ser	Lys	Pro	Ser	Glu	His 175
Asp	Lys	Glu	Thr	Arg 180	Ile	Asp	Ser	Glu 185	Ser	Ser	Arg	Thr	Asp 190	Ser	Asp
Ser	Ser	Met 195	Gln	Thr	Glu	Lys	Ile 200	Lys	Lys	Asp	Ser	Ser 205	Asp	Gly	Asn
Lys	Ser 210	Ser	Asn	Leu	Lys 215	Ser	Glu	Val	Ile	Ser 220	Asp	Lys	Ser	Asn	Thr
Val 225	Pro	Lys	Leu	Ser	Glu 230	Ser	Asp	Asp	Glu	Val 235	Asn	Asn	Gln	Lys	Pro 240
Leu	Thr	Leu	Pro	Glu 245	Glu	Gln	Lys	Leu	Lys 250	Arg	Gln	Gln	Ser	Gln	Asn 255
Glu	Gln	Thr	Lys 260	Thr	Tyr	Thr	Tyr	Gly 265	Asp	Ser	Glu	Gln	Asn 270	Asp	Lys
Ser	Asn	His 275	Glu	Asn	Asp	Leu	Ser 280	His	His	Ile	Pro	Ser 285	Ile	Ser	Asp
Asp	Lys 290	Asp	Asn	Val	Met 295	Arg	Glu	Asn	His	Ile	Val 300	Asp	Asp	Asn	Pro
Asp 305	Asn	Asp	Ile	Asn	Thr 310	Pro	Ser	Leu	Ser	Lys 315	Thr	Asp	Asp	Asp	Arg 320
Lys	Leu	Asp	Glu	Lys 325	Ile	His	Val	Glu	Asp 330	Lys	His	Lys	Gln	Asn	Ala 335
Asp	Ser	Ser	Glu 340	Thr	Val	Gly	Tyr	Gln 345	Ser	Gln	Ser	Thr	Ala 350	Ser	His
Arg	Ser	Thr 355	Glu	Lys	Arg	Asn	Ile 360	Ser	Ile	Asn	Asp	His 365	Asp	Lys	Leu
Asn	Gly 370	Gln	Lys	Thr	Asn	Thr 375	Lys	Thr	Ser	Ala	Asn 380	Asn	Asn	Gln	Lys
Lys 385	Ala	Thr	Ser	Lys	Leu 390	Asn	Lys	Gly	Arg	Ala 395	Thr	Asn	Asn	Asn	Tyr 400
Ser	Asp	Ile	Leu	Lys 405	Lys	Phe	Trp	Met	Met 410	Tyr	Trp	Pro	Lys	Leu	Val 415
Ile	Leu	Met	Gly 420	Ile	Ile	Ile	Leu	Ile 425	Val	Ile	Leu	Asn	Ala 430	Ile	Phe
Asn	Asn	Val 435	Asn	Lys	Asn	Asp	Arg 440	Met	Asn	Asp	Asn	Asn 445	Asp	Ala	Asp
Ala	Gln	Lys 450	Tyr	Thr	Thr	Thr 455	Met	Lys	Asn	Ala	Asn 460	Asn	Thr	Val	Lys
Ser 465	Val	Val	Thr	Val	Glu 470	Asn	Glu	Thr	Ser	Lys 475	Asp	Ser	Ser	Leu	Pro 480
Lys	Asp	Lys	Ala	Ser 485	Gln	Asp	Glu	Val	Gly 490	Ser	Gly	Val	Val	Tyr	Lys 495
Lys	Ser	Gly	Asp 500	Thr	Leu	Tyr	Ile	Val 505	Thr	Asn	Ala	His 510	Val	Val	Gly
Asp	Lys	Glu 515	Asn	Gln	Lys	Ile	Thr 520	Phe	Ser	Asn	Asn	Lys 525	Ser	Val	Val
Gly	Lys 530	Val	Leu	Gly	Lys 535	Asp	Lys	Trp	Ser	Asp	Leu 540	Ala	Val	Val	Lys
Ala 545	Thr	Ser	Ser	Asp	Ser 550	Ser	Val	Lys	Glu	Ile 555	Ala	Ile	Gly	Asp	Ser 560

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Asn Asn Leu Val Leu Gly Glu Pro Ile Leu Val Val Gly Asn Pro Leu
 565 570 575
 Gly Val Asp Phe Lys Gly Thr Val Thr Glu Gly Ile Ile Ser Gly Leu
 580 585 590
 Asn Arg Asn Val Pro Ile Asp Phe Asp Lys Asp Asn Lys Tyr Asp Met
 595 600 605
 Leu Met Lys Ala Phe Gln Ile Asp Ala Ser Val Asn Pro Gly Asn Ser
 610 615 620
 Gly Gly Ala Val Val Asn Arg Glu Gly Lys Leu Ile Gly Val Val Ala
 625 630 635 640
 Ala Lys Ile Ser Met Pro Asn Val Glu Asn Met Ser Phe Ala Ile Pro
 645 650 655
 Val Asn Glu Val Gln Lys Ile Val Lys Asp Leu Glu Thr Lys Gly Lys
 660 665 670
 Ile Asp Tyr Pro Asp Val Gly Val Lys Met Lys Asn Ile Val Ser Leu
 675 680 685
 Asn Ser Phe Glu Arg Gln Ala Val Lys Leu Pro Gly Lys Val Lys Asn
 690 695 700
 Gly Val Val Val Asp Gln Val Asp Asn Asn Gly Leu Ala Asp Gln Ser
 705 710 715 720
 Gly Leu Lys Lys Gly Asp Val Ile Thr Glu Leu Asp Gly Lys Leu Leu
 725 730 735
 Glu Asp Asp Leu Arg Phe Arg Gln Ile Ile Phe Ser His Lys Asp Asp
 740 745 750
 Leu Lys Ser Ile Thr Ala Lys Ile Tyr Arg Asp Gly Lys Glu Lys Glu
 755 760 765
 Ile Asn Ile Lys Leu Lys
 770

<210> SEQ ID NO 67

<211> LENGTH: 393

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 67

Met Asn Ser Ser Cys Lys Ser Arg Val Phe Asn Ile Ile Ser Ile Ile
 1 5 10 15
 Met Val Ser Met Leu Ile Leu Ser Leu Gly Ala Phe Ala Asn Asn Asn
 20 25 30
 Lys Ala Lys Ala Asp Ser His Ser Lys Gln Leu Glu Ile Asn Val Lys
 35 40 45
 Ser Asp Lys Val Pro Gln Lys Val Lys Asp Leu Ala Gln Gln Gln Phe
 50 55 60
 Ala Gly Tyr Ala Lys Ala Leu Asp Lys Gln Ser Asn Ala Lys Thr Gly
 65 70 75 80
 Lys Tyr Glu Leu Gly Glu Ala Phe Lys Ile Tyr Lys Phe Asn Gly Glu
 85 90 95
 Glu Asp Asn Ser Tyr Tyr Tyr Pro Val Ile Lys Asp Gly Lys Ile Val
 100 105 110
 Tyr Thr Leu Thr Leu Ser Pro Lys Asn Lys Asp Asp Leu Asn Lys Ser
 115 120 125
 Lys Glu Asp Met Asn Tyr Ser Val Lys Ile Ser Asn Phe Ile Ala Lys
 130 135 140
 Asp Leu Asp Gln Ile Lys Asp Lys Asn Ser Asn Ile Thr Val Leu Thr

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145	150	155	160
Asp Glu Lys Gly Phe Tyr Phe Glu Glu Asp Gly Lys Val Arg Leu Val	165	170	175
Lys Ala Thr Pro Leu Pro Gly Asn Val Lys Glu Lys Glu Ser Ala Lys	180	185	190
Thr Val Ser Ala Lys Leu Lys Gln Glu Leu Lys Asn Thr Val Thr Pro	195	200	205
Thr Lys Val Glu Glu Asn Glu Ala Ile Gln Glu Asp Gln Val Gln Tyr	210	215	220
Glu Asn Thr Leu Lys Asn Phe Lys Ile Arg Glu Gln Gln Phe Asp Asn	225	230	235
Ser Trp Cys Ala Gly Phe Ser Met Ala Ala Leu Leu Asn Ala Thr Lys	245	250	255
Asn Thr Asp Thr Tyr Asn Ala His Asp Ile Met Arg Thr Leu Tyr Pro	260	265	270
Glu Val Ser Glu Gln Asp Leu Pro Asn Cys Ala Thr Phe Pro Asn Gln	275	280	285
Met Ile Glu Tyr Gly Lys Ser Gln Gly Arg Asp Ile His Tyr Gln Glu	290	295	300
Gly Val Pro Ser Tyr Glu Gln Val Asp Gln Leu Thr Lys Asp Asn Val	305	310	315
Gly Ile Met Ile Leu Ala Gln Ser Val Ser Gln Asn Pro Asn Asp Pro	325	330	335
His Leu Gly His Ala Leu Ala Val Val Gly Asn Ala Lys Ile Asn Asp	340	345	350
Gln Glu Lys Leu Ile Tyr Trp Asn Pro Trp Asp Thr Glu Leu Ser Ile	355	360	365
Gln Asp Ala Asp Ser Ser Leu Leu His Leu Ser Phe Asn Arg Asp Tyr	370	375	380
Asn Trp Tyr Gly Ser Met Ile Gly Tyr	385	390	

<210> SEQ ID NO 68

<211> LENGTH: 336

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 68

Met Lys Gly Lys Phe Leu Lys Val Ser Ser Leu Phe Val Ala Thr Leu	1	5	10	15
Thr Thr Ala Thr Leu Val Ser Ser Pro Ala Ala Asn Ala Leu Ser Ser	20	25	30	
Lys Ala Met Asp Asn His Pro Gln Gln Thr Gln Ser Ser Lys Gln Gln	35	40	45	
Thr Pro Lys Ile Gln Lys Gly Gly Asn Leu Lys Pro Leu Glu Gln Arg	50	55	60	
Glu His Ala Asn Val Ile Leu Pro Asn Asn Asp Arg His Gln Ile Thr	65	70	75	80
Asp Thr Thr Asn Gly His Tyr Ala Pro Val Thr Tyr Ile Gln Val Glu	85	90	95	
Ala Pro Thr Gly Thr Phe Ile Ala Ser Gly Val Val Val Gly Lys Asp	100	105	110	
Thr Leu Leu Thr Asn Lys His Val Val Asp Ala Thr His Gly Asp Pro	115	120	125	

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His	Ala	Leu	Lys	Ala	Phe	Pro	Ser	Ala	Ile	Asn	Gln	Asp	Asn	Tyr	Pro
130						135					140				
Asn	Gly	Gly	Phe	Thr	Ala	Glu	Gln	Ile	Thr	Lys	Tyr	Ser	Gly	Glu	Gly
145					150					155					160
Asp	Leu	Ala	Ile	Val	Lys	Phe	Ser	Pro	Asn	Glu	Gln	Asn	Lys	His	Ile
			165						170					175	
Gly	Glu	Val	Val	Lys	Pro	Ala	Thr	Met	Ser	Asn	Asn	Ala	Glu	Thr	Gln
		180						185					190		
Val	Asn	Gln	Asn	Ile	Thr	Val	Thr	Gly	Tyr	Pro	Gly	Asp	Lys	Pro	Val
	195						200					205			
Ala	Thr	Met	Trp	Glu	Ser	Lys	Gly	Lys	Ile	Thr	Tyr	Leu	Lys	Gly	Glu
210						215					220				
Ala	Met	Gln	Tyr	Asp	Leu	Ser	Thr	Thr	Gly	Gly	Asn	Ser	Gly	Ser	Pro
225					230					235					240
Val	Phe	Asn	Glu	Lys	Asn	Glu	Val	Ile	Gly	Ile	His	Trp	Gly	Gly	Val
			245						250					255	
Pro	Asn	Glu	Phe	Asn	Gly	Ala	Val	Phe	Ile	Asn	Glu	Asn	Val	Arg	Asn
			260					265					270		
Phe	Leu	Lys	Gln	Asn	Ile	Glu	Asp	Ile	His	Phe	Ala	Asn	Asp	Asp	Gln
	275						280					285			
Pro	Asn	Asn	Pro	Asp	Asn	Pro	Asp	Asn	Pro	Asn	Asn	Pro	Asp	Asn	Pro
290					295						300				
Asn	Asn	Pro	Asp	Glu	Pro	Asn	Asn	Pro	Asp	Asn	Pro	Asn	Asn	Pro	Asp
305					310					315					320
Asn	Pro	Asp	Asn	Gly	Asp	Asn	Asn	Asn	Ser	Asp	Asn	Pro	Asp	Ala	Ala
			325					330						335	

<210> SEQ ID NO 69

<211> LENGTH: 397

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 69

Met	Lys	Phe	Asn	Lys	Val	Lys	Leu	Val	Ile	His	Ala	Cys	Val	Leu	Leu
1			5					10					15		
Phe	Ile	Ile	Ile	Ser	Ile	Ala	Leu	Ile	Phe	His	Arg	Leu	Gln	Thr	Lys
	20						25					30			
Thr	His	Ser	Ile	Asp	Pro	Ile	His	Lys	Glu	Thr	Lys	Leu	Ser	Asp	Asn
	35					40					45				
Glu	Lys	Tyr	Leu	Val	Asp	Arg	Asn	Lys	Glu	Lys	Val	Ala	Pro	Ser	Lys
50					55						60				
Leu	Lys	Glu	Val	Tyr	Asn	Ser	Lys	Asp	Pro	Lys	Tyr	Lys	Lys	Ile	Asp
65					70				75					80	
Lys	Tyr	Leu	Gln	Ser	Ser	Leu	Phe	Asn	Gly	Ser	Val	Ala	Ile	Tyr	Glu
		85						90					95		
Asn	Gly	Lys	Leu	Lys	Met	Ser	Lys	Gly	Tyr	Gly	Tyr	Gln	Asp	Phe	Glu
	100							105					110		
Lys	Gly	Ile	Lys	Asn	Thr	Pro	Asn	Thr	Met	Phe	Leu	Ile	Gly	Ser	Ala
	115						120					125			
Gln	Lys	Phe	Ser	Thr	Gly	Leu	Leu	Leu	Lys	Gln	Leu	Glu	Glu	Glu	His
130						135					140				
Lys	Ile	Asn	Ile	Asn	Asp	Pro	Val	Ser	Lys	Tyr	Leu	Pro	Trp	Phe	Lys
145					150					155					160
Thr	Ser	Lys	Pro	Ile	Pro	Leu	Lys	Asp	Leu	Met	Leu	His	Gln	Ser	Gly
			165						170					175	

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Leu Tyr Lys Tyr Lys Ser Ser Lys Asp Tyr Lys Asn Leu Asp Gln Ala
    180                      185                      190

Val Lys Ala Ile Gln Lys Arg Gly Ile Asp Pro Lys Lys Tyr Lys Lys
    195                      200                      205

His Met Tyr Asn Asp Gly Asn Tyr Leu Val Leu Ala Lys Val Ile Glu
    210                      215                      220

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

Asp Pro Leu Lys Leu Gln His Thr Ala Phe Tyr Asp Glu Gln Pro Phe
    245                      250                      255

Lys Lys Tyr Leu Ala Lys Gly Tyr Ala Tyr Asn Ser Thr Gly Leu Ser
    260                      265                      270

Phe Leu Arg Pro Asn Ile Leu Asp Gln Tyr Tyr Gly Ala Gly Asn Leu
    275                      280                      285

Tyr Met Thr Pro Thr Asp Met Gly Lys Leu Ile Thr Gln Ile Gln Gln
    290                      295                      300

Tyr Lys Leu Phe Ser Pro Lys Ile Thr Asn Pro Leu Leu His Glu Phe
    305                      310                      315                      320

Gly Thr Lys Lys Tyr Pro Asp Glu Tyr Arg Tyr Gly Phe Tyr Ala Lys
    325                      330                      335

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

Val Tyr Tyr Asn Asp Lys Tyr Val Val Val Leu Ala Leu Asn Val Lys
    355                      360                      365

Gly Asn Asn Glu Val Arg Ile Lys His Ile Tyr Asn Asp Ile Leu Lys
    370                      375                      380

Gln Asn Lys Pro Tyr Asn Thr Lys Gly Val Ile Val Gln
    385                      390                      395

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<210> SEQ ID NO 70

<211> LENGTH: 358

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 70

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Met Arg Asn Val Lys Gln Ile Ala Thr Lys Ser Ile Ile Ala Ile Ile
1      5      10      15

Ser Leu Gly Ile Leu Thr Tyr Thr Thr Met Ile Gly Ser Val Leu Ala
20     25     30

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

Asp Lys Thr Glu Leu Thr Thr Ser Ile Phe Asp Glu Lys Ile Lys Glu
50     55     60

Asn Lys Ala Leu Glu Leu Leu Ile Phe Asn Gln Glu Asn Lys Asn Val
65     70     75     80

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

Met Thr Gly Lys Ile Tyr Leu Gln Val Lys Leu Lys Gly Gln Ile Asp
100    105    110

Lys Glu Gln Leu Val Phe Gln Asn Asp Lys Asn Glu Glu Phe Pro Phe
115    120    125

Val Ile Lys Asp Glu Lys Asp Asp Thr Ile Val Arg Ile Leu Ile Glu
130    135    140

Gln His Met Asp Lys Ile Asn Met His Val Lys Thr Leu Ala Glu Lys

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145	150	155	160
Lys Asn Leu Asp Asn Lys Glu Met Val Tyr Ser Ile His Phe Lys Glu			
	165	170	175
Lys Lys Val Gln His Asp Asp Ala Lys Glu Val Pro Ser Lys His Gln			
	180	185	190
Asn Gln Glu Asn Asn Gln Asp Gln Leu Lys Lys Asp Ile Asp Asp Lys			
	195	200	205
Lys Asp Ser Gln Lys Ser Asp Thr Lys Glu Arg Arg Thr Ser Leu Phe			
	210	215	220
Thr Glu Lys Gly Leu Asn Asp Ile Pro Val Gln Lys Asp Lys Val Gln			
	225	230	235
Gln Asp Ser Asn Lys Lys Ile Glu Asn Glu Arg Pro Lys Ala Ser Gly			
	245	250	255
Thr Leu Lys Val Glu Asn Ser Pro Pro Thr Ile Lys Lys Val Glu Asn			
	260	265	270
Asn His Lys Glu Gln Pro Lys His Lys Asp Glu Lys Ser Lys Lys Glu			
	275	280	285
Lys Lys Lys Val Val Glu Lys Glu Lys Ala Leu Pro Ala Phe Asn Arg			
	290	295	300
Asp Asp Asp Ser Lys Asn Ser Ser Gln Leu Ser Ser Asp Ile Lys Glu			
	305	310	315
Leu Asp Glu Pro Asn His Lys Lys Gln Tyr Met Leu Phe Ala Ala Gly			
	325	330	335
Ile Val Leu Ala Thr Ile Leu Leu Ile Ser Ala His Leu Tyr Ser Arg			
	340	345	350
Lys Arg Gly Asn Gln Val			
	355		

<210> SEQ ID NO 71
 <211> LENGTH: 282
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 71

Met Ile Ser Val Val Ile Leu Thr Ser Cys Gln Ser Ser Ser Ser Gln			
1	5	10	15
Glu Ser Thr Lys Ser Gly Glu Phe Arg Ile Val Pro Thr Thr Val Ala			
	20	25	30
Leu Thr Met Thr Leu Asp Lys Leu Asp Leu Pro Ile Val Gly Lys Pro			
	35	40	45
Thr Ser Tyr Lys Thr Leu Pro Asn Arg Tyr Lys Asp Val Pro Glu Ile			
	50	55	60
Gly Gln Pro Met Glu Pro Asn Val Glu Ala Val Lys Lys Leu Lys Pro			
	65	70	75
Thr His Val Leu Ser Val Ser Thr Ile Lys Asp Glu Met Gln Pro Phe			
	85	90	95
Tyr Lys Gln Leu Asn Met Lys Gly Tyr Phe Tyr Asp Phe Asp Ser Leu			
	100	105	110
Lys Gly Met Gln Lys Ser Ile Thr Gln Leu Gly Asp Gln Phe Asn Arg			
	115	120	125
Lys Ala Gln Ala Lys Glu Leu Asn Asp His Leu Asn Ser Val Lys Gln			
	130	135	140
Lys Ile Glu Asn Lys Ala Ala Lys Gln Lys Lys His Pro Lys Val Leu			
	145	150	155
			160

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

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

Val Lys Asp Arg Gln Tyr Ile Ser Ser Asn Thr Glu Asn Leu Leu Asn
      195                      200                      205

Ile Asn Pro Asp Ile Ile Leu Arg Leu Pro His Gly Met Pro Glu Glu
      210                      215                      220

Val Lys Lys Met Phe Gln Lys Glu Phe Lys Gln Asn Asp Ile Trp Lys
      225                      230                      235                      240

His Phe Lys Ala Val Lys Asn Asn His Val Tyr Asp Leu Glu Glu Val
      245                      250                      255

Pro Phe Gly Ile Thr Ala Asn Val Asp Ala Asp Lys Ala Met Thr Gln
      260                      265                      270

Leu Tyr Asp Leu Phe Tyr Lys Asp Lys Lys
      275                      280

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<210> SEQ ID NO 72

<211> LENGTH: 244

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 72

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

Ile Ile Ile Ile Phe Gly Tyr Lys Ile Val Gln Thr Tyr Ile Glu Asp
 20      25      30

Lys Gln Glu Arg Ala Asn Tyr Glu Lys Leu Gln Gln Lys Phe Gln Met
 35      40      45

Leu Met Ser Lys His Gln Glu His Val Arg Pro Gln Phe Glu Ser Leu
 50      55      60

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

Ser Leu Asn Tyr Pro Val Leu Gln Gly Lys Thr Asn His Asp Tyr Leu
 85      90      95

Asn Leu Asp Phe Glu Arg Glu His Arg Arg Lys Gly Ser Ile Phe Met
100      105      110

Asp Phe Arg Asn Glu Leu Lys Asn Leu Asn His Asn Thr Ile Leu Tyr
115      120      125

Gly His His Val Gly Asp Asn Thr Met Phe Asp Val Leu Glu Asp Tyr
130      135      140

Leu Lys Gln Ser Phe Tyr Glu Lys His Lys Ile Ile Glu Phe Asp Asn
145      150      155      160

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

Thr Lys Asp Asn Tyr Ile Arg Thr Asp Phe Glu Asn Asp Gln Asp Tyr
180      185      190

Gln Gln Phe Leu Asp Glu Thr Lys Arg Lys Ser Val Ile Asn Ser Asp
195      200      205

Val Asn Val Thr Val Lys Asp Arg Ile Met Thr Leu Ser Thr Cys Glu
210      215      220

Asp Ala Tyr Ser Glu Thr Thr Lys Arg Ile Val Val Val Ala Lys Ile
225      230      235      240

Ile Lys Val Ser

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<210> SEQ ID NO 73
<211> LENGTH: 238
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 73

Met Ser Lys Asn Ile Thr Lys Asn Ile Ile Leu Thr Thr Thr Leu Leu
1      5      10      15
Leu Leu Gly Thr Val Leu Pro Gln Asn Gln Lys Pro Val Phe Ser Phe
20     25     30
Tyr Ser Glu Ala Lys Ala Tyr Ser Ile Gly Gln Asp Glu Thr Asn Ile
35     40     45
Asn Glu Leu Ile Lys Tyr Tyr Thr Gln Pro His Phe Ser Phe Ser Asn
50     55     60
Lys Trp Leu Tyr Gln Tyr Asp Asn Gly Asn Ile Tyr Val Glu Leu Lys
65     70     75     80
Arg Tyr Ser Trp Ser Ala His Ile Ser Leu Trp Gly Ala Glu Ser Trp
85     90     95
Gly Asn Ile Asn Gln Leu Lys Asp Arg Tyr Val Asp Val Phe Gly Leu
100    105    110
Lys Asp Lys Asp Thr Asp Gln Leu Trp Trp Ser Tyr Arg Glu Thr Phe
115    120    125
Thr Gly Gly Val Thr Pro Ala Ala Lys Pro Ser Asp Lys Thr Tyr Asn
130    135    140
Leu Phe Val Gln Tyr Lys Asp Lys Leu Gln Thr Ile Ile Gly Ala His
145    150    155    160
Lys Ile Tyr Gln Gly Asn Lys Pro Val Leu Thr Leu Lys Glu Ile Asp
165    170    175
Phe Arg Ala Arg Glu Ala Leu Ile Lys Asn Lys Ile Leu Tyr Asn Glu
180    185    190
Asn Arg Asn Lys Gly Lys Leu Lys Ile Thr Gly Gly Gly Asn Asn Tyr
195    200    205
Thr Ile Asp Leu Ser Lys Arg Leu His Ser Asp Leu Ala Asn Val Tyr
210    215    220
Val Lys Asn Pro Asn Lys Ile Thr Val Asp Val Leu Phe Asp
225    230    235

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<210> SEQ ID NO 74
<211> LENGTH: 241
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 74

Met Asn Asn Asn Ile Thr Lys Lys Ile Ile Leu Ser Thr Thr Leu Leu
1      5      10      15
Leu Leu Gly Thr Ala Ser Thr Gln Phe Pro Asn Thr Pro Ile Asn Ser
20     25     30
Ser Ser Glu Ala Lys Ala Tyr Tyr Ile Asn Gln Asn Glu Thr Asn Val
35     40     45
Asn Glu Leu Thr Lys Tyr Tyr Ser Gln Lys Tyr Leu Thr Phe Ser Asn
50     55     60
Ser Thr Leu Trp Gln Lys Asp Asn Gly Thr Ile His Ala Thr Leu Leu
65     70     75     80
Gln Phe Ser Trp Tyr Ser His Ile Gln Val Tyr Gly Pro Glu Ser Trp
85     90     95

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Gly	Asn	Ile	Asn	Gln	Leu	Arg	Asn	Lys	Ser	Val	Asp	Ile	Phe	Gly	Ile
			100					105					110		
Lys	Asp	Gln	Glu	Thr	Ile	Asp	Ser	Phe	Ala	Leu	Ser	Gln	Glu	Thr	Phe
		115					120					125			
Thr	Gly	Gly	Val	Thr	Pro	Ala	Ala	Thr	Ser	Asn	Asp	Lys	His	Tyr	Lys
	130					135					140				
Leu	Asn	Val	Thr	Tyr	Lys	Asp	Lys	Ala	Glu	Thr	Phe	Thr	Gly	Gly	Phe
	145				150					155					160
Pro	Val	Tyr	Glu	Gly	Asn	Lys	Pro	Val	Leu	Thr	Leu	Lys	Glu	Leu	Asp
			165						170					175	
Phe	Arg	Ile	Arg	Gln	Thr	Leu	Ile	Lys	Ser	Lys	Lys	Leu	Tyr	Asn	Asn
			180					185					190		
Ser	Tyr	Asn	Lys	Gly	Gln	Ile	Lys	Ile	Thr	Gly	Ala	Asp	Asn	Asn	Tyr
		195					200					205			
Thr	Ile	Asp	Leu	Ser	Lys	Arg	Leu	Pro	Ser	Thr	Asp	Ala	Asn	Arg	Tyr
	210					215					220				
Val	Lys	Lys	Pro	Gln	Asn	Ala	Lys	Ile	Glu	Val	Ile	Leu	Glu	Lys	Ser
	225				230					235					240

Asn

<210> SEQ ID NO 75

<211> LENGTH: 565

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 75

Met	Ala	Tyr	Asp	Gly	Leu	Phe	Thr	Lys	Lys	Met	Val	Glu	Ser	Leu	Gln
1				5					10					15	
Phe	Leu	Thr	Thr	Gly	Arg	Val	His	Lys	Ile	Asn	Gln	Pro	Asp	Asn	Asp
		20						25					30		
Thr	Ile	Leu	Met	Val	Val	Arg	Gln	Asn	Arg	Gln	Asn	His	Gln	Leu	Leu
		35				40						45			
Leu	Ser	Ile	His	Pro	Asn	Phe	Ser	Arg	Leu	Gln	Leu	Thr	Thr	Lys	Lys
	50					55					60				
Tyr	Asp	Asn	Pro	Phe	Asn	Pro	Pro	Met	Phe	Ala	Arg	Val	Phe	Arg	Lys
	65				70					75				80	
His	Leu	Glu	Gly	Gly	Ile	Ile	Glu	Ser	Ile	Lys	Gln	Ile	Gly	Asn	Asp
			85					90						95	
Arg	Arg	Ile	Glu	Ile	Asp	Ile	Lys	Ser	Lys	Asp	Glu	Ile	Gly	Asp	Thr
		100					105						110		
Ile	Tyr	Arg	Thr	Val	Ile	Leu	Glu	Ile	Met	Gly	Lys	His	Ser	Asn	Leu
	115					120						125			
Ile	Leu	Val	Asp	Glu	Asn	Arg	Lys	Ile	Ile	Glu	Gly	Phe	Lys	His	Leu
	130					135					140				
Thr	Pro	Asn	Thr	Asn	His	Tyr	Arg	Thr	Val	Met	Pro	Gly	Phe	Asn	Tyr
	145				150					155				160	
Glu	Ala	Pro	Pro	Thr	Gln	His	Lys	Ile	Asn	Pro	Tyr	Asp	Ile	Thr	Gly
			165					170						175	
Ala	Glu	Val	Leu	Lys	Tyr	Ile	Asp	Phe	Asn	Ala	Gly	Asn	Ile	Ala	Lys
			180					185					190		
Gln	Leu	Leu	Asn	Gln	Phe	Glu	Gly	Phe	Ser	Pro	Leu	Ile	Thr	Asn	Glu
	195						200					205			
Ile	Val	Ser	Arg	Arg	Gln	Phe	Met	Thr	Ser	Ser	Thr	Leu	Pro	Glu	Ala
	210					215					220				

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Phe	Asp	Glu	Val	Met	Ala	Glu	Thr	Lys	Leu	Pro	Pro	Thr	Pro	Ile	Phe	225	230	235	240
His	Lys	Asn	His	Glu	Thr	Gly	Lys	Glu	Asp	Phe	Tyr	Phe	Ile	Lys	Leu	245	250	255	
Asn	Gln	Phe	Asn	Asp	Asp	Thr	Val	Thr	Tyr	Asp	Ser	Leu	Asn	Asp	Leu	260	265	270	
Leu	Asp	Arg	Phe	Tyr	Asp	Ala	Arg	Gly	Glu	Arg	Glu	Arg	Val	Lys	Gln	275	280	285	
Arg	Ala	Asn	Asp	Leu	Val	Arg	Phe	Val	Gln	Gln	Gln	Leu	His	Lys	Tyr	290	295	300	
Gln	Asn	Lys	Leu	Ala	Lys	Leu	Ile	Glu	Glu	Tyr	Glu	Gln	Ser	Lys	Asn	305	310	315	320
Lys	Asp	Thr	Glu	Gln	Leu	Tyr	Gly	Glu	Leu	Ile	Thr	Ala	Asn	Ile	Tyr	325	330	335	
Arg	Ile	Lys	Gln	Gly	Asp	Lys	Glu	Val	Thr	Ala	Leu	Asn	Tyr	Tyr	Thr	340	345	350	
Asn	Glu	Glu	Val	Val	Ile	Pro	Leu	Asn	Pro	Thr	Lys	Ser	Pro	Ser	Ala	355	360	365	
Asn	Ala	Gln	Tyr	Tyr	Tyr	Lys	Gln	Tyr	Asn	Arg	Met	Lys	Thr	Arg	Glu	370	375	380	
Arg	Glu	Leu	Gln	His	Gln	Ile	Gln	Leu	Thr	Lys	Asp	Asn	Ile	Asp	Tyr	385	390	395	400
Phe	Ser	Thr	Ile	Glu	Gln	Gln	Leu	His	His	Ile	Ser	Val	His	Asp	Ile	405	410	415	
Asp	Glu	Ile	Arg	Asp	Glu	Leu	Ala	Glu	Gln	Gly	Phe	Met	Lys	Gln	Arg	420	425	430	
Lys	Asn	Gln	Thr	Lys	Lys	Lys	Lys	Ala	Gln	Ile	Gln	Leu	Gln	His	Tyr	435	440	445	
Val	Ser	Thr	Asp	Gly	Asp	Asp	Ile	Tyr	Val	Gly	Lys	Asn	Asn	Lys	Gln	450	455	460	
Asn	Asp	Tyr	Leu	Thr	Asn	Lys	Lys	Ala	Lys	Lys	Thr	His	Thr	Trp	Leu	465	470	475	480
His	Thr	Lys	Asp	Ile	Pro	Gly	Ser	His	Val	Val	Ile	Phe	Asn	Asp	Ala	485	490	495	
Pro	Ser	Asp	Thr	Thr	Ile	Lys	Glu	Ala	Ala	Met	Leu	Ala	Gly	Tyr	Phe	500	505	510	
Ser	Lys	Ala	Gly	Asn	Ser	Gly	Gln	Ile	Pro	Val	Asp	Tyr	Thr	Leu	Ile	515	520	525	
Lys	Asn	Val	His	Lys	Pro	Ser	Gly	Ala	Lys	Pro	Gly	Phe	Val	Thr	Tyr	530	535	540	
Asp	Asn	Gln	Lys	Thr	Leu	Tyr	Ala	Thr	Pro	Asp	Tyr	Glu	Leu	Ile	Gln	545	550	555	560
Lys	Met	Lys	Gln	Ser												565			

<210> SEQ ID NO 76

<211> LENGTH: 317

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 76

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

Ala	Gly	Cys	Ser	Phe	Gly	Gly	Asn	His	Lys	Leu	Ser	Ser	Lys	Lys	Ser	20	25	30	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	----	----	--

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Glu Glu Ser Lys Gln Glu Thr Val Lys Lys Glu Ser Glu Glu Glu Lys
 35 40 45
 Asp Pro Asp Leu Glu Lys Tyr Glu Glu Ile Glu Lys Lys Met Lys Gly
 50 55 60
 Ile Lys Asp Ala Pro Ser Leu Asp Lys Leu Asp Pro Leu Met Thr Glu
 65 70 75 80
 Lys Ser Phe Thr Asn Ser Lys Gly Ile Gln Gly Trp Lys Asp Tyr Lys
 85 90 95
 Glu Leu Met Gly Lys Val Glu Leu Ala Asp Tyr Arg Phe Thr Lys Asp
 100 105 110
 Ser Lys Gly Ser Ser Ile Lys Asp Val Asp Ala Phe Phe Lys Gly Lys
 115 120 125
 Lys Gly Ile Lys Arg Lys Val Ile Glu Thr His Asp Asp Val Lys Gln
 130 135 140
 Val Asp Tyr Trp Tyr Val Asp Pro Asp Gly Lys Lys Ile Gly Asn Ser
 145 150 155 160
 Asn Thr Pro Val Phe Tyr Ala Glu Ile Met Thr Lys Tyr Lys Asp Gly
 165 170 175
 Lys Leu Val Tyr Ala Ser Val Glu Pro Gly Ser Tyr Val Ile His Lys
 180 185 190
 Asp Asp Ala Ile Lys Tyr Asp Asp Tyr Ser Lys Leu Lys Lys Leu Ser
 195 200 205
 Gln Leu Thr Lys Leu Asp His Pro Lys Pro Val Pro Tyr Ser Val Ala
 210 215 220
 Gln Ile Lys Ser Phe Gly Val Pro Leu Thr Ser Val Ser Phe Met Thr
 225 230 235 240
 His Gly Ser Lys Asp Thr Lys Asp Glu Val Leu Pro Ala Leu Ala Tyr
 245 250 255
 Phe Thr Phe Ser Pro Lys Asn Tyr Glu Asp Lys Ser Asn Pro Asp Pro
 260 265 270
 Lys Val Leu Asn Leu Val His Met Asp Phe Leu Asn Ala Ser Ser Asp
 275 280 285
 Phe Gly Asn Ala His Phe Val Val Leu Ser Lys Tyr Ile Lys Glu Tyr
 290 295 300
 Glu Ser Asn Tyr Glu Thr Ala Ser Asp Asp Ser Leu Lys
 305 310 315

<210> SEQ ID NO 77

<211> LENGTH: 372

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 77

Met Asn Lys Gln Gln Ser Lys Val Arg Tyr Ser Ile Arg Lys Val Ser
 1 5 10 15
 Ile Gly Ile Leu Ser Ile Ser Ile Gly Met Phe Leu Ala Leu Gly Met
 20 25 30
 Ser Asn Lys Ala Tyr Ala Asp Glu Ile Asp Lys Ser Lys Asp Phe Thr
 35 40 45
 Arg Gly Tyr Glu Gln Asn Val Phe Ala Lys Ser Glu Leu Asn Ala Asn
 50 55 60
 Lys Asn Thr Thr Lys Asp Lys Ile Lys Asn Glu Gly Ala Val Lys Thr
 65 70 75 80
 Ser Asp Thr Ser Leu Lys Leu Asp Asn Lys Ser Ala Ile Ser Asn Gly

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85				90				95							
Asn	Glu	Ile	Asn	Gln	Asp	Ile	Lys	Ile	Ser	Asn	Thr	Pro	Lys	Asn	Ser
			100							105				110	
Ser	Gln	Gly	Asn	Asn	Leu	Val	Ile	Asn	Asn	Asn	Glu	Leu	Thr	Lys	Glu
		115					120						125		
Ile	Lys	Ile	Ala	Asn	Leu	Glu	Ala	Gln	Asn	Ser	Asn	Gln	Lys	Lys	Thr
		130				135					140				
Asn	Lys	Val	Thr	Asn	Asn	Tyr	Phe	Gly	Tyr	Tyr	Ser	Phe	Arg	Glu	Ala
					150						155				160
Pro	Lys	Thr	Gln	Ile	Tyr	Thr	Val	Lys	Lys	Gly	Asp	Thr	Leu	Ser	Ala
			165							170				175	
Ile	Ala	Leu	Lys	Tyr	Lys	Thr	Thr	Val	Ser	Asn	Ile	Gln	Asn	Thr	Asn
			180							185				190	
Asn	Ile	Ala	Asn	Pro	Asn	Leu	Ile	Phe	Ile	Gly	Gln	Lys	Leu	Lys	Val
			195				200						205		
Pro	Met	Thr	Pro	Leu	Val	Glu	Pro	Lys	Pro	Lys	Thr	Val	Ser	Ser	Asn
			210			215					220				
Asn	Lys	Ser	Asn	Ser	Asn	Ser	Ser	Thr	Leu	Asn	Tyr	Leu	Lys	Thr	Leu
			225		230					235					240
Glu	Asn	Arg	Gly	Trp	Asp	Phe	Asp	Gly	Ser	Tyr	Gly	Trp	Gln	Cys	Phe
			245						250					255	
Asp	Leu	Val	Asn	Val	Tyr	Trp	Asn	His	Leu	Tyr	Gly	His	Gly	Leu	Lys
			260				265						270		
Gly	Tyr	Gly	Ala	Lys	Asp	Ile	Pro	Tyr	Ala	Asn	Asn	Phe	Asn	Ser	Glu
		275					280						285		
Ala	Lys	Ile	Tyr	His	Asn	Thr	Pro	Thr	Phe	Lys	Ala	Glu	Pro	Gly	Asp
			290			295					300				
Leu	Val	Val	Phe	Ser	Gly	Arg	Phe	Gly	Gly	Gly	Tyr	Gly	His	Thr	Ala
			305		310					315					320
Ile	Val	Leu	Asn	Gly	Asp	Tyr	Asp	Gly	Lys	Leu	Met	Lys	Phe	Gln	Ser
			325						330					335	
Leu	Asp	Gln	Asn	Trp	Asn	Asn	Gly	Gly	Trp	Arg	Lys	Ala	Glu	Val	Ala
			340				345						350		
His	Lys	Val	Val	His	Asn	Tyr	Glu	Asn	Asp	Met	Ile	Phe	Ile	Arg	Pro
			355				360						365		
Phe	Lys	Lys	Ala												
			370												

<210> SEQ ID NO 78

<211> LENGTH: 304

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 78

Met	Leu	Lys	Lys	Ala	Lys	Phe	Ile	Leu	Met	Ala	Thr	Ile	Leu	Leu	Ser
1				5					10					15	
Gly	Cys	Ser	Thr	Thr	Asn	Asn	Glu	Ser	Asn	Lys	Glu	Thr	Lys	Ser	Val
			20						25				30		
Pro	Glu	Glu	Met	Asp	Ala	Ser	Lys	Tyr	Val	Gly	Gln	Gly	Phe	Gln	Pro
			35				40					45			
Pro	Ala	Glu	Lys	Asp	Ala	Ile	Glu	Phe	Ala	Lys	Lys	His	Lys	Asp	Lys
			50			55					60				
Ile	Ala	Lys	Arg	Gly	Glu	Gln	Phe	Phe	Met	Asp	Asn	Phe	Gly	Leu	Lys
			65		70					75				80	

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

Met 1	Lys	Lys	Leu	Val 5	Ser	Ile	Val	Gly	Ala 10	Thr	Leu	Leu	Leu	Ala 15	Gly	
Cys	Gly	Ser	Gln 20	Asn	Leu	Ala	Pro	Leu 25	Glu	Glu	Lys	Thr	Thr	Asp	Leu	
Arg	Glu	Asp 35	Asn	His	Gln	Leu	Lys 40	Leu	Asp	Ile	Gln	Glu 45	Leu	Asn	Gln	
Gln 50	Ile	Ser	Asp	Ser	Lys	Ser 55	Lys	Ile	Lys	Gly	Leu 60	Glu	Lys	Asp	Lys	
Glu 65	Asn	Ser	Lys	Lys	Thr 70	Ala	Ser	Asn	Asn	Thr 75	Lys	Ile	Lys	Leu	Met 80	
Asn	Val	Thr	Ser 85	Thr	Tyr	Tyr	Asp	Lys 90	Val	Ala	Lys	Ala	Leu	Lys 95	Ser	
Tyr	Asn	Asp	Ile 100	Glu	Lys	Asp	Val	Ser 105	Lys	Asn	Lys	Gly	Asp 110	Lys	Asn	
Val	Gln	Ser 115	Lys	Leu	Asn	Gln	Ile 120	Ser	Asn	Asp	Ile	Gln 125	Ser	Ala	His	
Thr 130	Ser	Tyr	Lys	Asp	Ala	Ile 135	Asp	Gly	Leu	Ser	Leu 140	Ser	Asp	Asp	Asp	
Lys 145	Lys	Thr	Ser	Lys	Asn 150	Ile	Asp	Lys	Leu	Asn 155	Ser	Asp	Leu	Asn	His 160	

Thr Glu Lys Gln Met Thr Pro Gln Glu Ala Glu Asp Ile Val Arg Asn
50 55 60

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Asp Tyr Lys Ala Arg Gly Val Asn Glu Tyr Gln Thr Leu Asn Tyr Lys
 65 70 75 80
 Thr Asn Leu Glu Arg Ser Asn Glu His Glu Tyr Tyr Val Glu His Leu
 85 90 95
 Val Arg Asp Ala Val Gly Thr Pro Leu Lys Arg Cys Ala Ile Val Asn
 100 105 110
 Arg His Asn Gly Thr Ile Ile Asn Ile Phe Asp Asp Met Ser Glu Lys
 115 120 125
 Asp Lys Glu Glu Phe Glu Ala Phe Lys Lys Arg Ser Pro Lys Tyr Asn
 130 135 140
 Pro Gly Met Asn Asn His Asp Glu Thr Asp Gly Glu Ser Glu Asp Ile
 145 150 155 160
 Gln His His Asp Ile Asp Asn Asn Lys Ala Ile Gln Asn Asp Ile Pro
 165 170 175
 Asp Gln Lys Val Asp Asp Lys Asn Asp Lys Asn Ala Val Asn Lys Glu
 180 185 190
 Glu Lys His Asp Asn Gly Ala Asn Asn Ser Glu Glu Thr Lys Val Lys
 195 200 205

 <210> SEQ ID NO 82
 <211> LENGTH: 457
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

 <400> SEQUENCE: 82

 Met Lys Ile Ile Lys Arg Ala Ile Ile Ser Leu Ile Ile Leu Ser Leu
 1 5 10 15
 Leu Ile Ser Ile Thr Met Ser Asn Ala Ser Ala Ser Glu Glu Leu Tyr
 20 25 30
 Tyr Ser Val Glu Tyr Lys Asn Thr Ala Thr Phe Asn Lys Leu Val Lys
 35 40 45
 Lys Lys Ser Leu Asn Val Val Tyr Asn Ile Pro Glu Leu His Val Ala
 50 55 60
 Gln Ile Lys Met Thr Lys Met His Ala Asn Ala Leu Ala Asn Tyr Lys
 65 70 75 80
 Asn Asp Ile Lys Tyr Ile Asn Ala Thr Cys Ser Thr Cys Ile Thr Ser
 85 90 95
 Glu Lys Thr Ile Asp Arg Thr Ser Asn Glu Ser Leu Phe Ser Arg Gln
 100 105 110
 Trp Asp Met Asn Lys Ile Thr Asn Asn Gly Ala Ser Tyr Asp Asp Leu
 115 120 125
 Pro Lys His Ala Asn Thr Lys Ile Ala Ile Ile Asp Thr Gly Val Met
 130 135 140
 Lys Asn His Asp Asp Leu Lys Asn Asn Phe Ser Thr Asp Ser Lys Asn
 145 150 155 160
 Leu Val Pro Leu Asn Gly Phe Arg Gly Thr Glu Pro Glu Glu Thr Gly
 165 170 175
 Asp Val His Asp Val Asn Asp Arg Lys Gly His Gly Thr Met Val Ser
 180 185 190
 Gly Gln Thr Ser Ala Asn Gly Lys Leu Ile Gly Val Ala Pro Asn Asn
 195 200 205
 Lys Phe Thr Met Tyr Arg Val Phe Gly Ser Lys Lys Thr Glu Leu Leu
 210 215 220
 Trp Val Ser Lys Ala Ile Val Gln Ala Ala Asn Asp Gly Asn Gln Val
 225 230 235 240

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Ile Asn Ile Ser Val Gly Ser Tyr Ile Ile Leu Asp Lys Asn Asp His
      245                      250                      255
Gln Thr Phe Arg Lys Asp Glu Lys Val Glu Tyr Asp Ala Leu Gln Lys
      260                      265                      270
Ala Ile Asn Tyr Ala Lys Lys Lys Lys Ser Ile Val Val Ala Ala Ala
      275                      280                      285
Gly Asn Asp Gly Ile Asp Val Asn Asp Lys Gln Lys Leu Lys Leu Gln
      290                      295                      300
Arg Glu Tyr Gln Gly Asn Gly Glu Val Lys Asp Val Pro Ala Ser Met
      305                      310                      315                      320
Asp Asn Val Val Thr Val Gly Ser Thr Asp Gln Lys Ser Asn Leu Ser
      325                      330                      335
Glu Phe Ser Asn Phe Gly Met Asn Tyr Thr Asp Leu Ala Ala Pro Gly
      340                      345                      350
Gly Ser Phe Ala Tyr Leu Asn Gln Phe Gly Val Asp Lys Trp Met Asn
      355                      360                      365
Glu Gly Tyr Met His Lys Glu Asn Ile Leu Thr Thr Ala Asn Asn Gly
      370                      375                      380
Arg Tyr Ile Tyr Gln Ala Gly Thr Ser Leu Ala Thr Pro Lys Val Ser
      385                      390                      395                      400
Gly Ala Leu Ala Leu Ile Ile Asp Lys Tyr His Leu Glu Lys His Pro
      405                      410                      415
Asp Lys Ala Ile Glu Leu Leu Tyr Gln His Gly Thr Ser Lys Asn Asn
      420                      425                      430
Lys Pro Phe Ser Arg Tyr Gly His Gly Glu Leu Asp Val Tyr Lys Ala
      435                      440                      445
Leu Asn Val Ala Asn Gln Lys Ala Ser
      450                      455

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<210> SEQ ID NO 83

<211> LENGTH: 320

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 83

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Met Lys Met Ile Asn Lys Leu Ile Val Pro Val Thr Ala Ser Ala Leu
1      5                      10                      15
Leu Leu Gly Ala Cys Gly Ala Ser Ala Thr Asp Ser Lys Glu Asn Thr
      20                      25                      30
Leu Ile Ser Ser Lys Ala Gly Asp Val Thr Val Ala Asp Thr Met Lys
      35                      40                      45
Lys Ile Gly Lys Asp Gln Ile Ala Asn Ala Ser Phe Thr Glu Met Leu
      50                      55                      60
Asn Lys Ile Leu Ala Asp Lys Tyr Lys Asn Lys Val Asn Asp Lys Lys
      65                      70                      75                      80
Ile Asp Glu Gln Ile Glu Lys Met Gln Lys Gln Tyr Gly Gly Lys Asp
      85                      90                      95
Lys Phe Glu Lys Ala Leu Gln Gln Gln Gly Leu Thr Ala Asp Lys Tyr
      100                     105                     110
Lys Glu Asn Leu Arg Thr Ala Ala Tyr His Lys Glu Leu Leu Ser Asp
      115                     120                     125
Lys Ile Lys Ile Ser Asp Ser Glu Ile Lys Glu Asp Ser Lys Lys Ala
      130                     135                     140
Ser His Ile Leu Ile Lys Val Lys Ser Lys Lys Ser Asp Lys Glu Gly

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145	150	155	160
Leu Asp Asp Lys Glu Ala Lys Gln Lys Ala Glu Glu Ile Gln Lys Glu	165	170	175
Val Ser Lys Asp Pro Ser Lys Phe Gly Glu Ile Ala Lys Lys Glu Ser	180	185	190
Met Asp Thr Gly Ser Ala Lys Lys Asp Gly Glu Leu Gly Tyr Val Leu	195	200	205
Lys Gly Gln Thr Asp Lys Asp Phe Glu Lys Ala Leu Phe Lys Leu Lys	210	215	220
Asp Gly Glu Val Ser Glu Val Val Lys Ser Ser Phe Gly Tyr His Leu	225	230	235
Leu Lys Ala Asp Lys Pro Thr Asp Phe Asn Ser Glu Lys Gln Ser Leu	245	250	255
Lys Glu Lys Leu Val Asp Gln Lys Val Gln Lys Asn Pro Lys Leu Leu	260	265	270
Thr Asp Ala Tyr Lys Asp Leu Leu Lys Glu Tyr Asp Val Asp Phe Lys	275	280	285
Asp Arg Asp Ile Lys Ser Val Val Glu Asp Lys Ile Leu Asn Pro Glu	290	295	300
Lys Leu Lys Gln Gly Gly Ala Gln Gly Gly Gln Ser Gly Met Ser Gln	305	310	315
			320

<210> SEQ ID NO 84

<211> LENGTH: 388

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 84

Met Lys Arg Asn Phe Pro Lys Leu Ile Ala Leu Ser Leu Ile Phe Ser	1	5	10	15
Leu Ser Val Thr Pro Ile Ala Asn Ala Glu Ser Asn Ser Asn Leu Lys	20	25	30	
Ala Lys Asp Lys Lys His Val Gln Val Asn Val Glu Asp Lys Ser Val	35	40	45	
Pro Thr Asp Val Arg Asn Leu Ala Gln Lys Asp Tyr Leu Ser Tyr Val	50	55	60	
Thr Ser Leu Asp Lys Ile Tyr Asn Lys Glu Lys Ala Ser Tyr Thr Leu	65	70	75	80
Gly Glu Pro Phe Lys Ile Tyr Lys Phe Asn Lys Lys Ser Asp Gly Asn	85	90	95	
Tyr Tyr Phe Pro Val Leu Asn Thr Glu Gly Asn Ile Asp Tyr Ile Val	100	105	110	
Thr Ile Ser Pro Lys Ile Thr Lys Tyr Ser Ser Ser Ser Ser Lys Tyr	115	120	125	
Thr Ile Asn Val Ser Pro Phe Leu Ser Lys Val Leu Asn Gln Tyr Lys	130	135	140	
Asp Gln Gln Ile Thr Ile Leu Thr Asn Ser Lys Gly Tyr Tyr Val Val	145	150	155	160
Thr Gln Asn His Lys Ala Lys Leu Val Leu Lys Thr Pro Arg Leu Glu	165	170	175	
Asp Lys Lys Leu Lys Lys Thr Glu Ser Ile Pro Thr Gly Asn Asn Val	180	185	190	
Thr Gln Leu Lys Gln Lys Ala Ser Val Thr Met Pro Thr Ser Gln Phe	195	200	205	

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

<210> SEQ ID NO 85
 <211> LENGTH: 280
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 85

Met Lys Lys Phe Phe Phe Ile Gly Leu Leu Val Phe Val Val Phe Phe
 1 5 10 15
 Thr Ala Ala Thr Ile Ile Trp Phe Ser Tyr Asp Lys Asn Lys Tyr Gly
 20 25 30
 Thr Lys Gln Tyr Asp Lys Thr Phe Lys Asp Asp Ala Phe Asp Asn Val
 35 40 45
 Ser Ile Asn Leu Asp Ser Thr Glu Leu Arg Ile Lys Arg Gly Asn Gln
 50 55 60
 Phe Arg Val Lys Tyr Asp Gly Asp Asn Asp Ile Leu Ile Asn Ile Val
 65 70 75 80
 Asp Lys Thr Leu Lys Ile Ser Asp Lys Arg Ser Lys Thr Arg Gly Tyr
 85 90 95
 Ala Ile Asp Met Asn Pro Phe His Glu Asn Lys Lys Thr Leu Thr Ile
 100 105 110
 Glu Met Pro Asp Lys Met Ile Lys Arg Leu Asn Leu Ser Ser Gly Ala
 115 120 125
 Gly Ser Val Arg Ile Ser Asp Val Asp Leu Glu Asn Thr Ser Ile Gln
 130 135 140
 Ser Ile Asn Gly Glu Val Val Ile Lys Asn Ser Asn Leu Asp Ala Leu
 145 150 155 160
 Asp Ser Lys Thr Asn Asn Ser Ser Thr Tyr Ile Ser Lys Ser Asn Ile
 165 170 175
 Lys Asn Ser Asn Ile Lys Val Val Ile Gly Thr Leu Gln Ile Asp Lys
 180 185 190

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Ser Gln Ile Lys Gln Ser Ile Phe Leu Asn Asp His Gly Asp Ile Glu
 195 200 205

Phe Lys Asn Met Pro Ser Lys Val Asp Ala Lys Ala Ser Thr Lys Gln
 210 215 220

Gly Asp Ile Arg Phe Lys Tyr Asp Ser Lys Pro Glu Asp Thr Ile Leu
 225 230 235 240

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

Thr Asn Gly Lys Val Gly Lys Ser Asp Asn Val Leu Glu Phe Tyr Thr
 260 265 270

Ile Asp Gly Asn Ile Lys Val Glu
 275 280

<210> SEQ ID NO 86

<211> LENGTH: 303

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 86

Met Lys Arg Leu Ile Gly Ile Leu Leu Cys Asn Leu Phe Ile Leu Thr
 1 5 10 15

Ala Cys Ser Ala Ser Val Asp Lys Thr Ser Asn Ser Thr Lys Thr Thr
 20 25 30

Asp Tyr Lys Ile Glu Asn Gly Glu Thr Leu Lys Val Pro Glu Lys Pro
 35 40 45

Lys Arg Val Ala Val Leu Thr Gly Phe Tyr Val Gly Asp Phe Ile Lys
 50 55 60

Leu Gly Ile Lys Pro Ile Ala Val Ser Asp Ile Thr Lys Asp Ser Ser
 65 70 75 80

Ile Leu Lys Pro Tyr Leu Lys Gly Val Asp Tyr Ile Gly Glu Asn Asp
 85 90 95

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

Met Asp Lys Asn Ile Lys Lys Tyr Gln Lys Ile Ala Pro Thr Ile Pro
 115 120 125

Tyr Thr Tyr Asn Lys Tyr Asn His Lys Glu Ile Leu Lys Glu Ile Gly
 130 135 140

Lys Leu Thr Asn Asn Glu Asp Lys Ala Lys Lys Trp Ile Glu Glu Trp
 145 150 155 160

Asp Asp Lys Thr Arg Lys Asp Lys Lys Glu Ile Gln Ser Lys Ile Gly
 165 170 175

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

Tyr Asn Ser Thr Trp Gly Arg Gly Leu Asp Ile Val His Asp Ala Phe
 195 200 205

Gly Met Pro Met Thr Lys Gln Tyr Lys Asp Lys Leu Gln Glu Asp Lys
 210 215 220

Lys Gly Tyr Ala Ser Ile Ser Lys Glu Asn Ile Ser Lys Tyr Ala Gly
 225 230 235 240

Asp Tyr Ile Phe Leu Ser Lys Pro Ser Tyr Gly Lys Phe Asp Phe Glu
 245 250 255

Lys Thr His Thr Trp Gln Asn Ile Glu Ala Val Lys Lys Gly His Val
 260 265 270

Ile Ser Tyr Lys Ala Glu Asp Tyr Trp Phe Thr Asp Pro Ile Thr Leu

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275	280	285
Glu His Leu Arg Ser Lys	Leu Lys Lys Glu Ile	Leu Asn Lys Lys
290	295	300
<210> SEQ ID NO 87 <211> LENGTH: 419 <212> TYPE: PRT <213> ORGANISM: Staphylococcus sp <400> SEQUENCE: 87		
Met Ser Tyr His Trp Phe Lys Lys Met	Leu Leu Ser Thr Ser Ile Leu	
1	5	10
Ile Leu Ser Ser Ser Ser	Leu Gly Leu Ala Thr His Thr Val Glu Ala	
20	25	30
Lys Asp Asn Leu Asn Gly Glu Lys Pro Thr Thr	Asn Leu Asn His Asn	
35	40	45
Ile Thr Ser Pro Ser Val Asn Ser Glu Met Asn Asn Asn Glu Thr Gly		
50	55	60
Thr Pro His Glu Ser Asn Gln Thr Gly Asn Glu Gly Thr Gly Ser Asn		
65	70	75
Ser Arg Asp Ala Asn Pro Asp Ser Asn Asn Val Lys Pro Asp Ser Asn		
85	90	95
Asn Gln Asn Pro Ser Thr Asp Ser Lys Pro Asp Pro Asn Asn Gln Asn		
100	105	110
Ser Ser Pro Asn Pro Lys Pro Asp Pro Asp Asn Pro Lys Pro Lys Pro		
115	120	125
Asp Pro Lys Pro Asp Pro Asp Lys Pro Lys Pro Asn Pro Asp Pro Lys		
130	135	140
Pro Asp Pro Asp Asn Pro Lys Pro Asn Pro Asp Pro Lys Pro Asp Pro		
145	150	155
Asp Lys Pro Lys Pro Asn Pro Asp Pro Lys Pro Asp Pro Lys Pro		
165	170	175
Lys Pro Asn Pro Asn Pro Lys Pro Asp Pro Asn Lys Pro Asn Pro Asn		
180	185	190
Pro Ser Pro Asp Pro Asp Gln Pro Gly Asp Ser Asn His Ser Gly Gly		
195	200	205
Ser Lys Asn Gly Gly Thr Trp Asn Pro Asn Ala Ser Asp Gly Ser Asn		
210	215	220
Gln Gly Gln Trp Gln Pro Asn Gly Asn Gln Gly Asn Ser Gln Asn Pro		
225	230	235
Thr Gly Asn Asp Phe Val Ser Gln Arg Phe Leu Ala Leu Ala Asn Gly		
245	250	255
Ala Tyr Lys Tyr Asn Pro Tyr Ile Leu Asn Gln Ile Asn Lys Leu Gly		
260	265	270
Lys Asp Tyr Gly Glu Val Thr Asp Glu Asp Ile Tyr Asn Ile Ile Arg		
275	280	285
Lys Gln Asn Phe Ser Gly Asn Ala Tyr Leu Asn Gly Leu Gln Gln Gln		
290	295	300
Ser Asn Tyr Phe Arg Phe Gln Tyr Phe Asn Pro Leu Lys Ser Glu Arg		
305	310	315
Tyr Tyr Arg Asn Leu Asp Glu Gln Val Leu Ala Leu Ile Thr Gly Glu		
325	330	335
Ile Gly Ser Met Pro Asp Leu Lys Lys Pro Glu Asp Lys Pro Asp Ser		
340	345	350

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Lys Gln Arg Ser Phe Glu Pro His Glu Lys Asp Asp Phe Thr Val Val
 355 360 365

Lys Lys Gln Glu Asp Asn Lys Lys Ser Ala Ser Thr Ala Tyr Ser Lys
 370 375 380

Ser Trp Leu Ala Ile Val Cys Ser Met Met Val Val Phe Ser Ile Met
 385 390 395 400

Leu Phe Leu Phe Val Lys Arg Asn Lys Lys Lys Asn Lys Asn Glu Ser
 405 410 415

Gln Arg Arg

<210> SEQ ID NO 88
 <211> LENGTH: 231
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 88

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

Val Ala Gly Asn Ala Gly His Glu Ala His Ala Ser Glu Ala Asp Leu
 20 25 30

Asn Lys Ala Ser Leu Ala Gln Met Ala Gln Ser Asn Asp Gln Thr Leu
 35 40 45

Asn Gln Lys Pro Ile Glu Ala Gly Ala Tyr Asn Tyr Thr Phe Asp Tyr
 50 55 60

Glu Gly Phe Thr Tyr His Phe Glu Ser Asp Gly Thr His Phe Ala Trp
 65 70 75 80

Asn Tyr His Ala Thr Gly Thr Asn Gly Ala Asp Met Ser Ala Gln Ala
 85 90 95

Pro Ala Thr Asn Asn Val Ala Pro Ser Ala Val Gln Ala Asn Gln Val
 100 105 110

Gln Ser Gln Glu Val Glu Ala Pro Gln Asn Ala Gln Thr Gln Gln Pro
 115 120 125

Gln Ala Ser Thr Ser Asn Asn Ser Gln Val Thr Ala Thr Pro Thr Glu
 130 135 140

Ser Lys Ser Ser Glu Gly Ser Ser Val Asn Val Asn Ala His Leu Lys
 145 150 155 160

Gln Ile Ala Gln Arg Glu Ser Gly Gly Asn Ile His Ala Val Asn Pro
 165 170 175

Thr Ser Gly Ala Ala Gly Lys Tyr Gln Phe Leu Gln Ser Thr Trp Asp
 180 185 190

Ser Val Ala Pro Ala Lys Tyr Lys Gly Val Ser Pro Ala Asn Ala Pro
 195 200 205

Glu Ser Val Gln Asp Ala Ala Ala Val Lys Leu Tyr Asn Thr Gly Gly
 210 215 220

Ala Gly His Trp Val Thr Ala
 225 230

<210> SEQ ID NO 89
 <211> LENGTH: 294
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 89

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

Leu Ala Val Ala Ile Ile Ile Gly Ser Ile Ile Met Val Val Phe Ser

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

<210> SEQ ID NO 90

<211> LENGTH: 807

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 90

Met	Thr	Tyr	Arg	Ile	Lys	Lys	Trp	Gln	Lys	Leu	Ser	Thr	Ile	Thr	Leu
1				5					10					15	
Leu	Met	Ala	Gly	Val	Ile	Thr	Leu	Asn	Gly	Gly	Glu	Phe	Arg	Ser	Val
		20						25					30		
Asp	Lys	His	Gln	Ile	Ala	Val	Ala	Asp	Thr	Asn	Val	Gln	Thr	Pro	Asp
		35						40					45		
Tyr	Glu	Lys	Leu	Arg	Asn	Thr	Trp	Leu	Asp	Val	Asn	Tyr	Gly	Tyr	Asp
	50					55					60				
Lys	Tyr	Asp	Glu	Asn	Asn	Pro	Asp	Met	Lys	Lys	Lys	Phe	Asp	Ala	Thr
65					70					75					80
Glu	Lys	Glu	Ala	Thr	Asn	Leu	Leu	Lys	Glu	Met	Lys	Thr	Glu	Ser	Gly
			85						90					95	

Arg	Lys	Tyr	Leu	Trp	Ser	Gly	Ala	Glu	Thr	Leu	Glu	Thr	Asn	Ser	Ser
			100					105					110		
His	Met	Thr	Arg	Thr	Tyr	Arg	Asn	Ile	Glu	Lys	Ile	Ala	Glu	Ala	Met
			115				120					125			
Arg	Asn	Pro	Lys	Thr	Thr	Leu	Asn	Thr	Asp	Glu	Asn	Lys	Lys	Lys	Val
			130			135					140				
Lys	Asp	Ala	Leu	Glu	Trp	Leu	His	Lys	Asn	Ala	Tyr	Gly	Lys	Glu	Pro
					150					155				160	
Asp	Lys	Lys	Val	Lys	Glu	Leu	Ser	Glu	Asn	Phe	Thr	Lys	Thr	Thr	Gly
				165					170					175	
Lys	Asn	Thr	Asn	Leu	Asn	Trp	Trp	Asp	Tyr	Glu	Ile	Gly	Thr	Pro	Lys
				180				185					190		
Ser	Leu	Thr	Asn	Thr	Leu	Ile	Leu	Leu	Asn	Asp	Gln	Phe	Ser	Asn	Glu
						200						205			
Glu	Lys	Lys	Lys	Phe	Thr	Ala	Pro	Ile	Lys	Thr	Phe	Ala	Pro	Asp	Ser
						215					220				
Asp	Lys	Ile	Leu	Ser	Ser	Val	Gly	Lys	Ala	Glu	Leu	Ala	Lys	Gly	Gly
					230					235				240	
Asn	Leu	Val	Asp	Ile	Ser	Lys	Val	Lys	Leu	Leu	Glu	Cys	Ile	Ile	Glu
				245					250					255	
Glu	Asp	Lys	Asp	Met	Met	Lys	Lys	Ser	Ile	Asp	Ser	Phe	Asn	Lys	Val
				260				265					270		
Phe	Thr	Tyr	Val	Gln	Asp	Ser	Ala	Thr	Gly	Lys	Glu	Arg	Asn	Gly	Phe
						280						285			
Tyr	Lys	Asp	Gly	Ser	Tyr	Ile	Asp	His	Gln	Asp	Val	Pro	Tyr	Thr	Gly
					295					300					
Ala	Tyr	Gly	Val	Val	Leu	Leu	Glu	Gly	Ile	Ser	Gln	Met	Met	Pro	Met
					310					315				320	
Ile	Lys	Glu	Thr	Pro	Phe	Asn	Asp	Lys	Thr	Gln	Asn	Asp	Thr	Thr	Leu
				325					330					335	
Lys	Ser	Trp	Ile	Asp	Asp	Gly	Phe	Met	Pro	Leu	Ile	Tyr	Lys	Gly	Glu
				340				345					350		
Met	Met	Asp	Leu	Ser	Arg	Gly	Arg	Ala	Ile	Ser	Arg	Glu	Asn	Glu	Thr
				355			360					365			
Ser	His	Ser	Ala	Ser	Ala	Thr	Val	Met	Lys	Ser	Leu	Leu	Arg	Leu	Ser
					375					380					
Asp	Ala	Met	Asp	Asp	Ser	Thr	Lys	Ala	Lys	Tyr	Lys	Lys	Ile	Val	Lys
					390					395				400	
Ser	Ser	Val	Glu	Ser	Asp	Ser	Ser	Tyr	Lys	Gln	Asn	Asp	Tyr	Leu	Asn
				405				410						415	
Ser	Tyr	Ser	Asp	Ile	Asp	Lys	Met	Lys	Ser	Leu	Met	Thr	Asp	Asn	Ser
				420				425					430		
Ile	Ser	Lys	Asn	Gly	Leu	Thr	Gln	Gln	Leu	Lys	Ile	Tyr	Asn	Asp	Met
				435			440					445			
Asp	Arg	Val	Thr	Tyr	His	Asn	Lys	Asp	Leu	Asp	Phe	Ala	Phe	Gly	Leu
					455					460		</			

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515					520					525					
Thr	Asp	Asp	Lys	Lys	Ser	Ser	Lys	Thr	Phe	Val	Gly	Gly	Thr	Lys	Val
530						535					540				
Asp	Asp	Gln	His	Ala	Ser	Ile	Gly	Met	Asp	Phe	Glu	Asn	Gln	Asp	Lys
545					550					555					560
Thr	Leu	Thr	Ala	Lys	Lys	Ser	Tyr	Phe	Ile	Leu	Asn	Asp	Lys	Ile	Val
				565					570					575	
Phe	Leu	Gly	Thr	Gly	Ile	Lys	Ser	Thr	Asp	Ser	Ser	Lys	Asn	Pro	Val
		580						585					590		
Thr	Thr	Ile	Glu	Asn	Arg	Lys	Ala	Asn	Gly	Tyr	Thr	Leu	Tyr	Thr	Asp
		595					600					605			
Asp	Lys	Gln	Thr	Thr	Asn	Ser	Asp	Asn	Gln	Glu	Asn	Asn	Ser	Val	Phe
	610					615					620				
Leu	Glu	Ser	Thr	Asp	Thr	Lys	Lys	Asn	Ile	Gly	Tyr	His	Phe	Leu	Asn
	625					630				635					640
Lys	Pro	Lys	Ile	Thr	Val	Lys	Lys	Glu	Ser	His	Thr	Gly	Lys	Trp	Lys
			645					650						655	
Glu	Ile	Asn	Lys	Ser	Gln	Lys	Asp	Thr	Gln	Lys	Thr	Asp	Glu	Tyr	Tyr
		660						665					670		
Glu	Val	Thr	Gln	Lys	His	Ser	Asn	Ser	Asp	Asn	Lys	Tyr	Gly	Tyr	Val
		675					680						685		
Leu	Tyr	Pro	Gly	Leu	Ser	Lys	Asp	Val	Phe	Lys	Thr	Lys	Lys	Asp	Glu
	690					695					700				
Val	Thr	Val	Val	Lys	Gln	Glu	Asp	Asp	Phe	His	Val	Val	Lys	Asp	Asn
	705				710					715					720
Glu	Ser	Val	Trp	Ala	Gly	Val	Asn	Tyr	Ser	Asn	Ser	Thr	Gln	Thr	Phe
			725					730						735	
Asp	Ile	Asn	Asn	Thr	Lys	Val	Glu	Val	Lys	Ala	Lys	Gly	Met	Phe	Ile
		740						745					750		
Leu	Lys	Lys	Lys	Asp	Asp	Asn	Thr	Tyr	Glu	Cys	Ser	Phe	Tyr	Asn	Pro
	755					760						765			
Glu	Ser	Thr	Asn	Ser	Ala	Ser	Asp	Ile	Glu	Ser	Lys	Ile	Ser	Met	Thr
	770					775					780				
Gly	Tyr	Ser	Ile	Thr	Asn	Lys	Asn	Thr	Ser	Thr	Ser	Asn	Glu	Ser	Gly
	785				790					795					800
Val	His	Phe	Glu	Leu	Thr	Lys									
				805											

<210> SEQ ID NO 91

<211> LENGTH: 166

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 91

Met	Lys	Lys	Leu	Val	Thr	Ala	Thr	Thr	Leu	Thr	Ala	Gly	Ile	Gly	Thr
1				5					10					15	
Ala	Leu	Val	Gly	Gln	Ala	His	His	Ala	Asp	Ala	Ala	Glu	Asn	Tyr	Thr
		20						25					30		
Asn	Tyr	Asn	Asn	Tyr	Asn	Tyr	Asn	Thr	Thr	Gln	Thr	Thr	Thr	Thr	Thr
		35					40					45			
Thr	Thr	Thr	Thr	Thr	Thr	Ser	Ser	Ile	Ser	His	Ser	Gly	Asn	Leu	Tyr
	50					55					60				
Thr	Ala	Gly	Gln	Cys	Thr	Trp	Tyr	Val	Tyr	Asp	Lys	Val	Gly	Gly	Glu
	65				70					75					80

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Ile Gly Ser Thr Trp Gly Asn Ala Asn Asn Trp Ala Ala Ala Ala Gln
      85                      90                      95
Gly Ala Gly Phe Thr Val Asn His Thr Pro Ser Lys Gly Ala Ile Leu
      100                    105                    110
Gln Ser Ser Glu Gly Pro Phe Gly His Val Ala Tyr Val Glu Ser Val
      115                    120                    125
Asn Ser Asp Gly Ser Val Thr Ile Ser Glu Met Asn Tyr Ser Gly Gly
      130                    135                    140
Pro Phe Ser Val Ser Ser Arg Thr Ile Ser Ala Ser Glu Ala Gly Asn
      145                    150                    155                    160
Tyr Asn Tyr Ile His Ile
      165

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<210> SEQ ID NO 92
<211> LENGTH: 516
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

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<400> SEQUENCE: 92

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Met Lys Lys Lys Leu Gly Met Leu Leu Leu Val Pro Ala Val Thr Leu
1      5      10      15
Ser Leu Ala Ala Cys Gly Asn Asp Asp Gly Lys Asp Lys Asp Gly Lys
      20      25      30
Val Thr Ile Lys Thr Thr Val Tyr Pro Leu Gln Ser Phe Ala Glu Gln
      35      40      45
Ile Gly Gly Lys His Val Lys Val Ser Ser Ile Tyr Pro Ala Gly Thr
      50      55      60
Asp Leu His Ser Tyr Glu Pro Thr Gln Lys Asp Ile Leu Ser Ala Ser
      65      70      75      80
Lys Ser Asp Leu Phe Met Tyr Thr Gly Asp Asn Leu Asp Pro Val Ala
      85      90      95
Lys Lys Val Ala Ser Thr Ile Lys Asp Lys Asp Lys Lys Leu Ser Leu
      100     105     110
Glu Asp Lys Leu Asp Lys Ala Lys Leu Leu Thr Asp Gln His Glu His
      115     120     125
Gly Glu Glu His Glu His Glu Gly His Asp His Glu Lys Glu Glu His
      130     135     140
His His His His Gly Gly Tyr Asp Pro His Val Trp Leu Asp Pro Lys
      145     150     155     160
Ile Asn Gln Thr Phe Ala Lys Glu Ile Lys Asp Glu Leu Val Lys Lys
      165     170     175
Asp Pro Lys His Lys Asp Asp Tyr Glu Lys Asn Tyr Lys Lys Leu Asn
      180     185     190
Asp Asp Leu Lys Lys Ile Asp Asn Asp Met Lys Gln Val Thr Lys Asp
      195     200     205
Lys Gln Gly Asn Ala Val Phe Ile Ser His Glu Ser Ile Gly Tyr Leu
      210     215     220
Ala Asp Cys Tyr Gly Phe Val Gln Lys Gly Ile Gln Asn Met Asn Ala
      225     230     235     240
Glu Asp Pro Ser Gln Lys Glu Leu Thr Lys Ile Val Lys Glu Ile Arg
      245     250     255
Asp Ser Asn Ala Lys Tyr Ile Leu Tyr Glu Asp Asn Val Ala Asn Lys
      260     265     270
Val Thr Glu Thr Ile Arg Lys Glu Thr Asp Ala Lys Pro Leu Lys Phe
      275     280     285

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Tyr Asn Met Glu Ser Leu Asn Lys Glu Gln Gln Lys Lys Asp Asn Ile
 290 295 300
 Thr Tyr Gln Ser Leu Met Lys Ser Asn Ile Glu Asn Ile Gly Lys Ala
 305 310 315 320
 Leu Asp Ser Gly Val Lys Val Lys Asp Asp Lys Ala Glu Ser Lys His
 325 330 335
 Asp Lys Ala Ile Ser Asp Gly Tyr Phe Lys Asp Glu Gln Val Lys Asp
 340 345 350
 Arg Glu Leu Ser Asp Tyr Ala Gly Glu Trp Gln Ser Val Tyr Pro Tyr
 355 360 365
 Leu Lys Asp Gly Thr Leu Asp Glu Val Met Glu His Lys Ala Glu Asn
 370 375 380
 Asp Pro Lys Lys Ser Ala Lys Asp Leu Lys Ala Tyr Tyr Asp Lys Gly
 385 390 395 400
 Tyr Lys Thr Asp Ile Thr Asn Ile Asp Ile Lys Gly Asn Glu Ile Thr
 405 410 415
 Phe Thr Lys Asp Gly Lys Lys His Thr Gly Lys Tyr Glu Tyr Asn Gly
 420 425 430
 Lys Lys Thr Leu Lys Tyr Pro Lys Gly Asn Arg Gly Val Arg Phe Met
 435 440 445
 Phe Lys Leu Val Asp Gly Asn Asp Lys Asp Leu Pro Lys Phe Ile Gln
 450 455 460
 Phe Ser Asp His Asn Ile Ala Pro Lys Lys Ala Glu His Phe His Ile
 465 470 475 480
 Phe Met Gly Asn Asp Asn Asp Ala Leu Leu Lys Glu Met Asp Asn Trp
 485 490 495
 Pro Thr Tyr Tyr Pro Ser Lys Leu Asn Lys Asp Gln Ile Lys Glu Glu
 500 505 510
 Met Leu Ala His
 515

<210> SEQ ID NO 93

<211> LENGTH: 309

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 93

Met Ile Lys Asn Lys Ile Leu Thr Ala Thr Leu Ala Val Gly Leu Ile
 1 5 10 15
 Ala Pro Leu Ala Asn Pro Phe Ile Glu Ile Ser Lys Ala Glu Asn Lys
 20 25 30
 Ile Glu Asp Ile Gly Gln Gly Ala Glu Ile Ile Lys Arg Thr Gln Asp
 35 40 45
 Ile Thr Ser Lys Arg Leu Ala Ile Thr Gln Asn Ile Gln Phe Asp Phe
 50 55 60
 Val Lys Asp Lys Lys Tyr Asn Lys Asp Ala Leu Val Val Lys Met Gln
 65 70 75 80
 Gly Phe Ile Ser Ser Arg Thr Thr Tyr Ser Asp Leu Lys Lys Tyr Pro
 85 90 95
 Tyr Ile Lys Arg Met Ile Trp Pro Phe Gln Tyr Asn Ile Ser Leu Lys
 100 105 110
 Thr Lys Asp Ser Asn Val Asp Leu Ile Asn Tyr Leu Pro Lys Asn Lys
 115 120 125
 Ile Asp Ser Ala Asp Val Ser Gln Lys Leu Gly Tyr Asn Ile Gly Gly

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130	135	140
Asn Phe Gln Ser Ala Pro Ser Ile Gly Gly Ser Gly Ser Phe Asn Tyr		
145	150	155 160
Ser Lys Thr Ile Ser Tyr Asn Gln Lys Asn Tyr Val Thr Glu Val Glu		
	165	170 175
Ser Gln Asn Ser Lys Gly Val Lys Trp Gly Val Lys Ala Asn Ser Phe		
	180	185 190
Val Thr Pro Asn Gly Gln Val Ser Ala Tyr Asp Gln Tyr Leu Phe Ala		
	195	200 205
Gln Asp Pro Thr Gly Pro Ala Ala Arg Asp Tyr Phe Val Pro Asp Asn		
	210	215 220
Gln Leu Pro Pro Leu Ile Gln Ser Gly Phe Asn Pro Ser Phe Ile Thr		
	225	230 235 240
Thr Leu Ser His Glu Arg Gly Lys Gly Asp Lys Ser Glu Phe Glu Ile		
	245	250 255
Thr Tyr Gly Arg Asn Met Asp Ala Thr Tyr Ala Tyr Val Thr Arg His		
	260	265 270
Arg Leu Ala Val Asp Arg Lys His Asp Ala Phe Lys Asn Arg Asn Val		
	275	280 285
Thr Val Lys Tyr Glu Val Asn Trp Lys Thr His Glu Val Lys Ile Lys		
	290	295 300
Ser Ile Thr Pro Lys		
305		
<210> SEQ ID NO 94		
<211> LENGTH: 532		
<212> TYPE: PRT		
<213> ORGANISM: Staphylococcus sp		
<400> SEQUENCE: 94		
Met Arg Lys Leu Thr Lys Met Ser Ala Met Leu Leu Ala Ser Gly Leu		
1	5	10 15
Ile Leu Thr Gly Cys Gly Gly Asn Lys Gly Leu Glu Glu Lys Lys Glu		
	20	25 30
Asn Lys Gln Leu Thr Tyr Thr Thr Val Lys Asp Ile Gly Asp Met Asn		
	35	40 45
Pro His Val Tyr Gly Gly Ser Met Ser Ala Glu Ser Met Ile Tyr Glu		
	50	55 60
Pro Leu Val Arg Asn Thr Lys Asp Gly Ile Lys Pro Leu Leu Ala Lys		
	65	70 75 80
Lys Trp Asp Val Ser Glu Asp Gly Lys Thr Tyr Thr Phe His Leu Arg		
	85	90 95
Asp Asp Val Lys Phe His Asp Gly Thr Pro Phe Asp Ala Asp Ala Val		
	100	105 110
Lys Lys Asn Ile Asp Ala Val Gln Glu Asn Lys Lys Leu His Ser Trp		
	115	120 125
Leu Lys Ile Ser Thr Leu Ile Asp Asn Val Lys Val Lys Asp Lys Tyr		
	130	135 140
Thr Val Glu Leu Asn Leu Lys Glu Ala Tyr Gln Pro Ala Leu Ala Glu		
	145	150 155 160
Leu Ala Met Pro Arg Pro Tyr Val Phe Val Ser Pro Lys Asp Phe Lys		
	165	170 175
Asn Gly Thr Thr Lys Asp Gly Val Lys Lys Phe Asp Gly Thr Gly Pro		
	180	185 190

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Phe Lys Leu Gly Glu His Lys Lys Asp Glu Ser Ala Asp Phe Asn Lys
 195 200 205
 Asn Asp Gln Tyr Trp Gly Glu Lys Ser Lys Leu Asn Lys Val Gln Ala
 210 215 220
 Lys Val Met Pro Ala Gly Glu Thr Ala Phe Leu Ser Met Lys Lys Gly
 225 230 235 240
 Glu Thr Asn Phe Ala Phe Thr Asp Asp Arg Gly Thr Asp Ser Leu Asp
 245 250 255
 Lys Asp Ser Leu Lys Gln Leu Lys Asp Thr Gly Asp Tyr Gln Val Lys
 260 265 270
 Arg Ser Gln Pro Met Asn Thr Lys Met Leu Val Val Asn Ser Gly Lys
 275 280 285
 Lys Asp Asn Ala Val Ser Asp Lys Thr Val Arg Gln Ala Ile Gly His
 290 295 300
 Met Val Asn Arg Asp Lys Ile Ala Lys Glu Ile Leu Asp Gly Gln Glu
 305 310 315 320
 Lys Pro Ala Thr Gln Leu Phe Ala Lys Asn Val Thr Asp Ile Asn Phe
 325 330 335
 Asp Met Pro Thr Arg Lys Tyr Asp Leu Lys Lys Ala Glu Ser Leu Leu
 340 345 350
 Asp Glu Ala Gly Trp Lys Lys Gly Lys Asp Ser Asp Val Arg Gln Lys
 355 360 365
 Asp Gly Lys Asn Leu Glu Met Ala Met Tyr Tyr Asp Lys Gly Ser Ser
 370 375 380
 Ser Gln Lys Glu Gln Ala Glu Tyr Leu Gln Ala Glu Phe Lys Lys Met
 385 390 395 400
 Gly Ile Lys Leu Asn Ile Asn Gly Glu Thr Ser Asp Lys Ile Ala Glu
 405 410 415
 Arg Arg Thr Ser Gly Asp Tyr Asp Leu Met Phe Asn Gln Thr Trp Gly
 420 425 430
 Leu Leu Tyr Asp Pro Gln Ser Thr Leu Ala Ala Phe Lys Glu Lys Asn
 435 440 445
 Gly Tyr Glu Ser Ala Thr Ser Gly Ile Glu Asn Lys Asp Lys Ile Tyr
 450 455 460
 Asn Ser Ile Asp Asp Ala Phe Lys Ile Gln Asn Gly Lys Glu Arg Ser
 465 470 475 480
 Asp Ala Tyr Lys Asn Ile Leu Lys Gln Ile Asp Asp Glu Gly Ile Phe
 485 490 495
 Ile Pro Ile Ser His Gly Ser Met Thr Val Val Ala Pro Lys Asp Leu
 500 505 510
 Glu Lys Val Ser Phe Thr Gln Ser Gln Tyr Glu Leu Pro Phe Asn Glu
 515 520 525
 Met Gln Tyr Lys
 530

<210> SEQ ID NO 95

<211> LENGTH: 264

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 95

Met Ile His Ser Lys Lys Leu Thr Leu Gly Ile Cys Leu Val Leu Leu
 1 5 10 15
 Ile Ile Leu Ile Val Gly Tyr Val Ile Met Thr Lys Thr Asn Gly Arg
 20 25 30

-continued

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

<210> SEQ ID NO 96

<211> LENGTH: 261

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 96

Met Ile His Ser Lys Lys Leu Thr Leu Gly Ile Cys Leu Val Leu Leu
 1 5 10 15
 Ile Ile Leu Ile Gly Gly Cys Val Ile Met Thr Lys Thr Asn Gly Arg
 20 25 30
 Asn Ala Gln Ile Lys Glu Asn Phe Asn Lys Thr Leu Ser Val Tyr Leu
 35 40 45
 Thr Lys Asn Leu Asp Asp Phe Tyr Asp Lys Glu Gly Phe Arg Asp Gln
 50 55 60
 Glu Phe Asp Lys Arg Asp Lys Gly Thr Trp Ile Ile Tyr Ser Glu Met
 65 70 75 80
 Val Ile Glu Pro Lys Gly Lys Asn Met Glu Ser Arg Gly Met Val Leu
 85 90 95
 Tyr Ile Asn Arg Asn Thr Arg Thr Thr Lys Gly Asn Phe Ile Val Thr
 100 105 110
 Glu Ile Thr Glu Asp Ser Lys Gly Tyr Ser Arg Ser Lys Glu Lys Lys
 115 120 125
 Tyr Pro Val Lys Met Glu Asn Asn Arg Ile Ile Pro Thr Lys Pro Ile

-continued

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

<210> SEQ ID NO 97

<211> LENGTH: 498

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 97

Met Ala Ala Leu Thr Leu Leu Ser Thr Leu Ser Pro Ala Ala Leu Ala		
1	5	10 15
Ile Asp Ser Lys Asn Lys Pro Ala Asn Ser Asp Ile Lys Phe Glu Val		
	20	25 30
Thr Gln Lys Ser Asp Ala Val Lys Ala Leu Lys Glu Leu Pro Lys Ser		
	35	40 45
Glu Asn Val Lys Asn Ile Tyr Gln Asp Tyr Ala Val Thr Asp Val Lys		
	50	55 60
Thr Asp Lys Lys Gly Phe Thr His Tyr Thr Leu Gln Pro Ser Val Asp		
	65	70 75 80
Gly Val His Ala Pro Asp Lys Glu Val Lys Val His Ala Asp Lys Ser		
	85	90 95
Gly Lys Val Val Leu Ile Asn Gly Asp Thr Asp Ala Lys Lys Val Lys		
	100	105 110
Pro Thr Asn Lys Val Thr Leu Ser Lys Asp Asp Ala Ala Asp Lys Ala		
	115	120 125
Phe Lys Ala Val Lys Ile Asp Lys Asn Lys Ala Lys Asn Leu Lys Asp		
	130	135 140
Lys Val Ile Lys Glu Asn Lys Val Glu Ile Asp Gly Asp Ser Asn Lys		
	145	150 155 160
Tyr Val Tyr Asn Val Glu Leu Ile Thr Val Thr Pro Glu Ile Ser His		
	165	170 175
Trp Lys Val Lys Ile Asp Ala Gln Thr Gly Glu Ile Leu Glu Lys Met		
	180	185 190
Asn Leu Val Lys Glu Ala Ala Glu Thr Gly Lys Gly Lys Gly Val Leu		
	195	200 205
Gly Asp Thr Lys Asp Ile Asn Ile Asn Ser Ile Asp Gly Gly Phe Ser		
	210	215 220
Leu Glu Asp Leu Thr His Gln Gly Lys Leu Ser Ala Phe Ser Phe Asn		
	225	230 235 240

[illegible]

<400> SEQUENCE: 98

Met	Lys	Ser	Gln	Asn	Lys	Tyr	Ser	Ile	Arg	Lys	Phe	Ser	Val	Gly	Ala
1				5					10					15	
Ser	Ser	Ile	Leu	Ile	Ala	Thr	Leu	Leu	Phe	Leu	Ser	Gly	Gly	Gln	Ala
			20					25					30		
Gln	Ala	Ala	Glu	Lys	Gln	Val	Asn	Met	Gly	Asn	Ser	Gln	Glu	Asp	Thr
		35					40					45			
Val	Thr	Ala	Gln	Ser	Ile	Gly	Asp	Gln	Gln	Thr	Arg	Glu	Asn	Ala	Asn
	50					55					60				
Tyr	Gln	Arg	Glu	Asn	Gly	Val	Asp	Glu	Gln	Gln	His	Thr	Glu	Asn	Leu
65					70					75					80
Thr	Lys	Asn	Leu	His	Asn	Asp	Lys	Thr	Ile	Ser	Glu	Glu	Asn	His	Arg
			85						90					95	
Lys	Thr	Asp	Asp	Leu	Asn	Lys	Asp	Gln	Leu	Lys	Asp	Asp	Lys	Lys	Ser
			100					105					110		

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Ser	Leu	Asn	Asn	Lys	Asn	Ile	Gln	Arg	Asp	Thr	Thr	Lys	Asn	Asn	Asn
		115					120					125			
Ala	Asn	Pro	Ser	Asp	Val	Asn	Gln	Gly	Leu	Glu	Gln	Ala	Ile	Asn	Asp
	130					135					140				
Gly	Lys	Gln	Ser	Lys	Val	Ala	Ser	Gln	Gln	Gln	Ser	Lys	Glu	Ala	Asp
	145				150					155					160
Asn	Ser	Gln	Asp	Ser	Asn	Ala	Asn	Asn	Asn	Leu	Pro	Ser	Gln	Ser	Arg
				165					170					175	
Ile	Lys	Glu	Ala	Pro	Ser	Leu	Asn	Lys	Leu	Asp	Gln	Thr	Ser	Gln	Arg
			180					185					190		
Glu	Ile	Val	Asn	Glu	Thr	Glu	Ile	Glu	Lys	Val	Gln	Pro	Gln	Gln	Asn
		195					200					205			
Asn	Gln	Ala	Asn	Asp	Lys	Ile	Thr	Asn	Tyr	Asn	Phe	Asn	Asn	Glu	Gln
	210					215					220				
Glu	Val	Lys	Pro	Gln	Lys	Asp	Glu	Lys	Thr	Leu	Ser	Val	Ser	Asp	Leu
	225				230					235					240
Lys	Asn	Asn	Gln	Lys	Ser	Pro	Val	Glu	Pro	Thr	Lys	Asp	Asn	Asp	Lys
				245					250					255	
Lys	Asn	Gly	Leu	Asn	Leu	Leu	Lys	Ser	Ser	Ala	Val	Ala	Thr	Leu	Pro
			260					265					270		
Asn	Lys	Gly	Thr	Lys	Glu	Leu	Thr	Ala	Lys	Ala	Lys	Asp	Asp	Gln	Thr
		275					280					285			
Asn	Lys	Val	Ala	Lys	Gln	Gly	Gln	Tyr	Lys	Asn	Gln	Asp	Pro	Ile	Val
	290					295					300				
Leu	Val	His	Gly	Phe	Asn	Gly	Phe	Thr	Asp	Asp	Ile	Asn	Pro	Ser	Val
	305				310					315					320
Leu	Ala	His	Tyr	Trp	Gly	Gly	Asn	Lys	Met	Asn	Ile	Arg	Gln	Asp	Leu
				325					330					335	
Glu	Glu	Asn	Gly	Tyr	Lys	Ala	Tyr	Glu	Ala	Ser	Ile	Ser	Ala	Phe	Gly
			340					345					350		
Ser	Asn	Tyr	Asp	Arg	Ala	Val	Glu	Leu	Tyr	Tyr	Tyr	Ile	Lys	Gly	Gly
		355					360					365			
Arg	Val	Asp	Tyr	Gly	Ala	Ala	His	Ala	Ala	Lys	Tyr	Gly	His	Glu	Arg
	370				375						380				
Tyr	Gly	Lys	Thr	Tyr	Glu	Gly	Ile	Tyr	Lys	Asp	Trp	Lys	Pro	Gly	Gln
	385				390					395					400
Lys	Val	His	Leu	Val	Gly	His	Ser	Met	Gly	Gly	Gln	Thr	Ile	Arg	Gln
			405						410					415	
Leu	Glu	Glu	Leu	Leu	Arg	Asn	Gly	Asn	Arg	Glu	Glu	Ile	Glu	Tyr	Gln
			420					425				430			
Lys	Lys	His	Gly	Gly	Glu	Ile	Ser	Pro	Leu	Phe	Lys	Gly	Asn	His	Asp
		435					440					445			
Asn	Met	Ile	Ser	Ser	Ile	Thr	Thr	Leu	Gly	Thr	Pro	His	Asn	Gly	Thr
	450					455					460				
His	Ala	Ser	Asp	Leu	Ala	Gly	Asn	Glu	Ala	Leu	Val	Arg	Gln	Ile	Val
	465				470					475					480
Phe	Asp	Ile	Gly	Lys	Met	Phe	Gly	Asn	Lys	Asn	Ser	Arg	Val	Asp	Phe
				485				490						495	
Gly	Leu	Ala	Gln	Trp	Gly	Leu	Lys	Gln	Lys	Pro	Asn	Glu	Ser	Tyr	Ile
		500					505					510			
Asp	Tyr	Val	Lys	Arg	Val	Lys	Gln	Ser	Asn	Leu	Trp	Lys	Ser	Lys	Asp
	515						520					525			
Asn	Gly	Phe	Tyr	Asp	Leu	Thr	Arg	Glu	Gly	Ala	Thr	Asp	Leu	Asn	Arg

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530	535	540
Lys Thr Ser Leu Asn Pro Asn Ile Val Tyr Lys Thr Tyr Thr Gly Glu		
545	550	555 560
Ala Thr His Lys Ala Leu Asn Ser Asp Arg Gln Lys Ala Asp Leu Asn		
	565	570 575
Met Phe Phe Pro Phe Val Ile Thr Gly Asn Leu Ile Gly Lys Ala Thr		
	580	585 590
Glu Lys Glu Trp Arg Glu Asn Asp Gly Leu Val Ser Val Ile Ser Ser		
	595	600 605
Gln His Pro Phe Asn Gln Ala Tyr Thr Lys Ala Thr Asp Lys Ile Gln		
610	615	620
Lys Gly Ile Trp Gln Val Thr Pro Thr Lys His Asp Trp Asp His Val		
625	630	635 640
Asp Phe Val Gly Gln Asp Ser Ser Asp Thr Val Arg Thr Arg Glu Glu		
	645	650 655
Leu Gln Asp Phe Trp His His Leu Ala Asp Asp Leu Val Lys Thr Glu		
	660	665 670
Lys Leu Thr Asp Thr Lys Gln Ala		
	675	680

<210> SEQ ID NO 99

<211> LENGTH: 328

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 99

Met Lys Lys Cys Ile Lys Thr Leu Phe Leu Ser Ile Ile Leu Val Val		
1	5	10 15
Met Ser Gly Trp Tyr His Ser Ala His Ala Ser Asp Ser Leu Ser Lys		
	20	25 30
Ser Pro Glu Asn Trp Met Ser Lys Leu Asp Asp Gly Lys His Leu Thr		
	35	40 45
Glu Ile Asn Ile Pro Gly Ser His Asp Ser Gly Ser Phe Thr Leu Lys		
50	55	60
Asp Pro Val Lys Ser Val Trp Ala Lys Thr Gln Asp Lys Asp Tyr Leu		
65	70	75 80
Thr Gln Met Lys Ser Gly Val Arg Phe Phe Asp Ile Arg Gly Arg Ala		
	85	90 95
Ser Ala Asp Asn Met Ile Ser Val His His Gly Met Val Tyr Leu His		
	100	105 110
His Glu Leu Gly Lys Phe Leu Asp Asp Ala Lys Tyr Tyr Leu Ser Ala		
	115	120 125
Tyr Pro Asn Glu Thr Ile Val Met Ser Met Lys Lys Asp Tyr Asp Ser		
130	135	140
Asp Ser Lys Val Thr Lys Thr Phe Glu Glu Ile Phe Arg Glu Tyr Tyr		
145	150	155 160
Tyr Asn Asn Pro Gln Tyr Gln Asn Leu Phe Tyr Thr Gly Ser Asn Ala		
	165	170 175
Asn Pro Thr Leu Lys Glu Thr Lys Gly Lys Ile Val Leu Phe Asn Arg		
	180	185 190
Met Gly Gly Thr Tyr Ile Lys Ser Gly Tyr Gly Ala Asp Thr Ser Gly		
	195	200 205
Ile Gln Trp Ala Asp Asn Ala Thr Phe Glu Thr Lys Ile Asn Asn Gly		
210	215	220

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Ser Leu Asn Leu Lys Val Gln Asp Glu Tyr Lys Asp Tyr Tyr Asp Lys
 225 230 235 240

Lys Val Glu Ala Val Lys Asn Leu Leu Ala Lys Ala Lys Thr Asp Ser
 245 250 255

Asn Lys Asp Asn Val Tyr Val Asn Phe Leu Ser Val Ala Ser Gly Gly
 260 265 270

Ser Ala Phe Asn Ser Thr Tyr Asn Tyr Ala Ser His Ile Asn Pro Glu
 275 280 285

Ile Ala Lys Thr Leu Lys Ala Asn Gly Lys Ala Arg Thr Gly Trp Leu
 290 295 300

Ile Val Asp Tyr Ala Gly Tyr Thr Trp Pro Gly Tyr Asp Asp Ile Val
 305 310 315 320

Ser Glu Ile Ile Asp Ser Asn Lys
 325

<210> SEQ ID NO 100

<211> LENGTH: 257

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 100

Met Lys Ala His Lys Ile Phe Trp Leu Asn Leu Ala Ala Ile Ile Ile
 1 5 10 15

Ile Ser Ile Val Val Ser Gly Asp Met Phe Leu Ala Met Lys Trp Glu
 20 25 30

Gln Ile His Leu Lys Asp Gly Leu Lys Lys Val Leu Ser Thr Tyr Pro
 35 40 45

Ile Lys Asn Leu Glu Thr Leu Tyr Glu Ile Asp Gly His Asp Asn Pro
 50 55 60

His Tyr Glu Asn Asn Asp Gln Asp Thr Trp Tyr Ile Glu Ser Ser Tyr
 65 70 75 80

Ser Val Val Gly Ser Asp Glu Leu Leu Lys Glu Asp Arg Met Leu Leu
 85 90 95

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

Thr Asn Asp Arg Lys Asn Ala Thr Asp Ser Thr Tyr Lys Ser Tyr Pro
 115 120 125

Val Lys Val Val Asn Asn Lys Ile Val Phe Thr Lys Asp Val Lys Asp
 130 135 140

Pro Ala Leu Lys Gln Lys Ile Glu Asn Asn Gln Phe Leu Ile Gln Ser
 145 150 155 160

Gly Asp Leu Thr Ser Ile Leu Asn Ser Asn Asp Leu Lys Val Thr His
 165 170 175

Asp Pro Thr Thr Asp Tyr Tyr Asn Leu Ser Gly Lys Leu Ser Asn Asp
 180 185 190

Asn Pro Asn Val Lys Gln Leu Lys Arg Arg Tyr Asn Ile Pro Lys Asn
 195 200 205

Ala Ser Thr Lys Val Glu Leu Lys Gly Met Ser Asp Leu Lys Gly Asn
 210 215 220

Asn His Gln Asp Gln Lys Leu Tyr Phe Tyr Phe Ser Ser Pro Gly Lys
 225 230 235 240

Asp Gln Ile Ile Tyr Lys Glu Ser Leu Thr Tyr Asn Lys Ile Ser Glu
 245 250 255

His

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<210> SEQ ID NO 101
<211> LENGTH: 423
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 101

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

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

Ala Leu Asn Lys Asp Asn Ser Lys Asp Lys Pro Asn Gln Leu Thr Met
35     40     45

Trp Val Asp Gly Asp Lys Gln Met Ala Phe Tyr Lys Lys Ile Thr Asp
50     55     60

Gln Tyr Thr Lys Lys Thr Gly Ile Lys Val Lys Leu Val Asn Ile Gly
65     70     75     80

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

Gly Pro Asp Ile Phe Phe Leu Ala His Asp Asn Thr Gly Ser Ala Tyr
100    105    110

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

Gly Phe Asn Lys Gln Ala Leu Lys Ala Met Asn Tyr Asp Asn Lys Gln
130    135    140

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

Lys Leu Val Lys Asn Ala Pro Gln Thr Leu Glu Glu Val Glu Ala Asn
165    170    175

Ala Ala Lys Leu Thr Asp Ser Lys Lys Lys Gln Tyr Gly Met Leu Phe
180    185    190

Asp Ala Lys Asn Phe Tyr Phe Asn Tyr Pro Phe Leu Phe Gly Asn Asp
195    200    205

Asp Tyr Ile Phe Lys Lys Asn Gly Ser Glu Tyr Asp Ile His Gln Leu
210    215    220

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

Trp Tyr Asp Lys Gly Tyr Leu Pro Lys Ala Ala Thr His Asp Val Met
245    250    255

Ile Gly Leu Phe Lys Glu Gly Lys Val Gly Gln Phe Val Thr Gly Pro
260    265    270

Trp Asn Ile Asn Glu Tyr Gln Glu Thr Phe Gly Lys Asp Leu Gly Val
275    280    285

Thr Thr Leu Pro Thr Asp Gly Gly Lys Pro Met Lys Pro Phe Leu Gly
290    295    300

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

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

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

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

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

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

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

Gln Asn Asp Lys Lys Gly Asp
 420

<210> SEQ ID NO 102

<211> LENGTH: 560

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 102

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

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

Asp Ala Lys Ser Ala Leu Ser Asn Asn Ser Ile Ser Asn Asp Asn Lys
 35 40 45

Gln Lys Ala Ile Glu Gln Val Val Ser Ala Val Lys Lys Leu Ser Leu
 50 55 60

Glu Asp Asn Ser Glu Ser Asn Ala Val Lys Ser Asp Val Arg Lys Leu
 65 70 75 80

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

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

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

Ala Met Thr Lys Ala Ile Lys Asp Lys Asn Lys Ala Glu Leu Glu Ser
 130 135 140

Leu Asn Asn Ser Leu Asn Gln Ile Trp Thr Ser Asn Glu Thr Val Ile
 145 150 155 160

Arg Asn Tyr Asp Ala Asn Gln Tyr Gly Gln Ile Glu Val Ala Leu Leu
 165 170 175

Gln Leu Arg Ile Ala Ile His Lys Ser Pro Leu Asp Thr Ala Lys Val
 180 185 190

Ser His Ala Trp Thr Thr Phe Lys Ser Asn Ile Asp His Val Asp Lys
 195 200 205

Lys Ser Asn Thr Ser Ala Asn Asp Gln Tyr His Val Ser Gln Leu Asn
 210 215 220

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

Asp Ala Asp Ala Ala Leu Thr His Phe Ile Glu Thr Trp Pro Tyr Val
 245 250 255

Glu Gly Gln Ile Gln Thr Lys Asp Gly Ala Leu Tyr Thr Lys Ile Glu
 260 265 270

Asp Lys Ile Pro Tyr Tyr Gln Ser Val Leu Asp Glu His Asn Lys Ala
 275 280 285

His Val Lys Asp Gly Leu Val Asp Leu Asn Asn Gln Ile Lys Glu Val
 290 295 300

Val Gly His Ser Tyr Ser Phe Val Asp Val Met Ile Ile Phe Leu Arg
 305 310 315 320

Glu Gly Leu Glu Val Leu Leu Ile Val Met Thr Leu Thr Thr Met Thr

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

<210> SEQ ID NO 103

<211> LENGTH: 334

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 103

Met	Gln	Lys	Lys	Val	Leu	Ala	Ala	Ile	Ile	Gly	Thr	Ser	Ala	Ile	Ser
1				5						10				15	
Ala	Val	Ala	Ala	Thr	Gln	Ala	Asn	Ala	Ala	Thr	Thr	His	Thr	Val	Lys
			20					25					30		
Pro	Gly	Glu	Ser	Val	Trp	Ala	Ile	Ser	Asn	Lys	Tyr	Gly	Ile	Ser	Ile
		35					40					45			
Ala	Lys	Leu	Lys	Ser	Leu	Asn	Asn	Leu	Thr	Ser	Asn	Leu	Ile	Phe	Pro
	50					55					60				
Asn	Gln	Val	Leu	Lys	Val	Ser	Gly	Ser	Ser	Asn	Ser	Thr	Ser	Asn	Ser
	65			70						75				80	
Ser	Arg	Pro	Ser	Thr	Asn	Ser	Gly	Gly	Gly	Ser	Tyr	Tyr	Thr	Val	Gln
			85					90						95	
Ala	Gly	Asp	Ser	Leu	Ser	Leu	Ile	Ala	Ser	Lys	Tyr	Gly	Thr	Thr	Tyr
		100						105					110		
Gln	Asn	Ile	Met	Arg	Leu	Asn	Gly	Leu	Asn	Asn	Phe	Phe	Ile	Tyr	Pro
	115						120					125			
Gly	Gln	Lys	Leu	Lys	Val	Ser	Gly	Thr	Ala	Ser	Ser	Ser	Asn	Ala	Ala
	130						135					140			

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Ser Asn Ser Ser Arg Pro Ser Thr Asn Ser Gly Gly Gly Ser Tyr Tyr
145          150          155          160

Thr Val Gln Ala Gly Asp Ser Leu Ser Leu Ile Ala Ser Lys Tyr Gly
          165          170          175

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

Ile Tyr Pro Gly Gln Lys Leu Lys Val Thr Gly Asn Ala Ser Thr Asn
          195          200          205

Ser Gly Ser Ala Thr Thr Thr Asn Arg Gly Tyr Asn Thr Pro Val Phe
210          215          220

Ser His Gln Asn Leu Tyr Thr Trp Gly Gln Cys Thr Tyr His Val Phe
225          230          235          240

Asn Arg Arg Ala Glu Ile Gly Lys Gly Ile Ser Thr Tyr Trp Trp Asn
          245          250          255

Ala Asn Asn Trp Asp Asn Ala Ala Ala Ala Asp Gly Tyr Thr Ile Asp
          260          265          270

Asn Arg Pro Thr Val Gly Ser Ile Ala Gln Thr Asp Val Gly Tyr Tyr
          275          280          285

Gly His Val Met Phe Val Glu Arg Val Asn Asn Asp Gly Ser Ile Leu
290          295          300

Val Ser Glu Met Asn Tyr Ser Ala Ala Pro Gly Ile Leu Thr Tyr Arg
305          310          315          320

Thr Val Pro Ala Tyr Gln Val Asn Asn Tyr Arg Tyr Ile His
          325          330

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<210> SEQ ID NO 104

<211> LENGTH: 279

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 104

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

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

Thr Pro Val Gln His Asn Tyr Val Ser Asn Val Gln Ala Gln Thr Gln
35     40     45

Ser Pro Thr Thr Tyr Thr Val Val Ala Gly Asp Ser Leu Tyr Lys Ile
50     55     60

Ala Leu Glu His His Leu Thr Leu Asn Gln Leu Tyr Ser Tyr Asn Pro
65     70     75     80

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

Gln Asn Lys Val Lys Gln Thr Lys Ala Val Lys Ser Pro Val Arg Lys
100    105    110

Ala Ser Gln Ala Lys Lys Val Val Lys Gln Pro Val Gln Gln Ala Ser
115    120    125

Lys Lys Val Val Val Lys Gln Ala Pro Lys Gln Ala Val Thr Lys Thr
130    135    140

Val Asn Val Ala Tyr Lys Pro Ala Gln Val Gln Lys Ser Val Pro Thr
145    150    155    160

Val Pro Val Ala His Asn Tyr Asn Lys Ser Val Ala Asn Arg Gly Asn
165    170    175

Leu Tyr Ala Tyr Gly Asn Cys Thr Tyr Tyr Ala Phe Asp Arg Arg Ala
180    185    190

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Gln Leu Gly Arg Ser Ile Gly Ser Leu Trp Gly Asn Ala Asn Asn Trp
 195 200 205

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

Val Gly Ala Ile Phe Gln Thr Ala Ala Gly Pro Tyr Gly His Val Gly
 225 230 235 240

Val Val Glu Ser Val Asn Pro Asn Gly Thr Ile Thr Val Ser Glu Met
 245 250 255

Asn Tyr Ala Gly Phe Asn Val Lys Ser Ser Arg Thr Ile Leu Asn Pro
 260 265 270

Gly Lys Tyr Asn Tyr Ile His
 275

<210> SEQ ID NO 105

<211> LENGTH: 346

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 105

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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275	280	285
Leu Ala Ile Val Leu Asp	Glu Phe Gly Gly Thr	Glu Ala Ile Val Ser
290	295	300
His Glu Asp Leu Ile Glu	Glu Leu Leu Gly Met	Glu Ile Glu Asp Glu
305	310	315
Met Asp Lys Lys Glu Lys	Glu Lys Leu Ser Gln	Gln Gln Ile Gln Phe
325	330	335
Gln Gln Arg Lys Asn Arg	Asn Val Ser Ile	
340	345	

<210> SEQ ID NO 106
 <211> LENGTH: 391
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 106

Met Lys Leu Lys Pro Phe	Leu Pro Ile Leu Ile Ser	Gly Ala Val Phe
1	5	10
Ile Val Phe Leu Leu Leu	Pro Ala Ser Trp Phe Thr	Gly Leu Val Asn
20	25	30
Glu Lys Thr Val Glu Asp	Asn Arg Thr Ser Leu Thr	Asp Gln Val Leu
35	40	45
Lys Gly Thr Leu Ile Gln	Asp Lys Leu Tyr Glu Ser	Asn Lys Tyr Tyr
50	55	60
Pro Ile Tyr Gly Ser Ser	Glu Leu Gly Lys Asp Asp	Pro Phe Asn Pro
65	70	75
Ala Ile Ala Leu Asn Lys	His Asn Ala Asn Lys Lys	Ala Phe Leu Leu
85	90	95
Gly Ala Gly Gly Ser Thr	Asp Leu Ile Asn Ala Val	Glu Leu Ala Ser
100	105	110
Gln Tyr Asp Lys Leu Lys	Gly Lys Lys Leu Thr Phe	Ile Ile Ser Pro
115	120	125
Gln Trp Phe Thr Asn His	Gly Leu Thr Asn Gln Asn	Phe Asp Ala Arg
130	135	140
Met Ser Gln Thr Gln Ile	Asn Gln Met Phe Gln Gln	Lys Asn Met Ser
145	150	155
Thr Glu Leu Lys Arg Arg	Tyr Ala Gln Arg Leu Leu	Gln Phe Pro His
165	170	175
Val His Asn Lys Glu Tyr	Leu Lys Ser Tyr Ala Lys	Asn Pro Lys Glu
180	185	190
Thr Lys Asp Ser Tyr Ile	Ser Gly Phe Lys Glu Asn	Gln Leu Ile Lys
195	200	205
Ile Glu Ala Ile Lys Ser	Leu Phe Ala Met Asp Lys	Ser Pro Leu Glu
210	215	220
His Val Lys Pro Ala Thr	Lys Pro Asp Ala Ser Trp	Asp Glu Met Lys
225	230	235
Gln Lys Ala Val Glu Ile	Gly Lys Ala Asp Thr Thr	Ser Asn Lys Phe
245	250	255
Gly Ile Arg Asp Gln Tyr	Trp Lys Leu Ile Gln Glu	Ser Lys Arg Lys
260	265	270
Val Arg Arg Asp Tyr Glu	Phe Asn Val Asn Ser Pro	Glu Phe Gln Asp
275	280	285
Leu Glu Leu Leu Val Lys	Thr Met Arg Ala Ala Gly	Ala Asp Val Gln
290	295	300

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Tyr Val Ser Ile Pro Ser Asn Gly Val Trp Tyr Asp His Ile Gly Ile
 305 310 315 320
 Asp Lys Glu Arg Arg Gln Ala Val Tyr Lys Lys Ile His Ser Thr Val
 325 330 335
 Val Asp Asn Gly Gly Lys Ile Tyr Asp Met Thr Asp Lys Asp Tyr Glu
 340 345 350
 Lys Tyr Val Ile Ser Asp Ala Val His Ile Gly Trp Lys Gly Trp Val
 355 360 365
 Tyr Met Asp Glu Gln Ile Ala Lys His Met Lys Gly Glu Pro Gln Pro
 370 375 380
 Glu Val Asp Lys Pro Lys Asn
 385 390

<210> SEQ ID NO 107

<211> LENGTH: 1256

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 107

Met Ala Lys Lys Phe Asn Tyr Lys Leu Pro Ser Met Val Ala Leu Thr
 1 5 10 15
 Leu Val Gly Ser Ala Val Thr Ala His Gln Val Gln Ala Ala Glu Thr
 20 25 30
 Thr Gln Asp Gln Thr Thr Asn Lys Asn Val Leu Asp Ser Asn Lys Val
 35 40 45
 Lys Ala Thr Thr Glu Gln Ala Lys Ala Glu Val Lys Asn Pro Thr Gln
 50 55 60
 Asn Ile Ser Gly Thr Gln Val Tyr Gln Asp Pro Ala Ile Val Gln Pro
 65 70 75 80
 Lys Thr Ala Asn Asn Lys Thr Gly Asn Ala Gln Val Ser Gln Lys Val
 85 90 95
 Asp Thr Ala Gln Val Asn Gly Asp Thr Arg Ala Asn Gln Ser Ala Thr
 100 105 110
 Thr Asn Asn Thr Gln Pro Val Ala Lys Ser Thr Ser Thr Thr Ala Pro
 115 120 125
 Lys Thr Asn Thr Asn Val Thr Asn Ala Gly Tyr Ser Leu Val Asp Asp
 130 135 140
 Glu Asp Asp Asn Ser Glu Asn Gln Ile Asn Pro Glu Leu Ile Lys Ser
 145 150 155 160
 Ala Ala Lys Pro Ala Ala Leu Glu Thr Gln Tyr Lys Thr Ala Ala Pro
 165 170 175
 Lys Ala Ala Thr Thr Ser Ala Pro Lys Ala Lys Thr Glu Ala Thr Pro
 180 185 190
 Lys Val Thr Thr Phe Ser Ala Ser Ala Gln Pro Arg Ser Val Ala Ala
 195 200 205
 Thr Pro Lys Thr Ser Leu Pro Lys Tyr Lys Pro Gln Val Asn Ser Ser
 210 215 220
 Ile Asn Asp Tyr Ile Cys Lys Asn Asn Leu Lys Ala Pro Lys Ile Glu
 225 230 235 240
 Glu Asp Tyr Thr Ser Tyr Phe Pro Lys Tyr Ala Tyr Arg Asn Gly Val
 245 250 255
 Gly Arg Pro Glu Gly Ile Val Val His Asp Thr Ala Asn Asp Arg Ser
 260 265 270
 Thr Ile Asn Gly Glu Ile Ser Tyr Met Lys Asn Asn Tyr Gln Asn Ala
 275 280 285

Phe	Val	His	Ala	Phe	Val	Asp	Gly	Asp	Arg	Ile	Ile	Glu	Thr	Ala	Pro
290						295					300				
Thr	Asp	Tyr	Leu	Ser	Trp	Gly	Val	Gly	Ala	Val	Gly	Asn	Pro	Arg	Phe
305					310					315					320
Ile	Asn	Val	Glu	Ile	Val	His	Thr	His	Asp	Tyr	Ala	Ser	Phe	Ala	Arg
				325					330					335	
Ser	Met	Asn	Asn	Tyr	Ala	Asp	Tyr	Ala	Ala	Thr	Gln	Leu	Gln	Tyr	Tyr
			340					345					350		
Gly	Leu	Lys	Pro	Asp	Ser	Ala	Glu	Tyr	Asp	Gly	Asn	Gly	Thr	Val	Trp
		355					360					365			
Thr	His	Tyr	Ala	Val	Ser	Lys	Tyr	Leu	Gly	Gly	Thr	Asp	His	Ala	Asp
	370					375					380				
Pro	His	Gly	Tyr	Leu	Arg	Ser	His	Asn	Tyr	Ser	Tyr	Asp	Gln	Leu	Tyr
385					390					395					400
Asp	Leu	Ile	Asn	Glu	Lys	Tyr	Leu	Ile	Lys	Met	Gly	Lys	Val	Ala	Pro
			405						410					415	
Trp	Gly	Thr	Gln	Ser	Thr	Thr	Thr	Pro	Thr	Thr	Pro	Ser	Lys	Pro	Thr
			420					425					430		
Thr	Pro	Ser	Lys	Pro	Ser	Thr	Gly	Lys	Leu	Thr	Val	Ala	Ala	Asn	Asn
	435						440					445			
Gly	Val	Ala	Gln	Ile	Lys	Pro	Thr	Asn	Ser	Gly	Leu	Tyr	Thr	Thr	Val
	450					455					460				
Tyr	Asp	Lys	Thr	Gly	Lys	Ala	Thr	Asn	Glu	Val	Gln	Lys	Thr	Phe	Ala
465					470					475					480
Val	Ser	Lys	Thr	Ala	Thr	Leu	Gly	Asn	Gln	Lys	Phe	Tyr	Leu	Val	Gln
				485					490					495	
Asp	Tyr	Asn	Ser	Gly	Asn	Lys	Phe	Gly	Trp	Val	Lys	Glu	Gly	Asp	Val
			500					505					510		
Val	Tyr	Asn	Thr	Ala	Lys	Ser	Pro	Val	Asn	Val	Asn	Gln	Ser	Tyr	Ser
		515					520					525			
Ile	Lys	Pro	Gly	Thr	Lys	Leu	Tyr	Thr	Val	Pro	Trp	Gly	Thr	Ser	Lys
	530					535					540				
Gln	Val	Ala	Gly	Ser	Val	Ser	Gly	Ser	Gly	Asn	Gln	Thr	Phe	Lys	Ala
545					550					555					560
Ser	Lys	Gln	Gln	Gln	Ile	Asp	Lys	Ser	Ile	Tyr	Leu	Tyr	Gly	Ser	Val
				565					570					575	
Asn	Gly	Lys	Ser	Gly	Trp	Val	Ser	Lys	Ala	Tyr	Leu	Val	Asp	Thr	Ala
			580					585					590		
Lys	Pro	Thr	Pro	Thr	Pro	Thr	Pro	Lys	Pro	Ser	Thr	Pro	Thr	Thr	Asn
		595					600					605			
Asn	Lys	Leu	Thr	Val	Ser	Ser	Leu	Asn	Gly	Val	Ala	Gln	Ile	Asn	Ala
	610					615					620				
Lys	Asn	Asn	Gly	Leu	Phe	Thr	Thr	Val	Tyr	Asp	Lys	Thr	Gly	Lys	Pro
625					630					635					640
Thr	Lys	Glu	Val												

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Tyr 705	Ser	Val	Pro	Trp	Gly 710	Thr	Tyr	Lys	Gln	Glu 715	Ala	Gly	Ala	Val	Ser 720
Gly	Thr	Gly	Asn 725	Gln	Thr	Phe	Lys	Ala	Thr 730	Lys	Gln	Gln	Gln	Ile 735	Asp
Lys	Ser	Ile	Tyr 740	Leu	Phe	Gly	Thr	Val 745	Asn	Gly	Lys	Ser	Gly	Trp	Val
Ser	Lys	Ala 755	Tyr	Leu	Ala	Val	Pro 760	Ala	Ala	Pro	Lys	Lys	Ala	Val	Ala
Gln	Pro 770	Lys	Thr	Ala	Val	Lys 775	Ala	Tyr	Thr	Val	Thr 780	Lys	Pro	Gln	Thr
Thr 785	Gln	Thr	Val	Ser	Lys 790	Ile	Ala	Gln	Val	Lys 795	Pro	Asn	Asn	Thr	Gly 800
Leu	Arg	Ala	Ser 805	Val	Tyr	Glu	Lys	Thr	Ala 810	Lys	Asn	Gly	Ala	Lys	Tyr 815
Ala	Asp	Arg	Thr 820	Phe	Tyr	Val	Thr	Lys 825	Glu	Arg	Ala	His	Gly	Asn	Glu
Thr	Tyr 835	Val	Leu	Leu	Asn	Asn	Thr 840	Ser	His	Asn	Ile	Pro 845	Leu	Gly	Trp
Phe 850	Asn	Val	Lys	Asp	Leu	Asn 855	Val	Gln	Asn	Leu	Gly 860	Lys	Glu	Val	Lys
Thr 865	Thr	Gln	Lys	Tyr	Thr 870	Val	Asn	Lys	Ser	Asn 875	Asn	Gly	Leu	Ser	Met 880
Val	Pro	Trp	Gly 885	Thr	Lys	Asn	Gln	Val	Ile 890	Leu	Thr	Gly	Asn	Asn	Ile 895
Ala	Gln	Gly	Thr 900	Phe	Asn	Ala	Thr	Lys 905	Gln	Val	Ser	Val	Gly	Lys	Asp
Val	Tyr 915	Leu	Tyr	Gly	Thr	Ile	Asn 920	Asn	Arg	Thr	Gly	Trp 925	Val	Asn	Ala
Lys 930	Asp	Leu	Thr	Ala	Pro	Thr 935	Ala	Val	Lys	Pro	Thr 940	Thr	Ser	Ala	Ala
Lys 945	Asp	Tyr	Asn	Tyr	Thr 950	Tyr	Val	Ile	Lys	Asn 955	Gly	Asn	Gly	Tyr	Tyr 960
Tyr	Val	Thr	Pro 965	Asn	Ser	Asp	Thr	Ala	Lys 970	Tyr	Ser	Leu	Lys	Ala	Phe 975
Asn	Glu	Gln	Pro 980	Phe	Ala	Val	Val	Lys 985	Glu	Gln	Val	Ile	Asn	Gly	Gln 990
Thr	Trp 995	Tyr	Tyr	Gly	Lys	Leu	Ser 1000	Asn	Gly	Lys	Leu	Ala	Trp	Ile	Lys 1005
Ser 1010	Thr	Asp	Leu	Ala	Lys	Glu 1015	Leu	Ile	Lys	Tyr	Asn 1020	Gln	Thr	Gly	
Met 1025	Thr	Leu	Asn	Gln	Val	Ala 1030	Gln	Ile	Gln	Ala	Gly 1035	Leu	Gln	Tyr	
Lys 1040	Pro	Gln	Val	Gln	Arg	Val 1045	Pro	Gly	Lys	Trp	Thr 1050	Asp	Ala	Lys	
Phe 1055	Asn	Asp	Val	Lys	His	Ala 1060	Met	Asp	Thr	Lys	Arg 1065	Leu	Ala	Gln	
Asp 1070	Pro	Ala	Leu	Lys	Tyr	Gln 1075	Phe	Leu	Arg	Leu	Asp 1080	Gln	Pro	Gln	
Asn 1085	Ile	Ser	Ile	Asp	Lys	Ile 1090	Asn	Gln	Phe	Leu	Lys 1095	Gly	Lys	Gly	
Val 1100	Leu	Glu	Asn	Gln	Gly	Ala 1105	Ala	Phe	Asn	Lys	Ala 1110	Ala	Gln	Met	
Tyr	Gly	Ile	Asn	Glu	Val	Tyr	Leu	Ile	Ser	His	Ala	Leu	Leu	Glu	

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1115	1120	1125
Thr Gly Asn Gly Thr Ser Gln Leu Ala Lys Gly Ala Asp Val Val		
1130	1135	1140
Asn Asn Lys Val Val Thr Asn Ser Asn Thr Lys Tyr His Asn Val		
1145	1150	1155
Phe Gly Leu Ala Ala Tyr Asp Asn Asp Pro Leu Arg Glu Gly Ile		
1160	1165	1170
Lys Tyr Ala Lys Gln Ala Gly Trp Asp Thr Val Ser Lys Ala Ile		
1175	1180	1185
Val Gly Gly Ala Lys Phe Ile Gly Asn Ser Tyr Val Lys Ala Gly		
1190	1195	1200
Gln Asn Thr Leu Tyr Lys Met Arg Trp Asn Pro Ala His Pro Gly		
1205	1210	1215
Thr His Gln Tyr Ala Thr Asp Val Asp Trp Ala Asn Ile Asn Ala		
1220	1225	1230
Lys Ile Ile Lys Gly Tyr Tyr Asp Lys Ile Gly Glu Val Gly Lys		
1235	1240	1245
Tyr Phe Asp Ile Pro Gln Tyr Lys		
1250	1255	
<210> SEQ ID NO 108		
<211> LENGTH: 413		
<212> TYPE: PRT		
<213> ORGANISM: Staphylococcus sp		
<400> SEQUENCE: 108		
Met Lys Phe Ser Thr Leu Ser Glu Glu Glu Phe Thr Asn Tyr Thr Lys		
1	5	10 15
Lys His Phe Lys His Tyr Thr Gln Ser Ile Glu Leu Tyr Asn Tyr Arg		
	20	25 30
Asn Lys Ile Asn His Glu Ala His Ile Val Gly Val Lys Asn Asp Lys		
	35	40 45
Asn Glu Val Leu Ala Ala Cys Leu Leu Thr Glu Ala Arg Ile Phe Lys		
	50	55 60
Phe Tyr Lys Tyr Phe Tyr Ser His Arg Gly Pro Leu Leu Asp Tyr Phe		
	65	70 75 80
Asp Ala Lys Leu Val Cys Tyr Phe Phe Lys Glu Leu Ser Lys Phe Ile		
	85	90 95
Tyr Lys Asn Arg Gly Val Phe Ile Leu Val Asp Pro Tyr Leu Ile Glu		
	100	105 110
Asn Leu Arg Asp Ala Asn Gly Arg Ile Ile Lys Asn Tyr Asn Asn Ser		
	115	120 125
Val Ile Val Lys Met Leu Gly Lys Ile Gly Tyr Leu His Gln Gly Tyr		
	130	135 140
Thr Thr Gly Tyr Ser Asn Lys Ser Gln Ile Arg Trp Ile Ser Val Leu		
	145	150 155 160
Asp Leu Lys Asp Lys Asp Glu Asn Gln Leu Leu Lys Glu Met Glu Tyr		
	165	170 175
Gln Thr Arg Arg Asn Ile Lys Lys Thr Ile Glu Ile Gly Val Lys Val		
	180	185 190
Glu Asp Leu Ser Ile Glu Glu Thr Asn Arg Phe Tyr Lys Leu Phe Gln		
	195	200 205
Met Ala Glu Glu Lys His Gly Phe His Phe Met Asn Glu Asp Tyr Phe		
	210	215 220

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

<210> SEQ ID NO 109

<211> LENGTH: 428

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 109

Met Lys Glu Arg Tyr Tyr Glu Leu Ile Asp Glu Arg Val Phe Glu Gln
 1 5 10 15
 Glu Leu Glu Asn Gly Leu Arg Leu Phe Ile Ile Pro Lys Pro Gly Phe
 20 25 30
 Gln Lys Thr Phe Val Thr Tyr Thr Thr Gln Phe Gly Ser Leu Asp Asn
 35 40 45
 Gln Phe Lys Pro Leu Gly Gln Asp Gln Phe Val Thr Val Pro Asp Gly
 50 55 60
 Val Ala His Phe Leu Glu His Lys Leu Phe Glu Lys Glu Glu Asp
 65 70 75 80
 Leu Phe Thr Ala Phe Ala Glu Asp Asn Ala Gln Ala Asn Ala Phe Thr
 85 90 95
 Ser Phe Asp Arg Thr Ser Tyr Leu Phe Ser Ala Thr Asp Asn Ile Glu
 100 105 110
 Asn Asn Ile Lys Arg Leu Leu Thr Met Val Glu Thr Pro Tyr Phe Thr
 115 120 125
 Lys Glu Thr Val Asp Lys Glu Lys Gly Ile Ile Ala Glu Glu Ile Lys
 130 135 140
 Met Tyr Gln Glu Gln Pro Gly Tyr Lys Leu Met Phe Asn Thr Leu Arg
 145 150 155 160
 Ala Met Tyr Gln Gln His Pro Ile Arg Val Asp Ile Ala Gly Ser Val
 165 170 175
 Glu Ser Ile Tyr Asp Ile Thr Lys Asp Asp Leu Tyr Leu Cys Tyr Glu
 180 185 190

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

<210> SEQ ID NO 110

<211> LENGTH: 519

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 110

Met Asn Leu Leu Ser Leu Leu Leu Ile Leu Leu Gly Ile Ile Leu Gly
 1 5 10 15
 Val Val Gly Gly Tyr Val Val Ala Arg Asn Leu Leu Leu Gln Lys Gln
 20 25 30
 Ser Gln Ala Arg Gln Thr Ala Glu Asp Ile Val Asn Gln Ala His Lys
 35 40 45
 Glu Ala Asp Asn Ile Lys Lys Glu Lys Leu Leu Glu Ala Lys Glu Glu
 50 55 60
 Asn Gln Ile Leu Arg Glu Gln Thr Glu Ala Glu Leu Arg Glu Arg Arg
 65 70 75 80
 Ser Glu Leu Gln Arg Gln Glu Thr Arg Leu Leu Gln Lys Glu Glu Asn
 85 90 95
 Leu Glu Arg Lys Ser Asp Leu Leu Asp Lys Lys Asp Glu Ile Leu Glu
 100 105 110
 Gln Lys Glu Ser Lys Ile Glu Glu Lys Gln Gln Gln Val Asp Ala Lys
 115 120 125
 Glu Ser Ser Val Gln Thr Leu Ile Met Lys His Glu Gln Glu Leu Glu

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130	135	140
Arg Ile Ser Gly Leu Thr Gln Glu Glu Ala Ile Asn Glu Gln Leu Gln		
145	150	155 160
Arg Val Glu Glu Glu Leu Ser Gln Asp Ile Ala Val Leu Val Lys Glu		
	165	170 175
Lys Glu Lys Glu Ala Lys Glu Lys Val Asp Lys Thr Ala Lys Glu Leu		
	180	185 190
Leu Ala Thr Ala Val Gln Arg Leu Ala Ala Asp His Thr Ser Glu Ser		
	195	200 205
Thr Val Ser Val Val Asn Leu Pro Asn Asp Glu Met Lys Gly Arg Ile		
	210	215 220
Ile Gly Arg Glu Gly Arg Asn Ile Arg Thr Leu Glu Thr Leu Thr Gly		
	225	230 235 240
Ile Asp Leu Ile Ile Asp Asp Thr Pro Glu Ala Val Ile Leu Ser Gly		
	245	250 255
Phe Asp Pro Ile Arg Arg Glu Ile Ala Arg Thr Ala Leu Val Asn Leu		
	260	265 270
Val Ser Asp Gly Arg Ile His Pro Gly Arg Ile Glu Asp Met Val Glu		
	275	280 285
Lys Ala Arg Lys Glu Val Asp Asp Ile Ile Arg Glu Ala Gly Glu Gln		
	290	295 300
Ala Thr Phe Glu Val Asn Ala His Asn Met His Pro Asp Leu Val Lys		
	305	310 315 320
Ile Val Gly Arg Leu Asn Tyr Arg Thr Ser Tyr Gly Gln Asn Val Leu		
	325	330 335
Lys His Ser Ile Glu Val Ala His Leu Ala Ser Met Leu Ala Ala Glu		
	340	345 350
Leu Gly Glu Asp Glu Thr Leu Ala Lys Arg Ala Gly Leu Leu His Asp		
	355	360 365
Val Gly Lys Ala Ile Asp His Glu Val Glu Gly Ser His Val Glu Ile		
	370	375 380
Gly Val Glu Leu Ala Lys Lys Tyr Gly Glu Asn Glu Thr Val Ile Asn		
	385	390 395 400
Ala Ile His Ser His His Gly Asp Val Glu Pro Thr Ser Ile Ile Ser		
	405	410 415
Ile Leu Val Ala Ala Ala Asp Ala Leu Ser Ala Ala Arg Pro Gly Ala		
	420	425 430
Arg Lys Glu Thr Leu Glu Asn Tyr Ile Arg Arg Leu Glu Arg Leu Glu		
	435	440 445
Thr Leu Ser Glu Ser Tyr Asp Gly Val Glu Lys Ala Phe Ala Ile Gln		
	450	455 460
Ala Gly Arg Glu Ile Arg Val Ile Val Ser Pro Glu Glu Ile Asp Asp		
	465	470 475 480
Leu Lys Ser Tyr Arg Leu Ala Arg Asp Ile Lys Asn Gln Ile Glu Asp		
	485	490 495
Glu Leu Gln Tyr Pro Gly His Ile Lys Val Thr Val Val Arg Glu Thr		
	500	505 510
Arg Ala Val Glu Tyr Ala Lys		
	515	

<210> SEQ ID NO 111

<211> LENGTH: 284

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

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<400> SEQUENCE: 111

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

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

Val Tyr Ala Arg Lys Gln Leu Ile Lys Lys Asn Lys Ala Leu Ser Ala
          35           40           45

Glu Asn Ala Glu Leu Arg Ser Gln Met Leu Ser Ser Asn Asn Asp Val
50           55           60

Gly His His Ala Tyr Lys Asn Ala Lys Arg Glu Leu Arg Lys Ile Leu
65           70           75           80

Asp Ser Tyr Leu Glu Asn Gly Lys Leu Lys Tyr Tyr Asp Ile Ile Val
          85           90           95

Thr Ser Asn Leu Ala Thr Lys His Pro Phe Phe Glu Tyr Ala Arg Ser
          100          105          110

Phe Asp Phe Ile Ile Val Ser Asp Ile Gly Leu Ile Asn Val Asp Val
          115          120          125

Lys Ser Trp Gly Glu Lys Thr Phe Tyr His Phe Asp Val Pro Asp Glu
130          135          140

His Asp Thr Glu Ile Ser Asn Ser Asn Ile Glu Lys Val Val Gly His
145          150          155          160

Tyr Ile Ser Gln Gln Tyr His Asp Gln Phe Asn Ser Ser Arg Lys Ser
          165          170          175

Ile Tyr Thr Phe Thr Glu Thr Val Gln Pro Asn Arg Val Ile Tyr Asp
          180          185          190

Phe Tyr Asp Tyr Asp Pro Tyr Gln Leu Ala Ala Asn Asn Ala Lys Ala
195          200          205

Leu Lys Asp His Ile Glu Gln Asn Phe Asn Phe Lys Val Gln Ser Thr
210          215          220

Gly Val Ile Tyr Phe Ser Asp Gly Thr Val Asn Ile Ile Gln Gly Ser
225          230          235          240

Glu Glu Arg Asp Lys Tyr Val Asp Thr Val Ser Thr Lys Ser Ser Leu
          245          250          255

Arg Arg Ile Ile Ser Glu Ala Ile Glu Leu Ser Lys His Pro Leu Asn
          260          265          270

Lys Glu Gln Val Asp Gln Ile Thr Ala Ile Phe Lys
275          280

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<210> SEQ ID NO 112

<211> LENGTH: 1274

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 112

```

Met Ser Trp Phe Asp Lys Leu Phe Gly Glu Asp Asn Asp Ser Asn Asp
1           5           10           15

Asp Leu Ile His Arg Lys Lys Lys Arg Arg Gln Glu Ser Gln Asn Ile
          20           25           30

Asp Asn Asp His Asp Ser Leu Leu Pro Gln Asn Asn Asp Ile Tyr Ser
          35           40           45

Arg Pro Arg Gly Lys Phe Arg Phe Pro Met Ser Val Ala Tyr Glu Asn
50           55           60

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

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Tyr His Arg Asp Tyr Arg Lys Gln Ser His Asp Ser Arg Ser Gln Lys
 85 90 95
 Arg His Arg Arg Arg Arg Asn Gln Thr Thr Glu Glu Gln Asn Tyr Ser
 100 105 110
 Glu Gln Arg Gly Asn Ser Lys Ile Ser Gln Gln Ser Ile Lys Tyr Lys
 115 120 125
 Asp His Ser His Tyr His Thr Asn Lys Pro Gly Thr Tyr Val Ser Ala
 130 135 140
 Ile Asn Gly Ile Glu Lys Glu Thr His Lys Pro Lys Thr His Asn Met
 145 150 155 160
 Tyr Ser Asn Asn Thr Asn His Arg Ala Lys Asp Ser Thr Pro Asp Tyr
 165 170 175
 His Lys Glu Ser Phe Lys Thr Ser Glu Val Pro Ser Ala Ile Phe Gly
 180 185 190
 Thr Met Lys Pro Lys Lys Leu Glu Asn Gly Arg Ile Pro Val Ser Lys
 195 200 205
 Pro Ser Glu Lys Val Glu Ser Asp Lys Gln Lys Tyr Asp Lys Tyr Val
 210 215 220
 Ala Lys Thr Gln Thr Ser Gln Asn Lys Gln Leu Glu Gln Glu Lys Gln
 225 230 235 240
 Asn Asp Ser Val Val Lys Gln Gly Thr Ala Ser Lys Ser Ser Asp Glu
 245 250 255
 Asn Val Ser Ser Thr Thr Lys Ser Met Pro Asn Tyr Ser Lys Val Asp
 260 265 270
 Asn Thr Ile Lys Ile Glu Asn Ile Tyr Ala Ser Gln Ile Val Glu Glu
 275 280 285
 Ile Arg Arg Glu Arg Glu Arg Lys Val Leu Gln Lys Arg Arg Phe Lys
 290 295 300
 Lys Ala Leu Gln Gln Lys Arg Glu Glu His Lys Asn Glu Glu Gln Asp
 305 310 315 320
 Ala Ile Gln Arg Ala Ile Asp Glu Met Tyr Ala Lys Gln Ala Glu Arg
 325 330 335
 Tyr Val Gly Asp Ser Ser Leu Asn Asp Asp Ser Asp Leu Thr Asp Asn
 340 345 350
 Ser Thr Asp Ala Ser Gln Leu His Thr Asn Gly Ile Glu Asn Glu Thr
 355 360 365
 Val Ser Asn Asp Glu Asn Lys Gln Ala Ser Ile Gln Asn Glu Asp Thr
 370 375 380
 Asn Asp Thr His Val Asp Glu Ser Pro Tyr Asn Tyr Glu Glu Val Ser
 385 390 395 400
 Leu Asn Gln Val Ser Thr Thr Lys Gln Leu Ser Asp Asp Glu Val Thr
 405 410 415
 Val Ser Asn Val Thr Ser Gln His Gln Ser Ala Leu Gln His Asn Val
 420 425 430
 Glu Val Asn Asp Lys Asp Glu Leu Lys Asn Gln Ser Arg Leu Ile Ala
 435 440 445
 Asp Ser Glu Glu Asp Gly Ala Thr Asn Lys Glu Glu Tyr Ser Gly Ser
 450 455 460
 Gln Ile Asp Asp Ala Glu Phe Tyr Glu Leu Asn Asp Thr Glu Val Asp
 465 470 475 480
 Glu Asp Thr Thr Ser Asn Ile Glu Asp Asn Thr Asn Arg Asn Ala Ser
 485 490 495

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Glu	Met	His	Val	Asp	Ala	Pro	Lys	Thr	Gln	Glu	Tyr	Ala	Val	Thr	Glu	
			500					505					510			
Ser	Gln	Val	Asn	Asn	Ile	Asp	Lys	Thr	Val	Asp	Asn	Glu	Ile	Glu	Leu	
		515					520					525				
Ala	Pro	Arg	His	Lys	Lys	Asp	Asp	Gln	Thr	Asn	Leu	Ser	Val	Asn	Ser	
	530					535					540					
Leu	Lys	Thr	Asn	Asp	Val	Asn	Asp	Asn	His	Val	Val	Glu	Asp	Ser	Ser	
545					550					555					560	
Met	Asn	Glu	Ile	Glu	Lys	Asn	Asn	Ala	Glu	Ile	Thr	Glu	Asn	Val	Gln	
			565						570					575		
Asn	Glu	Ala	Ala	Glu	Ser	Glu	Gln	Asn	Val	Glu	Glu	Lys	Thr	Ile	Glu	
			580					585					590			
Asn	Val	Asn	Pro	Lys	Lys	Gln	Thr	Glu	Lys	Val	Ser	Thr	Leu	Ser	Lys	
		595				600						605				
Arg	Pro	Phe	Asn	Val	Val	Met	Thr	Pro	Ser	Asp	Lys	Lys	Arg	Met	Met	
	610					615					620					
Asp	Arg	Lys	Lys	His	Ser	Lys	Val	Asn	Val	Pro	Glu	Leu	Lys	Pro	Val	
625					630					635					640	
Gln	Ser	Lys	Gln	Ala	Val	Ser	Glu	Arg	Met	Pro	Ala	Ser	Gln	Ala	Thr	
			645						650					655		
Pro	Ser	Ser	Arg	Ser	Asp	Ser	Gln	Glu	Ser	Asn	Thr	Asn	Ala	Tyr	Lys	
			660					665					670			
Thr	Asn	Asn	Met	Thr	Ser	Asn	Asn	Val	Glu	Asn	Asn	Gln	Leu	Ile	Gly	
		675					680					685				
His	Ala	Glu	Thr	Glu	Asn	Asp	Tyr	Gln	Asn	Ala	Gln	Gln	Tyr	Ser	Glu	
	690					695					700					
Gln	Lys	Pro	Ser	Val	Asp	Ser	Thr	Gln	Thr	Glu	Ile	Phe	Glu	Glu	Ser	
705					710					715					720	
Gln	Asp	Asp	Asn	Gln	Leu	Glu	Asn	Glu	Gln	Val	Asp	Gln	Ser	Thr	Ser	
			725						730					735		
Ser	Ser	Val	Ser	Glu	Val	Ser	Asp	Ile	Thr	Glu	Glu	Ser	Glu	Glu	Thr	
			740					745					750			
Thr	His	Pro	Asn	Asn	Thr	Ser	Gly	Gln	Gln	Asp	Asn	Asp	Asp	Gln	Gln	
		755					760					765				
Lys	Asp	Leu	Gln	Ser	Ser	Phe	Ser	Asn	Lys	Asn	Glu	Asp	Thr	Ala	Asn	
	770					775					780					
Glu	Asn	Arg	Pro	Arg	Thr	Asn	Gln	Gln	Asp	Val	Ala	Thr	Asn	Gln	Ala	
785					790					795					800	
Val	Gln	Thr	Ser	Lys	Pro	Met	Ile	Arg	Lys	Gly	Pro	Asn	Ile	Lys	Leu	
				805					810					815		
Pro	Ser	Val	Ser	Leu	Leu	Glu	Glu	Pro	Gln	Val	Ile	Glu	Ser	Asp	Glu	
			820					825					830			
Asp	Trp	Ile	Thr	Asp	Lys	Lys	Lys	Glu	Leu	Asn	Asp	Ala	Leu	Phe	Tyr	
	835						840					845				
Phe	Asn	Val	Pro	Ala	Glu	Val	Gln	Asp	Val	Thr	Glu	Gly	Pro	Ser	Val	
	850					855					860					
Thr	Arg	Phe	Glu	Leu	Ser	Val	Glu	Lys	Gly	Val	Lys	Val	Ser	Arg	Ile	
865					870					875					880	
Thr	Ala	Leu	Gln	Asp	Asp	Ile	Lys	Met	Ala	Leu	Ala	Ala	Lys	Asp	Ile	
				885				890						895		
Arg	Ile	Glu	Ala	Pro	Ile	Pro	Gly	Thr	Ser	Arg	Val	Gly	Ile	Glu	Val	
		900						905					910			
Pro	Asn	Gln	Asn	Pro	Thr	Thr	Val	Asn	Leu	Arg	Ser	Ile	Ile	Glu	Ser	

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915	920	925
Pro Ser Phe Lys Asn Ala	Glu Ser Lys Leu Thr	Val Ala Met Gly Tyr
930	935	940
Arg Ile Asn Asn Glu Pro	Leu Leu Met Asp Ile	Ala Lys Thr Pro His
945	950	955 960
Ala Leu Ile Ala Gly Ala	Thr Gly Ser Gly Lys	Ser Val Cys Ile Asn
	965	970 975
Ser Ile Leu Met Ser Leu	Leu Tyr Lys Asn His	Pro Glu Glu Leu Arg
	980	985 990
Leu Leu Leu Ile Asp Pro	Lys Met Val Glu Leu Ala	Pro Tyr Asn Gly
	995	1000 1005
Leu Pro His Leu Val Ala	Pro Val Ile Thr Asp	Val Lys Ala Ala
	1010	1015 1020
Thr Gln Ser Leu Lys Trp	Ala Val Glu Glu Met	Glu Arg Arg Tyr
	1025	1030 1035
Lys Leu Phe Ala His Tyr	His Val Arg Asn Ile	Thr Ala Phe Asn
	1040	1045 1050
Lys Lys Ala Pro Tyr Asp	Glu Arg Met Pro Lys	Ile Val Ile Val
	1055	1060 1065
Ile Asp Glu Leu Ala Asp	Leu Met Met Met Ala	Pro Gln Glu Val
	1070	1075 1080
Glu Gln Ser Ile Ala Arg	Ile Ala Gln Lys Ala	Arg Ala Cys Gly
	1085	1090 1095
Ile His Met Leu Val Ala	Thr Gln Arg Pro Ser	Val Asn Val Ile
	1100	1105 1110
Thr Gly Leu Leu Lys Ala	Asn Ile Pro Thr Arg	Ile Ala Phe Met
	1115	1120 1125
Val Ser Ser Ser Val Asp	Ser Arg Thr Ile Leu	Asp Ser Gly Gly
	1130	1135 1140
Ala Glu Arg Leu Leu Gly	Tyr Gly Asp Met Leu	Tyr Leu Gly Ser
	1145	1150 1155
Gly Met Asn Lys Pro Ile	Arg Val Gln Gly Thr	Phe Val Ser Asp
	1160	1165 1170
Asp Glu Ile Asp Asp Val	Val Asp Phe Ile Lys	Gln Gln Arg Glu
	1175	1180 1185
Pro Asp Tyr Leu Phe Glu	Glu Lys Glu Leu Leu	Lys Lys Thr Gln
	1190	1195 1200
Thr Gln Ser Gln Asp Glu	Leu Phe Asp Asp Val	Cys Ala Phe Met
	1205	1210 1215
Val Asn Glu Gly His Ile	Ser Thr Ser Leu Ile	Gln Arg His Phe
	1220	1225 1230
Gln Ile Gly Tyr Asn Arg	Ala Ala Arg Ile Ile	Asp Gln Leu Glu
	1235	1240 1245
Gln Leu Gly Tyr Val Ser	Ser Ala Asn Gly Ser	Lys Pro Arg Asp
	1250	1255 1260
Val Tyr Val Thr Glu Ala	Asp Leu Asn Lys Glu	
	1265	1270

<210> SEQ ID NO 113

<211> LENGTH: 239

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 113

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Met Asn Lys Asn Ile Ile Ile Lys Ser Leu Ala Ala Leu Thr Ile Leu
1      5      10      15
Thr Ser Ile Thr Gly Val Gly Thr Thr Met Val Glu Gly Ile Gln Gln
      20      25      30
Thr Ala Lys Ala Glu Asn Thr Val Lys Gln Ile Thr Asn Thr Asn Val
      35      40      45
Ala Pro Tyr Ser Gly Val Thr Trp Met Gly Ala Gly Thr Gly Phe Val
      50      55      60
Val Gly Asn His Thr Ile Ile Thr Asn Lys His Val Thr Tyr His Met
      65      70      75      80
Lys Val Gly Asp Glu Leu Lys Ala His Pro Asn Gly Phe Tyr Asn Asn
      85      90      95
Gly Gly Gly Leu Tyr Lys Val Thr Lys Ile Val Asp Tyr Pro Gly Lys
      100      105      110
Glu Asp Ile Ala Val Val Gln Val Glu Glu Lys Ser Thr Gln Pro Lys
      115      120      125
Gly Arg Lys Phe Lys Asp Phe Thr Ser Lys Phe Asn Ile Ala Ser Glu
      130      135      140
Ala Lys Glu Asn Glu Pro Ile Ser Val Ile Gly Tyr Pro Asn Pro Asn
      145      150      155      160
Gly Asn Lys Leu Gln Met Tyr Glu Ser Thr Gly Lys Val Leu Ser Val
      165      170      175
Asn Gly Asn Ile Val Ser Ser Asp Ala Ile Ile Gln Pro Gly Ser Ser
      180      185      190
Gly Ser Pro Ile Leu Asn Ser Lys His Glu Ala Ile Gly Val Ile Tyr
      195      200      205
Ala Gly Asn Lys Pro Ser Gly Glu Ser Thr Arg Gly Phe Ala Val Tyr
      210      215      220
Phe Ser Pro Glu Ile Lys Lys Phe Ile Ala Asp Asn Leu Asp Lys
      225      230      235

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<210> SEQ ID NO 114

<211> LENGTH: 238

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 114

```

Met Asn Lys Asn Ile Ile Ile Lys Ser Leu Ala Ala Leu Thr Ile Leu
1      5      10      15
Thr Ser Val Thr Gly Val Gly Thr Thr Val Val Glu Gly Ile Gln Gln
      20      25      30
Thr Ala Lys Ala Glu His Asn Val Lys Leu Ile Lys Asn Thr Asn Val
      35      40      45
Ala Pro Tyr Asn Gly Val Val Ser Ile Gly Ser Gly Thr Gly Phe Ile
      50      55      60
Val Gly Lys Asn Thr Ile Val Thr Asn Lys His Val Val Ala Gly Met
      65      70      75      80
Glu Ile Gly Ala His Ile Ile Ala His Pro Asn Gly Glu Tyr Asn Asn
      85      90      95
Gly Gly Phe Tyr Lys Val Lys Lys Ile Val Arg Tyr Ser Gly Gln Glu
      100      105      110
Asp Ile Ala Ile Leu His Val Glu Asp Lys Ala Val His Pro Lys Asn
      115      120      125
Arg Asn Phe Lys Asp Tyr Thr Gly Ile Leu Lys Ile Ala Ser Glu Ala
      130      135      140

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Lys Glu Asn Glu Arg Ile Ser Ile Val Gly Tyr Pro Glu Pro Tyr Ile
 145 150 155 160

Asn Lys Phe Gln Met Tyr Glu Ser Thr Gly Lys Val Leu Ser Val Lys
 165 170 175

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

Ser Ala Val Phe Asn Ser Lys Tyr Glu Val Val Gly Val His Phe Gly
 195 200 205

Gly Asn Gly Pro Gly Asn Lys Ser Thr Lys Gly Tyr Gly Val Tyr Phe
 210 215 220

Ser Pro Glu Ile Lys Lys Phe Ile Ala Asp Asn Thr Asp Lys
 225 230 235

<210> SEQ ID NO 115
 <211> LENGTH: 239
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 115

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

Thr Ser Ile Thr Gly Val Gly Thr Thr Val Val Asp Gly Ile Gln Gln
 20 25 30

Thr Ala Lys Ala Glu Asn Ser Val Lys Leu Ile Thr Asn Thr Asn Val
 35 40 45

Ala Pro Tyr Ser Gly Val Thr Trp Met Gly Ala Gly Thr Gly Phe Val
 50 55 60

Val Gly Asn His Thr Ile Ile Thr Asn Lys His Val Thr Tyr His Met
 65 70 75 80

Lys Val Gly Asp Glu Leu Lys Ala His Pro Asn Gly Phe Tyr Asn Asn
 85 90 95

Gly Gly Gly Leu Tyr Lys Val Thr Lys Ile Val Asp Tyr Pro Gly Lys
 100 105 110

Glu Asp Ile Ala Val Val Gln Val Glu Glu Lys Ser Thr Gln Pro Lys
 115 120 125

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

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

Gly Asn Lys Leu Gln Met Tyr Glu Ser Thr Gly Lys Val Leu Ser Val
 165 170 175

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

Gly Ser Pro Ile Leu Asn Ser Lys Arg Glu Ala Ile Gly Val Met Tyr
 195 200 205

Ala Ser Asp Lys Pro Thr Gly Glu Ser Thr Arg Ser Phe Ala Val Tyr
 210 215 220

Phe Ser Pro Glu Ile Lys Lys Phe Ile Ala Asp Asn Leu Asp Lys
 225 230 235

<210> SEQ ID NO 116
 <211> LENGTH: 239
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 116

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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

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<210> SEQ ID NO 117

<211> LENGTH: 240

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 117

```

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

Thr Ser Val Thr Gly Ile Gly Thr Thr Leu Val Glu Glu Val Gln Gln
           20           25           30

Thr Ala Lys Ala Glu Asn Asn Val Thr Lys Val Lys Asp Thr Asn Ile
           35           40           45

Phe Pro Tyr Thr Gly Val Val Ala Phe Lys Ser Ala Thr Gly Phe Val
           50           55           60

Val Gly Lys Asn Thr Ile Leu Thr Asn Lys His Val Ser Lys Asn Tyr
65           70           75           80

Lys Val Gly Asp Arg Ile Thr Ala His Pro Asn Ser Asp Lys Gly Asn
           85           90           95

Gly Gly Ile Tyr Ser Ile Lys Lys Ile Ile Asn Tyr Pro Gly Lys Glu
           100          105          110

Asp Val Ser Val Ile Gln Val Glu Glu Arg Ala Ile Glu Arg Gly Pro
           115          120          125

Lys Gly Phe Asn Phe Asn Asp Asn Val Thr Pro Phe Lys Tyr Ala Ala

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130	135	140													
Gly	Ala	Lys	Ala	Gly	Glu	Arg	Ile	Lys	Val	Ile	Gly	Tyr	Pro	His	Pro
145				150						155					160
Tyr	Lys	Asn	Lys	Tyr	Val	Leu	Tyr	Glu	Ser	Thr	Gly	Pro	Val	Met	Ser
			165						170					175	
Val	Glu	Gly	Ser	Ser	Ile	Val	Tyr	Ser	Ala	His	Thr	Glu	Ser	Gly	Asn
			180					185					190		
Ser	Gly	Ser	Pro	Val	Leu	Asn	Ser	Asn	Asn	Glu	Leu	Val	Gly	Ile	His
		195					200					205			
Phe	Ala	Ser	Asp	Val	Lys	Asn	Asp	Asp	Asn	Arg	Asn	Ala	Tyr	Gly	Val
210					215						220				
Tyr	Phe	Thr	Pro	Glu	Ile	Lys	Lys	Phe	Ile	Ala	Glu	Asn	Ile	Asp	Lys
225					230					235					240

<210> SEQ ID NO 118

<211> LENGTH: 235

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 118

Met	Asn	Lys	Asn	Val	Met	Val	Lys	Gly	Leu	Thr	Ala	Leu	Thr	Ile	Leu
1			5						10					15	
Thr	Ser	Leu	Gly	Phe	Ala	Glu	Asn	Ile	Ser	Asn	Gln	Pro	His	Ser	Ile
		20						25					30		
Ala	Lys	Ala	Glu	Lys	Asn	Val	Lys	Glu	Ile	Thr	Asp	Ala	Thr	Lys	Glu
		35				40						45			
Pro	Tyr	Asn	Ser	Val	Val	Ala	Phe	Val	Gly	Gly	Thr	Gly	Val	Val	Val
	50					55					60				
Gly	Lys	Asn	Thr	Ile	Val	Thr	Asn	Lys	His	Ile	Ala	Lys	Ser	Asn	Asp
65				70						75					80
Ile	Phe	Lys	Asn	Arg	Val	Ser	Ala	His	His	Ser	Ser	Lys	Gly	Lys	Gly
			85						90					95	
Gly	Gly	Asn	Tyr	Asp	Val	Lys	Asp	Ile	Val	Glu	Tyr	Pro	Gly	Lys	Glu
		100						105					110		
Asp	Leu	Ala	Ile	Val	His	Val	His	Glu	Thr	Ser	Thr	Glu	Gly	Leu	Asn
		115				120						125			
Phe	Asn	Lys	Asn	Val	Ser	Tyr	Thr	Lys	Phe	Ala	Asp	Gly	Ala	Lys	Val
	130					135					140				
Lys	Asp	Arg	Ile	Ser	Val	Ile	Gly	Tyr	Pro	Lys	Gly	Ala	Gln	Thr	Lys
145				150						155					160
Tyr	Lys	Met	Phe	Glu	Ser	Thr	Gly	Thr	Ile	Asn	His	Ile	Ser	Gly	Thr
			165					170						175	
Phe	Met	Glu	Phe	Asp	Ala	Tyr	Ala	Gln	Pro	Gly	Asn	Ser	Gly	Ser	Pro
		180						185					190		
Val	Leu	Asn	Ser	Lys	His	Glu	Leu	Ile	Gly	Ile	Leu	Tyr	Ala	Gly	Ser
	195						200					205			
Gly	Lys	Asp	Glu	Ser	Glu	Lys	Asn	Phe	Gly	Val	Tyr	Phe	Thr	Pro	Gln
210					215						220				
Leu	Lys	Glu	Phe	Ile	Gln	Asn	Asn	Ile	Glu	Lys					
225					230				235						

<210> SEQ ID NO 119

<211> LENGTH: 163

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

-continued

<400> SEQUENCE: 119

```

Met Leu Lys Arg Ser Leu Leu Phe Leu Thr Val Leu Leu Leu Leu Phe
1           5           10           15
Ser Phe Ser Ser Ile Thr Asn Glu Val Ser Ala Ser Ser Ser Phe Asp
          20           25           30
Lys Gly Lys Tyr Lys Lys Gly Asp Asp Ala Ser Tyr Phe Glu Pro Thr
          35           40           45
Gly Pro Tyr Leu Met Val Asn Val Thr Gly Val Asp Gly Lys Gly Asn
          50           55           60
Glu Leu Leu Ser Pro His Tyr Val Glu Phe Pro Ile Lys Pro Gly Thr
          65           70           75           80
Thr Leu Thr Lys Glu Lys Ile Glu Tyr Tyr Val Glu Trp Ala Leu Asp
          85           90           95
Ala Thr Ala Tyr Lys Glu Phe Arg Val Val Glu Leu Asp Pro Ser Ala
          100          105          110
Lys Ile Glu Val Thr Tyr Tyr Asp Lys Asn Lys Lys Lys Glu Glu Thr
          115          120          125
Lys Ser Phe Pro Ile Thr Glu Lys Gly Phe Val Val Pro Asp Leu Ser
          130          135          140
Glu His Ile Lys Asn Pro Gly Phe Asn Leu Ile Thr Lys Val Ile Ile
          145          150          155          160
Glu Lys Lys

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<210> SEQ ID NO 120

<211> LENGTH: 290

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 120

```

Met Lys Lys Lys Ala Leu Leu Pro Leu Phe Leu Gly Ile Met Val Phe
1           5           10           15
Leu Ala Gly Cys Asp Tyr Ser Lys Pro Glu Lys Arg Ser Gly Phe Phe
          20           25           30
Tyr Asn Thr Phe Val Asp Pro Met Lys Asn Val Leu Asp Trp Leu Gly
          35           40           45
Asn Asn Leu Leu Asn Asp Asn Tyr Gly Leu Ala Ile Ile Ile Leu Val
          50           55           60
Leu Val Ile Arg Ile Ile Leu Leu Pro Phe Met Leu Ser Asn Tyr Lys
          65           70           75           80
Asn Ser His Met Met Arg Gln Lys Met Lys Val Ala Lys Pro Glu Val
          85           90           95
Glu Lys Ile Gln Glu Lys Val Lys Arg Ala Arg Thr Gln Glu Glu Lys
          100          105          110
Met Ala Ala Asn Gln Glu Leu Met Gln Val Tyr Lys Lys Tyr Asp Met
          115          120          125
Asn Pro Ile Lys Ser Met Leu Gly Cys Leu Pro Met Leu Ile Gln Leu
          130          135          140
Pro Ile Ile Met Gly Leu Tyr Phe Val Leu Lys Asp Gln Leu Val Asp
          145          150          155          160
Gly Leu Phe Lys Tyr Pro His Phe Leu Trp Phe Asp Leu Gly Arg Pro
          165          170          175
Asp Ile Trp Ile Thr Ile Ile Ala Gly Val Leu Tyr Phe Ile Gln Ala
          180          185          190
Tyr Val Ser Ser Lys Thr Met Pro Asp Glu Gln Arg Gln Met Gly Tyr

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195					200					205					
Met	Met	Met	Val	Ile	Ser	Pro	Ile	Met	Ile	Ile	Trp	Ile	Ser	Leu	Ser
210						215					220				
Ser	Ala	Ser	Ala	Leu	Gly	Leu	Tyr	Trp	Ser	Val	Ser	Ala	Ala	Phe	Leu
225					230					235					240
Val	Val	Gln	Thr	His	Phe	Ala	Asn	Ile	Tyr	Tyr	Glu	Lys	Val	Ala	Lys
				245					250					255	
Lys	Glu	Val	Gln	Pro	Phe	Ile	Glu	Ala	Tyr	Glu	Arg	Glu	His	Asn	Gly
		260					265						270		
Gly	Ser	Asn	Lys	Lys	Gly	Lys	Asn	Thr	Gln	Val	Val	Ser	Lys	Lys	Lys
		275					280					285			
Lys	Lys														
		290													
<210> SEQ ID NO 121															
<211> LENGTH: 460															
<212> TYPE: PRT															
<213> ORGANISM: Staphylococcus sp															
<400> SEQUENCE: 121															
Met	Lys	Ser	Cys	Pro	Lys	Cys	Gly	Gln	Gln	Ala	Gln	Asp	Asp	Val	Gln
1				5				10						15	
Ile	Cys	Thr	Gln	Cys	Gly	His	Lys	Phe	Asp	Ser	Arg	Gln	Ala	Leu	Tyr
		20						25					30		
Arg	Lys	Ser	Thr	Asp	Glu	Asp	Ile	Gln	Thr	Asn	Asn	Ile	Lys	Met	Arg
		35				40						45			
Lys	Met	Val	Pro	Trp	Ala	Ile	Gly	Phe	Phe	Ile	Leu	Ile	Leu	Ile	Ile
	50					55				60					
Ile	Leu	Phe	Phe	Leu	Leu	Arg	Asn	Phe	Asn	Ser	Pro	Glu	Ala	Gln	Thr
65				70						75				80	
Lys	Ile	Leu	Val	Asn	Ala	Ile	Glu	Asn	Asn	Asp	Lys	Gln	Lys	Val	Ala
			85					90						95	
Thr	Leu	Leu	Ser	Thr	Lys	Asp	Asn	Lys	Val	Asp	Ser	Glu	Glu	Ala	Lys
		100						105					110		
Val	Tyr	Ile	Asn	Tyr	Ile	Lys	Asp	Glu	Val	Gly	Leu	Lys	Gln	Phe	Val
		115				120					125				
Ser	Asp	Leu	Lys	Asn	Thr	Val	His	Lys	Leu	Asn	Lys	Ser	Lys	Thr	Ser
	130					135					140				
Val	Ala	Ser	Tyr	Ile	Gln	Thr	Arg	Ser	Gly	Gln	Asn	Ile	Leu	Arg	Val
145					150					155				160	
Ser	Lys	Asn	Gly	Thr	Arg	Tyr	Ile	Phe	Phe	Asp	Asn	Met	Ser	Phe	Thr
			165						170					175	
Ala	Pro	Thr	Lys	Gln	Pro	Ile	Val	Lys	Pro	Lys	Glu	Lys	Thr	Lys	Tyr
			180					185					190		
Glu	Phe	Lys	Ser	Gly	Gly	Lys	Lys	Lys	Met	Val	Ile	Ala	Glu	Ala	Asn
		195				200					205				
Lys	Val	Thr	Pro	Ile	Gly	Asn	Phe	Ile	Pro	Gly	Thr	Tyr	Arg	Ile	Pro
	210					215					220				
Ala	Met	Lys	Ser	Thr	Glu	Asn	Gly	Asp	Phe	Ala	Gly	His	Leu	Lys	Phe
225					230					235				240	
Asp	Phe	Arg	Gln	Ser	Asn	Ser	Glu	Thr	Val	Asp	Val	Thr	Glu	Asp	Phe
			245					250						255	
Glu	Glu	Ala	Asn	Ile	Ser	Val	Thr	Leu	Lys	Gly	Asp	Thr	Lys	Leu	Asn
		260						265					270		

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Asp Ser Ser Lys Lys Val Thr Ile Asn Asp His Glu Met Ala Phe Ser
    275                                280                285

Ser Ser Lys Thr Tyr Gly Pro Tyr Pro Gln Asn Lys Asp Ile Thr Ile
    290                                295                300

Ser Ala Ser Gly Lys Ala Lys Asp Lys Thr Phe Thr Thr Gln Thr Lys
    305                                310                315                320

Thr Leu Lys Ala Ser Asp Leu Lys Tyr Asn Thr Glu Ile Thr Leu Asn
    325                                330                335

Phe Asp Ser Glu Asp Ile Glu Asp Tyr Val Glu Lys Lys Glu Lys Glu
    340                                345                350

Glu Asn Ser Leu Lys Asn Lys Leu Ile Glu Phe Phe Ala Gly Tyr Ser
    355                                360                365

Leu Ala Asn Asn Ala Ala Phe Asn Gln Ser Asp Phe Asp Phe Val Ser
    370                                375                380

Ser Tyr Ile Lys Lys Gly Ser Ser Phe Tyr Asp Asp Val Lys Lys Arg
    385                                390                395                400

Val Ser Lys Gly Ser Leu Met Met Ile Ser Ser Pro Gln Ile Ile Asp
    405                                410                415

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

Glu Asn Gly Lys Gln Val Asp Lys Glu Tyr Glu Leu Glu Gln Gly Ser
    435                                440                445

Gln Asp Arg Leu Gln Leu Ile Lys Thr Ser Glu Lys
    450                                455                460

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<210> SEQ ID NO 122

<211> LENGTH: 322

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 122

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

Tyr Ala His Ile Arg Ile Lys Glu Lys Arg Ser Val Lys Ser Tyr Met
  20      25      30

Leu Glu Gln Gly Ile Arg Leu Ser Arg Ala Lys Arg Arg Phe Met Tyr
  35      40      45

Lys Glu Glu Ala Met Lys Ala Leu Glu Lys Met Ala Pro Gln Thr Ala
  50      55      60

Gly Glu Tyr Glu Gly Thr Asn Tyr Gln Phe Lys Met Pro Val Lys Val
  65      70      75      80

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

Lys His Gln Arg Val Val Leu Tyr Ala His Gly Gly Ala Trp Phe Gln
  100     105     110

Asp Pro Leu Lys Ile His Phe Glu Phe Ile Asp Glu Leu Ala Glu Thr
  115     120     125

Leu Asn Ala Lys Val Ile Met Pro Val Tyr Pro Lys Ile Pro His Gln
  130     135     140

Asp Tyr Gln Ala Thr Tyr Val Leu Phe Glu Lys Leu Tyr His Asp Leu
  145     150     155     160

Leu Asn Gln Val Ala Asp Ser Lys Gln Ile Val Val Met Gly Asp Ser
  165     170     175

Ala Gly Gly Gln Ile Ala Leu Ser Phe Ala Gln Leu Leu Lys Glu Lys
  180     185     190

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His Ile Val Gln Pro Gly His Ile Val Leu Ile Ser Pro Val Leu Asp
 195 200 205
 Ala Thr Met Gln His Pro Glu Ile Pro Asp Tyr Leu Lys Lys Asp Pro
 210 215 220
 Met Val Gly Val Asp Gly Ser Val Phe Leu Ala Glu Gln Trp Ala Gly
 225 230 235 240
 Asp Thr Pro Leu Asp Asn Tyr Lys Val Ser Pro Ile Asn Gly Asp Leu
 245 250 255
 Asp Gly Leu Gly Arg Ile Thr Leu Thr Val Gly Thr Lys Glu Val Leu
 260 265 270
 Tyr Pro Asp Ala Leu Asn Leu Ser Gln Leu Leu Ser Ala Lys Gly Ile
 275 280 285
 Glu His Asp Phe Ile Pro Gly Tyr Tyr Gln Phe His Ile Tyr Pro Val
 290 295 300
 Phe Pro Ile Pro Glu Arg Arg Arg Phe Leu Tyr Gln Val Lys Asn Ile
 305 310 315 320
 Ile Asn

<210> SEQ ID NO 123
 <211> LENGTH: 143
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 123

Met Glu Tyr Lys Lys Ile Leu Ile Arg Leu Leu Ile Ala Phe Ala Val
 1 5 10 15
 Leu Phe Ser Ala Asp Phe Thr Tyr Gln Ser Val Glu Gln Thr His Gln
 20 25 30
 Ser His Ala Ala Val Asn Tyr Tyr Ser Lys Asn Gln Cys Thr Trp Trp
 35 40 45
 Ala Phe Lys Arg Arg Ala Gln Val Gly Lys Pro Val Ser Asn Arg Trp
 50 55 60
 Gly Asn Ala Lys Asn Trp Tyr Tyr Asn Ala Arg Lys Ser Lys Tyr Ala
 65 70 75 80
 Thr Gly Arg Thr Pro Arg Lys Phe Ala Val Met Gln Ser Thr Ala Gly
 85 90 95
 Tyr Tyr Gly His Val Ala Val Val Glu Gln Val Tyr Lys Asn Gly Ser
 100 105 110
 Ile Lys Val Ser Glu Tyr Asn Phe Tyr Arg Pro Leu Lys Tyr Asn Thr
 115 120 125
 Arg Val Leu Ser Lys Lys Ala Ala Arg Asn Phe Asn Tyr Ile Tyr
 130 135 140

<210> SEQ ID NO 124
 <211> LENGTH: 255
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 124

Met Lys Lys Ile Val Thr Ala Thr Ile Ala Thr Ala Gly Leu Ala Thr
 1 5 10 15
 Ile Ala Phe Ala Gly His Asp Ala Gln Ala Ala Glu Gln Asn Asn Asn
 20 25 30
 Gly Tyr Asn Ser Asn Asp Ala Gln Ser Tyr Ser Tyr Thr Tyr Thr Ile
 35 40 45

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

Ser Gln Leu Thr Gln Asn Asn Thr Tyr Tyr Tyr Asn Asn Tyr Asn Thr
 65          70          75          80

Tyr Ser Tyr Asn Asn Ala Ser Tyr Asn Asn Tyr Tyr Asn His Ser Tyr
          85          90          95

Gln Tyr Asn Asn Tyr Thr Asn Asn Ser Gln Thr Ala Thr Asn Asn Tyr
          100          105          110

Tyr Thr Gly Gly Ser Gly Ala Ser Tyr Ser Thr Thr Ser Asn Asn Val
          115          120          125

His Val Thr Thr Thr Ala Ala Pro Ser Ser Asn Gly Arg Ser Ile Ser
          130          135          140

Asn Gly Tyr Ala Ser Gly Ser Asn Leu Tyr Thr Ser Gly Gln Cys Thr
          145          150          155          160

Tyr Tyr Val Phe Asp Arg Val Gly Gly Lys Ile Gly Ser Thr Trp Gly
          165          170          175

Asn Ala Ser Asn Trp Ala Asn Ala Ala Ala Ser Ser Gly Tyr Thr Val
          180          185          190

Asn Asn Thr Pro Lys Val Gly Ala Ile Met Gln Thr Thr Gln Gly Tyr
          195          200          205

Tyr Gly His Val Ala Tyr Val Glu Gly Val Asn Ser Asn Gly Ser Val
          210          215          220

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

Arg Thr Ile Ser Ala Asn Gln Ala Gly Ser Tyr Asn Phe Ile His
          245          250          255

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<210> SEQ ID NO 125
<211> LENGTH: 131
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

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<400> SEQUENCE: 125

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

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

Asn Leu Gln Lys Glu Asn Lys Glu Leu Lys Asp Lys Lys Glu Lys Leu
          35          40          45

Gln Gln Glu Lys Glu Lys Leu Ala Asp Lys Gln Lys Asp Leu Glu Lys
          50          55          60

Glu Val Lys Asp Leu Lys Pro Ser Lys Glu Asp Asn Lys Asp Asp Lys
          65          70          75          80

Lys Asp Glu Asp Lys Asn Lys Asp Lys Asp Lys Asp Lys Glu Ala Ser
          85          90          95

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

His Lys Lys Pro Thr Ser Ala Asp Lys Asp Gln Lys Ala Asn Asp Lys
          115          120          125

His Gln Ser
          130

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<210> SEQ ID NO 126
<211> LENGTH: 192
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

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<400> SEQUENCE: 126

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

Ser Leu Leu Phe Thr Ile Ile Tyr Ile Asp Asp Ile Gln Lys Trp Phe
      20           25           30

Asn Gln Tyr Thr Asp Lys Leu Thr Gln Asn His Lys Gly Gln Gly His
      35           40           45

Ser Lys Trp Glu Asp Phe Phe Arg Gly Ser Arg Ile Thr Glu Thr Phe
      50           55           60

Gly Lys Tyr Gln His Ser Pro Phe Asp Gly Lys His Tyr Gly Ile Asp
      65           70           75           80

Phe Ala Leu Pro Lys Gly Thr Pro Leu Lys Ala Pro Thr Asn Gly Lys
      85           90           95

Val Thr Arg Ile Phe Asn Asn Glu Leu Gly Gly Lys Val Leu Gln Ile
      100          105          110

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

Tyr Asn Val Lys Val Gly Asp Arg Val Lys Ala Gly Asp Ile Ile Ala
      130          135          140

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

Gln Arg Met Lys Gly Gly Val Gly Asn Ala Tyr Ala Glu Asp Pro Lys
      165          170          175

Pro Phe Ile Asp Gln Leu Pro Asp Gly Glu Arg Ser Leu Tyr Asp Leu
      180          185          190

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<210> SEQ ID NO 127

<211> LENGTH: 505

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 127

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Met Thr Gln Gln Gln Asn Asp Lys Arg Thr Leu Lys Asn Lys His Thr
 1           5           10           15

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

Ile Thr Gly Ala Leu Val Gly Ser Ala Leu Gly Leu Tyr Phe Lys Asn
      35           40           45

Lys Val Tyr Gln Lys Ala Asp Asp Leu Lys Val Lys Glu Gln Glu Leu
      50           55           60

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

Tyr Thr Lys Glu Arg Val Glu Gly Phe Leu Asn Lys Ser Lys Asn Glu
      85           90           95

Gln Ala Ala Leu Lys Ala Gln Gln Ala Ala Ile Lys Glu Glu Ala Ser
      100          105          110

Ala Asn Asn Leu Ser Asp Thr Ser Gln Glu Ala Gln Glu Ile Gln Glu
      115          120          125

Ala Lys Arg Glu Ala Gln Ala Glu Ala Asp Lys Ser Val Ala Val Ser
      130          135          140

Asn Lys Glu Ser Lys Ala Val Ala Leu Lys Ala Gln Gln Ala Ala Ile
      145          150          155          160

Lys Glu Glu Ala Ser Ala Asn Asn Leu Ser Asp Thr Ser Gln Glu Ala
      165          170          175

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Gln Glu Ile Gln Glu Ala Lys Lys Glu Ala Gln Ala Glu Thr Asp Lys
 180 185 190
 Ser Ala Ala Val Ser Asn Glu Glu Pro Lys Ala Val Ala Leu Lys Ala
 195 200 205
 Gln Gln Ala Ala Ile Lys Glu Glu Ala Ser Ala Asn Asn Leu Ser Asp
 210 215 220
 Thr Ser Gln Glu Ala Gln Glu Val Gln Glu Ala Lys Lys Glu Ala Gln
 225 230 235 240
 Ala Glu Thr Asp Lys Ser Ala Ala Val Ser Asn Glu Glu Pro Lys Ala
 245 250 255
 Val Ala Leu Lys Ala Gln Gln Ala Ala Ile Lys Glu Glu Ala Ser Ala
 260 265 270
 Asn Asn Leu Ser Asp Ile Ser Gln Glu Ala Gln Glu Val Gln Glu Ala
 275 280 285
 Lys Lys Glu Ala Gln Ala Glu Lys Asp Ser Asp Thr Leu Thr Lys Asp
 290 295 300
 Ala Ser Ala Ala Lys Val Glu Val Ser Lys Pro Glu Ser Gln Ala Glu
 305 310 315 320
 Arg Leu Ala Asn Ala Ala Lys Gln Lys Gln Ala Lys Leu Thr Pro Gly
 325 330 335
 Ser Lys Glu Ser Gln Leu Thr Glu Ala Leu Phe Ala Glu Lys Pro Val
 340 345 350
 Ala Lys Asn Asp Leu Lys Glu Ile Pro Gln Leu Val Thr Lys Lys Asn
 355 360 365
 Asp Val Ser Glu Thr Glu Thr Val Asn Ile Asp Asn Lys Asp Thr Val
 370 375 380
 Lys Gln Lys Glu Ala Lys Phe Glu Asn Gly Val Ile Thr Arg Lys Ala
 385 390 395 400
 Asp Glu Lys Thr Thr Asn Asn Thr Ala Val Asp Lys Lys Ser Gly Lys
 405 410 415
 Gln Ser Lys Lys Thr Thr Pro Ser Asn Lys Arg Asn Ala Ser Lys Ala
 420 425 430
 Ser Thr Asn Lys Thr Ser Gly Gln Lys Lys Gln His Asn Lys Lys Ser
 435 440 445
 Ser Gln Gly Ala Lys Lys Gln Ser Ser Ser Ser Lys Ser Thr Gln Lys
 450 455 460
 Asn Asn Gln Thr Ser Asn Lys Asn Ser Lys Thr Thr Asn Ala Lys Ser
 465 470 475 480
 Ser Asn Ala Ser Lys Thr Pro Asn Ala Lys Val Glu Lys Ala Lys Ser
 485 490 495
 Lys Ile Glu Lys Arg Thr Phe Asn Asp
 500 505

<210> SEQ ID NO 128

<211> LENGTH: 305

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 128

Met Phe Lys Arg Thr Lys Leu Ile Leu Ile Ala Thr Leu Leu Leu Ser
 1 5 10 15
 Gly Cys Ser Thr Thr Asn Asn Glu Ser Asn Lys Glu Thr Lys Ser Val
 20 25 30
 Pro Glu Glu Met Glu Ala Ser Lys Tyr Val Gly Gln Gly Phe Gln Pro

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35	40	45
Pro Ala Glu Lys Asp Val	Val Glu Phe Ala Lys	Lys His Lys Asp Lys
50	55	60
Ile Ala Lys Arg Gly Glu	Gln Phe Phe Met Asp	Asn Phe Gly Leu Lys
65	70	75 80
Val Lys Ala Thr Asn Val	Val Gly Ser Gly Lys	Gly Val Glu Val Phe
	85	90 95
Val His Cys Asp Asp His	Asp Ile Val Phe Asn Ala	Ser Ile Pro Phe
	100	105 110
Asp Lys Ser Ile Ile Glu	Ser Asp Ser Ser Leu Arg	Ser Glu Asp Lys
	115	120 125
Gly Asp Asp Met Ser Thr	Leu Val Gly Thr Val	Leu Ser Gly Phe Glu
	130	135 140
Tyr Arg Thr Gln Lys Glu	Lys Tyr Asp Asn Leu	Tyr Lys Phe Phe Lys
	145	150 155 160
Asp Asn Glu Glu Lys Tyr	Gln Tyr Thr Gly Phe	Thr Lys Glu Ala Ile
	165	170 175
Asn Lys Thr Gln Asn Val	Gly Tyr Lys Asn Glu	Tyr Phe Tyr Ile Thr
	180	185 190
Tyr Ser Ser Arg Ser Leu	Lys Glu Tyr Arg Lys	Tyr Tyr Glu Pro Leu
	195	200 205
Ile His Lys Asn Asp Lys	Glu Phe Lys Glu Gly	Met Glu Gln Ala Arg
	210	215 220
Lys Glu Val Asn Tyr Ala	Ala Asn Thr Asp Thr	Val Thr Thr Leu Phe
	225	230 235 240
Ser Thr Lys Glu Asn Phe	Thr Lys Asp Asn Thr	Val Asp Asp Val Ile
	245	250 255
Glu Leu Ser Asp Lys Leu	Tyr Asn Phe Lys Asn	Lys Pro Glu Lys Ser
	260	265 270
Thr Ile Thr Ile Gln Ile	Gly Lys Pro Thr Ile	Asn Thr Lys Lys Ala
	275	280 285
Phe Tyr Asp Asp Asn Asp	Pro Ile Glu Tyr Gly	Val Tyr Arg Lys Asp
	290	295 300
Glu		
305		

<210> SEQ ID NO 129

<211> LENGTH: 226

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 129

Met Lys Phe Lys Ala Ile	Ala Lys Ala Ser Leu	Ala Leu Gly Met Leu
1	5	10 15
Ala Thr Gly Val Ile Thr	Ser Asn Val Gln Ser	Val Gln Ala Lys Ala
	20	25 30
Glu Val Lys Gln Gln Ser	Glu Ser Glu Leu Lys	His Tyr Tyr Asn Lys
	35	40 45
Pro Ile Leu Glu Arg Lys	Asn Val Thr Gly Phe	Lys Tyr Thr Asp Glu
	50	55 60
Gly Lys His Tyr Leu Glu	Val Thr Val Gly Gln	Gln His Ser Arg Ile
	65	70 75 80
Thr Leu Leu Gly Ser Asp	Lys Asp Lys Phe Lys	Asp Gly Glu Asn Ser
	85	90 95

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Asn Ile Asp Val Phe Ile Leu Arg Glu Gly Asp Ser Arg Gln Ala Thr
    100                      105                      110

Asn Tyr Ser Ile Gly Gly Val Thr Lys Ser Asn Ser Val Gln Tyr Ile
    115                      120                      125

Asp Tyr Ile Asn Thr Pro Ile Leu Glu Ile Lys Lys Asp Asn Glu Asp
    130                      135                      140

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

Glu Leu Asp Tyr Arg Leu Arg Glu Arg Ala Ile Lys Gln His Gly Leu
                      165                      170                      175

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

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

Met Gly Glu Ser Ile Asp Gly Thr Lys Ile Asn Lys Ile Leu Val Glu
    210                      215                      220

Met Lys
225

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<210> SEQ ID NO 130
<211> LENGTH: 231
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

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<400> SEQUENCE: 130

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

Ala Thr Gly Val Asn Thr Thr Thr Glu Lys Pro Val His Ala Glu Lys
20     25     30

Lys Pro Ile Val Ile Ser Glu Asn Ser Lys Lys Leu Lys Ala Tyr Tyr
35     40     45

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

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

Asn Asn Ile Ala Leu Ile Gly Lys Asp Lys Gln His Tyr His Thr Gly
85     90     95

Val His Arg Asn Leu Asn Ile Phe Tyr Val Asn Glu Asp Lys Arg Phe
100    105    110

Glu Gly Ala Lys Tyr Ser Ile Gly Gly Ile Thr Ser Ala Asn Asp Lys
115    120    125

Ala Val Asp Leu Ile Ala Glu Ala Arg Val Ile Lys Glu Asp His Thr
130    135    140

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

Met Ser Leu Lys Glu Ile Asp Phe Lys Leu Arg Lys Tyr Leu Ile Asp
165    170    175

Asn Tyr Gly Leu Tyr Gly Glu Met Ser Thr Gly Lys Ile Thr Val Lys
180    185    190

Lys Lys Tyr Tyr Gly Lys Tyr Thr Phe Glu Leu Asp Lys Lys Leu Gln
195    200    205

Glu Asp Arg Met Ser Asp Val Ile Asn Val Thr Asp Ile Asp Arg Ile
210    215    220

Glu Ile Lys Val Leu Lys Ala
225    230

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<210> SEQ ID NO 131
<211> LENGTH: 356
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 131

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

Thr Thr Gly Ala Ile Thr Val Thr Thr Gln Ser Val Lys Ala Glu Lys
 20             25             30

Ile Gln Ser Thr Lys Val Asp Lys Val Pro Thr Leu Lys Ala Glu Arg
 35             40             45

Leu Ala Met Ile Asn Ile Thr Ala Gly Ala Asn Ser Ala Thr Thr Gln
 50             55             60

Ala Ala Asn Thr Arg Gln Glu Arg Thr Pro Lys Leu Glu Lys Ala Pro
 65             70             75             80

Asn Thr Asn Glu Glu Lys Thr Ser Ala Ser Lys Ile Glu Lys Ile Ser
 85             90             95

Gln Pro Lys Gln Glu Glu Gln Lys Thr Leu Asn Ile Ser Ala Thr Pro
100             105             110

Ala Pro Lys Gln Glu Gln Ser Gln Thr Thr Thr Glu Ser Thr Thr Pro
115             120             125

Lys Thr Lys Val Thr Thr Pro Pro Ser Thr Asn Thr Pro Gln Pro Met
130             135             140

Gln Ser Thr Lys Ser Asp Thr Pro Gln Ser Pro Thr Ile Lys Gln Ala
145             150             155             160

Gln Thr Asp Met Thr Pro Lys Tyr Glu Asp Leu Arg Ala Tyr Tyr Thr
165             170             175

Lys Pro Ser Phe Glu Phe Glu Lys Gln Phe Gly Phe Met Leu Lys Pro
180             185             190

Trp Thr Thr Val Arg Phe Met Asn Val Ile Pro Asn Arg Phe Ile Tyr
195             200             205

Lys Ile Ala Leu Val Gly Lys Asp Glu Lys Lys Tyr Lys Asp Gly Pro
210             215             220

Tyr Asp Asn Ile Asp Val Phe Ile Val Leu Glu Asp Asn Lys Tyr Gln
225             230             235             240

Leu Lys Lys Tyr Ser Val Gly Gly Ile Thr Lys Thr Asn Ser Lys Lys
245             250             255

Val Asn His Lys Val Glu Leu Ser Ile Thr Lys Lys Asp Asn Gln Gly
260             265             270

Met Ile Ser Arg Asp Val Ser Glu Tyr Met Ile Thr Lys Glu Glu Ile
275             280             285

Ser Leu Lys Glu Leu Asp Phe Lys Leu Arg Lys Gln Leu Ile Glu Lys
290             295             300

His Asn Leu Tyr Gly Asn Met Gly Ser Gly Thr Ile Val Ile Lys Met
305             310             315             320

Lys Asn Gly Gly Lys Tyr Thr Phe Glu Leu His Lys Lys Leu Gln Glu
325             330             335

His Arg Met Ala Asp Val Ile Asp Gly Thr Asn Ile Asp Asn Ile Glu
340             345             350

Val Asn Ile Lys
355

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<210> SEQ ID NO 132
<211> LENGTH: 308
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 132

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

Thr Thr Gly Val Ile Thr Thr Thr Thr Gln Ala Ala Asn Ala Thr Thr
      20             25             30

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

Lys Ile Glu Ala Pro Gln Ser Lys Pro Asn Ala Thr Thr Pro Pro Ser
 50             55             60

Thr Lys Val Glu Ala Pro Gln Gln Thr Ala Asn Ala Thr Thr Pro Pro
65             70             75             80

Ser Thr Lys Val Thr Thr Pro Pro Ser Thr Asn Thr Pro Gln Pro Met
      85             90             95

Gln Ser Thr Lys Ser Asp Thr Pro Gln Ser Pro Thr Thr Lys Gln Val
      100             105             110

Pro Thr Glu Ile Asn Pro Lys Phe Lys Asp Leu Arg Ala Tyr Tyr Thr
      115             120             125

Lys Pro Ser Leu Glu Phe Lys Asn Glu Ile Gly Ile Ile Leu Lys Lys
      130             135             140

Trp Thr Thr Ile Arg Phe Met Asn Val Val Pro Asp Tyr Phe Ile Tyr
      145             150             155             160

Lys Ile Ala Leu Val Gly Lys Asp Asp Lys Lys Tyr Gly Glu Gly Val
      165             170             175

His Arg Asn Val Asp Val Phe Val Val Leu Glu Glu Asn Asn Tyr Asn
      180             185             190

Leu Glu Lys Tyr Ser Val Gly Gly Ile Thr Lys Ser Asn Ser Lys Lys
      195             200             205

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

Thr Ile Ser His Asp Val Ser Glu Phe Lys Ile Thr Lys Glu Gln Ile
      225             230             235             240

Ser Leu Lys Glu Leu Asp Phe Lys Leu Arg Lys Gln Leu Ile Glu Lys
      245             250             255

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

Lys Asn Gly Gly Lys Tyr Thr Phe Glu Leu His Lys Lys Leu Gln Glu
      275             280             285

Asn Arg Met Ala Asp Val Ile Asp Gly Thr Asn Ile Asp Asn Ile Glu
      290             295             300

Val Asn Ile Lys
305

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<210> SEQ ID NO 133
<211> LENGTH: 234
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 133

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

Ala Thr Gly Thr Ile Thr Ser Leu His Gln Thr Val Asn Ala Ser Glu

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20					25					30					
His	Lys	Ala	Lys	Tyr	Glu	Asn	Val	Thr	Lys	Asp	Ile	Phe	Asp	Leu	Arg
	35						40					45			
Asp	Tyr	Tyr	Ser	Gly	Ala	Ser	Lys	Glu	Leu	Lys	Asn	Val	Thr	Gly	Tyr
	50					55					60				
Arg	Tyr	Ser	Lys	Gly	Gly	Lys	His	Tyr	Leu	Ile	Phe	Asp	Lys	Asn	Arg
	65			70					75					80	
Lys	Phe	Thr	Arg	Val	Gln	Ile	Phe	Gly	Lys	Asp	Ile	Glu	Arg	Phe	Lys
			85					90						95	
Ala	Arg	Lys	Asn	Pro	Gly	Leu	Asp	Ile	Phe	Val	Val	Lys	Glu	Ala	Glu
			100					105					110		
Asn	Arg	Asn	Gly	Thr	Val	Phe	Ser	Tyr	Gly	Gly	Val	Thr	Lys	Lys	Asn
		115					120					125			
Gln	Asp	Ala	Tyr	Tyr	Asp	Tyr	Ile	Asn	Ala	Pro	Arg	Phe	Gln	Ile	Lys
	130					135					140				
Arg	Asp	Glu	Gly	Asp	Gly	Ile	Ala	Thr	Tyr	Gly	Arg	Val	His	Tyr	Ile
	145			150					155					160	
Tyr	Lys	Glu	Glu	Ile	Ser	Leu	Lys	Glu	Leu	Asp	Phe	Lys	Leu	Arg	Gln
			165					170						175	
Tyr	Leu	Ile	Gln	Asn	Phe	Asp	Leu	Tyr	Lys	Lys	Phe	Pro	Lys	Asp	Ser
		180					185						190		
Lys	Ile	Lys	Val	Ile	Met	Lys	Asp	Gly	Gly	Tyr	Tyr	Thr	Phe	Glu	Leu
	195					200						205			
Asn	Lys	Lys	Leu	Gln	Thr	Asn	Arg	Met	Ser	Asp	Val	Ile	Asp	Gly	Arg
	210					215					220				
Asn	Ile	Glu	Lys	Ile	Glu	Ala	Asn	Ile	Arg						
	225			230											

<210> SEQ ID NO 134
 <211> LENGTH: 231
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 134

Met	Lys	Leu	Lys	Thr	Leu	Ala	Lys	Ala	Thr	Leu	Val	Leu	Gly	Leu	Leu
1			5						10					15	
Ala	Thr	Gly	Val	Ile	Thr	Thr	Glu	Ser	Gln	Thr	Val	Lys	Ala	Ala	Glu
		20					25					30			
Ser	Thr	Gln	Gly	Gln	His	Asn	Tyr	Lys	Ser	Leu	Lys	Tyr	Tyr	Tyr	Ser
	35					40					45				
Lys	Pro	Ser	Ile	Glu	Leu	Lys	Asn	Leu	Asp	Gly	Leu	Tyr	Arg	Gln	Lys
	50				55					60					
Val	Thr	Asp	Lys	Gly	Val	Tyr	Val	Trp	Lys	Asp	Arg	Lys	Asp	Tyr	Phe
	65			70					75					80	
Val	Gly	Leu	Leu	Gly	Lys	Asp	Ile	Glu	Lys	Tyr	Pro	Gln	Gly	Glu	His
		85					90						95		
Asp	Lys	Gln	Asp	Ala	Phe	Leu	Val	Ile	Glu	Glu	Glu	Thr	Val	Asn	Gly
		100					105						110		
Arg	Gln	Tyr	Ser	Ile	Gly	Gly	Leu	Ser	Lys	Thr	Asn	Ser	Lys	Glu	Phe
	115						120					125			
Ser	Lys	Glu	Val	Asp	Val	Lys	Val	Thr	Arg	Lys	Ile	Asp	Glu	Ser	Ser
	130					135					140				
Glu	Lys	Ser	Lys	Asp	Ser	Lys	Phe	Lys	Ile	Thr	Lys	Glu	Glu	Ile	Ser
	145			150					155					160	

[illegible]

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<210> SEQ ID NO 135
<211> LENGTH: 231
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp
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<400> SEQUENCE: 135

[illegible]

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<210> SEQ ID NO 136
<211> LENGTH: 232
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp
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<400> SEQUENCE: 136

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

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Thr	Thr	Ser	Val	Met	Ile	Thr	Glu	Asn	Gln	Ser	Val	Asn	Ala	Lys	Gly
			20					25					30		
Lys	Tyr	Glu	Lys	Met	Asn	Arg	Leu	Tyr	Asp	Thr	Asn	Lys	Leu	His	Gln
	35						40				45				
Tyr	Tyr	Ser	Gly	Pro	Ser	Tyr	Glu	Leu	Thr	Asn	Val	Ser	Gly	Gln	Ser
	50					55					60				
Gln	Gly	Tyr	Tyr	Asp	Ser	Asn	Val	Leu	Leu	Phe	Asn	Gln	Gln	Asn	Gln
65					70					75					80
Lys	Phe	Gln	Val	Phe	Leu	Leu	Gly	Lys	Asp	Glu	Asn	Lys	Tyr	Lys	Glu
			85					90						95	
Lys	Thr	His	Gly	Leu	Asp	Val	Phe	Ala	Val	Pro	Glu	Leu	Val	Asp	Leu
		100						105					110		
Asp	Gly	Arg	Ile	Phe	Ser	Val	Ser	Gly	Val	Thr	Lys	Lys	Asn	Val	Lys
	115						120					125			
Ser	Ile	Phe	Glu	Ser	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Val	Lys	Lys	Ile
	130					135					140				
Asp	Asp	Lys	Asp	Gly	Phe	Ser	Ile	Asp	Glu	Phe	Phe	Phe	Ile	Gln	Lys
145					150					155					160
Glu	Glu	Val	Ser	Leu	Lys	Glu	Leu	Asp	Phe	Lys	Ile	Arg	Lys	Leu	Leu
			165					170						175	
Ile	Lys	Lys	Tyr	Lys	Leu	Tyr	Glu	Gly	Ser	Ala	Asp	Lys	Gly	Arg	Ile
		180						185					190		
Val	Ile	Asn	Met	Lys	Asp	Glu	Asn	Lys	Tyr	Glu	Ile	Asp	Leu	Ser	Asp
		195					200					205			
Lys	Leu	Asp	Phe	Glu	Arg	Met	Ala	Asp	Val	Ile	Asn	Ser	Glu	Gln	Ile
	210					215					220				
Lys	Asn	Ile	Glu	Val	Asn	Leu	Lys								
225					230										

<210> SEQ ID NO 137

<211> LENGTH: 232

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 137

Met	Lys	Leu	Thr	Thr	Ile	Ala	Lys	Ala	Thr	Leu	Ala	Leu	Gly	Ile	Leu
1			5						10					15	
Thr	Thr	Gly	Val	Phe	Thr	Ala	Glu	Ser	Gln	Thr	Gly	His	Ala	Lys	Val
		20						25				30			
Glu	Leu	Asp	Glu	Thr	Gln	Arg	Lys	Tyr	Tyr	Ile	Asn	Met	Leu	His	Gln
	35					40					45				
Tyr	Tyr	Ser	Glu	Glu	Ser	Phe	Glu	Pro	Thr	Asn	Ile	Ser	Val	Lys	Ser
	50				55					60					
Glu	Asp	Tyr	Tyr	Gly	Ser	Asn	Val	Leu	Asn	Phe	Lys	Gln	Arg	Asn	Lys
65					70					75					80
Ala	Phe	Lys	Val	Phe	Leu	Leu	Gly	Asp	Asp	Lys	Asn	Lys	Tyr	Lys	Glu
			85					90						95	
Lys	Thr	His	Gly	Leu	Asp	Val	Phe	Ala	Val	Pro	Glu	Leu	Ile	Asp	Ile
		100						105					110		
Lys	Gly	Gly	Ile	Tyr	Ser	Val	Gly	Gly	Ile	Thr	Lys	Lys	Asn	Val	Arg
	115						120					125			
Ser	Val	Phe	Gly	Phe	Val	Ser	Asn	Pro	Ser	Leu	Gln	Val	Lys	Lys	Val
	130					135					140				
Asp	Ala	Lys	Asn	Gly	Phe	Ser	Ile	Asn	Glu	Leu	Phe	Phe	Ile	Gln	Lys
145					150					155					160

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Glu Glu Val Ser Leu Lys Glu Leu Asp Phe Lys Ile Arg Lys Leu Leu
 165 170 175
 Ile Glu Lys Tyr Arg Leu Tyr Lys Gly Thr Ser Asp Lys Gly Arg Ile
 180 185 190
 Val Ile Asn Met Lys Asp Glu Lys Lys His Glu Ile Asp Leu Ser Glu
 195 200 205
 Lys Leu Ser Phe Glu Arg Met Phe Asp Val Met Asp Ser Lys Gln Ile
 210 215 220
 Lys Asn Ile Glu Val Asn Leu Asn
 225 230

<210> SEQ ID NO 138
 <211> LENGTH: 227
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 138

Met Lys Phe Thr Ala Leu Ala Lys Ala Thr Leu Ala Leu Gly Ile Leu
 1 5 10 15
 Thr Thr Gly Thr Leu Thr Thr Glu Val His Ser Gly His Ala Lys Gln
 20 25 30
 Asn Gln Lys Ser Val Asn Lys His Asp Lys Glu Ala Leu Tyr Arg Tyr
 35 40 45
 Tyr Thr Gly Lys Thr Met Glu Met Lys Asn Ile Ser Ala Leu Lys His
 50 55 60
 Gly Lys Asn Asn Leu Arg Phe Lys Phe Arg Gly Ile Lys Ile Gln Val
 65 70 75 80
 Leu Leu Pro Gly Asn Asp Lys Ser Lys Phe Gln Gln Arg Ser Tyr Glu
 85 90 95
 Gly Leu Asp Val Phe Phe Val Gln Glu Lys Arg Asp Lys His Asp Ile
 100 105 110
 Phe Tyr Thr Val Gly Gly Val Ile Gln Asn Asn Lys Thr Ser Gly Val
 115 120 125
 Val Ser Ala Pro Ile Leu Asn Ile Ser Lys Glu Lys Gly Glu Asp Ala
 130 135 140
 Phe Val Lys Gly Tyr Pro Tyr Tyr Ile Lys Lys Glu Lys Ile Thr Leu
 145 150 155 160
 Lys Glu Leu Asp Tyr Lys Leu Arg Lys His Leu Ile Glu Lys Tyr Gly
 165 170 175
 Leu Tyr Lys Thr Ile Ser Lys Asp Gly Arg Val Lys Ile Ser Leu Lys
 180 185 190
 Asp Gly Ser Phe Tyr Asn Leu Asp Leu Arg Ser Lys Leu Lys Phe Lys
 195 200 205
 Tyr Met Gly Glu Val Ile Glu Ser Lys Gln Ile Lys Asp Ile Glu Val
 210 215 220
 Asn Leu Lys
 225

<210> SEQ ID NO 139
 <211> LENGTH: 225
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 139

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

-continued

Thr Thr Gly Met Ile Thr Thr Thr Ala Gln Pro Val Lys Ala Ser Thr
 20 25 30
 Leu Glu Val Arg Ser Gln Ala Thr Gln Asp Leu Ser Glu Tyr Tyr Asn
 35 40 45
 Arg Pro Phe Phe Glu Tyr Thr Asn Gln Ser Gly Tyr Lys Glu Glu Gly
 50 55 60
 Lys Val Thr Phe Thr Pro Asn Tyr Gln Leu Ile Asp Val Thr Leu Thr
 65 70 75 80
 Gly Asn Glu Lys Gln Asn Phe Gly Glu Asp Ile Ser Asn Val Asp Ile
 85 90 95
 Phe Val Val Arg Glu Asn Ser Asp Arg Ser Gly Asn Thr Ala Ser Ile
 100 105 110
 Gly Gly Ile Thr Lys Thr Asn Gly Ser Asn Tyr Ile Asp Lys Val Lys
 115 120 125
 Asp Val Asn Leu Ile Ile Thr Lys Asn Ile Asp Ser Val Thr Ser Thr
 130 135 140
 Ser Thr Ser Ser Thr Tyr Thr Ile Asn Lys Glu Glu Ile Ser Leu Lys
 145 150 155 160
 Glu Leu Asp Phe Lys Leu Arg Lys His Leu Ile Asp Lys His Asn Leu
 165 170 175
 Tyr Lys Thr Glu Pro Lys Asp Ser Lys Ile Arg Ile Thr Met Lys Asp
 180 185 190
 Gly Gly Phe Tyr Thr Phe Glu Leu Asn Lys Lys Leu Gln Thr His Arg
 195 200 205
 Met Gly Asp Val Ile Asp Gly Arg Asn Ile Glu Lys Ile Glu Val Asn
 210 215 220
 Leu
 225

<210> SEQ ID NO 140
 <211> LENGTH: 116
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 140

Met Lys Phe Lys Lys Tyr Ile Leu Thr Gly Thr Leu Ala Leu Leu Leu
 1 5 10 15
 Ser Ser Thr Gly Ile Ala Thr Ile Glu Gly Asn Lys Ala Asp Ala Ser
 20 25 30
 Ser Leu Asp Lys Tyr Leu Thr Glu Ser Gln Phe His Asp Lys Arg Ile
 35 40 45
 Ala Glu Glu Leu Arg Thr Leu Leu Asn Lys Ser Asn Val Tyr Ala Leu
 50 55 60
 Ala Ala Gly Ser Leu Asn Pro Tyr Tyr Lys Arg Thr Ile Met Met Asn
 65 70 75 80
 Glu Tyr Arg Ala Lys Ala Ala Leu Lys Lys Asn Asp Phe Val Ser Met
 85 90 95
 Ala Asp Ala Lys Val Ala Leu Glu Lys Ile Tyr Lys Glu Ile Asp Glu
 100 105 110
 Ile Ile Asn Arg
 115

<210> SEQ ID NO 141
 <211> LENGTH: 203
 <212> TYPE: PRT

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<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 141

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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

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<210> SEQ ID NO 142

<211> LENGTH: 146

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 142

```

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

Ala Leu Gly Ala Cys Gly Asn Ser Asn Ser Gln Asp Gln Gly Asn Lys
      20             25             30

Thr Glu Gln Lys Thr Lys Ser Glu Asp Ser Asn Val Lys Thr Asp Lys
      35             40             45

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

Glu Gly Lys Ala Glu Ile Lys Asn Gly Lys Leu Met Leu Thr Asn Tyr
 65             70             75             80

Lys Ser Ser Lys Gly Pro Asp Leu Tyr Val Tyr Leu Thr Lys Asn Gly
      85             90             95

Asp Ile Lys Asn Gly Lys Glu Ile Ala Met Val Asp Tyr Asp Lys Glu
      100            105            110

Lys Gln Thr Phe Asp Leu Lys Asn Val Asp Leu Ser Lys Tyr Asp Glu
      115            120            125

Val Thr Ile Tyr Cys Lys Lys Ala His Val Ile Phe Gly Gly Ala Lys
      130            135            140

Leu Lys

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145

<210> SEQ ID NO 143

<211> LENGTH: 619

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 143

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

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

Asp Thr Thr Ala Lys Thr Thr Ser His Asp Ser Lys Lys Ser Asn Asp
      35           40           45

Asp Glu Thr Ser Lys Asp Thr Thr Ser Lys Asp Ile Asp Lys Ala Asp
      50           55           60

Lys Asn Asn Thr Ser Asn Gln Asp Asn Asn Asp Lys Lys Phe Lys Thr
      65           70           75           80

Ile Asp Asp Ser Thr Ser Asp Ser Asn Asn Ile Ile Asp Phe Ile Tyr
      85           90           95

Lys Asn Leu Pro Gln Thr Asn Ile Asn Gln Leu Leu Thr Lys Asn Lys
      100          105          110

Tyr Asp Asp Asn Tyr Ser Leu Thr Thr Leu Ile Gln Asn Leu Phe Asn
      115          120          125

Leu Asn Ser Asp Ile Ser Asp Tyr Glu Gln Pro Arg Asn Gly Glu Lys
      130          135          140

Ser Thr Asn Asp Ser Asn Lys Asn Ser Asp Asn Ser Ile Lys Asn Asp
      145          150          155          160

Thr Asp Thr Gln Ser Ser Lys Gln Asp Lys Ala Asp Asn Gln Lys Ala
      165          170          175

Pro Lys Ser Asn Asn Thr Lys Pro Ser Thr Ser Asn Lys Gln Pro Asn
      180          185          190

Ser Pro Lys Pro Thr Gln Pro Asn Gln Ser Asn Ser Gln Pro Ala Ser
      195          200          205

Asp Asp Lys Ala Asn Gln Lys Ser Ser Ser Lys Asp Asn Gln Ser Met
      210          215          220

Ser Asp Ser Ala Leu Asp Ser Ile Leu Asp Gln Tyr Ser Glu Asp Ala
      225          230          235          240

Lys Lys Thr Gln Lys Asp Tyr Ala Ser Gln Ser Lys Lys Asp Lys Asn
      245          250          255

Glu Lys Ser Asn Thr Lys Asn Pro Gln Leu Pro Thr Gln Asp Glu Leu
      260          265          270

Lys His Lys Ser Lys Pro Ala Gln Ser Phe Asn Asn Asp Val Asn Gln
      275          280          285

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

Asn Asn Asp Asp Ser Gly Gln Phe Asn Val Val Asp Ser Lys Asp Thr
      305          310          315          320

Arg Gln Phe Val Lys Ser Ile Ala Lys Asp Ala His Arg Ile Gly Gln
      325          330          335

Asp Asn Asp Ile Tyr Ala Ser Val Met Ile Ala Gln Ala Ile Leu Glu
      340          345          350

Ser Asp Ser Gly Arg Ser Ala Leu Ala Lys Ser Pro Asn His Asn Leu
      355          360          365

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

Leu Glu Ala Asp Gly Asn Gln Leu Tyr Ser Ile Asn Ala Gly Phe Arg
 385          390          395          400

Lys Tyr Pro Ser Thr Lys Glu Ser Leu Lys Asp Tyr Ser Asp Leu Ile
          405          410          415

Lys Asn Gly Ile Asp Gly Asn Arg Thr Ile Tyr Lys Pro Thr Trp Lys
          420          425          430

Ser Glu Ala Asp Ser Tyr Lys Asp Ala Thr Ser His Leu Ser Lys Thr
          435          440          445

Tyr Ala Thr Asp Pro Asn Tyr Ala Lys Lys Leu Asn Ser Ile Ile Lys
          450          455          460

His Tyr Gln Leu Thr Gln Phe Asp Asp Glu Arg Met Pro Asp Leu Asp
 465          470          475          480

Lys Tyr Glu Arg Ser Ile Lys Asp Tyr Asp Asp Ser Ser Asp Glu Phe
          485          490          495

Lys Pro Phe Arg Glu Val Ser Asp Ser Met Pro Tyr Pro His Gly Gln
          500          505          510

Cys Thr Trp Tyr Val Tyr Asn Arg Met Lys Gln Phe Gly Thr Ser Ile
          515          520          525

Ser Gly Asp Leu Gly Asp Ala His Asn Trp Asn Asn Arg Ala Gln Tyr
 530          535          540

Arg Asp Tyr Gln Val Ser His Thr Pro Lys Arg His Ala Ala Val Val
 545          550          555          560

Phe Glu Ala Gly Gln Phe Gly Ala Asp Gln His Tyr Gly His Val Ala
          565          570          575

Phe Val Glu Lys Val Asn Ser Asp Gly Ser Ile Val Ile Ser Glu Ser
          580          585          590

Asn Val Lys Gly Leu Gly Ile Ile Ser His Arg Thr Ile Asn Ala Ala
 595          600          605

Ala Ala Glu Glu Leu Ser Tyr Ile Thr Gly Lys
 610          615

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<210> SEQ ID NO 144

<211> LENGTH: 208

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 144

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

Leu Ala Gly Cys Thr Thr Asp Lys Lys Glu Ile Lys Ala Tyr Leu Lys
 20          25          30

Gln Val Asp Lys Ile Lys Asp Asp Glu Glu Pro Ile Lys Thr Val Gly
 35          40          45

Lys Lys Ile Ala Glu Leu Asp Glu Lys Lys Lys Lys Leu Thr Glu Asp
 50          55          60

Val Asn Ser Lys Asp Thr Ala Val Arg Gly Lys Ala Val Lys Asp Leu
 65          70          75          80

Ile Lys Asn Ala Asp Asp Arg Leu Lys Glu Phe Glu Lys Glu Glu Asp
          85          90          95

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

Asp Asn Ile Asp Asn Asp Val Lys Arg Lys Glu Val Lys Gln Leu Asp
          115          120          125

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Asp Val Leu Lys Glu Lys Tyr Lys Leu His Ser Asp Tyr Ala Lys Ala
 130                      135                      140

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

Gln Asn Asp Ala Thr Gln Gln Gly Val Asn Glu Lys Ser Lys Ala Ile
                      165                      170                      175

Glu Gln Asn Tyr Lys Lys Leu Lys Glu Val Ser Asp Lys Tyr Thr Lys
                      180                      185                      190

Val Leu Asn Lys Val Gly Lys Glu Lys Gln Asp Val Asp Gln Phe Lys
 195                      200                      205

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<210> SEQ ID NO 145
<211> LENGTH: 105
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

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<400> SEQUENCE: 145

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

Leu Val Thr Pro Asn Leu Asn Ala Asp Ala Thr Thr Asn Thr Thr Pro
                      20                      25                      30

Gln Ile Lys Gly Ala Asn Asp Ile Val Ile Lys Lys Gly Gln Asp Tyr
 35                      40                      45

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

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

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

Ile Ser Thr Arg Tyr Ile Glu Val Lys
 100                      105

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<210> SEQ ID NO 146
<211> LENGTH: 312
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

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<400> SEQUENCE: 146

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Met Lys Lys Leu Val Pro Leu Leu Leu Ala Leu Leu Leu Val Ala
 1                      5                      10                      15

Ala Cys Gly Thr Gly Gly Lys Gln Ser Ser Asp Lys Ser Asn Gly Lys
 20                      25                      30

Leu Lys Val Val Thr Thr Asn Ser Ile Leu Tyr Asp Met Ala Lys Asn
 35                      40                      45

Val Gly Gly Asp Asn Val Asp Ile His Ser Ile Val Pro Val Gly Gln
 50                      55                      60

Asp Pro His Glu Tyr Glu Val Lys Pro Lys Asp Ile Lys Lys Leu Thr
 65                      70                      75                      80

Asp Ala Asp Val Ile Leu Tyr Asn Gly Leu Asn Leu Glu Thr Gly Asn
 85                      90                      95

Gly Trp Phe Glu Lys Ala Leu Glu Gln Ala Gly Lys Ser Leu Lys Asp
 100                      105                      110

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

Gly Glu Glu Gly Asn Lys Asp Lys Gln Asp Pro His Ala Trp Leu Ser
 130                      135                      140

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Leu Asp Asn Gly Ile Lys Tyr Val Lys Thr Ile Gln Gln Thr Phe Ile
145             150             155             160

Asp Asn Asp Lys Lys His Lys Ala Asp Tyr Glu Lys Gln Gly Asn Lys
             165             170             175

Tyr Ile Ala Gln Leu Glu Lys Leu Asn Asn Asp Ser Lys Asp Ser Lys
             180             185             190

Asp Lys Phe Asn Asp Ile Pro Lys Glu Gln Arg Ala Met Ile Thr Ser
             195             200             205

Glu Gly Ala Phe Lys Tyr Phe Ser Lys Gln Tyr Gly Ile Thr Pro Gly
210             215             220

Tyr Ile Trp Glu Ile Asn Thr Glu Lys Gln Gly Thr Pro Glu Gln Met
225             230             235             240

Arg Gln Ala Ile Glu Phe Val Lys Lys His Lys Leu Lys His Leu Leu
             245             250             255

Val Glu Thr Ser Val Asp Lys Lys Ala Met Glu Ser Leu Ser Glu Glu
             260             265             270

Thr Lys Lys Asp Ile Phe Gly Glu Val Tyr Thr Asp Ser Ile Gly Lys
             275             280             285

Glu Gly Thr Lys Gly Asp Ser Tyr Tyr Lys Met Met Lys Ser Asn Ile
290             295             300

Glu Thr Val His Gly Ser Met Lys
305             310

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<210> SEQ ID NO 147

<211> LENGTH: 646

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 147

```

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

Thr Val Ile Thr Ile Thr Leu Lys Thr Tyr Phe Ser Tyr Tyr Val Asp
             20             25             30

Phe Ser Leu Gly Val Lys Gly Leu Val Gln Asn Leu Ile Leu Leu Met
             35             40             45

Asn Pro Tyr Ser Leu Val Ala Leu Val Leu Ser Val Phe Leu Phe Phe
50             55             60

Lys Gly Lys Lys Ala Phe Trp Phe Met Phe Ile Gly Gly Phe Leu Leu
65             70             75             80

Thr Phe Leu Leu Tyr Ala Asn Val Val Tyr Phe Arg Phe Phe Ser Asp
             85             90             95

Phe Leu Thr Phe Ser Thr Leu Asn Gln Val Gly Asn Val Glu Ser Met
             100            105            110

Gly Gly Ala Val Ser Ala Ser Phe Lys Trp Tyr Asp Phe Val Tyr Phe
             115            120            125

Ile Asp Thr Leu Val Tyr Leu Phe Ile Leu Ile Phe Lys Thr Lys Trp
130            135            140

Leu Asp Thr Lys Ala Phe Ser Lys Lys Phe Val Pro Val Val Met Ala
145            150            155            160

Ala Ser Val Ala Leu Phe Phe Leu Asn Leu Ala Phe Ala Glu Thr Asp
             165             170             175

Arg Pro Glu Leu Leu Thr Arg Thr Phe Asp His Lys Tyr Leu Val Lys
             180            185             190

Tyr Leu Gly Pro Tyr Asn Phe Thr Val Tyr Asp Gly Val Lys Thr Ile

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195					200					205					
Glu	Asn	Asn	Gln	Gln	Lys	Ala	Leu	Ala	Ser	Glu	Asp	Asp	Leu	Thr	Lys
210						215					220				
Val	Leu	Asn	Tyr	Thr	Lys	Gln	Arg	Gln	Thr	Glu	Pro	Asn	Pro	Glu	Tyr
225					230					235				240	
Tyr	Gly	Val	Ala	Lys	Lys	Lys	Asn	Ile	Ile	Lys	Ile	His	Leu	Glu	Ser
				245					250					255	
Phe	Gln	Thr	Phe	Leu	Ile	Asn	Lys	Lys	Val	Asn	Gly	Lys	Glu	Val	Thr
			260					265					270		
Pro	Phe	Leu	Asn	Lys	Leu	Ser	Ser	Gly	Lys	Glu	Gln	Phe	Thr	Tyr	Phe
		275					280					285			
Pro	Asn	Phe	Phe	His	Gln	Thr	Gly	Gln	Gly	Lys	Thr	Ser	Asp	Ser	Glu
	290					295					300				
Phe	Thr	Met	Asp	Asn	Ser	Leu	Tyr	Gly	Leu	Pro	Gln	Gly	Ser	Ala	Phe
305					310					315					320
Ser	Leu	Lys	Gly	Asp	Asn	Thr	Tyr	Gln	Ser	Leu	Pro	Ala	Ile	Leu	Asp
				325					330					335	
Gln	Lys	Gln	Gly	Tyr	Lys	Ser	Asp	Val	Met	His	Gly	Asp	Tyr	Lys	Thr
			340					345					350		
Phe	Trp	Asn	Arg	Asp	Gln	Val	Tyr	Lys	His	Phe	Gly	Ile	Asp	Lys	Phe
		355					360					365			
Tyr	Asp	Ala	Thr	Tyr	Tyr	Asp	Met	Ser	Asp	Lys	Asn	Val	Val	Asn	Leu
	370					375					380				
Gly	Leu	Lys	Asp	Lys	Ile	Phe	Phe	Lys	Asp	Ser	Ala	Asn	Tyr	Gln	Ala
385					390					395					400
Lys	Met	Lys	Ser	Pro	Phe	Tyr	Ser	His	Leu	Ile	Thr	Leu	Thr	Asn	His
				405					410					415	
Tyr	Pro	Phe	Thr	Leu	Asp	Glu	Lys	Asp	Ala	Thr	Ile	Glu	Lys	Ser	Asn
			420					425					430		
Thr	Gly	Asp	Ala	Thr	Val	Asp	Gly	Tyr	Ile	Gln	Thr	Ala	Arg	Tyr	Leu
		435					440					445			
Asp	Glu	Ala	Leu	Glu	Glu	Tyr	Ile	Asn	Asp	Leu	Lys	Lys	Lys	Gly	Leu
	450					455					460				
Tyr	Asp	Asn	Ser	Val	Ile	Met	Ile	Tyr	Gly	Asp	His	Tyr	Gly	Ile	Ser
465					470					475					480
Glu	Asn	His	Asn	Asn	Ala	Met	Glu	Lys	Leu	Leu	Gly	Glu	Lys	Ile	Thr
				485					490					495	
Pro	Ala	Lys	Phe	Thr	Asp	Leu	Asn	Arg	Thr	Gly	Phe	Trp	Ile	Lys	Ile
			500					505					510		
Pro	Gly	Lys	Ser	Gly	Gly	Ile	Asn	Asn	Glu	Tyr	Ala	Gly	Gln	Val	Asp
		515					520					525			
Val	Met	Pro	Thr	Ile	Leu	His	Leu	Ala	Gly	Ile	Asp	Thr	Lys	Asn	Tyr
	530					535					540				
Leu	Met	Phe	Gly	Thr	Asp	Leu	Phe	Ser	Lys	Gly	His	Asn	Gln	Val	Val
545					550					555					560
Pro	Phe	Arg	Asn	Gly	Asp	Phe	Ile	Thr	Lys	Asp	Tyr	Lys	Tyr	Val	Asn
				565					570					575	
Gly	Lys	Ile	Tyr	Ser	Asn	Lys	Asn	Asn	Glu	Leu	Ile	Thr	Thr	Gln	Pro
			580					585					590		
Ala	Asp	Phe	Glu	Lys	Asn	Lys	Lys	Gln	Val	Glu	Lys	Asp	Leu	Glu	Met
		595					600					605			
Ser	Asp	Asn	Val	Leu	Asn	Gly	Asp	Leu	Phe	Arg	Phe	Tyr	Lys	Asn	Pro
	610					615					620				

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Asp Phe Lys Lys Val Asn Pro Ser Lys Tyr Lys Tyr Glu Thr Gly Pro
625 630 635 640

Lys Ala Asn Ser Lys Lys
645

<210> SEQ ID NO 148
<211> LENGTH: 173
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 148

Met Ile Asn Ile Ile Ser Ala Ile Gly Ser Ile Gly Thr Phe Ile Met
1 5 10 15

Ala Leu Phe Tyr Phe Val Ser Val Ser Val Gln Leu Tyr Gln Met Lys
20 25 30

Ile Ser Phe Leu Pro Ala Leu Gly Phe Asn Gln Ile Leu Leu Glu Arg
35 40 45

Glu Glu Asp Gln Leu Asn Ile Met Asn Ser Ala Thr Glu Glu His His
50 55 60

His Lys Asp Tyr Ile Lys Leu Tyr Asn Leu Gly Gly Gly Ala Ala Lys
65 70 75 80

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

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

Asn Lys Asn Val Tyr Glu Glu Leu Glu Arg Thr Ile Glu Asn Asn Gly
115 120 125

His Glu Ala Asp Leu Asn Val Arg Met Thr Tyr Tyr His Asn Val Ser
130 135 140

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

Thr Tyr Asn Asn Lys Glu Ile Tyr Asp Leu Gln Phe Ile
165 170

<210> SEQ ID NO 149
<211> LENGTH: 156
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 149

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

Gln Leu Trp His Ser Asn His Ala Asn Ala Leu Val Thr Glu Ser Gly
20 25 30

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

Ile Thr Val Glu His Ala Gln Ile Asn Ile Phe Gln Ser Asn Ser Asn
50 55 60

Ser Asn Leu Met Glu Phe Asn Ile Leu Thr Met Gly Gly Lys Ser Gly
65 70 75 80

Ala Met Val Gly Tyr Ser Glu Ile Asp Ser Ser His Phe Thr Asp Arg
85 90 95

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

Val Glu Asn Tyr Lys Asp Thr Gln Ser Ala Asp Ala Arg Met Lys Ala
115 120 125

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Lys Gln Lys Val Asn Thr Leu Ser Lys Pro His Gln Asn Tyr Phe Asn
130 135 140

Lys Gln Ile Asp Lys Val Tyr Asn Gly Leu Gln Arg
145 150 155

<210> SEQ ID NO 150

<211> LENGTH: 133

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 150

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

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

Glu Trp Lys Gly Leu Glu Ile Ala Lys Asn Leu Ala Asp Gln Ala Lys
35 40 45

Lys Asp Asp Glu Arg Ile Asp Lys Leu Met Lys Glu Ser Asp Lys Asn
50 55 60

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

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

Asp Gly Gly Pro Arg Asp Tyr Tyr Thr Phe Asp Leu Thr Arg Pro Leu
100 105 110

Glu Glu Asn Arg Lys Asn Ile Lys Val Val Lys Asn Gly Glu Ile Asp
115 120 125

Ser Ile Thr Trp Tyr
130

<210> SEQ ID NO 151

<211> LENGTH: 274

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 151

Met Tyr Pro Asn Trp Gly Gln Tyr Lys Arg Ala Asp Leu Ile Gly Gln
1 5 10 15

Ser Ser Tyr Ile Lys Asn Asn Asp Val Val Ile Phe Asn Glu Ala Phe
20 25 30

Asp Asn Gly Ala Ser Asp Lys Leu Leu Ser Asn Val Lys Lys Glu Tyr
35 40 45

Pro Tyr Gln Thr Pro Val Leu Gly Arg Ser Gln Ser Gly Trp Asp Lys
50 55 60

Thr Glu Gly Ser Tyr Ser Ser Thr Val Ala Glu Asp Gly Gly Val Ala
65 70 75 80

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

Ser Gly Cys Gly Phe Asp Asn Asp Ser Asn Lys Gly Phe Val Tyr Thr
100 105 110

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

Gln Ser Glu Asp Ser Arg Cys Gly Ala Gly His Asp Arg Lys Ile Arg
130 135 140

Ala Glu Gln Met Lys Glu Ile Ser Asp Phe Val Lys Lys Lys Asn Ile
145 150 155 160

Met 1	Leu	Glu	Phe 5	Glu	Gln	Gly	Phe	Asn 10	His	Leu	Ala	Thr	Leu	Lys 15	Val
Ile	Gly	Val	Gly 20	Gly	Gly	Gly	Asn 25	Asn	Ala	Val	Asn	Arg 30	Met	Ile	Asp
His	Gly 35	Met	Asn	Asn	Val	Glu	Phe 40	Ile	Ala	Ile	Asn	Thr 45	Asp	Gly	Gln
Ala 50	Leu	Asn	Leu	Ser	Lys	Ala 55	Glu	Ser	Lys	Ile	Gln 60	Ile	Gly	Glu	Lys
Leu 65	Thr	Arg	Gly	Leu	Gly 70	Ala	Gly	Ala	Asn 75	Pro	Glu	Ile	Gly	Lys	Lys 80
Ala	Ala	Glu	Glu	Ser 85	Arg	Glu	Gln	Ile	Glu 90	Asp	Ala	Ile	Gln	Gly 95	Ala
Asp	Met	Val	Phe 100	Val	Thr	Ser	Gly	Met 105	Gly	Gly	Gly	Thr 110	Gly	Thr	Gly
Ala 115	Ala	Pro	Val	Val	Ala	Lys	Ile 120	Ala	Lys	Glu	Met	Gly 125	Ala	Leu	Thr
Val 130	Gly	Val	Val	Thr	Arg	Pro 135	Phe	Ser	Phe	Glu	Gly 140	Arg	Lys	Arg	Gln
Thr 145	Gln	Ala	Ala	Ala 150	Gly	Val	Glu	Ala	Met 155	Lys	Ala	Ala	Val	Asp	Thr 160
Leu	Ile	Val	Ile 165	Pro	Asn	Asp	Arg	Leu 170	Leu	Asp	Ile	Val	Asp	Lys 175	Ser
Thr	Pro	Met	Met 180	Glu	Ala	Phe	Lys	Glu 185	Ala	Asp	Asn	Val 190	Leu	Arg	Gln
Gly	Val	Gln	Gly 195	Ile	Ser	Asp	Leu 200	Ile	Ala	Val	Ser	Gly 205	Glu	Val	Asn
Leu 210	Asp	Phe	Ala	Asp	Val	Lys 215	Thr	Ile	Met	Ser	Asn 220	Gln	Gly	Ser	Ala
Leu 225	Met	Gly	Ile	Gly 230	Val	Ser	Ser	Gly	Glu 235	Asn	Arg	Ala	Val	Glu	Ala 240
Ala	Lys	Lys	Ala 245	Ile	Ser	Ser	Pro	Leu 250	Leu	Glu	Thr	Ser	Ile	Val	Gly 255

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His Lys Ala Trp His Asp His Ser Asp Ala Ile Ser Lys Ile Thr Tyr
      85              90              95

Thr Met Ile Gly Asp Pro Ser Gln Thr Ile Thr Arg Asn Phe Asp Val
      100              105              110

Leu Asp Glu Ala Thr Gly Leu Ala Gln Arg Gly Thr Phe Ile Ile Asp
      115              120              125

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

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

Arg Lys Asn Pro Gly Glu Val Cys Pro Ala Lys Trp Glu Glu Gly Ala
      165              170              175

Lys Thr Leu Gln Pro Gly Leu Asp Leu Val Gly Lys Ile
      180              185

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<210> SEQ ID NO 155

<211> LENGTH: 207

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp

<400> SEQUENCE: 155

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

Ser Tyr Gly Gln Gly Ser Asp Gln Ile Arg Gln Ile Leu Ser Asp Leu
      20              25              30

Thr Arg Ala Gln Gly Glu Leu Ala Ala Asn Trp Glu Gly Gln Ala Phe
      35              40              45

Ser Arg Phe Glu Glu Gln Phe Gln Gln Leu Ser Pro Lys Val Glu Lys
      50              55              60

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

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

Gln Ala Ser Gly Gly Gly Ser Met Gly Gly Tyr Lys Gly Leu Lys Ala
      100              105              110

Asp Gly Gly Lys Val Asp Gln Ala Lys Gln Leu Ala Ala Lys Thr Ala
      115              120              125

Lys Asp Ile Glu Ala Cys Gln Lys Gln Thr Gln Gln Leu Ala Glu Tyr
      130              135              140

Ile Glu Gly Ser Asp Trp Glu Gly Gln Phe Ala Asn Lys Val Lys Asp
      145              150              155              160

Val Leu Leu Leu Met Ala Lys Phe Gln Glu Glu Leu Val Gln Pro Met
      165              170              175

Ala Asp His Gln Lys Ala Ile Asp Asn Leu Ser Gln Asn Leu Ala Lys
      180              185              190

Tyr Asp Thr Leu Ser Ile Lys Gln Gly Leu Asp Arg Val Asn Pro
      195              200              205

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What is claimed is:

1. A method for enhancing a subject's ability to mount an immune response to a *Staphylococcus aureus* antigen comprising providing to the subject a composition comprising an isolated antibody that specifically binds to a nontoxicogenic *Staphylococcus aureus* protein (SpA) variant, the SpA variant having

60 (a) amino acid substitutions in an IgG Fc binding sub-domain of each of SpA domains A, B, C, D, and E that disrupt or decrease binding to IgG Fc, wherein the amino acid substitutions are in SpA domain A at position 7 and 8 of SEQ ID NO:4, in SpA domain B at position 7 and 8 of SEQ ID NO:6, in SpA domain C at position 7 and 8 of SEQ ID NO:5, in SpA domain D at

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position 9 and 10 of SEQ ID NO:2; and in SpA domain E at position 6 and 7 of SEQ ID NO:3; and

(b) amino acid substitutions in a V_H 3 binding sub-domain of each of SpA domains A, B, C, D, and E that disrupt or decrease binding to VH3, wherein the amino acid substitutions are in SpA domain A at position 34 and 35 of SEQ ID NO:4, in SpA domain B at position 34 and 35 of SEQ ID NO:6, in SpA domain C at position 34 and 35 of SEQ ID NO:5, in SpA domain D at position 36 and 37 of SEQ ID NO:2; in SpA domain E at position 33 and 34 of SEQ ID NO:3

wherein the antibody enhances the subject's ability to mount an immune response to a *Staphylococcus aureus* antigen selected from the group consisting of FnBpA, FnBpB, LukD, LukE, LukF, SasA, SasD, SasG, SasI, SasK, Ebh, Emp, EsaB, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, ClfA, ClfB, Coa, Hla, IsdC, SasF, vWbp, and vWh.

2. The method of claim 1, wherein the *Staphylococcus aureus* antigen is present in or on a *Staphylococcus aureus* bacterium.

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3. The method of claim 1, further comprising providing to the subject a *Staphylococcus aureus* antigen.

4. The method of claim 3, wherein the *Staphylococcus aureus* antigen is present in or on a *Staphylococcus aureus* bacterium.

5. The method of claim 3, wherein the *Staphylococcus aureus* antigen is selected from the group consisting of FnBpA, FnBpB, LukD, LukE, LukF, SasA, SasD, SasG, SasI, SasK, Eap, Ebh, Emp, EsaB, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, Coa, Hla, IsdC, SasF, vWbp, and vWh.

6. The method of claim 1, wherein the antibody is a polyclonal antibody, a monoclonal antibody, or an antibody fragment.

7. The method of claim 1, wherein the antibody was generated using the nontoxigenic SpA variant as an antigen.

8. The method of claim 1, wherein the subject is at risk of developing a *Staphylococcus aureus* infection.

9. The method of claim 1, wherein the subject has a *Staphylococcus aureus* infection.

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