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(54) **COMPOSITIONS AND METHODS RELATED TO PROTEIN A (SPA) VARIANTS**

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(57) **ABSTRACT**

Related U.S. Application Data

(63) Continuation of application No. 14/466,514, filed on Aug. 22, 2014, now Pat. No. 9,315,554, which is a continuation of application No. 13/807,598, filed on Mar. 19, 2013, now Pat. No. 8,821,894, filed as application No. PCT/US2011/042845 on Jul. 1, 2011.

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-toxigenic Protein A (SpA) variant.

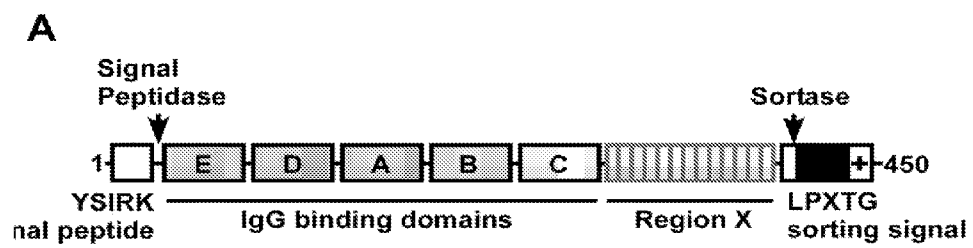


FIG. 1A

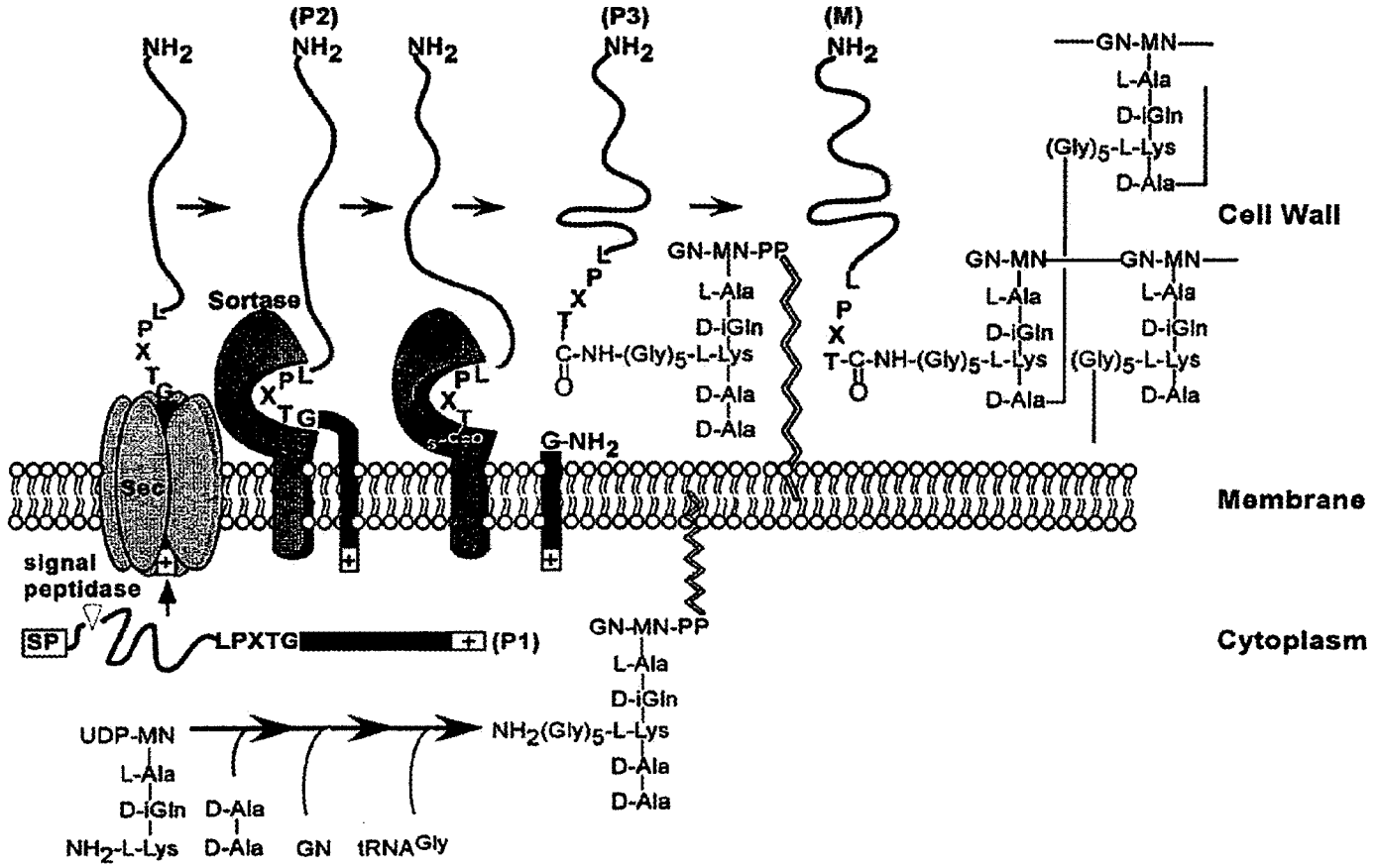
B

FIG. 1B

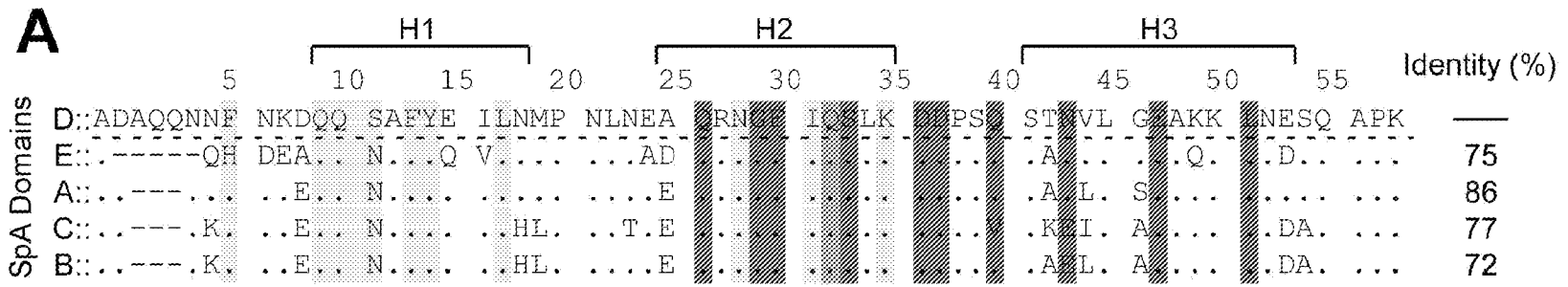


FIG. 2A

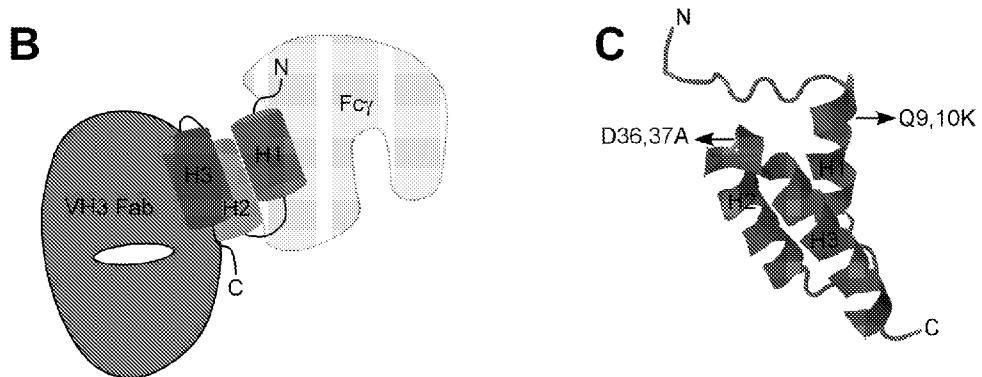


FIG. 2B-2C

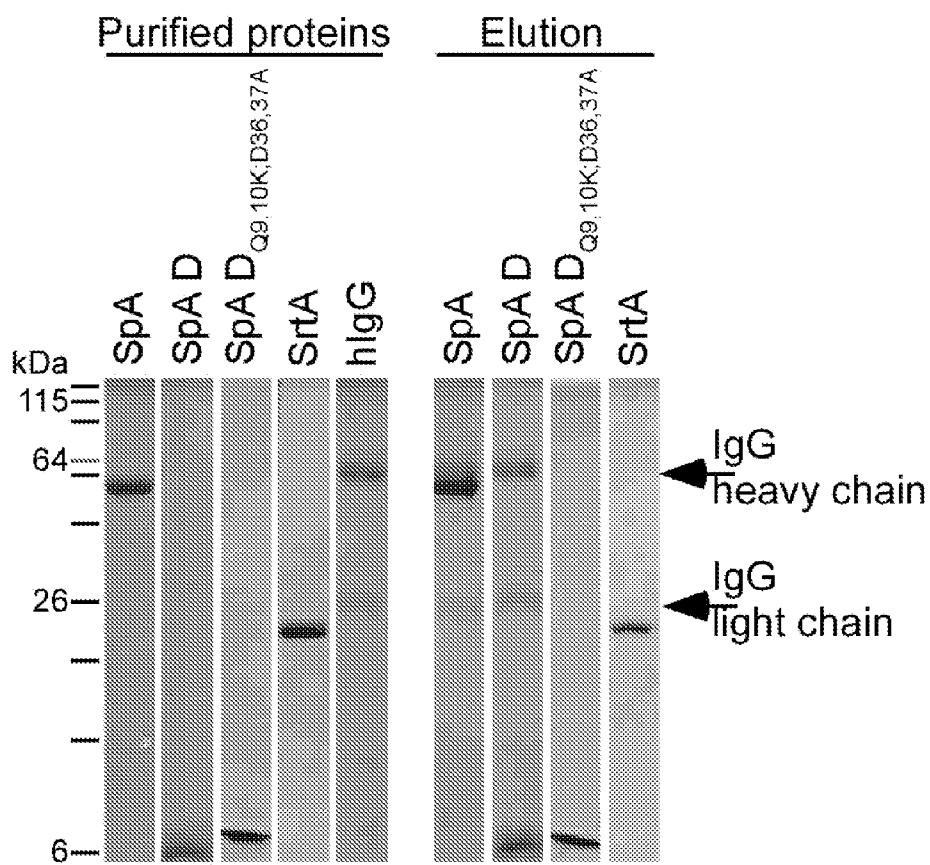


FIG. 3

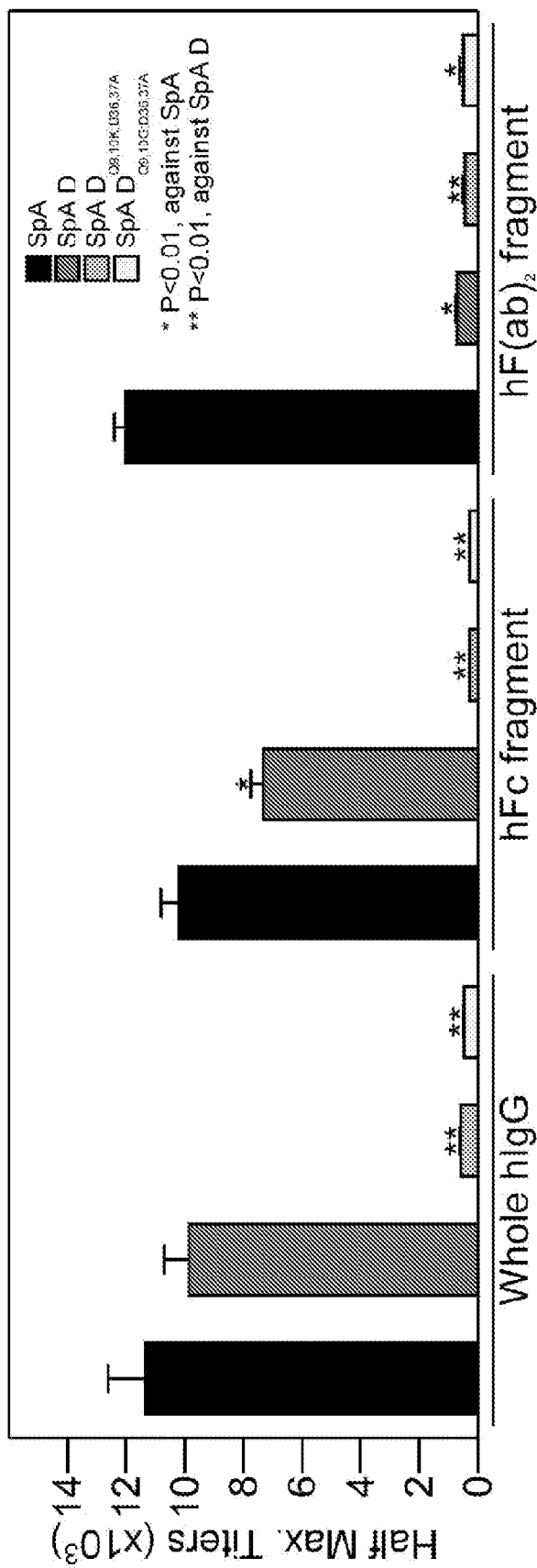


FIG. 4

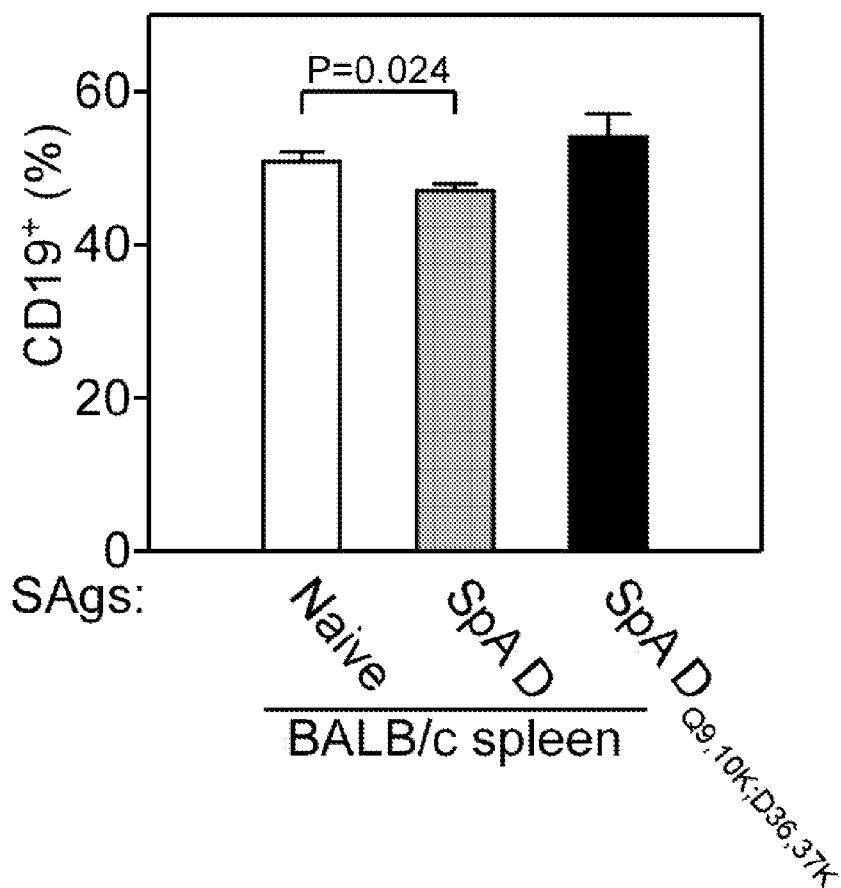


FIG. 5

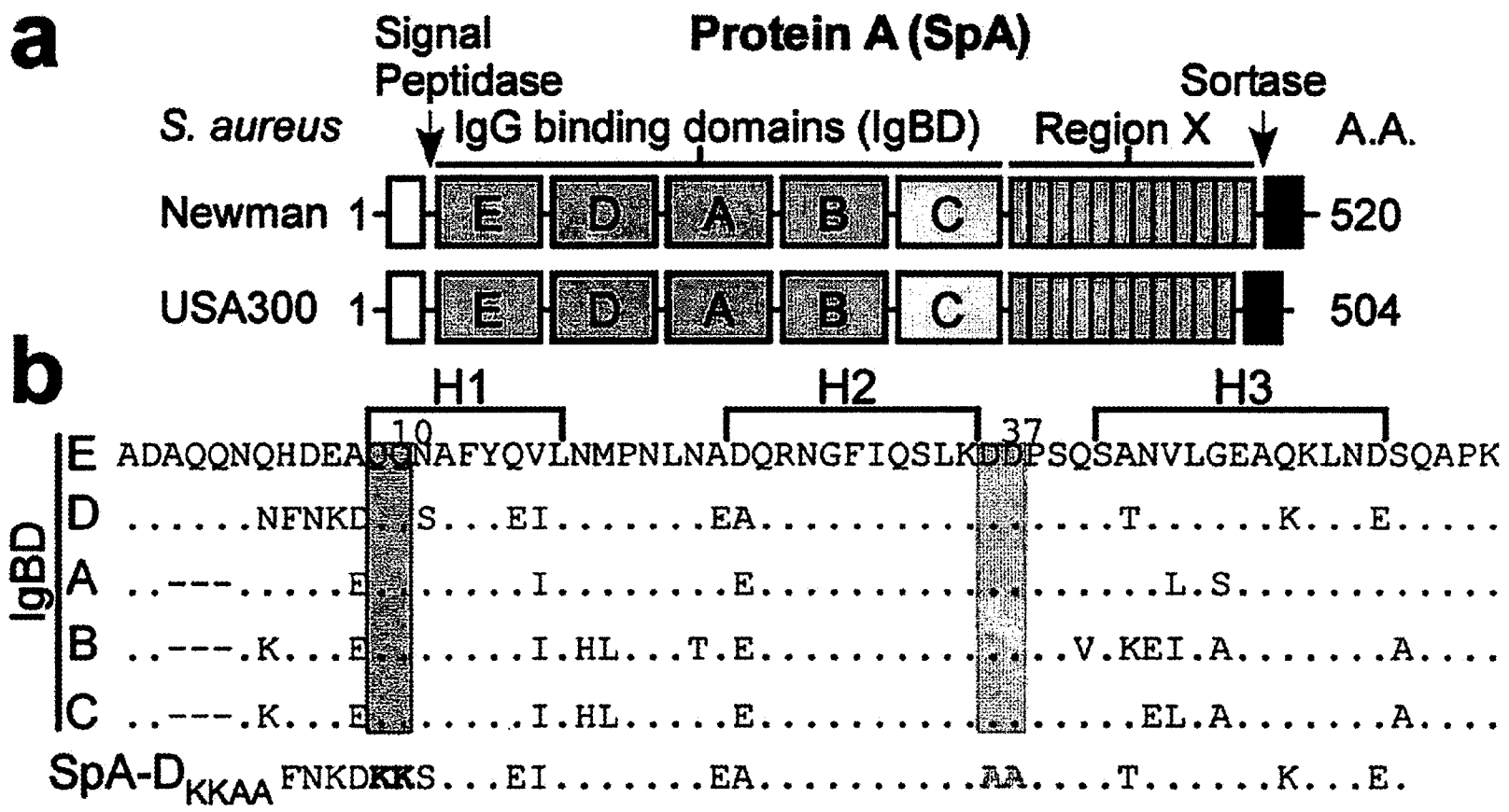


FIG. 6A-6B

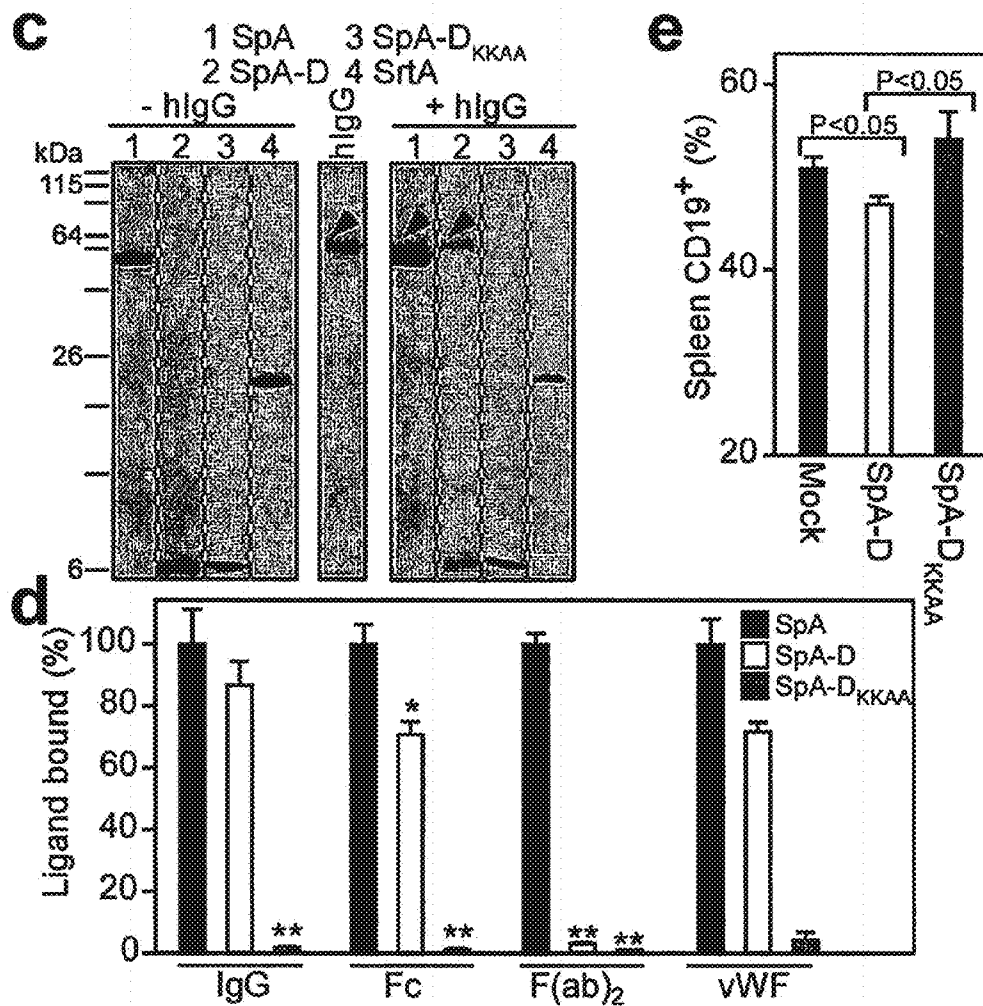


FIG. 6C-6E

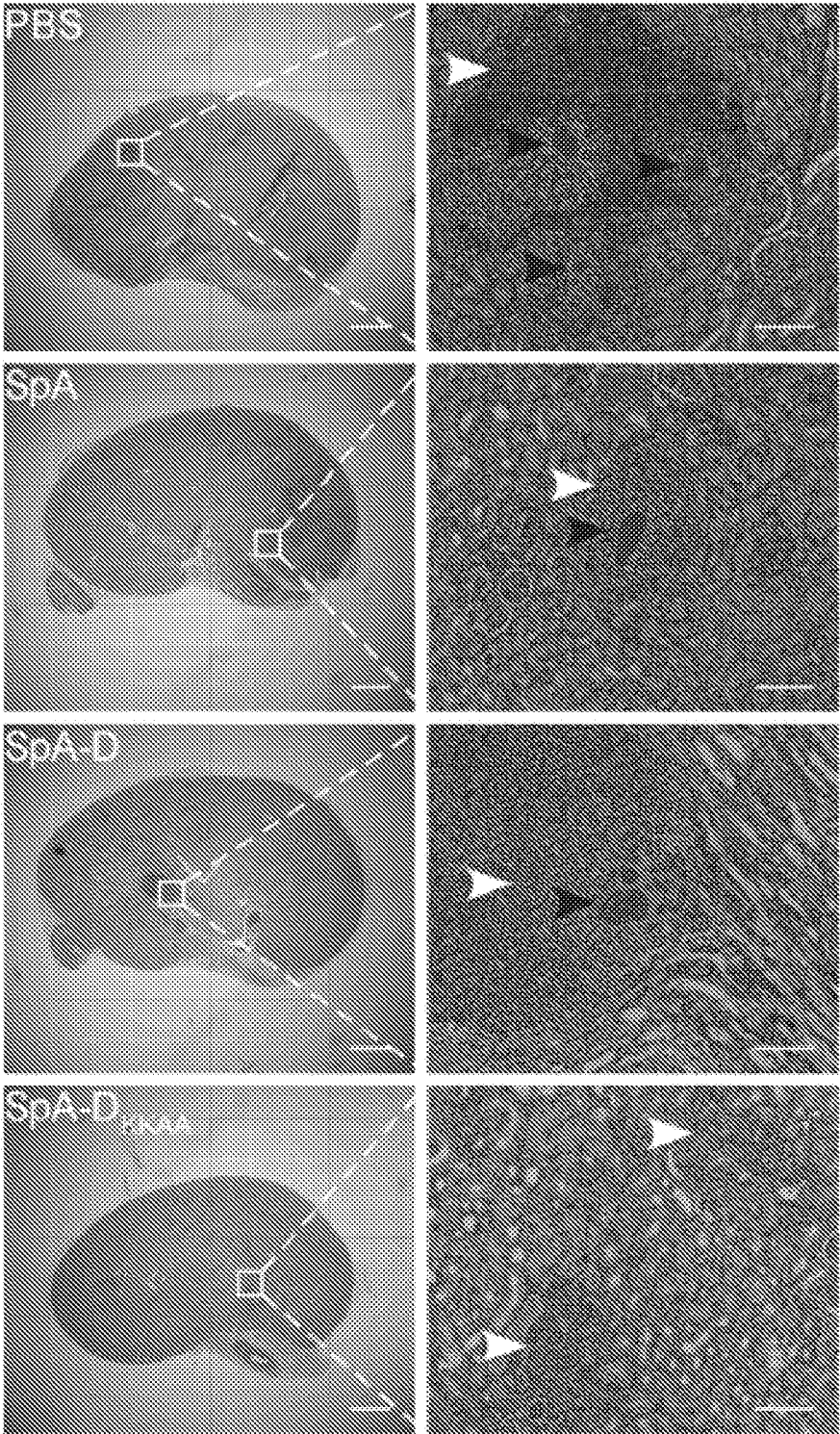


FIG. 7

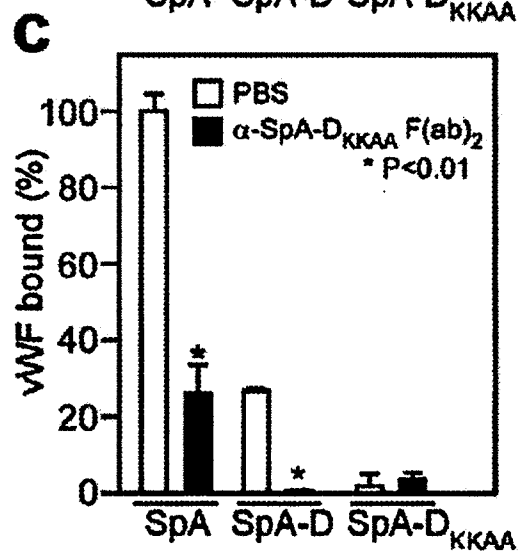
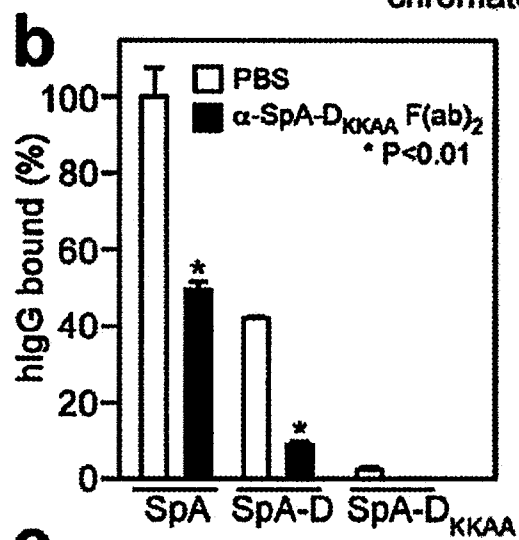
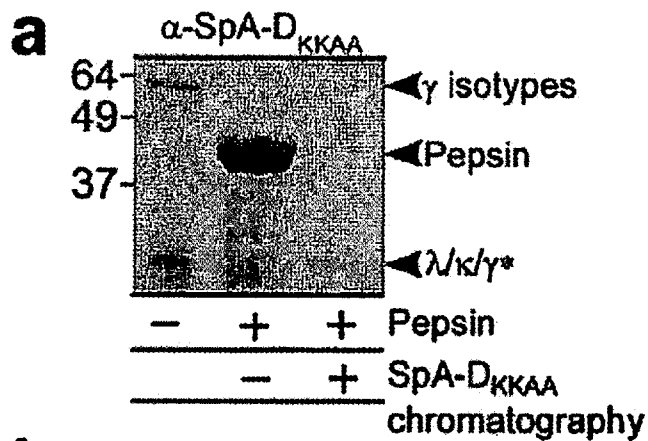


FIG. 8A-8C

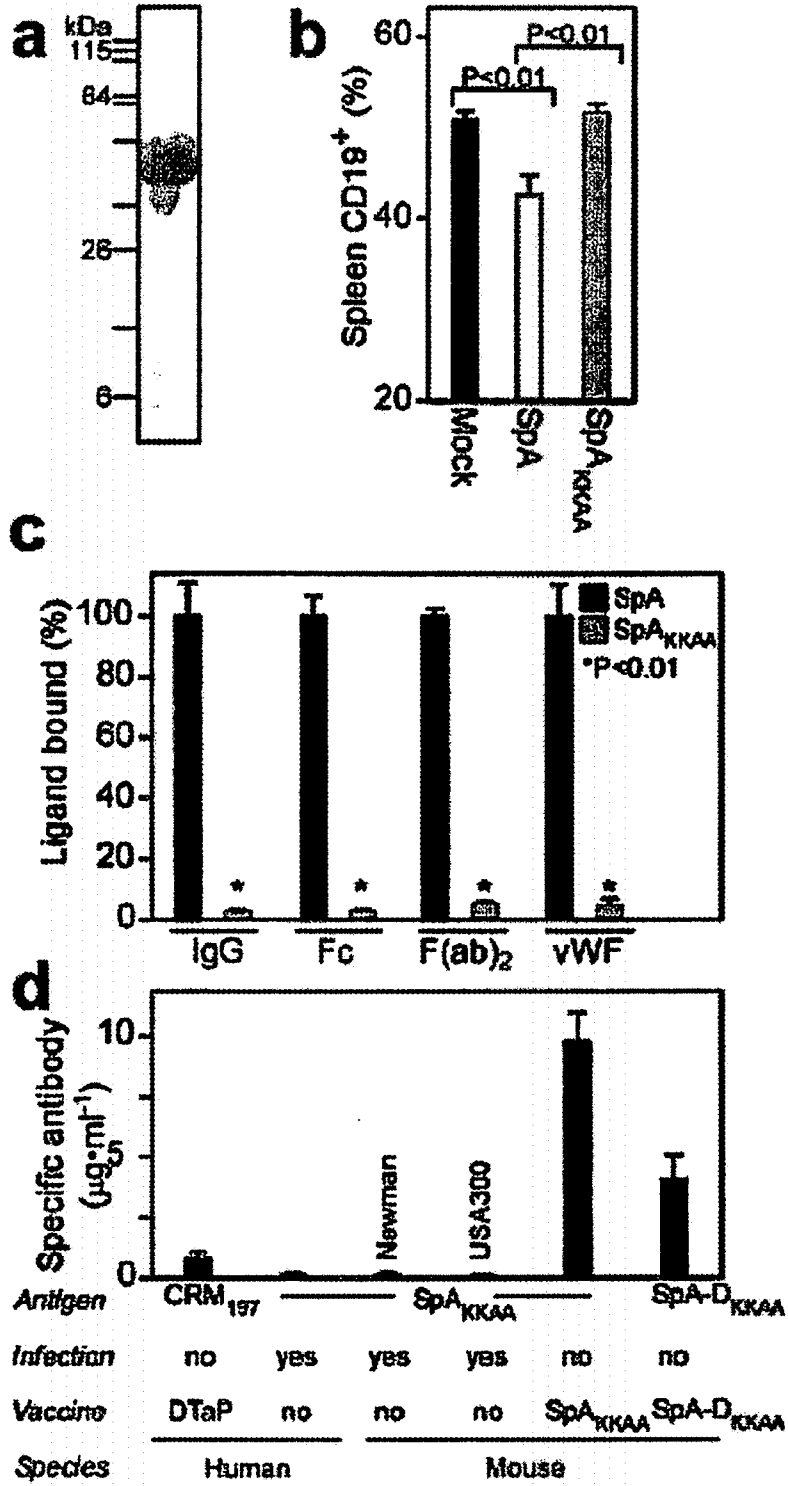


FIG. 9A-9D

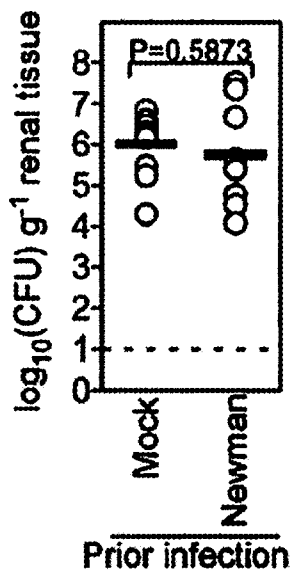


FIG. 10

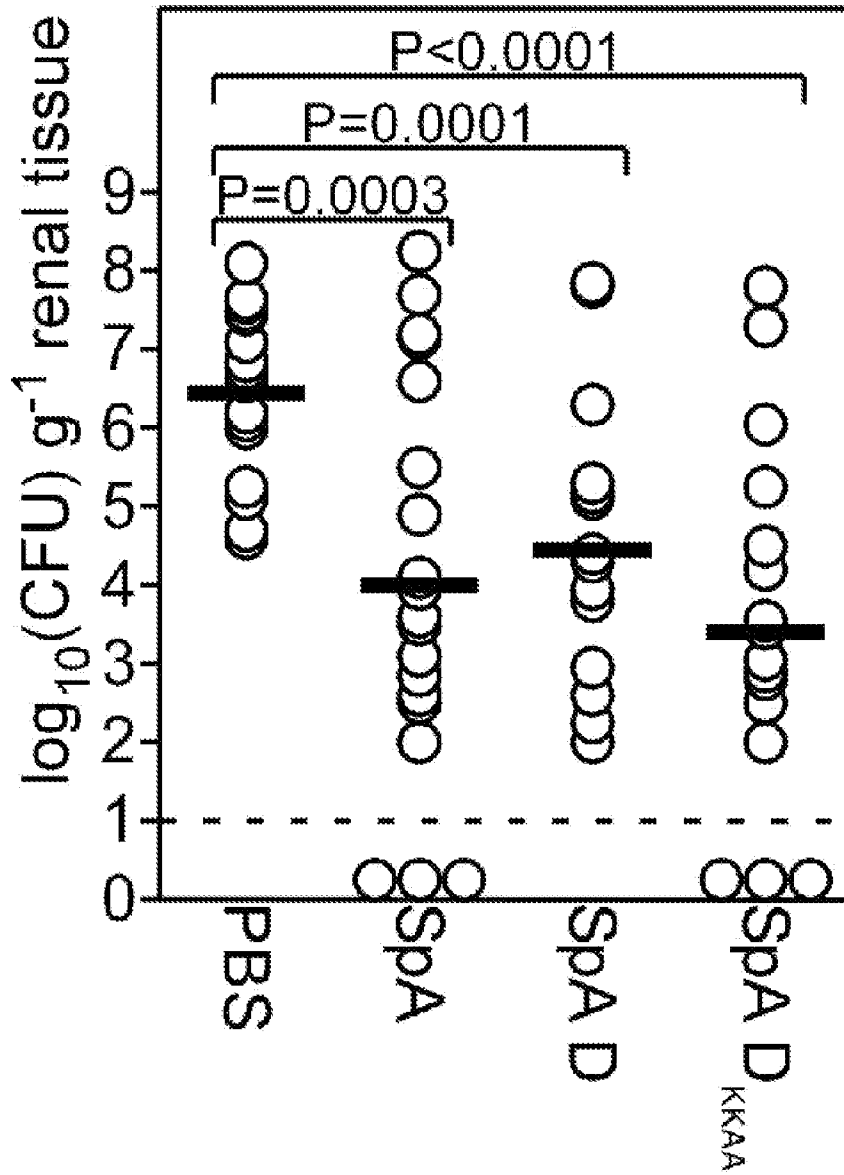


FIG. 11

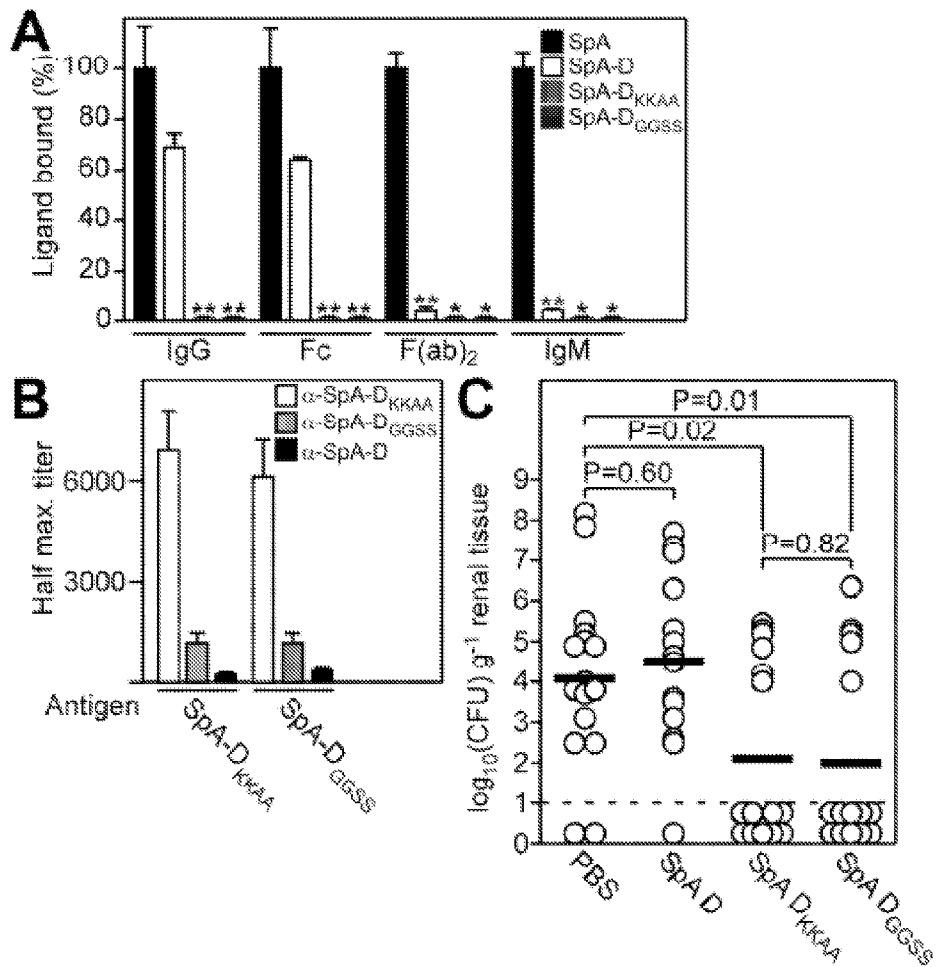


FIG. 12A-12C

COMPOSITIONS AND METHODS RELATED TO PROTEIN A (SPA) VARIANTS

[0001] This application is a continuation of U.S. patent application Ser. No. 14/466,514, filed Aug. 22, 2014, which is a continuation of U.S. patent application Ser. No. 13/807,598, filed Mar. 19, 2013, now U.S. Pat. No. 8,821,894, which is a national phase application under 35 U.S.C. §371 of International Application No. PCT/US2011/042845, filed Jul. 1, 2011, which claims the benefit of priority to U.S. Provisional Patent Application Ser. No. 61/361,218 filed Jul. 2, 2010, and 61/370,725 filed Aug. 4, 2010. The entire contents of each of the above-referenced disclosures are specifically incorporated herein by reference without disclaimer.

[0002] This invention was made with government support under AI057153, AI052474, and GM007281 awarded by the National Institutes of Health. The government has certain rights in the invention.

BACKGROUND OF THE INVENTION

[0003] I. Field of the Invention

[0004] The present invention relates generally to the fields of immunology, microbiology, and pathology. More particularly, it concerns methods and compositions involving bacterial Protein A variants, which can be used to invoke an immune response against the bacteria.

[0005] II. Background

[0006] 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%) (Emorl and Gaynes, 1993).

[0007] 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.

[0008] 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.

[0009] *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.

[0010] *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* infec-

tion 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.

[0011] *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.

[0012] 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).

[0013] 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).

[0014] *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 Snm 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).

[0015] 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

[0016] 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 por-

tion, 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 Protein A variants no longer able to bind to immunoglobulins, which are thereby removed of their toxigenic potential, i.e., are non-toxicogenic, stimulate humoral immune responses that protect against staphylococcal disease.

[0017] 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.

[0018] 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.

[0019] 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.

[0020] 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.

[0021] 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.

[0022] 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 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.

[0023] 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.

[0024] 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.

[0025] 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.

[0026] 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.

[0027] 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.

[0028] 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, QQNNFNKDKQSAFYEILNMPNLNEAQRNGFIQSLKDDPSQSTNVLGAEAKKLNES) 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, for example see FIG. 2A. 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.

[0029] 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.

[0030] Embodiments include the use of Protein A variants in methods and compositions for the treatment of bacterial and/or staphylococcal infection. This application also provides an immunogenic composition comprising a Protein A variant or immunogenic fragment thereof. In certain aspects, the immunogenic fragment is a Protein A domain D segment. 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) or prevent bacterial infection. In some cases, methods for stimulating an immune response involve administering to the subject an effective amount of a composition including or encoding all or part of a Protein A variant polypeptide or antigen, and in certain aspects other bacterial proteins. Other bacterial proteins 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.

[0031] In other aspects, the subject can be administered all or part of a Protein A variant, such as a variant Protein A domain D segment. The polypeptide of the invention can be formulated in a pharmaceutically acceptable composition. The composition can further comprise 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 (e.g., Eap, Ebh, Emp, EsaB, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, CIfA, CHB, Coa, Hla (e.g., H35 mutants), IsdC, SasF, vWbp, or vWh). Additional staphylococcal antigens that can be used in combination with a Protein A variant include, but are not limited to 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),

[0034] In still further aspects, the isolated Protein A variant 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. SpA polypeptides 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 Eap, Ebh, Emp, EsaB, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, CHB, Coa, Hla, IsdC, SasF, vWbp, vWh or immunogenic fragments thereof. Additional staphylococcal antigens that can be used in combination with a Protein A variant 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.

[0035] The term "Protein A variant" or "SpA variant" refers to polypeptides that include a SpA IgG domain having two or more amino acid substitutions that disrupt binding to Fc and V_H3. In certain aspect, a SpA variant includes a variant domain D peptide, as well as variants of SpA polypeptides and segments thereof that are non-toxicogenic and stimulate an immune response against *staphylococcus* bacteria Protein A and/or bacteria expressing such.

[0036] Embodiments of the present invention include methods for eliciting an immune response against a *staphylococcus* bacterium or staphylococci in a subject comprising providing to the subject an effective amount of a Protein A variant or a segment thereof. In certain aspects, the methods for eliciting an immune response against a *staphylococcus* bacterium or staphylococci in a subject comprising providing to the subject an effective amount of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or more secreted proteins and/or cell surface proteins or segments/fragments thereof. A secreted protein or cell surface protein includes, but is not limited to Eap, Ebh, Emp, EsaB, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, Coa, Hla, IsdC, SasF, vWbp, and/or vWh proteins and immunogenic fragments thereof. Additional staphylococcal antigens that can be used in combination with a Protein A variant 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, Immun-

odominant 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.

[0037] 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 Protein A, or a second protein or peptide that is a secreted bacterial protein or a bacterial cell surface protein. In a further embodiment 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 Protein A domain D polypeptide (SEQ ID NO:2), domain E (SEQ ID NO:3), domain A (SEQ ID NO:4), domain C (SEQ ID NO:5), domain B (SEQ ID NO:6), or a nucleic acid sequence encoding a Protein A domain D, domain E, domain A, domain C, or domain B polypeptide. In certain aspects a Protein A polypeptide segment will have an amino acid sequence of SEQ ID NO:8. Similarity or identity, with identity being preferred, is known in the art and a number of different programs can be used to identify whether a protein (or nucleic acid) has sequence identity or similarity to a known sequence. Sequence identity and/or similarity is determined using standard techniques known in the art, including, but not limited to, the local sequence identity algorithm of Smith & Waterman (1981), by the sequence identity alignment algorithm of Needleman & Wunsch (1970), by the search for similarity method of Pearson & Lipman (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, Wis.), the Best Fit sequence program described by Devereux et al. (1984), preferably using the default settings, or by inspection. Preferably, percent identity is calculated by using alignment tools known to and readily ascertainable to those of skill in the art. Percent identity is essentially the number of identical amino acids divided by the total number of amino acids compared times one hundred.

[0038] Still further embodiments include methods for stimulating in a subject a protective or therapeutic immune response against a *staphylococcus* bacterium comprising administering to the subject an effective amount of a composition including (i) a SpA variant, e.g., a variant SpA domain D polypeptide or peptide thereof; or, (ii) a nucleic acid molecule encoding such a SpA variant polypeptide or peptide thereof, or (iii) administering a SpA variant domain D polypeptide with any combination or permutation of bacterial proteins described herein. In a preferred embodiment the composition is not a *staphylococcus* bacterium. In certain aspects the subject is a human or a cow. In a further aspect the composition is formulated in a pharmaceutically acceptable formulation. The staphylococci may be *Staphylococcus aureus*.

[0039] Yet still further embodiments include vaccines comprising a pharmaceutically acceptable composition having an isolated SpA variant polypeptide, or any other combination or permutation of protein(s) or peptide(s) described herein, wherein the composition is capable of stimulating an immune

response against a *staphylococcus* bacterium. The vaccine may comprise an isolated SpA variant polypeptide, or any other combination or permutation of protein(s) or peptide(s) described. In certain aspects of the invention the isolated SpA variant polypeptide, 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 non-SpA polypeptide. Typically the vaccine comprises an adjuvant. In certain aspects a protein or peptide of the invention is linked (covalently or non-covalently) to the adjuvant, preferably the adjuvant is chemically conjugated to the protein.

[0040] In still yet further embodiments, a vaccine composition is a pharmaceutically acceptable composition having a recombinant nucleic acid encoding all or part of a SpA variant polypeptide, or any other combination or permutation of protein(s) or peptide(s) described herein, wherein the composition is capable of stimulating an immune response against a *staphylococcus* bacteria. The vaccine composition may comprise a recombinant nucleic acid encoding all or part of a SpA variant polypeptide, or any other combination or permutation of protein(s) or peptide(s) described herein. In certain embodiments the recombinant nucleic acid contains a heterologous promoter. Preferably the recombinant nucleic acid is a vector. More preferably the vector is a plasmid or a viral vector. In some aspects the vaccine includes a recombinant, non-*staphylococcus* bacterium containing the nucleic acid. The recombinant non-staphylococci may be *Salmonella* or another gram-positive bacteria. The vaccine may comprise a pharmaceutically acceptable excipient, more preferably an adjuvant.

[0041] Still further embodiments include methods for stimulating in a subject a protective or therapeutic immune response against a *staphylococcus* bacterium comprising administering to the subject an effective amount of a composition of a SpA variant polypeptide or segment/fragment thereof and further comprising one or more of a Eap, Ebh, Emp, EsaB, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, Coa, Hla, IsdC, SasF, vWbp, or vWh protein or peptide thereof. In a preferred embodiment the composition comprises a non-*staphylococcus* bacterium. In a further aspect the composition is formulated in a pharmaceutically acceptable formulation. The staphylococci for which a subject is being treated may be *Staphylococcus aureus*. Methods of the invention also include SpA variant compositions that contain 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or more secreted virulence factors and/or cell surface proteins, such as Eap, Ebh, Emp, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, Coa, Hla, IsdC, SasF, vWbp, or vWh in various combinations. In certain aspects a vaccine formulation includes Eap, Ebh, Emp, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, Coa, Hla, IsdC, SasF, vWbp, and vWh. In certain aspects an antigen combination can include (1) a SpA variant and IsdA; (2) SpA variant and ClfB; (3) SpA variant and SdrD; (4) SpA variant and Hla or Hla variant; (5) SpA variant and ClfB, SdrD, and Hla or Hla variant; (6) SpA variant, IsdA, SdrD, and Hla or Hla variant; (7) SpA variant, IsdA, ClfB, and Hla or Hla variant; (8) SpA variant, IsdA, ClfB, and SdrD; (9) SpA variant, IsdA, ClfB, SdrD and Hla or Hla variant; (10) SpA variant, IsdA, ClfB, and SdrD; (11) SpA variant, IsdA,

SdrD, and Hla or Hla variant; (12) SpA variant, IsdA, and Hla or Hla variant; (13) SpA variant, IsdA, ClfB, and Hla or Hla variant; (14) SpA variant, ClfB, and SdrD; (15) SpA variant, ClfB, and Hla or Hla variant; or (16) SpA variant, SdrD, and Hla or Hla variant.

[0042] 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, SpA variant(s) can be overexpressed in an attenuated bacterium to further enhance or supplement an immune response or vaccine formulation.

[0043] 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.

[0044] 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.

[0045] 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.

[0046] 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.

[0047] 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.

[0048] 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.

[0049] 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.

[0050] 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.

[0051] 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.

[0052] 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.

[0053] The term “EsaC protein” refers to a protein that includes isolated wild-type EsaC polypeptides from *staphy-*

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

[0054] 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.

[0055] 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.

[0056] 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.

[0057] 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.

[0058] 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.

[0059] 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.

[0060] 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.

[0061] 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.

[0062] 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.

[0063] 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.

[0064] 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.

[0065] 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.

[0066] 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.

[0067] 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.

[0068] 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.

[0069] 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.

[0070] 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 an EsaB protein. In certain aspects the EsaB protein will have all or part of the amino acid sequence of SEQ ID NO:17.

[0071] 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.

[0072] 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.

[0073] 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.

[0074] 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.

[0075] 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.

[0076] 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.

[0077] 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.

[0078] 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.

[0079] 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.

[0080] 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.

[0081] 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.

[0082] 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.

[0083] 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.

[0084] 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.

[0085] 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:32-34.

[0086] A polypeptide segment 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:33-34.

[0087] The compositions may be formulated in a pharmaceutically acceptable composition. In certain aspects of the invention the *staphylococcus* bacterium is an *S. aureus* bacterium.

[0088] 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.

[0089] 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 mol-

ecule 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.

[0090] In further embodiments a composition comprises a recombinant nucleic acid molecule encoding all or part of one or more of a Eap, Ebh, Emp, 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.

[0091] 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 *staphylococcus* bacterium is contemplated, particularly cattle, horses, goats, sheep and other domestic animals, i.e., mammals.

[0092] 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.

[0093] 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 or peptide or nucleic acid may be implemented with respect to other antigens, such as 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 GehD, MAP, Mg2+ transporter, MEW 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), and vice versa. It is also understood that any 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 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 can be specifically excluded from a claimed composition.

[0094] 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.

[0095] 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.

[0096] 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.

[0097] 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.

[0098] The subject will have (e.g., are diagnosed with a staphylococcal infection), will be suspected of having, or will 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.

[0099] The embodiments in the Example section are understood to be embodiments of the invention that are applicable to all aspects of the invention.

[0100] 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.

[0101] 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.

[0102] 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.

[0103] 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

[0104] 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.

[0105] FIGS. 1A-1B. (FIG. 1A) Primary structure of the Protein A precursor with an N-terminal YSIRK motif signal peptide, five immunoglobulin binding domains as tandem repeats designated E, D, A, B, C, region X, and the LPXTG sorting signal. (FIG. 1B) Following synthesis of the Protein A precursor, staphylococci secrete this product via the Sec pathway, and sortase A cleaves the LPXTG sorting signal between the T and G residues. Nucleophilic attack of the amino group within lipid II at the sortase-Protein A thioester-linked intermediate forms the amide bond that links Protein A to the cell wall envelope and enables its display on the bacterial surface.

[0106] FIG. 2A-2C. Three dimensional model of the molecular interactions between the SpA-domain D of Protein A, the VH3 Fab domain of the B cell receptor, and of the Fc γ domain of immunoglobulin. The model is derived from two crystal structures (Graille et al., 2000 and Gouda et al., 1992) that revealed side chain residues involved in the formation of ionic bonds that enable these complexes. Gln-9 and Gln-10 of SpA-D promote binding to Fc γ , whereas Asp-36 and Asp-37 enable complex formation with VH3 Fab.

[0107] FIG. 3. Left panel—Coomassie Blue stained SDS-PAGE reveals the migrational position of purified His-tagged SpA, SpA-D, SpA-D_{Q9,10K;D36,37A}, human IgG, and sortase A (SrtA), a control protein. Right panel—Coomassie Blue stained SDS-PAGE to reveal the elution of Protein A immunoglobulin complexes eluted following affinity chromatography of human IgG on Ni-NTA columns pre-charged with His-tagged SpA, SpA-D, SpA-D_{Q9,10K;D36,37A} or SrtA.

[0108] FIG. 4. ELISA assays to quantify human immunoglobulin (hIgG), human F(ab)₂ IgG fragments and human Fc fragments of immunoglobulin (hFc). Plates were coated with equal amounts of His-tagged SpA, SpA-D, SpA-D_{Q9,10K;D36,37A} or SrtA. hIgG-HRP, F(ab)₂-HRP and hFc-HRP were added onto the plates and incubated for an hour. Absorbance at 450 nm was recorded and plotted to determine the half maximal titers.

[0109] FIG. 5. Purified SpA-D, SpA-D_{Q9,10K;D36,37A} or a PBS mock control were injected into the peritoneum of mice and analyzed for their ability to reduce the B cell population in the spleen of experimental BALB/c mice. Animals were killed 4 hours following injection, their spleen removed, tissue homogenized and stained with CD19 antibodies directed against B cells. The number of B cells was quantified by FACS sorting.

[0110] FIG. 6A-6E. Generation of a non-toxicogenic protein A vaccine. a, Translational protein A (SpA) product of S.

aureus Newman and USA300 LAC with an N-terminal signal peptide (white box), five immunoglobulin binding domains (IgBDs designated E, D, A, B and C), variable region X and C-terminal sorting signal (black box). b, Amino acid sequence of the five IgBDs as well as nontoxicogenic SpA-D_{KKAA} with the positions of triple α -helical bundles (H1, H2 and H3) as well as glutamine (Q) 9, 10 and aspartate (D) 36, 37 indicated. c, Coomassie Blue-stained SDS-PAGE of SpA, SpA-D, SpA-D_{KKAA} or SrtA purified on Ni-NTA sepharose in the presence or absence of human immunoglobulin (hIgG). d, ELISA examining the association of immobilized SpA, SpA-D or SpA-D_{KKAA} with human IgG as well as its Fc or F(ab)₂ fragments and von Willebrand factor (vWF). e, CD19+ B lymphocytes in splenic tissue of BALB/c mice that had been mock immunized or treated with SpA-D or SpA-D_{KKAA} were quantified by FACS.

[0111] FIG. 7. Non-toxicogenic protein A vaccine prevents abscess formation. Histopathology of renal tissue isolated during necropsy of BALB/c mice that had been mock immunized (PBS) or vaccinated with SpA, SpA-D as well as SpA-D_{KKAA} and challenged with *S. aureus* Newman. Thin sectioned tissues were stained with hematoxylin-eosin. White arrows identify polymorphonuclear leukocyte (PMN) infiltrates. Dark arrows identify staphylococcal abscess communities.

[0112] FIG. 8A-8C. Antibodies raised by the non-toxicogenic protein A vaccine block the B cell superantigen function of SpA. a, Rabbit antibodies raised against SpA-D_{KKAA} were purified on a matrix with immobilized antigen and analyzed by Coomassie Blue-stained SDS-PAGE. Antibodies were cleaved with pepsin and F(ab)₂ fragments were purified by a second round of affinity chromatography on SpA-D_{KKAA} matrix. b, SpA-D_{KKAA} specific F(ab)₂ interfere with the binding of SpA or SpA-D to human immunoglobulin (hIgG) or, c, to von Willebrand Factor (vWF).

[0113] FIG. 9A-9D. Full-length non-toxicogenic protein A generates improved immune responses. a, Full-length SpA_{KKAA} was purified on Ni-NTA sepharose and analyzed by Coomassie-Blue stained SDS-PAGE. b, CD19+ B lymphocytes in splenic tissue of BALB/c mice that had been mock immunized or treated with SpA or SpA_{KKAA} were quantified by FACS. c, ELISA examining the association of immobilized SpA or SpA_{KKAA} with human IgG as well as its Fc or F(ab)₂ fragments or von Willebrand factor (vWF). d, Human or mouse serum antibody titers to diphtheria toxoid (CRM197) and non-toxicogenic SpA_{KKAA} or SpA-D_{KKAA}. Human volunteers with a history of DTaP immunization and staphylococcal infection (n=16) as well as mice (n=20) that had been infected with *S. aureus* Newman or USA 300 LAC or immunized with SpA_{KKAA} or SpA-D_{KKAA} were examined by quantitative dot blot.

[0114] FIG. 10. Staphylococcal infection does not generate protective immunity. BALB/c mice (n=20) were infected with *S. aureus* Newman or mock challenged (PBS) for thirty days and infection cleared with chloramphenicol treatment. Both cohorts of animals were then challenged with *S. aureus* Newman and bacterial load (CFU) in kidney tissue homogenate analyzed following necropsy on day 4.

[0115] FIG. 11. Comparison of abscess formation in mice treated with PBS, SpA, SpA-D, and SpA-D_{KKAA}.

[0116] FIGS. 12A-12C. (A) ELISA examining the association of immobilized SpA, SpA-D, SpA-DKKAA or SpA-DGGSS with human IgG as well as its Fc or F(ab)₂ fragments and IgM. Statistical significance of SpA-DKKAA and SpA-

DGGSS binding to each ligand was compared against SpA-D; SpA-D binding was compared against SpA (n=3); * signifies P<0.05; ** signifies P<0.01. (B) ELISA examining the level of cross-reactive antibodies of hyperimmune sera samples collected from actively immunized mice (n=5) with SpA-D, SpA-DKKAA and SpA-DGGSS. (C) Abscess formation in mice treated with PBS, SpA-D, SpA-D_{KKAA} and SpA-D_{GGSS}.

DETAILED DESCRIPTION

[0117] *Staphylococcus aureus* is a commensal of the human skin and nares, and the leading cause of bloodstream, skin and soft tissue infections (Klevens 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 (Klevens et al., 2007). The annual health care costs for 94,300 MRSA infected individuals in the United States exceed \$2.4 billion (Klevens 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.

[0118] 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).

II. Staphylococcal Antigens

[0119] A. Staphylococcal Protein A (SpA)

[0120] 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 Willibrand factor at its A1 domain [vWF A1 is a ligand for platelets] (O'Seaghda et al., 2006) and the tumor necrosis factor α (TNF- α) receptor I (TNFR1) (Gomez et al., 2006), which is displayed on surfaces of airway epithelia (Gomez et al., 2004; Gomez et al., 2007).

[0121] 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 Willibrand factor A1 domains (Hartleib et al., 2000). Plasma proteins such as fibrinogen and fibronectin act as bridges between staphylococci (C1fA and C1fB) 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'Seaghda et al., 2006). SpA also binds TNFR1 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- κ B. 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).

[0122] 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. Staphylococcal variants lacking Protein A are unable to establish the histopathology features of abscesses and are cleared during infection.

[0123] 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.

[0124] 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.

[0125] 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.

[0126] O'Seaghda 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'Seaghda 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.

[0127] 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.

[0128] 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'Seaghda 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).

[0129] Molecular Basis of Protein a Surface Display and Function.

[0130] 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 crossbridges 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).

[0131] 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).

[0132] 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 C0 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.

[0133] 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.

[0134] In contrast, occupancy of the Fc portion of IgG on the domain D blocks its interaction with vWF A1 and probably also TNFR1 (O'Seaghda et al., 2006). Mutations in residues essential for IgG Fc binding (F5, Q9, Q10, S11, F13, Y14, L17, N28, I31 and K35) are also required for vWF A1 and TNFR1 binding (O'Seaghda 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.

[0135] 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 AI 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. (See Examples section below).

[0136] B. Staphylococcal Coagulases

[0137] 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).

[0138] Fibrinogen is a large glycoprotein (Mr~340,000), formed by three pairs of α -, β -, 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 β - 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.

[0139] 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.

[0140] 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.

[0141] Earlier studies revealed a requirement of coagulase for resisting phagocytosis in blood (Smith et al., 1947) and the inventors observed a similar phenotype for Δ coa 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 Δ vWbp 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, Δ coa 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.

[0142] C. Other Staphylococcal Antigens

[0143] 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 micro-organisms 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.

[0144] 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 esaB esaB essB 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, esaA, esaB, and esaC 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).

[0145] 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.

[0146] 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.

[0147] 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.

[0148] 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 (gi|68565539), 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 (gi|68565532), 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.

[0149] 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 (gi|15926240), 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.

[0150] 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.

[0151] 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.

[0152] 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.).

[0153] 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.

[0154] 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.

[0155] 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.

[0156] 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.

[0157] 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.

[0158] 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 2

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
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

[0159] 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.

[0160] 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 3

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	

TABLE 3-continued

Codon Table					
Amino Acids		Codons			
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

TABLE 3-continued

Codon Table					
Amino Acids		Codons			
Threonine	Thr	T	ACA	ACC	ACG ACU
Valine	Val	V	GUA	GUC	GUG GUU
Tryptophan	Trp	W	UGG		
Tyrosine	Tyr	Y	UAC	UAU	

[0161] 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.

[0162] 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.

[0163] 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.

[0164] 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.

[0165] 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.

[0166] D. Polypeptides and Polypeptide Production

[0167] 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.

[0168] 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.

[0169] 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.

[0170] 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.

[0171] A number of selection systems may be used including, but not limited to HSV thymidine kinase, hypoxanthine-guanine phosphoribosyltransferase, and adenine phosphori-

bosyltransferase genes, in tk-, hgp^rt- or ap^rt-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 mycophenolic acid; neo, which confers resistance to the aminoglycoside G418; and hyg^r, which confers resistance to hygromycin.

[0172] 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).

[0173] 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.

[0174] 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.

[0175] 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

[0176] 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.

[0177] 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.

[0178] 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 3 above).

[0179] 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.

[0180] 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.

[0181] 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.

[0182] 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.

[0183] 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).

[0184] The invention also contemplates the use of polynucleotides which are complementary to all the above described polynucleotides.

[0185] A. Vectors

[0186] 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.

[0187] 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.

[0188] 1. Promoters and Enhancers

[0189] 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.

[0190] 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.

[0191] 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 (Transthyretin) (Costa et al., 1988), Elastase I (Ornitz et al., 1987), Metal-

lothionein (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; Miksicek 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; Laspia 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).

[0192] 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; McNeill 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).

[0193] 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.

[0194] 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.

[0195] 2. Initiation Signals and Internal Ribosome Binding Sites (IRES)

[0196] 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.

[0197] 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 Sarnow, 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).

[0198] 3. Selectable and Screenable Markers

[0199] 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.

[0200] B. Host Cells

[0201] 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.

[0202] 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).

[0203] C. Expression Systems

[0204] 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.

[0205] 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®.

[0206] 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

[0207] 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.

[0208] A. PIA (PNAG)

[0209] 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.

[0210] 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.

[0211] 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→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.

[0212] 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.

[0213] 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 NH₄OH. 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.

[0214] The polysaccharide(s) can be conjugated or unconjugated to a carrier protein.

[0215] B. Type 5 and Type 8 Polysaccharides from *S. aureus*

[0216] 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 FucNAcp in their repeat unit as well as ManNAcA which can be used to introduce a sulfhydryl group. The structures are:

[0217] Type 5

[0218] $\rightarrow 4$)- β -D-ManNAcA(3OAc)-(1 \rightarrow 4)- α -L-FucNAc (1 \rightarrow 3)- β -D-FucNAc-(1 \rightarrow

[0219] Type 8

[0220] $\rightarrow 3$)- β -D-ManNAcA(4OAc)-(1 \rightarrow 3)- α -L-FucNAc (1 \rightarrow 3)- β -D-FucNAc-(1 \rightarrow

[0221] Recently (Jones, 2005) NMR spectroscopy revised the structures to:

[0222] Type 5

[0223] $\rightarrow 4$)- β -D-ManNAcA-(1 \rightarrow 4)- α -L-FucNAc (3OAc)-(1 \rightarrow 3)- β -D-FucNAc-(1 \rightarrow

[0224] Type 8

[0225] $\rightarrow 3$)- β -D-ManNAcA(4OAc)-(1 \rightarrow 3)- α -L-FucNAc (1 \rightarrow 3)- α -D-FucNAc(1 \rightarrow

[0226] Polysaccharides may be extracted from the appropriate strain of *S. aureus* using method well known to 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.

[0227] 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.

[0228] C. *S. aureus* 336 Antigen

[0229] 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.

[0230] D. Type I, II and III Polysaccharides from *S. epidermidis*

[0231] 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. influenzae* will preferably contain the N-terminal $\frac{1}{3}$ 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.

[0232] 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.

[0233] 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.

[0234] 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

[0235] 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.

[0236] A. Immunoassays

[0237] 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.

[0238] Immunoassays generally are binding assays. Certain preferred immunoassays are the various types of enzyme linked immunosorbent assays (ELISAs) and radioimmunoassays (MA) 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 com-

plexes, 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.

[0239] 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.

[0240] 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.

[0241] B. Diagnosis of Bacterial Infection

[0242] 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 bind-

ing to the polypeptides, proteins, and/or peptides, or polypeptides, proteins, and/or peptides binding to the antibodies in the sample.

[0243] 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.

[0244] 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).

[0245] C. Protective Immunity

[0246] In some embodiments of the invention, proteinaeous 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.

[0247] 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.

[0248] 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.

[0249] 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.

[0250] 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.

[0251] 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 reso-

nance. 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.

[0252] 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.

[0253] 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.

[0254] 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.

[0255] 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.

[0256] 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).

[0257] 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.

[0258] 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.

[0259] 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.

[0260] D. Treatment Methods

[0261] 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.

[0262] 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.

[0263] 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.

[0264] 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

[0265] A. Vaccines

[0266] 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.

[0267] 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.

[0268] 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.

[0269] 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, polyalkalene 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%.

[0270] 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.

[0271] 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.

[0272] 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.

[0273] 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.

[0274] 1. Carriers

[0275] 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-biazo-tized benzidine.

[0276] 2. Adjuvants

[0277] 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.

[0278] 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, GMCSF, 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).

[0279] 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 mono-oleate (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.

[0280] 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.

[0281] 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.

[0282] 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.

[0283] 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 suppresser 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.

[0284] B. Lipid Components and Moieties

[0285] 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.

[0286] 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.

[0287] 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.

[0288] 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.

[0289] C. Combination Therapy

[0290] 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.

[0291] 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.

[0292] 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/B B/A/A/A A/B/A/A A/A/B/A

[0293] 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.

[0294] D. General Pharmaceutical Compositions

[0295] 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.

[0296] 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.

[0297] 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 mol-

ecule 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.

[0298] 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.

[0299] 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.

[0300] 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.

[0301] 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.

[0302] 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.

[0303] 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 orthotopic, 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.

[0304] 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.

[0305] 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.

[0306] 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.

[0307] 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.

[0308] E. In Vitro, Ex Vivo, or In Vivo Administration

[0309] 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.

[0310] 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.

[0311] F. Antibodies and Passive Immunization

[0312] 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.

[0313] Inocula for polyclonal antibody production are typically prepared by persping 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.

[0314] 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.

[0315] 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.

[0316] 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.

[0317] An additional aspect of the invention is a pharmaceutical composition comprising two or more monoclonal antibodies (or fragments thereof; preferably human or humanized) 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.

[0318] 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

[0319] 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

Non-Toxicogenic Protein A Variants as Subunit Vaccines to Prevent *Staphylococcus aureus* Infections

[0320] A. Results

[0321] An Animal Model for *S. aureus* Infection

[0322] BALB/c mice were infected by intravenous injection with 1×10^7 CFU of the human clinical isolate *S. aureus* Newman (Baba et al., 2007). Within 6 hours following infection, 99.999% of staphylococci disappeared from the blood stream and were distributed via the vasculature. Staphylococcal dissemination to peripheral tissues occurred rapidly, as the bacterial load in kidney and other peripheral organ tissues reached 1×10^5 CFU g^{-1} within the first three hours. The staphylococcal load in kidney tissues increased by 1.5 log CFU within twenty-four hours. Forty-eight hours following infection, mice developed disseminated abscesses in multiple organs, detectable by light microscopy of hematoxylin-eosin stained, thin-sectioned kidney tissue. The initial abscess diameter was 524 μ M (\pm 65 μ M); lesions were initially marked

by an influx of polymorphonuclear leukocytes (PMNs) and harbored no discernable organization of staphylococci, most of which appeared to reside within PMNs. On day 5 of infection, abscesses increased 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. A rim of necrotic PMNs were observed at the periphery of abscess lesions, bordering eosi-

red blood cells were located among the bacteria. Bacterial populations at the abscess center, designated staphylococcal abscess communities (SAC), appeared homogenous and coated by an electron-dense, granular material. The kinetics of the appearance of infectious lesions and the morphological attributes of abscesses formed by *S. aureus* Newman were similar to those observed following mouse infection with *S. aureus* USA300 (LAC), the current epidemic community-acquired methicillin-resistant *S. aureus* (CA-MRSA) clone in the United States (Diep et al., 2006).

TABLE 4

Genotype	Genetic requirements for <i>S. aureus</i> Newman abscess formation in mice			Abscess formation in kidney tissue		
	Staphylococcal load in kidney tissue			^d Surface	^e Number of	^f Significance (P-value)
	^a log ₁₀ CFU g ⁻¹ tissue	^b Significance (P-value)	^c Reduction (log ₁₀ CFU g ⁻¹)	abscesses (%)	abscesses per kidney	
wild-type	6.141 ± 0.192	—	—	70	4.364 ± 0.889	—
ΔsrtA	4.095 ± 0.347	6.7 × 10 ⁻⁶	2.046	0	0.000 ± 0.000	0.0216
spa	5.137 ± 0.374	0.0144	1.004	13	0.375 ± 0.374	0.0356

^aMeans of staphylococcal load calculated as log₁₀ CFU g⁻¹ in homogenized renal tissues 5 days following infection in cohorts of fifteen BALB/c mice per challenge strain. Standard error of the means (±SEM) is indicated.

^bStatistical significance was calculated with the Students t-test and P-values recorded; P-values < 0.05 were deemed significant.

^cReduction in bacterial load calculated as log₁₀ CFU g⁻¹.

^dAbscess formation in kidney tissues five days following infection was measured by macroscopic inspection (% positive)

^eHistopathology of hematoxylin-eosin stained, thin sectioned kidneys from eight to ten animals; the average number of abscesses per kidney was recorded and averaged again for the final mean (±SEM).

^fStatistical significance was calculated with the Students t-test and P-values recorded; P-values < 0.05 were deemed significant.

nophilic, amorphous material that separates healthy renal tissue from lesions. Abscesses eventually reached a diameter of ≥1,524 μm on day 15 or 36. At later time intervals, the staphylococcal load was increased to 10⁴-10⁶ CFU g⁻¹ and growing abscess lesions migrated towards the organ capsule. Peripheral lesions were prone to rupture, thereby releasing necrotic material and staphylococci into the peritoneal cavity or the retroperitoneal space. These events resulted in bacteremia as well as a secondary wave of abscesses, eventually precipitating a lethal outcome.

[0323] To enumerate staphylococcal load in renal tissue, animals were killed, their kidneys excised and tissue homogenate spread on agar media for colony formation. On day 5 of infection, a mean of 1×10⁶ CFU g⁻¹ renal tissue for *S. aureus* Newman was observed. To quantify abscess formation, kidneys were visually inspected, and each individual organ was given a score of one or zero. The final sum was divided by the total number of kidneys to calculate percent surface abscesses (Table 4). In addition, randomly chosen kidneys were fixed in formalin, embedded, thin sectioned, and stained with hematoxylin-eosin. For each kidney, four sagittal sections at 200 μm intervals were viewed by microscopy. The numbers of lesions were counted for each section and averaged to quantify the number of abscesses within the kidneys. *S. aureus* Newman caused 4.364±0.889 abscesses per kidney, and surface abscesses were observed on 14 out of 20 kidneys (70%) (Table 4).

[0324] When examined by scanning electron microscopy, *S. aureus* Newman was located in tightly associated lawns at the center of abscesses. Staphylococci were contained by an amorphous pseudocapsule that separated bacteria from the cuff of abscesses leukocytes. No immune cells were observed in these central nests of staphylococci, however occasional

[0325] *S. aureus* Protein A (spa) Mutants are Avirulent and Cannot Form Abscesses

[0326] Sortase A is a transpeptidase that immobilizes nineteen surface proteins in the envelope of *S. aureus* strain Newman (Mazmanian et al., 1999; Mazmanian et al., 2000). Earlier work identified sortase A as a virulence factor in multiple animal model systems, however the contributions of this enzyme and its anchored surface proteins to abscess formation or persistence have not yet been revealed (Jonsson et al., 2002; Weiss et al., 2004). Compared to the wild-type parent (Baba et al., 2007), an isogenic srtA variant (AsrtA) failed to form abscess lesions on either macroscopic or histopathology examination on days 2, 5, or 15. In mice infected with the strA mutant, only 1×10⁴ CFU g⁻¹ was recovered from kidney tissue on day 5 of infection, which is a 2.046 log₁₀ CFU g⁻¹ reduction compared to the wild-type parent strain (P=6.73×10⁻⁶). A similar defect was observed for the srtA mutant of MRSA strain USA300 (data not shown). Scanning electron microscopy showed that srtA mutants were highly dispersed and often associated with leukocytes in otherwise healthy renal tissue. On day fifteen following infection, srtA mutants were cleared from renal tissues, a ≥3.5 log₁₀ CFU g⁻¹ reduction compared to the wild-type (Table 3). Thus, sortase A anchored surface proteins enable the formation of abscess lesions and the persistence of bacteria in host tissues, wherein staphylococci replicate as communities embedded in an extracellular matrix and shielded from surrounding leukocytes by an amorphous pseudocapsule.

[0327] Sortase A anchors a large spectrum of proteins with LPXTG motif sorting signals to the cell wall envelope, thereby providing for the surface display of many virulence factors (Mazmanian et al., 2002). To identify surface proteins required for staphylococcal abscess formation, bursa aurealis insertions were introduced in 5' coding sequences of genes that encode polypeptides with LPXTG motif proteins (Bae et

al., 2004) and these mutations were transduced into *S. aureus* Newman. Mutations in the structural gene for Protein A (*spa*) reduced the staphylococcal load in infected mouse kidney tissues by $1.004 \log_{10}$ ($P=0.0144$). When analyzed for their ability to form abscesses in kidney tissues by histopathology, we observed that the *spa* mutants were unable to form abscesses as compared with the wild-type parent strain *S. aureus* Newman (wild-type *S. aureus* Newman 4.364 ± 0.889 abscesses per kidney vs. the isogenic *spa* mutant with 0.375 ± 0.374 lesions; $P=0.0356$).

[0328] Protein A Blocks Innate and Adaptive Immune Responses.

[0329] Studies identified Protein A as a critical virulence factor during the pathogenesis of *S. aureus* infections. Earlier work demonstrated that Protein A impedes phagocytosis of staphylococci by binding the Fc component of immunoglobulin (Jensen 1958; Uhlén et al., 1984), activates platelet aggregation via the von Willebrand factor (Hartleib et al., 2000), functions as a B cell superantigen by capturing the F(ab)₂ region of VH3 bearing IgM (Roben et al., 1995), and, through its activation of TNFR1, can initiate staphylococcal pneumonia (Gomez et al., 2004). 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. The inventors demonstrate for the first time that Protein A variants no longer able to bind to immunoglobulins, vWF and TNFR-1 are removed of their toxigenic potential and are able to stimulate humoral immune responses that protect against staphylococcal disease.

[0330] Molecular Basis of Protein A Surface Display and Function.

[0331] 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 crossbridges by sortase A (Schneewind et al., 1995; Mazmanian et al., 1999; Mazmanian et al., 2000). Protein A is the most abundant surface protein of staphylococci; the molecule is expressed by virtually all *S. aureus* strains (Said-Salim et al., 2003; Cespedes et al., 2005; Kennedy et al., 2008). 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).

[0332] 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 and Silverman 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 (Schneewind et al., 1992; Said-Salim et al., 2003). 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 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 et al., 2000).

[0333] 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 et al., 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 C0 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 as well as Asp-37 and Gln-40 in the loop between helix II and helix III, in addition to several other residues with SpA-D (Graille et al., 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, these residues were selected for mutagenesis.

[0334] 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 B primarily involves residues in helix I with lesser involvement of helix II (Deisenhofer 1981; Gouda et al., 1992). 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), a 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.

[0335] 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, 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 critical for the V_H3 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 VH3 family related IgM on their surface, i.e. these molecules function as VH3 type 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 2003; Goodyear and Silver-

man 2004). It is important to note that more than 40% of circulating B cells are targeted by the Protein A interaction and the VH3 family represents the largest family of human B cell receptors to impart protective humoral responses against pathogens (Goodyear and Silverman 2003; Goodyear and Silverman 2004). 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.

[0336] Non-Toxicogenic Variant of Protein A.

[0337] The inventors have developed a non-toxicogenic variant of staphylococcal Protein A and, with this reagent in hand, aimed for the first time to measure the immune response of animals to Protein A immunization. Further, the inventors address whether immunization of animals with a non-toxicogenic variant of Protein A could generate immune responses that raise protective immunity against staphylococcal infection.

[0338] To perturb the IgG Fc, vWF A1 and TNFR1 binding activities of Protein A, glutamine (Q) residues 9 and 10 [the numbering here is derived from that established for the SpA domain D] were modified generating lysine or glycine substitutions for both glutamines with the expectation that these substitutions abolish the ion bonds formed between wild-type Protein A and its ligands. The added effect of the dual lysine substitutions may be that these positively charged residues institute a repellent charge for immunoglobulins. To perturb IgM Fab VH3 binding, the inventors selected the aspartate (D) residues 36 and 37 of SpA-D, each of which is required for the association of Protein A with the B cell receptor. D36 and D37 were both substituted with alanine. The Q9,10K and D36,37A mutations were combined in the recombinant molecule SpA-D_{Q9,10K;D36,37A} and examined for the binding attributes of Protein A.

[0339] In brief, the Protein A (spa) genomic sequence of *Staphylococcus aureus* N315 was PCR amplified with the primers (GCTGCACATATGGCGCAACACGATGAAGCTCAAC [5' primer] (SEQ ID NO:35) and AGTGATCCTTATGCTTTGTTAGCATCTGC [3' primer] (SEQ ID NO:36)), cloned into the pET15b vector (pYSJ1, codons 48-486) (Stranger-Jones, et al., 2006) and recombinant plasmid transformed into *E. coli* BL21(DE3) (Studier et al., 1990). The Protein A product derived from pYSJ1 harbors SpA residues 36-265 fused to the N-terminal His tag (MGSSHHHHHSSGLVPRGS (SEQ ID NO:37)). Following IPTG inducible expression, recombinant N-terminal His₆-tagged SpA was purified by affinity chromatography on Ni-NTA resin (Stranger-Jones et al., 2006). The domain D of SpA (SpA-D) was PCR amplified with a pair of specific primers (AACATATGTTCAACAAAGATCAACAAAGC [5' primer] (SEQ ID NO:38) and AAGGATCCAGATTCGTTAAATTTTTAGC [3' primer] (SEQ ID NO:39)), sub-cloned into the pET15b vector (pHAN1, spa codons 212-261) and recombinant plasmid transformed into *E. coli* BL21(DE3) to express and purify recombinant N-terminal His₆-tagged protein. To generate mutations in the SpA-D coding sequence, sets of two pairs of primers were synthesized (for D to A substitutions: CTTCAATCAAAGTCTTAAAGCCGC-

CCCAAGCCAAAGCACTAAC [5' primer] (SEQ ID NO:40) and GTTAGTGCTTTGGCTTGGGGCGGCTTAAAGACTTTGAATGAAG [3' primer] (SEQ ID NO:41); for Q to K substitutions CATATGTTCAACAAAGATAAAAAAAGCGCCTTCTATGAAATC [5' primer] (SEQ ID NO:42) and GATTTTCATAGAAGGCGCTTTTTTATCCTTTGTTGAACATATG [3' primer] (SEQ ID NO:43); for Q to G substitutions CATATGTTCAACAAAGATGGAGGAAGCGCCTTCTATGAAATC [5' primer] (SEQ ID NO:44) and GATTTTCATAGAAGGCGCTTCCTCATCTTTGTTGAACATATG [3' primer] (SEQ ID NO:45). Primers were used for quick-change mutagenesis protocols. Following mutagenesis, DNA sequences were confirmed for each of the recombinant proteins: SpA, SpA-D and SpA-D_{Q9,10K;D36,37A} and SpA-D_{Q9,10K;D36,37A}. All proteins were purified from lysates of recombinant *E. coli* using Ni-NTA chromatography and subsequently dialyzed against PBS and stored at 4° C.

[0340] To measure binding of immunoglobulin to Protein A and its variants, 200 µg of purified protein was diluted into a 1 ml volume using column buffer (50 mM Tris-HCl, 150 mM NaCl, pH7.5) and then loaded onto a pre-equilibrated Ni-NTA column (1 ml bed volume). Columns were washed with 10 ml of column buffer. 200 µg of purified human IgG was diluted in a total volume of 1 ml column buffer and then applied to each of the columns charged with Protein A and its variants. The columns were subsequently washed with 5 ml wash buffer (10 mM imidazole in column buffer) and 5 ml column buffer. Protein samples were eluted with 2 ml elution buffer (500 mM imidazole in column buffer), fractions collected and aliquots subjected to SDS-PAGE gel electrophoresis, followed by Coomassie-Blue staining. As shown in FIG. 3, wild-type Protein A (SpA) and its SpA-domain D both retained immunoglobulin during chromatography. In contrast, the SpA-D_{Q9,10K;D36,37A} variant did not bind to immunoglobulin.

[0341] To quantify the binding of Protein A and its variants to the Fc portion of immunoglobulin and the VH3 domain of Fab, HRP conjugated human immunoglobulin G [hIgG], the Fc portion of human IgG [hFc] and the F(ab)₂ portion of human IgG [hF(ab)₂] as well as ELISA assays were used to quantify the relative amount binding to Protein A and its variants. The data in FIG. 4 demonstrate the binding of SpA and SpA-D to hIgG and hFc, whereas SpA-D_{Q9,10K;D36,37A} and SpA-D_{Q9,10K;D36,37A} displayed only background binding activities. SpA bound similar amounts of hFc and hF(ab)₂, however the binding of SpA-D to hF(ab)₂ was reduced compared to full length SpA. This result suggests that the presence of multiple IgG binding domains may cooperatively increase the ability of Protein A to bind to the B cell receptor. When compared with the reduced binding power of SpA-D for hF(ab)₂, of the two variants only SpA-D_{Q9,10K;D36,37A} displayed a significant reduction in the ability to bind the VH3 domain of immunoglobulin. To examine the toxicogenic attributes of SpA-D and its variants, purified proteins were injected into mice, which were sacrificed after 4 hours to remove their spleens. Organ tissue was homogenized, capsular material removed and B cells stained with fluorescent CD19 antibodies. Following FACS analysis to quantify the abundance of B cells in splenic tissues, it was observed that SpA-D caused a 5% drop in the B cell count compared to a mock (PBS) control (FIG. 5). In contrast, SpA-D_{Q9,10K;D36,37A} did not cause a reduction in B-cell counts, indicating that the mutant molecule had lost its toxicogenic attributes of stimu-

lating B cell proliferation and death (FIG. 5). In summary, amino acid substitutions in the SpA-D residues Q9, Q10, D36, and D37 abolished the ability of Protein A domains to bind immunoglobulins or exert toxigenic functions in human and animal tissues.

[0342] Non-Toxigenic Protein A Variants Elicit Vaccine Protection.

[0343] To test whether or not Protein A and its variants can function as vaccine antigens, SpA, SpA-D, SpA-D_{Q9,10K;D36,37A}, and SpA-D_{Q9,10K;D36,37A} were emulsified with complete or incomplete Freund's adjuvant and immunized 4 week old BALB/c mice on day 1 and day 11 with 50 µg of purified protein. Cohort of animals (n=5) were analyzed for humoral immune responses to immunization by bleeding the animals before (day 0) and after the immunization schedule (day 21). Table 5 indicates that immunized mice generated only a modest humoral immune response directed at wild-type Protein A or its SpA-D module, whereas the amount of antibody raised following immunization with SpA-D_{Q9,10K;D36,37A} or SpA-D_{Q9,10K;D36,37A} was increased four to five fold. Following intravenous challenge with 1×10⁷ CFU *S. aureus* Newman, animals were killed on day 4, their kidneys removed and either analyzed for staphylococcal load (by plating tissue

D36,37A generated significant protection from staphylococcal abscess formation, as only 0.5 (±0.4) and 0.8 (±0.5) infectious lesions per organ (P=0.02 and P=0.04) were identified. Thus, immunization with non-toxigenic Protein A variants generates increased humoral immune responses for Protein A and provides protective immunity against staphylococcal challenge. These data indicate that Protein A is an ideal candidate for a human vaccine that prevents *S. aureus* disease.

[0344] These exciting results have several implications for the design of a human vaccine. First, the generation of substitution mutations that affect the ability of the immunoglobulin binding domains of Protein A, either alone or in combination of two or more domains, can generate non-toxigenic variants suitable for vaccine development. It seems likely that a combination of mutant IgG binding domains closely resembling the structure of Protein A can generate even better humoral immune responses as is reported here for the SpA-domain D alone. Further, a likely attribute of Protein A specific antibodies may be that the interaction of antigen binding sites with the microbial surface can neutralize the ability of staphylococci to capture immunoglobulins via their Fc portion or to stimulate the B cell receptor via the VH3 binding activities.

TABLE 5

Non-toxigenic Protein A variants as vaccine antigens that prevent <i>S. aureus</i> disease									
Antigen	Bacterial load in kidney (n = number of mice)			IgG titer	Abscess formation in mice (n = number of mice)				
	^a log ₁₀ CFU g ⁻¹	Reduction	^c P value		^d Surface abscess	Reduction	^e Histopathology	Reduction	^f P value
Mock	6.46 ± 0.25 (n = 19)	—	—	<100	14/19 (70%)	—	3.7 ± 1.2 (n = 10)	—	—
SpA	3.95 ± 0.56 (n = 20)	2.51	0.0003	1706 ± 370	10/20 (50%)	32%	2.1 ± 1.2 (n = 10)	2.2	0.35
SpA-D	4.43 ± 0.41 (n = 18)	2.03	0.0001	381 ± 27	10/18 (55%)	25%	1.5 ± 0.8 (n = 10)	2.2	0.15
SpA-D1	3.39 ± 0.50 (n = 19)	3.07	<0.0001	5600 ± 801	6/20 (30%)	59%	0.5 ± 0.4 (n = 10)	3.2	0.02
SpA-D2	3.43 ± 0.46 (n = 19)	3.03	<0.0001	3980 ± 676	6/19 (32%)	57%	0.8 ± 0.5 (n = 10)	2.9	0.04

^aMeans of staphylococcal load calculated as log₁₀ CFU g⁻¹ in homogenized renal tissues 4 days following infection in cohorts of 18 to 20 BALB/c mice. Standard error of the means (±SEM) is indicated.

^cStatistical significance was calculated with the Students t-test and P-values recorded; P-values < 0.05 were deemed significant.

^bReduction in bacterial load calculated as log₁₀ CFU g⁻¹.

^dAbscess formation in kidney tissues four days following infection was measured by macroscopic inspection (% positive)

^eHistopathology of hematoxylin-eosin stained, thin sectioned kidneys from ten animals; the number of abscesses per kidney was recorded and averaged for the final mean (±SEM).

^fStatistical significance was calculated with the Students t-test and P-values recorded; P-values < 0.05 were deemed significant.

SpA-D1 and SpA-D2 represent SpA-D_{Q9,10K;D36,37A} and SpA-D_{Q9,10K;D36,37A}, respectively.

homogenate on agar plates and enumerating colony forming units, CFU) or histopathology. As expected, mock (PBS) immunized mice (n=19) harbored 6.46 log₁₀ (±0.25) CFU in kidney tissue and infectious lesions were organized into 3.7 (±1.2) abscesses per organ (n=10)(Table 5). Immunization of animals with SpA led to a 2.51 log₁₀ CFU reduction on day 5 (P=0.0003) with 2.1 (±1.2) abscesses per organ. The latter data indicate that there was no significant reduction in abscess formation (P=0.35). Immunization with SpA-D generated similar results: a 2.03 log₁₀ CFU reduction on day 5 (P=0.0001) with 1.5 (±0.8) abscesses per organ (P=0.15). In contrast, immunization with SpA-D_{Q9,10K;D36,37A} or SpA-D_{Q9,10K;D36,37A} created increased protection, with 3.07 log₁₀ and 3.03 log₁₀ CFU reduction on day 4, respectively (statistical significance P<0.0001 for both observations). Further, immunization with both SpA-D_{Q9,10K;D36,37A} and SpA-D_{Q9,10K;}

[0345] Vaccine Protection in Murine Abscess, Murine Lethal Infection, and Murine Pneumonia Models.

[0346] Three animal models have been established for the study of *S. aureus* infectious disease. These models are used here to examine the level of protective immunity provided via the generation of Protein A specific antibodies.

[0347] Murine Abscess—

[0348] BALB/c mice (24-day-old female, 8-10 mice per group, Charles River Laboratories, Wilmington, Mass.) are immunized by intramuscular injection into the hind leg with purified protein (Chang et al., 2003; Schneewind et al., 1992). Purified SpA, SpA-D or SpA-D_{Q9,10K;D36,37A} (50 µg protein) is administered on days 0 (emulsified 1:1 with complete Freund's adjuvant) and 11 (emulsified 1:1 with incomplete Freund's adjuvant). Blood samples are drawn by retroorbital

bleeding on days 0, 11, and 20. Sera are examined by ELISA for IgG titers for specific SpA-D and SpA-D_{Q9,10K;D36,37A} binding activity. Immunized animals are challenged on day 21 by retroorbital injection of 100 μ l of *S. aureus* Newman or *S. aureus* USA300 suspension (1×10^7 cfu). For this, overnight cultures of *S. aureus* Newman are diluted 1:100 into fresh tryptic soy broth and grown for 3 h at 37° C. Staphylococci are centrifuged, washed twice, and diluted in PBS to yield an A₆₀₀ of 0.4 (1×10^8 cfu per ml). Dilutions are verified experimentally by agar plating and colony formation. Mice are anesthetized by intraperitoneal injection of 80-120 mg of ketamine and 3-6 mg of xylazine per kilogram of body weight and infected by retroorbital injection. On day 5 or 15 following challenge, mice are euthanized by compressed CO₂ inhalation. Kidneys are removed and homogenized in 1% Triton X-100. Aliquots are diluted and plated on agar medium for triplicate determination of cfu. For histology, kidney tissue is incubated at room temperature in 10% formalin for 24 h. Tissues are embedded in paraffin, thin-sectioned, stained with hematoxylin/eosin, and examined by microscopy.

[0349] Murine Lethal Infection—

[0350] BALB/c mice (24-day-old female, 8-10 mice per group, Charles River Laboratories, Wilmington, Mass.) are immunized by intramuscular injection into the hind leg with purified SpA, SpA-D or SpA-D_{Q9,10K;D36,37A} (50 μ g protein). Vaccine is administered on days 0 (emulsified 1:1 with complete Freund's adjuvant) and 11 (emulsified 1:1 with incomplete Freund's adjuvant). Blood samples are drawn by retroorbital bleeding on days 0, 11, and 20. Sera are examined by ELISA for IgG titers with specific SpA-D and SpA-D_{Q9,10K;D36,37A} binding activity. Immunized animals are challenged on day 21 by retroorbital injection of 100 μ l of *S. aureus* Newman or *S. aureus* USA300 suspension (15×10^7 cfu) (34). For this, overnight cultures of *S. aureus* Newman are diluted 1:100 into fresh tryptic soy broth and grown for 3 h at 37° C. Staphylococci are centrifuged, washed twice, diluted in PBS to yield an A₆₀₀ of 0.4 (1×10^8 cfu per ml) and concentrated. Dilutions are verified experimentally by agar plating and colony formation. Mice are anesthetized by intraperitoneal injection of 80-120 mg of ketamine and 3-6 mg of xylazine per kilogram of body weight. Immunized animals are challenged on day 21 by intraperitoneal inject with 2×10^{10} cfu of *S. aureus* Newman or $3-10 \times 10^9$ cfu of clinical *S. aureus* isolates. Animals are monitored for 14 days, and lethal disease is recorded.

[0351] Murine Pneumonia Model—

[0352] *S. aureus* strains Newman or USA300 (LAC) are grown at 37° C. in tryptic soy broth/agar to OD₆₆₀ 0.5. 50-ml culture aliquots are centrifuged, washed in PBS, and suspended in 750 μ l PBS for mortality studies ($3-4 \times 10^8$ CFU per 30- μ l volume), or 1,250 μ l PBS (2×10^8 CFU per 30- μ l volume) for bacterial load and histopathology experiments (2, 3). For lung infection, 7-wk-old C57BL/6J mice (The Jackson Laboratory) are anesthetized before inoculation of 30 μ l of *S. aureus* suspension into the left nare. Animals are placed into the cage in a supine position for recovery and observed for 14 days. For active immunization, 4-wk-old mice receive 20 μ g SpA-D or SpA-D_{Q9,10K;D36,37A} in CFA on day 0 via the i.m. route, followed by a boost with 20 μ g SpA-D or SpA-D_{Q9,10K;D36,37A} in incomplete Freund's adjuvant (IFA) on day 10. Animals are challenged with *S. aureus* on day 21. Sera are collected before immunization and on day 20 to assess specific antibody production. For passive immunization studies, 7-wk-old mice receive 100 μ l of either NRS (normal

rabbit serum) or SpA-D-specific rabbit antisera via i.p. injection 24 h before challenge. To assess the pathological correlates of pneumonia, infected animals are killed via forced CO₂ inhalation before removal of both lungs. The right lung is homogenized for enumeration of lung bacterial load. The left lung is placed in 1% formalin and paraffin embedded, thin sectioned, stained with hematoxylin-eosin, and analyzed by microscopy.

[0353] Rabbit Antibodies—

[0354] Purified 200 μ g SpA-D or SpA-D_{Q9,10K;D36,37A} is used as an immunogen for the production of rabbit antisera. 200 μ g protein is emulsified with CFA for injection at day 0, followed by booster injections with 200 μ g protein emulsified with IFA on days 21 and 42. Rabbit antibody titers are determined by ELISA. Purified antibodies are obtained by affinity chromatography of rabbit serum on SpA-D or SpA-D_{Q9,10K;D36,37A} sepharose. The concentration of eluted antibodies is measured by absorbance at A₂₈₀ and specific antibody titers are determined by ELISA.

[0355] Active Immunization with SpA-Domain D Variants.—

[0356] To determine vaccine efficacy, animals are actively immunized with purified SpA-D or SpA-D_{Q9,10K;D36,37A}. As a control, animals are immunized with adjuvant alone. Antibody titers against Protein A preparations are determined using SpA-D or SpA-D_{Q9,10K;D36,37A} as antigens; note that the SpA-D_{Q9,10K;D36,37A} variant cannot bind the Fc or Fab portion of IgG. Using infectious disease models described above, any reduction in bacterial load (murine abscess and pneumonia), histopathology evidence of staphylococcal disease (murine abscess and pneumonia) and protection from lethal disease (murine lethal challenge and pneumonia) is measured.

[0357] Passive Immunization with Affinity Purified Rabbit Polyclonal Antibodies Generated Against SpA-Domain D Variants.

[0358] To determine protective immunity of Protein A specific rabbit antibodies, mice are passively immunized with 5 mg/kg of purified SpA-D or SpA-D_{Q9,10K;D36,37A} derived rabbit antibodies. Both of these antibody preparations are purified by affinity chromatography using immobilized SpA-D or SpA-D_{Q9,10K;D36,37A}. As a control, animals are passively immunized with rV10 antibodies (a plague protective antigen that has no impact on the outcome of staphylococcal infections). Antibody titers against all Protein A preparations are determined using SpA-D_{Q9,10K;D36,37A} as an antigen, as this variant cannot bind the Fc or Fab portion of IgG. Using the infectious disease models described above, the reduction in bacterial load (murine abscess and pneumonia), histopathology evidence of staphylococcal disease (murine abscess and pneumonia), and the protection from lethal disease (murine lethal challenge and pneumonia) is measured.

Example 2

Non-Toxicogenic Protein A Vaccine for
Methicillin-Resistant *Staphylococcus aureus*
Infection

[0359] Clinical isolates of *S. aureus* express protein A (Shopsin et al., 1999, whose primary translational product is comprised of an N-terminal signal peptide (DeDent et al., 2008), five IgBDs (designated E, D, A, B and C)(Sjodahl, 1977), region X with variable repeats of an eight residue peptide (Guss et al., 1984), and C-terminal sorting signal for

the cell wall anchoring of SpA (Schneewind et al., 1992; Schneewind et al., 1995) (FIG. 6). Guided by amino acid homology (Uhlen et al., 1984), the triple α -helical bundle structure of IgBDs (Deisenhofer et al., 1978; Deisenhofer et al., 1981) and their atomic interactions with Fab V_{H3} (Graille et al., 2000) or Fc γ (Gouda et al., 1998), glutamine 9 and 10 were selected as well as aspartate 36 and 37 as critical for the association of SpA with antibodies or B cell receptor, respectively. Substitutions Gln9Lys, Gln10Lys, Asp36Ala and Asp37Ala were introduced into the D domain to generate SpA-D_{KKAA} (FIG. 6). The ability of isolated SpA-D or SpA-D_{KKAA} to bind human IgG was analyzed by affinity chromatography (FIG. 6). Polyhistidine tagged SpA-D as well as full-length SpA retained human IgG on Ni-NTA, whereas SpA-D_{KKAA} and a negative control (SrtA) did not (FIG. 6). A similar result was observed with von Willebrand factor (Hartleib et al., 2000), which, along with tumor necrosis factor receptor 1 (TNFR1) (Gomez et al., 2004), can also bind protein A via glutamine 9 and 10 (FIG. 6). Human immunoglobulin encompasses 60-70% V_{H3} -type IgG. The inventors distinguish between Fc domain and B cell receptor activation of Igs and measured association of human Fc γ and F(ab)₂ fragments, both of which bound to full-length SpA or SpA-D, but not to SpA-D_{KKAA} (FIG. 6). Injection of SpA-D into the peritoneal cavity of mice resulted in B cell expansion followed by apoptotic collapse of CD19+ lymphocytes in spleen tissue of BALB/c mice (Goodyear and Silverman, 2003)(FIG. 6). B cell superantigen activity was not observed following injection with SpA-D_{KKAA}, and TUNEL-staining of splenic tissue failed to detect the increase in apoptotic cells that follows injection of SpA or SpA-D (FIG. 6).

[0360] Naive six week old BALB/c mice were injected with 50 μ g each of purified SpA, SpA-D or SpA-D_{KKAA} emulsified in CFA and boosted with the same antigen emulsified in IFA. In agreement with the hypothesis that SpA-D promotes the apoptotic collapse of activated clonal B cell populations, the inventors observed a ten-fold higher titer of SpA-D_{KKAA} specific antibodies following immunization of mice with the non-toxicogenic variant as compared to the B cell superantigen (SpA-D vs. SpA-D_{KKAA} $P < 0.0001$, Table 6). Antibody titers raised by immunization with full-length SpA were higher than those elicited by SpA-D ($P = 0.0022$), which is likely due to the larger size and reiterative domain structure of this antigen (Table 6). Nevertheless, even SpA elicited lower antibody titers than SpA-D_{KKAA} ($P = 0.0003$), which encompasses only 50 amino acids of protein A (520 residues, SEQ ID NO:33). Immunized mice were challenged by intravenous inoculation with *S. aureus* Newman and the ability of staphylococci to seed abscesses in renal tissues was examined by necropsy four days after challenge. In homogenized renal tissue of mock (PBS/adjuvant) immunized mice, an average staphylococcal load of 6.46 \log_{10} CFU g^{-1} was enumerated (Table 6). Immunization of mice with SpA or SpA-D led to a reduction in staphylococcal load, however SpA-D_{KKAA} vaccinated animals displayed an even greater, 3.07 \log_{10} CFU g^{-1} reduction of *S. aureus* Newman in renal tissues ($P < 0.0001$, Table 6). Abscess formation in kidneys was analyzed by histopathology (FIG. 7). Mock immunized animals harbored an average of 3.7 (± 1.2) abscesses per kidney (Table 6). Vaccination with SpA-D_{KKAA} reduced the average number of abscesses to 0.5 (± 0.4) ($P = 0.0204$), whereas immunization with SpA or SpA-D did not cause a significant reduction in the number of abscess lesions (Table 6). Lesions from SpA-D_{KKAA} vaccinated animals were smaller in size, with fewer

infiltrating PMNs and characteristically lacked staphylococcal abscess communities (Cheng et al., 2009) (FIG. 7). Abscesses in animals that had been immunized with SpA or SpA-D displayed the same overall structure of lesions in mock immunized animals (FIG. 7).

[0361] The inventors examined whether SpA-D_{KKAA} immunization can protect mice against MRSA strains and selected the USA300 LAC isolate for animal challenge (Diep et al., 2006). This highly virulent CA-MRSA strain spread rapidly throughout the United States, causing significant human morbidity and mortality (Kennedy et al., 2008). Compared to adjuvant control mice, SpA-D_{KKAA} immunized animals harbored a 1.07 \log_{10} CFU g^{-1} reduction in bacterial load of infected kidney tissues. Histopathology examination of renal tissue following *S. aureus* USA300 challenge revealed that the average number of abscesses was reduced from 4.04 (± 0.8) to 1.6 (± 0.6) ($P = 0.02774$). In contrast, SpA or SpA-D immunization did not cause a significant reduction in bacterial load or abscess formation (Table 6).

[0362] Rabbits were immunized with SpA-D_{KKAA} and specific antibodies were purified on SpA-D_{KKAA} affinity column followed by SDS-PAGE (FIG. 8). SpA-D_{KKAA} specific IgG was cleaved with pepsin to generate Fc γ and F(ab)₂ fragments, the latter of which were purified by chromatography on SpA-D_{KKAA} column (FIG. 8). Binding of human IgG or vWF to SpA or SpA-D was perturbed by SpA-D_{KKAA} specific F(ab)₂, indicating that SpA-D_{KKAA} derived antibodies neutralize the B cell superantigen function of protein A as well as its interactions with Ig (FIG. 8).

[0363] To further improve the vaccine properties for non-toxicogenic protein A, the inventors generated SpA_{KKAA} which includes all five IgBDs with four amino acid substitutions—substitutions corresponding to Gln9Lys, Gln10Lys, Asp36Ala and Asp37Ala of domain D—in each of its five domains (E, D, A, B and C). Polyhistidine tagged SpA_{KKAA} was purified by affinity chromatography and analyzed by Coomassie Blue-stained SDS-PAGE (FIG. 9). Unlike full-length SpA, SpA_{KKAA} did not bind human IgG, Fc and F(ab)₂ or vWF (FIG. 9). SpA_{KKAA} failed to display B cell superantigen activity, as injection of the variant into BALB/c mice did not cause a depletion of CD19+ B cells in splenic tissue (FIG. 9). SpA_{KKAA} vaccination generated higher specific antibody titers than SpA-D_{KKAA} immunization and provided mice with elevated protection against *S. aureus* USA300 challenge (Table 6). Four days following challenge, SpA_{KKAA} vaccinated animals harbored 3.54 \log_{10} CFU g^{-1} fewer staphylococci in renal tissues ($P = 0.0001$) and also caused a greater reduction in the number of abscess lesions ($P = 0.0109$) (Table 6).

[0364] SpA_{KKAA} was used to immunize rabbits. Rabbit antibodies specific for SpA-D_{KKAA} or SpA_{KKAA} were affinity purified on matrices with immobilized cognate antigen and injected at a concentration of 5 mg kg^{-1} body weight into the peritoneal cavity of BALB/c mice (Table 7). Twenty-four hours later, specific antibody titers were determined in serum and animals challenged by intravenous inoculation with *S. aureus* Newman. Passive transfer reduced the staphylococcal load in kidney tissues for SpA-D_{KKAA} ($P = 0.0016$) or SpA_{KKAA} ($P = 0.0005$) specific antibodies. On histopathology examination, both antibodies reduced the abundance of abscess lesions in the kidneys of mice challenged with *S. aureus* Newman (Table 7). Together these data reveal that vaccine protection following immunization with SpA-D_{KKAA} or SpA_{KKAA} is conferred by antibodies that neutralize protein A.

TABLE 6

Immunization of mice with protein A vaccines.						
Staphylococcal load and abscess formation in renal tissue						
Antigen	^a log ₁₀ CFU g ⁻¹	^b P-value	^c Reduction (log ₁₀ CFU g ⁻¹)	^d IgG Titer	^e Number of abscesses	^b P-value
<i>S. aureus</i> Newman challenge						
Mock	6.46 ± 0.25	—	—	<100	3.7 ± 1.2	—
SpA	3.95 ± 0.56	0.0003	2.51	1706 ± 370	2.1 ± 1.2	0.3581
SpA-D	4.43 ± 0.41	0.0001	2.03	381 ± 27	1.5 ± 0.8	0.1480
SpA D _{KKAA}	3.39 ± 0.50	<0.0001	3.07	5600 ± 801	0.5 ± 0.4	0.0204
<i>S. aureus</i> USA300 (LAC) challenge						
Mock	7.20 ± 0.24	—	—	<100	4.0 ± 0.8	—
SpA	6.81 ± 0.26	0.2819	0.39	476 ± 60	3.3 ± 1.0	0.5969
SpA-D	6.34 ± 0.52	0.1249	0.85	358 ± 19	2.2 ± 0.6	0.0912
SpA-D _{KKAA}	6.00 ± 0.42	0.0189	1.20	3710 ± 1147	1.6 ± 0.6	0.0277
SpA _{KKAA}	3.66 ± 0.76	0.0001	3.54	10200 ± 2476	1.2 ± 0.5	0.0109

^aMeans of staphylococcal load calculated as log₁₀ CFU g⁻¹ in homogenized renal tissues 4 days following infection in cohorts of fifteen to twenty BALB/c mice per immunization. Representative of two independent and reproducible animal experiments is shown. Standard error of the means (±SEM) is indicated.

^bStatistical significance was calculated with the unpaired two-tailed Students t-test and P-values recorded; P-values < 0.05 were deemed significant.

^cReduction in bacterial load calculated as log₁₀ CFU g⁻¹.

^dMeans of five randomly chosen serum IgG titers were measured prior to staphylococcal infection by ELISA

^eHistopathology of hematoxyline-eosin stained, thin sectioned kidneys from ten animals; the average number of abscesses per kidney was recorded and averaged again for the final mean (±SEM).

TABLE 7

Passive immunization of mice with antibodies against protein A.						
Staphylococcal load and abscess formation in renal tissue						
^a Antibody	^b log ₁₀ CFU g ⁻¹	^c P-value	^d Reduction (log ₁₀ CFU g ⁻¹)	^e IgG Titer	^f Number of abscesses	^b P-value
Mock	7.10 ± 0.14	—	—	<100	4.5 ± 0.8	—
α-SpA-D _{KKAA}	5.53 ± 0.43	0.0016	1.57	466 ± 114	1.9 ± 0.7	0.0235
α-SpA _{KKAA}	5.69 ± 0.34	0.0005	1.41	1575 ± 152	1.6 ± 0.5	0.0062

^aAffinity purified antibodies were injected into the peritoneal cavity of BALB/c mice at a concentration of 5 mg · kg⁻¹ twenty-four hours prior to intravenous challenge with 1 × 10⁷ CFU *S. aureus* Newman.

^bMeans of staphylococcal load calculated as log₁₀ CFU g⁻¹ in homogenized renal tissues 4 days following infection in cohorts of fifteen BALB/c mice per immunization. Representative of two independent and reproducible animal experiments is shown. Standard error of the means (±SEM) is indicated.

^cStatistical significance was calculated with the unpaired two-tailed Students t-test and P-values recorded; P-values < 0.05 were deemed significant.

^dReduction in bacterial load calculated as log₁₀ CFU g⁻¹.

^eMeans of five randomly chosen serum IgG titers were measured prior to staphylococcal infection by ELISA

^fHistopathology of hematoxyline-eosin stained, thin sectioned kidneys from ten animals; the average number of abscesses per kidney was recorded and averaged again for the final mean (±SEM).

[0365] Following infection with virulent *S. aureus*, mice do not develop protective immunity against subsequent infection with the same strain (Burts et al., 2008)(FIG. 10). The average abundance of SpA-D_{KKAA} specific IgG in these animals was determined by dot blot as 0.20 μg ml⁻¹ (±0.04) and 0.14 μg ml⁻¹ (±0.01) for strains Newman and USA300 LAC, respectively (FIG. 9). The minimal concentration of protein A-specific IgG required for disease protection in SpA_{KKAA} or SpA-D_{KKAA} vaccinated animals (P 0.05 log₁₀ reduction in staphylococcal CFU g⁻¹ renal tissue) was calculated as 4.05 μg ml⁻¹ (±0.88). Average serum concentration of SpA-specific IgG in adult healthy human volunteers (n=16) was 0.21 μg ml⁻¹ (±0.02). Thus, *S. aureus* infections in mice or humans are not associated with immune responses that raise significant levels of neutralizing antibodies directed against protein A, which is likely due to the B cell superantigen attributes of this molecule. In contrast, the average serum concentration of IgG specific for diphtheria toxin in human volunteers, 0.068 μg ml⁻¹ (±0.20), was within range for protective immunity against diphtheria (Behring, 1890; Lagergard et al., 1992).

[0366] Clinical *S. aureus* isolates express protein A, an essential virulence factor whose B cell superantigen activity and evasive attributes towards opsono-phagocytic clearance are absolutely required for staphylococcal abscess formation (Palmqvist et al., 2005; Cheng et al., 2009; Silverman and Goodyear, 2006). Protein A can thus be thought of as a toxin, essential for pathogenesis, whose molecular attributes must be neutralized in order to achieve protective immunity. By generating non-toxic variants unable to bind Igs via Fcγ or VH₃-Fab domains, the inventors measure here for the first time protein A neutralizing immune responses as a correlate for protective immunity against *S. aureus* infection. In contrast to many methicillin-sensitive strains, CA-MRSA isolate USA300 LAC is significantly more virulent (Cheng et al., 2009). For example, immunization of experimental animals with the surface protein IsdB (Kuklin et al., 2006; Stranger-Jones et al., 2006) raises antibodies that confer protection against *S. aureus* Newman (Stranger-Jones et al., 2009) but not against USA300 challenge.

[0367] The methods utilized include:

[0368] Bacterial Strains and Growth.

[0369] *Staphylococcus aureus* strains Newman and USA300 were grown in tryptic soy broth (TSB) at 37° C. *Escherichia coli* strains DH5 α and BL21 (DE3) were grown in Luria-Bertani (LB) broth with 100 $\mu\text{g ml}^{-1}$ ampicillin at 37° C.

[0370] Rabbit Antibodies.

[0371] The coding sequence for SpA was PCR-amplified with two primers, gctgcacatatggcgcaacacgatgaagctcaac (SEQ ID NO:35) and agtggatccttatgcttgagcttggtagcatctgc (SEQ ID NO:36) using *S. aureus* Newman template DNA. SpA-D was PCR-amplified with two primers, aacatattgcaacaagatcaacaagc (SEQ ID NO:38) and aaggatccagattcgtttaatttttagc (SEQ ID NO:39). The sequence for SpA-D_{KKAA} was mutagenized with two sets of primers catatgttcaacaaagataaaaaagcgctctatgaaatc (SEQ ID NO:42) and gatttcata-gaagcgctttttttatcttggtaacatg (SEQ ID NO:43) for Q9K, Q10K as well as cttcattcaaaagtctaaagccgc-ccaaagcacaagcactaac (SEQ ID NO:40) and gttagtcttggct-tggcgctttaaagacttgaatgaag (SEQ ID NO:41) for D36A, D37A. The sequence of SpA_{KKAA} was synthesized by Integrated DNA Technologies, Inc. PCR products were cloned into pET-15b generating N-terminal His₆ tagged recombinant protein. Plasmids were transformed into BL21 (DE3). Overnight cultures of transformants were diluted 1:100 into fresh media and grown at 37° C. to an OD₆₀₀ 0.5, at which point cultures were induced with 1 mM isopropyl β -D-1-thiogalactopyranoside (IPTG) and grown for an additional three hours. Bacterial cells were sedimented by centrifugation, suspended in column buffer (50 mM Tris-HCl, pH 7.5, 150 mM NaCl) and disrupted with a French pressure cell at 14,000 psi. Lysates were cleared of membrane and insoluble components by ultracentrifugation at 40,000 \times g. Proteins in the soluble lysate were subjected to nickel-nitrilotriacetic acid (Ni-NTA, Qiagen) affinity chromatography. Proteins were eluted in column buffer containing successively higher concentrations of imidazole (100-500 mM). Protein concentrations were determined by bicinchonic acid (BCA) assay (Thermo Scientific). For antibody generation, rabbits (6 month old New-Zealand white, female, Charles River Laboratories) were immunized with 500 μg protein emulsified in Complete Freund's Adjuvant (Difco) by subscapular injection. For booster immunizations, proteins emulsified in Incomplete Freund's Adjuvant and injected 24 or 48 days following the initial immunization. On day 60, rabbits were bled and serum recovered.

[0372] Purified antigen (5 mg protein) was covalently linked to HiTrap NETS-activated HP columns (GE Healthcare). Antigen-matrix was used for affinity chromatography of 10-20 ml of rabbit serum at 4° C. Charged matrix was washed with 50 column volumes of PBS, antibodies eluted with elution buffer (1 M glycine, pH 2.5, 0.5 M NaCl) and immediately neutralized with 1M Tris-HCl, pH 8.5. Purified antibodies were dialyzed overnight against PBS at 4° C.

[0373] F(Ab)₂ Fragments.

[0374] Affinity purified antibodies were mixed with 3 mg of pepsin at 37° C. for 30 minutes. The reaction was quenched with 1 M Tris-HCl, pH 8.5 and F(ab)₂ fragments were affinity purified with specific antigen-conjugated HiTrap NETS-activated HP columns. Purified antibodies were dialyzed overnight against PBS at 4° C., loaded onto SDS-PAGE gel and visualized with Coomassie Blue staining.

[0375] Active and Passive Immunization.

[0376] BALB/c mice (3 week old, female, Charles River Laboratories) were immunized with 50 μg protein emulsified in Complete Freund's Adjuvant (Difco) by intramuscular injection. For booster immunizations, proteins were emulsified in Incomplete Freund's Adjuvant and injected 11 days following the initial immunization. On day 20 following immunization, 5 mice were bled to obtain sera for specific antibody titers by enzyme-linked immunosorbent assay (ELISA).

[0377] Affinity purified antibodies in PBS were injected at a concentration 5 mg kg⁻¹ of experimental animal weight into the peritoneal cavity of BALB/c mice (6 week old, female, Charles River Laboratories) 24 hours prior to challenge with *S. aureus*. Animal blood was collected via periorbital vein puncture. Blood cells were removed with heparinized micro-hematocrit capillary tubes (Fisher) and Z-gel serum separation micro tubes (Sarstedt) were used to collect and measure antigen specific antibody titers by ELISA.

[0378] Mouse Renal Abscess.

[0379] Overnight cultures of *S. aureus* Newman or USA300 (LAC) were diluted 1:100 into fresh TSB and grown for 2 hours at 37° C. Staphylococci were sedimented, washed and suspended PBS at OD₆₀₀ of 0.4 ($\sim 1 \times 10^8$ CFU ml⁻¹). Inocula were quantified by spreading sample aliquots on TSA and enumerating colonies formed. BALB/c mice (6 week old, female, Charles River Laboratories) were anesthetized via intraperitoneal injection with 100 mg ml⁻¹ ketamine and 20 mg ml⁻¹ xylazine per kilogram of body weight. Mice were infected by retro-orbital injection with 1×10^7 CFU of *S. aureus* Newman or 5×10^6 CFU of *S. aureus* USA300. On day 4 following challenge, mice were killed by CO₂ inhalation. Both kidneys were removed, and the staphylococcal load in one organ was analyzed by homogenizing renal tissue with PBS, 1% Triton X-100. Serial dilutions of homogenate were spread on TSA and incubated for colony formation. The remaining organ was examined by histopathology. Briefly, kidneys were fixed in 10% formalin for 24 hours at room temperature. Tissues were embedded in paraffin, thin-sectioned, stained with hematoxylin-eosin, and inspected by light microscopy to enumerate abscess lesions. All mouse experiments were performed in accordance with the institutional guidelines following experimental protocol review and approval by the Institutional Biosafety Committee (IBC) and the Institutional Animal Care and Use Committee (IACUC) at the University of Chicago.

[0380] Protein A Binding.

[0381] For human IgG binding, Ni-NTA affinity columns were pre-charged with 200 μg of purified proteins (SpA, SpA-D, SpA-D_{KKAA}, and SrtA) in column buffer. After washing, 200 μg of human IgG (Sigma) was loaded onto the column. Protein samples were collected from washes and elutions and subjected to SDS-PAGE gel electrophoresis, followed by Coomassie Blue staining. Purified proteins (SpA, SpA_{KKAA}, SpA-D and SpA-D_{KKAA}) were coated onto MaxiSorp ELISA plates (NUNC) in 0.1M carbonate buffer (pH 9.5) at 1 $\mu\text{g ml}^{-1}$ concentration overnight at 4° C. Plates were next blocked with 5% whole milk followed by incubation with serial dilutions of peroxidase-conjugated human IgG, Fc or F(ab)₂ fragments for one hour. Plates were washed and developed using OptEIA ELISA reagents (BD). Reactions were quenched with 1 M phosphoric acid and A₄₅₀ readings were used to calculate half maximal titer and percent binding.

[0382] von Willebrand Factor (vWF) Binding Assays.
[0383] Purified proteins (SpA, SpA_{KKAA}, SpA D and SpA-D_{KKAA}) were coated and blocked as described above. Plates were incubated with human vWF at 1 $\mu\text{g ml}^{-1}$ concentration for two hours, then washed and blocked with human IgG for another hour. After washing, plates were incubated with serial dilution of peroxidase-conjugated antibody directed against human vWF for one hour. Plates were washed and developed using OptEIA ELISA reagents (BD). Reactions were quenched with 1 M phosphoric acid and A₄₅₀ readings were used to calculate half maximal titer and percent binding. For inhibition assays, plates were incubated with affinity purified F(ab)₂ fragments specific for SpA-D_{KKAA} at 10 $\mu\text{g ml}^{-1}$ concentration for one hour prior to ligand binding assays.

[0384] Splenocyte Apoptosis.

[0385] Affinity purified proteins (150 μg of SpA, SpA-D, SpA_{KKAA}, and SpA-D_{KKAA}) were injected into the peritoneal cavity of BALB/c mice (6 week old, female, Charles River Laboratories). Four hours following injection, animals were killed by CO₂ inhalation. Their spleens were removed and homogenized. Cell debris were removed using cell strainer and suspended cells were transferred to ACK lysis buffer (0.15 M NH₄Cl, 10 mM KHCO₃, 0.1 mM EDTA) to lyse red blood cells. White blood cells were sedimented by centrifugation, suspended in PBS and stained with 1:250 diluted R-PE conjugated anti-CD19 monoclonal antibody (Invitrogen) on ice and in the dark for one hour. Cells were washed with 1% FBS and fixed with 4% formalin overnight at 4° C. The following day, cells were diluted in PBS and analyzed by flow cytometry. The remaining organ was examined for histopathology. Briefly, spleens were fixed in 10% formalin for 24 hours at room temperature. Tissues were embedded in paraffin, thin-sectioned, stained with the Apoptosis detection kit (Millipore), and inspected by light microscopy.

[0386] Antibody Quantification.

[0387] Sera were collected from healthy human volunteers or BALB/c mice that had been either infected with *S. aureus* Newman or USA300 for 30 days or that had been immunized with SpA-D_{KKAA}/SpA_{KKAA} as described above. Human/mouse IgG (Jackson Immunology Laboratory), SpA_{KKAA}, and CRM₁₉₇ were blotted onto nitrocellulose membrane. Membranes were blocked with 5% whole milk, followed by incubation with either human or mouse sera. IRDye 700DX conjugated affinity purified anti-human/mouse IgG (Rockland) was used to quantify signal intensities using the Odyssey™ infrared imaging system (Li-cor). Experiments with blood from human volunteers involved protocols that were reviewed, approved and performed under regulatory supervision of The University of Chicago's Institutional Review Board (IRB).

[0388] Statistical Analysis.

[0389] Two tailed Student's t tests were performed to analyze the statistical significance of renal abscess, ELISA, and B cell superantigen data.

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[0390] The following references, to the extent that they provide exemplary procedural or other details supplementary to those set forth herein, are specifically incorporated herein by reference.

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

<400> SEQUENCE: 2

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

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

Lys Lys Leu Asn Glu Ser
 50

<210> SEQ ID NO 3
 <211> LENGTH: 51
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 3

Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr Gln Val Leu Asn Met
 1 5 10 15

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
 50

<210> SEQ ID NO 4
 <211> LENGTH: 52
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 4

Asn Asn Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu Asn
 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
 50

<210> SEQ ID NO 5
 <211> LENGTH: 52
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 5

Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His
 1 5 10 15

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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
50

<210> SEQ ID NO 6
<211> LENGTH: 52
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 6

Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His
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
50

<210> SEQ ID NO 7
<211> LENGTH: 52
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp.
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (7)..(8)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (34)..(35)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 7

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
50

<210> SEQ ID NO 8
<211> LENGTH: 52
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp.
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (7)..(8)
<223> OTHER INFORMATION: where X is any amino acid other than Q
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (12)..(35)
<223> OTHER INFORMATION: where Y is any amion acid other than D

<400> SEQUENCE: 8

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

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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
      50

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<210> SEQ ID NO 9
<211> LENGTH: 450
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp.

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<400> SEQUENCE: 9

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Val Ser Lys Glu Ile Leu
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     320

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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
 385 390 395 400

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

<210> SEQ ID NO 10
 <211> LENGTH: 450
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 10

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

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

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

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

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

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

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

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

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

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

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

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

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

Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe

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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
	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	310 315 320
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	390 395 400
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		

<210> SEQ ID NO 11

<211> LENGTH: 97

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 11

Met Ala Met Ile Lys Met Ser Pro Glu Glu Ile Arg Ala Lys Ser Gln	1	5	10	15
Ser Tyr Gly Gln Gly Ser Asp Gln Ile Arg Gln Ile Leu Ser Asp Leu	20	25	30	
Thr Arg Ala Gln Gly Glu Ile Ala Ala Asn Trp Glu Gly Gln Ala Phe	35	40	45	
Ser Arg Phe Glu Glu Gln Phe Gln Gln Leu Ser Pro Lys Val Glu Lys	50	55	60	
Phe Ala Gln Leu Leu Glu Glu Ile Lys Gln Gln Leu Asn Ser Thr Ala	65	70	75	80
Asp Ala Val Gln Glu Gln Asp Gln Gln Leu Ser Asn Asn Phe Gly Leu	85	90	95	

Gln

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<210> SEQ ID NO 12
 <211> LENGTH: 102
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp.
 <400> SEQUENCE: 12
 Met Gly Gly Tyr Lys Gly Ile Lys Ala Asp Gly Gly Lys Val Asn Gln
 1 5 10 15
 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

<210> SEQ ID NO 13
 <211> LENGTH: 1385
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus sp.
 <400> SEQUENCE: 13
 Met Leu Asn Arg Glu Asn Lys Thr Ala Ile Thr Arg Lys Gly Met Val
 1 5 10 15
 Ser Asn Arg Leu Asn Lys Phe Ser Ile Arg Lys Tyr Thr Val Gly Thr
 20 25 30
 Ala Ser Ile Leu Val Gly Thr Thr Leu Ile Phe Gly Leu Gly Asn Gln
 35 40 45
 Glu Ala Lys Ala Ala Glu Ser Thr Asn Lys Glu Leu Asn Glu Ala Thr
 50 55 60
 Thr Ser Ala Ser Asp Asn Gln Ser Ser Asp Lys Val Asp Met Gln Gln
 65 70 75 80
 Leu Asn Gln Glu Asp Asn Thr Lys Asn Asp Asn Gln Lys Glu Met Val
 85 90 95
 Ser Ser Gln Gly Asn Glu Thr Thr Ser Asn Gly Asn Lys 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
 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

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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 Asn Lys	Ser Val Ser	Thr Gly Asn	Ala Leu Gly	Phe Thr Asn	Asn			
545		550	555		560			
Gln Ser Gly	Gly Ala Gly	Gln Glu Val	Tyr Lys Ile	Gly Asn Tyr	Val			
	565		570		575			
Trp Glu Asp	Thr Asn Lys	Asn Gly Val	Gln Glu Leu	Gly Glu Lys	Gly			
	580		585		590			
Val Gly Asn	Val Thr Val	Thr Val Phe	Asp Asn Asn	Thr Asn Thr	Lys			
	595		600		605			
Val Gly Glu	Ala Val Thr	Lys Glu Asp	Gly Ser Tyr	Leu Ile Pro	Asn			
	610		615		620			

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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
 740 745 750
 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

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

<400> SEQUENCE: 14

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

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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

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

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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	Ser	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		

<210> SEQ ID NO 15

<211> LENGTH: 350

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp.

-continued

<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
 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

-continued

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 Ala Glu Glu Thr Gly Gly Thr
 35 40 45
 Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
 50 55 60
 Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
 65 70 75 80
 Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
 85 90 95
 Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Ala Val Lys
 100 105 110
 Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
 115 120 125
 Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
 130 135 140
 Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Glu Asn Gly
 145 150 155 160
 Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val
 165 170 175
 Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
 180 185 190
 Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
 195 200 205
 Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
 210 215 220
 Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr
 225 230 235 240
 His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
 245 250 255
 Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
 260 265 270
 Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
 275 280 285
 Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu
 290 295 300
 Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
 305 310 315 320
 Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
 325 330 335
 Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
 340 345 350
 Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
 355 360 365
 His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
 370 375 380
 Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
 385 390 395 400

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Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
      405
      410
      415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
      420
      425
      430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
      435
      440
      445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
      450
      455
      460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
      465
      470
      475
      480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
      485
      490
      495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
      500
      505
      510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
      515
      520
      525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
      530
      535
      540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
      545
      550
      555
      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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-continued

<400> SEQUENCE: 18

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
 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

-continued

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 Ile Tyr Tyr	Glu His Pro Asn Val Ala Ser Ile Lys Phe Gly Asp		
	465	470	475
Ile Thr Lys Thr	Tyr Val Val Leu Val Glu Gly His Tyr Asp Asn Thr		
	485	490	495
Gly Lys Asn Leu	Lys Thr Gln Val Ile Gln Glu Asn Val Asp Pro Val		
	500	505	510
Thr Asn Arg Asp	Tyr Ser Ile Phe Gly Trp Asn Asn Glu Asn Val Val		
	515	520	525
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
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 Asp Ser		
	610	615	620
Asp Ser Asp Ser	Glu Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser		
	625	630	635
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 Asp Ser Asp Ser Asp Ser Asp 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 Asp Ser Asp Ser Asp Ser Asp Ser		
	705	710	715
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

-continued

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
 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

-continued

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
 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
 210 215 220
 Ser Gly His Val Val Leu Asn Lys Phe Leu Ser Asn Glu Glu Asn Gln
 225 230 235 240
 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
 290 295 300
 Glu Val Asn Lys Thr Lys Glu Arg Ile Lys Ser Gln Arg Asn Ile Ile
 305 310 315 320
 Leu Glu Glu Leu Ala Arg Thr Asp Asp Lys Lys Tyr Ala Thr Gln Ser
 325 330 335
 Ile Leu Glu Ser Ile Phe Asn Lys Asp Glu Ala 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
 370 375 380
 Thr Ser Leu Ile Asp Gln Ser Gln Asp Lys Ser Leu Leu Ile Ser Gln
 385 390 395 400

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Ile Leu Gln Thr Lys Leu Gly Lys Ala Glu Ala Asp Lys Leu Ala Lys
      405
Asp Trp Thr Asn Lys Gly Leu Ser Asn Arg Gln Ile Val Asp Gln Leu
      420
Lys Lys His Phe Ala Ser Thr Gly Asp Thr Ser Ser Asp Asp Ile Leu
      435
Lys Ala Ile Leu Asn Asn Ala Lys Asp Lys Lys Gln Ala Ile Glu Thr
      450
Ile Leu Ala Thr Arg Ile Glu Arg Gln Lys Ala Lys Leu Leu Ala Asp
      465
Leu Ile Thr Lys Ile Glu Thr Asp Gln Asn Lys Ile Phe Asn Leu Val
      485
Lys Ser Ala Leu Asn Gly Lys Ala Asp Asp Leu Leu Asn Leu Gln Lys
      500
Arg Leu Asn Gln Thr Lys Lys Asp Ile Asp Tyr Ile Leu Ser Pro Ile
      515
Val Asn Arg Pro Ser Leu Leu Asp Arg Leu Asn Lys Asn Gly Lys Thr
      530
Thr Asp Leu Asn Lys Leu Ala Asn Leu Met Asn Gln Gly Ser Asn Leu
      545
Leu Asp Ser Ile Pro Asp Ile Pro Thr Pro Lys Pro Glu Lys Thr Leu
      565
Thr Leu Gly Lys Gly Asn Gly Leu Leu Ser Gly Leu Leu Asn Ala Asp
      580
Gly Asn Val Ser Leu Pro Lys Ala Gly Glu Thr Ile Lys Glu His Trp
      595
Leu Pro Ile Ser Val Ile Val Gly Ala Met Gly Val Leu Met Ile Trp
      610
Leu Ser Arg Arg Asn Lys Leu Lys Asn Lys Ala
      625

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<210> SEQ ID NO 21

<211> LENGTH: 953

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 21

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Met Asn Asn Lys Lys Thr Ala Thr Asn Arg Lys Gly Met Ile Pro Asn
1      5      10
Arg Leu Asn Lys Phe Ser Ile Arg Lys Tyr Ser Val Gly Thr Ala Ser
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

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-continued

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
 325 330 335
 Asn Gln Lys Gly Gln Gln Leu Ile Ser Ser Thr Asn Tyr Ile Asn Asn
 340 345 350
 Glu Asp Leu Ser Arg Asn Met Thr Val Tyr Val Asn Gln Pro Lys Lys
 355 360 365
 Thr Tyr Thr Lys Glu Thr Phe Val Thr Asn Leu Thr Gly Tyr Lys Phe
 370 375 380
 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

-continued

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			
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	Asn	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	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

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          930          935          940
Phe Gly Arg Arg Lys Lys Gln Asn Lys
945          950

<210> SEQ ID NO 22
<211> LENGTH: 989
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 22

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
          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

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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

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

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740				745				750					
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
	770				775				780				
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
			805				810						815
Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Glu
			820				825						830
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp
			835				840						845
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Glu	Ser	Asp	Ser	Asp	Ser	Asp
			850				855						860
Ser	Asp	Ser	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp
			865				870						875
Ser	Ala	Ser	Asp	Ser	Asp	Ser	Gly	Ser	Asp	Ser	Ser	Ser	Asp
			885				890						895
Ser	Asp	Ser	Asp	Ser	Thr	Ser	Asp	Thr	Gly	Ser	Asp	Asn	Asp
			900				905						910
Ser	Asp	Ser	Asn	Ser	Asp	Ser	Glu	Ser	Gly	Ser	Asn	Asn	Val
			915				920						925
Pro	Pro	Asn	Ser	Pro	Lys	Asn	Gly	Thr	Asn	Ala	Ser	Asn	Lys
			930				935						940
Ala	Lys	Asp	Ser	Lys	Glu	Pro	Leu	Pro	Asp	Thr	Gly	Ser	Glu
			945				950						955
Ala	Asn	Thr	Ser	Leu	Ile	Trp	Gly	Leu	Leu	Ala	Ser	Leu	Gly
			965				970						975
Leu	Leu	Phe	Arg	Arg	Lys	Lys	Glu	Asn	Lys	Asp	Lys	Lys	
			980				985						

<210> SEQ ID NO 23

<211> LENGTH: 584

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 23

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	

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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
 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

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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.

<400> SEQUENCE: 24

Met	Asn	Tyr	Arg	Asp	Lys	Ile	Gln	Lys	Phe	Ser	Ile	Arg	Lys	Tyr	Thr
1			5						10					15	
Val	Gly	Thr	Phe	Ser	Thr	Val	Ile	Ala	Thr	Leu	Val	Phe	Leu	Gly	Phe
			20					25					30		
Asn	Thr	Ser	Gln	Ala	His	Ala	Ala	Glu	Thr	Asn	Gln	Pro	Ala	Ser	Val
		35				40						45			
Val	Lys	Gln	Lys	Gln	Gln	Ser	Asn	Asn	Glu	Gln	Thr	Glu	Asn	Arg	Glu
	50					55					60				
Ser	Gln	Val	Gln	Asn	Ser	Gln	Asn	Ser	Gln	Asn	Gly	Gln	Ser	Leu	Ser
65				70						75				80	
Ala	Thr	His	Glu	Asn	Glu	Gln	Pro	Asn	Ile	Ser	Gln	Ala	Asn	Leu	Val
			85					90						95	
Asp	Gln	Lys	Val	Ala	Gln	Ser	Ser	Thr	Thr	Asn	Asp	Glu	Gln	Pro	Ala
			100					105					110		
Ser	Gln	Asn	Val	Asn	Thr	Lys	Lys	Asp	Ser	Ala	Thr	Ala	Ala	Thr	Thr
		115				120						125			
Gln	Pro	Asp	Lys	Glu	Gln	Ser	Lys	His	Lys	Gln	Asn	Glu	Ser	Gln	Ser
	130					135					140				
Ala	Asn	Lys	Asn	Gly	Asn	Asp	Asn	Arg	Ala	Ala	His	Val	Glu	Asn	His
145				150					155					160	
Glu	Ala	Asn	Val	Val	Thr	Ala	Ser	Asp	Ser	Ser	Asp	Asn	Gly	Asn	Val
			165					170						175	
Gln	His	Asp	Arg	Asn	Glu	Leu	Gln	Ala	Phe	Phe	Asp	Ala	Asn	Tyr	His
			180					185					190		
Asp	Tyr	Arg	Phe	Ile	Asp	Arg	Glu	Asn	Ala	Asp	Ser	Gly	Thr	Phe	Asn
		195					200					205			
Tyr	Val	Lys	Gly	Ile	Phe	Asp	Lys	Ile	Asn	Thr	Leu	Leu	Gly	Ser	Asn
	210					215					220				
Asp	Pro	Ile	Asn	Asn	Lys	Asp	Leu	Gln	Leu	Ala	Tyr	Lys	Glu	Leu	Glu
225					230					235					240
Gln	Ala	Val	Ala	Leu	Ile	Arg	Thr	Met	Pro	Gln	Arg	Gln	Gln	Thr	Ser
				245					250					255	
Arg	Arg	Ser	Asn	Arg	Ile	Gln	Thr	Arg	Ser	Val	Glu	Ser	Arg	Ala	Ala
			260					265					270		
Glu	Pro	Arg	Ser	Val	Ser	Asp	Tyr	Gln	Asn	Ala	Asn	Ser	Ser	Tyr	Tyr
		275					280						285		

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Val	Glu	Asn	Ala	Asn	Asp	Gly	Ser	Gly	Tyr	Pro	Val	Gly	Thr	Tyr	Ile
	290					295					300				
Asn	Ala	Ser	Ser	Lys	Gly	Ala	Pro	Tyr	Asn	Leu	Pro	Thr	Thr	Pro	Trp
305					310					315					320
Asn	Thr	Leu	Lys	Ala	Ser	Asp	Ser	Lys	Glu	Ile	Ala	Leu	Met	Thr	Ala
				325					330					335	
Lys	Gln	Thr	Gly	Asp	Gly	Tyr	Gln	Trp	Val	Ile	Lys	Phe	Asn	Lys	Gly
			340					345					350		
His	Ala	Pro	His	Gln	Asn	Met	Ile	Phe	Trp	Phe	Ala	Leu	Pro	Ala	Asp
		355					360					365			
Gln	Val	Pro	Val	Gly	Arg	Thr	Asp	Phe	Val	Thr	Val	Asn	Ser	Asp	Gly
	370					375					380				
Thr	Asn	Val	Gln	Trp	Ser	His	Gly	Ala	Gly	Ala	Gly	Ala	Asn	Lys	Pro
385					390					395					400
Leu	Gln	Gln	Met	Trp	Glu	Tyr	Gly	Val	Asn	Asp	Pro	His	Arg	Ser	His
				405					410					415	
Asp	Phe	Lys	Ile	Arg	Asn	Arg	Ser	Gly	Gln	Val	Ile	Tyr	Asp	Trp	Pro
			420					425					430		
Thr	Val	His	Ile	Tyr	Ser	Leu	Glu	Asp	Leu	Ser	Arg	Ala	Ser	Asp	Tyr
		435					440					445			
Phe	Ser	Glu	Ala	Gly	Ala	Thr	Pro	Ala	Thr	Lys	Ala	Phe	Gly	Arg	Gln
	450					455					460				
Asn	Phe	Glu	Tyr	Ile	Asn	Gly	Gln	Lys	Pro	Ala	Glu	Ser	Pro	Gly	Val
465					470					475					480
Pro	Lys	Val	Tyr	Thr	Phe	Ile	Gly	Gln	Gly	Asp	Ala	Ser	Tyr	Thr	Ile
				485					490					495	
Ser	Phe	Lys	Thr	Gln	Gly	Pro	Thr	Val	Asn	Lys	Leu	Tyr	Tyr	Ala	Ala
			500					505					510		
Gly	Gly	Arg	Ala	Leu	Glu	Tyr	Asn	Gln	Leu	Phe	Met	Tyr	Ser	Gln	Leu
		515					520					525			
Tyr	Val	Glu	Ser	Thr	Gln	Asp	His	Gln	Gln	Arg	Leu	Asn	Gly	Leu	Arg
	530					535						540			
Gln	Val	Val	Asn	Arg	Thr	Tyr	Arg	Ile	Gly	Thr	Thr	Lys	Arg	Val	Glu
545					550					555					560
Val	Ser	Gln	Gly	Asn	Val	Gln	Thr	Lys	Lys	Val	Leu	Glu	Ser	Thr	Asn
				565					570					575	
Leu	Asn	Ile	Asp	Asp	Phe	Val	Asp	Asp	Pro	Leu	Ser	Tyr	Val	Lys	Thr
			580					585					590		
Pro	Ser	Asn	Lys	Val	Leu	Gly	Phe	Tyr	Ser	Asn	Asn	Ala	Asn	Thr	Asn
		595					600					605			
Ala	Phe	Arg	Pro	Gly	Gly	Ala	Gln	Gln	Leu	Asn	Glu	Tyr	Gln	Leu	Ser
	610					615						620			
Gln	Leu	Phe	Thr	Asp	Gln	Lys	Leu	Gln	Glu	Ala	Ala	Arg	Thr	Arg	Asn
625					630					635					640
Pro	Ile	Arg	Leu	Met	Ile	Gly	Phe	Asp	Tyr	Pro	Asp	Ala	Tyr	Gly	Asn
				645					650					655	
Ser	Glu	Thr	Leu	Val	Pro	Val	Asn	Leu	Thr	Val	Leu	Pro	Glu	Ile	Gln
			660					665					670		
His	Asn	Ile	Lys	Phe	Phe	Lys	Asn	Asp	Asp	Thr	Gln	Asn	Ile	Ala	Glu
		675					680					685			
Lys	Pro	Phe	Ser	Lys	Gln	Ala	Gly	His	Pro	Val	Phe	Tyr	Val	Tyr	Ala

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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											765
Gly	Asn	Leu	Leu	Pro	Gly	Asp	Tyr	Phe	Gly	Thr	Ile	Arg	Phe	Gly	Arg
															770
Lys	Glu	Gln	Leu	Phe	Glu	Ile	Arg	Val	Lys	Pro	His	Thr	Pro	Thr	Ile
785					790										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											830
Val	Ala	Pro	Thr	Asn	Gln	Thr	Thr	Asn	Gly	Gly	Ser	Glu	Ala	Asp	Gln
															835
Ile	Pro	Ser	Gly	Tyr	Thr	Ile	Leu	Ala	Thr	Gly	Thr	Pro	Asp	Gly	Val
															850
His	Asn	Thr	Ile	Thr	Ile	Arg	Pro	Gln	Asp	Tyr	Val	Val	Phe	Ile	Pro
865					870										880
Pro	Val	Gly	Lys	Gln	Ile	Arg	Ala	Val	Val	Tyr	Tyr	Asn	Lys	Val	Val
															885
Ala	Ser	Asn	Met	Ser	Asn	Ala	Val	Thr	Ile	Leu	Pro	Asp	Asp	Ile	Pro
															900
Pro	Thr	Ile	Asn	Asn	Pro	Val	Gly	Ile	Asn	Ala	Lys	Tyr	Tyr	Arg	Gly
															915
Asp	Glu	Val	Asn	Phe	Thr	Met	Gly	Val	Ser	Asp	Arg	His	Ser	Gly	Ile
															930
Lys	Asn	Thr	Thr	Ile	Thr	Thr	Leu	Pro	Asn	Gly	Trp	Thr	Ser	Asn	Leu
945					950										960
Thr	Lys	Ala	Asp	Lys	Asn	Asn	Gly	Ser	Leu	Ser	Ile	Thr	Gly	Arg	Val
															965
Ser	Met	Asn	Gln	Ala	Phe	Asn	Ser	Asp	Ile	Thr	Phe	Lys	Val	Ser	Ala
															980
Thr	Asp	Asn	Val	Asn	Asn	Thr	Thr	Asn	Asp	Ser	Gln	Ser	Lys	His	Val
															995
Ser	Ile	His	Val	Gly	Lys	Ile	Ser	Glu	Asp	Ala	His	Pro	Ile	Val	
															1010
Leu	Gly	Asn	Thr	Glu	Lys	Val	Val	Val	Val	Asn	Pro	Thr	Ala	Val	
															1025
Ser	Asn	Asp	Glu	Lys	Gln	Ser	Ile	Ile	Thr	Ala	Phe	Met	Asn	Lys	
															1040
Asn	Gln	Asn	Ile	Arg	Gly	Tyr	Leu	Ala	Ser	Thr	Asp	Pro	Val	Thr	
															1055
Val	Asp	Asn	Asn	Gly	Asn	Val	Thr	Leu	His	Tyr	Arg	Asp	Gly	Ser	
															1070
Ser	Thr	Thr	Leu	Asp	Ala	Thr	Asn	Val	Met	Thr	Tyr	Glu	Pro	Val	
															1085

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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
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

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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			
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

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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
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

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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	
2600		2605		2610

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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

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2990	2995	3000
Ser Thr Ala Asn Gln Ala Lys Ser Asp Leu Asp His Ala Arg Gln 3005 3010 3015		
Ala Leu Thr Pro Asp Lys Ala Pro Leu Gln Thr Ala Lys Thr Gln 3020 3025 3030		
Leu Glu Gln Ser Ile Asn Gln Pro Thr Asp Thr Thr Gly Met Thr 3035 3040 3045		
Thr Ala Ser Leu Asn Ala Tyr Asn Gln Lys Leu Gln Ala Ala Arg 3050 3055 3060		
Gln Lys Leu Thr Glu Ile Asn Gln Val Leu Asn Gly Asn Pro Thr 3065 3070 3075		
Val Gln Asn Ile Asn Asp Lys Val Thr Glu Ala Asn Gln Ala Lys 3080 3085 3090		
Asp Gln Leu Asn Thr Ala Arg Gln Gly Leu Thr Leu Asp Arg Gln 3095 3100 3105		
Pro Ala Leu Thr Thr Leu His Gly Ala Ser Asn Leu Asn Gln Ala 3110 3115 3120		
Gln Gln Asn Asn Phe Thr Gln Gln Ile Asn Ala Ala Gln Asn His 3125 3130 3135		
Ala Ala Leu Glu Thr Ile Lys Ser Asn Ile Thr Ala Leu Asn Thr 3140 3145 3150		
Ala Met Thr Lys Leu Lys Asp Ser Val Ala Asp Asn Asn Thr Ile 3155 3160 3165		
Lys Ser Asp Gln Asn Tyr Thr Asp Ala Thr Pro Ala Asn Lys Gln 3170 3175 3180		
Ala Tyr Asp Asn Ala Val Asn Ala Ala Lys Gly Val Ile Gly Glu 3185 3190 3195		
Thr Thr Asn Pro Thr Met Asp Val Asn Thr Val Asn Gln Lys Ala 3200 3205 3210		
Ala Ser Val Lys Ser Thr Lys Asp Ala Leu Asp Gly Gln Gln Asn 3215 3220 3225		
Leu Gln Arg Ala Lys Thr Glu Ala Thr Asn Ala Ile Thr His Ala 3230 3235 3240		
Ser Asp Leu Asn Gln Ala Gln Lys Asn Ala Leu Thr Gln Gln Val 3245 3250 3255		
Asn Ser Ala Gln Asn Val Gln Ala Val Asn Asp Ile Lys Gln Thr 3260 3265 3270		
Thr Gln Ser Leu Asn Thr Ala Met Thr Gly Leu Lys Arg Gly Val 3275 3280 3285		
Ala Asn His Asn Gln Val Val Gln Ser Asp Asn Tyr Val Asn Ala 3290 3295 3300		
Asp Thr Asn Lys Lys Asn Asp Tyr Asn Asn Ala Tyr Asn His Ala 3305 3310 3315		
Asn Asp Ile Ile Asn Gly Asn Ala Gln His Pro Val Ile Thr Pro 3320 3325 3330		
Ser Asp Val Asn Asn Ala Leu Ser Asn Val Thr Ser Lys Glu His 3335 3340 3345		
Ala Leu Asn Gly Glu Ala Lys Leu Asn Ala Ala Lys Gln Glu Ala 3350 3355 3360		
Asn Thr Ala Leu Gly His Leu Asn Asn Leu Asn Asn Ala Gln Arg 3365 3370 3375		

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Gln Asn	Leu Gln Ser Gln	Ile	Asn Gly Ala His	Gln	Ile Asp Ala
3380		3385		3390	
Val Asn	Thr Ile Lys Gln	Asn	Ala Thr Asn Leu	Asn	Ser Ala Met
3395		3400		3405	
Gly Asn	Leu Arg Gln Ala	Val	Ala Asp Lys Asp	Gln	Val Lys Arg
3410		3415		3420	
Thr Glu	Asp Tyr Ala Asp	Ala	Asp Thr Ala Lys	Gln	Asn Ala Tyr
3425		3430		3435	
Asn Ser	Ala Val Ser Ser	Ala	Glu Thr Ile Ile	Asn	Gln Thr Thr
3440		3445		3450	
Asn Pro	Thr Met Ser Val	Asp	Asp Val Asn Arg	Ala	Thr Ser Ala
3455		3460		3465	
Val Thr	Ser Asn Lys Asn	Ala	Leu Asn Gly Tyr	Glu	Lys Leu Ala
3470		3475		3480	
Gln Ser	Lys Thr Asp Ala	Ala	Arg Ala Ile Asp	Ala	Leu Pro His
3485		3490		3495	
Leu Asn	Asn Ala Gln Lys	Ala	Asp Val Lys Ser	Lys	Ile Asn Ala
3500		3505		3510	
Ala Ser	Asn Ile Ala Gly	Val	Asn Thr Val Lys	Gln	Gln Gly Thr
3515		3520		3525	
Asp Leu	Asn Thr Ala Met	Gly	Asn Leu Gln Gly	Ala	Ile Asn Asp
3530		3535		3540	
Glu Gln	Thr Thr Leu Asn	Ser	Gln Asn Tyr Gln	Asp	Ala Thr Pro
3545		3550		3555	
Ser Lys	Lys Thr Ala Tyr	Thr	Asn Ala Val Gln	Ala	Ala Lys Asp
3560		3565		3570	
Ile Leu	Asn Lys Ser Asn	Gly	Gln Asn Lys Thr	Lys	Asp Gln Val
3575		3580		3585	
Thr Glu	Ala Met Asn Gln	Val	Asn Ser Ala Lys	Asn	Asn Leu Asp
3590		3595		3600	
Gly Thr	Arg Leu Leu Asp	Gln	Ala Lys Gln Thr	Ala	Lys Gln Gln
3605		3610		3615	
Leu Asn	Asn Met Thr His	Leu	Thr Thr Ala Gln	Lys	Thr Asn Leu
3620		3625		3630	
Thr Asn	Gln Ile Asn Ser	Gly	Thr Thr Val Ala	Gly	Val Gln Thr
3635		3640		3645	
Val Gln	Ser Asn Ala Asn	Thr	Leu Asp Gln Ala	Met	Asn Thr Leu
3650		3655		3660	
Arg Gln	Ser Ile Ala Asn	Lys	Asp Ala Thr Lys	Ala	Ser Glu Asp
3665		3670		3675	
Tyr Val	Asp Ala Asn Asn	Asp	Lys Gln Thr Ala	Tyr	Asn Asn Ala
3680		3685		3690	
Val Ala	Ala Ala Glu Thr	Ile	Ile Asn Ala Asn	Ser	Asn Pro Glu
3695		3700		3705	
Met Asn	Pro Ser Thr Ile	Thr	Gln Lys Ala Glu	Gln	Val Asn Ser
3710		3715		3720	
Ser Lys	Thr Ala Leu Asn	Gly	Asp Glu Asn Leu	Ala	Ala Ala Lys
3725		3730		3735	
Gln Asn	Ala Lys Thr Tyr	Leu	Asn Thr Leu Thr	Ser	Ile Thr Asp
3740		3745		3750	

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Ala Gln	Lys Asn Asn Leu Ile	Ser Gln Ile Thr Ser	Ala Thr Arg
3755	3760	3765	
Val Ser	Gly Val Asp Thr Val	Lys Gln Asn Ala Gln	His Leu Asp
3770	3775	3780	
Gln Ala	Met Ala Ser Leu Gln	Asn Gly Ile Asn Asn	Glu Ser Gln
3785	3790	3795	
Val Lys	Ser Ser Glu Lys Tyr	Arg Asp Ala Asp Thr	Asn Lys Gln
3800	3805	3810	
Gln Glu	Tyr Asp Asn Ala Ile	Thr Ala Ala Lys Ala	Ile Leu Asn
3815	3820	3825	
Lys Ser	Thr Gly Pro Asn Thr	Ala Gln Asn Ala Val	Glu Ala Ala
3830	3835	3840	
Leu Gln	Arg Val Asn Asn Ala	Lys Asp Ala Leu Asn	Gly Asp Ala
3845	3850	3855	
Lys Leu	Ile Ala Ala Gln Asn	Ala Ala Lys Gln His	Leu Gly Thr
3860	3865	3870	
Leu Thr	His Ile Thr Thr Ala	Gln Arg Asn Asp Leu	Thr Asn Gln
3875	3880	3885	
Ile Ser	Gln Ala Thr Asn Leu	Ala Gly Val Glu Ser	Val Lys Gln
3890	3895	3900	
Asn Ala	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

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Val	Gln	Gln	Ala	Gln	Asn	Val	Ala	Gly	Val	Asp	Thr	Val	Lys	Ser
4520						4525						4530		
Ser	Ala	Asn	Thr	Leu	Asn	Gly	Ala	Met	Gly	Thr	Leu	Arg	Asn	Ser
4535						4540						4545		
Ile	Gln	Asp	Asn	Thr	Ala	Thr	Lys	Asn	Gly	Gln	Asn	Tyr	Leu	Asp
4550						4555						4560		
Ala	Thr	Glu	Arg	Asn	Lys	Thr	Asn	Tyr	Asn	Asn	Ala	Val	Asp	Ser
4565						4570						4575		
Ala	Asn	Gly	Val	Ile	Asn	Ala	Thr	Ser	Asn	Pro	Asn	Met	Asp	Ala
4580						4585						4590		
Asn	Ala	Ile	Asn	Gln	Ile	Ala	Thr	Gln	Val	Thr	Ser	Thr	Lys	Asn
4595						4600						4605		
Ala	Leu	Asp	Gly	Thr	His	Asn	Leu	Thr	Gln	Ala	Lys	Gln	Thr	Ala
4610						4615						4620		
Thr	Asn	Ala	Ile	Asp	Gly	Ala	Thr	Asn	Leu	Asn	Lys	Ala	Gln	Lys
4625						4630						4635		
Asp	Ala	Leu	Lys	Ala	Gln	Val	Thr	Ser	Ala	Gln	Arg	Val	Ala	Asn
4640						4645						4650		
Val	Thr	Ser	Ile	Gln	Gln	Thr	Ala	Asn	Glu	Leu	Asn	Thr	Ala	Met
4655						4660						4665		
Gly	Gln	Leu	Gln	His	Gly	Ile	Asp	Asp	Glu	Asn	Ala	Thr	Lys	Gln
4670						4675						4680		
Thr	Gln	Lys	Tyr	Arg	Asp	Ala	Glu	Gln	Ser	Lys	Lys	Thr	Ala	Tyr
4685						4690						4695		
Asp	Gln	Ala	Val	Ala	Ala	Ala	Lys	Ala	Ile	Leu	Asn	Lys	Gln	Thr
4700						4705						4710		
Gly	Ser	Asn	Ser	Asp	Lys	Ala	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		

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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
4970						4975					4980			
Thr	Lys	Ala	Ala	Leu	Asn	Gly	Ala	Gln	Asn	Leu	Ala	Gln	Ala	Lys
4985						4990					4995			
Thr	Asn	Ala	Thr	Asn	Thr	Ile	Asn	Asn	Ala	His	Asp	Leu	Asn	Gln
5000						5005					5010			
Lys	Gln	Lys	Asp	Ala	Leu	Lys	Thr	Gln	Val	Asn	Asn	Ala	Gln	Arg
5015						5020					5025			
Val	Ser	Asp	Ala	Asn	Asn	Val	Gln	His	Thr	Ala	Thr	Glu	Leu	Asn
5030						5035					5040			
Ser	Ala	Met	Thr	Ala	Leu	Lys	Ala	Ala	Ile	Ala	Asp	Lys	Glu	Arg
5045						5050					5055			
Thr	Lys	Ala	Ser	Gly	Asn	Tyr	Val	Asn	Ala	Asp	Gln	Glu	Lys	Arg
5060						5065					5070			
Gln	Ala	Tyr	Asp	Ser	Lys	Val	Thr	Asn	Ala	Glu	Asn	Ile	Ile	Ser
5075						5080					5085			
Gly	Thr	Pro	Asn	Ala	Thr	Leu	Thr	Val	Asn	Asp	Val	Asn	Ser	Ala
5090						5095					5100			
Ala	Ser	Gln	Val	Asn	Ala	Ala	Lys	Thr	Ala	Leu	Asn	Gly	Asp	Asn
5105						5110					5115			
Asn	Leu	Arg	Val	Ala	Lys	Glu	His	Ala	Asn	Asn	Thr	Ile	Asp	Gly
5120						5125					5130			
Leu	Ala	Gln	Leu	Asn	Asn	Ala	Gln	Lys	Ala	Lys	Leu	Lys	Glu	Gln
5135						5140					5145			
Val	Gln	Ser	Ala	Thr	Thr	Leu	Asp	Gly	Val	Gln	Thr	Val	Lys	Asn
5150						5155					5160			
Ser	Ser	Gln	Thr	Leu	Asn	Thr	Ala	Met	Lys	Gly	Leu	Arg	Asp	Ser
5165						5170					5175			
Ile	Ala	Asn	Glu	Ala	Thr	Ile	Lys	Ala	Gly	Gln	Asn	Tyr	Thr	Asp
5180						5185					5190			
Ala	Ser	Pro	Asn	Asn	Arg	Asn	Glu	Tyr	Asp	Ser	Ala	Val	Thr	Ala
5195						5200					5205			
Ala	Lys	Ala	Ile	Ile	Asn	Gln	Thr	Ser	Asn	Pro	Thr	Met	Glu	Pro
5210						5215					5220			
Asn	Thr	Ile	Thr	Gln	Val	Thr	Ser	Gln	Val	Thr	Thr	Lys	Glu	Gln
5225						5230					5235			
Ala	Leu	Asn	Gly	Ala	Arg	Asn	Leu	Ala	Gln	Ala	Lys	Thr	Thr	Ala
5240						5245					5250			
Lys	Asn	Asn	Leu	Asn	Asn	Leu	Thr	Ser	Ile	Asn	Asn	Ala	Gln	Lys
5255						5260					5265			
Asp	Ala	Leu	Thr	Arg	Ser	Ile	Asp	Gly	Ala	Thr	Thr	Val	Ala	Gly

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5270	5275	5280
Val Asn Gln Glu Thr Ala Lys Ala Thr Glu Leu Asn Asn Ala Met		
5285	5290	5295
His Ser Leu Gln Asn Gly Ile Asn Asp Glu Thr Gln Thr Lys Gln		
5300	5305	5310
Thr Gln Lys Tyr Leu Asp Ala Glu Pro Ser Lys Lys Ser Ala Tyr		
5315	5320	5325
Asp Gln Ala Val Asn Ala Ala Lys Ala Ile Leu Thr Lys Ala Ser		
5330	5335	5340
Gly Gln Asn Val Asp Lys Ala Ala Val Glu Gln Ala Leu Gln Asn		
5345	5350	5355
Val Asn Ser Thr Lys Thr Ala Leu Asn Gly Asp Ala Lys Leu Asn		
5360	5365	5370
Glu Ala Lys Ala Ala Ala Lys Gln Thr Leu Gly Thr Leu Thr His		
5375	5380	5385
Ile Asn Asn Ala Gln Arg Thr Ala Leu Asp Asn Glu Ile Thr Gln		
5390	5395	5400
Ala Thr Asn Val Glu Gly Val Asn Thr Val Lys Ala Lys Ala Gln		
5405	5410	5415
Gln Leu Asp Gly Ala Met Gly Gln Leu Glu Thr Ser Ile Arg Asp		
5420	5425	5430
Lys Asp Thr Thr Leu Gln Ser Gln Asn Tyr Gln Asp Ala Asp Asp		
5435	5440	5445
Ala Lys Arg Thr Ala Tyr Ser Gln Ala Val Asn Ala Ala Ala Thr		
5450	5455	5460
Ile Leu Asn Lys Thr Ala Gly Gly Asn Thr Pro Lys Ala Asp Val		
5465	5470	5475
Glu Arg Ala Met Gln Ala Val Thr Gln Ala Asn Thr Ala Leu Asn		
5480	5485	5490
Gly Ile Gln Asn Leu Asp Arg Ala Lys Gln Ala Ala Asn Thr Ala		
5495	5500	5505
Ile Thr Asn Ala Ser Asp Leu Asn Thr Lys Gln Lys Glu Ala Leu		
5510	5515	5520
Lys Ala Gln Val Thr Ser Ala Gly Arg Val Ser Ala Ala Asn Gly		
5525	5530	5535
Val Glu His Thr Ala Thr Glu Leu Asn Thr Ala Met Thr Ala Leu		
5540	5545	5550
Lys Arg Ala Ile Ala Asp Lys Ala Glu Thr Lys Ala Ser Gly Asn		
5555	5560	5565
Tyr Val Asn Ala Asp Ala Asn Lys Arg Gln Ala Tyr Asp Glu Lys		
5570	5575	5580
Val Thr Ala Ala Glu Asn Ile Val Ser Gly Thr Pro Thr Pro Thr		
5585	5590	5595
Leu Thr Pro Ala Asp Val Thr Asn Ala Ala Thr Gln Val Thr Asn		
5600	5605	5610
Ala Lys Thr Gln Leu Asn Gly Asn His Asn Leu Glu Val Ala Lys		
5615	5620	5625
Gln Asn Ala Asn Thr Ala Ile Asp Gly Leu Thr Ser Leu Asn Gly		
5630	5635	5640
Pro Gln Lys Ala Lys Leu Lys Glu Gln Val Gly Gln Ala Thr Thr		
5645	5650	5655

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Leu	Pro	Asn	Val	Gln	Thr	Val	Arg	Asp	Asn	Ala	Gln	Thr	Leu	Asn
5660						5665					5670			
Thr	Ala	Met	Lys	Gly	Leu	Arg	Asp	Ser	Ile	Ala	Asn	Glu	Ala	Thr
5675						5680					5685			
Ile	Lys	Ala	Gly	Gln	Asn	Tyr	Thr	Asp	Ala	Ser	Gln	Asn	Lys	Gln
5690						5695					5700			
Thr	Asp	Tyr	Asn	Ser	Ala	Val	Thr	Ala	Ala	Lys	Ala	Ile	Ile	Gly
5705						5710					5715			
Gln	Thr	Thr	Ser	Pro	Ser	Met	Asn	Ala	Gln	Glu	Ile	Asn	Gln	Ala
5720						5725					5730			
Lys	Asp	Gln	Val	Thr	Ala	Lys	Gln	Gln	Ala	Leu	Asn	Gly	Gln	Glu
5735						5740					5745			
Asn	Leu	Arg	Thr	Ala	Gln	Thr	Asn	Ala	Lys	Gln	His	Leu	Asn	Gly
5750						5755					5760			
Leu	Ser	Asp	Leu	Thr	Asp	Ala	Gln	Lys	Asp	Ala	Val	Lys	Arg	Gln
5765						5770					5775			
Ile	Glu	Gly	Ala	Thr	His	Val	Asn	Glu	Val	Thr	Gln	Ala	Gln	Asn
5780						5785					5790			
Asn	Ala	Asp	Ala	Leu	Asn	Thr	Ala	Met	Thr	Asn	Leu	Lys	Asn	Gly
5795						5800					5805			
Ile	Gln	Asp	Gln	Asn	Thr	Ile	Lys	Gln	Gly	Val	Asn	Phe	Thr	Asp
5810						5815					5820			
Ala	Asp	Glu	Ala	Lys	Arg	Asn	Ala	Tyr	Thr	Asn	Ala	Val	Thr	Gln
5825						5830					5835			
Ala	Glu	Gln	Ile	Leu	Asn	Lys	Ala	Gln	Gly	Pro	Asn	Thr	Ser	Lys
5840						5845					5850			
Asp	Gly	Val	Glu	Thr	Ala	Leu	Glu	Asn	Val	Gln	Arg	Ala	Lys	Asn
5855						5860					5865			
Glu	Leu	Asn	Gly	Asn	Gln	Asn	Val	Ala	Asn	Ala	Lys	Thr	Thr	Ala
5870						5875					5880			
Lys	Asn	Ala	Leu	Asn	Asn	Leu	Thr	Ser	Ile	Asn	Asn	Ala	Gln	Lys
5885						5890					5895			
Glu	Ala	Leu	Lys	Ser	Gln	Ile	Glu	Gly	Ala	Thr	Thr	Val	Ala	Gly
5900						5905					5910			
Val	Asn	Gln	Val	Ser	Thr	Thr	Ala	Ser	Glu	Leu	Asn	Thr	Ala	Met
5915						5920					5925			
Ser	Asn	Leu	Gln	Asn	Gly	Ile	Asn	Asp	Glu	Ala	Ala	Thr	Lys	Ala
5930						5935					5940			
Ala	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			

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Gly Thr 6035	Thr Val Ala Gly Val 6040	Gln Gly Ile Gln Ala 6045	Asn Ala Gly
Thr Leu 6050	Asp Gln Ala Met Asn 6055	Gln Leu Arg Gln Ser 6060	Ile Ala Ser
Lys Asp 6065	Ala Thr Lys Ser Ser 6070	Glu Asp Tyr Gln Asp 6075	Ala Asn Ala
Asp Leu 6080	Gln Asn Ala Tyr Asn 6085	Asp Ala Val Thr Asn 6090	Ala Glu Gly
Ile Ile 6095	Ser Ala Thr Asn Asn 6100	Pro Glu Met Asn Pro 6105	Asp Thr Ile
Asn Gln 6110	Lys Ala Ser Gln Val 6115	Asn Ser Ala Lys Ser 6120	Ala Leu Asn
Gly Asp 6125	Glu Lys Leu Ala Ala 6130	Ala Lys Gln Thr Ala 6135	Lys Ser Asp
Ile Gly 6140	Arg Leu Thr Asp Leu 6145	Asn Asn Ala Gln Arg 6150	Thr Ala Ala
Asn Ala 6155	Glu Val Asp Gln Ala 6160	Pro Asn Leu Ala Ala 6165	Val Thr Ala
Ala Lys 6170	Asn Lys Ala Thr Ser 6175	Leu Asn Thr Ala Met 6180	Gly Asn Leu
Lys His 6185	Ala Leu Ala Glu Lys 6190	Asp Asn Thr Lys Arg 6195	Ser Val Asn
Tyr Thr 6200	Asp Ala Asp Gln Pro 6205	Lys Gln Gln Ala Tyr 6210	Asp Thr Ala
Val Thr 6215	Gln Ala Glu Ala Ile 6220	Thr Asn Ala Asn Gly 6225	Ser Asn Ala
Asn Glu 6230	Thr Gln Val Gln Ala 6235	Ala Leu Asn Gln Leu 6240	Asn Gln Ala
Lys Asn 6245	Asp Leu Asn Gly Asp 6250	Asn Lys Val Ala Gln 6255	Ala Lys Glu
Ser Ala 6260	Lys Arg Ala Leu Ala 6265	Ser Tyr Ser Asn Leu 6270	Asn Asn Ala
Gln Ser 6275	Thr Ala Ala Ile Ser 6280	Gln Ile Asp Asn Ala 6285	Thr Thr Val
Ala Gly 6290	Val Thr Ala Ala Gln 6295	Asn Thr Ala Asn Glu 6300	Leu Asn Thr
Ala Met 6305	Gly Gln Leu Gln Asn 6310	Gly Ile Asn Asp Gln 6315	Asn Thr Val
Lys Gln 6320	Gln Val Asn Phe Thr 6325	Asp Ala Asp Gln Gly 6330	Lys Lys Asp
Ala Tyr 6335	Thr Asn Ala Val Thr 6340	Asn Ala Gln Gly Ile 6345	Leu Asp Lys
Ala His 6350	Gly Gln Asn Met Thr 6355	Lys Ala Gln Val Glu 6360	Ala Ala Leu
Asn Gln 6365	Val Thr Thr Ala Lys 6370	Asn Ala Leu Asn Gly 6375	Asp Ala Asn
Val Arg 6380	Gln Ala Lys Ser Asp 6385	Ala Lys Ala Asn Leu 6390	Gly Thr Leu
Thr His 6395	Leu Asn Asn Ala Gln 6400	Lys Gln Asp Leu Thr 6405	Ser Gln Ile
Glu Gly	Ala Thr Thr Val Asn	Gly Val Asn Gly Val	Lys Thr Lys

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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
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

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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	
Leu Gly	Ser Gln Asn Phe	Ala	Asp Ala Asp Pro	Glu	Lys Lys Asn
6950		6955		6960	
Ala Tyr	Asn Glu Ala Val	His	Asn Ala Glu Asn	Ile	Leu Asn Lys
6965		6970		6975	
Ser Thr	Gly Thr Asn Val	Pro	Lys Asp Gln Val	Glu	Ala Ala Met
6980		6985		6990	
Asn Gln	Val Asn Ala Thr	Lys	Ala Ala Leu Asn	Gly	Thr Gln Asn
6995		7000		7005	
Leu Glu	Lys Ala Lys Gln	His	Ala Asn Thr Ala	Ile	Asp Gly Leu
7010		7015		7020	
Ser His	Leu Thr Asn Ala	Gln	Lys Glu Ala Leu	Lys	Gln Leu Val
7025		7030		7035	
Gln Gln	Ser Thr Thr Val	Ala	Glu Ala Gln Gly	Asn	Glu Gln Lys
7040		7045		7050	
Ala Asn	Asn Val Asp Ala	Ala	Met Asp Lys Leu	Arg	Gln Ser Ile
7055		7060		7065	
Ala Asp	Asn Ala Thr Thr	Lys	Gln Asn Gln Asn	Tyr	Thr Asp Ala
7070		7075		7080	
Ser Gln	Asn Lys Lys Asp	Ala	Tyr Asn Asn Ala	Val	Thr Thr Ala
7085		7090		7095	
Gln Gly	Ile Ile Asp Gln	Thr	Thr Ser Pro Thr	Leu	Asp Pro Thr
7100		7105		7110	
Val Ile	Asn Gln Ala Ala	Gly	Gln Val Ser Thr	Thr	Lys Asn Ala
7115		7120		7125	
Leu Asn	Gly Asn Glu Asn	Leu	Glu Ala Ala Lys	Gln	Gln Ala Ser
7130		7135		7140	
Gln Ser	Leu Gly Ser Leu	Asp	Asn Leu Asn Asn	Ala	Gln Lys Gln
7145		7150		7155	
Thr Val	Thr Asp Gln Ile	Asn	Gly Ala His Thr	Val	Asp Glu Ala
7160		7165		7170	

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Asn	Gln	Ile	Lys	Gln	Asn	Ala	Gln	Asn	Leu	Asn	Thr	Ala	Met	Gly
7175						7180					7185			
Asn	Leu	Lys	Gln	Ala	Ile	Ala	Asp	Lys	Asp	Ala	Thr	Lys	Ala	Thr
7190						7195					7200			
Val	Asn	Phe	Thr	Asp	Ala	Asp	Gln	Ala	Lys	Gln	Gln	Ala	Tyr	Asn
7205						7210					7215			
Thr	Ala	Val	Thr	Asn	Ala	Glu	Asn	Ile	Ser	Lys	Ala	Asn	Gly	Asn
7220						7225					7230			
Ala	Thr	Gln	Ala	Glu	Val	Glu	Gln	Ala	Ile	Lys	Gln	Val	Asn	Ala
7235						7240					7245			
Ala	Lys	Gln	Ala	Leu	Asn	Gly	Asn	Ala	Asn	Val	Gln	His	Ala	Lys
7250						7255					7260			
Asp	Glu	Ala	Thr	Ala	Leu	Ile	Asn	Ser	Ser	Asn	Asp	Leu	Asn	Gln
7265						7270					7275			
Ala	Gln	Lys	Asp	Ala	Leu	Lys	Gln	Gln	Val	Gln	Asn	Ala	Thr	Thr
7280						7285					7290			
Val	Ala	Gly	Val	Asn	Asn	Val	Lys	Gln	Thr	Ala	Gln	Glu	Leu	Asn
7295						7300					7305			
Asn	Ala	Met	Thr	Gln	Leu	Lys	Gln	Gly	Ile	Ala	Asp	Lys	Glu	Gln
7310						7315					7320			
Thr	Lys	Ala	Asp	Gly	Asn	Phe	Val	Asn	Ala	Asp	Pro	Asp	Lys	Gln
7325						7330					7335			
Asn	Ala	Tyr	Asn	Gln	Ala	Val	Ala	Lys	Ala	Glu	Ala	Leu	Ile	Ser
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

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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
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

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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			
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			

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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
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

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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			
Leu	Asp	Asn	Ala	Met	Gly	Ala	Val	Gln	Gln	Tyr	Ile	Asp	Glu	Gln
9320						9325					9330			
His	Leu	Gly	Val	Ile	Ser	Ser	Thr	Asn	Tyr	Ile	Asn	Ala	Asp	Asp
9335						9340					9345			
Asn	Leu	Lys	Ala	Asn	Tyr	Asp	Asn	Ala	Ile	Ala	Asn	Ala	Ala	His
9350						9355					9360			
Glu	Leu	Asp	Lys	Val	Gln	Gly	Asn	Ala	Ile	Ala	Lys	Ala	Glu	Ala
9365						9370					9375			
Glu	Gln	Leu	Lys	Gln	Asn	Ile	Ile	Asp	Ala	Gln	Asn	Ala	Leu	Asn
9380						9385					9390			
Gly	Asp	Gln	Asn	Leu	Ala	Asn	Ala	Lys	Asp	Lys	Ala	Asn	Ala	Phe
9395						9400					9405			
Val	Asn	Ser	Leu	Asn	Gly	Leu	Asn	Gln	Gln	Gln	Gln	Asp	Leu	Ala
9410						9415					9420			
His	Lys	Ala	Ile	Asn	Asn	Ala	Asp	Thr	Val	Ser	Asp	Val	Thr	Asp
9425						9430					9435			
Ile	Val	Asn	Asn	Gln	Ile	Asp	Leu	Asn	Asp	Ala	Met	Glu	Thr	Leu
9440						9445					9450			

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Lys 9455	His	Leu	Val	Asp	Asn	Glu 9460	Ile	Pro	Asn	Ala	Glu 9465	Gln	Thr	Val
Asn 9470	Tyr	Gln	Asn	Ala	Asp	Asp 9475	Asn	Ala	Lys	Thr	Asn 9480	Phe	Asp	Asp
Ala 9485	Lys	Arg	Leu	Ala	Asn	Thr 9490	Leu	Leu	Asn	Ser	Asp 9495	Asn	Thr	Asn
Val 9500	Asn	Asp	Ile	Asn	Gly	Ala 9505	Ile	Gln	Ala	Val	Asn 9510	Asp	Ala	Ile
His 9515	Asn	Leu	Asn	Gly	Asp	Gln 9520	Arg	Leu	Gln	Asp	Ala 9525	Lys	Asp	Lys
Ala 9530	Ile	Gln	Ser	Ile	Asn	Gln 9535	Ala	Leu	Ala	Asn	Lys 9540	Leu	Lys	Glu
Ile 9545	Glu	Ala	Ser	Asn	Ala	Thr 9550	Asp	Gln	Asp	Lys	Leu 9555	Ile	Ala	Lys
Asn 9560	Lys	Ala	Glu	Glu	Leu	Ala 9565	Asn	Ser	Ile	Ile	Asn 9570	Asn	Ile	Asn
Lys 9575	Ala	Thr	Ser	Asn	Gln	Ala 9580	Val	Ser	Gln	Val	Gln 9585	Thr	Ala	Gly
Asn 9590	His	Ala	Ile	Glu	Gln	Val 9595	His	Ala	Asn	Glu	Ile 9600	Pro	Lys	Ala
Lys 9605	Ile	Asp	Ala	Asn	Lys	Asp 9610	Val	Asp	Lys	Gln	Val 9615	Gln	Ala	Leu
Ile 9620	Asp	Glu	Ile	Asp	Arg	Asn 9625	Pro	Asn	Leu	Thr	Asp 9630	Lys	Glu	Lys
Gln 9635	Ala	Leu	Lys	Asp	Arg	Ile 9640	Asn	Gln	Ile	Leu	Gln 9645	Gln	Gly	His
Asn 9650	Gly	Ile	Asn	Asn	Ala	Met 9655	Thr	Lys	Glu	Glu	Ile 9660	Glu	Gln	Ala
Lys 9665	Ala	Gln	Leu	Ala	Gln	Ala 9670	Leu	Gln	Asp	Ile	Lys 9675	Asp	Leu	Val
Lys 9680	Ala	Lys	Glu	Asp	Ala	Lys 9685	Gln	Asp	Val	Asp	Lys 9690	Gln	Val	Gln
Ala 9695	Leu	Ile	Asp	Glu	Ile	Asp 9700	Gln	Asn	Pro	Asn	Leu 9705	Thr	Asp	Lys
Glu 9710	Lys	Gln	Ala	Leu	Lys	Tyr 9715	Arg	Ile	Asn	Gln	Ile 9720	Leu	Gln	Gln
Gly 9725	His	Asn	Asp	Ile	Asn	Asn 9730	Ala	Leu	Thr	Lys	Glu 9735	Glu	Ile	Glu
Gln 9740	Ala	Lys	Ala	Gln	Leu	Ala 9745	Gln	Ala	Leu	Gln	Asp 9750	Ile	Lys	Asp
Leu 9755	Val	Lys	Ala	Lys	Glu	Asp 9760	Ala	Lys	Asn	Ala	Ile 9765	Lys	Ala	Leu
Ala 9770	Asn	Ala	Lys	Arg	Asp	Gln 9775	Ile	Asn	Ser	Asn	Pro 9780	Asp	Leu	Thr
Pro 9785	Glu	Gln	Lys	Ala	Lys	Ala 9790	Leu	Lys	Glu	Ile	Asp 9795	Glu	Ala	Glu
Lys 9800	Arg	Ala	Leu	Gln	Asn	Val 9805	Glu	Asn	Ala	Gln	Thr 9810	Ile	Asp	Gln
Leu 9815	Asn	Arg	Gly	Leu	Asn	Leu 9820	Gly	Leu	Asp	Asp	Ile 9825	Arg	Asn	Thr
His 9830	Val	Trp	Glu	Val	Asp	Glu 9835	Gln	Pro	Ala	Val	Asn 9840	Glu	Ile	Phe

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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 Asp Glu Lys Gln Ala Ala Met Asn Gln Ile Asn Glu Ile		
10115	10120	10125
Val Leu Glu Thr Ile Arg Asp Ile Asn Asn Ala His Thr Leu Gln		
10130	10135	10140
Gln Val Glu Ala Ala Leu Asn Asn Gly Ile Ala Arg Ile Ser Ala		
10145	10150	10155
Val Gln Ile Val Thr Ser Asp Arg Ala Lys Gln Ser Ser Ser Thr		
10160	10165	10170
Gly Asn Glu Ser Asn Ser His Leu Thr Ile Gly Tyr Gly Thr Ala		
10175	10180	10185
Asn His Pro Phe Asn Ser Ser Thr Ile Gly His Lys Lys Lys Leu		
10190	10195	10200
Asp Glu Asp Asp Asp Ile Asp Pro Leu His Met Arg His Phe Ser		
10205	10210	10215

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Asn Asn  Phe Gly Asn Val Ile  Lys Asn Ala Ile Gly  Val Val Gly
10220                                10225                    10230

Ile Ser  Gly Leu Leu Ala Ser  Phe Trp Phe Phe Ile  Ala Lys Arg
10235                                10240                    10245

Arg Arg  Lys Glu Asp Glu Glu  Glu Glu Leu Glu Ile  Arg Asp Asn
10250                                10255                    10260

Asn Lys  Asp Ser Ile Lys Glu  Thr Leu Asp Asp Thr  Lys His Leu
10265                                10270                    10275

Pro Leu  Leu Phe Ala Lys Arg  Arg Arg Lys Glu Asp  Glu Glu Asp
10280                                10285                    10290

Val Thr  Val Glu Glu Lys Asp  Ser Leu Asn Asn Gly  Glu Ser Leu
10295                                10300                    10305

Asp Lys  Val Lys His Thr Pro  Phe Phe Leu Pro Lys  Arg Arg Arg
10310                                10315                    10320

Lys Glu  Asp Glu Glu Asp Val  Glu Val Thr Asn Glu  Asn Thr Asp
10325                                10330                    10335

Glu Lys  Val Leu Lys Asp Asn  Glu His Ser Pro Leu  Leu Phe Ala
10340                                10345                    10350

Lys Arg  Arg Lys Asp Lys Glu  Glu Asp Val Glu Thr  Thr Thr Ser
10355                                10360                    10365

Ile Glu  Ser Lys Asp Glu Asp  Val Pro Leu Leu Leu  Ala Lys Lys
10370                                10375                    10380

Lys Asn  Gln Lys Asp Asn Gln  Ser Lys Asp Lys Lys  Ser Ala Ser
10385                                10390                    10395

Lys Asn  Thr Ser Lys Lys Val  Ala Ala Lys Lys Lys  Lys Lys Lys
10400                                10405                    10410

Ala Lys  Lys Asn Lys Lys
10415

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<210> SEQ ID NO 25

<211> LENGTH: 340

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 25

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

Gln Ile Met Asn Ser Asn His Ala Lys Ala Ser Val Thr Glu Ser Val
20     25     30

Asp Lys Lys Phe Val Val Pro Glu Ser Gly Ile Asn Lys Ile Ile Pro
35     40     45

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

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

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

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

Asn Arg Val Asn Val Ala Thr Asn Asn Pro Ala Ser Gln Gln Val Asp
115    120    125

Lys His Phe Val Ala Lys Gly Pro Glu Val Asn Arg Phe Ile Thr Gln

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<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

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

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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

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<210> SEQ ID NO 28

<211> LENGTH: 745

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 28

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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
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                               80

Val Asp Thr Gln Gln Ala Ser Thr Gln Lys Pro Thr His Thr Ala Thr

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85				90				95							
Phe	Lys	Leu	Ser	Asn	Ala	Lys	Thr	Ala	Ser	Leu	Ser	Pro	Arg	Met	Phe
			100							105				110	
Ala	Ala	Asn	Ala	Pro	Gln	Thr	Thr	Thr	His	Lys	Ile	Leu	His	Thr	Asn
		115					120					125			
Asp	Ile	His	Gly	Arg	Leu	Ala	Glu	Glu	Lys	Gly	Arg	Val	Ile	Gly	Met
	130					135					140				
Ala	Lys	Leu	Lys	Thr	Val	Lys	Glu	Gln	Glu	Lys	Pro	Asp	Leu	Met	Leu
145					150					155				160	
Asp	Ala	Gly	Asp	Ala	Phe	Gln	Gly	Leu	Pro	Leu	Ser	Asn	Gln	Ser	Lys
			165						170					175	
Gly	Glu	Glu	Met	Ala	Lys	Ala	Met	Asn	Ala	Val	Gly	Tyr	Asp	Ala	Met
			180						185					190	
Ala	Val	Gly	Asn	His	Glu	Phe	Asp	Phe	Gly	Tyr	Asp	Gln	Leu	Lys	Lys
		195					200					205			
Leu	Glu	Gly	Met	Leu	Asp	Phe	Pro	Met	Leu	Ser	Thr	Asn	Val	Tyr	Lys
	210					215					220				
Asp	Gly	Lys	Arg	Ala	Phe	Lys	Pro	Ser	Thr	Ile	Val	Thr	Lys	Asn	Gly
225					230					235				240	
Ile	Arg	Tyr	Gly	Ile	Ile	Gly	Val	Thr	Thr	Pro	Glu	Thr	Lys	Thr	Lys
			245						250					255	
Thr	Arg	Pro	Glu	Gly	Ile	Lys	Gly	Val	Glu	Phe	Arg	Asp	Pro	Leu	Gln
			260						265					270	
Ser	Val	Thr	Ala	Glu	Met	Met	Arg	Ile	Tyr	Lys	Asp	Val	Asp	Thr	Phe
		275					280					285			
Val	Val	Ile	Ser	His	Leu	Gly	Ile	Asp	Pro	Ser	Thr	Gln	Glu	Thr	Trp
		290				295					300				
Arg	Gly	Asp	Tyr	Leu	Val	Lys	Gln	Leu	Ser	Gln	Asn	Pro	Gln	Leu	Lys
305					310					315				320	
Lys	Arg	Ile	Thr	Val	Ile	Asp	Gly	His	Ser	His	Thr	Val	Leu	Gln	Asn
			325						330					335	
Gly	Gln	Ile	Tyr	Asn	Asn	Asp	Ala	Leu	Ala	Gln	Thr	Gly	Thr	Ala	Leu
			340						345					350	
Ala	Asn	Ile	Gly	Lys	Ile	Thr	Phe	Asn	Tyr	Arg	Asn	Gly	Glu	Val	Ser
		355					360					365			
Asn	Ile	Lys	Pro	Ser	Leu	Ile	Asn	Val	Lys	Asp	Val	Glu	Asn	Val	Thr
		370				375					380				
Pro	Asn	Lys	Ala	Leu	Ala	Glu	Gln	Ile	Asn	Gln	Ala	Asp	Gln	Thr	Phe
385					390					395				400	
Arg	Ala	Gln	Thr	Ala	Glu	Val	Ile	Ile	Pro	Asn	Asn	Thr	Ile	Asp	Phe
			405						410					415	
Lys	Gly	Glu	Arg	Asp	Asp	Val	Arg	Thr	Arg	Glu	Thr	Asn	Leu	Gly	Asn
			420						425					430	
Ala	Ile	Ala	Asp	Ala	Met	Glu	Ala	Tyr	Gly	Val	Lys	Asn	Phe	Ser	Lys
		435					440					445			
Lys	Thr	Asp	Phe	Ala	Val	Thr	Asn	Gly	Gly	Gly	Ile	Arg	Ala	Ser	Ile
		450				455					460				
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	

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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
85 90 95

Phe Lys His Pro Lys Phe Tyr Gln Gln Leu Phe Lys Leu Leu Glu Asp

-continued

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	

-continued

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

-continued

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
 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

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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 32

<211> LENGTH: 508

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 32

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

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Ala Asn Lys Lys Ala Val Asn Lys Arg Met Leu Glu Asn Lys Lys Glu
 210 215 220

Asp Leu Glu Thr Ile Ile Asp Glu Phe Phe Ser Asp Ile Asp Lys Thr
 225 230 235 240

Arg Pro Asn Asn Ile Pro Val Leu Glu Asp Glu Lys Gln Glu Glu Lys
 245 250 255

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

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

Gln Asn His Lys Pro Ala Ser Gln Glu Val Ser Glu Gln Gln Lys Ala
 290 295 300

Glu Tyr Asp Lys Arg Ala Glu Glu Arg Lys Ala Arg Phe Leu Asp Asn
 305 310 315 320

Gln Lys Ile Lys Lys Thr Pro Val Val Ser Leu Glu Tyr Asp Phe Glu
 325 330 335

His Lys Gln Arg Ile Asp Asn Glu Asn Asp Lys Lys Leu Val Val Ser
 340 345 350

Ala Pro Thr Lys Lys Pro Thr Ser Pro Thr Thr Tyr Thr Glu Thr Thr
 355 360 365

Thr Gln Val Pro Met Pro Thr Val Glu Arg Gln Thr Gln Gln Gln Ile
 370 375 380

Ile Tyr Asn Ala Pro Lys Gln Leu Ala Gly Leu Asn Gly Glu Ser His
 385 390 395 400

Asp Phe Thr Thr Thr His Gln Ser Pro Thr Thr Ser Asn His Thr His
 405 410 415

Asn Asn Val Val Glu Phe Glu Glu Thr Ser Ala Leu Pro Gly Arg Lys
 420 425 430

Ser Gly Ser Leu Val Gly Ile Ser Gln Ile Asp Ser Ser His Leu Thr
 435 440 445

Glu Arg Glu Lys Arg Val Ile Lys Arg Glu His Val Arg Glu Ala Gln
 450 455 460

Lys Leu Val Asp Asn Tyr Lys Asp Thr His Ser Tyr Lys Asp Arg Ile
 465 470 475 480

Asn Ala Gln Gln Lys Val Asn Thr Leu Ser Glu Gly His Gln Lys Arg
 485 490 495

Phe Asn Lys Gln Ile Asn Lys Val Tyr Asn Gly Lys
 500 505

<210> 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

-continued

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
		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						460			

-continued

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

<210> SEQ ID NO 34
 <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
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Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln
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Ala Pro Lys

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290

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<400> SEQUENCE: 35

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<400> SEQUENCE: 36

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<400> SEQUENCE: 37

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Arg Gly Ser

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<400> SEQUENCE: 39

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 <211> LENGTH: 43
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<210> SEQ ID NO 41
 <211> LENGTH: 43
 <212> TYPE: DNA
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<400> SEQUENCE: 41

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<210> SEQ ID NO 42
<211> LENGTH: 42
<212> TYPE: DNA
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<210> SEQ ID NO 43
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: *Staphylococcus* sp.
<400> SEQUENCE: 43
gatttcataag aaggcgcttt ttttatcttt gttgaacata tg 42

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<211> LENGTH: 42
<212> TYPE: DNA
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<400> SEQUENCE: 44
catatgttca acaaagatgg aggaagcgcc ttctatgaaa tc 42

<210> SEQ ID NO 45
<211> LENGTH: 42
<212> TYPE: DNA
<213> ORGANISM: *Staphylococcus* sp.
<400> SEQUENCE: 45
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<210> SEQ ID NO 46
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<212> TYPE: DNA
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<212> TYPE: DNA
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aaggatcccc tccaaaatgt aattgccc 28

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<400> SEQUENCE: 51

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<400> SEQUENCE: 52

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<213> ORGANISM: Staphylococcus sp.

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<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 54

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<210> SEQ ID NO 55
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<400> SEQUENCE: 55

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<400> SEQUENCE: 56

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<211> LENGTH: 33

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gtaggatcct gggatagagt taaaaac 27

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<400> SEQUENCE: 61

gaactcgagg cattatgtgt atcaciaaatt tggg 34

<210> SEQ ID NO 62
<211> LENGTH: 43
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 62

gaactcgaga tagaaggcag agtggtttct ggggagaaga atc 43

<210> SEQ ID NO 63
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 63

gaactcgagg cagccatgca ttaattattt gcc 33

<210> SEQ ID NO 64
<211> LENGTH: 677
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 64

Met Lys Ser Asn Leu Arg Tyr Gly Ile Arg Lys His Lys Leu Gly Ala

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Ala Ser Val Phe Leu Gly Thr Met Ile Val Val Gly Met Gly Gln Glu 20 25 30			
Lys Glu Ala Ala Ala Ser Glu Gln Asn Asn Thr Thr Val Glu Glu Ser 35 40 45			
Gly Ser Ser Ala Thr Glu Ser Lys Ala Ser Glu Thr Gln Thr Thr Thr 50 55 60			
Asn Asn Val Asn Thr Ile Asp Glu Thr Gln Ser Tyr Ser Ala Thr Ser 65 70 75 80			
Thr Glu Gln Pro Ser Gln Ser Thr Gln Val Thr Thr Glu Glu Ala Pro 85 90 95			
Lys Thr Val Gln Ala Pro Lys Val Glu Thr Ser Arg Val Asp Leu Pro 100 105 110			
Ser Glu Lys Val Ala Asp Lys Glu Thr Thr Gly Thr Gln Val Asp Ile 115 120 125			
Ala Gln Pro Ser Asn Val Ser Glu Ile Lys Pro Arg Met Lys Arg Ser 130 135 140			
Thr Asp Val Thr Ala Val Ala Glu Lys Glu Val Val Glu Glu Thr Lys 145 150 155 160			
Ala Thr Gly Thr Asp Val Thr Asn Lys Val Glu Val Glu Glu Gly Ser 165 170 175			
Glu Ile Val Gly His Lys Gln Asp Thr Asn Val Val Asn Pro His Asn 180 185 190			
Ala Glu Arg Val Thr Leu Lys Tyr Lys Trp Lys Phe Gly Glu Gly Ile 195 200 205			
Lys Ala Gly Asp Tyr Phe Asp Phe Thr Leu Ser Asp Asn Val Glu Thr 210 215 220			
His Gly Ile Ser Thr Leu Arg Lys Val Pro Glu Ile Lys Ser Thr Asp 225 230 235 240			
Gly Gln Val Met Ala Thr Gly Glu Ile Ile Gly Glu Arg Lys Val Arg 245 250 255			
Tyr Thr Phe Lys Glu Tyr Val Gln Glu Lys Lys Asp Leu Thr Ala Glu 260 265 270			
Leu Ser Leu Asn Leu Phe Ile Asp Pro Thr Thr Val Thr Gln Lys Gly 275 280 285			
Asn Gln Asn Val Glu Val Lys Leu Gly Glu Thr Thr Val Ser Lys Ile 290 295 300			
Phe Asn Ile Gln Tyr Leu Gly Gly Val Arg Asp Asn Trp Gly Val Thr 305 310 315 320			
Ala Asn Gly Arg Ile Asp Thr Leu Asn Lys Val Asp Gly Lys Phe Ser 325 330 335			
His Phe Ala Tyr Met Lys Pro Asn Asn Gln Ser Leu Ser Ser Val Thr 340 345 350			
Val Thr Gly Gln Val Thr Lys Gly Asn Lys Pro Gly Val Asn Asn Pro 355 360 365			
Thr Val Lys Val Tyr Lys His Ile Gly Ser Asp Asp Leu Ala Glu Ser 370 375 380			
Val Tyr Ala Lys Leu Asp Asp Val Ser Lys Phe Glu Asp Val Thr Asp 385 390 395 400			
Asn Met Ser Leu Asp Phe Asp Thr Asn Gly Gly Tyr Ser Leu Asn Phe 405 410 415			

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Asn Asn Leu Asp Gln Ser Lys Asn Tyr Val Ile Lys Tyr Glu Gly Tyr
    420                                425                                430

Tyr Asp Ser Asn Ala Ser Asn Leu Glu Phe Gln Thr His Leu Phe Gly
    435                                440                                445

Tyr Tyr Asn Tyr Tyr Tyr Thr Ser Asn Leu Thr Trp Lys Asn Gly Val
    450                                455                                460

Ala Phe Tyr Ser Asn Asn Ala Gln Gly Asp Gly Lys Asp Lys Leu Lys
    465                                470                                475                                480

Glu Pro Ile Ile Glu His Ser Thr Pro Ile Glu Leu Glu Phe Lys Ser
    485                                490                                495

Glu Pro Pro Val Glu Lys His Glu Leu Thr Gly Thr Ile Glu Glu Ser
    500                                505                                510

Asn Asp Ser Lys Pro Ile Asp Phe Glu Tyr His Thr Ala Val Glu Gly
    515                                520                                525

Ala Glu Gly His Ala Glu Gly Thr Ile Glu Thr Glu Glu Asp Ser Ile
    530                                535                                540

His Val Asp Phe Glu Glu Ser Thr His Glu Asn Ser Lys His His Ala
    545                                550                                555                                560

Asp Val Val Glu Tyr Glu Glu Asp Thr Asn Pro Gly Gly Gly Gln Val
    565                                570                                575

Thr Thr Glu Ser Asn Leu Val Glu Phe Asp Glu Asp Ser Thr Lys Gly
    580                                585                                590

Ile Val Thr Gly Ala Val Ser Asp His Thr Thr Ile Glu Asp Thr Lys
    595                                600                                605

Glu Tyr Thr Thr Glu Ser Asn Leu Ile Glu Leu Val Asp Glu Leu Pro
    610                                615                                620

Glu Glu His Gly Gln Ala Gln Gly Pro Ile Glu Glu Ile Thr Glu Asn
    625                                630                                635                                640

Asn His His Ile Ser His Ser Gly Leu Gly Thr Glu Asn Gly His Gly
    645                                650                                655

Asn Tyr Gly Val Ile Glu Glu Ile Glu Glu Asn Ser His Val Asp Ile
    660                                665                                670

Lys Ser Glu Leu Gly
    675

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1-77. (canceled)

78. An isolated polypeptide comprising a *Staphylococcus aureus* Protein A (SpA) D variant domain segment comprising (a) at least one amino acid substitution that disrupts Fc binding and (b) at least one amino acid substitution that disrupts VH3 binding and (c) an amino acid sequence that is at least 70% identical to the amino acid sequence of SEQ ID NO: 2, wherein the amino acid substitutions correspond to at least amino acids at position 9, 10, 36 and/or 37 of SEQ ID NO: 2.

79. The isolated polypeptide of claim 78, wherein the SpA D domain segment is at least 90% identical to the amino acid sequence of SEQ ID NO: 2.

80. The isolated polypeptide of claim 78, further comprising one or more variant domain segments having substitutions in the SpA E domain, A domain, B domain and/or C domain.

81. The isolated polypeptide of claim 78, further comprising a non-Protein A segment.

82. The isolated polypeptide of claim 78, further comprising a second antigen segment, wherein the second antigen segment is a staphylococcal antigen segment selected from Emp, EsxA, EsxB, EsaC, Eap, Ebh, EsaB, Coa, vWbp, vWh, Hla, SdrC, SdrD, SdrE, IsdA, IsdB, IsdC, ClfA, ClfB, and/or SasF segment.

83. The isolated polypeptide of claim 78, wherein the substitutions at amino acids corresponding to positions 9 and 10 are with a lysine residue and the substitutions at amino acids corresponding to positions 36 and 37 are with an alanine residue.

84. A method of making the polypeptide of claim 78, comprising isolating the polypeptide from a host cell expressing the polypeptide.

85. A composition comprising the isolated polypeptide of claim 78.

86. A vaccine comprising the isolated polypeptide of claim 78 and a pharmaceutically acceptable excipient.

87. A method of preventing or treating staphylococcal infection comprising the step of administering the vaccine of claim **86** to a patient in need thereof.

88. A method for eliciting an immune response against a *staphylococcus* bacterium in a subject comprising providing to the subject an effective amount of the composition of claim **85**.

89. The method of claim **88**, further comprising administering to the subject a composition comprising a second staphylococcal antigen.

90. The method of claim **89**, wherein the second staphylococcal antigen is one or more of Emp, EsxA, EsxB, EsaC, Eap, Ebh, EsaB, Coa, vWbp, vWh, Hla, SdrC, SdrD, SdrE, IsdA, IsdB, IsdC, ClfA, ClfB, and SasF.

91. An isolated polypeptide comprising a *Staphylococcus aureus* Protein A (SpA) D variant domain segment having amino acid substitutions corresponding to amino acids at position 9, 10, 36 and 37 of SEQ ID NO: 2; wherein the substitutions at amino acids corresponding to positions 9 and 10 are with a lysine residue and the substitutions at amino acids corresponding to positions 36 and 37 are with an alanine residue and wherein the amino acid sequence is at least 70% identical to the amino acid sequence of SEQ ID NO: 2; and optionally wherein the peptide further comprises one or more

variant domain segments having substitutions in the SpA E domain, A domain, B domain and/or C domain.

92. The isolated polypeptide of claim **92**, wherein the amino acid sequence is at least 90% identical to the amino acid sequence of SEQ ID NO: 2

93. A method of preventing or treating staphylococcal infection comprising the step of administering the isolated polypeptide of claim **91** to a patient in need thereof.

94. A method for eliciting an immune response against a *staphylococcus* bacterium in a subject comprising providing to the subject an effective amount of the isolated polypeptide of claim **91**.

95. The method of claim **94**, further comprising administering to the subject a composition comprising a second staphylococcal antigen.

96. The method of claim **95**, wherein the second staphylococcal antigen is one or more of Emp, EsxA, EsxB, EsaC, Eap, Ebh, EsaB, Coa, vWbp, vWh, Hla, SdrC, SdrD, SdrE, IsdA, IsdB, IsdC, ClfA, ClfB, and SasF.

97. A vaccine composition comprising the isolated polypeptide of claim **91** and a pharmaceutically acceptable excipient.

* * * * *