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

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(58) **Field of Classification Search**

None  
See application file for complete search history.

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(57) **ABSTRACT**

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

**14 Claims, 12 Drawing Sheets**

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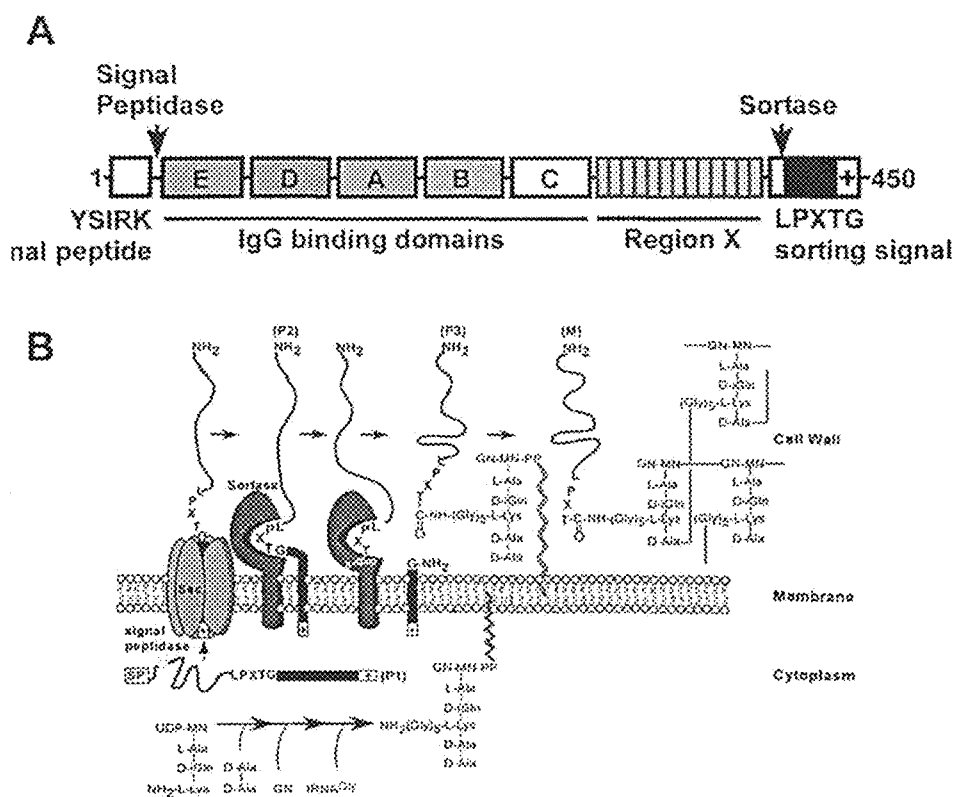
Zhou et al., "An immunogenicity study of a newly fusion protein Cna-FnBP vaccinated against *Staphylococcus aureus* infections in a mice model," *Vaccine*, 24 (22): 4830-4837, 2006.

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FIGs. 1A-1B

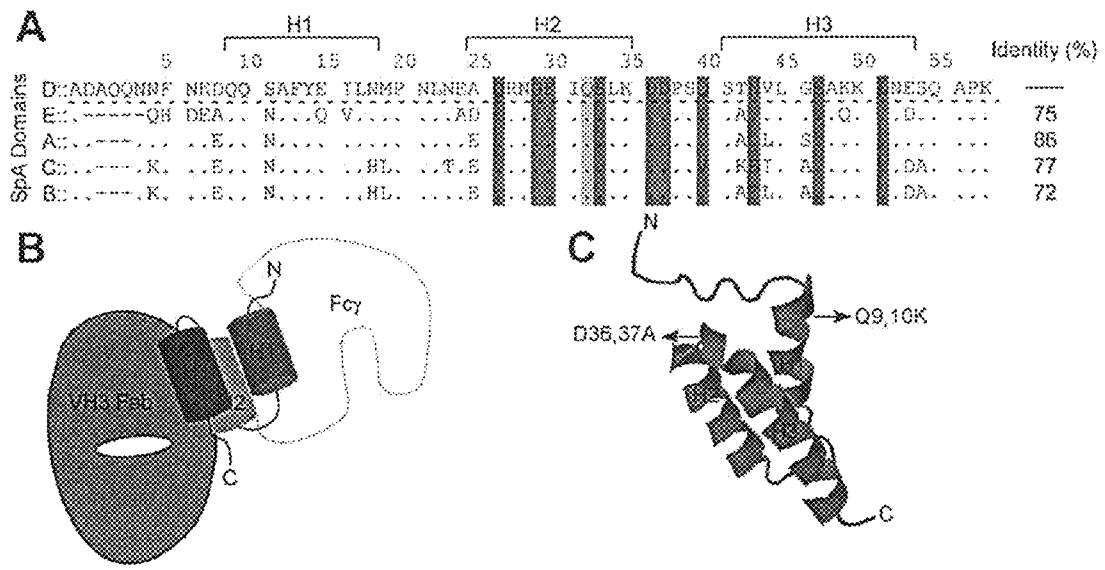


FIG. 2

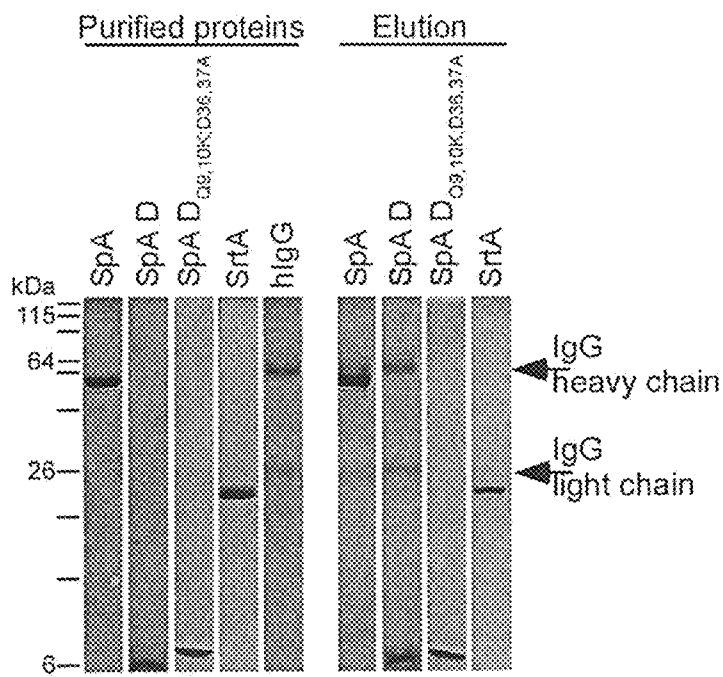


FIG. 3

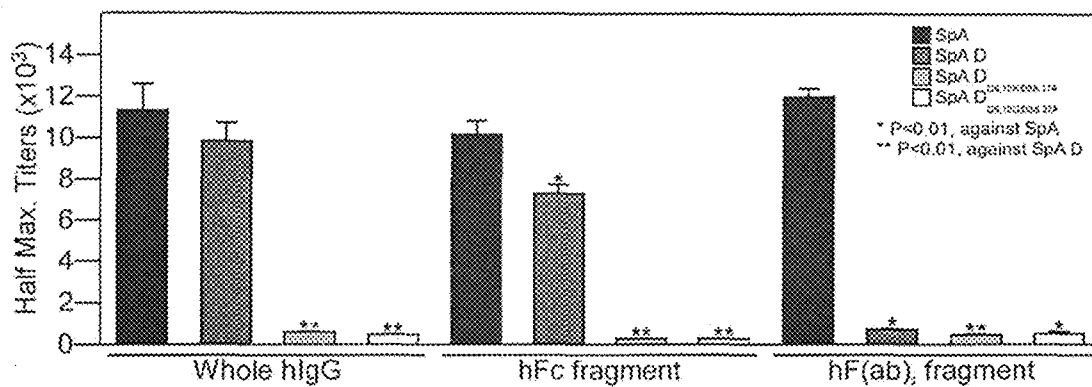


FIG. 4

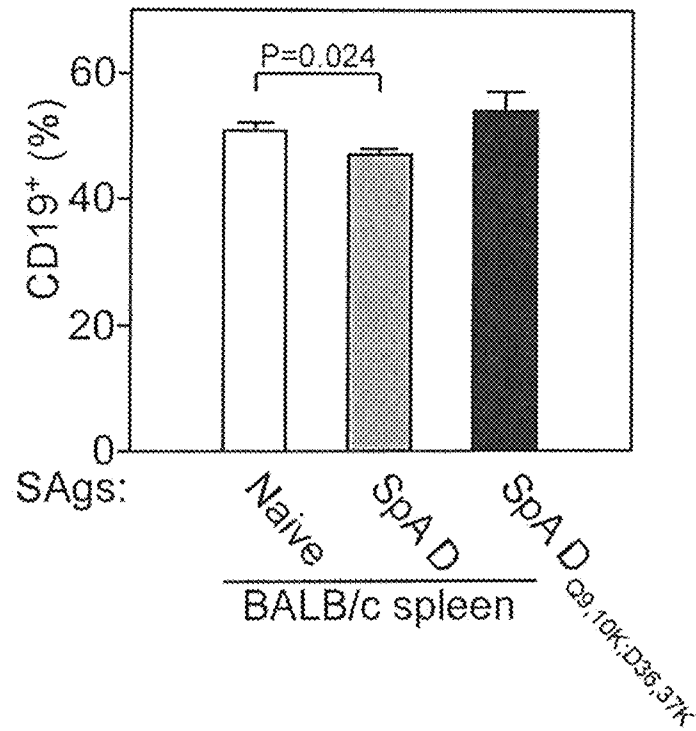


FIG. 5

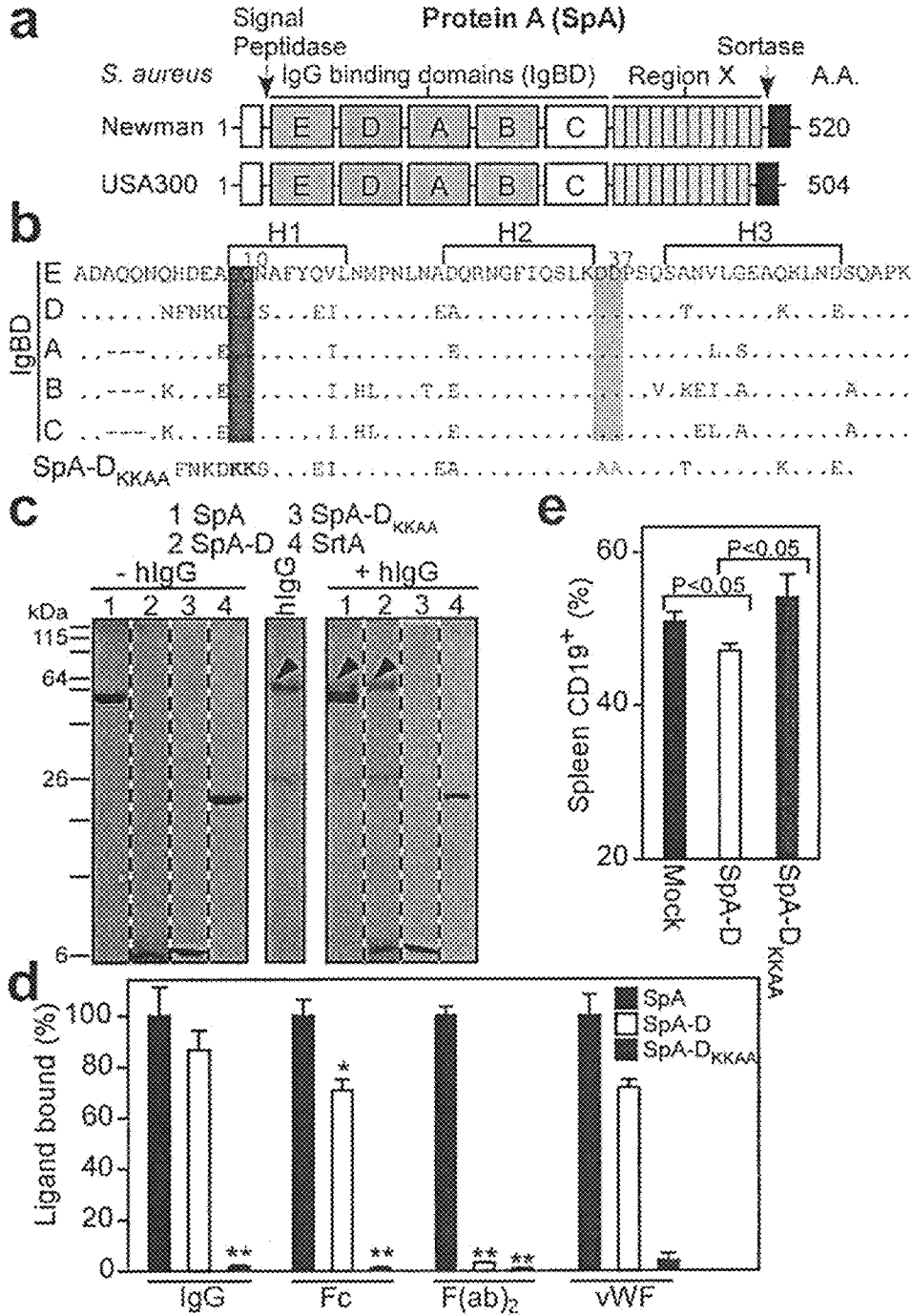


FIG. 6

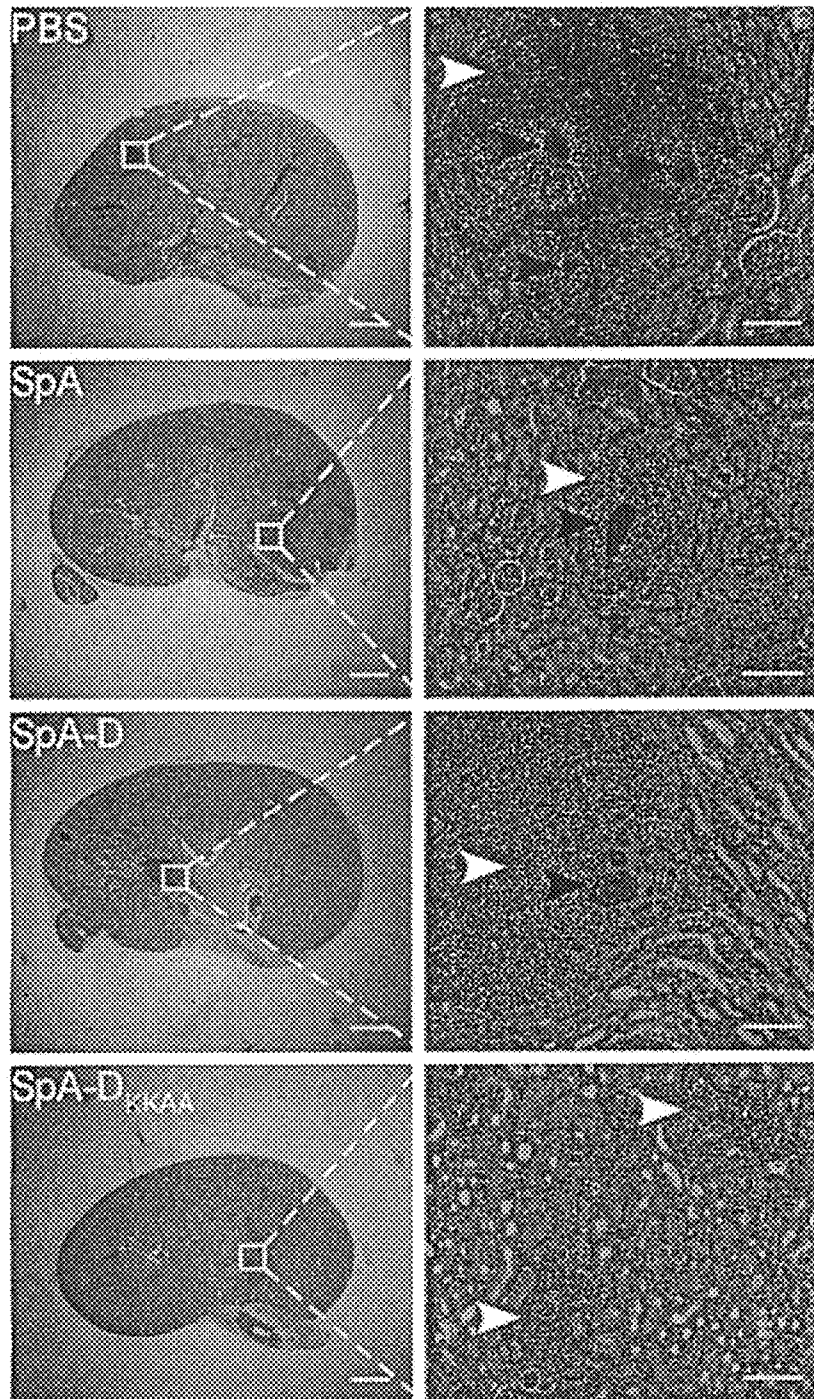


FIG. 7

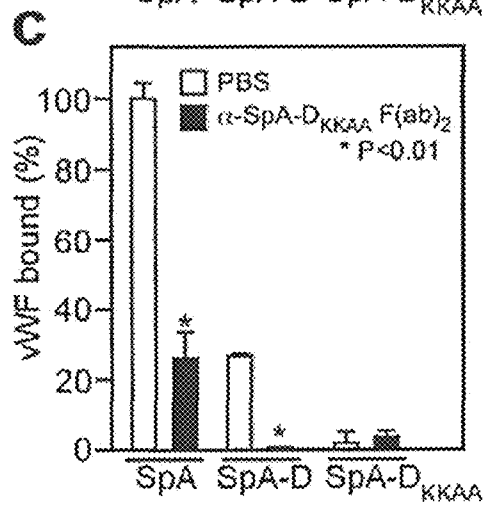
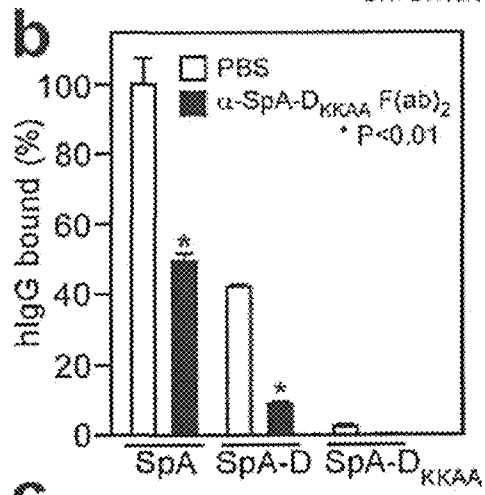
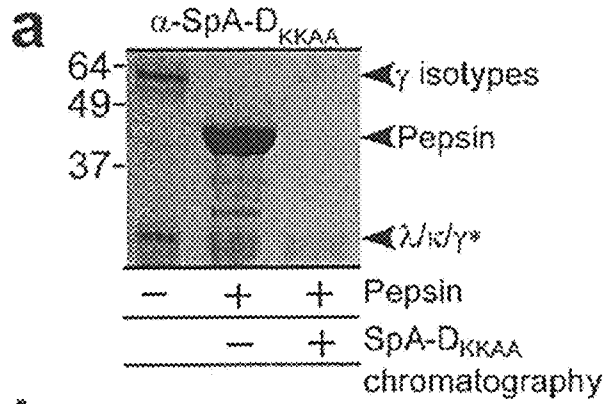


FIG. 8



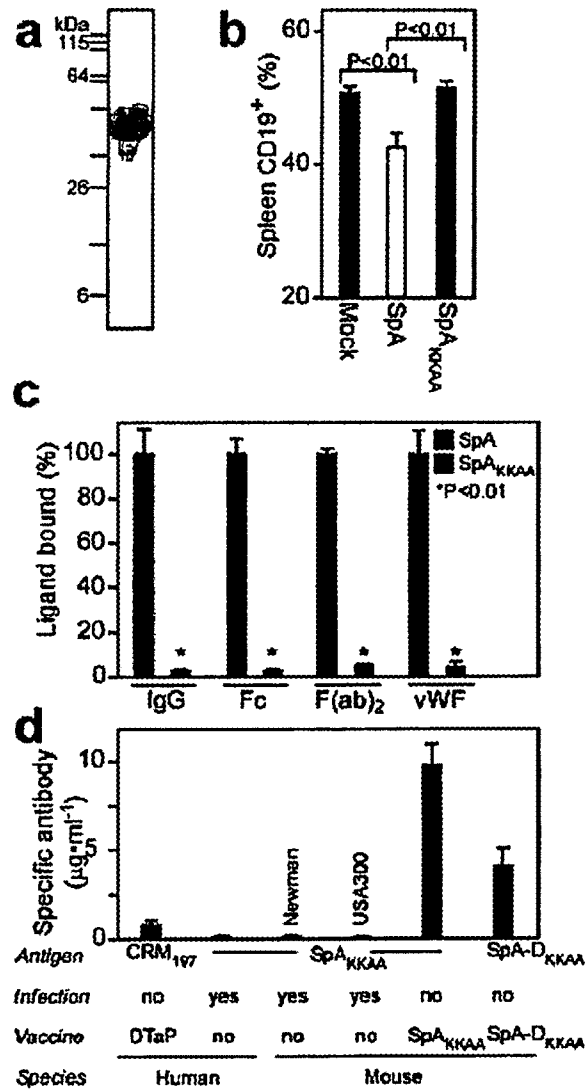


FIG. 9

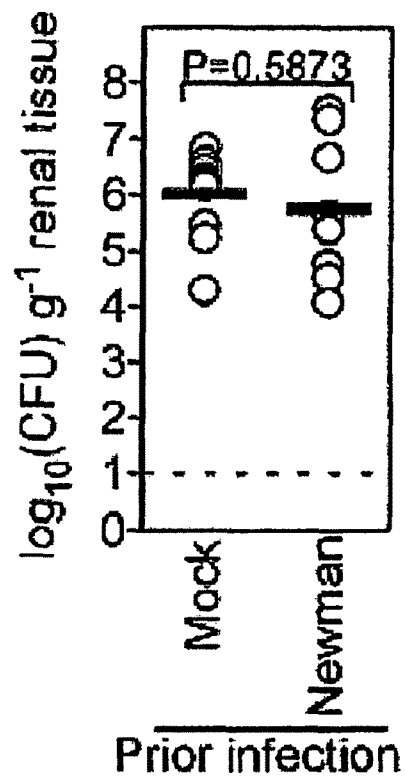


FIG. 10

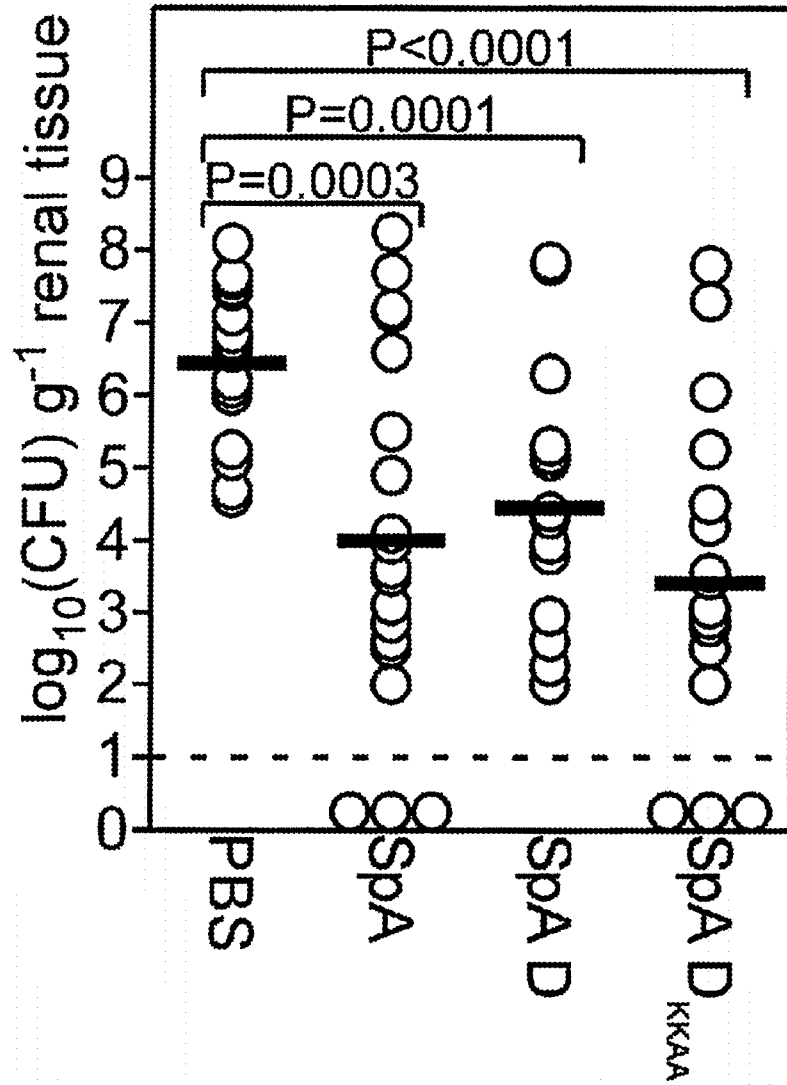


FIG. 11

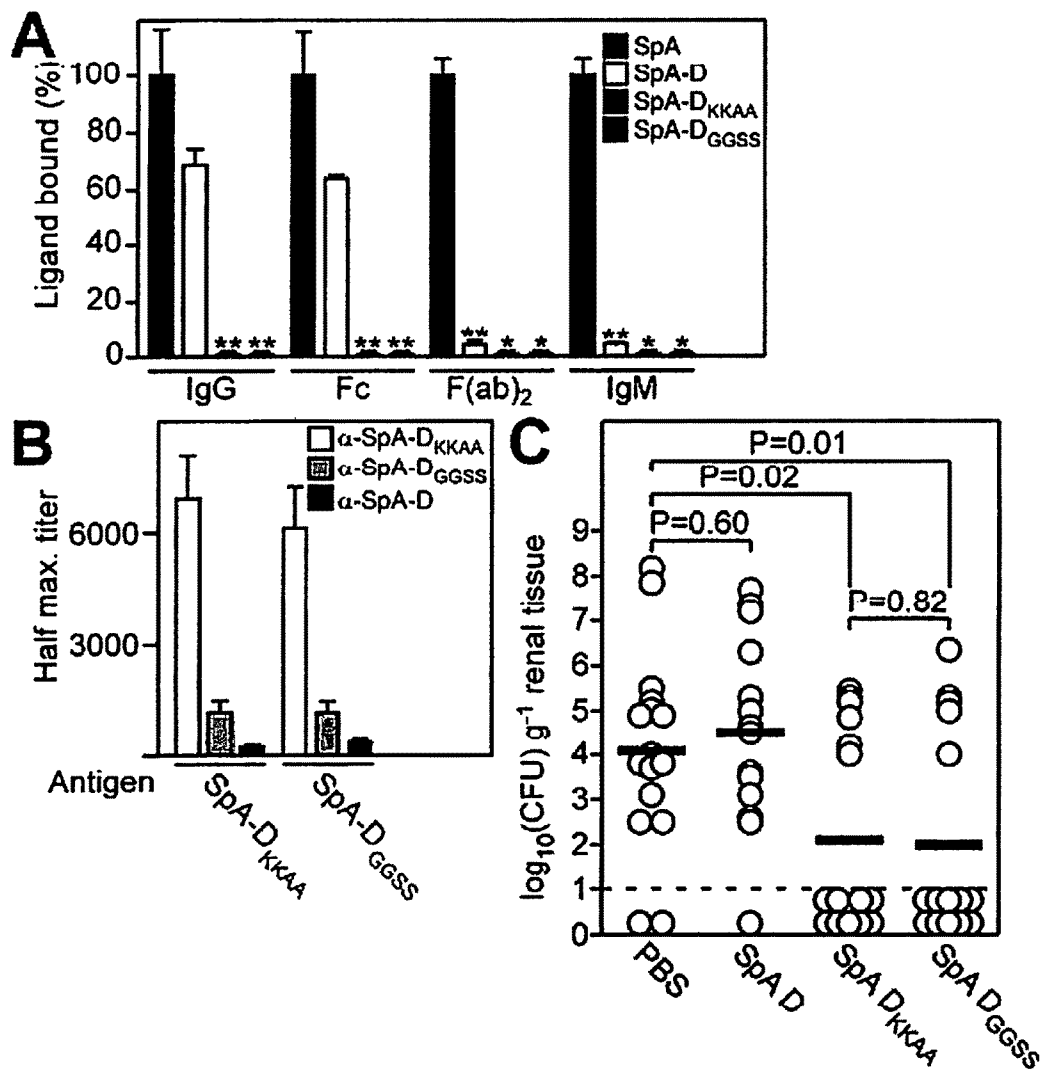


FIG. 12A-12C

## COMPOSITIONS AND METHODS RELATED TO PROTEIN A (SPA) VARIANTS

The present application is a continuation of U.S. patent application Ser. No. 13/807,598, now U.S. Pat. No. 8,821,894 filed Mar. 19, 2013, which is a national phase application under 35 U.S.C. §371 of International Patent 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, all of which are hereby incorporated by reference in their entirety.

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

#### I. Field of the Invention

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

#### II. Background

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

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

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

*Staphylococcus epidermidis* is a normal skin commensal which is also an important opportunistic pathogen responsible for infections of impaired medical devices and infections at sites of surgery. Medical devices infected by *S. epidermidis* include cardiac pacemakers, cerebrospinal fluid shunts, continuous ambulatory peritoneal dialysis catheters, orthopedic devices and prosthetic heart valves.

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

ing. Problematically, Methicillin-resistant *Staphylococcus aureus* (MRSA) has become a major cause of hospital-acquired infections.

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

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

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

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

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

### SUMMARY OF THE INVENTION

Protein A (SpA)(SEQ ID NO:33), a cell wall anchored surface protein of *Staphylococcus aureus*, provides for bacterial evasion from innate and adaptive immune responses. Protein A binds immunoglobulins at their Fc portion, interacts with the VH3 domain of B cell receptors inappropriately stimulating B cell proliferation and apoptosis, binds to von Willebrand factor A1 domains to activate intracellular clotting, and also binds to the TNF Receptor-1 to contribute to the pathogenesis of staphylococcal pneumonia. Due to the fact that Protein A captures immunoglobulin and displays toxic

attributes, the possibility that this surface molecule may function as a vaccine in humans has not been rigorously pursued. Here the inventors demonstrate that Protein A variants no longer able to bind to immunoglobulins, which are thereby removed of their toxigenic potential, i.e., are non-toxigenic, stimulate humoral immune responses that protect against staphylococcal disease.

In certain embodiments the SpA variant is a full length SpA variant comprising a variant A, B, C, D, and/or E domain. In certain aspects, the SpA variant comprises or consists of the amino acid sequence that is 80, 90, 95, 98, 99, or 100% identical to the amino acid sequence of SEQ ID NO:34. In other embodiments the SpA variant comprises a segment of SpA. The SpA segment can comprise at least or at most 1, 2, 3, 4, 5 or more IgG binding domains. The IgG domains can be at least or at most 1, 2, 3, 4, 5 or more variant A, B, C, D, or E domains. In certain aspects the SpA variant comprises at least or at most 1, 2, 3, 4, 5, or more variant A domains. In a further aspect the SpA variant comprises at least or at most 1, 2, 3, 4, 5, or more variant B domains. In still a further aspect the SpA variant comprises at least or at most 1, 2, 3, 4, 5, or more variant C domains. In yet a further aspect the SpA variant comprises at least or at most 1, 2, 3, 4, 5, or more variant D domains. In certain aspects the SpA variant comprises at least or at most 1, 2, 3, 4, 5, or more variant E domains. In a further aspect the SpA variant comprises a combination of A, B, C, D, and E domains in various combinations and permutations. The combinations can include all or part of a SpA signal peptide segment, a SpA region X segment, and/or a SpA sorting signal segment. In other aspects the SpA variant does not include a SpA signal peptide segment, a SpA region X segment, and/or a SpA sorting signal segment. In certain aspects a variant A domain comprises a substitution at position(s) 7, 8, 34, and/or 35 of SEQ ID NO:4. In another aspect a variant B domain comprises a substitution at position(s) 7, 8, 34, and/or 35 of SEQ ID NO:6. In still another aspect a variant C domain comprises a substitution at position(s) 7, 8, 34, and/or 35 of SEQ ID NO:5. In certain aspects a variant D domain comprises a substitution at position(s) 9, 10, 36, and/or 37 of SEQ ID NO:2. In a further aspect a variant E domain comprises a substitution at position(s) 6, 7, 33, and/or 34 of SEQ ID NO:3.

In certain aspects, an SpA domain D variant or its equivalent can comprise a mutation at position 9 and 36; 9 and 37; 9 and 10; 36 and 37; 10 and 36; 10 and 37; 9, 36, and 37; 10, 36, and 37; 9, 10 and 36; or 9, 10 and 37 of SEQ ID NO:2. In a further aspect, analogous mutations can be included in one or more of domains A, B, C, or E.

In further aspects, the amino acid glutamine (Q) at position 9 of SEQ ID NO:2 (or its analogous amino acid in other SpA domains) can be replaced with an alanine (A), an asparagine (N), an aspartic acid (D), a cysteine (C), a glutamic acid (E), a phenylalanine (F), a glycine (G), a histidine (H), an isoleucine (I), a lysine (K), a leucine (L), a methionine (M), a proline (P), a serine (S), a threonine (T), a valine (V), a tryptophane (W), or a tyrosine (Y). In some aspects the glutamine at position 9 can be substituted with an arginine (R). In a further aspect, the glutamine at position 9 of SEQ ID NO:2, or its equivalent, can be substituted with a lysine or a glycine. Any 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more of the substitutions can be explicitly excluded.

In another aspect, the amino acid glutamine (Q) at position 10 of SEQ ID NO:2 (or its analogous amino acid in other SpA domains) can be replaced with an alanine (A), an asparagine (N), an aspartic acid (D), a cysteine (C), a glutamic acid (E), a phenylalanine (F), a glycine (G), a histidine (H), an isoleucine (I), a lysine (K), a leucine (L), a methionine (M), a

proline (P), a serine (S), a threonine (T), a valine (V), a tryptophane (W), or a tyrosine (Y). In some aspects the glutamine at position 10 can be substituted with an arginine (R). In a further aspect, the glutamine at position 10 of SEQ ID NO:2, or its equivalent, can be substituted with a lysine or a glycine. Any 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more of the substitutions can be explicitly excluded.

In certain aspects, the aspartic acid (D) at position 36 of SEQ ID NO:2 (or its analogous amino acid in other SpA domains) can be replaced with an alanine (A), an asparagine (N), an arginine (R), a cysteine (C), a phenylalanine (F), a glycine (G), a histidine (H), an isoleucine (I), a lysine (K), a leucine (L), a methionine (M), a proline (P), a glutamine (Q), a serine (S), a threonine (T), a valine (V), a tryptophane (W), or a tyrosine (Y). In some aspects the aspartic acid at position 36 can be substituted with a glutamic acid (E). In certain aspects, an aspartic acid at position 36 of SEQ ID NO:2, or its equivalent, can be substituted with an alanine or a serine. Any 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more of the substitutions can be explicitly excluded.

In another aspect, the aspartic acid (D) at position 37 of SEQ ID NO:2 (or its analogous amino acid in other SpA domains) can be replaced with an alanine (A), an asparagine (N), an arginine (R), a cysteine (C), a phenylalanine (F), a glycine (G), a histidine (H), an isoleucine (I), a lysine (K), a leucine (L), a methionine (M), a proline (P), a glutamine (Q), a serine (S), a threonine (T), a valine (V), a tryptophane (W), or a tyrosine (Y). In some aspects the aspartic acid at position 37 can be substituted with a glutamic acid (E). In certain aspects, an aspartic acid at position 37 of SEQ ID NO:2, or its equivalent, can be substituted with an alanine or a serine. Any 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more of the substitutions can be explicitly excluded.

In a particular embodiment the amino at position 9 of SEQ ID NO:2 (or an analogous amino acid in another SpA domain) is replaced by an alanine (A), a glycine (G), an isoleucine (I), a leucine (L), a proline (P), a serine (S), or a valine (V). In certain aspects the amino acid at position 9 of SEQ ID NO:2 is replaced by a glycine. In a further aspect the amino acid at position 9 of SEQ ID NO:2 is replaced by a lysine.

In a particular embodiment the amino at position 10 of SEQ ID NO:2 (or an analogous amino acid in another SpA domain) is replaced by an alanine (A), a glycine (G), an isoleucine (I), a leucine (L), a proline (P), a serine (S), or a valine (V). In certain aspects the amino acid at position 10 of SEQ ID NO:2 is replaced by a glycine. In a further aspect the amino acid at position 10 of SEQ ID NO:2 is replaced by a lysine.

In a particular embodiment the amino at position 36 of SEQ ID NO:2 (or an analogous amino acid in another SpA domain) is replaced by an alanine (A), a glycine (G), an isoleucine (I), a leucine (L), a proline (P), a serine (S), or a valine (V). In certain aspects the amino acid at position 36 of SEQ ID NO:2 is replaced by a serine. In a further aspect the amino acid at position 36 of SEQ ID NO:2 is replaced by an alanine.

In a particular embodiment the amino at position 37 of SEQ ID NO:2 (or an analogous amino acid in another SpA domain) is replaced by an alanine (A), a glycine (G), an isoleucine (I), a leucine (L), a proline (P), a serine (S), or a valine (V). In certain aspects the amino acid at position 37 of SEQ ID NO:2 is replaced by a serine. In a further aspect the amino acid at position 37 of SEQ ID NO:2 is replaced by an alanine.

In certain aspects the SpA variant includes a substitution of (a) one or more amino acid substitution in an IgG Fc binding sub-domain of SpA domain A, B, C, D, and/or E that disrupts or decreases binding to IgG Fc, and (b) one or more amino acid substitution in a  $V_H3$  binding sub-domain of SpA domain A, B, C, D, and/or E that disrupts or decreases binding

to  $V_H3$ . In still further aspects the amino acid sequence of a SpA variant comprises an amino acid sequence that is at least 50%, 60%, 70%, 80%, 90%, 95%, or 100% identical, including all values and ranges there between, to the amino acid sequence of SEQ ID NOs:2-6.

In a further aspect the SpA variant includes (a) one or more amino acid substitution in an IgG Fc binding sub-domain of SpA domain D, or at a corresponding amino acid position in other IgG domains, that disrupts or decreases binding to IgG Fc, and (b) one or more amino acid substitution in a  $V_H3$  binding sub-domain of SpA domain D, or at a corresponding amino acid position in other IgG domains, that disrupts or decreases binding to  $V_H3$ . In certain aspects amino acid residue F5, Q9, Q10, S11, F13, Y14, L17, N28, I31, and/or K35 (SEQ ID NO:2, QQNFNKDDQSAFYELNMPNL-NEAQRNGFIQSLKDDPSQSTNVLGEAKKLNES) 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.

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) Fc $\gamma$  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 infec-

tion 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.

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.

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, Ehb, Emp, EsaB, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, 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), FnbA, FnbB, GehD (US 2002/0169288), HarA, HBP, Immunodominant ABC transporter, IsaA/PisA, laminin receptor, Lipase GehD, MAP, Mg2+ transporter, MHC II analogue (U.S. Pat. No. 5,648,240), MRPII, Npase, RNA III activating protein (RAP), SasA, SasB, SasC, SasD, SasK, SBI, SdrF (WO 00/12689), SdrG/Fig (WO 00/12689), SdrH (WO 00/12689), SEA exotoxins (WO 00/02523), SEB exotoxins (WO 00/02523), SitC and Ni ABC transporter, SitC/MntC/saliva binding protein (U.S. Pat. No. 5,801,234), SsaA, SSP-1, SSP-2, and/or Vitronectin binding protein (see PCT publications WO2007/113222, WO2007/113223, WO2006/032472, WO2006/032475, WO2006/032500, each of which is incorporated herein by reference in their entirety). The staphylococcal antigen or immunogenic fragment can be administered concurrently with the Protein A variant. The staphylococcal antigen or immunogenic fragment and the Protein A variant can be administered in the same composition. The Protein A variant can also be a recombinant nucleic acid molecule encoding a Protein A variant. A recombinant nucleic acid molecule can encode the Protein A variant and at least one staphylococcal antigen or immunogenic fragment thereof. As used herein, the term “modulate” or “modulation” encompasses the meanings of the words “enhance,” or









TABLE 1-continued

SpA and staphylococcal antigen combinations.							
ClfA	+	+	+	+	+	+	+
ClfB		+	+	+	+	+	+
Coa			+	+	+	+	+
Hla				+	+	+	+
Hla <sub>H35.4</sub>					+	+	+
IsdC					+	+	+
SasF						+	+
vWbp							+
vWh							+
ClfB		+	+	+	+	+	+
Coa			+	+	+	+	+
Hla				+	+	+	+
Hla <sub>H35.4</sub>					+	+	+
IsdC					+	+	+
SasF						+	+
vWbp							+
vWh							+
Coa			+	+	+	+	+
Hla				+	+	+	+
Hla <sub>H35.4</sub>					+	+	+
IsdC					+	+	+
SasF						+	+
vWbp							+
vWh							+
Hla				+	+	+	+
Hla <sub>H35.4</sub>					+	+	+
IsdC					+	+	+
SasF						+	+
vWbp							+
vWh							+
Hla <sub>H35.4</sub>				+	+	+	+
IsdC					+	+	+
SasF						+	+
vWbp							+
vWh							+
IsdC					+	+	+
SasF						+	+
vWbp							+
vWh							+
SasF						+	+
vWbp							+
vWh							+
vWbp						+	+
vWh							+
vWh							+

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, ClfB, 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, Mg<sup>2+</sup> 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.

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.

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, Ehb, 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, 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.

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.

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*.

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.

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.

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, Ehb, 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 com-

prises 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.

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.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

In yet still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an SdrD protein. In certain aspects the SdrD protein will have all or part of the amino acid sequence of SEQ ID NO:13.

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

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

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

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

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

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

In yet further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or

99% identical or similar to a SasF protein. In certain aspects the SasF protein will have all or part of the amino acid sequence of SEQ ID NO:20.

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

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

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

In yet still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an Ehb protein. In certain aspects the Ehb protein will have all or part of the amino acid sequence of SEQ ID NO:24.

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

In yet still further embodiments of the invention a composition may include a polypeptide, peptide, or protein that is or is at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical or similar to an EsaC protein. In certain aspects the EsaC protein will have all or part of the amino acid sequence of SEQ ID NO:26. Sequence of EsaC polypeptides can be found in the protein databases and include, but are not limited to accession numbers ZP\_02760162 (GI:168727885), NP\_645081.1 (GI:21281993), and NP\_370813.1 (GI:15923279), each of which is incorporated herein by reference as of the priority date of this application.

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

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

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

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

aspects the vWbp protein will have all or part of the amino acid sequence of SEQ ID NO:32.

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

The 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.

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.

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

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

In still further embodiments, a composition comprises a recombinant nucleic acid molecule encoding a polypeptide described herein or segments/fragments thereof. Typically a

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

In further embodiments a composition comprises a recombinant nucleic acid molecule encoding all or part of one or more of a Eap, Ebh, Emp, EsaB, EsaC, EsxA, EsxB, SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, Coa, Hla, IsdC, SasF, SpA, vWbp, or vWh protein or peptide or variant thereof. Additional staphylococcal antigens that can be used in combination with the polypeptides described herein include, but are not limited to 52 kDa vitronectin binding protein (WO 01/60852), Aaa, Aap, Ant, autolysin glucosaminidase, autolysin amidase, Cna, collagen binding protein (U.S. Pat. No. 6,288,214), EFB (FIB), Elastin binding protein (EbpS), EPB, FbpA, fibrinogen binding protein (U.S. Pat. No. 6,008,341), Fibronectin binding protein (U.S. Pat. No. 5,840,846), FnbA, FnbB, GehD (US 2002/0169288), HarA, HBP, Immunodominant ABC transporter, IsaA/PisA, laminin receptor, Lipase GehD, MAP, Mg2+ transporter, MHC II analogue (U.S. Pat. No. 5,648,240), MRPII, Npase, RNA III activating protein (RAP), SasA, SasB, SasC, SasD, SasK, SBI, SdrF (WO 00/12689), SdrG/Fig (WO 00/12689), SdrH (WO 00/12689), SEA exotoxins (WO 00/02523), SEB exotoxins (WO 00/02523), SitC and Ni ABC transporter, SitC/MntC/saliva binding protein (U.S. Pat. No. 5,801,234), SsaA, SSP-1, SSP-2, and/or Vitronectin binding protein. In particular aspects, a bacteria is a recombinant non-*staphylococcus* bacteria, such as a *Salmonella* or other gram-positive bacteria.

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.

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

Any embodiment discussed with respect to one aspect of the invention applies to other aspects of the invention as well. In particular, any embodiment discussed in the context of a SpA variant polypeptide 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, MHC II analogue (U.S. Pat. No. 5,648,240), MRPII, Npase, RNA III activating protein (RAP), SasA, SasB, SasC, SasD, SasK, SBI, SdrF (WO 00/12689), SdrG/ Fig (WO 00/12689), SdrH (WO 00/12689), SEA exotoxins (WO 00/02523), SEB exotoxins (WO 00/02523), SitC and Ni ABC transporter, SitC/MntC/saliva binding protein (U.S. Pat. No. 5,801,234), SsaA, SSP-1, SSP-2, and/or Vitronectin binding protein (or nucleic acids), 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.

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

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

Moieties of the invention, such as polypeptides, peptides, antigens, or immunogens, may be conjugated or linked covalently or noncovalently to other moieties such as adjuvants, proteins, peptides, supports, fluorescence moieties, or labels. The term "conjugate" or "immunoconjugate" is broadly used to define the operative association of one moiety

with another agent and is not intended to refer solely to any type of operative association, and is particularly not limited to chemical "conjugation." Recombinant fusion proteins are particularly contemplated. Compositions of the invention may further comprise an adjuvant or a pharmaceutically acceptable excipient. An adjuvant may be covalently or non-covalently coupled to a polypeptide or peptide of the invention. In certain aspects, the adjuvant is chemically conjugated to a protein, polypeptide, or peptide.

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

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

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

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

Throughout this application, the term "about" is used to indicate that a value includes the standard deviation of error for the device or method being employed to determine the value.

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

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

#### DESCRIPTION OF THE DRAWINGS

So that the matter in which the above-recited features, advantages and objects of the invention as well as others



which will become clear are attained and can be understood in detail, more particular descriptions and certain embodiments of the invention briefly summarized above are illustrated in the appended drawings. These drawings form a part of the specification. It is to be noted, however, that the appended drawings illustrate certain embodiments of the invention and therefore are not to be considered limiting in their scope.

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.

FIG. 2. 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 $\gamma$  domain of immunoglobulin. The model is derived from two crystal structures (Graillie 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 $\gamma$ , whereas Asp-36 and Asp-37 enable complex formation with VH3 Fab.

FIG. 3. Left panel—Coomassie Blue stained SDS-PAGE reveals the migrational position of purified His-tagged SpA, SpA-D, SpA-D<sub>Q9,10K;D36,37A</sub>, 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<sub>Q9,10K;D36,37A</sub> or SrtA.

FIG. 4. ELISA assays to quantify human immunoglobulin (hIgG), human F(ab)<sub>2</sub> IgG fragments and human Fc fragments of immunoglobulin (hFc). Plates were coated with equal amounts of His-tagged SpA, SpA-D, SpA-D<sub>Q9,10K;D36,37A</sub> or SrtA. hIgG-HRP, F(ab)<sub>2</sub>-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.

FIG. 5. Purified SpA-D, SpA-D<sub>Q9,10K;D36,37A</sub> 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.

FIG. 6 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<sub>KKAA</sub>, with the positions of triple  $\alpha$ -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<sub>KKAA</sub> 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<sub>KKAA</sub> with human IgG as well as its Fc or F(ab)<sub>2</sub> fragments and von Willebrand factor (vWF). e, CD19+B lympho-

cytes in splenic tissue of BALB/c mice that had been mock immunized or treated with SpA-D or SpA-D<sub>KKAA</sub> were quantified by FACS.

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<sub>KKAA</sub> 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.

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

FIG. 9 Full-length non-toxicogenic protein A generates improved immune responses. a, Full-length SpA<sub>KKAA</sub> 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<sub>KKAA</sub> were quantified by FACS. c, ELISA examining the association of immobilized SpA or SpA<sub>KKAA</sub> with human IgG as well as its Fc or F(ab)<sub>2</sub> fragments or von Willebrand factor (vWF). d, Human or mouse serum antibody titers to diphtheria toxoid (CRM197) and non-toxicogenic SpA<sub>KKAA</sub> or SpA-D<sub>KKAA</sub>. 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<sub>KKAA</sub> or SpA-D<sub>KKAA</sub> were examined by quantitative dot blot.

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.

FIG. 11 Comparison of abscess formation in mice treated with PBS, SpA, SpA-D, and SpA-D<sub>KKAA</sub>.

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)<sub>2</sub> 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 hyper-immune 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<sub>KKAA</sub> and SpA-D<sub>GGSS</sub>.

#### DETAILED DESCRIPTION

*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.

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

### A. Staphylococcal Protein A (SpA)

All *Staphylococcus aureus* strains express the structural gene for Protein A (*spa*) (Jensen, 1958; Said-Salim et al., 2003), a well characterized virulence factor whose cell wall anchored surface protein product (SpA) encompasses five highly homologous immunoglobulin binding domains designated E, D, A, B, and C (Sjodahl, 1977). These domains display ~80% identity at the amino acid level, are 56 to 61 residues in length, and are organized as tandem repeats (Uhlen et al., 1984). SpA is synthesized as a precursor protein with an N-terminal YSIRK/GS signal peptide and a C-terminal LPXTG motif sorting signal (DeDent et al., 2008; Schneewind et al., 1992). Cell wall anchored Protein A is displayed in great abundance on the staphylococcal surface (DeDent et al., 2007; Sjoquist et al., 1972). Each of its immunoglobulin binding domains is composed of anti-parallel  $\alpha$ -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  $\alpha$  (TNF- $\alpha$ ) receptor I (TNFRI) (Gomez et al., 2006), which is displayed on surfaces of airway epithelia (Gomez et al., 2004; Gomez et al., 2007).

SpA impedes neutrophil phagocytosis of staphylococci through its attribute of binding the Fc component of IgG (Jensen, 1958; Uhlen et al., 1984). Moreover, SpA is able to activate intravascular clotting via its binding to von Willibrand factor A1 domains (Hartleib et al., 2000). Plasma proteins such as fibrinogen and fibronectin act as bridges between staphylococci (ClfA and ClfB) and the platelet integrin GPIIb/IIIa (O'Brien et al., 2002), an activity that is supplemented through Protein A association with vWF A1,

which allows staphylococci to capture platelets via the GPIIb- $\alpha$  platelet receptor (Foster, 2005; O'Seaghda et al., 2006). SpA also binds TNFRI and this interaction contributes to the pathogenesis of staphylococcal pneumonia (Gomez et al., 2004). SpA activates proinflammatory signaling through TNFR1 mediated activation of TRAF2, the p38/c-Jun kinase, mitogen activate protein kinase (MAPK) and the Rel-transcription factor NF-KB. SpA binding further induces TNFR1 shedding, an activity that appears to require the TNF-converting enzyme (TACE) (Gomez et al., 2007). All of the aforementioned SpA activities are mediated through its five IgG binding domains and can be perturbed by the same amino acid substitutions, initially defined by their requirement for the interaction between Protein A and human IgG1 (Cedergren et al., 1993).

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

In previous studies, Cedergren et al. (1993) engineered five individual substitutions in the Fc fragment binding sub-domain of the B domain of SpA, L17D, N28A, I31A and K35A. These authors created these proteins to test data gathered from a three dimensional structure of a complex between one domain of SpA and Fc<sub>1</sub>. Cedergren et al. determined the effects of these mutations on stability and binding, but did not contemplate use of such substitutions for the production of a vaccine antigen.

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

Graille et al. (2000) describe a crystal structure of domain D of SpA and the Fab fragment of a human IgM antibody. Graille et al. define by analysis of a crystal structure the D

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

O'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.

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

Recombinant affinity tagged Protein A, a polypeptide encompassing the five IgG domains (EDCAB) (Sjodahl, 1977) but lacking the C-terminal Region X (Guss et al., 1984), was purified from recombinant *E. coli* and used as a vaccine antigen (Stranger-Jones et al., 2006). Because of the attributes of SpA in binding the Fc portion of IgG, a specific humoral immune response to Protein A could not be measured (Stranger-Jones et al., 2006). The inventors have overcome this obstacle through the generation of SpA-DQ9,10K; D36,37A. BALB/c mice immunized with recombinant Protein A (SpA) displayed significant protection against intravenous challenge with *S. aureus* strains: a 2.951 log reduction in staphylococcal load as compared to the wild-type ( $P > 0.005$ ; Student's t-test) (Stranger-Jones et al., 2006). SpA specific antibodies may cause phagocytic clearance prior to abscess formation and/or impact the formation of the aforementioned eosinophilic barrier in abscesses that separate staphylococcal communities from immune cells since these do not form during infection with Protein A mutant strains. Each of the five SpA domains (i.e., domains formed from three helix bundles designated E, D, A, B, and C) exerts similar binding properties (Jansson et al., 1998). The solution and crystal structure of the domain D has been solved both with and without the Fc and VH3 (Fab) ligands, which bind Protein A in a non-competitive manner at distinct sites (Graille et al., 2000). Mutations in residues known to be involved in IgG binding (FS, Q9, Q10, S11, F13, Y14, L17, N28, I31 and K35) are also required for vWF AI 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).

Molecular Basis of Protein A Surface Display and Function.

Protein A is synthesized as a precursor in the bacterial cytoplasm and secreted via its YSIRK signal peptide at the cross wall, i.e. the cell division septum of staphylococci (FIG. 1) (DeDent et al., 2007; DeDent et al., 2008). Following cleavage of the C-terminal LPXTG sorting signal, Protein A is anchored to bacterial peptidoglycan 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).

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<sub>H</sub>3 (Fab) ligands, which bind Protein A in a non-competitive manner at distinct sites (Graille 2000).

In the crystal structure complex, the Fab interacts with helix II and helix III of domain D via a surface composed of four VH region  $\beta$ -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.

The SpA-D sites responsible for Fab binding are structurally separate from the domain surface that mediates Fc $\gamma$  binding. The interaction of Fc $\gamma$  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 $\gamma$  interaction are involved in Fab binding. To examine the spatial relationship between these different Ig-binding sites, the SpA domains in these com-

plexes have been superimposed to construct a model of a complex between Fab, the SpA-domain D, and the Fc $\gamma$  molecule. In this ternary model, Fab and Fc $\gamma$  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 $\gamma$  are Gln-9 and Gln-10.

In contrast, occupancy of the Fc portion of IgG on the domain D blocks its interaction with vWF A1 and probably also TNFR1 (O'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<sub>H</sub>3 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<sub>H</sub>3 family represents the largest family of human B cell receptors to impart protective humoral responses against pathogens (Goodyear and Silverman, 2004; Goodyear and Silverman, 2003). Thus, Protein A functions analogously to staphylococcal superantigens (Roben et al., 1995), albeit that the latter class of molecules, for example SEB, TSST-1, TSST-2, form complexes with the T cell receptor to inappropriately stimulate host immune responses and thereby precipitating characteristic disease features of staphylococcal infections (Roben et al., 1995; Tiedemann et al., 1995). Together these findings document the contributions of Protein A in establishing staphylococcal infections and in modulating host immune responses.

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

rabbits and analyzed for [1] the production of specific antibodies (SpA-D Ab); [2] the ability of SpA-D Ab to block the association between Protein A and its four different ligands; and, [3] the attributes of SpA-D Ab to generate protective immunity against staphylococcal infections. (See Examples section below).

### B. Staphylococcal Coagulases

Coagulases are enzymes produced by *Staphylococcus* bacteria that convert fibrinogen to fibrin. Coa and vW<sub>B</sub> 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-Val<sup>2</sup> N-terminus into the Ile<sup>16</sup> pocket, inducing a functional active site in the zymogen through conformational change (Friedrich et al., 2003). Exosite I of  $\alpha$ -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)<sub>2</sub> complex binds fibrinogen at a new site with high affinity (Panizzi et al., 2006). This model explains the coagulant properties and efficient fibrinogen conversion by coagulase (Panizzi et al., 2006).

Fibrinogen is a large glycoprotein (Mr ~340,000), formed by three pairs of  $\alpha$ -,  $\beta$ -, and  $\gamma$ -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  $\beta$ - and  $\gamma$ -chains. These globular domains are connected by long triple-helical structures. Coagulase-prothrombin complexes, which convert human fibrinogen to the self-polymerizing fibrin, are not targeted by circulating thrombin inhibitors (Panizzi et al., 2006). Thus, staphylococcal coagulases bypass the physiological blood coagulation pathway.

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

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

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

Earlier studies revealed a requirement of coagulase for resisting phagocytosis in blood (Smith et al., 1947) and the inventors observed a similar phenotype for  $\Delta$ 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  $\Delta$ 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,  $\Delta$ 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.

### C. Other Staphylococcal Antigens

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

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

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

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

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

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

The Esx polypeptides include the amino acid sequence of Esx proteins from bacteria in the *Staphylococcus* genus. The

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

The sortase substrate polypeptides include, but are not limited to the amino acid sequence of SdrC, SdrD, SdrE, IsdA, IsdB, ClfA, ClfB, IsdC or SasF proteins from bacteria in the *Staphylococcus* genus. The sortase substrate polypeptide sequence may be from a particular *staphylococcus* species, such as *Staphylococcus aureus*, and may be from a particular strain, such as Newman. In certain embodiments, the SdrD sequence is from strain N315 and can be accessed using Genbank Accession Number NP\_373773.1 (gil15926240), which is incorporated by reference. In other embodiments, the SdrE sequence is from strain N315 and can be accessed using Genbank Accession Number NP\_373774.1 (gil15926241), which is incorporated by reference. In other embodiments, the IsdA sequence is SAV1130 from strain Mu50 (which is the same amino acid sequence for Newman) and can be accessed using Genbank Accession Number NP\_371654.1 (gil15924120), which is incorporated by reference. In other embodiments, the IsdB sequence is SAV1129 from strain Mu50 (which is the same amino acid sequence for Newman) and can be accessed using Genbank Accession Number NP\_371653.1 (gil15924119), which is incorporated by reference. In further embodiments, other polypeptides transported by the Ess pathway or processed by sortase may be used, the sequences of which may be identified by one of skill in the art using databases and internet accessible resources.

Examples of various proteins that can be used in the context of the present invention can be identified by analysis of database submissions of bacterial genomes, including but not limited to accession numbers NC\_002951 (GI:57650036 and GenBank CP000046), NC\_002758 (GI:57634611 and GenBank BA000017), NC\_002745 (GI:29165615 and GenBank BA000018), NC\_003923 (GI:21281729 and GenBank BA000033), NC\_002952 (GI:49482253 and GenBank BX571856), NC\_002953 (GI:49484912 and GenBank BX571857), NC\_007793 (GI:87125858 and GenBank CP000255), NC\_007795 (GI:87201381 and GenBank CP000253) each of which are incorporated by reference.

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

that a modified/variant protein or polypeptide may be altered with respect to one activity or function yet retain a wild-type activity or function in other respects, such as immunogenicity.

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

As used herein, an "amino molecule" refers to any amino acid, amino acid derivative, or amino acid mimic known in the art. In certain embodiments, the residues of the proteinaceous molecule are sequential, without any non-amino molecule interrupting the sequence of amino molecule residues. In other embodiments, the sequence may comprise one or more non-amino molecule moieties. In particular embodiments, the sequence of residues of the proteinaceous molecule may be interrupted by one or more non-amino molecule moieties. Accordingly, the term "proteinaceous composition" encompasses amino molecule sequences comprising at least one of the 20 common amino acids in naturally synthesized proteins, or at least one modified or unusual amino acid.

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

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

tide processed or secreted by the Ess pathway or other surface proteins (see Table 1) or sortase substrates from any *staphylococcus* species and strain are contemplated for use in compositions and methods described herein.

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

Substitutional variants typically contain the exchange of one amino acid for another at one or more sites within the protein, and may be designed to modulate one or more properties of the polypeptide, with or without the loss of other functions or properties. Substitutions may be conservative, that is, one amino acid is replaced with one of similar shape and charge. Conservative substitutions are well known in the art and include, for example, the changes of: alanine to serine; arginine to lysine; asparagine to glutamine or histidine; aspartate to glutamate; cysteine to serine; glutamine to asparagine; glutamate to aspartate; glycine to proline; histidine to asparagine or glutamine; isoleucine to leucine or valine; leucine to valine or isoleucine; lysine to arginine; methionine to leucine or isoleucine; phenylalanine to tyrosine, leucine or methionine; serine to threonine; threonine to serine; tryptophan to tyrosine; tyrosine to tryptophan or phenylalanine; and valine to isoleucine or leucine. Alternatively, substitutions may be non-conservative such that a function or activity of the polypeptide is affected. Non-conservative changes typically involve substituting a residue with one that is chemically dissimilar, such as a polar or charged amino acid for a non-polar 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	Can	1183	—	—	—	1183	1183
SAV0561	SA0519	SdrC	955	953	953	947	906	957
SAV0562	SA0520	SdrD	1347	1385	1385	1315	—	1365
SAV0563	SA0521	SdrE	1141	1141	1141	1166	1137	1141
Np	Np	Pls	—	—	—	—	—	—
SAV2654	SA2447	SasA	2275	2271	2271	2271	1351	2275
SAV2160	SA1964	SasB	686	2481	2481	2481	2222	685
	SA1577	SasC	2186	213	2186	2186	2189	2186
SAV0134	SA0129	SasD	241	241	241	241	221	241
SAV1130	SA0977	SasE/IsdA	350	350	350	350	354	350
SAV2646	SA2439	SasF	635	635	635	635	627	635
SAV2496		SasG	1371	525	927	—	—	1371
SAV0023	SA0022	SasH	772	—	772	772	786	786
SAV1731	SA1552	SasI	895	891	891	891	534	895
SAV1129	SA0976	SasJ/IsdB	645	645	645	645	652	645
	SA2381	SasK	198	211	211	—	—	197
	Np	SasL	—	232	—	—	—	—
SAV1131	SA0978	IsdC	227	227	227	227	227	227

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

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

TABLE 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

TABLE 3-continued

Codon Table	
Amino Acids	Codons
Asparagine	AsnN AAC AAU
Proline	ProP CCA CCC CCG CCU
Glutamine	GlnQ CAA CAG
Arginine	ArgR AGA AGG CGA CGC CGG CGU
Serine	SerS AGC AGU UCA UCC UCG UCU
Threonine	ThrT ACA ACC ACG ACU
Valine	ValV GUA GUC GUG GUU
Tryptophan	TrpW UGG
Tyrosine	TyrY UAC UAU

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

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

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

The present invention contemplates the administration of variant SpA polypeptides or peptides to effect a preventative

therapy or therapeutic effect against the development of a disease or condition associated with infection by a *staphylococcus* pathogen.

In certain aspects, combinations of staphylococcal antigens are used in the production of an immunogenic composition that is effective at treating or preventing staphylococcal infection. Staphylococcal infections progress through several different stages. For example, the staphylococcal life cycle involves commensal colonization, initiation of infection by accessing adjoining tissues or the bloodstream, and/or anaerobic multiplication in the blood. The interplay between *S. aureus* virulence determinants and the host defense mechanisms can induce complications such as endocarditis, metastatic abscess formation, and sepsis syndrome. Different molecules on the surface of the bacterium are involved in different steps of the infection cycle. Combinations of certain antigens can elicit an immune response which protects against multiple stages of staphylococcal infection. The effectiveness of the immune response can be measured either in animal model assays and/or using an opsonophagocytic assay.

#### D. Polypeptides and Polypeptide Production

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

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

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

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



priate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed.

A number of selection systems may be used including, but not limited to HSV thymidine kinase, hypoxanthine-guanine phosphoribosyltransferase, and adenine phosphoribosyltransferase genes, in tk-, hgprt- or aprt-cells, respectively. Also, anti-metabolite resistance can be used as the basis of selection: for dhfr, which confers resistance to trimethoprim and methotrexate; gpt, which confers resistance to mycophenolic acid; neo, which confers resistance to the aminoglycoside G418; and hygro, which confers resistance to hygromycin.

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

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

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

Also included in immunogenic compositions of the invention are fusion proteins composed of one or more Staphylococcal proteins, or immunogenic fragments of staphylococcal proteins. Such fusion proteins may be made recombinantly and may comprise one portion of at least 1, 2, 3, 4, 5, or 6 staphylococcal proteins or segments. Alternatively, a fusion protein may comprise multiple portions of at least 1, 2, 3, 4 or 5 staphylococcal proteins. These may combine different Staphylococcal proteins and/or multiples of the same protein or protein fragment, or immunogenic fragments in the same protein (forming a multimer or a concatamer). Alternatively, the invention also includes individual fusion proteins of Staphylococcal proteins or immunogenic frag-

ments thereof, as a fusion protein with heterologous sequences such as a provider of T-cell epitopes or purification tags, for example:  $\beta$ -galactosidase, glutathione-S-transferase, green fluorescent proteins (GFP), epitope tags such as FLAG, myc tag, poly histidine, or viral surface proteins such as influenza virus haemagglutinin, or bacterial proteins such as tetanus toxoid, diphtheria toxoid, or CRM197.

## II. NUCLEIC ACIDS

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

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

In this respect, the term "gene," "polynucleotide," or "nucleic acid" is used to refer to a nucleic acid that encodes a protein, polypeptide, or peptide (including any sequences required for proper transcription, post-translational modification, or localization). As will be understood by those in the art, this term encompasses genomic sequences, expression cassettes, cDNA sequences, and smaller engineered nucleic acid segments that express, or may be adapted to express, proteins, polypeptides, domains, peptides, fusion proteins, and mutants. A nucleic acid encoding all or part of a polypeptide may contain a contiguous nucleic acid sequence of: 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 441, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, 1000, 1010, 1020, 1030, 1040, 1050, 1060, 1070, 1080, 1090, 1095, 1100, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 9000, 10000, or more nucleotides, nucleosides, or base pairs, including all values and ranges therebetween, of a polynucleotide encoding one or more amino acid sequence described or referenced herein. It also is contemplated that a particular polypeptide may be encoded by nucleic acids containing variations having slightly different nucleic acid sequences but, nonetheless, encode the same or substantially similar protein (see Table 3 above).

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

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

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

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

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

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

#### A. Vectors

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

ing peptide. Useful vectors encoding such fusion proteins include pIN vectors (Inouye et al., 1985), vectors encoding a stretch of histidines, and pGEX vectors, for use in generating glutathione S-transferase (GST) soluble fusion proteins for later purification and separation or cleavage.

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

#### 1. Promoters and Enhancers

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

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

Various elements/promoters may be employed in the context of the present invention to regulate the expression of a gene. Examples of such inducible elements, which are regions of a nucleic acid sequence that can be activated in response to a specific stimulus, include but are not limited to Immunoglobulin Heavy Chain (Banerji et al., 1983; Gilles et al., 1983; Grosschedl et al., 1985; Atchinson et al., 1986, 1987; Imler et al., 1987; Weinberger et al., 1984; Kiledjian et al., 1988; Porton et al.; 1990), Immunoglobulin Light Chain (Queen et al., 1983; Picard et al., 1984), T Cell Receptor (Luria et al., 1987; Winoto et al., 1989; Redondo et al.; 1990), HLA DQ a and/or DQ 13 (Sullivan et al., 1987), (3 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-DRa (Sherman et al., 1989),  $\beta$ -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), Metallothionein (MTII) (Karin et al., 1987; Culotta et al., 1989), Collagenase (Pinkert et al., 1987; Angel et al., 1987), Albumin (Pinkert et al., 1987; Tronche et al., 1989, 1990),  $\alpha$ -Fetoprotein (Godbout et al., 1988; Campere et al., 1989),

$\gamma$ -Globin (Bodine et al., 1987; Perez-Stable et al., 1990),  $\beta$ -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),  $\alpha$ 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).

Inducible elements include, but are not limited to MT II—Phorbol Ester (TFA)/Heavy metals (Palmiter et al., 1982; Haslinger et al., 1985; Searle et al., 1985; Stuart et al., 1985; Imagawa et al., 1987; Karin et al., 1987; Angel et al., 1987b; McNeall et al., 1989); MMTV (mouse mammary tumor virus)—Glucocorticoids (Huang et al., 1981; Lee et al., 1981; Majors et al., 1983; Chandler et al., 1983; Lee et al., 1984; Ponta et al., 1985; Sakai et al., 1988);  $\beta$ -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);  $\alpha$ -2-Macroglobulin—IL-6 (Kunz et al., 1989); Vimentin—Serum (Rittling et al., 1989); MHC Class I Gene H-2kb—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 a Gene—Thyroid Hormone (Chatterjee et al., 1989).

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

of being expressed in a human cell. Generally speaking, such a promoter might include either a bacterial, human or viral promoter.

In embodiments in which a vector is administered to a subject for expression of the protein, it is contemplated that a desirable promoter for use with the vector is one that is not down-regulated by cytokines or one that is strong enough that even if down-regulated, it produces an effective amount of a variant SpA for eliciting an immune response. Non-limiting examples of these are CMV IE and RSV LTR. Tissue specific promoters can be used, particularly if expression is in cells in which expression of an antigen is desirable, such as dendritic cells or macrophages. The mammalian MHC I and MHC II promoters are examples of such tissue-specific promoters.

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

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

In certain embodiments of the invention, the use of internal ribosome entry sites (IRES) elements are used to create multi-gene, 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).

## 3. Selectable and Screenable Markers

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

## B. Host Cells

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

Host cells may be derived from prokaryotes or eukaryotes, including bacteria, yeast cells, insect cells, and mammalian cells for replication of the vector or expression of part or all of the nucleic acid sequence(s). Numerous cell lines and cultures are available for use as a host cell, and they can be obtained through the American Type Culture Collection (ATCC), which is an organization that serves as an archive for living cultures and genetic materials (www.atcc.org).

### C. Expression Systems

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

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

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

### III. POLYSACCHARIDES

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

#### A. PIA (PNAG)

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

PIA is a polysaccharide intercellular adhesin and is composed of a polymer of  $\beta$ -(1 $\rightarrow$ 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- $\beta$ -(1 $\rightarrow$ 6)-glucosamine (PNSG) was recently shown not to have the expected structure since the identification of N-succinylation was incorrect (Maira-Litran et al., 2002). Therefore the polysaccharide formally known as PNSG and now found to be PNAG is also encompassed by the term PIA.

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

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

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

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

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

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

Type 5  
 $\rightarrow$ 4)- $\beta$ -D-ManNAcA(3OAc)-(1 $\rightarrow$ 4)- $\alpha$ -L-FucNAc  
 (1 $\rightarrow$ 3)- $\beta$ -D-FucNAc-(1 $\rightarrow$   
 Type 8  
 $\rightarrow$ 3)- $\beta$ -D-ManNAcA(4OAc)-(1 $\rightarrow$ 3)- $\alpha$ -L-FucNAc  
 (1 $\rightarrow$ 3)- $\beta$ -D-FucNAc-(1 $\rightarrow$

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

Type 5  
 →4)-β-D-ManNAcA-(1→4)-α-L-FucNAc(3OAc)-  
 (1→3)-β-D-FucNAc-(1→  
 Type 8  
 →3)-β-D-ManNAcA(4OAc)-(1→3)-α-L-FucNAc  
 (1→3)-α-D-FucNAc(1→

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.

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

#### C. *S. aureus* 336 Antigen

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

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

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

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

detoxified alpha toxin is optionally chemically detoxified, preferably by treatment with a cross-linking reagent, formaldehyde or glutaraldehyde to further reduce toxicity.

The polysaccharides may be linked to the carrier protein(s) by any known method (for example those methods described in U.S. Pat. Nos. 4,372,945, 4,474,757, and 4,356,170). Preferably, CDAP conjugation chemistry is carried out (see WO95/08348). In CDAP, the cyanating reagent 1-cyanodimethylaminopyridinium tetrafluoroborate (CDAP) is preferably used for the synthesis of polysaccharide-protein conjugates. The cyanilation reaction can be performed under relatively mild conditions, which avoids hydrolysis of the alkaline sensitive polysaccharides. This synthesis allows direct coupling to a carrier protein.

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

## IV. IMMUNE RESPONSE AND ASSAYS

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

### A. Immunoassays

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

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

Competition ELISAs are also possible implementations in which test samples compete for binding with known amounts

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

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

#### B. Diagnosis of Bacterial Infection

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

Accordingly, antibodies in accordance with the invention may be used for the prevention of infection from staphylococcal bacteria (i.e., passive immunization), for the treatment of an ongoing infection, or for use as research tools. The term "antibodies" as used herein includes monoclonal, polyclonal, chimeric, single chain, bispecific, simianized, and humanized or primatized antibodies as well as Fab fragments, such as those fragments which maintain the binding specificity of the antibodies, including the products of an Fab immunoglobulin

expression library. Accordingly, the invention contemplates the use of single chains such as the variable heavy and light chains of the antibodies. Generation of any of these types of antibodies or antibody fragments is well known to those skilled in the art. Specific examples of the generation of an antibody to a bacterial protein can be found in U.S. Patent Application Pub. No. 20030153022, which is incorporated herein by reference in its entirety.

Any of the above described polypeptides, proteins, peptides, and/or antibodies may be labeled directly with a detectable label for identification and quantification of staphylococcal bacteria. Labels for use in immunoassays are generally known to those skilled in the art and include enzymes, radioisotopes, and fluorescent, luminescent and chromogenic substances, including colored particles such as colloidal gold or latex beads. Suitable immunoassays include enzyme-linked immunosorbent assays (ELISA).

#### C. Protective Immunity

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

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

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

As used herein "passive immunity" refers to any immunity conferred upon a subject without administration of an antigen to the subject. "Passive immunity" therefore includes, but is not limited to, administration of activated immune effectors including cellular mediators or protein mediators (e.g., monoclonal and/or polyclonal antibodies) of an immune response. A monoclonal or polyclonal antibody composition

may be used in passive immunization for the prevention or treatment of infection by organisms that carry the antigen recognized by the antibody. An antibody composition may include antibodies that bind to a variety of antigens that may in turn be associated with various organisms. The antibody component can be a polyclonal antiserum. In certain aspects the antibody or antibodies are affinity purified from an animal or second subject that has been challenged with an antigen(s). Alternatively, an antibody mixture may be used, which is a mixture of monoclonal and/or polyclonal antibodies to antigens present in the same, related, or different microbes or organisms, such as gram-positive bacteria, gram-negative bacteria, including but not limited to *staphylococcus* bacteria.

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

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

The presence of a cell-mediated immunological response can be determined by proliferation assays (CD4 (+) T cells) or CTL (cytotoxic T lymphocyte) assays. The relative contributions of humoral and cellular responses to the protective or therapeutic effect of an immunogen can be distinguished by

separately isolating IgG and T-cells from an immunized syngeneic animal and measuring protective or therapeutic effect in a second subject.

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

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

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

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

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

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

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

#### D. Treatment Methods

A method of the present invention includes treatment for a disease or condition caused by a *staphylococcus* pathogen. An immunogenic polypeptide of the invention can be given to induce an immune response in a person infected with *staphylococcus* or suspected of having been exposed to *staphylococcus*. Methods may be employed with respect to individu-



als who have tested positive for exposure to *staphylococcus* or who are deemed to be at risk for infection based on possible exposure.

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

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

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

## V. VACCINE AND OTHER PHARMACEUTICAL COMPOSITIONS AND ADMINISTRATION

### A. Vaccines

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

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

The preparation of vaccines that contain polypeptide or peptide sequence(s) as active ingredients is generally well understood in the art, as exemplified by U.S. Pat. Nos. 4,608,251; 4,601,903; 4,599,231; 4,599,230; 4,596,792; and 4,578,770, all of which are incorporated herein by reference. Typically, such vaccines are prepared as injectables either as liquid solutions or suspensions: solid forms suitable for solution in or suspension in liquid prior to injection may also be prepared. The preparation may also be emulsified. The active immunogenic ingredient is often mixed with excipients that

are pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like and combinations thereof. In addition, if desired, the vaccine may contain amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, or adjuvants that enhance the effectiveness of the vaccines. In specific embodiments, vaccines are formulated with a combination of substances, as described in U.S. Pat. Nos. 6,793,923 and 6,733,754, which are incorporated herein by reference.

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

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

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

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

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

#### 1. Carriers

A given composition may vary in its immunogenicity. It is often necessary therefore to boost the host immune system, as



may be achieved by coupling a peptide or polypeptide to a carrier. Exemplary and preferred carriers are keyhole limpet hemocyanin (KLH) and bovine serum albumin (BSA). Other albumins such as ovalbumin, mouse serum albumin, or rabbit serum albumin can also be used as carriers. Means for conjugating a polypeptide to a carrier protein are well known in the art and include glutaraldehyde, m-maleimidobencoyl-N-hydroxysuccinimide ester, carbodiimide, and bis-biazotized benzidine.

## 2. Adjuvants

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

Adjuvants include, but are not limited to, oil-in-water emulsions, water-in-oil emulsions, mineral salts, polynucleotides, and natural substances. Specific adjuvants that may be used include IL-1, IL-2, IL-4, IL-7, IL-12,  $\gamma$ -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).

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.

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

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

The distinction of Th1 and Th2-type immune response is not absolute. In reality an individual will support an immune response which is described as being predominantly Th1 or

predominantly Th2. However, it is often convenient to consider the families of cytokines in terms of that described in murine CD4+ T cell clones by Mosmann and Coffman (Mosmann, and Coffman, 1989). Traditionally, Th1-type responses are associated with the production of the INF- $\gamma$  and IL-2 cytokines by T-lymphocytes. Other cytokines often directly associated with the induction of Th1-type immune responses are not produced by T-cells, such as IL-12. In contrast, Th2-type responses are associated with the secretion of IL-4, IL-5, IL-6, IL-10.

In addition to adjuvants, it may be desirable to co-administer biologic response modifiers (BRM) to enhance immune responses. BRMs have been shown to upregulate T cell immunity or downregulate 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/m<sup>2</sup>) (Johnson/Mead, NJ) and cytokines such as  $\gamma$ -interferon, IL-2, or IL-12 or genes encoding proteins involved in immune helper functions, such as B-7.

## B. Lipid Components and Moieties

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

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

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

In certain embodiments, a composition may comprise about 1%, about 2%, about 3%, about 4% about 5%, about 6%, about 7%, about 8%, about 9%, about 10%, about 11%, about 12%, about 13%, about 14%, about 15%, about 16%, about 17%, about 18%, about 19%, about 20%, about 21%, about 22%, about 23%, about 24%, about 25%, about 26%, about 27%, about 28%, about 29%, about 30%, about 31%, about 32%, about 33%, about 34%, about 35%, about 36%, about 37%, about 38%, about 39%, about 40%, about 41%, about 42%, about 43%, about 44%, about 45%, about 46%, about 47%, about 48%, about 49%, about 50%, about 51%, about 52%, about 53%, about 54%, about 55%, about 56%, about 57%, about 58%, about 59%, about 60%, about 61%, about 62%, about 63%, about 64%, about 65%, about 66%, about 67%, about 68%, about 69%, about 70%, about 71%,

about 72%, about 73%, about 74%, about 75%, about 76%, about 77%, about 78%, about 79%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or any range therebetween, of a particular lipid, lipid type, or non-lipid component such as an adjuvant, antigen, peptide, polypeptide, sugar, nucleic acid or other material disclosed herein or as would be known to one of skill in the art. In a non-limiting example, a composition may comprise about 10% to about 20% neutral lipids, and about 33% to about 34% of a cerebroside, and about 1% cholesterol. In another non-limiting example, a liposome may comprise about 4% to about 12% terpenes, wherein about 1% of the micelle is specifically lycopene, leaving about 3% to about 11% of the liposome as comprising other terpenes; and about 10% to about 35% phosphatidyl choline, and about 1% of a non-lipid component. Thus, it is contemplated that compositions of the present invention may comprise any of the lipids, lipid types or other components in any combination or percentage range.

### C. Combination Therapy

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

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

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

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

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

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

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

Administration of the immunogenic compositions of the present invention to a patient/subject will follow general protocols for the administration of such compounds, taking into account the toxicity, if any, of the SpA composition, or other compositions described herein. It is expected that the treat-

ment cycles would be repeated as necessary. It also is contemplated that various standard therapies, such as hydration, may be applied in combination with the described therapy.

### D. General Pharmaceutical Compositions

In some embodiments, pharmaceutical compositions are administered to a subject. Different aspects of the present invention involve administering an effective amount of a composition to a subject. In some embodiments of the present invention, staphylococcal antigens, members of the Ess pathway, including polypeptides or peptides of the Esa or Esx class, and/or members of sortase substrates may be administered to the patient to protect against infection by one or more *staphylococcus* pathogens. Alternatively, an expression vector encoding one or more such polypeptides or peptides may be given to a patient as a preventative treatment. Additionally, such compounds can be administered in combination with an antibiotic or an antibacterial. Such compositions will generally be dissolved or dispersed in a pharmaceutically acceptable carrier or aqueous medium.

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

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

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

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

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

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

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

Administration of the compositions according to the present invention will typically be via any common route. This includes, but is not limited to oral, nasal, or buccal administration. Alternatively, administration may be by 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.

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

subject. The person responsible for administration will, in any event, determine the appropriate dose for the individual subject.

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

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

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

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

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

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

#### F. Antibodies And Passive Immunization

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

Inocula for polyclonal antibody production are typically prepared by dispersing the antigenic composition in a physiologically tolerable diluent such as saline or other adjuvants

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suitable for human use to form an aqueous composition. An immunostimulatory amount of inoculum is administered to a mammal and the inoculated mammal is then maintained for a time sufficient for the antigenic composition to induce protective antibodies.

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

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

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

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

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

## VI. EXAMPLES

The following examples are given for the purpose of illustrating various embodiments of the invention and are not meant to limit the present invention in any fashion. One skilled in the art will appreciate readily that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those objects, 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

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spirit of the invention as defined by the scope of the claims will occur to those skilled in the art.

### Example 1

#### Non-Toxicigenic Protein a Variants as Subunit Vaccines to Prevent *Staphylococcus Aureus* Infections

##### A. Results

##### An Animal Model for *S. aureus* Infection

BAL.B/c mice were infected by intravenous injection with  $1 \times 10^7$  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  $1 \times 10^5$  CFU g<sup>-1</sup> 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 μm (±65 μm); 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 eosinophilic, 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  $10^4$ - $10^6$  CFU g<sup>-1</sup> 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.

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  $1 \times 10^6$  CFU g<sup>-1</sup> 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  $4.364 \pm 0.889$  abscesses per kidney, and surface abscesses were observed on 14 out of 20 kidneys (70%) (Table 4).

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 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	Staphylococcal load in kidney tissue				Abscess formation in kidney tissue	
	<sup>a</sup> log <sub>10</sub> CFU g <sup>-1</sup>	<sup>b</sup> Significance (P-value)	<sup>c</sup> Reduction (log <sub>10</sub> CFU g <sup>-1</sup> )	<sup>d</sup> Surface abscesses (%)	<sup>e</sup> Number of abscesses per kidney	<sup>f</sup> Significance (P-value)
	wild-type	6.141 ± 0.192	—	—	70	4.364 ± 0.889
ΔsrtA	4.095 ± 0.347	6.7 × 10 <sup>-6</sup>	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

<sup>a</sup>Means of staphylococcal load calculated as log<sub>10</sub> CFU g<sup>-1</sup> 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.

<sup>b</sup>Statistical significance was calculated with the Students t-test and P-values recorded; P-values < 0.05 were deemed significant.

<sup>c</sup>Reduction in bacterial load calculated as log<sub>10</sub> CFU g<sup>-1</sup>.

<sup>d</sup>Abscess formation in kidney tissues five days following infection was measured by macroscopic inspection (% positive)

<sup>e</sup>Histopathology 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).

<sup>f</sup>Statistical significance was calculated with the Students t-test and P-values recorded; P-values < 0.05 were deemed significant.

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

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 (ΔsrtA) failed to form abscess lesions on either macroscopic or histopathology examination on days 2, 5, or 15. In mice infected with the ΔsrtA mutant, only 1 × 10<sup>4</sup> CFU g<sup>-1</sup> was recovered from kidney tissue on day 5 of infection, which is a 2.046 log<sub>10</sub> CFU g<sup>-1</sup> reduction compared to the wild-type parent strain (P=6.73 × 10<sup>-6</sup>). 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, ΔsrtA mutants were cleared from renal tissues, a ≥3.5 log<sub>10</sub> CFU g<sup>-1</sup> 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.

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<sub>10</sub> (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).

#### Protein A Blocks Innate and Adaptive Immune Responses.

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)<sub>2</sub> 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.

#### Molecular Basis of Protein A Surface Display and Function.

Protein A is synthesized as a precursor in the bacterial cytoplasm and secreted via its YSIRK signal peptide at the cross wall, i.e., the cell division septum of staphylococci (FIG. 1). (DeDent et al., 2007; DeDent et al., 2008). Following cleavage of the C-terminal LPXTG sorting signal, Protein A is anchored to bacterial peptidoglycan 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 (Saïd-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). 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; Saïd-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 (Sjödahl 1977; Jansson et al., 1998). The solution and crystal structure of domain D has been solved both with and without the Fc and V<sub>H</sub>3 (Fab) ligands, which bind Protein A in a non-competitive manner at distinct sites (Graille et al., 2000).

In the crystal structure complex, the Fab interacts with helix II and helix III of domain D via a surface composed of four VH region  $\beta$ -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.

The SpA-D sites responsible for Fab binding are structurally separate from the domain surface that mediates Fey binding. The interaction of Fey 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 Fey 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 Fey molecule. In this ternary model, Fab and Fey 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 Fey are Gln-9 and Gln-10.

In contrast, occupancy of the Fc portion of IgG on the domain D blocks its interaction with vWF A1 and probably also TNFR1 (O'Seaghdha et al., 2006). Mutations in residues

essential for IgG Fc binding (F5, Q9, Q10, S11, F13, Y14, L17, N28, 131 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<sub>H</sub>3 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 Silverman 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.

#### Non-Toxicogenic Variant of Protein A.

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.

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<sup>Q9,10K;D36,37A</sup> and examined for the binding attributes of Protein A.

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 AGTGGATCCTTATGCTTTGTTAGCATCTGC [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 (MGSSHHHHHHHSSGLVPRGS (SEQ ID NO:37)). Following IPTG inducible expression, recombinant N-terminal His<sub>6</sub>-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 (AA-CATATGTTCAACAAAGATCAACAAAGC [5' primer] (SEQ ID NO:38) and AAGGATCCAGATTCGTT-TAATTTTTTAGC [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 His<sub>6</sub>-tagged protein. To generate mutations in the SpA-D coding sequence, sets of two pairs of primers were synthesized (for D to A substitutions: CTTTCATTCAAAGTCTTAAAGCCGC-CCCAAGCCAAAGCACTAAC [5' primer] (SEQ ID NO:40) and GTTAGTGCTTTGGCTTGGGGCGGCTT-TAAGACTTTGAATGAAG [3' primer] (SEQ ID NO:41); for Q to K substitutions CATATGTTCAACAAA-GATAAAAAAAGCGCCTTCTATGAAATC [5' primer] (SEQ ID NO:42) and GATTTCATAGAAGGCGCTTTTTT-TATCTTTGTTGAACATATG [3' primer] (SEQ ID NO:43); for Q to G substitutions CATATGTTCAACAAAGATG-GAGGAAGCGCCTTCTATGAAATC [5' primer] (SEQ ID NO:44) and GATTTCATAGAAGGCGCTTCTC-CATCTTTGTTGAACATATG [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<sub>Q9,10G;D36,37A</sub> and SpA-D<sub>Q9,10K;D36,37A</sub>. All proteins were purified from lysates of recombinant *E. coli* using Ni-NTA chromatography and subsequently dialyzed against PBS and stored at 4° C.

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<sub>Q9,10K;D36,37A</sub> variant did not bind to immunoglobulin.

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)<sub>2</sub> portion of human IgG [hF(ab)<sub>2</sub>] 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<sub>Q9,10G;D36,37A</sub> and SpA-D<sub>Q9,10K;D36,37A</sub> displayed only background binding activities. SpA bound similar amounts of hFc and hF(ab)<sub>2</sub>, however the binding of SpA-D to hF(ab)<sub>2</sub> 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)<sub>2</sub>, of the two variants only SpA-D<sub>Q9,10K;D36,37A</sub> displayed a significant reduction in the ability to bind the VH3 domain of immunoglobulin. To examine the toxigenic 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<sub>Q9,10K;D36,37A</sub> did not cause a reduction in B-cell counts, indicating that the mutant molecule had lost its toxigenic attributes of stimulating 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 toxic functions in human and animal tissues.

Non-Toxicogenic Protein a Variants Elicit Vaccine Protection.

To test whether or not Protein A and its variants can function as vaccine antigens, SpA, SpA-D, SpA-D<sub>Q9,10K;D36,37A</sub>, and SpA-D<sub>Q9,10G;D36,37A</sub>, 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<sub>Q9,10K;D36,37A</sub> or SpA-D<sub>Q9,10G;D36,37A</sub> was increased four to five fold. Following intravenous challenge with 1×10<sup>7</sup> CFU *S. aureus* Newman, animals were killed on day 4, their kidneys removed and either analyzed for staphylococcal load (by plating tissue homogenate on agar plates and enumerating colony forming units, CFU) or histopathology. As expected, mock (PBS) immunized mice (n=19) harbored 6.46 log<sub>10</sub> (±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 log<sub>10</sub> 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 log<sub>10</sub> 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<sub>Q9,10K;D36,37A</sub> or SpA-D<sub>Q9,10G;D36,37A</sub> created increased protection, with 3.07 log<sub>10</sub> and 3.03 log<sub>10</sub> CFU reduction on day 4, respectively (statistical significance P<0.0001 for both observations). Further, immunization with both SpA-D<sub>Q9,10K;D36,37A</sub> and SpA-D<sub>Q9,10G;D36,37A</sub> 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-toxicogenic 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.

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-toxicogenic 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.

nized by intramuscular injection into the hind leg with purified SpA, SpA-D or SpA-D<sub>Q9,10K;D36,37A</sub> (50 µg protein). Vaccine is administered on days 0 (emulsified 1:1 with com-

TABLE 5

Non-toxicogenic 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)				
	<sup>a</sup> log <sub>10</sub> CFU g <sup>-1</sup>	<sup>b</sup> Reduction	<sup>c</sup> P value		<sup>d</sup> Surface abscess	Reduction	<sup>e</sup> Histopathology	Reduction	<sup>f</sup> 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

<sup>a</sup>Means of staphylococcal load calculated as log<sub>10</sub> CFU g<sup>-1</sup> 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.

<sup>c</sup>Statistical significance was calculated with the Students t-test and P-values recorded; P-values < 0.05 were deemed significant.

<sup>b</sup>Reduction in bacterial load calculated as log<sub>10</sub> CFU g<sup>-1</sup>.

<sup>d</sup>Abscess formation in kidney tissues four days following infection was measured by macroscopic inspection (% positive)

<sup>e</sup>Histopathology 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).

<sup>f</sup>Statistical 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<sub>Q9, 10K; D36, 37A</sub> and SpA-D<sub>Q9, 10K; D36, 37A</sub>, respectively.

### Vaccine Protection in Murine Abscess, Murine Lethal Infection, and Murine Pneumonia Models.

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.

#### Murine Abscess—

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<sub>Q9,10K;D36,37A</sub> (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<sub>Q9,10K;D36,37A</sub> binding activity. Immunized animals are challenged on day 21 by retroorbital injection of 100 µl of *S. aureus* Newman or *S. aureus* USA300 suspension (1×10<sup>7</sup> 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 A<sub>600</sub> of 0.4 (1×10<sup>8</sup> 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 CO<sub>2</sub> 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.

#### Murine Lethal Infection—

BALB/c mice (24-day-old female, 8-10 mice per group, Charles River Laboratories, Wilmington, Mass.) are immu-

plete 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<sub>Q9,10K;D36,37A</sub> binding activity. Immunized animals are challenged on day 21 by retroorbital injection of 100 µl of *S. aureus* Newman or *S. aureus* USA300 suspension (15×10<sup>7</sup> 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 A<sub>600</sub> of 0.4 (1×10<sup>8</sup> 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<sup>10</sup> cfu of *S. aureus* Newman or 3-10×10<sup>9</sup> cfu of clinical *S. aureus* isolates. Animals are monitored for 14 days, and lethal disease is recorded.

#### Murine Pneumonia Model—

*S. aureus* strains Newman or USA300 (LAC) are grown at 37° C. in tryptic soy broth/agar to OD<sub>600</sub> 0.5. 50-ml culture aliquots are centrifuged, washed in PBS, and suspended in 750 µl PBS for mortality studies (3-4×10<sup>8</sup> CFU per 30-µl volume), or 1,250 µl PBS (2×10<sup>8</sup> CFU per 30-µl 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 µl 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 µg SpA-D or SpA-D<sub>Q9,10K;D36,37A</sub> in CFA on day 0 via the i.m. route, followed by a boost with 20 µg SpA-D or SpA-D<sub>Q9,10K;D36,37A</sub> 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 µl 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 CO<sub>2</sub> 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.

#### Rabbit Antibodies—

Purified 200 µg SpA-D or SpA-D<sub>Q9,10K;D36,37A</sub> is used as an immunogen for the production of rabbit antisera. 200 µg protein is emulsified with CFA for injection at day 0, followed by booster injections with 200 µg 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<sub>Q9,10K;D36,37A</sub> sepharose. The concentration of eluted antibodies is measured by absorbance at A<sub>280</sub> and specific antibody titers are determined by ELISA.

#### Active Immunization with SpA-Domain D Variants.—

To determine vaccine efficacy, animals are actively immunized with purified SpA-D or SpAD<sub>Q9,10K;D36,37A</sub>. As a control, animals are immunized with adjuvant alone. Antibody titers against Protein A preparations are determined using SpA-D or SpA-D<sub>Q9,10K;D36,37A</sub> as antigens; note that the SpA-D<sub>Q9,10K;D36,37A</sub> 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.

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

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<sub>Q9,10K;D36,37A</sub> derived rabbit antibodies. Both of these antibody preparations are purified by affinity chromatography using immobilized SpA-D or SpA-D<sub>Q9,10K;D36,37A</sub>. 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<sub>Q9,10K;D36,37A</sub> 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-Toxicigenic Protein a Vaccine for Methicillin-Resistant *Staphylococcus aureus* Infection

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 Ig-BDs (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  $\alpha$ -helical bundle structure of IgBDs (Deisenhofer et al., 1978; Deisenhofer et al., 1981) and their atomic interactions with Fab V<sub>H3</sub> (Graille et al., 2000) or Fc $\gamma$  (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<sub>KKAA</sub> (FIG. 6). The ability of isolated SpA-D or SpA-D<sub>KKAA</sub> to bind human IgG was analyzed by affinity chromatography (FIG. 6). Poly-histidine tagged SpA-D as well as full-length SpA retained human IgG on Ni-NTA, whereas SpA-D<sub>KKAA</sub> 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<sub>H3</sub>-type IgG. The inventors distinguish between Fc domain and B cell receptor activation of Igs and measured association of human Fc $\gamma$  and F(ab)<sub>2</sub> fragments, both of which bound to full-length SpA or SpA-D, but not to SpA-D<sub>KKAA</sub> (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<sub>KKAA</sub>, and TUNEL-staining of splenic tissue failed to detect the increase in apoptotic cells that follows injection of SpA or SpA-D (FIG. 6).

Naive six week old BALB/c mice were injected with 50 µg each of purified SpA, SpA-D or SpA-D<sub>KKAA</sub> 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<sub>KKAA</sub> specific antibodies following immunization of mice with the non-toxicigenic variant as compared to the B cell superantigen (Spa-D vs. SpA-D<sub>KKAA</sub> 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<sub>KKAA</sub> (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<sub>10</sub> CFU g<sup>-1</sup> was enumerated (Table 6). Immunization of mice with SpA or SpA-D led to a reduction in staphylococcal load, however SpA-D<sub>KKAA</sub> vaccinated animals displayed an even greater, 3.07 log<sub>10</sub> CFU g<sup>-1</sup> 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<sub>KKAA</sub> reduced the average number of

abscesses to 0.5 ( $\pm 0.4$ ) ( $P=0.0204$ ), 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<sub>KKAA</sub> 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).

The inventors examined whether SpA-D<sub>KKAA</sub> 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<sub>KKAA</sub> 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 ( $\pm 0.8$ ) to 1.6 ( $\pm 0.6$ ) ( $P=0.02774$ ). In contrast, SpA or SpA-D immunization did not cause a significant reduction in bacterial load or abscess formation (Table 6).

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

To further improve the vaccine properties for non-toxic protein A, the inventors generated SpA<sub>KKAA</sub>, 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<sub>KKAA</sub> was purified by affinity chromatography and analyzed by Coomassie Blue-stained SDS-PAGE (FIG. 9). Unlike full-length SpA, SpA<sub>KKAA</sub> did not bind human IgG, Fc and F(ab)<sub>2</sub> or vWF (FIG. 9). SpA<sub>KKAA</sub> 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<sub>KKAA</sub> vaccination generated higher specific antibody titers than SpA-D<sub>KKAA</sub> immunization and provided mice with elevated protection against *S. aureus* USA300 challenge (Table 6). Four days following challenge, SpA<sub>KKAA</sub> 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).

SpA<sub>KKAA</sub> was used to immunize rabbits. Rabbit antibodies specific for SpA-D<sub>KKAA</sub> or SpA<sub>KKAA</sub> 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<sub>KKAA</sub> ( $P=0.0016$ ) or SpA<sub>KKAA</sub> ( $P=0.0005$ ) 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<sub>KKAA</sub> or SpA<sub>KKAA</sub> 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	<sup>a</sup> $\log_{10}$ CFU $g^{-1}$	<sup>b</sup> P-value	<sup>c</sup> Reduction ( $\log_{10}$ CFU $g^{-1}$ )	<sup>d</sup> IgG Titer	<sup>e</sup> Number of abscesses	<sup>f</sup> P-value
<i>S. aureus</i> Newman challenge						
Mock	6.46 $\pm$ 0.25	—	—	<100	3.7 $\pm$ 1.2	—
SpA	3.95 $\pm$ 0.56	0.0003	2.51	1706 $\pm$ 370	2.1 $\pm$ 1.2	0.3531
SpA-D	4.43 $\pm$ 0.41	0.0001	2.03	381 $\pm$ 27	1.5 $\pm$ 0.8	0.1430
SpA-D <sub>KKAA</sub>	3.39 $\pm$ 0.50	<0.0001	3.07	5600 $\pm$ 801	0.5 $\pm$ 0.4	0.0204
<i>S. aureus</i> USA300 (LAC) challenge						
Mock	7.20 $\pm$ 0.24	—	—	<100	4.0 $\pm$ 0.8	—
SpA	6.81 $\pm$ 0.26	0.2819	0.39	476 $\pm$ 60	3.3 $\pm$ 1.0	0.5959
SpA-D	6.34 $\pm$ 0.52	0.1249	0.86	358 $\pm$ 19	2.2 $\pm$ 0.6	0.0912
SpA-D <sub>KKAA</sub>	6.00 $\pm$ 0.42	0.0189	1.20	3710 $\pm$ 1147	1.6 $\pm$ 0.6	0.0277
SpA <sub>KKAA</sub>	3.66 $\pm$ 0.76	0.0001	3.54	10200 $\pm$ 2476	1.2 $\pm$ 0.5	0.0109

<sup>a</sup>Means of staphylococcal load calculated as  $\log_{10}$  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 ( $\pm$ SEM) is indicated.

<sup>b</sup>Statistical significance was calculated with the unpaired two-tailed Students t-test and P-values recorded; P-values < 0.05 were deemed significant.

<sup>c</sup>Reduction in bacterial load calculated as  $\log_{10}$  CFU  $g^{-1}$ .

<sup>d</sup>Means of five randomly chosen serum IgG titers were measured prior to staphylococcal infection by ELISA.

<sup>e</sup>Histopathology of hematoxyline-cosin stained, thin sectioned kidneys from ten animals; the average number of abscesses per kidney was recorded and averaged again for the final mean ( $\pm$ SEM).

TABLE 7

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

<sup>a</sup>Affinity purified antibodies were injected into the peritoneal cavity of BALB/c mice at a concentration of 5 mg · kg<sup>-1</sup> twenty-four hours prior to intravenous challenge with 1 × 10<sup>7</sup> CFU *S. aureus* Newman.

<sup>b</sup>Means of staphylococcal load calculated as log<sub>10</sub> CFU g<sup>-1</sup> 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.

<sup>c</sup>Statistical significance was calculated with the unpaired two-tailed Students t-test and P-values recorded; P-values < 0.05 were deemed significant.

<sup>d</sup>Reduction in bacterial load calculated as log<sub>10</sub> CFU g<sup>-1</sup>.

<sup>e</sup>Means of five randomly chosen serum IgG titers were measured prior to staphylococcal infection by ELISA.

<sup>f</sup>Histopathology 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).

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<sub>KKAA</sub> specific IgG in these animals was determined by dot blot as 0.20 μg ml<sup>-1</sup> (±0.04) and 0.14 μg ml<sup>-1</sup> (±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<sub>KKAA</sub> or SpA-D<sub>KKAA</sub> vaccinated animals (P 0.05 log<sub>10</sub> reduction in staphylococcal CFU g<sup>-1</sup> renal tissue) was calculated as 4.05 μg ml<sup>-1</sup> (±0.88). Average serum concentration of SpA-specific IgG in adult healthy human volunteers (n=16) was 0.21 μg ml<sup>-1</sup> (±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<sup>-1</sup> (±0.20), was within range for protective immunity against diphtheria (Behring, 1890; Lagergard et al., 1992).

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 VH<sub>3</sub>-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.

The methods utilized include:

Bacterial Strains and Growth.

*Staphylococcus aureus* strains Newman and USA300 were grown in tryptic soy broth (TSB) at 37° C. *Escherichia coli* strains DH5a and BL21 (DE3) were grown in Luria-Bertani (LB) broth with 100 μg ml<sup>-1</sup> ampicillin at 37° C.

Rabbit Antibodies.

The coding sequence for SpA was PCR-amplified with two primers, gctgcacatgatggcgcaacacgatgaagctcaac (SEQ ID NO:35) and agtggatcctatgcttgagctttgttagcatctgc (SEQ ID NO:36) using *S. aureus* Newman template DNA. SpA-D was PCR-amplified with two primers, aacatggttcaacaagaatcaacaaagc (SEQ ID NO:38) and aaggatccagattcgtttaattttttgac (SEQ ID NO:39). The sequence for SpA-D<sub>KKAA</sub> was mutagenized with two sets of primers catatgttcaacaagataaaaaaagcgcttctatgaaatc (SEQ ID NO:42) and gatttcata-gaaggcgctttttatcttggtaacatag (SEQ ID NO:43) for Q9K, Q10K as well as ctccattcaagctttaaagccgc-cccaagccaagcactaac (SEQ ID NO:40) and gttagtgtttggct-tggggcgctttaaagactttgaatgaag (SEQ ID NO:41) for D36A, D37A. The sequence of SpA<sub>KKAA</sub> was synthesized by Integrated DNA Technologies, Inc. PCR products were cloned into pET-15b generating N-terminal His<sub>6</sub> 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 OD<sub>600</sub> 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×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.

Purified antigen (5 mg protein) was covalently linked to HiTrap NHS-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.

F(Ab)<sub>2</sub> Fragments.

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)<sub>2</sub> fragments were affinity purified with specific antigen-conjugated HiTrap NHS-activated HP columns. Purified antibodies were dialyzed overnight against PBS at 4° C., loaded onto SDS-PAGE gel and visualized with Coomassie Blue staining.

Active and Passive Immunization.

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).

Affinity purified antibodies in PBS were injected at a concentration 5 mg kg<sup>-1</sup> 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 microhematocrit capillary tubes (Fisher) and Z-gel serum separation micro tubes (Sarstedt) were used to collect and measure antigen specific antibody titers by ELISA.

Mouse Renal Abscess.

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 in PBS at OD<sub>600</sub> of 0.4 (~1×10<sup>8</sup> CFU ml<sup>-1</sup>). 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<sup>-1</sup> ketamine and 20 mg ml<sup>-1</sup> xylazine per kilogram of body weight. Mice were infected by retro-orbital injection with 1×10<sup>7</sup> CFU of *S. aureus* Newman or 5×10<sup>6</sup> CFU of *S. aureus* USA300. On day 4 following challenge, mice were killed by CO<sub>2</sub> 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.

Protein A Binding.

For human IgG binding, Ni-NTA affinity columns were pre-charged with 200 µg of purified proteins (SpA, SpA-D, SpA-D<sub>KKAA</sub>, 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<sub>KKAA</sub>, SpA-D and SpA-D<sub>KKAA</sub>) were coated onto MaxiSorp ELISA plates (NUNC) in 0.1M carbonate buffer (pH 9.5) at 1 µg ml<sup>-1</sup> 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)<sub>2</sub> fragments for one hour. Plates were washed and developed using

OptEIA ELISA reagents (BD). Reactions were quenched with 1 M phosphoric acid and A<sub>450</sub> readings were used to calculate half maximal titer and percent binding.

von Willebrand Factor (vWF) Binding Assays.

Purified proteins (SpA, SpA<sub>KKAA</sub>, SpA-D and SpA-D<sub>KKAA</sub>) were coated and blocked as described above. Plates were incubated with human vWF at 1 µg ml<sup>-1</sup> 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 A<sub>450</sub> readings were used to calculate half maximal titer and percent binding. For inhibition assays, plates were incubated with affinity purified F(ab)<sub>2</sub> fragments specific for SpA-D<sub>KKAA</sub> at 10 µg ml<sup>-1</sup> concentration for one hour prior to ligand binding assays.

Splenocyte Apoptosis.

Affinity purified proteins (150 µg of SpA, SpA-D, SpA<sub>KKAA</sub>, and SpA-D<sub>KKAA</sub>) 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 CO<sub>2</sub> 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 NH<sub>4</sub>Cl, 10 mM KHCO<sub>3</sub>, 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.

Antibody Quantification.

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<sub>KKAA</sub>/SpA<sub>KKAA</sub> as described above. Human/mouse IgG (Jackson Immunology Laboratory), SpA<sub>KKAA</sub>, and CRM<sub>197</sub> 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).

Statistical Analysis.

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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&lt;221&gt; NAME/KEY: MISC\_FEATURE

&lt;222&gt; LOCATION: (12)..(35)

&lt;223&gt; OTHER INFORMATION: where Y is any amion acid other than D

&lt;400&gt; SEQUENCE: 8

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Asn Asn Phe Asn Lys Asp Xaa Xaa Ser Ala Phe Tyr Glu Ile Leu Asn
1           5           10           15
Met Pro Asn Leu Asn Glu Ala Gln Arg Asn Gly Phe Ile Gln Ser Leu
          20           25           30
Lys 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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&lt;210&gt; SEQ ID NO 9

&lt;211&gt; LENGTH: 450

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Staphylococcus sp.

&lt;400&gt; 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 Asn 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

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420					425					430							
Gly	Leu	Ser	Leu	Ala	Leu	Gly	Ala	Ala	Leu	Leu	Ala	Gly	Arg	Arg	Arg	Arg	Arg
		435					440					445					
Glu Leu																	
450																	
<p>&lt;210&gt; SEQ ID NO 10                  &lt;211&gt; LENGTH: 450                  &lt;212&gt; TYPE: PRT                  &lt;213&gt; ORGANISM: Staphylococcus sp.                  &lt;400&gt; SEQUENCE: 10</p>																	
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		
Gly	Asn	Lys	Pro	Gly	Lys	Glu	Asp	Asn	Asn	Lys	Pro	Gly	Lys	Glu	Asp		
				325						330					335		

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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

<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

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<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
 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

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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						
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		

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785		790				795			800
Glu Asp Thr	Asn Lys	Asp Gly Lys	Gln Asp	Ser Thr	Glu Lys	Gly Ile			
	805		810			815			
Ser Gly Val	Thr Val	Thr Leu Lys	Asn Glu	Asn Gly	Glu Val	Leu Gln			
	820		825			830			
Thr Thr Lys	Thr Asp	Lys Asp	Gly Lys	Tyr Gln	Phe Thr	Gly Leu	Glu		
	835		840			845			
Asn Gly Thr	Tyr Lys	Val Glu	Phe Glu	Thr Pro	Ser Gly	Tyr Thr	Pro		
	850		855			860			
Thr Gln Val	Gly Ser	Gly Thr	Asp Glu	Gly Ile	Asp Ser	Asn Gly	Thr		
865		870		875		880			
Ser Thr Thr	Gly Val	Ile Lys	Asp Lys	Asp Asn	Asp Thr	Ile Asp	Ser		
	885		890			895			
Gly Phe Tyr	Lys Pro	Thr Tyr	Asn Leu	Gly Asp	Tyr Val	Trp Glu	Asp		
	900		905			910			
Thr Asn Lys	Asn Gly	Val Gln	Asp Lys	Asp Glu	Lys Gly	Ile Ser	Gly		
	915		920			925			
Val Thr Val	Thr Leu	Lys Asp	Glu Asn	Asp Lys	Val Leu	Lys Thr	Val		
	930		935			940			
Thr Thr Asp	Glu Asn	Gly Lys	Tyr Gln	Phe Thr	Asp Leu	Asn Asn	Gly		
945		950		955		960			
Thr Tyr Lys	Val Glu	Phe Glu	Thr Pro	Ser Gly	Tyr Thr	Pro Thr	Ser		
	965			970		975			
Val Thr Ser	Gly Asn	Asp Thr	Glu Lys	Asp Ser	Asn Gly	Leu Thr	Thr		
	980		985			990			
Thr Gly Val	Ile Lys	Asp Ala	Asp Asn	Met Thr	Leu Asp	Ser Gly	Phe		
	995		1000			1005			
Tyr Lys Thr	Pro Lys	Tyr Ser	Leu Gly	Asp Tyr	Val Trp	Tyr Asp			
	1010		1015			1020			
Ser Asn Lys	Asp Gly	Lys Gln	Asp Ser	Thr Glu	Lys Gly	Ile Lys			
	1025		1030			1035			
Asp Val Lys	Val Ile	Leu Leu	Asn Glu	Lys Gly	Glu Val	Ile Gly			
	1040		1045			1050			
Thr Thr Lys	Thr Asp	Glu Asn	Gly Lys	Tyr Arg	Phe Asp	Asn Leu			
	1055		1060			1065			
Asp Ser Gly	Lys Tyr	Lys Val	Ile Phe	Glu Lys	Pro Thr	Gly Leu			
	1070		1075			1080			
Thr Gln Thr	Gly Thr	Asn Thr	Thr Glu	Asp Asp	Lys Asp	Ala Asp			
	1085		1090			1095			
Gly Gly Glu	Val Asp	Val Thr	Ile Thr	Asp His	Asp Asp	Phe Thr			
	1100		1105			1110			
Leu Asp Asn	Gly Tyr	Tyr Glu	Glu Glu	Thr Ser	Asp Ser	Asp Ser			
	1115		1120			1125			
Asp Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp			
	1130		1135			1140			
Ser Asp Ser	Asp Ser	Asp Ser	Ser Asp	Ser Asp	Ser Asp	Ser Asp			
	1145		1150			1155			
Asp Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp			
	1160		1165			1170			
Ser Asp Ser	Asp Ser	Asp Ser	Ser Asp	Ser Asp	Ser Asp	Ser Asp			
	1175		1180			1185			
Asp Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp			
	1190		1195			1200			



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Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
1205                1210                1215

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
1220                1225                1230

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
1235                1240                1245

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
1250                1255                1260

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
1265                1270                1275

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
1280                1285                1290

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
1295                1300                1305

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
1310                1315                1320

Ser Asp Ala Gly Lys His Thr Pro Val Lys Pro Met Ser Thr Thr
1325                1330                1335

Lys Asp His His Asn Lys Ala Lys Ala Leu Pro Glu Thr Gly Asn
1340                1345                1350

Glu Asn Ser Gly Ser Asn Asn Ala Thr Leu Phe Gly Gly Leu Phe
1355                1360                1365

Ala Ala Leu Gly Ser Leu Leu Leu Phe Gly Arg Arg Lys Lys Gln
1370                1375                1380

Asn Lys
1385

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

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<400> SEQUENCE: 14

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

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

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

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

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

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

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

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

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

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

Thr Asn Asn Asp Val Thr Thr Lys Pro Ser Thr Ser Glu Ile Gln Thr

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



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Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 1010          1015          1020

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 1025          1030          1035

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 1040          1045          1050

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 1055          1060          1065

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ala Gly
 1070          1075          1080

Lys His Thr Pro Val Lys Pro Met Ser Thr Thr Lys Asp His His
 1085          1090          1095

Asn Lys Ala Lys Ala Leu Pro Glu Thr Gly Ser Glu Asn Asn Gly
 1100          1105          1110

Ser Asn Asn Ala Thr Leu Phe Gly Gly Leu Phe Ala Ala Leu Gly
 1115          1120          1125

Ser Leu Leu Leu Phe Gly Arg Arg Lys Lys Gln Asn Lys
 1130          1135          1140

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<210> SEQ ID NO 15
<211> LENGTH: 350
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp.

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<400> SEQUENCE: 15

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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

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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

&lt;210&gt; SEQ ID NO 16

&lt;211&gt; LENGTH: 645

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Staphylococcus sp.

&lt;400&gt; SEQUENCE: 16

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

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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
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												

&lt;210&gt; SEQ ID NO 17

&lt;211&gt; LENGTH: 80

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Staphylococcus sp.

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&lt;400&gt; SEQUENCE: 17

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

&lt;210&gt; SEQ ID NO 18

&lt;211&gt; LENGTH: 877

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Staphylococcus sp.

&lt;400&gt; 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





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Asp Ser Asp Ser Asp Ser Asp Ser Glu Ser Asp Ser Asp Ser Asp Ser
705                               710                               715                               720

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
725                               730                               735

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
740                               745                               750

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

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

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

Asp Ser Asp Ser Arg Val Thr Pro Pro Asn Asn Glu Gln Lys Ala Pro
805                               810                               815

Ser Asn Pro Lys Gly Glu Val Asn His Ser Asn Lys Val Ser Lys Gln
820                               825                               830

His Lys Thr Asp Ala Leu Pro Glu Thr Gly Asp Lys Ser Glu Asn Thr
835                               840                               845

Asn Ala Thr Leu Phe Gly Ala Met Met Ala Leu Leu Gly Ser Leu Leu
850                               855                               860

Leu Phe Arg Lys Arg Lys Gln Asp His Lys Glu Lys Ala
865                               870                               875

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<210> SEQ ID NO 19
<211> LENGTH: 227
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus sp.

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<400> SEQUENCE: 19

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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

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Ala Leu Leu Ile Ala Ile Thr Leu Phe Val Arg Lys Lys Ser Lys Gly  
 210 215 220

Asn Val Glu  
 225

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

<400> SEQUENCE: 20

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

Cys Ser Thr Met Met Ala Ser Ser Ile Ile Leu Thr Asn Ile Leu Pro  
 20 25 30

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

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

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

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

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

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

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

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

Ala Thr Thr Lys Tyr Gly Glu Lys Asp Asp Lys Asn Asp Glu Ala Met  
 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

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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			
Ile	Leu	Gln	Thr	Lys	Leu	Gly	Lys	Ala	Glu	Ala	Asp	Lys	Leu	Ala	Lys
				405					410					415	
Asp	Trp	Thr	Asn	Lys	Gly	Leu	Ser	Asn	Arg	Gln	Ile	Val	Asp	Gln	Leu
			420						425					430	
Lys	Lys	His	Phe	Ala	Ser	Thr	Gly	Asp	Thr	Ser	Ser	Asp	Asp	Ile	Leu
		435							440					445	
Lys	Ala	Ile	Leu	Asn	Asn	Ala	Lys	Asp	Lys	Lys	Gln	Ala	Ile	Glu	Thr
		450							455					460	
Ile	Leu	Ala	Thr	Arg	Ile	Glu	Arg	Gln	Lys	Ala	Lys	Leu	Leu	Ala	Asp
		465							470					475	
Leu	Ile	Thr	Lys	Ile	Glu	Thr	Asp	Gln	Asn	Lys	Ile	Phe	Asn	Leu	Val
				485					490					495	
Lys	Ser	Ala	Leu	Asn	Gly	Lys	Ala	Asp	Asp	Leu	Leu	Asn	Leu	Gln	Lys
			500						505					510	
Arg	Leu	Asn	Gln	Thr	Lys	Lys	Asp	Ile	Asp	Tyr	Ile	Leu	Ser	Pro	Ile
		515							520					525	
Val	Asn	Arg	Pro	Ser	Leu	Leu	Asp	Arg	Leu	Asn	Lys	Asn	Gly	Lys	Thr
		530							535					540	
Thr	Asp	Leu	Asn	Lys	Leu	Ala	Asn	Leu	Met	Asn	Gln	Gly	Ser	Asn	Leu
		545							550					555	
Leu	Asp	Ser	Ile	Pro	Asp	Ile	Pro	Thr	Pro	Lys	Pro	Glu	Lys	Thr	Leu
				565					570					575	
Thr	Leu	Gly	Lys	Gly	Asn	Gly	Leu	Leu	Ser	Gly	Leu	Leu	Asn	Ala	Asp
			580						585					590	
Gly	Asn	Val	Ser	Leu	Pro	Lys	Ala	Gly	Glu	Thr	Ile	Lys	Glu	His	Trp
		595							600					605	
Leu	Pro	Ile	Ser	Val	Ile	Val	Gly	Ala	Met	Gly	Val	Leu	Met	Ile	Trp
		610							615					620	
Leu	Ser	Arg	Arg	Asn	Lys	Leu	Lys	Asn	Lys	Ala					
		625							630					635	

&lt;210&gt; SEQ ID NO 21

&lt;211&gt; LENGTH: 953

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Staphylococcus sp.

&lt;400&gt; SEQUENCE: 21

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

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

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

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

Phe Gly Arg Arg Lys Lys Gln Asn Lys  
 945 950

<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

Ala Tyr Ile Asp Pro Glu Asn Val Thr Lys Thr Gly Asn Val Thr Leu



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Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp  
 770 775 780  
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp  
 785 790 795 800  
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp  
 805 810 815  
 Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Glu  
 820 825 830  
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp  
 835 840 845  
 Ser Asp Ser Asp Ser Asp Ser Glu Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp  
 850 855 860  
 Ser Asp Ser Glu Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp  
 865 870 875 880  
 Ser Ala Ser Asp Ser Asp Ser Gly Ser Asp Ser Asp Ser Ser Ser Asp  
 885 890 895  
 Ser Asp Ser Asp Ser Thr Ser Asp Thr Gly Ser Asp Asn Asp Ser Asp  
 900 905 910  
 Ser Asp Ser Asn Ser Asp Ser Glu Ser Gly Ser Asn Asn Asn Val Val  
 915 920 925  
 Pro Pro Asn Ser Pro Lys Asn Gly Thr Asn Ala Ser Asn Lys Asn Glu  
 930 935 940  
 Ala Lys Asp Ser Lys Glu Pro Leu Pro Asp Thr Gly Ser Glu Asp Glu  
 945 950 955 960  
 Ala Asn Thr Ser Leu Ile Trp Gly Leu Leu Ala Ser Leu Gly Ser Leu  
 965 970 975  
 Leu Leu Phe Arg Arg Lys Lys Glu Asn Lys Asp Lys Lys  
 980 985

<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  
 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



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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 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			

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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

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

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355					360					365					
Gln	Val	Pro	Val	Gly	Arg	Thr	Asp	Phe	Val	Thr	Val	Asn	Ser	Asp	Gly
	370					375					380				
Thr	Asn	Val	Gln	Trp	Ser	His	Gly	Ala	Gly	Ala	Gly	Ala	Asn	Lys	Pro
	385					390					395				400
Leu	Gln	Gln	Met	Trp	Glu	Tyr	Gly	Val	Asn	Asp	Pro	His	Arg	Ser	His
			405						410					415	
Asp	Phe	Lys	Ile	Arg	Asn	Arg	Ser	Gly	Gln	Val	Ile	Tyr	Asp	Trp	Pro
		420						425					430		
Thr	Val	His	Ile	Tyr	Ser	Leu	Glu	Asp	Leu	Ser	Arg	Ala	Ser	Asp	Tyr
		435					440					445			
Phe	Ser	Glu	Ala	Gly	Ala	Thr	Pro	Ala	Thr	Lys	Ala	Phe	Gly	Arg	Gln
	450					455					460				
Asn	Phe	Glu	Tyr	Ile	Asn	Gly	Gln	Lys	Pro	Ala	Glu	Ser	Pro	Gly	Val
	465					470					475				480
Pro	Lys	Val	Tyr	Thr	Phe	Ile	Gly	Gln	Gly	Asp	Ala	Ser	Tyr	Thr	Ile
				485					490					495	
Ser	Phe	Lys	Thr	Gln	Gly	Pro	Thr	Val	Asn	Lys	Leu	Tyr	Tyr	Ala	Ala
			500					505					510		
Gly	Gly	Arg	Ala	Leu	Glu	Tyr	Asn	Gln	Leu	Phe	Met	Tyr	Ser	Gln	Leu
		515					520					525			
Tyr	Val	Glu	Ser	Thr	Gln	Asp	His	Gln	Gln	Arg	Leu	Asn	Gly	Leu	Arg
	530					535					540				
Gln	Val	Val	Asn	Arg	Thr	Tyr	Arg	Ile	Gly	Thr	Thr	Lys	Arg	Val	Glu
	545					550					555				560
Val	Ser	Gln	Gly	Asn	Val	Gln	Thr	Lys	Lys	Val	Leu	Glu	Ser	Thr	Asn
				565					570					575	
Leu	Asn	Ile	Asp	Asp	Phe	Val	Asp	Asp	Pro	Leu	Ser	Tyr	Val	Lys	Thr
			580					585					590		
Pro	Ser	Asn	Lys	Val	Leu	Gly	Phe	Tyr	Ser	Asn	Asn	Ala	Asn	Thr	Asn
		595					600					605			
Ala	Phe	Arg	Pro	Gly	Gly	Ala	Gln	Gln	Leu	Asn	Glu	Tyr	Gln	Leu	Ser
	610					615					620				
Gln	Leu	Phe	Thr	Asp	Gln	Lys	Leu	Gln	Glu	Ala	Ala	Arg	Thr	Arg	Asn
	625					630					635				640
Pro	Ile	Arg	Leu	Met	Ile	Gly	Phe	Asp	Tyr	Pro	Asp	Ala	Tyr	Gly	Asn
			645						650					655	
Ser	Glu	Thr	Leu	Val	Pro	Val	Asn	Leu	Thr	Val	Leu	Pro	Glu	Ile	Gln
			660					665					670		
His	Asn	Ile	Lys	Phe	Phe	Lys	Asn	Asp	Asp	Thr	Gln	Asn	Ile	Ala	Glu
	675						680					685			
Lys	Pro	Phe	Ser	Lys	Gln	Ala	Gly	His	Pro	Val	Phe	Tyr	Val	Tyr	Ala
	690					695					700				
Gly	Asn	Gln	Gly	Asn	Ala	Ser	Val	Asn	Leu	Gly	Gly	Ser	Val	Thr	Ser
	705					710					715				720
Ile	Gln	Pro	Leu	Arg	Ile	Asn	Leu	Thr	Ser	Asn	Glu	Asn	Phe	Thr	Asp
				725					730					735	
Lys	Asp	Trp	Gln	Ile	Thr	Gly	Ile	Pro	Arg	Thr	Leu	His	Ile	Glu	Asn
			740					745					750		
Ser	Thr	Asn	Arg	Pro	Asn	Asn	Ala	Arg	Glu	Arg	Asn	Ile	Glu	Leu	Val
		755					760					765			
Gly	Asn	Leu	Leu	Pro	Gly	Asp	Tyr	Phe	Gly	Thr	Ile	Arg	Phe	Gly	Arg
	770					775						780			

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Lys Glu Gln Leu Phe Glu Ile Arg Val Lys Pro His Thr Pro Thr Ile  
 785 790 795 800  
 Thr Thr Thr Ala Glu Gln Leu Arg Gly Thr Ala Leu Gln Lys Val Pro  
 805 810 815  
 Val Asn Ile Ser Gly Ile Pro Leu Asp Pro Ser Ala Leu Val Tyr Leu  
 820 825 830  
 Val Ala Pro Thr Asn Gln Thr Thr Asn Gly Gly Ser Glu Ala Asp Gln  
 835 840 845  
 Ile Pro Ser Gly Tyr Thr Ile Leu Ala Thr Gly Thr Pro Asp Gly Val  
 850 855 860  
 His Asn Thr Ile Thr Ile Arg Pro Gln Asp Tyr Val Val Phe Ile Pro  
 865 870 875 880  
 Pro Val Gly Lys Gln Ile Arg Ala Val Val Tyr Tyr Asn Lys Val Val  
 885 890 895  
 Ala Ser Asn Met Ser Asn Ala Val Thr Ile Leu Pro Asp Asp Ile Pro  
 900 905 910  
 Pro Thr Ile Asn Asn Pro Val Gly Ile Asn Ala Lys Tyr Tyr Arg Gly  
 915 920 925  
 Asp Glu Val Asn Phe Thr Met Gly Val Ser Asp Arg His Ser Gly Ile  
 930 935 940  
 Lys Asn Thr Thr Ile Thr Thr Leu Pro Asn Gly Trp Thr Ser Asn Leu  
 945 950 955 960  
 Thr Lys Ala Asp Lys Asn Asn Gly Ser Leu Ser Ile Thr Gly Arg Val  
 965 970 975  
 Ser Met Asn Gln Ala Phe Asn Ser Asp Ile Thr Phe Lys Val Ser Ala  
 980 985 990  
 Thr Asp Asn Val Asn Asn Thr Thr Asn Asp Ser Gln Ser Lys His Val  
 995 1000 1005  
 Ser Ile His Val Gly Lys Ile Ser Glu Asp Ala His Pro Ile Val  
 1010 1015 1020  
 Leu Gly Asn Thr Glu Lys Val Val Val Val Asn Pro Thr Ala Val  
 1025 1030 1035  
 Ser Asn Asp Glu Lys Gln Ser Ile Ile Thr Ala Phe Met Asn Lys  
 1040 1045 1050  
 Asn Gln Asn Ile Arg Gly Tyr Leu Ala Ser Thr Asp Pro Val Thr  
 1055 1060 1065  
 Val Asp Asn Asn Gly Asn Val Thr Leu His Tyr Arg Asp Gly Ser  
 1070 1075 1080  
 Ser Thr Thr Leu Asp Ala Thr Asn Val Met Thr Tyr Glu Pro Val  
 1085 1090 1095  
 Val Lys Pro Glu Tyr Gln Thr Val Asn Ala Ala Lys Thr Ala Thr  
 1100 1105 1110  
 Val Thr Ile Ala Lys Gly Gln Ser Phe Ser Ile Gly Asp Ile Lys  
 1115 1120 1125  
 Gln Tyr Phe Thr Leu Ser Asn Gly Gln Pro Ile Pro Ser Gly Thr  
 1130 1135 1140  
 Phe Thr Asn Ile Thr Ser Asp Arg Thr Ile Pro Thr Ala Gln Glu  
 1145 1150 1155  
 Val Ser Gln Met Asn Ala Gly Thr Gln Leu Tyr His Ile Thr Ala  
 1160 1165 1170  
 Thr Asn Ala Tyr His Lys Asp Ser Glu Asp Phe Tyr Ile Ser Leu  
 1175 1180 1185

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Lys 1190	Ile	Asp	Val	Lys	Gln 1195	Pro	Glu	Gly	Asp	Gln 1200	Arg	Val	Tyr
Arg 1205	Thr	Ser	Thr	Tyr	Asp	Leu 1210	Thr	Thr	Asp	Glu 1215	Ile	Ser	Lys
Lys 1220	Gln	Ala	Phe	Ile	Asn 1225	Ala	Asn	Arg	Asp	Val 1230	Ile	Thr	Leu
Glu 1235	Gly	Asp	Ile	Ser	Val	Thr 1240	Asn	Thr	Pro	Asn 1245	Gly	Ala	Asn
Ser 1250	Thr	Ile	Thr	Val	Asn 1255	Ile	Asn	Lys	Gly	Arg 1260	Leu	Thr	Lys
Phe 1265	Ala	Ser	Asn	Leu	Ala 1270	Asn	Met	Asn	Phe	Leu 1275	Arg	Trp	Val
Phe 1280	Pro	Gln	Asp	Tyr	Thr 1285	Val	Thr	Trp	Thr	Asn 1290	Ala	Lys	Ile
Asn 1295	Arg	Pro	Thr	Asp	Gly 1300	Gly	Leu	Ser	Trp	Ser 1305	Asp	His	Lys
Ser 1310	Leu	Ile	Tyr	Arg	Tyr 1315	Asp	Ala	Thr	Leu	Gly 1320	Thr	Gln	Ile
Thr 1325	Asn	Asp	Ile	Leu	Thr 1330	Met	Leu	Lys	Ala	Thr 1335	Thr	Val	Pro
Gly 1340	Leu	Arg	Asn	Asn	Ile 1345	Thr	Gly	Asn	Glu	Lys 1350	Ser	Gln	Ala
Ala 1355	Gly	Gly	Arg	Pro	Asn 1360	Phe	Arg	Thr	Thr	Gly 1365	Tyr	Ser	Gln
Asn 1370	Ala	Thr	Thr	Asp	Gly 1375	Gln	Arg	Gln	Phe	Thr 1380	Leu	Asn	Gly
Val 1385	Ile	Gln	Val	Leu	Asp 1390	Ile	Ile	Asn	Pro	Ser 1395	Asn	Gly	Tyr
Gly 1400	Gln	Pro	Val	Thr	Asn 1405	Ser	Asn	Thr	Arg	Ala 1410	Asn	His	Ser
Ser 1415	Thr	Val	Val	Asn	Val 1420	Asn	Glu	Pro	Ala	Ala 1425	Asn	Gly	Ala
Ala 1430	Phe	Thr	Ile	Asp	His 1435	Val	Val	Lys	Ser	Asn 1440	Ser	Thr	His
Ala 1445	Ser	Asp	Ala	Val	Tyr 1450	Lys	Ala	Gln	Leu	Tyr 1455	Leu	Thr	Pro
Gly 1460	Pro	Lys	Gln	Tyr	Val 1465	Glu	His	Leu	Asn	Gln 1470	Asn	Thr	Gly
Thr 1475	Thr	Asp	Ala	Ile	Asn 1480	Ile	Tyr	Phe	Val	Pro 1485	Ser	Asp	Leu
Asn 1490	Pro	Thr	Ile	Ser	Val 1495	Gly	Asn	Tyr	Thr	Asn 1500	His	Gln	Val
Ser 1505	Gly	Glu	Thr	Phe	Thr 1510	Asn	Thr	Ile	Thr	Ala 1515	Asn	Asp	Asn
Gly 1520	Val	Gln	Ser	Val	Thr 1525	Val	Pro	Asn	Thr	Ser 1530	Gln	Ile	Thr
Thr 1535	Val	Asp	Asn	Asn	His 1540	Gln	His	Val	Ser	Ala 1545	Thr	Ala	Pro
Val 1550	Thr	Ser	Ala	Thr	Asn 1555	Lys	Thr	Ile	Asn	Leu 1560	Leu	Ala	Thr
Thr 1565	Ser	Gly	Asn	Thr	Ala 1570	Thr	Thr	Ser	Phe	Asn 1575	Val	Thr	Val
Pro 1580	Leu	Arg	Asp	Lys	Tyr 1585	Arg	Val	Gly	Thr	Ser 1590	Ser	Thr	Ala

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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					
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							

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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		
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		

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Lys Thr 2375	Ile Asn Val Val Arg 2380	Gly Gln Asn Asn Gln Trp Thr Ile 2385
Ala Asn 2390	Lys Pro Asp Tyr Val 2395	Thr Leu Asp Ala Gln Thr Gly Lys 2400
Val Thr 2405	Phe Asn Ala Asn Thr 2410	Ile Lys Pro Asn Ser Ser Ile Thr 2415
Ile Thr 2420	Pro Lys Ala Gly Thr 2425	Gly His Ser Val Ser Ser Asn Pro 2430
Ser Thr 2435	Leu Thr Ala Pro Ala 2440	Ala His Thr Val Asn Thr Thr Glu 2445
Ile Val 2450	Lys Asp Tyr Gly Ser 2455	Asn Val Thr Ala Ala Glu Ile Asn 2460
Asn Ala 2465	Val Gln Val Ala Asn 2470	Lys Arg Thr Ala Thr Ile Lys Asn 2475
Gly Thr 2480	Ala Met Pro Thr Asn 2485	Leu Ala Gly Gly Ser Thr Thr Thr 2490
Ile Pro 2495	Val Thr Val Thr Tyr 2500	Asn Asp Gly Ser Thr Glu Glu Val 2505
Gln Glu 2510	Ser Ile Phe Thr Lys 2515	Ala Asp Lys Arg Glu Leu Ile Thr 2520
Ala Lys 2525	Asn His Leu Asp Asp 2530	Pro Val Ser Thr Glu Gly Lys Lys 2535
Pro Gly 2540	Thr Ile Thr Gln Tyr 2545	Asn Asn Ala Met His Asn Ala Gln 2550
Gln Gln 2555	Ile Asn Thr Ala Lys 2560	Thr Glu Ala Gln Gln Val Ile Asn 2565
Asn Glu 2570	Arg Ala Thr Pro Gln 2575	Gln Val Ser Asp Ala Leu Thr Lys 2580
Val Arg 2585	Ala Ala Gln Thr Lys 2590	Ile Asp Gln Ala Lys Ala Leu Leu 2595
Gln Asn 2600	Lys Glu Asp Asn Ser 2605	Gln Leu Val Thr Ser Lys Asn Asn 2610
Leu Gln 2615	Ser Ser Val Asn Gln 2620	Val Pro Ser Thr Ala Gly Met Thr 2625
Gln Gln 2630	Ser Ile Asp Asn Tyr 2635	Asn Ala Lys Lys Arg Glu Ala Glu 2640
Thr Glu 2645	Ile Thr Ala Ala Gln 2650	Arg Val Ile Asp Asn Gly Asp Ala 2655
Thr Ala 2660	Gln Gln Ile Ser Asp 2665	Glu Lys His Arg Val Asp Asn Ala 2670
Leu Thr 2675	Ala Leu Asn Gln Ala 2680	Lys His Asp Leu Thr Ala Asp Thr 2685
His Ala 2690	Leu Glu Gln Ala Val 2695	Gln Gln Leu Asn Arg Thr Gly Thr 2700
Thr Thr 2705	Gly Lys Lys Pro Ala 2710	Ser Ile Thr Ala Tyr Asn Asn Ser 2715
Ile Arg 2720	Ala Leu Gln Ser Asp 2725	Leu Thr Ser Ala Lys Asn Ser Ala 2730
Asn Ala 2735	Ile Ile Gln Lys Pro 2740	Ile Arg Thr Val Gln Glu Val Gln 2745
Ser Ala 2750	Leu Thr Asn Val Asn 2755	Arg Val Asn Glu Arg Leu Thr Gln 2760
Ala Ile	Asn Gln Leu Val Pro	Leu Ala Asp Asn Ser Ala Leu Lys





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Lys Ser Asp Gln Asn Tyr Thr Asp Ala Thr Pro Ala Asn Lys Gln 3170 3175 3180
Ala Tyr Asp Asn Ala Val Asn Ala Ala Lys Gly Val Ile Gly Glu 3185 3190 3195
Thr Thr Asn Pro Thr Met Asp Val Asn Thr Val Asn Gln Lys Ala 3200 3205 3210
Ala Ser Val Lys Ser Thr Lys Asp Ala Leu Asp Gly Gln Gln Asn 3215 3220 3225
Leu Gln Arg Ala Lys Thr Glu Ala Thr Asn Ala Ile Thr His Ala 3230 3235 3240
Ser Asp Leu Asn Gln Ala Gln Lys Asn Ala Leu Thr Gln Gln Val 3245 3250 3255
Asn Ser Ala Gln Asn Val Gln Ala Val Asn Asp Ile Lys Gln Thr 3260 3265 3270
Thr Gln Ser Leu Asn Thr Ala Met Thr Gly Leu Lys Arg Gly Val 3275 3280 3285
Ala Asn His Asn Gln Val Val Gln Ser Asp Asn Tyr Val Asn Ala 3290 3295 3300
Asp Thr Asn Lys Lys Asn Asp Tyr Asn Asn Ala Tyr Asn His Ala 3305 3310 3315
Asn Asp Ile Ile Asn Gly Asn Ala Gln His Pro Val Ile Thr Pro 3320 3325 3330
Ser Asp Val Asn Asn Ala Leu Ser Asn Val Thr Ser Lys Glu His 3335 3340 3345
Ala Leu Asn Gly Glu Ala Lys Leu Asn Ala Ala Lys Gln Glu Ala 3350 3355 3360
Asn Thr Ala Leu Gly His Leu Asn Asn Leu Asn Asn Ala Gln Arg 3365 3370 3375
Gln Asn Leu Gln Ser Gln Ile Asn Gly Ala His Gln Ile Asp Ala 3380 3385 3390
Val Asn Thr Ile Lys Gln Asn Ala Thr Asn Leu Asn Ser Ala Met 3395 3400 3405
Gly Asn Leu Arg Gln Ala Val Ala Asp Lys Asp Gln Val Lys Arg 3410 3415 3420
Thr Glu Asp Tyr Ala Asp Ala Asp Thr Ala Lys Gln Asn Ala Tyr 3425 3430 3435
Asn Ser Ala Val Ser Ser Ala Glu Thr Ile Ile Asn Gln Thr Thr 3440 3445 3450
Asn Pro Thr Met Ser Val Asp Asp Val Asn Arg Ala Thr Ser Ala 3455 3460 3465
Val Thr Ser Asn Lys Asn Ala Leu Asn Gly Tyr Glu Lys Leu Ala 3470 3475 3480
Gln Ser Lys Thr Asp Ala Ala Arg Ala Ile Asp Ala Leu Pro His 3485 3490 3495
Leu Asn Asn Ala Gln Lys Ala Asp Val Lys Ser Lys Ile Asn Ala 3500 3505 3510
Ala Ser Asn Ile Ala Gly Val Asn Thr Val Lys Gln Gln Gly Thr 3515 3520 3525
Asp Leu Asn Thr Ala Met Gly Asn Leu Gln Gly Ala Ile Asn Asp 3530 3535 3540
Glu Gln Thr Thr Leu Asn Ser Gln Asn Tyr Gln Asp Ala Thr Pro 3545 3550 3555

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Ser	Lys	Lys	Thr	Ala	Tyr	Thr	Asn	Ala	Val	Gln	Ala	Ala	Lys	Asp
3560						3565					3570			
Ile	Leu	Asn	Lys	Ser	Asn	Gly	Gln	Asn	Lys	Thr	Lys	Asp	Gln	Val
3575						3580					3585			
Thr	Glu	Ala	Met	Asn	Gln	Val	Asn	Ser	Ala	Lys	Asn	Asn	Leu	Asp
3590						3595					3600			
Gly	Thr	Arg	Leu	Leu	Asp	Gln	Ala	Lys	Gln	Thr	Ala	Lys	Gln	Gln
3605						3610					3615			
Leu	Asn	Asn	Met	Thr	His	Leu	Thr	Thr	Ala	Gln	Lys	Thr	Asn	Leu
3620						3625					3630			
Thr	Asn	Gln	Ile	Asn	Ser	Gly	Thr	Thr	Val	Ala	Gly	Val	Gln	Thr
3635						3640					3645			
Val	Gln	Ser	Asn	Ala	Asn	Thr	Leu	Asp	Gln	Ala	Met	Asn	Thr	Leu
3650						3655					3660			
Arg	Gln	Ser	Ile	Ala	Asn	Lys	Asp	Ala	Thr	Lys	Ala	Ser	Glu	Asp
3665						3670					3675			
Tyr	Val	Asp	Ala	Asn	Asn	Asp	Lys	Gln	Thr	Ala	Tyr	Asn	Asn	Ala
3680						3685					3690			
Val	Ala	Ala	Ala	Glu	Thr	Ile	Ile	Asn	Ala	Asn	Ser	Asn	Pro	Glu
3695						3700					3705			
Met	Asn	Pro	Ser	Thr	Ile	Thr	Gln	Lys	Ala	Glu	Gln	Val	Asn	Ser
3710						3715					3720			
Ser	Lys	Thr	Ala	Leu	Asn	Gly	Asp	Glu	Asn	Leu	Ala	Ala	Ala	Lys
3725						3730					3735			
Gln	Asn	Ala	Lys	Thr	Tyr	Leu	Asn	Thr	Leu	Thr	Ser	Ile	Thr	Asp
3740						3745					3750			
Ala	Gln	Lys	Asn	Asn	Leu	Ile	Ser	Gln	Ile	Thr	Ser	Ala	Thr	Arg
3755						3760					3765			
Val	Ser	Gly	Val	Asp	Thr	Val	Lys	Gln	Asn	Ala	Gln	His	Leu	Asp
3770						3775					3780			
Gln	Ala	Met	Ala	Ser	Leu	Gln	Asn	Gly	Ile	Asn	Asn	Glu	Ser	Gln
3785						3790					3795			
Val	Lys	Ser	Ser	Glu	Lys	Tyr	Arg	Asp	Ala	Asp	Thr	Asn	Lys	Gln
3800						3805					3810			
Gln	Glu	Tyr	Asp	Asn	Ala	Ile	Thr	Ala	Ala	Lys	Ala	Ile	Leu	Asn
3815						3820					3825			
Lys	Ser	Thr	Gly	Pro	Asn	Thr	Ala	Gln	Asn	Ala	Val	Glu	Ala	Ala
3830						3835					3840			
Leu	Gln	Arg	Val	Asn	Asn	Ala	Lys	Asp	Ala	Leu	Asn	Gly	Asp	Ala
3845						3850					3855			
Lys	Leu	Ile	Ala	Ala	Gln	Asn	Ala	Ala	Lys	Gln	His	Leu	Gly	Thr
3860						3865					3870			
Leu	Thr	His	Ile	Thr	Thr	Ala	Gln	Arg	Asn	Asp	Leu	Thr	Asn	Gln
3875						3880					3885			
Ile	Ser	Gln	Ala	Thr	Asn	Leu	Ala	Gly	Val	Glu	Ser	Val	Lys	Gln
3890						3895					3900			
Asn	Ala	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

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3950	3955	3960
Thr Ala Val Glu Gln Ala Leu Asn Asn Val Asn Asn Ala Lys His		
3965	3970	3975
Ala Leu Asn Gly Thr Gln Asn Leu Asn Asn Ala Lys Gln Ala Ala		
3980	3985	3990
Ile Thr Ala Ile Asn Gly Ala Ser Asp Leu Asn Gln Lys Gln Lys		
3995	4000	4005
Asp Ala Leu Lys Ala Gln Ala Asn Gly Ala Gln Arg Val Ser Asn		
4010	4015	4020
Ala Gln Asp Val Gln His Asn Ala Thr Glu Leu Asn Thr Ala Met		
4025	4030	4035
Gly Thr Leu Lys His Ala Ile Ala Asp Lys Thr Asn Thr Leu Ala		
4040	4045	4050
Ser Ser Lys Tyr Val Asn Ala Asp Ser Thr Lys Gln Asn Ala Tyr		
4055	4060	4065
Thr Thr Lys Val Thr Asn Ala Glu His Ile Ile Ser Gly Thr Pro		
4070	4075	4080
Thr Val Val Thr Thr Pro Ser Glu Val Thr Ala Ala Ala Asn Gln		
4085	4090	4095
Val Asn Ser Ala Lys Gln Glu Leu Asn Gly Asp Glu Arg Leu Arg		
4100	4105	4110
Glu Ala Lys Gln Asn Ala Asn Thr Ala Ile Asp Ala Leu Thr Gln		
4115	4120	4125
Leu Asn Thr Pro Gln Lys Ala Lys Leu Lys Glu Gln Val Gly Gln		
4130	4135	4140
Ala Asn Arg Leu Glu Asp Val Gln Thr Val Gln Thr Asn Gly Gln		
4145	4150	4155
Ala Leu Asn Asn Ala Met Lys Gly Leu Arg Asp Ser Ile Ala Asn		
4160	4165	4170
Glu Thr Thr Val Lys Thr Ser Gln Asn Tyr Thr Asp Ala Ser Pro		
4175	4180	4185
Asn Asn Gln Ser Thr Tyr Asn Ser Ala Val Ser Asn Ala Lys Gly		
4190	4195	4200
Ile Ile Asn Gln Thr Asn Asn Pro Thr Met Asp Thr Ser Ala Ile		
4205	4210	4215
Thr Gln Ala Thr Thr Gln Val Asn Asn Ala Lys Asn Gly Leu Asn		
4220	4225	4230
Gly Ala Glu Asn Leu Arg Asn Ala Gln Asn Thr Ala Lys Gln Asn		
4235	4240	4245
Leu Asn Thr Leu Ser His Leu Thr Asn Asn Gln Lys Ser Ala Ile		
4250	4255	4260
Ser Ser Gln Ile Asp Arg Ala Gly His Val Ser Glu Val Thr Ala		
4265	4270	4275
Thr Lys Asn Ala Ala Thr Glu Leu Asn Thr Gln Met Gly Asn Leu		
4280	4285	4290
Glu Gln Ala Ile His Asp Gln Asn Thr Val Lys Gln Ser Val Lys		
4295	4300	4305
Phe Thr Asp Ala Asp Lys Ala Lys Arg Asp Ala Tyr Thr Asn Ala		
4310	4315	4320
Val Ser Arg Ala Glu Ala Ile Leu Asn Lys Thr Gln Gly Ala Asn		
4325	4330	4335
Thr Ser Lys Gln Asp Val Glu Ala Ala Ile Gln Asn Val Ser Ser		
4340	4345	4350

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Ala Lys Asn Ala Leu Asn Gly Asp Gln Asn Val Thr Asn Ala Lys	4355	4360	4365
Asn Ala Ala Lys Asn Ala Leu Asn Asn Leu Thr Ser Ile Asn Asn	4370	4375	4380
Ala Gln Lys Arg Asp Leu Thr Thr Lys Ile Asp Gln Ala Thr Thr	4385	4390	4395
Val Ala Gly Val Glu Ala Val Ser Asn Thr Ser Thr Gln Leu Asn	4400	4405	4410
Thr Ala Met Ala Asn Leu Gln Asn Gly Ile Asn Asp Lys Thr Asn	4415	4420	4425
Thr Leu Ala Ser Glu Asn Tyr His Asp Ala Asp Ser Asp Lys Lys	4430	4435	4440
Thr Ala Tyr Thr Gln Ala Val Thr Asn Ala Glu Asn Ile Leu Asn	4445	4450	4455
Lys Asn Ser Gly Ser Asn Leu Asp Lys Thr Ala Val Glu Asn Ala	4460	4465	4470
Leu Ser Gln Val Ala Asn Ala Lys Gly Ala Leu Asn Gly Asn His	4475	4480	4485
Asn Leu Glu Gln Ala Lys Ser Asn Ala Asn Thr Thr Ile Asn Gly	4490	4495	4500
Leu Gln His Leu Thr Thr Ala Gln Lys Asp Lys Leu Lys Gln Gln	4505	4510	4515
Val Gln Gln Ala Gln Asn Val Ala Gly Val Asp Thr Val Lys Ser	4520	4525	4530
Ser Ala Asn Thr Leu Asn Gly Ala Met Gly Thr Leu Arg Asn Ser	4535	4540	4545
Ile Gln Asp Asn Thr Ala Thr Lys Asn Gly Gln Asn Tyr Leu Asp	4550	4555	4560
Ala Thr Glu Arg Asn Lys Thr Asn Tyr Asn Asn Ala Val Asp Ser	4565	4570	4575
Ala Asn Gly Val Ile Asn Ala Thr Ser Asn Pro Asn Met Asp Ala	4580	4585	4590
Asn Ala Ile Asn Gln Ile Ala Thr Gln Val Thr Ser Thr Lys Asn	4595	4600	4605
Ala Leu Asp Gly Thr His Asn Leu Thr Gln Ala Lys Gln Thr Ala	4610	4615	4620
Thr Asn Ala Ile Asp Gly Ala Thr Asn Leu Asn Lys Ala Gln Lys	4625	4630	4635
Asp Ala Leu Lys Ala Gln Val Thr Ser Ala Gln Arg Val Ala Asn	4640	4645	4650
Val Thr Ser Ile Gln Gln Thr Ala Asn Glu Leu Asn Thr Ala Met	4655	4660	4665
Gly Gln Leu Gln His Gly Ile Asp Asp Glu Asn Ala Thr Lys Gln	4670	4675	4680
Thr Gln Lys Tyr Arg Asp Ala Glu Gln Ser Lys Lys Thr Ala Tyr	4685	4690	4695
Asp Gln Ala Val Ala Ala Ala Lys Ala Ile Leu Asn Lys Gln Thr	4700	4705	4710
Gly Ser Asn Ser Asp Lys Ala 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

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Glu Ala 4745	Lys Ala Ala Ala 4750	Lys Gln Asn Leu Gly 4750	Thr Leu Asn His 4755
Ile Thr 4760	Asn Ala Gln Arg 4765	Asp Leu Glu Gly 4770	Gln Ile Asn Gln 4770
Ala Thr 4775	Thr Val Asp Gly 4780	Val Asn Thr Val Lys 4785	Thr Asn Ala Asn 4785
Thr Leu 4790	Asp Gly Ala Met 4795	Asn Ser Leu Gln Gly 4800	Ile Asn Asp 4800
Lys Asp 4805	Ala Thr Leu Arg 4810	Asn Gln Asn Tyr Leu 4815	Ala Asp Glu 4815
Ser Lys 4820	Arg Asn Ala Tyr 4825	Thr Gln Ala Val Thr 4830	Ala Ala Glu Gly 4830
Ile Leu 4835	Asn Lys Gln Thr 4840	Gly Gly Asn Thr Ser 4845	Lys Ala Asp Val 4845
Asp Asn 4850	Ala Leu Asn Ala 4855	Val Thr Arg Ala Lys 4860	Ala Ala Leu Asn 4860
Gly Ala 4865	Asp Asn Leu Arg 4870	Asn Ala Lys Thr Ser 4875	Ala Thr Asn Thr 4875
Ile Asp 4880	Gly Leu Pro Asn 4885	Leu Thr Gln Leu Gln 4890	Lys Asp Asn Leu 4890
Lys His 4895	Gln Val Glu Gln 4900	Ala Gln Asn Val Ala 4905	Gly Val Asn Gly 4905
Val Lys 4910	Asp Lys Gly Asn 4915	Thr Leu Asn Thr Ala 4920	Met Gly Ala Leu 4920
Arg Thr 4925	Ser Ile Gln Asn 4930	Asp Asn Thr Thr Lys 4935	Thr Ser Gln Asn 4935
Tyr Leu 4940	Asp Ala Ser Asp 4945	Ser Asn Lys Asn Asn 4950	Tyr Asn Thr Ala 4950
Val Asn 4955	Asn Ala Asn Gly 4960	Val Ile Asn Ala Thr 4965	Asn Asn Pro Asn 4965
Met Asp 4970	Ala Asn Ala Ile 4975	Asn Gly Met Ala Asn 4980	Gln Val Asn Thr 4980
Thr Lys 4985	Ala Ala Leu Asn 4990	Gly Ala Gln Asn Leu 4995	Ala Gln Ala Lys 4995
Thr Asn 5000	Ala Thr Asn Thr 5005	Ile Asn Asn Ala His 5010	Asp Leu Asn Gln 5010
Lys Gln 5015	Lys Asp Ala Leu 5020	Lys Thr Gln Val Asn 5025	Asn Ala Gln Arg 5025
Val Ser 5030	Asp Ala Asn Asn 5035	Val Gln His Thr Ala 5040	Thr Glu Leu Asn 5040
Ser Ala 5045	Met Thr Ala Leu 5050	Lys Ala Ala Ile Ala 5055	Asp Lys Glu Arg 5055
Thr Lys 5060	Ala Ser Gly Asn 5065	Tyr Val Asn Ala Asp 5070	Gln Glu Lys Arg 5070
Gln Ala 5075	Tyr Asp Ser Lys 5080	Val Thr Asn Ala Glu 5085	Asn Ile Ile Ser 5085
Gly Thr 5090	Pro Asn Ala Thr 5095	Leu Thr Val Asn Asp 5100	Val Asn Ser Ala 5100
Ala Ser 5105	Gln Val Asn Ala 5110	Ala Lys Thr Ala Leu 5115	Asn Gly Asp Asn 5115
Asn Leu 5120	Arg Val Ala Lys 5125	Glu His Ala Asn Asn 5130	Thr Ile Asp Gly 5130
Leu Ala	Gln Leu Asn Asn Ala	Gln Lys Ala Lys Leu	Lys Glu Gln

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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	
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			

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Val	Glu	His	Thr	Ala	Thr	Glu	Leu	Asn	Thr	Ala	Met	Thr	Ala	Leu
5540						5545					5550			
Lys	Arg	Ala	Ile	Ala	Asp	Lys	Ala	Glu	Thr	Lys	Ala	Ser	Gly	Asn
5555						5560					5565			
Tyr	Val	Asn	Ala	Asp	Ala	Asn	Lys	Arg	Gln	Ala	Tyr	Asp	Glu	Lys
5570						5575					5580			
Val	Thr	Ala	Ala	Glu	Asn	Ile	Val	Ser	Gly	Thr	Pro	Thr	Pro	Thr
5585						5590					5595			
Leu	Thr	Pro	Ala	Asp	Val	Thr	Asn	Ala	Ala	Thr	Gln	Val	Thr	Asn
5600						5605					5610			
Ala	Lys	Thr	Gln	Leu	Asn	Gly	Asn	His	Asn	Leu	Glu	Val	Ala	Lys
5615						5620					5625			
Gln	Asn	Ala	Asn	Thr	Ala	Ile	Asp	Gly	Leu	Thr	Ser	Leu	Asn	Gly
5630						5635					5640			
Pro	Gln	Lys	Ala	Lys	Leu	Lys	Glu	Gln	Val	Gly	Gln	Ala	Thr	Thr
5645						5650					5655			
Leu	Pro	Asn	Val	Gln	Thr	Val	Arg	Asp	Asn	Ala	Gln	Thr	Leu	Asn
5660						5665					5670			
Thr	Ala	Met	Lys	Gly	Leu	Arg	Asp	Ser	Ile	Ala	Asn	Glu	Ala	Thr
5675						5680					5685			
Ile	Lys	Ala	Gly	Gln	Asn	Tyr	Thr	Asp	Ala	Ser	Gln	Asn	Lys	Gln
5690						5695					5700			
Thr	Asp	Tyr	Asn	Ser	Ala	Val	Thr	Ala	Ala	Lys	Ala	Ile	Ile	Gly
5705						5710					5715			
Gln	Thr	Thr	Ser	Pro	Ser	Met	Asn	Ala	Gln	Glu	Ile	Asn	Gln	Ala
5720						5725					5730			
Lys	Asp	Gln	Val	Thr	Ala	Lys	Gln	Gln	Ala	Leu	Asn	Gly	Gln	Glu
5735						5740					5745			
Asn	Leu	Arg	Thr	Ala	Gln	Thr	Asn	Ala	Lys	Gln	His	Leu	Asn	Gly
5750						5755					5760			
Leu	Ser	Asp	Leu	Thr	Asp	Ala	Gln	Lys	Asp	Ala	Val	Lys	Arg	Gln
5765						5770					5775			
Ile	Glu	Gly	Ala	Thr	His	Val	Asn	Glu	Val	Thr	Gln	Ala	Gln	Asn
5780						5785					5790			
Asn	Ala	Asp	Ala	Leu	Asn	Thr	Ala	Met	Thr	Asn	Leu	Lys	Asn	Gly
5795						5800					5805			
Ile	Gln	Asp	Gln	Asn	Thr	Ile	Lys	Gln	Gly	Val	Asn	Phe	Thr	Asp
5810						5815					5820			
Ala	Asp	Glu	Ala	Lys	Arg	Asn	Ala	Tyr	Thr	Asn	Ala	Val	Thr	Gln
5825						5830					5835			
Ala	Glu	Gln	Ile	Leu	Asn	Lys	Ala	Gln	Gly	Pro	Asn	Thr	Ser	Lys
5840						5845					5850			
Asp	Gly	Val	Glu	Thr	Ala	Leu	Glu	Asn	Val	Gln	Arg	Ala	Lys	Asn
5855						5860					5865			
Glu	Leu	Asn	Gly	Asn	Gln	Asn	Val	Ala	Asn	Ala	Lys	Thr	Thr	Ala
5870						5875					5880			
Lys	Asn	Ala	Leu	Asn	Asn	Leu	Thr	Ser	Ile	Asn	Asn	Ala	Gln	Lys
5885						5890					5895			
Glu	Ala	Leu	Lys	Ser	Gln	Ile	Glu	Gly	Ala	Thr	Thr	Val	Ala	Gly
5900						5905					5910			
Val	Asn	Gln	Val	Ser	Thr	Thr	Ala	Ser	Glu	Leu	Asn	Thr	Ala	Met
5915						5920					5925			



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Ser	Asn	Leu	Gln	Asn	Gly	Ile	Asn	Asp	Glu	Ala	Ala	Thr	Lys	Ala
5930						5935					5940			
Ala	Gln	Lys	Tyr	Thr	Asp	Ala	Asp	Arg	Glu	Lys	Gln	Thr	Ala	Tyr
5945						5950					5955			
Asn	Asp	Ala	Val	Thr	Ala	Ala	Lys	Thr	Leu	Leu	Asp	Lys	Thr	Ala
5960						5965					5970			
Gly	Ser	Asn	Asp	Asn	Lys	Ala	Ala	Val	Glu	Gln	Ala	Leu	Gln	Arg
5975						5980					5985			
Val	Asn	Thr	Ala	Lys	Thr	Ala	Leu	Asn	Gly	Asp	Glu	Arg	Leu	Asn
5990						5995					6000			
Glu	Ala	Lys	Asn	Thr	Ala	Lys	Gln	Gln	Val	Ala	Thr	Met	Ser	His
6005						6010					6015			
Leu	Thr	Asp	Ala	Gln	Lys	Ala	Asn	Leu	Thr	Ser	Gln	Ile	Glu	Ser
6020						6025					6030			
Gly	Thr	Thr	Val	Ala	Gly	Val	Gln	Gly	Ile	Gln	Ala	Asn	Ala	Gly
6035						6040					6045			
Thr	Leu	Asp	Gln	Ala	Met	Asn	Gln	Leu	Arg	Gln	Ser	Ile	Ala	Ser
6050						6055					6060			
Lys	Asp	Ala	Thr	Lys	Ser	Ser	Glu	Asp	Tyr	Gln	Asp	Ala	Asn	Ala
6065						6070					6075			
Asp	Leu	Gln	Asn	Ala	Tyr	Asn	Asp	Ala	Val	Thr	Asn	Ala	Glu	Gly
6080						6085					6090			
Ile	Ile	Ser	Ala	Thr	Asn	Asn	Pro	Glu	Met	Asn	Pro	Asp	Thr	Ile
6095						6100					6105			
Asn	Gln	Lys	Ala	Ser	Gln	Val	Asn	Ser	Ala	Lys	Ser	Ala	Leu	Asn
6110						6115					6120			
Gly	Asp	Glu	Lys	Leu	Ala	Ala	Ala	Lys	Gln	Thr	Ala	Lys	Ser	Asp
6125						6130					6135			
Ile	Gly	Arg	Leu	Thr	Asp	Leu	Asn	Asn	Ala	Gln	Arg	Thr	Ala	Ala
6140						6145					6150			
Asn	Ala	Glu	Val	Asp	Gln	Ala	Pro	Asn	Leu	Ala	Ala	Val	Thr	Ala
6155						6160					6165			
Ala	Lys	Asn	Lys	Ala	Thr	Ser	Leu	Asn	Thr	Ala	Met	Gly	Asn	Leu
6170						6175					6180			
Lys	His	Ala	Leu	Ala	Glu	Lys	Asp	Asn	Thr	Lys	Arg	Ser	Val	Asn
6185						6190					6195			
Tyr	Thr	Asp	Ala	Asp	Gln	Pro	Lys	Gln	Gln	Ala	Tyr	Asp	Thr	Ala
6200						6205					6210			
Val	Thr	Gln	Ala	Glu	Ala	Ile	Thr	Asn	Ala	Asn	Gly	Ser	Asn	Ala
6215						6220					6225			
Asn	Glu	Thr	Gln	Val	Gln	Ala	Ala	Leu	Asn	Gln	Leu	Asn	Gln	Ala
6230						6235					6240			
Lys	Asn	Asp	Leu	Asn	Gly	Asp	Asn	Lys	Val	Ala	Gln	Ala	Lys	Glu
6245						6250					6255			
Ser	Ala	Lys	Arg	Ala	Leu	Ala	Ser	Tyr	Ser	Asn	Leu	Asn	Asn	Ala
6260						6265					6270			
Gln	Ser	Thr	Ala	Ala	Ile	Ser	Gln	Ile	Asp	Asn	Ala	Thr	Thr	Val
6275						6280					6285			
Ala	Gly	Val	Thr	Ala	Ala	Gln	Asn	Thr	Ala	Asn	Glu	Leu	Asn	Thr
6290						6295					6300			
Ala	Met	Gly	Gln	Leu	Gln	Asn	Gly	Ile	Asn	Asp	Gln	Asn	Thr	Val
6305						6310					6315			
Lys	Gln	Gln	Val	Asn	Phe	Thr	Asp	Ala	Asp	Gln	Gly	Lys	Lys	Asp

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6320	6325	6330
Ala Tyr Thr Asn Ala Val Thr Asn Ala Gln Gly Ile Leu Asp Lys 6335 6340 6345		
Ala His Gly Gln Asn Met Thr Lys Ala Gln Val Glu Ala Ala Leu 6350 6355 6360		
Asn Gln Val Thr Thr Ala Lys Asn Ala Leu Asn Gly Asp Ala Asn 6365 6370 6375		
Val Arg Gln Ala Lys Ser Asp Ala Lys Ala Asn Leu Gly Thr Leu 6380 6385 6390		
Thr His Leu Asn Asn Ala Gln Lys Gln Asp Leu Thr Ser Gln Ile 6395 6400 6405		
Glu Gly Ala Thr Thr Val Asn Gly Val Asn Gly Val Lys Thr Lys 6410 6415 6420		
Ala Gln Asp Leu Asp Gly Ala Met Gln Arg Leu Gln Ser Ala Ile 6425 6430 6435		
Ala Asn Lys Asp Gln Thr Lys Ala Ser Glu Asn Tyr Ile Asp Ala 6440 6445 6450		
Asp Pro Thr Lys Lys Thr Ala Phe Asp Asn Ala Ile Thr Gln Ala 6455 6460 6465		
Glu Ser Tyr Leu Asn Lys Asp His Gly Ala Asn Lys Asp Lys Gln 6470 6475 6480		
Ala Val Glu Gln Ala Ile Gln Ser Val Thr Ser Thr Glu Asn Ala 6485 6490 6495		
Leu Asn Gly Asp Ala Asn Leu Gln Arg Ala Lys Thr Glu Ala Ile 6500 6505 6510		
Gln Ala Ile Asp Asn Leu Thr His Leu Asn Thr Pro Gln Lys Thr 6515 6520 6525		
Ala Leu Lys Gln Gln Val Asn Ala Ala Gln Arg Val Ser Gly Val 6530 6535 6540		
Thr Asp Leu Lys Asn Ser Ala Thr Ser Leu Asn Asn Ala Met Asp 6545 6550 6555		
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		

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Ile Asn	Ala Thr Ser Gln	Pro Thr Leu Asp Pro Ser	Ala Val Thr
6725		6730	6735
Gln Ala	Ala Asn Gln Val Ser	Thr Asn Lys Thr Ala	Leu Asn Gly
6740		6745	6750
Ala Gln	Asn Leu Ala Asn Lys	Lys Gln Glu Thr Thr	Ala Asn Ile
6755		6760	6765
Asn Gln	Leu Ser His Leu Asn	Asn Ala Gln Lys Gln	Asp Leu Asn
6770		6775	6780
Thr Gln	Val Thr Asn Ala Pro	Asn Ile Ser Thr Val	Asn Gln Val
6785		6790	6795
Lys Thr	Lys Ala Glu Gln Leu	Asp Gln Ala Met Glu	Arg Leu Ile
6800		6805	6810
Asn Gly	Ile Gln Asp Lys Asp	Gln Val Lys Gln Ser	Val Asn Phe
6815		6820	6825
Thr Asp	Ala Asp Pro Glu Lys	Gln Thr Ala Tyr Asn	Asn Ala Val
6830		6835	6840
Thr Ala	Ala Glu Asn Ile Ile	Asn Gln Ala Asn Gly	Thr Asn Ala
6845		6850	6855
Asn Gln	Ser Gln Val Glu Ala	Ala Leu Ser Thr Val	Thr Thr Thr
6860		6865	6870
Lys Gln	Ala Leu Asn Gly Asp	Arg Lys Val Thr Asp	Ala Lys Asn
6875		6880	6885
Asn Ala	Asn Gln Thr Leu Ser	Thr Leu Asp Asn Leu	Asn Asn Ala
6890		6895	6900
Gln Lys	Gly Ala Val Thr Gly	Asn Ile Asn Gln Ala	His Thr Val
6905		6910	6915
Ala Glu	Val Thr Gln Ala Ile	Gln Thr Ala Gln Glu	Leu Asn Thr
6920		6925	6930
Ala Met	Gly Asn Leu Lys Asn	Ser Leu Asn Asp Lys	Asp Thr Thr
6935		6940	6945
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

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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
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

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7505	7510	7515
Lys Thr Thr Leu Gly Thr	Leu Asp His Leu Asn	Asp Ala Gln Lys
7520	7525	7530
Gln Ala Leu Thr Thr Gln	Val Glu Gln Ala Pro	Asp Ile Ala Thr
7535	7540	7545
Val Asn Asn Val Lys Gln	Asn Ala Gln Asn Leu	Asn Asn Ala Met
7550	7555	7560
Thr Asn Leu Asn Asn Ala	Leu Gln Asp Lys Thr	Glu Thr Leu Asn
7565	7570	7575
Ser Ile Asn Phe Thr Asp	Ala Asp Gln Ala Lys	Lys Asp Ala Tyr
7580	7585	7590
Thr Asn Ala Val Ser His	Ala Glu Gly Ile Leu	Ser Lys Ala Asn
7595	7600	7605
Gly Ser Asn Ala Ser Gln	Thr Glu Val Glu Gln	Ala Met Gln Arg
7610	7615	7620
Val Asn Glu Ala Lys Gln	Ala Leu Asn Gly Asn	Asp Asn Val Gln
7625	7630	7635
Arg Ala Lys Asp Ala Ala	Lys Gln Val Ile Thr	Asn Ala Asn Asp
7640	7645	7650
Leu Asn Gln Ala Gln Lys	Asp Ala Leu Lys Gln	Gln Val Asp Ala
7655	7660	7665
Ala Gln Thr Val Ala Asn	Val Asn Thr Ile Lys	Gln Thr Ala Gln
7670	7675	7680
Asp Leu Asn Gln Ala Met	Thr Gln Leu Lys Gln	Gly Ile Ala Asp
7685	7690	7695
Lys Asp Gln Thr Lys Ala	Asn Gly Asn Phe Val	Asn Ala Asp Thr
7700	7705	7710
Asp Lys Gln Asn Ala Tyr	Asn Asn Ala Val Ala	His Ala Glu Gln
7715	7720	7725
Ile Ile Ser Gly Thr Pro	Asn Ala Asn Val Asp	Pro Gln Gln Val
7730	7735	7740
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

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

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Ser	Ser	Asp	Ile	Ala	Ala	Val	Asn	Gly	His	Lys	Gln	Thr	Ala	Glu
8300						8305					8310			
Ser	Leu	Asn	Thr	Ala	Met	Gly	Asn	Leu	Ile	Asn	Ala	Ile	Ala	Asp
8315						8320					8325			
His	Gln	Ala	Val	Glu	Gln	Arg	Gly	Asn	Phe	Ile	Asn	Ala	Asp	Thr
8330						8335					8340			
Asp	Lys	Gln	Thr	Ala	Tyr	Asn	Thr	Ala	Val	Asn	Glu	Ala	Ala	Ala
8345						8350					8355			
Met	Ile	Asn	Lys	Gln	Thr	Gly	Gln	Asn	Ala	Asn	Gln	Thr	Glu	Val
8360						8365					8370			
Glu	Gln	Ala	Ile	Thr	Lys	Val	Gln	Thr	Thr	Leu	Gln	Ala	Leu	Asn
8375						8380					8385			
Gly	Asp	His	Asn	Leu	Gln	Val	Ala	Lys	Thr	Asn	Ala	Thr	Gln	Ala
8390						8395					8400			
Ile	Asp	Ala	Leu	Thr	Ser	Leu	Asn	Asp	Pro	Gln	Lys	Thr	Ala	Leu
8405						8410					8415			
Lys	Asp	Gln	Val	Thr	Ala	Ala	Thr	Leu	Val	Thr	Ala	Val	His	Gln
8420						8425					8430			
Ile	Glu	Gln	Asn	Ala	Asn	Thr	Leu	Asn	Gln	Ala	Met	His	Gly	Leu
8435						8440					8445			
Arg	Gln	Ser	Ile	Gln	Asp	Asn	Ala	Ala	Thr	Lys	Ala	Asn	Ser	Lys
8450						8455					8460			
Tyr	Ile	Asn	Glu	Asp	Gln	Pro	Glu	Gln	Gln	Asn	Tyr	Asp	Gln	Ala
8465						8470					8475			
Val	Gln	Ala	Ala	Asn	Asn	Ile	Ile	Asn	Glu	Gln	Thr	Ala	Thr	Leu
8480						8485					8490			
Asp	Asn	Asn	Ala	Ile	Asn	Gln	Ala	Ala	Thr	Thr	Val	Asn	Thr	Thr
8495						8500					8505			
Lys	Ala	Ala	Leu	His	Gly	Asp	Val	Lys	Leu	Gln	Asn	Asp	Lys	Asp
8510						8515					8520			
His	Ala	Lys	Gln	Thr	Val	Ser	Gln	Leu	Ala	His	Leu	Asn	Asn	Ala
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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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			
Lys	His	Leu	Val	Asp	Asn	Glu	Ile	Pro	Asn	Ala	Glu	Gln	Thr	Val
9455						9460					9465			
Asn	Tyr	Gln	Asn	Ala	Asp	Asp	Asn	Ala	Lys	Thr	Asn	Phe	Asp	Asp
9470						9475					9480			

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Ala Lys Arg Leu Ala Asn Thr Leu Leu Asn Ser Asp Asn Thr Asn 9485 9490 9495
Val Asn Asp Ile Asn Gly Ala Ile Gln Ala Val Asn Asp Ala Ile 9500 9505 9510
His Asn Leu Asn Gly Asp Gln Arg Leu Gln Asp Ala Lys Asp Lys 9515 9520 9525
Ala Ile Gln Ser Ile Asn Gln Ala Leu Ala Asn Lys Leu Lys Glu 9530 9535 9540
Ile Glu Ala Ser Asn Ala Thr Asp Gln Asp Lys Leu Ile Ala Lys 9545 9550 9555
Asn Lys Ala Glu Glu Leu Ala Asn Ser Ile Ile Asn Asn Ile Asn 9560 9565 9570
Lys Ala Thr Ser Asn Gln Ala Val Ser Gln Val Gln Thr Ala Gly 9575 9580 9585
Asn His Ala Ile Glu Gln Val His Ala Asn Glu Ile Pro Lys Ala 9590 9595 9600
Lys Ile Asp Ala Asn Lys Asp Val Asp Lys Gln Val Gln Ala Leu 9605 9610 9615
Ile Asp Glu Ile Asp Arg Asn Pro Asn Leu Thr Asp Lys Glu Lys 9620 9625 9630
Gln Ala Leu Lys Asp Arg Ile Asn Gln Ile Leu Gln Gln Gly His 9635 9640 9645
Asn Gly Ile Asn Asn Ala Met Thr Lys Glu Glu Ile Glu Gln Ala 9650 9655 9660
Lys Ala Gln Leu Ala Gln Ala Leu Gln Asp Ile Lys Asp Leu Val 9665 9670 9675
Lys Ala Lys Glu Asp Ala Lys Gln Asp Val Asp Lys Gln Val Gln 9680 9685 9690
Ala Leu Ile Asp Glu Ile Asp Gln Asn Pro Asn Leu Thr Asp Lys 9695 9700 9705
Glu Lys Gln Ala Leu Lys Tyr Arg Ile Asn Gln Ile Leu Gln Gln 9710 9715 9720
Gly His Asn Asp Ile Asn Asn Ala Leu Thr Lys Glu Glu Ile Glu 9725 9730 9735
Gln Ala Lys Ala Gln Leu Ala Gln Ala Leu Gln Asp Ile Lys Asp 9740 9745 9750
Leu Val Lys Ala Lys Glu Asp Ala Lys Asn Ala Ile Lys Ala Leu 9755 9760 9765
Ala Asn Ala Lys Arg Asp Gln Ile Asn Ser Asn Pro Asp Leu Thr 9770 9775 9780
Pro Glu Gln Lys Ala Lys Ala Leu Lys Glu Ile Asp Glu Ala Glu 9785 9790 9795
Lys Arg Ala Leu Gln Asn Val Glu Asn Ala Gln Thr Ile Asp Gln 9800 9805 9810
Leu Asn Arg Gly Leu Asn Leu Gly Leu Asp Asp Ile Arg Asn Thr 9815 9820 9825
His Val Trp Glu Val Asp Glu Gln Pro Ala Val Asn Glu Ile Phe 9830 9835 9840
Glu Ala Thr Pro Glu Gln Ile Leu Val Asn Gly Glu Leu Ile Val 9845 9850 9855
His Arg Asp Asp Ile Ile Thr Glu Gln Asp Ile Leu Ala His Ile 9860 9865 9870
Asn Leu Ile Asp Gln Leu Ser Ala Glu Val Ile Asp Thr Pro Ser

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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
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

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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

<210> SEQ ID NO 25  
 <211> LENGTH: 340  
 <212> TYPE: PRT  
 <213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 25

Met Lys Lys Lys Leu Leu Val Leu Thr Met Ser Thr Leu Phe Ala Thr  
 1 5 10 15  
 Gln Ile Met Asn Ser Asn His Ala Lys Ala Ser Val Thr Glu Ser Val  
 20 25 30  
 Asp Lys Lys Phe Val Val Pro Glu Ser Gly Ile Asn Lys Ile Ile Pro  
 35 40 45  
 Ala Tyr Asp Glu Phe Lys Asn Ser Pro Lys Val Asn Val Ser Asn Leu  
 50 55 60  
 Thr Asp Asn Lys Asn Phe Val Ala Ser Glu Asp Lys Leu Asn Lys Ile  
 65 70 75 80  
 Ala Asp Ser Ser Ala Ala Ser Lys Ile Val Asp Lys Asn Phe Val Val  
 85 90 95  
 Pro Glu Ser Lys Leu Gly Asn Ile Val Pro Glu Tyr Lys Glu Ile Asn  
 100 105 110  
 Asn Arg Val Asn Val Ala Thr Asn Asn Pro Ala Ser Gln Gln Val Asp  
 115 120 125  
 Lys His Phe Val Ala Lys Gly Pro Glu Val Asn Arg Phe Ile Thr Gln  
 130 135 140  
 Asn Lys Val Asn His His Phe Ile Thr Thr Gln Thr His Tyr Lys Lys  
 145 150 155 160  
 Val Ile Thr Ser Tyr Lys Ser Thr His Val His Lys His Val Asn His  
 165 170 175  
 Ala Lys Asp Ser Ile Asn Lys His Phe Ile Val Lys Pro Ser Glu Ser  
 180 185 190  
 Pro Arg Tyr Thr His Pro Ser Gln Ser Leu Ile Ile Lys His His Phe  
 195 200 205  
 Ala Val Pro Gly Tyr His Ala His Lys Phe Val Thr Pro Gly His Ala

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210	215	220
Ser Ile Lys Ile Asn His Phe Cys Val Val Pro Gln Ile Asn Ser Phe		
225	230	235 240
Lys Val Ile Pro Pro Tyr Gly His Asn Ser His Arg Met His Val Pro		
	245	250 255
Ser Phe Gln Asn Asn Thr Thr Ala Thr His Gln Asn Ala Lys Val Asn		
	260	265 270
Lys Ala Tyr Asp Tyr Lys Tyr Phe Tyr Ser Tyr Lys Val Val Lys Gly		
	275	280 285
Val Lys Lys Tyr Phe Ser Phe Ser Gln Ser Asn Gly Tyr Lys Ile Gly		
	290	295 300
Lys Pro Ser Leu Asn Ile Lys Asn Val Asn Tyr Gln Tyr Ala Val Pro		
305	310	315 320
Ser Tyr Ser Pro Thr His Tyr Val Pro Glu Phe Lys Gly Ser Leu Pro		
	325	330 335
Ala Pro Arg Val		
	340	

<210> SEQ ID NO 26  
 <211> LENGTH: 130  
 <212> TYPE: PRT  
 <213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 26

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

<210> 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		

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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			
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

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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

&lt;210&gt; SEQ ID NO 28

&lt;211&gt; LENGTH: 745

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Staphylococcus sp.

&lt;400&gt; SEQUENCE: 28

Ala Glu Gln His Thr Pro Met Lys Ala His Ala Val Thr Thr Ile Asp  
1 5 10 15

Lys Ala Thr Thr Asp Lys Gln Gln Val Pro Pro Thr Lys Glu Ala Ala  
20 25 30

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

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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
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



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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

&lt;210&gt; SEQ ID NO 29

&lt;211&gt; LENGTH: 628

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Staphylococcus sp.

&lt;400&gt; 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  
 Phe Lys His Pro Lys Phe Tyr Gln Gln Leu Phe Lys Leu Leu Glu Asp  
                   100                  105                  110  
 Met Arg Val Leu Asn Ser Ile Lys Val Glu Arg Pro Ser Thr Ala Lys  
                   115                  120                  125  
 Leu Ile Asp Leu Arg Leu Asp Thr Arg Ile Ser Tyr Thr Glu Ser Gln  
                   130                  135                  140  
 Ile Lys Val Tyr Arg Thr Lys Thr Gln Tyr Thr Asp Leu Leu Phe Leu  
   145                  150                  155                  160  
 Tyr Leu Glu His Ala Phe Leu Ser Gln Asp Phe Phe Asp Ile Pro Ser  
                   165                  170                  175  
 Ile His Ser Asp Leu Asp Asp Ile Leu Val Asn Met Phe Leu Tyr Leu  
                   180                  185                  190  
 Pro Asn Phe Phe Gln Asn Gln Asn Ser Glu Asp Asn Met Tyr Leu Ala  
                   195                  200                  205  
 Gln Arg Ile Met Tyr Gln Val Asp Asp Ile Leu Lys Glu Asp Met Leu  
                   210                  215                  220  
 Asn Glu Tyr Tyr Tyr Leu Pro Lys Thr Leu Tyr Asn Thr Leu Ala Ser  
   225                  230                  235                  240  
 Pro Glu Phe Asp Asp Leu Lys Arg Thr Asp Ala Ser Gln Val Asp Gly  
                   245                  250                  255  
 Gln Asp Asp Thr Ser Glu Asp Asp Asp Asn Glu Ser Glu Lys Ala Asp

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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	
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														

&lt;210&gt; SEQ ID NO 30

&lt;211&gt; LENGTH: 154

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Staphylococcus sp.

&lt;400&gt; SEQUENCE: 30

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

<210> SEQ ID NO 31  
 <211> LENGTH: 584  
 <212> TYPE: PRT  
 <213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 31

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

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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  
 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

&lt;210&gt; SEQ ID NO 32

&lt;211&gt; LENGTH: 508

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Staphylococcus sp.

&lt;400&gt; SEQUENCE: 32

Met Lys Asn Lys Leu Leu Val Leu Ser Leu Gly Ala Leu Cys Val Ser

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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	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	160
Gln Leu Lys	Cys Asp Leu Glu Leu Asn	Lys Leu Glu Asn Gln	Ile Leu
	165	170	175
Met Leu Gly	Lys Thr Phe Tyr Gln	Asn Tyr Arg Asp Asp	Val Glu Ser
	180	185	190
Leu Tyr Ser	Lys Leu Asp Leu Ile Met	Gly Tyr Lys Asp	Glu Glu Arg
	195	200	205
Ala Asn Lys	Lys Ala Val Asn Lys Arg	Met Leu Glu Asn Lys	Lys Glu
	210	215	220
Asp Leu Glu	Thr Ile Ile Asp Glu Phe	Phe Ser Asp Ile Asp	Lys Thr
	225	230	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	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	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

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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

&lt;210&gt; SEQ ID NO 33

&lt;211&gt; LENGTH: 520

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Staphylococcus sp.

&lt;400&gt; SEQUENCE: 33

Met Leu Thr Leu Gln Ile His Thr Gly Gly Ile Asn Leu Lys Lys Lys  
 1 5 10 15

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

Leu Gly Thr Leu Leu Ile Ser Gly Gly Val Thr Pro Ala Ala Asn Ala  
 35 40 45

Ala Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr Gln Val Leu Asn  
 50 55 60

Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser Leu  
 65 70 75 80

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

Leu Asn Asp Ser Gln Ala Pro Lys Ala Asp Ala Gln Gln Asn Asn Phe  
 100 105 110

Asn Lys Asp Gln Gln Ser Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn  
 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



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

<210> SEQ ID NO 35  
 <211> LENGTH: 34  
 <212> TYPE: DNA  
 <213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 35

gctgcacata tggcgcaaca cgatgaagct caac

34

<210> SEQ ID NO 36  
 <211> LENGTH: 30  
 <212> TYPE: DNA  
 <213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 36

agtggatcct tatgctttgt tagcatctgc

30

<210> SEQ ID NO 37  
 <211> LENGTH: 19  
 <212> TYPE: PRT  
 <213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 37

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
 1 5 10 15

Arg Gly Ser

<210> SEQ ID NO 38  
 <211> LENGTH: 29  
 <212> TYPE: DNA  
 <213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 38

aacatatggt caacaaagat caacaaagc

29

<210> SEQ ID NO 39  
 <211> LENGTH: 29  
 <212> TYPE: DNA  
 <213> ORGANISM: Staphylococcus sp.



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<400> SEQUENCE: 39  
aaggatccag attcgtttaa ttttttagc 29

<210> SEQ ID NO 40  
<211> LENGTH: 43  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 40  
cttcattcaa agtcttaaag cgcgcccaag ccaaagcact aac 43

<210> SEQ ID NO 41  
<211> LENGTH: 43  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 41  
gttagtgcct tggcttgggg cggetttaag actttgaatg aag 43

<210> SEQ ID NO 42  
<211> LENGTH: 42  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 42  
catatgttca acaaagataa aaaaagcgcc ttctatgaaa tc 42

<210> SEQ ID NO 43  
<211> LENGTH: 42  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 43  
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<210> SEQ ID NO 44  
<211> LENGTH: 42  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 44  
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<210> SEQ ID NO 45  
<211> LENGTH: 42  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 45  
gatttcatag aaggcgcttc ctccatcttt gttgaacata tg 42

<210> SEQ ID NO 46  
<211> LENGTH: 52  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 46  
ggggacaagt ttgtacaaaa aagcaggctg atgactaagt tgaaaaaaga ag 52

<210> SEQ ID NO 47  
<211> LENGTH: 28  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.

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<400> SEQUENCE: 47  
aaggatcccc tccaaaatgt aattgccc 28

<210> SEQ ID NO 48  
<211> LENGTH: 30  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 48  
aaggatccgt ttgtaactct atccaaagac 30

<210> SEQ ID NO 49  
<211> LENGTH: 49  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 49  
ggggaccact ttgtacaaga aagctgggtg acacctattg cagcattcg 49

<210> SEQ ID NO 50  
<211> LENGTH: 50  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 50  
ggggacaagt ttgtacaaaa aagcaggctc agatagcgat tcagattcag 50

<210> SEQ ID NO 51  
<211> LENGTH: 31  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 51  
aaggatccct gtattttctc cttaattttc c 31

<210> SEQ ID NO 52  
<211> LENGTH: 30  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 52  
aaggatccca tggctgcaaa gcaaataatg 30

<210> SEQ ID NO 53  
<211> LENGTH: 51  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 53  
ggggaccact ttgtacaaga aagctgggtg ccctgggtgta acaaatttat g 51

<210> SEQ ID NO 54  
<211> LENGTH: 37  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.

<400> SEQUENCE: 54  
gaaggatccg tttattctag ttaatatata gttaatg 37

<210> SEQ ID NO 55  
<211> LENGTH: 33  
<212> TYPE: DNA

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<213> ORGANISM: Staphylococcus sp.  
<400> SEQUENCE: 55  
gaactgcagc tgtatgtctt tggatagagt tac 33

<210> SEQ ID NO 56  
<211> LENGTH: 33  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.  
<400> SEQUENCE: 56  
gaaggatccg gtggcttttt tacttggatt ttc 33

<210> SEQ ID NO 57  
<211> LENGTH: 33  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.  
<400> SEQUENCE: 57  
gaactgcagc gacaaactca ttatttgctt tgc 33

<210> SEQ ID NO 58  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.  
<400> SEQUENCE: 58  
gaactcgagt ctagcttatt tacatgg 27

<210> SEQ ID NO 59  
<211> LENGTH: 45  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.  
<400> SEQUENCE: 59  
gaactcgaga tagaaggcag aatagtaaca aaggattata gtggg 45

<210> SEQ ID NO 60  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.  
<400> SEQUENCE: 60  
gtaggatcct gggatagagt tacaaac 27

<210> SEQ ID NO 61  
<211> LENGTH: 34  
<212> TYPE: DNA  
<213> ORGANISM: Staphylococcus sp.  
<400> SEQUENCE: 61  
gaactcgagg cattatgtgt atcacaaatt 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

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&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Staphylococcus sp.

&lt;400&gt; SEQUENCE: 63

gaactcgagg cagccatgca ttaattattt gcc

33

&lt;210&gt; SEQ ID NO 64

&lt;211&gt; LENGTH: 677

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Staphylococcus sp.

&lt;400&gt; SEQUENCE: 64

Met Lys Ser Asn Leu Arg Tyr Gly Ile Arg Lys His Lys Leu Gly Ala  
1 5 10 15Ala Ser Val Phe Leu Gly Thr Met Ile Val Val Gly Met Gly Gln Glu  
20 25 30Lys Glu Ala Ala Ala Ser Glu Gln Asn Asn Thr Thr Val Glu Glu Ser  
35 40 45Gly Ser Ser Ala Thr Glu Ser Lys Ala Ser Glu Thr Gln Thr Thr Thr  
50 55 60Asn Asn Val Asn Thr Ile Asp Glu Thr Gln Ser Tyr Ser Ala Thr Ser  
65 70 75 80Thr Glu Gln Pro Ser Gln Ser Thr Gln Val Thr Thr Glu Glu Ala Pro  
85 90 95Lys Thr Val Gln Ala Pro Lys Val Glu Thr Ser Arg Val Asp Leu Pro  
100 105 110Ser Glu Lys Val Ala Asp Lys Glu Thr Thr Gly Thr Gln Val Asp Ile  
115 120 125Ala Gln Pro Ser Asn Val Ser Glu Ile Lys Pro Arg Met Lys Arg Ser  
130 135 140Thr Asp Val Thr Ala Val Ala Glu Lys Glu Val Val Glu Glu Thr Lys  
145 150 155 160Ala Thr Gly Thr Asp Val Thr Asn Lys Val Glu Val Glu Glu Gly Ser  
165 170 175Glu Ile Val Gly His Lys Gln Asp Thr Asn Val Val Asn Pro His Asn  
180 185 190Ala Glu Arg Val Thr Leu Lys Tyr Lys Trp Lys Phe Gly Glu Gly Ile  
195 200 205Lys Ala Gly Asp Tyr Phe Asp Phe Thr Leu Ser Asp Asn Val Glu Thr  
210 215 220His Gly Ile Ser Thr Leu Arg Lys Val Pro Glu Ile Lys Ser Thr Asp  
225 230 235 240Gly Gln Val Met Ala Thr Gly Glu Ile Ile Gly Glu Arg Lys Val Arg  
245 250 255Tyr Thr Phe Lys Glu Tyr Val Gln Glu Lys Lys Asp Leu Thr Ala Glu  
260 265 270Leu Ser Leu Asn Leu Phe Ile Asp Pro Thr Thr Val Thr Gln Lys Gly  
275 280 285Asn Gln Asn Val Glu Val Lys Leu Gly Glu Thr Thr Val Ser Lys Ile  
290 295 300Phe Asn Ile Gln Tyr Leu Gly Gly Val Arg Asp Asn Trp Gly Val Thr  
305 310 315 320Ala 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

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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	400
Asn Met Ser Leu Asp Phe Asp Thr Asn Gly Gly Tyr Ser Leu Asn Phe		
	405	410
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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What is claimed is:

1. A recombinant nucleic acid molecule comprising a nucleic acid sequence encoding a *Staphylococcus aureus* Protein A (SpA) D domain segment having (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 amino acids at position 9, 10, 36 and/or 37 of SEQ ID NO: 2; and wherein the substitutions at amino acids corresponding to positions 9 and 10 are with a glycine residue and the substitutions at amino acids corresponding to positions 36 and 37 are with a serine residue; or 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.

2. The nucleic acid molecule of claim 1, wherein the SpA D domain segment is at least 90% identical to the amino acid sequence of SEQ ID NO: 2.

3. The nucleic acid molecule of claim 1, further comprising a nucleic acid sequence encoding one or more SpA E domain, A domain, B domain or C domain.

4. The nucleic acid molecule of claim 1, further comprising a nucleic acid sequence encoding a non-Protein A segment.

5. The nucleic acid molecule of claim 1, further comprising a nucleic acid sequence encoding 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.

6. The nucleic acid molecule of claim 1, wherein the (SpA) D domain segment has glycine substitutions at amino acids corresponding to positions 9 and 10 and serine substitutions at amino acids corresponding to positions 36 and 37 of SEQ ID NO:2.

7. The nucleic acid molecule of claim 1, wherein the (SpA) D domain segment has lysine substitutions at amino acids corresponding to positions 9 and 10 and alanine substitutions at amino acids corresponding to positions 36 and 37 of SEQ ID NO:2.

8. A host cell comprising the nucleic acid molecule of claim 1.

9. A method of making an isolated polypeptide comprising expressing the recombinant nucleic acid molecule of claim 1 in a host cell.

10. The method of claim 9, wherein the host cell is a bacterial cell or eukaryotic cell.

11. The method of claim 9, wherein the method comprises culturing the host cell.

12. The method of claim 11, wherein the host cell is induced to express the polypeptide.

13. The method of claim 9, wherein the (SpA) D domain segment has glycine substitutions at amino acids corresponding to positions 9 and 10 and serine substitutions at amino acids corresponding to positions 36 and 37 of SEQ ID NO:2.

14. The method of claim 9, wherein the (SpA) D domain segment has lysine substitutions at amino acids corresponding to positions 9 and 10 and alanine substitutions at amino acids corresponding to positions 36 and 37 of SEQ ID NO:2.

\* \* \* \* \*