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(54) **Titre : COMPOSITION IMMUNOGENE COMPORTANT DES POLYPEPTIDES ISSUS DE LEUCOCIDINE DE PANTON-VALENTINE (PVL)**
(54) **Title: IMMUNOGENIC COMPOSITION COMPRISING PANTON-VALENTINE LEUKOCIDIN (PVL) DERIVED POLYPEPTIDES**

(57) **Abrégé/Abstract:**
The present disclosure provides immunogenic compositions useful in prevention and treatment of Staphylococcus aureus infection. In particular, the disclosure provides methods of inducing an immune response against a panton-valentine leukocidin (PVL)-expressing S. aureus, methods of preventing or treating S. aureus infections, and composition for preventing or treating S. aureus infections.

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(54) Title: IMMUNOGENIC COMPOSITION COMPRISING PANTON-VALENTINE LEUKOCIDIN (PVL) DERIVED POLYPEPTIDES

(57) Abstract: The present disclosure provides immunogenic compositions useful in prevention and treatment of Staphylococcus aureus infection. In particular, the disclosure provides methods of inducing an immune response against a panton-valentine leukocidin (PVL)-expressing S. aureus, methods of preventing or treating S. aureus infections, and composition for preventing or treating S. aureus infections.

IMMUNOGENIC COMPOSITION COMPRISING PANTON-VALENTINE LEUKOCIDIN (PVL) DERIVED POLYPEPTIDES

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BACKGROUND

Field of the Disclosure

[0002] This disclosure relates to the treatment and prevention of *Staphylococcus aureus* (*S. aureus*) infection. In particular, the disclosure provides compositions and methods for preventing *S. aureus* infection and treating a disease caused by a leukocidin, *e.g.*, Panton-Valentine leukocidin (PVL) or gamma-hemolysin expressing *S. aureus* infection.

Background of the Disclosure

[0003] *Staphlyococcus aureus* (SA) is a gram positive human pathogen that is associated with or causes a wide range of pathologies ranging from skin and soft tissue infections to life-threatening systemic infections, *e.g.*, minor skin infections such as pimples, impetigo, boils (furuncles), cellulitis folliculitis, carbuncles, scalded skin syndrome, and abscesses, to life-threatening deep infections such as pneumonia, sepsis, endocarditis, meningitis, post-operative wound infections, septicemia, and toxic shock syndrome (Nizet, V., J Allergy Clin Immunol, 2007. 120(1): p. 13-22; Kotzin, *et al.*, Adv Immunol, 1993. 54: p. 99-166; Meyer *et al.*, Int J Infect Dis, 2001. 5(3): p. 163-6; Schuberth *et al.*, Vet Microbiol, 2001. 82(2): p. 187-99; and Silverstein *et al.*, in Microbiology, Davis *et al.*, eds. (Lippincott, Philadelphia, 1990), pp. 485-506).

[0004] Pneumonia is one of the most severe and prominent complications of *S. aureus* infection leading with 50,000 cases per year in the U.S. alone (Kuehnert, *et al.*, *Emerg. Infect. Dis.* 11:868-872, 2005). *S. aureus* pneumonia has been traditionally ventilator associated but

in recent years it has been recognized also as a major cause of community acquired pneumonia primarily in otherwise healthy children and young individuals.

[0005] The range of SA-associated pathologies reflects the diverse abilities of this microbe to escape the innate and adaptive immune response using multiple virulence factors including coagulase, capsular polysaccharides, adhesins, proteases, exoproteins that inactivate the complement system, pore-forming toxins, and other innate response mediators (Nizet, V., J Allergy Clin Immunol, 2007. 120(1): p. 13-22; Tristan *et al.*, J Hosp Infect, 2007. 65 Suppl 2: p. 105-9). The rapid spread of methicillin resistant SA (MRSA) underscores the importance of developing vaccines for prevention or reduction of severity of MRSA infections. Most previous approaches for vaccine development have ignored the importance of including attenuated toxin components to disarm the immune evasion strategies of SA.

[0006] A significant increase in *S. aureus* isolates that exhibit resistance to most of the antibiotics currently available to treat infections has been observed in hospitals throughout the world. While MRSA strains were initially limited to health care settings, recent epidemics of community associated *S. aureus* (CA-MRSA) have been reported that cause severe disease in an otherwise healthy population. To date, five CA-MRSA clonal lineages are associated with these outbreaks: the Midwest clone (USA400, CC1), the European clone (CC80), the Southwest-Pacific Oceania clone (CC30), the Pacific clone (CC59), and the Pandemic clone (USA300, CC8). In addition to SCC*mec* IV, a characteristic feature of these major CA-MRSA lineages is that they have the *luk*PV operon encoding the Panton Valentine Leukocidin (PVL) (Diep, B.A. and M. Otto, Trends Microbiol, 2008. 16(8): p. 361-9), carried by the lysogenic phages ϕSLT, ϕPVL, ϕSA2MW and ϕSA2usa (Diep *et al.*, Lancet, 2006. 367(9512): p. 731-9; Kaneko *et al.*, Gene, 1998. 215(1): p. 57-67; Narita *et al.*, Gene, 2001. 268(1-2): p. 195-206). The development of penicillin to combat *S. aureus* was a major advance in infection control and treatment. Unfortunately, penicillin-resistant organisms quickly emerged and the need for new antibiotics was paramount. With the introduction of every new antibiotic, *S. aureus* has been able to counter with β-lactamases, altered penicillin-binding proteins, and mutated cell membrane proteins allowing the bacterium to persist. Consequently, methicillin-resistant *S. aureus* (MRSA) and multidrug resistant organisms have emerged and established major footholds in hospitals and nursing homes around the world.

(Chambers, H. F., *Clin Microbiol Rev.,* 1:173, 1988; and Mulligan, M. E., *et al.*, *Am J Med.,* 94:313, 1993). Today, almost half of the Staphylococcal strains causing nosocomial infections are resistant to all antibiotics except vancomycin and linezolid. Since many vancomycin intermediate resistant *S. aureus* (VISA) among MRSA, and a few vancomycin resistant *S. aureus*, have been reported in the literature, it appears to be only a matter of time before vancomycin will become ineffective as well. (Appelbaum PC., *Clin Microbiol Infect.*, 12 Suppl 1:16-23, 2006).

[0007] Natural immunity to *S. aureus* infections remains poorly understood. Typically, healthy humans and animals exhibit a high degree of innate resistance to *S. aureus* infections. Protection is attributed to intact epithelial and mucosal barriers and normal cellular and humoral responses. Titers of antibodies to *S. aureus* components are elevated after severe infections (Ryding *et al.*, *J Med Microbiol,* 43(5):328-334, 1995), however to date there is no serological evidence of a correlation between these acquired antibody titers and human immunity.

[0008] Pore forming toxins that are secreted by *S. aureus* are crucial to its immune evasion. These toxins may create a survival advantage for the bacteria by forming pores into the membrane of target cells, inducing cell death and weakening the host during the first stages of infection. Because of the limited treatment modalities for *S. aureus* infection, the emergence of methicillin-resistant *S. aureus* poses a tremendous public health threat. While the molecular basis of the disease remains unclear, community-associated MRSA infection is closely linked to the presence of a Panton-Valentine leukocidin (PVL), a bipartite toxin consisting of the ~34 kDa LukF-PV and the ~32 kDa LukS-PV proteins (H. F. Chambers. *The New England Journal of Medicine 352*, 1485-1487, 2005). The function of the two PVL components (LukF-PV and LukS-PV) is synergistic and requires a sequence of events at the membrane surface of the target cell (J. Kaneko and Y. Kamio. *Bioscience, Biotechnology, and Biochemistry 68*, 981-1003, 2004). In the first step, the secreted, water-soluble LukF-PV and LukS-PV monomers aggregate on the membrane surface, and subsequently assemble into heterodimers. In a stepwise fashion, these heterodimers further oligomerize into heterotetramers that are characterized by alternating LukF-PV and LukS-PV subunits. These heterotetramers further assemble into an octameric, disc-like structure that is comprised of alternating LukS-PV and LukF-PV subunits in a 1:1 stoichiometry (L. Jayasinghe and H. Bayley. *Protein Sci 14*, 2550-2561,

2005). At this stage, experimental data indicates that PVL exists as an octamer in pre-pore conformation that is not fully functional and not transversing the cell membrane. Subsequently, the pre-pore structure undergoes major conformational changes that result in the formation of a single transmembrane pore that allows the influx of calcium ions, leading to cell death (V. T. Nguyen, Y. Kamio, and H. Higuchi. *The EMBO Journal 22*, 4968-4979, 2003). PVL causes cytolysis resulting in loss of immune cells such as neutrophils and may also cause tissue damage promoting bacterial dissemination. PVL is believed to be involved in pathogenesis of invasive pneumonia and skin infections.

[0009] Accordingly, there remains a need in the art for compositions and methods that can safely confer immunity to PVL-expressing *S. aureus*.

BRIEF SUMMARY

[0010] The present disclosure provides methods of inducing an immune response against a PVL-expressing *S. aureus*, methods of preventing or treating a PVL-expressing *S. aureus* infections, and compositions for preventing or treating a PVL-expressing *S. aureus* infections. In certain embodiments, the disclosure provides attenuated mutants of LukS-PV and LukF-PV as vaccines for *S. aureus* infections.

[0011] Some embodiments include an isolated mutant staphylococcal leukocidin subunit polypeptide comprising a wild-type staphylococcal leukocidin subunit except for one to five amino acid substitutions at conserved residues, which reduce toxicity of the mutant leukocidin subunit relative to the corresponding wild-type leukocidin subunit; where the wild-type leukocidin subunit comprises three consecutive regions designated A-B-C arranged from amino terminus to carboxy terminus, and wherein region B comprises the amino acid sequence of SEQ ID NO: 2.

[0012] Also disclosed is the mutant leukocidin subunit described herein, where region A of the wild-type leukocidin subunit comprises the amino acid sequence of SEQ ID NO: 1 and where region C of the wild-type leukocidin subunit comprises the amino acid sequence of SEQ ID NO: 3.

[0013] Also disclosed is the mutant leukocidin subunit as described herein, which comprises an amino acid substitution at position K24 of SEQ ID NO: 2. In certain embodiments, K24 is substituted with alanine.

[0014] Some embodiments include the mutant leukocidin subunit as described herein, which comprises an amino acid substitution at position S18 of SEQ ID NO: 3. In certain embodiments S18 is substituted with alanine.

[0015] Some embodiments include the mutant leukocidin as described herein, which comprises an amino acid substitution at position Y58 of SEQ ID NO:2. In certain embodiments Y58 is substituted with alanine.

[0016] Some embodiments include the mutant leukocidin subunit as described herein, which comprises an amino acid substitution at position T11 of SEQ ID NO: 1. In certain embodiments T11 is substituted with phenylalanine.

[0017] Some embodiments include the mutant leukocidin subunit as described herein, which comprises an amino acid substitution at position D28 of SEQ ID NO: 2. In certain embodiments D28 is substituted with alanine.

[0018] In some embodiments the wild-type leukocidin subunit is a Panton-Valentine leukocidin (PVL) LukS-PV. In certain embodiments, the wild-type leukocidin subunit comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 5, SEQ ID NO: 15, and SEQ ID NO: 16. In some embodiments the mutant LukS-PV subunit comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, and SEQ ID NO: 14. In certain embodiments the mutant leukocidin subunit as described herein, comprises the amino acid of SEQ ID NO: 14.

[0019] In some embodiments the mutant leukocidin subunit as described herein, comprises a calculated molecular energy between 600 kcal/mol and 7500 kcal/mol, or between 900 kcal/mol and 3900 kcal/mol, or between 2000 kcal/mol and 3650 kcal/mol in complex with a wild-type Panton-Valentine leukocidin (PVL) LukF-PV subunit.

[0020] Some embodiments include an isolated mutant staphylococcal leukocidin subunit polypeptide comprising a wild-type staphylococcal leukocidin subunit except for one to five amino acid substitutions at conserved residues, which reduce toxicity of the mutant leukocidin subunit relative to the corresponding wild-type leukocidin subunit; wherein the wild-type leukocidin subunit comprises the amino acid sequence of SEQ ID NO: 4.

[0021] In some embodiments the mutant leukocidin subunit as described herein, comprises an amino acid substitution at position K8. In certain embodiments K8 is substituted with alanine.

[0022] In some embodiments the mutant leukocidin subunit as described herein, comprises an amino acid substitution at position D28. In certain embodiments D28 is substituted with alanine.

[0023] In some embodiments the mutant leukocidin subunit as described herein, comprises an amino acid substitution at position E53. In certain embodiments E53 is substituted with alanine.

[0024] In some embodiments the wild-type leukocidin subunit is a Panton-Valentine leukocidin (PVL) LukF-PV. In certain embodiments the wild-type leukocidin subunit comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 16, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, and SEQ ID NO: 27. In some embodiments, the mutant LukF-PV subunit comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 18, SEQ ID NO: 19, and SEQ ID NO: 20. In one embodiment, the mutant LukF-PV subunit comprises an amino acid sequence of SEQ ID NO: 18.

[0025] In some embodiments the mutant leukocidin subunit as described herein, comprises a calculated molecular energy between 900 kcal/mol and 1500 kcal/mol in complex with a wild-type Panton-Valentine leukocidin (PVL) LukS-PV.

[0026] Some embodiments include the mutant leukocidin subunit as described herein, which is less toxic in a neutrophil toxicity assay compared to the corresponding wild-type leukocidin subunit.

[0027] Some embodiments include the mutant leukocidin subunit as described herein, which does not oligomerize with a wild-type leukocidin component. In certain embodiments, the wild-type leukocidin component is selected from the group consisting of a LukS-PV subunit, a LukF-PV subunit, Gamma hemolysin A, Gamma hemolysin B, Gamma hemolysin C, LukE and LukD subunit, or any combination thereof.

[0028] Also disclosed is a polypeptide complex comprising the mutant leukocidin subunits as described herein.

[0029] Also disclosed is an isolated polynucleotide comprising a nucleic acid which encodes the mutant leukocidin subunit described herein. In some embodiments, the polynucleotide further comprises a heterologous nucleic acid. In some embodiments, the heterologous nucleic acid comprises a promoter operably associated with the nucleic acid encoding the polypeptide described herein.

[0030] Also included is a vector comprising the polunucleotide described herein, or a host cell comprising the vector. In some embodiments, the vector is a plasmid. In some embodiments, the host cell is a bacterium, an insect cell, a mammalian cell, yeast or a plant cell. In certain embodiments, the bacterium is *Escherichia coli*.

[0031] Also disclosed is a method of producing a mutant staphylococcal leukocidin subunit polypeptide, comprising culturing the host cell described herein and recovering the polypeptide.

[0032] Further disclosed is a composition comprising the mutant leukocidin subunit or the polypeptide complex, as described herein, and a carrier. The composition can further comprise an adjuvant. Further disclosed is a composition comprising an additional staphylococcal antigen. In certain embodiments, the additional staphylococcal antigen is an alpha-hemolysin subunit polypeptide.

[0033] Also disclosed is a method of inducing a host immune response against a *Staphylococcus aureus* strain, comprising administering to a subject in need of the immune response an effective amount of the composition described herein. In certain embodiments the immune response is an antibody response. In some embodiments the the immune response selected from the group consisting of an innate response, a humoral response, an antibody response a T cell response, and a combination of two or more of said immune responses.

[0034] Also disclosed is a method of preventing or treating a Staphylococcal disease or infection in a subject comprising administering to a subject in need thereof the composition described herein. The infection can be localized or systemic infection of skin, soft tissue, blood, or an organ, or is auto-immune in nature, and disease can be a respiratory disease, such as pneumonia. The subject can be an animal, a vertebrate, a mammal, or a human. The composition described herein can be administered via intramuscular injection, intradermal injection, intraperitoneal injection, subcutaneous injection, intravenous injection, oral administration, mucosal administration, intranasal administration, or pulmonary administration.

[0035] Also included is a method of producing a vaccine against *S. aureus* infection comprising isolating the mutant leukocidin subunit or the polypeptide complex, as described herein, and combining the mutant leukocidin subunit or polypeptide complex with an adjuvant.

In certain embodiments, the method discloses further comprising combining the mutant leukocidin subunit or polypeptide complex with an additional staphylococcal antigen.

BRIEF DESCRIPTION OF THE DRAWING

[0036] Figure 1-Interface interactions between Thr28 of LukS-PV and Asn158 and Phe159 of LukF-PV.

[0037] Figure 2-Interface interaction between Ser209 of LukS-PV and Lys102 of LukF-PV.

[0038] Figure 3-Percent (%) survival of HL-60 derived neutrophils in the presence of 3000 or 300 ng/ml of LukS-PV mutants (K97A, D101A, S209A, T28F, T28F/Y131A, T28F/S209A, or T28F/K97A/S209A) or the wild-type LukS-PV along with the same concentrations of the wild-type LukF-PV. Cells only bar represents the control with no toxin added. Data are shown as average of 3-5 experiments with standard deviation shown as error bars.

[0039] Figure 4-Percent (%) survival of HL-60 derived neutrophils in the presence of 3000 or 300 ng/ml of LukF-PV mutants (K102A, D121A, or E147A) or the wild-type LukF-PV along with the same concentrations of the wild-type LukS-PV or triple mutant of LukS-PV as defined in Figure 3. Cells only bar represents the control with no toxin added.

[0040] Figure 5-Alignment of S subunits of leukocidins amino acid sequences.

[0041] Figure 6-Percent (%) survivial of polymorphonuclear neutrophils (PMN) in supernatants of PVL positive (USA300&400) and PVL negative (Newman, 8325-4) SA strains treated with anti-LukS-PV or control (rabbit total IgG). PVL: purified PVL; BHI: medium control; and Cells only: control with no toxin added.

[0042] Figure 7-(**A**) SDS-PAGE and (**B**) Western blot analysis of mutant PVL subunits. M: MW marker; Lane 1: LukS-PV Mut9; Lane 2: LukF-PV Mut1. **(C)** SDS-PAGE (Lane 1) and Western blot (Lane 2) analysis of LukF-PV triple mutant (K102A/D121A/E147A); M: MW marker.

[0043] Figure 8-(**A**) Percent (%) survival of HL-60 derived neutrophils treated with increasing concentrations of wild-type or mutant LukS in combination with wild-type LukF. Results are from 5 independent experiments. STDV is shown only for wild-type and triple mutant. (**B**) % survival of HL-60 derived neutrophils treated with increasing concentrations of wild-type or mutant LukF in combination with wild-type LukS or LukS Triple mutant (Mut9). (**C**) % survival of HL-60 with increasing concentrations of wild-

type or triple mutant LukF or LukF mutant 1 in combination with wild-type LukS or LukS Triple mutant (Mut9).

[0044] Figure 9-Thermal unfolding of LukS-PV and LukF-PV proteins as monitored by thermofluor assay using Sypro Orange dye. (**A**) Plot of fluorescence intensity of PVL proteins (wild-type LukS-PV, LukS-PV Mut 8, LukS-PV Mut 9, wild-type LukF-PV, and LukF-PV Mut 1) at 588 nm against temperature. Data was collected for every 5°C. (**B**) Plot of unfolded fraction calculated from the thermal denaturation curve for PVL proteins (wild-type LukS-PV, LukS-PV Mut 8, LukS-PV Mut 9, wild-type LukF-PV, and LukF-PV Mut 1).

[0045] Figure 10-Immunogenicity of LukS-Mut9, wild-type LukS-PV, and control (STEBVax) in mice with different adjuvants. Doses used: antigens: 10 ug; Al(OH)3: 34 ug, AlPO4: 70 ug, IDC-1001: 20 ug, and CpG: 10 ug/mouse. (**A**) Total antibody titers determined by ELISA for individual mouse sera (EC50; i.e. dilution of serum with 50% maximal signal on ELISA plates coated with wild type LukS-PV). (**B**) Neutralization determined in HL-60 toxin neutralization assay using wild type LukS-PV and LukF-PV toxins. Percent neutralization of wild type toxin is shown at 1:100 dilution of serum from vaccinated mice (sera pooled from 5 mice in each group).

[0046] Figure 11-Bacterial CFU in blood and organs (liver, spleen, lung, and kidneys) after treatment of mice with 2 mg naïve IgG (N), 2 mg AT62-IgG (AT) or the combination of 2mg AT62-IgG and 0.25 mg of LukS-PV IgG (AT+S).

[0047] Figure 12-Survival curves showing protection against (**A**) bacteremia/sepsis and (**B**) pneumonia with Luk (LukS Mut 9, LukF Mut1, and LukS Mut 9 + LukF Mut1) and Hla (AT-62aa) vaccine candidates as well as the combination of LukS Mut 9 + LukF Mut1 + AT-62aa and BSA control. No further lethality was observed after the time points shown.

[0048] Figure 13-(**A**) Specificity of LukS-PV mutant-9 mouse sera to homologous antigen, (**B**) Cross-reactivity of LukS-PV mutant-9 mouse sera to HlgB antigen, (**C**) Cross-reactivity of LukS-PV mutant-9 mouse sera to HlgC antigen. (**D**) Neutralization efficacy of LukS-PV mutant-9 mouse sera against 200 ng/ml of PVL and or gamma-hemolysin toxins in invitro XTT cytotoxicity assay based on human neutrophil cell line HL-60.

[0049] Figure 14-(**A**) MPD based oligomerization assay. Lane 1: Molecular weight marker; Lane 2: LukS wt+LukFwt; Lane 3: LukS wt +Lukf mut1; Lane 4: LukS wt+ Gamma B; Lane 5: LukF wt+ LukS mut9; Lane 6: LukS mut9 + LukF mut1; Lane 7: LukS mut9 +

Gamma B. **(B)** Inhibition of oligomeric band by anti LukS specific polyclonal antibody. Lane 1: Marker; Lanes 2-8: LukS+LukF + anti-LukS pAbs at 2-fold decreasing concentrations (5.5mg/ml to 0.85mg/ml); Lane 9: LukS+LukF without pAbs; Lane 10: LukS+LukF+ pAbs without MPD; Lane 11: pAbs + MPD only. **(C)** Inhibition of oligomeric band formed by LukS-PV + hlgB by anti LukS specific polyclonal antibody. Lane 1: Marker; Lanes 2-8: LukS-PV + hlgB (940 ng each) + anti-LukS pAbs at 2-fold decreasing concentrations (34.5 ug/ml to 0.5mg/ml); Lane 9: LukS-PV + hlgB without pAbs; Lane 10: LukS-PV + hlgB + pAbs without MPD; Lanes 11-14 Naïve Rabbit pAbs (34.5 ug/ml to 4.3 mg/ml) + LukS-PV + hlgB (940 ng each) and Lane 15: Naïve Rabbit pAbs+ MPD only.

DETAILED DESCRIPTION

[0050] Disclosed herein are mutant staphylococcal leukocidin subunit polypeptides, *e.g.*, a mutant LukS-PV subunit polypeptide or a mutant LukF-PV subunit polypeptide, compositions comprising one or more mutant leukocidin subunits as disclosed herein, and methods of eliciting an immune response against staphylococci, e.g. *S. aureus*, or treating or preventing a staphylococcal infection in a subject, comprising administering to a subject an effective amount of a mutant staphylococcal leukocidin subunit polypeptide as disclosed herein.

[0051] It is to be noted that the term "a" or "an" entity refers to one or more of that entity; for example, "a polynucleotide," is understood to represent one or more polynucleotides. As such, the terms "a" (or "an"), "one or more," and "at least one" can be used interchangeably herein.

[0052] The terms "nucleic acid" or "nucleic acid fragment" refers to any one or more nucleic acid segments, *e.g.*, DNA or RNA fragments, present in a polynucleotide or construct. Two or more nucleic acids of the disclosure can be present in a single polynucleotide construct, *e.g.*, on a single plasmid, or in separate (non-identical) polynucleotide constructs, *e.g.*, on separate plasmids. Furthermore, any nucleic acid or nucleic acid fragment can encode a single polypeptide, *e.g.*, a single antigen, cytokine, or regulatory polypeptide, or can encode more than one polypeptide, *e.g.*, a nucleic acid can encode two or more polypeptides. In addition, a nucleic acid can encode a regulatory element such as a promoter or a transcription terminator, or can encode a specialized element or

motif of a polypeptide or protein, such as a secretory signal peptide or a functional domain.

[0053] The term "polynucleotide" is intended to encompass a singular nucleic acid or nucleic acid fragment as well as plural nucleic acids or nucleic acid fragments, and refers to an isolated molecule or construct, *e.g.*, a virus genome (*e.g.*, a non-infectious viral genome), messenger RNA (mRNA), plasmid DNA (pDNA), or derivatives of pDNA (*e.g.*, minicircles as described in (Darquet, A-M *et al.*, *Gene Therapy* 4:1341-1349, 1997) comprising a polynucleotide. A polynucleotide can be provided in linear (*e.g.*, mRNA), circular (*e.g.*, plasmid), or branched form as well as double-stranded or single-stranded forms. A polynucleotide can comprise a conventional phosphodiester bond or a non-conventional bond (*e.g.*, an amide bond, such as found in peptide nucleic acids (PNA)).

[0054] As used herein, the term "polypeptide" is intended to encompass a singular "polypeptide" as well as plural "polypeptides," and comprises any chain or chains of two or more amino acids. Thus, as used herein, a "peptide," an "oligopeptide," a "dipeptide," a "tripeptide," a "protein," an "amino acid chain," an "amino acid sequence," or any other term used to refer to a chain or chains of two or more amino acids, are included in the definition of a "polypeptide," (even though each of these terms can have a more specific meaning) and the term "polypeptide" can be used instead of, or interchangeably with any of these terms. The term further includes polypeptides which have undergone post-translational modifications, for example, glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, or modification by non-naturally occurring amino acids.

[0055] The terms "staphylococcal leukocidin subunit," "LukS-PV polypeptide," and "LukF-PV polypeptide," as used herein, encompass mature or full length staphylococcal leukocidin subunits (*e.g.*, LukS-PV or LukF-PV), and fragments, variants or derivatives of mature or full length staphylococcal leukocidin subunits (*e.g.*, LukS-PV and LukF-PV), and chimeric and fusion polypeptides comprising mature or full length staphylococcal leukocidin subunits (*e.g.*, LukS-PV and LukF-PV) or one or more fragments of mature or full length staphylococcal leukocidin subunits (*e.g.*, LukS-PV and LukF-PV). In certain embodiments, staphylococcal leukocidin subunits as disclosed herein are mutant staphylococcal leukocidin subunits, which are reduced in toxicity relative to a corresponding wild-type leukocidin subunit. By "corresponding wild-type leukocidin

subunit" is meant the native leukocidin subunit from which the mutant leukocidin subunit was derived.

[0056] Pore forming toxins, *e.g.*, single-component alpha-hemolysin and the bi-component hemolysins and leukotoxins, play an important role in staphylococcal immune evasion. These toxins kill key immune cells and cause tissue destruction, thereby often weakening the host during the first stage of infection and promoting bacterial dissemination and metastatic growth. The two PVL components, LukS-PV and LukF-PV, are secreted separately and form the pore-forming octameric complex upon binding of LukS-PV to its receptor and subsequent binding of LukF-PV to LukS-PV (Miles *et al.*, Protein Sci, 2002. 11(4): p. 894-902; Pedelacq *et al.*, Int J Med Microbiol, 2000. 290(4-5): p. 395-401). Targets of PVL include, *e.g.*, polymorphonuclear neutrophils (PMN), monocytes, and macrophages.

[0057] Other bi-component toxins have been characterized in *S. aureus*: S components HlgA and HlgC and the F component HlgB for γ-hemolysin; lukE (S) and lukD (F); and lukM (S) and lukF-PV-like (F). Due to their close similarity, these S components can combine with a F component and form an active toxin with different target specificity (Ferreras *et al.*, Biochim Biophys Acta, 1998. 1414(1-2): p. 108-26; Prevost *et al.*, Infect Immun, 1995. 63(10): p. 4121-9). γ-Hemolysin is strongly hemolytic and 90% less leukotoxic than PVL, while PVL is non-hemolytic. However, HlgA or HlgC paired with lukF-PV promotes leukotoxic activity (Prevost *et al.*, Infect Immun, 1995. **63**(10): p. 4121-9). Luk and PVL lyse neutrophils, and Hlg is hemolytic (Kaneko *et al.,* Biosci Biotechnol Biochem, 2004. 68(5): p. 981-1003) and was also reported to lyse neutrophils (Malachowa et al., PLoS One, 2011. 6(4): p. e18617). While PVL subunits are phage derived (the F&S leukocidin), Hlg proteins are derived from Hlg locus (*hlg*) and found in 99% of clinical isolates (Kaleko *et al.*). Hlg subunits are strongly upregulated during *S. aureus* growth in blood (Malachowa *et al.*), and Hlg was shown to be involved in survival of *S. aureus* in blood (Malachowa *et al.*, Virulence, 2011. 2(6)). The mutant USA300 Δ-hlgABC has reduced capacity to cause mortality in a mouse bacteremia model (Malachowa *et al.*, PLoS One, 2011. 6(4): p. e18617). *Alonzo et al.* have shown that LukED toxin is critical for bloodstream infections in mice (Alonzo *et al.*, Mol Microbiol, 2012. 83(2): p. 423-35). Another novel *S. aureus* leukotoxin, LukGH, has also

been described, which synergizes with PVL to enhance human PMN lysis (Ventura *et al.*, PLoS One, 2010. 5(7): p. e11634).

[0058] The terms "fragment," "analog," "derivative," or "variant" when referring to a staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV) of the present disclosure include any polypeptide which retains at least some of the immunogenicity or antigenicity of the source protein. Fragments of staphylococcal leukocidin subunits (*e.g.*, LukS-PV or LukF-PV) as described herein include proteolytic fragments, deletion fragments and in particular, fragments of staphylococcal leukocidin subunits (*e.g.*, LukS-PV or LukF-PV) which exhibit increased solubility during expression, purification, or administration to an animal. Fragments of staphylococcal leukocidin subunits (*e.g.*, LukS-PV or LukF-PV) as described herein further include proteolytic fragments or deletion fragments which exhibit reduced pathogenicity or toxicity when delivered to a subject. Polypeptide fragments further include any portion of the polypeptide which comprises an antigenic or immunogenic epitope of the source polypeptide, including linear as well as three-dimensional epitopes.

[0059] An "epitopic fragment" of a polypeptide antigen is a portion of the antigen that contains an epitope. An "epitopic fragment" can, but need not, contain amino acid sequence in addition to one or more epitopes.

[0060] The term "variant," as used herein, refers to a polypeptide that differs from the recited polypeptide due to amino acid substitutions, deletions, insertions, and/or modifications. Non-naturally occurring variants can be produced using art-known mutagenesis techniques. In some embodiments, variant polypeptides differ from an identified sequence by substitution, deletion or addition of three amino acids or fewer. Such variants can generally be identified by modifying a polypeptide sequence, and evaluating the antigenic or pathogenic properties of the modified polypeptide using, for example, the representative procedures described herein. In some embodiments, variants of a wild-type staphylococcal leukocidin subunit (*e.g.*, LukS-PV, or LukF-PV, or both) form a protein complex which is less toxic than the wild-type complex.

[0061] Polypeptide variants disclosed herein exhibit at least about 85%, 90%, 94%, 95%, 96%, 97%, 98%, 99% or 99.9% sequence identity with identified polypeptide. Variant polypeptides can comprise conservative or non-conservative amino acid substitutions, deletions or insertions. Variants can comprise staphylococcal leukocidin subunits (*e.g.*,

LukS-PV or LukF-PV, or both) identical to a wild-type leukocidin subunit except for at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, or more amino acid substitutions, where the substitutions render a leukocidin complex comprising the variant leukocidin subunit less toxic than a corresponding wild-type protein complex. Derivatives of staphylococcal leukocidin subunits (*e.g.*, LukS-PV and LukF-PV) as described herein are polypeptides which have been altered so as to exhibit additional features not found on the native polypeptide. Examples include fusion proteins. An analog is another form of a staphylococcal leukocidin subunit (*e.g.*, LukS-PV and LukF-PV) described herein. An example is a proprotein which can be activated by cleavage of the proprotein to produce an active mature polypeptide.

[0062] Variants can also, or alternatively, contain other modifications, whereby, for example, a polypeptide can be conjugated or coupled, *e.g.*, fused to a heterologous amino acid sequence, *e.g.*, a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide can also be conjugated or produced coupled to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, 6-His), or to enhance binding of the polypeptide to a solid support. For example, the polypeptide can be conjugated or coupled to an immunoglobulin Fc region. The polypeptide can also be conjugated or coupled to a sequence that imparts or modulates the immune response to the polypeptide (*e.g.*, a T-cell epitope, B-cell epitope, cytokine, chemokine, etc.) and/or enhances uptake and/or processing of the polypeptide by antigen presenting cells or other immune system cells. The polypeptide can also be conjugated or coupled to other polypeptides/epitopes from *Staphylococcus sp.* and/or from other bacteria and/or other viruses to generate a hybrid immunogenic protein that alone or in combination with various adjuvants can elicit protective immunity to other pathogenic organisms. The polypeptide can also be conjugated or coupled to moieties which confer greater stability or improve half life such as, but not limited to albumin, an immunoglobulin Fc region, polyethylene glycol (PEG), and the like. The polypeptide can also be conjugated or coupled to moieties (*e.g.*, immunogenic carbohydrates, *e.g.*, a capsular polysaccharide or a surface polysaccharide) from *Staphylococcus sp.* and/or from other bacteria and/or other viruses to generate a modified immunogenic protein that alone or in combination with one or more adjuvants can enhance and/or synergize protective immunity. In certain

embodiments, the polypeptide described herein further comprises an immunogenic carbohydrate. In one embodiment, the immunogenic carbohydrate is a saccharide.

[0063] The term "saccharide" throughout this specification may indicate polysaccharide or oligosaccharide and includes both. Polysaccharides of the invention may be isolated from bacteria and may be sized by known methods. For example, full length polysaccharides may be "sized" (*e.g.*, their size may be reduced by various methods such as acid hydrolysis treatment, hydrogen peroxide treatment, sizing by EMULSIFLEX® followed by a hydrogen peroxide treatment to generate oligosaccharide fragments or microfluidization). Polysaccharides can be sized in order to reduce viscosity in polysaccharide samples and/or to improve filterability for conjugated products. Oligosaccharides have a low number of repeat units (*e.g.*, 5-30 repeat units) and are typically hydrolysed polysaccharides. Polysaccharides of the invention may be produced recombinantly.

[0064] *S. aureus* capsular antigens are surface associated, limited in antigenic specificity, and highly conserved among clinical isolates. In one embodiment, the immunogenic carbohydrate of the invention is a capsular polysaccharide (CP) of *S. aureus*. In one embodiment, a capsular saccharide may be a full length polysaccharide, however in other embodiments it may be one oligosaccharide unit, or a shorter than native length saccharide chain of repeating oligosaccharide units. Serotyping studies of staphylococcal isolates have revealed several putative capsular serotypes, with types 5 and 8 (CP5 and CP8) being the most prevalent among isolates from clinical infections, accounting for about 25% and 50% of isolates recovered from humans, respectively (O'Riordan and Lee, Clinical Microbiology Reviews, January 2004, p. 218-234, Vol. 17, No. 1; Poutrel and Sutra , J Clin Microbiol. 1993 Feb;31(2):467-9). The same isolates were also recovered from poultry, cows, horses and pigs (Tollersrud *et al.*, J Clin Microbiol. 2000 Aug;38(8):2998-3003; Cunnion KM *et al.*, Infect Immun. 2001 Nov;69(11):6796-803). Type 5 and 8 capsular polysaccharides purified from the prototype strains Reynolds and Becker, respectively, are structurally very similar to each other and to the capsule made by strain T, described previously by Wu and Park (Wu and Park. 1971. J. Bacteriol. 108:874-884). Type 5 has the structure (→4)-3-O-Ac-ß-D-ManNAcA-(1→4)-«-L-FucNAc-(1→3)-ß-D-FucNAc-(1→)$_n$ (Fournier, J. M., *et al.*, 1987. Ann. Inst. Pasteur Microbiol. 138:561-567; Moreau, M., *et al.*, 1990. Carbohydr. Res. 201:285-297), and

type 8 has the structure (→3)-4-O-Ac-ß-D-ManNAcA-(1→3)-α-L-FucNAc-(1→3)-ß-D-FucNAc-(1→)$_n$ (Fournier, J. M., *et al.*, 1984. Infect. Immun. 45:87-93). Type 5 and 8 polysaccharides differ only in the linkages between the sugars and in the sites of O-acetylation of the mannosaminuronic acid residues, yet they are serologically distinct.

[0065] Type 5 and 8 CP conjugated to a detoxified recombinant *Pseudomonas aeruginosa* exotoxin A carrier were shown to be highly immunogenic and protective in a mouse model (A Fattom *et al.*, Infect Immun. 1993 March; 61(3): 1023–1032; A Fattom et al., Infect Immun. 1996 May; 64(5): 1659–1665) and passive transfer of the CP5-specific antibodies from the immunized animals induced protection against systemic infection in mice (Lee *et al.*, Infect Immun. 1997 October; 65(10): 4146–4151) and against endocarditis in rats challenged with a serotype 5 *S. aureus* (Shinefield H *et al.*, N Engl J Med. 2002 Feb 14;346(7):491-6). A bivalent CP5 and CP8 conjugate vaccine (StaphVAX®, Nabi Biopharmaceutical) was developed that provided 75% protection in mice against *S. aureus* challenge. The vaccine has been tested on humans (Fattom AI *et al.*, Vaccine. 2004 Feb 17;22(7):880-7; Maira-Litrán T *et al.,* Infect Immun. 2005 Oct;73(10):6752-62). In certain embodiments, the oligopeptide of the invention is combined with or conjugated to an immunogenic carbohydrate (*e.g.*, CP5, CP8, a CP fragment or a combination thereof).

[0066] Immunization with poly-N-acetylglucosamine (PNAG) (McKenney D. *et al.*, Science. 1999 May 28;284(5419):1523-7) or poly-N-succinyl glucosamine (PNSG) (Tuchscherr LP. *et al.*, Infect Immun. 2008 Dec;76(12):5738-44. Epub 2008 Sep 22), both *S. aureus* surface carbohydrates, has been shown to generate at least partial protection against *S. aureus* challenge in experimental animal models. PNSG was identified as the chemical form of the *S. epidermidis* capsular polysaccharide/adhesin (PS/A) which mediates adherence of coagulase-negative staphylococci (CoNS) to biomaterials, serves as the capsule for strains of CoNS that express PS/A, and is a target for protective antibodies. PNSG is also made by *S. aureus*, where it is an environmentally regulated, *in vivo*-expressed surface polysaccharide and similarly serves as a target for protective immunity (McKenney D. *et al.*, J. Biotechnol. 2000 Sept 29;83(1-2): 37-44). In certain embodiments of the invention, the immunogenic carbohydrate is a surface polysaccharide, *e.g.*, poly-N-acetylglucosamine (PNAG), poly-N-succinyl glucosamine (PNSG), a surface polysaccharide fragment or a combination thereof.

[0067] Wall Teichoic Acid (WTA) is a prominent polysaccharide widely expressed on *S. aureus* strains (Neuhaus, F.C. and J. Baddiley, Microbiol Mol Biol Rev, 2003. 67(4):686-723) and antisera to WTA have been shown to induce opsonophagocytic killing alone and in presence of complement ((Thakker, M., et al., Infect Immun, 1998. 66(11):5183-9), *and Fattom et al, US Patent 7,754,225*). WTA is linked to peptidoglycans and protrudes through the cell wall becoming prominently exposed on non-encapsulated strains such as USA300 responsible for most cases of community acquired MRSA (CA MRSA) in the US (Hidron, A.I., et al., Lancet Infect Dis, 2009. 9(6):384-92).

[0068] Lipoteichoic acid (LTA) is a constituent of the cell wall of Gram-positive bacteria, *e.g.*, *Staphylococcus aureus*. LTA may bind to target cells non-specifically through membrane phospholipids, or specifically to CD14 and to Toll-like receptors. Target-bound LTA can interact with circulating antibodies and activate the complement cascade to induce a passive immune kill phenomenon. It also triggers the release from neutrophils and macrophages of reactive oxygen and nitrogen species, acid hydrolases, highly cationic proteinases, bactericidal cationic peptides, growth factors, and cytotoxic cytokines, which may act in synergy to amplify cell damage.

[0069] In certain embodiments, a surface polysaccharide is combined with or conjugated to a polypeptide of the disclosure. In certain embodiments the surface polysaccharide is, *e.g.*, poly-N-acetylglucosamine (PNAG), poly-N-succinyl glucosamine (PNSG), Wall Teichoic Acid (WTA), Lipoteichoic acid (LPA), a fragment of any of said surface polysaccharides, or a combination of two or more of said surface polysaccharides.

[0070] The term "sequence identity" as used herein refers to a relationship between two or more polynucleotide sequences or between two or more polypeptide sequences. When a position in one sequence is occupied by the same nucleic acid base or amino acid in the corresponding position of the comparator sequence, the sequences are said to be "identical" at that position. The percentage "sequence identity" is calculated by determining the number of positions at which the identical nucleic acid base or amino acid occurs in both sequences to yield the number of "identical" positions. The number of "identical" positions is then divided by the total number of positions in the comparison window and multiplied by 100 to yield the percentage of "sequence identity." Percentage of "sequence identity" is determined by comparing two optimally aligned sequences over a comparison window and a homologous polypeptide from another isolate. In order to

optimally align sequences for comparison, the portion of a polynucleotide or polypeptide sequence in the comparison window can comprise additions or deletions termed gaps while the reference sequence is kept constant. An optimal alignment is that alignment which, even with gaps, produces the greatest possible number of "identical" positions between the reference and comparator sequences. Percentage "sequence identity" between two sequences can be determined using the version of the program "BLAST 2 Sequences" which is available from the National Center for Biotechnology Information as of September 1, 2004, which program incorporates the programs BLASTN (for nucleotide sequence comparison) and BLASTP (for polypeptide sequence comparison), which programs are based on the algorithm of Karlin and Altschul (*Proc. Natl. Acad. Sci. USA* 90(12):5873-5877, 1993). When utilizing "BLAST 2 Sequences," parameters that were default parameters as of September 1, 2004, can be used for word size (3), open gap penalty (11), extension gap penalty (1), gap drop-off (50), expect value (10) and any other required parameter including but not limited to matrix option.

[0071] The term "epitope," as used herein, refers to portions of a polypeptide having antigenic or immunogenic activity in an animal, for example a mammal, for example, a human. An "immunogenic epitope," as used herein, is defined as a portion of a protein that elicits an immune response in an animal, as determined by any method known in the art. The term "antigenic epitope," as used herein, is defined as a portion of a protein to which an antibody or T-cell receptor can immunospecifically bind its antigen as determined by any method well known in the art. Immunospecific binding excludes non-specific binding but does not necessarily exclude cross-reactivity with other antigens. Whereas all immunogenic epitopes are antigenic, antigenic epitopes need not be immunogenic.

[0072] As used herein, a "coding region" is a portion of nucleic acid which consists of codons translated into amino acids. Although a "stop codon" (TAG, TGA, or TAA) is not translated into an amino acid, it can be considered to be part of a coding region, but any flanking sequences, for example promoters, ribosome binding sites, transcriptional terminators, and the like, are outside the coding region.

[0073] The term "codon optimization" is defined herein as modifying a nucleic acid sequence for enhanced expression in the cells of the host of interest by replacing at least one, more than one, or a significant number, of codons of the native sequence with codons that are

more frequently or most frequently used in the genes of that host. Various species exhibit particular bias for certain codons of a particular amino acid.

[0074] The term "composition," or "pharmaceutical composition" can include compositions containing immunogenic polypeptides of the disclosure along with *e.g.*, adjuvants or pharmaceutically acceptable carriers, excipients, or diluents, which are administered to an individual already suffering from *S. aureus* infection or an individual in need of immunization against *S. aureus* infection.

[0075] The term "pharmaceutically acceptable" refers to compositions that are, within the scope of sound medical judgment, suitable for contact with the tissues of human beings and animals without excessive toxicity or other complications commensurate with a reasonable benefit/risk ratio. In some embodiments, the polypeptides, polynucleotides, compositions, and vaccines described herein are pharmaceutically acceptable.

[0076] An "effective amount" is that amount the administration of which to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. An amount is effective, for example, when its administration results in a reduced incidence of *S. aureus* infection relative to an untreated individual, as determined, *e.g.*, after infection or challenge with infectious *S. aureus*, including, but is not limited to reduced bacteremia, reduced toxemia, reduced sepsis, reduced symptoms, increased immune response, modulated immune response, or reduced time required for recovery. This amount varies depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated (*e.g.*, human, nonhuman primate, primate, etc.), the responsive capacity of the individual's immune system, the extent of treatment or protection desired, the formulation of the vaccine, a professional assessment of the medical situation, and other relevant factors. It is expected that the effective amount will fall in a relatively broad range that can be determined through routine trials. Typically a single dose is from about 10 μg to 10 mg/kg body weight of purified polypeptide or an amount of a modified carrier organism or virus, or a fragment or remnant thereof, sufficient to provide a comparable quantity of recombinantly expressed mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein. The term "peptide vaccine" or "subunit vaccine" refers to a composition comprising one or more polypeptides described herein, which when administered to an

animal are useful in stimulating an immune response against staphylococcal (*e.g., S. aureus*) infection.

[0077] The term "subject" is meant any subject, particularly a mammalian subject, for whom diagnosis, prognosis, immunization, or therapy is desired. Mammalian subjects include, but are not limited to, humans, domestic animals, farm animals, zoo animals such as bears, sport animals, pet animals such as dogs, cats, guinea pigs, rabbits, rats, mice, horses, cattle, bears, cows; primates such as apes, monkeys, orangutans, and chimpanzees; canids such as dogs and wolves; felids such as cats, lions, and tigers; equids such as horses, donkeys, and zebras; food animals such as cows, pigs, and sheep; ungulates such as deer and giraffes; rodents such as mice, rats, hamsters and guinea pigs; and so on. In one embodiment, the subject is a human subject.

[0078] As used herein, a "subject in need thereof" refers to an individual for whom it is desirable to treat, *i.e.*, to prevent, cure, retard, or reduce the severity of staphylococcal (*e.g., S. aureus*) disease symptoms, or result in no worsening of disease cause by *S. aureus* over a specified period of time, or both.

[0079] The terms "priming" or "primary" and "boost" or "boosting" as used herein to refer to the initial and subsequent immunizations, respectively, *i.e.*, in accordance with the definitions these terms normally have in immunology. However, in certain embodiments, *e.g.*, where the priming component and boosting component are in a single formulation, initial and subsequent immunizations may not be necessary as both the "prime" and the "boost" compositions are administered simultaneously.

Polypeptides

[0080] Disclosed is an isolated mutant staphylococcal leukocidin subunit polypeptide comprising, consisting of, or consisting essentially of a wild-type staphylococcal leukocidin subunit except for 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20 or more amino acid substitutions at conserved residues, which reduce toxicity of the mutant leukocidin subunit relative to the corresponding wild-type leukocidin subunit; where the wild-type leukocidin subunit comprises, consists of, or consists essentially of three consecutive regions designated A-B-C arranged from amino terminus to carboxy terminus, and where region B comprises the amino acid consensus sequence presented here as SEQ ID NO: 2:

FQYNI**X1**L**X2X3X4**D**X5X6X7X8**LIN**X9X10X11**LPK**X12**KI**X13X14X15X16**V**X17**Q**X18**LGYN**X19**G**X20X21X22X23X24X25X26X27X28X29**G**X30**G**X31**F**X32**YSK; where

X1=Glycine(G), Serine(S) or Alanine(A)

X2=Lysine(K),Threonine(T), Serine(S) or Methionine(M)

X3=Threonine(T) or Serine(S)

X4=Asparagine(N) or Lysine(K)

X5=Proline(P), Lysine(K), Serine(S) or Glutamine(Q)

X6=Asparagine(N) or Tyrosine(Y)

X7=Valine(V), Threonine(T) or Isoleucine(I)

X8=Aspartic acid(D),Serine(S) or Phenylalanine(F)

X9=Serine(S) or no amino acid

X10=Isoleucine(I) or no amino acid

X11=Tyrosine(Y), Histidine(H) or Threonine(T)

X12=Asparagine(N) or Threonine(T)

X13=Aspartic acid(D) or Glutamic acid (E)

X14=Serine(S) or Threonine(T)

X15=Valine(V), Threonine(T), Alanine(A) or Isoleucine(I)

X16=Asparagine(N) or Aspartic acid(D)

X17=Serine(S) or Glycine(G)

X18=Threonine(T) or Lysine(K)

X19=Isoleucine(I) orValine(V)

X20= Glycine(G)or no amino acid

X21= Asparagine(N), Lysine(K) or no amino acid

X22= Phenylalanine(F) or no amino acid

X23= Asparagine(N), Glutamine(Q) or no amino acid

X24=Serine(S), Threonine(T) or no amino acid

X25=Glycine(G), Alanine(A), Valine(V) or no amino acid

X26=Proline(P) or no amino acid

X27=Serine(S), Leucine(L) or no amino acid

X28=Threonine(T), Leucine(L), Isoleucine(I) or no amino acid

X29=Glycine(G), Alanine(A) or no amino acid

X30=Asparagine(N), Serine(S) or Lysine(K)

X31=Serine(S), Alanine(A)or Glutamic acid (E); and

X32=Asparagine(N) or Serine(S).

[0081] In some embodiments, region A of the wild-type leukocidin subunit comprises the amino acid consensus sequence presented here as SEQ ID NO: 1:

X1X2X3X4S**X5X6X7X8X9**TQN**X10**QF**X11**F**X12**KD**X13**KYNK**X14**AL**X15X16**KMQ GFI**X17**S**X18**T**X19X20X21X22X23**K**X24X25X26X27X28X29X30**K**X31X32X33**WP; where

X1=Glutamic acid (E), Glutamine(Q) or no amino acid

X2=Aspartic acid(D), Glycine(G)or no amino acid

X3=Threonine(T), Lysine(K), Isoleucine(I), Valine(V)or no amino acid

X4=Serine(S), Threonine(T), Alanine(A) or no amino acid

X5=Aspartic acid(D), Lysine(K), Asparagine(N), Arginine(R) or no amino acid

X6=Lysine(K), Arginine(R) or no amino acid

X7=Tryptophan(W), Leucine(L) or no amino acid

X8=Glycine(G), Alanine(A) or no amino acid

X9=Valine(V), Isoleucine(I) or no amino acid

X10=Isoleucine(I),Valine(V) or no amino acid

X11=Aspartic acid(D), Glycine(G) or no amino acid

X12=Valine(V) or Methionine(M)

X13=Lysine(K), Threonine(T) or Proline(P)

X14=Aspartic acid(D), Asparagine(N) orValine(V)

X15=Isoleucine(I) or Valine(V)

X16=Leucine(L), Valine(V) or Isoleucine(I)

X17=Asparagine(N), Serine(S) or Lysine(K)

X18=Lysine(K) or Arginine(R)

X19=Threonine(T), Serine(S) or Alanine(A)

X20=Tyrosine(Y) or Phenylalanine(F)

X21=Tyrosine(Y), Serine(S), Asparagine(N) or Threonine(T)

X22=Asparagine(N) or Aspartic acid(D)

X23=Tyrosine(Y),Valine(V), Leucine(L),Phenylalanine(F) or Serine(S)

X24=Asparagine(N), Lysine(K), Glycine(G) or Glutamine(Q)

X25=Threonine(T), Tyrosine(Y), Serine(S), Asparagine(N), Lysine(K) or Arginine(R)

X26=Glycine(G) or no amino acid

X27=Tyrosine(Y) or no amino acid

X28=Aspartic acid(D), Asparagine(N), Glutamic acid (E), Proline(P) orArginine(R)

X29=Histidine(H), Tyrosine(Y), Leucine(L) or Alanine(A)

X30=Isoleucine(I), Threonine(T),Valine(V) or Asparagine(N)

X31=Alanine(A), Arginine(R) or Serine(S)

X32=Methionine(M), Isoleucine(I) or Leucine(L); and

X33=Arginine(R), Isoleucine(I), Valine(V) or Leucine(L).

[0082] In some embodiments, region C of the wild-type leukocidin subunit comprises the amino acid consensus sequence presented here as SEQ ID NO: 3:

F**X1X2X3X4X5**LPPL**X6X7**SGFNPSFI**X8TX9**SHE**X10X11X12X13X14X15X16X17X18X19X20X21X22**YGRN**X23**D**X24TX25**A**X26X27X28X29X30X31X32X33X34X35X36;** where

X1=Valine(V) or Alanine(A)

X2=Proline(P) or Aspartic acid(D)

X3=Aspartic acid(D) or Asparagine(N)

X4=Asparagine(N), Serine(S) or Aspartic acid(D)

X5=Glutamic acid (E) or Glutamine(Q)

X6=Valine(V) or Isoleucine(I)

X7=Histidine(H), Glutamine(Q) or Threonine(T)

X8=Alanine(A) or Threonine(T)

X9=Valine(V) or Leucine(L)

X10=Lysine(K) or Arginine(R)

X11=Glycine(G) or Aspartic acid(D)

X12=Serine(S), Lysine(K) or Threonine(T)

X13=Glycine(G), Serine(S) or Lysine(K)

X14=Aspartic acid(D), Glutamic acid (E) or Leucine(L)

X15=Threonine(T), Lysine(K) or Isoleucine(I)

X16=Arginine(R)or no amino acid

X17=Serine(S) or Valine(V)

X18=Glutamic acid (E), Aspartic acid(D) or Asparagine(N)

X19=Phenylalanine(F) or Leucine(L)

X20=Glutamic acid (E) or Lysine(K)

X21=Isoleucine(I) or Phenylalanine(F)

X22=Threonine(T), Serine(S) or Alanine(A)

X23=Methionine(M) or Leucine(L)

X24=Valine(V), Alanine(A), Isoleucine(I) or Threonine(T)

X25=Histidine(H) or Tyrosine(Y)

X26=Threonine(T), Isoleucine(I) or Tyrosine(Y)

X27=Arginine(R), Lysine(K), Valine(V), Leucine(L) or Phenylalanine(F)

X28=Arginine(R), Threonine(T), Phenylalanine(F) or Leucine(L)

X29=Threonine(T), Serine(S), Arginine(R) or Proline(P)

X30=Threonine(T), Histidine(H), Arginine(R), Lysine(K) or Proline(P)

X31=Histidine(H), Arginine(R), Threonine(T), Leucine(L) or Glutamine(Q)

X32=Tyrosine(Y) or no amino acid

X33=Glycine(G) or no amino acid

X34=Asparagine(N) or no amino acid

X35=Serine(S) or no amino acid; and

X36=Tyrosine(Y) or Glycine(G).

[0083] In some embodiments the mutant leukocidin subunit comprises amino acid substitutions at positions T11, K24, D28, Y58, S18, or any combination thereof. In certain embodiments, the substitutions can be with any amino acid which maintains the antigenicity of the mutant staphylococcal leukocidin subunit. In certain embodiments T11, K24, D28, Y58, or S18 is substituted with alanine or phenylalanine.

[0084] Also disclosed is the mutant leukocidin subunit, as described herein, which comprises an amino acid substitution at position K24 of SEQ ID NO: 2. The substitution can be with any amino acid which maintains the antigenicity of the mutant staphylococcal leukocidin subunit. In certain embodiments K24 is substituted with alanine.

[0085] Also disclosed is the mutant leukocidin subunit, as described herein, which comprises an amino acid substitution at position S18 of SEQ ID NO: 3. The substitution can be with any amino acid which maintains the antigenicity of the mutant staphylococcal leukocidin subunit. In certain embodiments S18 is substituted with alanine.

[0086] Some embodiments include the mutant leukocidin subunit, as described herein, which comprises an amino acid substitution at position Y58 of SEQ ID NO:2. The substitution can be with any amino acid which maintains the antigenicity of the mutant staphylococcal leukocidin subunit. In certain embodiments Y58 is substituted with alanine.

[0087] Some embodiments include the mutant leukocidin subunit, as described herein, which comprises an amino acid substitution at position T11 of SEQ ID NO: 1. The substitution can be with any amino acid which maintains the antigenicity of the mutant staphylococcal leukocidin subunit. In certain embodiments T11 is substituted with phenylalanine.

[0088] Some embodiments include the mutant leukocidin subunit, as described herein, which comprises amino acid substitutions at positions T11 and Y58. The substitutions can be with any amino acid which maintains the antigenicity of the mutant staphylococcal leukocidin subunit. In certain embodiments T11 and Y58 are substituted with phenylalanine and alanine, respectively.

[0089] Some embodiments include the mutant leukocidin subunit, as described herein, which comprises amino acid substitutions at positions T11 and S18. The substitutions can be with any amino acid which maintains the antigenicity of the mutant staphylococcal leukocidin subunit. In certain embodiments T11 and S18 are substituted with phenylalanine and alanine, respectively.

[0090] Some embodiments include the mutant leukocidin subunit, as described herein, which comprises amino acid substitutions at positions T11, K24, and S18. The substitutions can be with any amino acid which maintains the antigenicity of the mutant staphylococcal leukocidin subunit. In certain embodiments T11 is substituted with phenylalanine, and K24 and S18 are substituted with alanine.

[0091] Also disclosed is the mutant leukocidin subunit, as described herein, which comprises an amino acid substitution at position D28 of SEQ ID NO: 2. The substitution can be with any amino acid which maintains the antigenicity of the mutant staphylococcal leukocidin subunit. In certain embodiments D28 is substituted with alanine.

[0092] Also disclosed is an isolated mutant staphylococcal leukocidin subunit polypeptide comprising, consisting of, or consisting essentially of a wild-type staphylococcal leukocidin subunit except for 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, or more amino acid substitutions at conserved residues, which reduce toxicity of the mutant leukocidin subunit relative to the corresponding wild-type leukocidin subunit; where the wild-type leukocidin is a Panton-Valentine leukocidin (PVL) LukS-PV. In some embodiments, the wild-type LukS-PV comprises an amino acid sequence selected from the group consisting

of SEQ ID NO: 5, SEQ ID NO: 15, and SEQ ID NO: 16. In certain embodiments the wild-type LukS-PV comprises an amino acid sequence of SEQ ID NO: 5:

mvkkrllaat lslgiitpia tsfheskadn nienigdgae vvkrtedtss dkwgvtqniq fdfvkdkkyn kdalilkmqg finskttyyn yknidhikam rwpfqynigl ktndpnvdli nylpknkids vnvsqtlgyn iggnfnsgps tggngsfnys ktisynqqny isevehqnsk svqwgikans fitslgkmsg hdpnlfvgyk pysqnprdyf vpdnelpplv hsgfnpsfia tvshekgsgd tsefeitygr nmdvthatrr tthygnsyle gsrihnafvn rnytvkyevn wktheikvkg hn

(precursor protein sequence for LukS-PV. GenBank accession number: NP_058465.1; 28 amino acid signal peptide (amino acids 1-28) is underlined).

[0093] In some embodiments the mutant LukS-PV subunit comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, and SEQ ID NO: 14. In certain embodiments the mutant leukocidin subunit as described herein, comprises the amino acid of SEQ ID NO: 14.

[0094] Also disclosed is an isolated mutant staphylococcal leukocidin subunit polypeptide comprising, consisting of, or consisting essentially of a wild-type staphylococcal leukocidin subunit except for 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, or more amino acid substitutions at conserved residues, which reduce toxicity of the mutant leukocidin subunit relative to the corresponding wild-type leukocidin subunit; where the wild-type leukocidin subunit comprises, consists of, or consists essentially of the amino acid consensus sequence presented here as SEQ ID NO: 4:

N**X1**V**X2**YAPKNQNEEFQVQ**X3**T**X4**GY**X5X6**GGDI**X7**I**X8X9**GL**X10**GG**X11**NG**X12X13X14**FSETINYKQESYR**X15X16X17X18;** where

X1=Valine(V), Isoleucine(I) or Alanine(A)

X2=Aspartic acid(D) or Histidine(H)

X3=Asparagine(N) or Glutamine(Q)

X4=Leucine(L) or Valine(V)

X5=Serine(S) or Threonine(T)

X6=Phenylalanine(F) or Tyrosine(Y)

X7=Serine(S) or Asparagine(N)

X8=Serine(S), Isoleucine(I), Asparagine(N) or Threonine(T)

X9=Lysine(K) or Asparagine(N)

X10=Serine(S) or Threonine(T)

X11=Leucine(L) or Glycine(G)

X12=Serine(S) or Asparagine(N)

X13=Glutamic acid (E), Threonine(T) or Lysine(K)

X14=Serine(S) or Alanine(A)

X15=Threonine(T) or no amino acid

X16=Threonine(T) or Serine(S)

X17=Isoleucine(I) or Leucine(L); and

X18=Aspartic acid(D) or Serine(S).

[0095] In some embodiments the mutant leukocidin subunit comprises amino acid substitutions at positions K8, D28, E53, or any combination thereof. In certain embodiments, the substitutions can be with any amino acid which maintains the antigenicity of the mutant staphylococcal leukocidin subunit. In certain embodiments K8, D28, or E53 is substituted with alanine.

[0096] Also disclosed is an isolated mutant staphylococcal leukocidin subunit polypeptide comprising, consisting of, or consisting essentially of a wild-type staphylococcal leukocidin subunit except for 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, or more amino acid substitutions at conserved residues, which reduce toxicity of the mutant leukocidin subunit relative to the corresponsing wild-type leukocidin subunit; where the wild-type leukocidin is a Panton-Valentine leukocidin (PVL) LukF-PV. In some embodiments the wild-type LukF-PV comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 16, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, and SEQ ID NO: 27. In certain embodiments the wild-type LukF-PV comprises an amino acid sequence of SEQ ID NO: 16:

mkkivkssvv tsiallllsn tvdaaqhitp vsekkvddki tlykttatsd sdklkisqil
tfnfikdksy dkdtlilkaa gniysgytkp npkdtissqf ywgskynisi nsdsndsvnv
vdyapknqne efqvqqtvgy syggdinisn glsgggngsk sfsetinykq esyrtsldkr
tnfkkigwdv eahkimnngw gpygrdsyhs tygnemflgs rqsnlnagqn fleyhkmpvl
srgnfnpefi gvlsrkqnaa kkskitvtyq remdrytnfw nqlhwignny kdenraths
iyevdwenht vklidtqske knpms

(precursor protein sequence for LukF-PV. GenBank accession number: NP_058466.1; 24 amino acid signal peptide (amino acids 1-24) is underlined).

[0097] In some embodiments, the mutant LukF-PV subunit comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, and SEQ ID NO: 136. In certain embodiments the mutant LukF-PV subunit comprises an amino acid sequence of SEQ ID NO: 18. In certain embodiments the mutant LukF-PV subunit comprises an amino acid sequence of SEQ ID NO: 136.

[0098] Also disclosed is a polypeptide complex comprising the mutant leukocidin subunits as described herein. The substitution can be any amino acid that maintains structure and conformation of the the mutant leukocidin subunit complex.

[0099] In another embodiment, the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein, can be attached to a heterologous polypeptide. Various heterologous polypeptides can be used, including, but not limited to an N- or C-terminal peptide imparting stabilization, secretion, or simplified purification, such as a hexa-Histidine-tag, a ubiquitin tag, a NusA tag, a chitin binding domain, ompT, ompA, pelB, DsbA, DsbC, c-myc, KSI, polyaspartic acid, (Ala-Trp-Trp-Pro)n, polyphenyalanine, polycysteine, polyarginine, a B-tag, a HSB-tag, green fluorescent protein (GFP), influenza virus hemagglutinin (HAI), a calmodulin binding protein (CBP), a galactose-binding protein, a maltose binding protein (MBP), a cellulose binding domains (CBD's), dihydrofolate reductase (DHFR), glutathione-S-transferase (GST), streptococcal protein G, staphylococcal protein A, T7gene10, an avidin/streptavidin/Strep-tag complex, trpE, chloramphenicol acetyltransferase, lacZ (β-Galactosidase), His-patch thioredoxin, thioredoxin, a FLAG™ peptide (Sigma-Aldrich), an S-tag, or a T7-tag. *See, e.g.*, Stevens, R.C., Structure, 8:R177-R185 (2000). Heterologous polypeptides can also include any pre- and/or pro- sequences that facilitate the transport, translocations, processing and/or purification of LukS-PV and/or LukF-PV polypeptide as described herein from a host cell or any useful immunogenic sequence, including but not limited to sequences that encode a T-cell epitope of a microbial pathogen, or other immunogenic proteins and/or epitopes.

[0100] In some embodiments, the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), attached to a heterologous polypeptide, as described herein, can include a peptide linker sequence joining sequences that comprise two or more peptide

regions. Suitable peptide linker sequences can be chosen based on their ability to adopt a flexible, extended conformation, or a secondary structure that could interact with joined epitopes, or based on their ability to increase overall solubility of the fusion polypeptide, or based on their lack of electrostatic or water-interaction effects that influence joined peptide regions.

[0101] In some embodiments, the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein, is isolated. An "isolated" polypeptide is one that has been removed from its natural milieu. The term "isolated" does not connote any particular level of purification. Recombinantly produced mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein, expressed in non-native host cells is considered isolated for purposes of the disclosure, as is the polypeptide which have been separated, fractionated, or partially or substantially purified by any suitable technique, including by filtration, chromatography, centrifugation, and the like.

[0102] Production of the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein, can be achieved by culturing a host cell comprising a polynucleotide which operably encodes the polypeptide of the disclosure, and recovering the polypeptide. Determining conditions for culturing such a host cell and expressing the polynucleotide are generally specific to the host cell and the expression system and are within the knowledge of one of skill in the art. Likewise, appropriate methods for recovering the polypeptide of the disclosure are known to those in the art, and include, but are not limited to, chromatography, filtration, precipitation, or centrifugation.

[0103] In certain embodiments, the mutant staphylococcal leukocidin subunit, as described herein, comprises a calculated molecular energy of less than 7000 kcal/mol, or less than 4000 kcal/mol, or less than 2000 kcal/mol, or between 600 kcal/mol and 7500 kcal/mol, or between 900 kcal/mol and 3900 kcal/mol, or between 900 kcal/mol and 1500 kcal/mol, or between 2000 kcal/mol and 3650 kcal/mol. Specific calculated molecular energies for the heterodimer complex structure for LukS-PV and LukF-PV mutants are represented in Table 1. These measurements are explained in detail in the examples section.

Table 1: Calculated molecular energies for the heterodimer complex structure for LukS-PV and LukF-PV mutants

LukS-PV Mutants (numbering according to mature (*i.e.*, without signal peptide) wild-type LukS-PV sequence of SEQ ID NO: 6)	Energy (kcal/mol)	LukS-PV Mutants (corresponding numbers according to consensus wild-type LukS-PV sequences of SEQ ID NO: 1, SEQ ID NO: 2 or SEQ ID NO: 3)
T28F	2535	T11F of SEQ ID NO: 1
K97A	655	K24A of SEQ ID NO: 2
D101A	3200	D28A of SEQ ID NO: 2
Y131A	1027	Y58A of SEQ ID NO: 2
S209A	7399	S18A of SEQ ID NO: 3
T28F/Y131A	2032	T11F/Y58A
T28F/S209A	3187	T11F/S18A
T28F/K97A/S209A	3595	T11F/K24A/S18A
LukF-PV Mutants (numbering according to mature (*i.e.*, without signal peptide) wild-type LukF-PV sequence of SEQ ID NO: 17)	Energy (kcal/mol)	LukF-PV Mutants (corresponding numbers according to consensus wild-type LukF-PV sequence of SEQ ID NO: 4)
K102A	1209	K8A
D121A	989	D28A
E147A	1384	E53A
K102A/D121A/E147A	n/a	K8A/D28A/E53A

Polynucleotides

[0104] The disclosure is further directed to an isolated polynucleotide comprising a nucleic acid encoding an isolated mutant staphylococcal leukocidin subunit polypeptide comprising, consisting of, or consisting essentially of a wild-type staphylococcal leukocidin subunit except for 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, or more amino acid substitutions at conserved residues, which reduce toxicity of the mutant leukocidin subunit relative to the corresponding wild-type leukocidin subunit; where the wild-type leukocidin subunit comprises, consists of, or consists essentially of three consecutive regions designated A-B-C arranged from amino terminus to carboxy terminus, and where region B comprises the amino acid consensus sequence of SEQ ID NO: 2.

[0105] Also disclosed is an isolated polynucleotide comprising a nucleic acid encoding an isolated mutant staphylococcal leukocidin subunit polypeptide comprising, consisting of, or consisting essentially of a wild-type staphylococcal leukocidin subunit except for 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, or more amino acid substitutions at conserved residues, which reduce toxicity of the mutant leukocidin subunit relative to the corresponding wild-type leukocidin subunit; where the wild-type leukocidin subunit comprises, consists of, or consists essentially of the amino acid consensus sequence presented here as SEQ ID NO: 4.

[0106] In certain embodiments, the isolated polynucleotide as described herein further comprises non-coding regions such as promoters, operators, or transcription terminators as described elsewhere herein. In some embodiments, the disclosure is directed to the polynucleotide as described herein, and further comprising a heterologous nucleic acid. The heterologous nucleic acid can, in some embodiments, encode a heterologous polypeptide fused to the polypeptide as described herein. For example, the isolated polynucleotide as described herein can comprise additional coding regions encoding, *e.g.*, a heterologous polypeptide fused to the polypeptide as described herein, or coding regions encoding heterologous polypeptides separate from the polypeptide as described herein such as, but not limited to, selectable markers, additional immunogens, immune enhancers, and the like.

[0107] Also provided are expression constructs, vectors, and/or host cells comprising the polynucleotides described herein.

[0108] An example of an isolated polynucleotide is a recombinant polynucleotide contained in a vector. Further examples of an isolated polynucleotide include recombinant polynucleotides maintained in heterologous host cells or purified (partially or substantially) polynucleotides in solution. In certain embodiments of the disclosure a polynucleotide is "recombinant." Isolated polynucleotides or nucleic acids according to the disclosure further include such molecules produced synthetically. The relative degree of purity of a polynucleotide or polypeptide described herein is easily determined by well-known methods.

Codon Optimization

[0109] Also included within the scope of the disclosure are genetically engineered polynucleotides encoding the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or

LukF-PV, or both), as described herein. Modifications of nucleic acids encoding the mutant staphylococcal leukocidin subunit *e.g.*, (LukS-PV or LukF-PV, or both), as described herein, can readily be accomplished by those skilled in the art, for example, by oligonucleotide-directed site-specific mutagenesis or de novo nucleic acid synthesis.

[0110] Some embodiments disclose an isolated polynucleotide comprising a nucleic acid fragment, which encodes the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein, where the coding region encoding the polypeptide has been codon-optimized. As appreciated by one of ordinary skill in the art, various nucleic acid coding regions will encode the same polypeptide due to the redundancy of the genetic code. Deviations in the nucleotide sequence that comprise the codons encoding the amino acids of any polypeptide chain allow for variations in the sequence of the coding region. Since each codon consists of three nucleotides, and the nucleotides comprising DNA are restricted to four specific bases, there are 64 possible combinations of nucleotides, 61 of which encode amino acids (the remaining three codons encode signals ending translation). The "genetic code" which shows which codons encode which amino acids is reproduced herein as Table 2. As a result, many amino acids are designated by more than one codon. For example, the amino acids alanine and proline are coded for by four triplets, serine and arginine by six, whereas tryptophan and methionine are coded by just one triplet. This degeneracy allows for DNA base composition to vary over a wide range without altering the amino acid sequence of the polypeptides encoded by the DNA.

TABLE 2: The Standard Genetic Code

	T	C	A	G
T	TTT Phe (F) TTC " TTA Leu (L) TTG "	TCT Ser (S) TCC " TCA " TCG "	TAT Tyr (Y) TAC " TAA **Ter** TAG **Ter**	TGT Cys (C) TGC TGA **Ter** TGG Trp (W)
C	CTT Leu (L) CTC " CTA " CTG "	CCT Pro (P) CCC " CCA " CCG "	CAT His (H) CAC " CAA Gln (Q) CAG "	CGT Arg (R) CGC " CGA " CGG "
A	ATT Ile (I) ATC " ATA " **ATG** Met (M)	ACT Thr (T) ACC " ACA " ACG "	AAT Asn (N) AAC " AAA Lys (K) AAG "	AGT Ser (S) AGC " AGA Arg (R) AGG "
G	GTT Val (V) GTC " GTA " GTG "	GCT Ala (A) GCC " GCA " GCG "	GAT Asp (D) GAC " GAA Glu (E) GAG "	GGT Gly (G) GGC " GGA " GGG "

[0111] It is to be appreciated that any polynucleotide that encodes a polypeptide in accordance with the disclosure falls within the scope of this disclosure, regardless of the codons used.

[0112] Many organisms display a bias for use of particular codons to code for insertion of a particular amino acid in a growing polypeptide chain. Codon preference or codon bias, differences in codon usage between organisms, is afforded by degeneracy of the genetic code, and is well documented among many organisms.

[0113] Different factors have been proposed to contribute to codon usage preference, including translational selection, GC composition, strand-specific mutational bias, amino acid conservation, protein hydropathy, transcriptional selection and even RNA stability. One factor that determines codon usage is mutational bias that shapes genome GC composition. This factor is most significant in genomes with extreme base composition: species with high GC content (*e.g.*, gram positive bacteria). Mutational bias is responsible not only for intergenetic difference in codon usage but also for codon usage bias within the same genome (Ermolaeva M, *Curr. Issues Mol. Biol.* 3(4):91-97, 2001).

[0114] Codon bias often correlates with the efficiency of translation of messenger RNA (mRNA), which is in turn believed to be dependent on, *inter alia*, the properties of the codons being translated and the availability of particular transfer RNA (tRNA) molecules. The predominance of selected tRNAs in a cell is generally a reflection of the codons used most frequently in peptide synthesis. Accordingly, genes can be tailored for optimal gene expression in a given organism based on codon optimization.

[0115] The present disclosure relates to a polynucleotide comprising a codon-optimized coding region which encodes the mutant staphylococcal leukocidin subunit polypeptide (*e.g.*, LukS-PV or LukF-PV, or both), as described herein. The codon usage is adapted for optimized expression in a given prokaryotic or eukaryotic host cell.

[0116] Codon-optimized polynucleotides are prepared by incorporating codons preferred for use in the genes of a given species into the DNA sequence. Also provided are polynucleotide expression constructs, vectors, host cells comprising polynucleotides comprising codon-optimized coding regions which encode the mutant staphylococcal leukocidin subunit polypeptide (*e.g.*, LukS-PV or LukF-PV, or both), as described herein.

[0117] Given the large number of gene sequences available for a wide variety of animal, plant and microbial species, it is possible to calculate the relative frequencies of codon usage. Codon usage tables are readily available, for example, at the "Codon Usage Database" available at http://www.kazusa.or.jp/codon/ (visited October 12, 2011), and these tables can be adapted in a number of ways. (Nakamura, Y., *et al.,* "Codon usage tabulated from the international DNA sequence databases: status for the year 2000" *Nucl. Acids Res.* 28:292, 2000).

[0118] By utilizing available tables, one of ordinary skill in the art can apply the frequencies to any given polypeptide sequence, and produce a nucleic acid fragment of a codon-optimized coding region which encodes a desired polypeptide, but which uses codons optimal for a given species. For example, in some embodiments of the disclosure, the coding region is codon-optimized for expression in *E. coli*.

DNA Synthesis

[0119] A number of options are available for synthesizing codon optimized coding regions designed by any of the methods described above, using standard and routine molecular biological manipulations well known to those of ordinary skill in the art. In addition, gene synthesis is readily available commercially.

Vectors and Expression Systems

[0120] Further disclosed is a vector comprising the polynucleotide as described herein. The term "vector," as used herein, refers to *e.g.*, any of a number of nucleic acids into which a desired sequence can be inserted, *e.g.*, by restriction and ligation, for transport between different genetic environments or for expression in a host cell. Nucleic acid vectors can be DNA or RNA. Vectors include, but are not limited to, plasmids, phage, phagemids, bacterial genomes, and virus genomes. A cloning vector is one which is able to replicate in a host cell, and which is further characterized by one or more endonuclease restriction sites at which the vector can be cut in a determinable fashion and into which a desired DNA sequence can be ligated such that the new recombinant vector retains its ability to replicate in the host cell. In the case of plasmids, replication of the desired sequence can occur many times as the plasmid increases in copy number within the host bacterium or just a single time per host before the host reproduces by mitosis. In the case of phage, replication can occur actively during a lytic phase or passively during a lysogenic phase. Certain vectors are capable of autonomous replication in a host cell into which they are introduced. Other vectors are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome.

[0121] Any of a wide variety of suitable cloning vectors are known in the art and commercially available which can be used with appropriate hosts. As used herein, the term "plasmid" refers to a circular, double-stranded construct made up of genetic material (*i.e.*, nucleic acids), in which the genetic material is extrachromosomal and in some instances, replicates autonomously. A polynucleotide described herein can be in a circular or linearized plasmid or in any other sort of vector. Procedures for inserting a nucleotide sequence into a vector, *e.g.*, an expression vector, and transforming or transfecting into an appropriate host cell and cultivating under conditions suitable for expression are generally known in the art.

[0122] In accordance with one aspect of the disclosure, provided is a vector comprising a nucleic acid sequence encoding the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein. In certain embodiments the vector is an expression vector capable of expressing the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein in a suitable host cell. The term "expression vector" refers to a vector that is capable of expressing the polypeptide

described herein, *i.e.*, the vector sequence contains the regulatory sequences required for transcription and translation of a polypeptide, including, but not limited to promoters, operators, transcription termination sites, ribosome binding sites, and the like. The term "expression" refers to the biological production of a product encoded by a coding sequence. In most cases a DNA sequence, including the coding sequence, is transcribed to form a messenger-RNA (mRNA). The messenger-RNA is then translated to form a polypeptide product which has a relevant biological activity. Also, the process of expression can involve further processing steps to the RNA product of transcription, such as splicing to remove introns, and/or post-translational processing of a polypeptide product.

[0123] Vector-host systems include, but are not limited to, systems such as bacterial, mammalian, yeast, insect or plant cell systems, either *in vivo*, *e.g.*, in an animal or *in vitro*, *e.g.*, in bacteria or in cell cultures. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein. In certain embodiments, the host cell is a bacterium, *e.g.*, *E. coli*.

[0124] Host cells are genetically engineered (infected, transduced, transformed, or transfected) with vectors of the disclosure. Thus, one aspect of the disclosure is directed to a host cell comprising a vector which contains the polynucleotide as describe herein. The engineered host cell can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the polynucleotides. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan. The term "transfect," as used herein, refers to any procedure whereby eukaryotic cells are induced to accept and incorporate into their genome isolated DNA, including but not limited to DNA in the form of a plasmid. The term "transform," as used herein, refers to any procedure whereby bacterial cells are induced to accept and incorporate into their genome isolated DNA, including but not limited to DNA in the form of a plasmid.

[0125] Bacterial host-expression vector systems include, but are not limited to, a prokaryote (*e.g.*, *E. coli),* transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA. In some embodiments, the plasmids used with *E. coli* use the T7 promoter-driven system regulated by the LacI protein *via* IPTG induction. A large number of

suitable vectors are known to those of skill in the art, and are commercially available. The following bacterial vectors are provided by way of example: pET (Novagen), pET28, pBAD, pTrcHIS, pBR322,pQE70, pQE60, pQE-9 (Qiagen), phagescript, psiX174, pBluescript SK, pbsks, pNH8A, pNH16a, pNH18A, pNH46A (Stratagene), ptrc99a, pKK223-3, pKK243-3, pDR540, pBR322, pPS10, RSF1010, pRIT5 (Pharmacia); pCR (Invitrogen); pLex (Invitrogen), and pUC plasmid derivatives.

[0126] A suitable expression vector contains regulatory sequences which can be operably joined to an inserted nucleotide sequence encoding the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein. As used herein, the term "regulatory sequences" means nucleotide sequences which are necessary for or conducive to the transcription of an inserted sequence coding the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein by a host cell and/or which are necessary for or conducive to the translation by a host cell of the resulting transcript into the desired mutant leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both). Regulatory sequences include, but are not limited to, 5' sequences such as operators, promoters and ribosome binding sequences, and 3' sequences such as polyadenylation signals or transcription terminators. Regulatory sequences can also include enhancer sequences or upstream activator sequences.

[0127] Generally, bacterial vectors will include origins of replication and selectable markers, *e.g.*, the ampicillin, tetracycline, kanamycin, resistance genes of *E. coli*, permitting transformation of the host cell and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Suitable promoters include, but are not limited to, the T7 promoter, lambda (λ) promoter, T5 promoter, and lac promoter, or promoters derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), acid phosphatase, or heat shock proteins, or inducible promoters like cadmium (pcad), and beta-lactamase (pbla).

[0128] Once an expression vector is selected, the polynucleotide as described herein can be cloned downstream of the promoter, for example, in a polylinker region. The vector is transformed into an appropriate bacterial strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the polynucleotide as well as all other elements included in the vector, are confirmed using restriction mapping, DNA sequence

analysis, and/or PCR analysis. Bacterial cells harboring the correct plasmid can be stored as cell banks.

Immunogenic and Pharmaceutical Compositions

[0129] Further disclosed are compositions, *e.g.*, immunogenic or pharmaceutical compositions, that contain an effective amount of the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein, or a polynucleotide encoding the polypeptide of the disclosure. Compositions as described herein can further comprise additional immunogenic components, *e.g.*, as a multivalent vaccine, as well as carriers, excipients or adjuvants.

[0130] Compositions as described herein can be formulated according to known methods. Suitable preparation methods are described, for example, in *Remington's Pharmaceutical Sciences*, 19th Edition, A.R. Gennaro, ed., Mack Publishing Co., Easton, PA (1995). Composition can be in a variety of forms, including, but not limited to an aqueous solution, an emulsion, a gel, a suspension, lyophilized form, or any other form known in the art. In addition, the composition can contain pharmaceutically acceptable additives including, for example, diluents, binders, stabilizers, and preservatives. Once formulated, compositions of the disclosure can be administered directly to the subject. The subjects to be treated can be animals; in particular, human subjects can be treated.

[0131] Carriers that can be used with compositions of the disclosure are well known in the art, and include, without limitation, *e.g.*, thyroglobulin, albumins such as human serum albumin, tetanus toxoid, and polyamino acids such as poly L-lysine, poly L-glutamic acid, influenza, hepatitis B virus core protein, and the like. A variety of aqueous carriers can be used, *e.g.*, water, buffered water, 0.8% saline, 0.3% glycine, hyaluronic acid and the like. Compositions can be sterilized by conventional, well known sterilization techniques, or can be sterile filtered. A resulting composition can be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. Compositions can contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH adjusting and buffering agents, tonicity adjusting agents, wetting agents and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamineoleate, etc.

[0132] Certain compositions as described herein further include one or more adjuvants, a substance added to an immunogenic composition to, for example, enhance, sustain, localize, or modulate an immune response to an immunogen. The term "adjuvant" refers to any material having the ability to (1) alter or increase the immune response to a particular antigen or (2) increase or aid an effect of a pharmacological agent. Any compound which can increase the expression, antigenicity or immunogenicity of the polypeptide is a potential adjuvant. The term "immunogenic carrier" as used herein refers to a first moiety, *e.g.*, a polypeptide or fragment, variant, or derivative thereof which enhances the immunogenicity of a second polypeptide or fragment, variant, or derivative thereof.

[0133] A great variety of materials have been shown to have adjuvant activity through a variety of mechanisms. For example, an increase in humoral immunity is typically manifested by a significant increase in the titer of antibodies raised to the antigen, and an increase in T-cell activity is typically manifested in increased cell proliferation, or cellular cytotoxicity, or cytokine secretion. An adjuvant can also alter or modulate an immune response, for example, by changing a primarily humoral or Th_2 response into a primarily cellular, or Th_1 response. Immune responses to a given antigen can be tested by various immunoassays well known to those of ordinary skill in the art, and/or described elsewhere herein.

[0134] A wide number of adjuvants are familiar to persons of ordinary skill in the art, and are described in numerous references. Adjuvants which can be used in compositions described herein include, but are not limited to: inert carriers, such as alum, bentonite, latex, and acrylic particles; incomplete Freund's adjuvant, complete Freund's adjuvant; aluminum-based salts such as aluminum hydroxide; Alhydrogel ($Al(OH_3)$); aluminum phosphate ($AlPO_4$); calcium-based salts; silica; any TLR biological ligand(s); IDC-1001 (also known as GLA-SE; glucopyranosyl lipid adjuvant stable emulsion) (Coler et al., PLoS One, 2010. **5**(10): p. e13677; Coler et al., PLoS One, 2011. **6**(1): p. e16333); CpG (Mullen et al., PLoS One, 2008. **3**(8): p. e2940), or any combination thereof. The amount of adjuvant, how it is formulated, and how it is administered all parameters which are well within the purview of a person of ordinary skill in the art.

[0135] In some embodiments, a composition of the disclosure further comprises a liposome or other particulate carrier, which can serve, *e.g.*, to stabilize a formulation, to target the

formulation to a particular tissue, such as lymphoid tissue, or to increase the half-life of the polypeptide composition. Such particulate carriers include emulsions, foams, micelles, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers, iscoms, and the like. In these preparations, the polypeptide described herein can be incorporated as part of a liposome or other particle, or can be delivered in conjunction with a liposome. Liposomes for use in accordance with the disclosure can be formed from standard vesicle-forming lipids, which generally include neutral and negatively charged phospholipids and a sterol, such as cholesterol. A composition comprising a liposome or other particulate suspension as well as the polypeptide as described herein can be administered intravenously, locally, topically, *etc.* in a dose which varies according to, *inter alia*, the manner of administration, the polypeptide being delivered, and the stage of the disease being treated.

[0136] For solid compositions, conventional nontoxic solid carriers can be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, the polypeptide as described herein, often at a concentration of 25%-75%.

[0137] For aerosol or mucosal administration, the polypeptide as described herein can be supplied in finely divided form, optionally along with a surfactant and, propellant and/or a mucoadhesive, *e.g.*, chitosan. The surfactant must, of course, be pharmaceutically acceptable, and in some embodiments soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides can be employed. The surfactant can constitute 0.1%-20% by weight of the composition, in some embodiments 0.25-5% by weight. The balance of the composition is ordinarily propellant, although an atomizer can be used in which no propellant is necessary and other percentages are adjusted accordingly. In some embodiments, the immunogenic polypeptides can be incorporated within an aerodynamically light particle, such as those particles described in U.S. Pat. No.

6,942,868 or U.S. Pat. Pub. No. 2005/0008633. A carrier can also be included, *e.g.*, lecithin for intranasal delivery.

[0138] The disclosure is also directed to a method of producing the composition according to the disclosure. In some embodiments, the method of producing the composition comprises (a) isolating a polypeptide according to the disclosure; and (b) adding an adjuvant, carrier and/or excipient to the isolated polypeptide. Some embodiments disclose further combining the polypeptide with other staphylococcal antigens. staphylococcal antigens.

[0139] Some embodiments include a multivalent vaccine. A multivalent vaccine of the present disclosure comprises the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein, or a polynucleotide encoding one or both subunits, and one or more additional immunogenic components. Such components can be additional immunogens of the same infectious agent, *e.g.*, *S. aureus*, or from other staphylococci, or can be immunogens derived from other infectious agents which can be effectively, conveniently, or economically administered together. In certain embodiments, the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein, can be combined with other toxins or other virulent component-based vaccines to make a broad toxin-based multivalent vaccine capable of targeting multiple bacterial virulence determinants. In other embodiments, the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein, can be fused to other immunogenic, biologically significant, or protective epitope containing polypeptides to generate a multivalent vaccine in a single chain and induce an immune response against multiple antigens. In yet another embodiment, the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein, can be fused to one or more T cell epitopes to induce T cell immunity along with anti PVL antibodies.

Methods of Treatment/Prevention and Regimens

[0140] Also provided is a method of treating or preventing *Staphylococcus* infection, *e.g.* ,*S. aureus* infection or treating or preventing a disease caused by *Staphylococcus*, *e.g* , *S. aureus* in a subject, comprising administering to a subject in need thereof a composition as described herein comprising the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein, or polynucleotides, vectors, or host cells

encoding same. In certain embodiments, the subject is an animal, *e.g.*, a vertebrate, *e.g.*, a mammal, *e.g.*, a human. Some embodiments include a method of inducing an immune response against a *S. aureus* strain, comprising administering to a subject in need of said immune response an effective amount of a composition as described herein comprising the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein, or polynucleotides, vectors, or host cells encoding same.

[0141] In some embodiments, a subject is administered a composition as described herein comprising the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein, or polynucleotides, vectors, or host cells encoding same prophylactically, *e.g.*, as a prophylactic vaccine, to establish or enhance immunity to *Staphylococcus*, *e.g., S. aureus,* in a healthy animal prior to potential or actual exposure to *Staphylococcus*, *e.g., S. aureus* or contraction of a *Staphylococcus*-related symptom, thus preventing disease, alleviating symptoms, reducing symptoms, or reducing the severity of disease symptoms. In one embodiment the disease is a respiratory disease, *e.g.*, pneumonia. Other diseases or conditions to be treated or prevented include, but are not limited to, bacteremia, sepsis, skin infections, wound infections, endocarditis, bone and joint infections, osteomyelitis, and/or meningitis. One or more compositions, polypeptides, polynucleotides, vectors, or host cells as described herein can also be used to treat a subject already exposed to *Staphylococcus*, *e.g., S. aureus*, or already suffering from a *Staphylococcus* related symptom to further stimulate the immune system of the animal, thus reducing or eliminating the symptoms associated with that exposure. As defined herein, "treatment of an animal" refers to the use of one or more compositions, polypeptides, polynucleotides, vectors, or host cells of the disclosure to prevent, cure, retard, or reduce the severity of *S. aureus* symptoms in an animal, and/or result in no worsening of *S. aureus* symptoms over a specified period of time. It is not required that any composition, polypeptide, polynucleotide, a vector, or a host cell as described herein provides total protection against a staphylococcal infection or totally cure or eliminate all *Staphylococcus* related symptoms.

[0142] As used herein, "a subject in need of therapeutic and/or preventative immunity" refers to a subject in which it is desirable to treat, *i.e.*, to prevent, cure, retard, or reduce the severity of *Staphylococcus* related symptoms, or result in no worsening of *Staphylococcus* related symptoms over a specified period of time. As used herein, "a subject in need of

the immune response" refers to a subject for which an immune response(s) against any of PVL expressing Staphylococcal strains is desired.

[0143] Treatment with pharmaceutical compositions comprising an immunogenic composition, polypeptide or polynucleotide as described herein can occur separately or in conjunction with other treatments, as appropriate.

[0144] In therapeutic applications, a composition, polypeptide or polynucleotide of the disclosure is administered to a patient in an amount sufficient to elicit an effective innate, humoral or cellular response, or both, to the *S. aureus* PVL derived polypeptide to cure or at least partially arrest symptoms or complications.

[0145] An amount adequate to accomplish this is defined as "therapeutically effective dose" or "unit dose." Amounts effective for this use will depend on, *e.g.,* the polypeptide or polynucleotide composition, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician, but generally range for the initial immunization for polypeptide vaccines is (that is for therapeutic or prophylactic administration) from about *e.g.*, 0.1 μg to about 5000 μg of polypeptide, depending upon the patient's response and condition by measuring, for example, antibody levels in the patient's blood. In some embodiments, a priming dose is followed by a boosting dose over a period of time.

[0146] In non-limiting embodiments of the disclosure, an effective amount of a composition as disclosed herein produces an elevation of antibody titer to at least 2, 5, 10, 50, 100, 500, 1000, 5000, 10^4, 5x10^4, or 10^5 times the antibody titer prior to administration.

[0147] In alternative embodiments, generally for humans an initial immunization (that is for therapeutic or prophylactic administration) is administered followed by boosting dosages in the same dose range pursuant to a boosting regimen over weeks to months depending upon the patient's response and condition by measuring the antibody or T lymphocyte response in the patient's blood.

[0148] It must be kept in mind that the polypeptides and compositions as described herein can generally be employed in serious disease states, that is, life-threatening or potentially life threatening situations. In such cases, in view of the minimization of extraneous substances and the relative nontoxic nature of the polypeptides, it is possible and can be felt desirable by the treating physician to administer substantial excesses of these polypeptide compositions.

[0149] For therapeutic use, administration should begin at the first sign of *S. aureus* infection or risk factors. In certain embodiments, the initial dose is followed by boosting doses until, *e.g.*, symptoms are substantially abated and for a period thereafter. In frequent infection, loading doses followed by boosting doses can be required.

[0150] In certain embodiments, the composition as described herein is delivered to a subject by methods described herein, thereby achieving an effective immune response, and/or an effective therapeutic or preventative immune response. Any mode of administration can be used so long as the mode results in the delivery and/or expression of the desired polypeptide in the desired tissue, in an amount sufficient to generate an immune response to *Staphylococcus*, *e.g., S. aureus,* and/or to generate a prophylactically or therapeutically effective immune response to *Staphylococcus*, *e.g.,* to *S. aureus,* in an animal in need of such response. According to the disclosed methods, a composition described herein can be administered by mucosal delivery, transdermal delivery, subcutaneous injection, intravenous injection, oral administration, pulmonary administration, intramuscular (i.m.) administration, or via intraperitoneal injection. Other suitable routes of administration include, but not limited to intratracheal, transdermal, intraocular, intranasal, inhalation, intracavity, intraductal (*e.g.*, into the pancreas) and intraparenchymal (*i.e.*, into any tissue) administration. Transdermal delivery includes, but not limited to intradermal (*e.g.*, into the dermis or epidermis), transdermal (*e.g.*, percutaneous) and transmucosal administration (*i.e.,* into or through skin or mucosal tissue). Intracavity administration includes, but not limited to administration into oral, vaginal, rectal, nasal, peritoneal, or intestinal cavities as well as, intrathecal (*i.e.*, into spinal canal), intraventricular (*i.e.*, into the brain ventricles or the heart ventricles), intra-arterial (*i.e.*, into the heart atrium) and sub arachnoidal (*i.e.*, into the sub arachnoid spaces of the brain) administration.

[0151] Any mode of administration can be used so long as the mode results in the delivery and/or expression of the desired polypeptide in an amount sufficient to generate an immune response to *Staphylococcus*, *e.g., S. aureus,* and/or to generate a prophylactically or therapeutically effective immune response to *Staphylococcus*, *e.g., S. aureus,* in an animal in need of such response. Administration as described herein can be by *e.g.*, needle injection, or other delivery or devices known in the art.

[0152] In some embodiments, a composition comprising the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein, or polynucleotides,

vectors, or host cells encoding same, stimulate an antibody response or a cell-mediated immune response sufficient for protection of an animal against *Staphylococcus*, *e.g., S. aureus* infection. In other embodiments, a composition comprising the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein, or polynucleotides, vectors, or host cells encoding same, stimulate both a humoral and a cell-mediated response, the combination of which is sufficient for protection of an animal against *Staphylococcus*, *e.g., S. aureus* infection. In some embodiments, a composition comprising the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein, or polynucleotides, vectors, or host cells encoding same, further stimulates an innate, an antibody, and/or a cellular immune response.

[0153] In some embodiments, a composition comprising the mutant staphylococcal leukocidin subunit (*e.g.*, LukS-PV or LukF-PV, or both), as described herein, or polynucleotides, vectors, or host cells encoding same, induce antibody responses to *S. aureus* PVL. In certain embodiments, components that induce T cell responses (*e.g.*, T cell epitopes) are combined with components such as the polypeptides as described herein that primarily induce an antibody response.

[0154] Further disclosed is a method for generating, enhancing, or modulating a protective and/or therapeutic immune response to *S. aureus* infection in a subject, comprising administering to a subject in need of therapeutic and/or preventative immunity one or more of the compositions as described herein.

[0155] The compositions as described herein can be administered to an animal at any time during the lifecycle of the animal to which it is being administered. In humans, administration of the composition as described herein can, and often advantageously occurs while other vaccines are being administered, *e.g.*, as a multivalent vaccine as described elsewhere herein.

[0156] Furthermore, the composition as described herein can be used in any desired immunization or administration regimen; *e.g.*, in a single administration or alternatively as part of periodic vaccination regimes such as annual vaccinations, or as in a prime-boost regime in which composition or polypeptide or polynucleotide of the disclosure is administered either before or after the administration of the same or of a different polypeptide or polynucleotide. Recent studies have indicated that a prime-boost protocol

is often a suitable method of administering vaccines. In a prime-boost protocol, one or more compositions as described herein can be utilized in a "prime boost" regimen. An example of a "prime boost" regimen can be found in Yang, Z. *et al. J. Virol.* 77:799-803, 2002.

[0157] Infections to be treated include, but are not limited to a localized or systemic infection of skin, soft tissue, blood, or an organ or an auto-immune disease. Specific diseases or conditions to be treated or prevented include, but are not limited to, respiratory diseases, *e.g.*, pneumonia, sepsis, skin infections, wound infections, endocarditis, bone and joint infections, osteomyelitis, and/or meningitis.

Immune correlates

[0158] A number of animal models for *S. aureus* infection are known in the art, and can be used with the methods disclosed herein without undue experimentation. For example, a hamster model of methicillin-resistant *Staphylococcus aureus* (MRSA) pneumonia has been described for the testing of antimicrobials. (Verghese A. *et al.*, *Chemotherapy.* 34:497-503 (1988), Kephart PA. *et al.* J Antimicrob *Chemother.* 21:33-9, (1988)). Further, a model of *S. aureus*-induced pneumonia in adult, immunocompetent C57BL/6J mice is described, which closely mimics the clinical and pathological features of pneumonia in human patients. (Bubeck-Wardenburg J. *et al.*, *Infect Immun.* 75:1040-4 (2007)). Additionally, virulence has been tested in a rat model of *S. aureus* pneumonia as described in McElroy *et al.* (McElroy MC. *et al.*, *Infect Immun.* 67:5541-4 (1999)). Finally, a standardized and reproducible model of MRSA-induced septic pneumonia to evaluate new therapies was established in sheep. (Enkhbaatar P. *et al.*, *Shock.* 29(5):642-9 (2008)).

[0159] The practice of the disclosure will employ, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. *See*, for example, Molecular Cloning A Laboratory Manual, 2nd Ed., Sambrook *et al.*, ed., Cold Spring Harbor Laboratory Press: (1989); Molecular Cloning: A Laboratory Manual, Sambrook *et al.*, ed., Cold Springs Harbor Laboratory, New York (1992), DNA Cloning, D. N. Glover ed., Volumes I and II (1985); Oligonucleotide Synthesis, M. J. Gait ed., (1984); Mullis *et al.* U.S. Pat. No: 4,683,195; Nucleic Acid Hybridization, B. D. Hames & S. J. Higgins eds. (1984);

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[0160] Standard reference works setting forth general principles of immunology include Current Protocols in Immunology, John Wiley & Sons, New York; Klein, J., Immunology: The Science of Self-Nonself Discrimination, John Wiley & Sons, New York (1982); Roitt, I., Brostoff, J. and Male D., Immunology, 6th ed. London: Mosby (2001); Abbas A., Abul, A. and Lichtman, A., Cellular and Molecular Immunology, Ed. 5, Elsevier Health Sciences Division (2005); and Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Press (1988).

EXAMPLES

Example 1: Molecular modeling and design of vaccine candidates

[0161] This example describes molecular modeling (computer based) techniques for deriving, analyzing and manipulating the structure of Panton-Valentine leukocidin (PVL) LukF-PV and LukS-PV subunits in order to design vaccine candidates.

[0162] To develop a vaccine that is composed of attenuated forms of LukF-PV and/or LukS-PV, the subunits were modified to avoid *in vivo* pore assembly and the cytolytic and inflammatory effects that occur upon pore formation. To identify regions on the LukF-PV and LukS-PV protein surfaces that may be amenable to mutations that abolish pore-formation without disrupting the structural integrity of each subunit, the structure of the LukF-PV/LukS-PV heterodimer and octamer was modeled as described in Aman *et al. J Biomol Struct Dyn* 28, 1-12, 2010. Briefly, LukF-PV and LukS-PV monomers were extracted from the 1PVL and 1T5R crystal structures, respectively. Missing residues in

each structure were modeled into the polypeptide. The resulting structures were energy refined using tethered minimization. Since each subunit possesses two interacting faces in the octamer ring-like structure, it was necessary to construct two different LukF-PV/LukS-PV heterodimer models to fully elucidate the binding interactions on each subunit. These two molecular models were identified as F_R-S_L, and S_L-F_R. This nomenclature is based on the side-by-side relationship of the LukF-PV and LukS-PV constituents in the octameric ring-like structure. F and S represent the two classes, and subscript R and L denote right and left faces, respectively. If one views the two subunits from inside the channel lumen, in the FR-SL model, the right side of LukF-PV (F_R) is bound with the left side of LukS-PV (S_L) and alternatively, in the S_L-F_R model, the right side of LukS-PV (S_L) is bound with the left side of LukF-PV (F_R). The Discovery Studio 2.1 (Accelrys, Inc) program running on a Dell Precision 690 with Red Hat Enterprise Linux 4 was used to build, visualize, and analyze the protein models. Simulations were performed *in vacuo* using a distance-dependent dielectric of 1 and nonbonded interactions limited to within 14 Å in a CHARMM force-field. The template in the model building is disclosed in Aman *et al.*

[0163] The F_R-S_L model shows that the Thr28 side chain is tightly packed against the polypeptide backbone of residues Asn158 and Phe159 in the neighboring LukF-PV subunit (**Figure 1**).

[0164] To identify other interaction sites that may be crucial to oligomerization, molecular modeling as described above was used to scan the F_R-S_L and S_R-F_L interfaces in the PVL octamer model for hotspots that, if mutated, would significantly shift the monomer-dimer equilibrium constant in favor of monomer. In mature LukS-PV, these sites were Tyr131 and Ser209, which were identified from the F_R-S_L interface model and Lys97 and Asp101 from the S_R-F_L model. The corresponding sites in mature LukF-PV were Lys102 and Asp121 in the F_R-S_L model and Glu147 and Asn220 in the S_R-F_L model.

[0165] As one of the metrics used to determine the effect of each mutant on dimerization, the positions were mutated to alanine *in silico* for residues outside of Thr28 and to phenylalanine for Thr28. The single- and double-point mutant complexes were energy minimized, and their molecular energies were calculated relative to wild-type. Similar alanine mutations of Lys97, Asp101 and Tyr131 in LukS-PV and of Lys102, Asp121, and Glu147 in LukF-PV in the molecular models resulted in significant increases in the

calculated energy of the complex relative to wild-type (see **Table 1** above). The most dramatic increase in destabilization energy was observed for the Ser209Ala mutant of LukS-PV. Ser209 connects loop and strand structures in LukS-PV and is buried near the middle of the dimer interface between Ser209 of LukS-PV and Lys 102 of LukF-PV (**Figure 2**).

[0166] Single point mutations at the above-described sites were predicted to shift the monomer-heterodimer equilibrium of PVL in favor of monomers, and these mutants were selected as candidates for vaccine development.

[0167] Thr28 on LukS-PV has been reported in the literature to play a role in dimerization (V. Guillet *et al.*, *The Journal of Biological Chemistry 279*: 41028-41037 (2004)). The potential utility of Thr28 in double mutants was examined. In this preliminary analysis, the double mutants Thr28Phe/Tyr131Ala and Thr28Phe/Ser209Ala as well as a triple mutant Thr28Phe/Tyr131Ala/Ser209Ala was investigated *in silico*. Based on energy calculations, the Thr28Phe/Ser209Ala mutant followed by the triple mutant had the most significant effect. **Table 1** also lists the calculated energy increase in the heterodimer complex structure as a result of the different proposed single and double mutations of LukS-PV.

Example 2: Generation of LukS-PV and LukF-PV mutants

[0168] Mutations were designed based on the octameric model and were introduced into cDNA constructs for LukS-PV and LukF-PV that carried a N-Terminal 6xHis tag for purification purposes. Wild-type LukS-PV and LukF-PV DNA fragments encoding the respective mature protein sequences were synthesized by PCR, treated by BamHI and KpnI restriction enzymes to create cohesive ends, and cloned into pQE30 vector (Qiagen) digested by BamHI and KpnI restriction enzymes. Mutations were introduced into DNA by using the QickChange^{R} II Site-Directed Mutagenesis Kit (Stratagene). The nucleotide sequence of the plasmid construct encoding the wild-type LukS-PV is presented as SEQ ID NO: 123. The nucleotide sequence of the plasmid construct encoding the mutant (K97A) LukS-PV is presented as SEQ ID NO: 124. The nucleotide sequence of the plasmid construct encoding the mutant (D102A) LukS-PV is presented as SEQ ID NO: 125. The nucleotide sequence of the plasmid construct encoding the mutant (Y131A) LukS-PV is presented as SEQ ID NO: 126. The nucleotide sequence of the plasmid construct encoding the mutant (S209A) LukS-PV is presented as SEQ ID NO: 127. The

nucleotide sequence of the plasmid construct encoding the mutant (T28F) LukS-PV is presented as SEQ ID NO: 128. The nucleotide sequence of the plasmid construct encoding the mutant (T28F/Y131A) LukS-PV is presented as SEQ ID NO: 129. The nucleotide sequence of the plasmid construct encoding the mutant (T28F/S209A) LukS-PV is presented as SEQ ID NO: 130. The nucleotide sequence of the plasmid construct encoding the mutant (T28F/K97A/S209A) LukS-PV is presented as SEQ ID NO: 131. The nucleotide sequence of the plasmid construct encoding the wild-type LukF-PV is presented as SEQ ID NO: 132. The nucleotide sequence of the plasmid construct encoding the mutant (K102A) LukF-PV is presented as SEQ ID NO: 133. The nucleotide sequence of the plasmid construct encoding the mutant (D121A) LukF-PV is presented as SEQ ID NO: 134. The nucleotide sequence of the plasmid construct encoding the mutant (E147A) LukF-PV is presented as SEQ ID NO: 135.

[0169] A plasmid construct encoding the LukF-PV triple mutant (K102A/D121A/E147A) listed in **Table 1** was also generated as described above. The mature protein sequence of the LukF-PV Triple Mutant (Lys102Ala (K102A)/Asp121Ala (D121A)/Glu147Ala (E147A)) is shown below with the mutated amino acids underlined and presented as SEQ ID NO: 136:

```
1    aqhitpvsek kvddkitlyk ttatsdsdkl kisqiltfnf ikdksydkdt lilkaagniy
61   sgytkpnpkd tissqfywgs kynisinsds ndsvnvvdya panqneefqv qqtvgysygg
121  ainisnglsg ggngsksfse tinykqasyr tsldkrtnfk kigwdveahk imnngwgpyg
181  rdsyhstygn emflgsrqsn lnagqnfley hkmpvlsrgn fnpefigvls rkqnaakksk
241  itvtyqremd rytnfwnqlh wignnykden rathtsiyev dwenhtvkli dtqskeknpm
301  s
```

[0170] The nucleotide sequence of the plasmid construct encoding the triple mutant (K102A/D121A/E147A) LukF-PV is shown below (cloning sites BamHI and KpnI are underlined, the mutations are double underlined, and the termination codon is in italics) and presented as SEQ ID NO: 137:

ATGAGAGGATCGCATCACCATCACCATCACGGATCCGCTCAACATATCACACCTGTAAGTGAGAAAAAGG
TTGATGATAAAATTACTTTGTACAAAACAACTGCAACATCAGATTCCGATAAGTTAAAAATTTCTCAGATTT
TAACTTTTAATTTTATTAAAGATAAAAGTTATGATAAAGATACATTAATACTCAAAGCTGCTGGAAACATTT
ATTCTGGCTATACAAAGCCAAATCCAAAAGACACTATTAGTTCTCAATTTTATTGGGGTTCTAAGTACAAC
ATTTCAATTAATTCAGATTCTAATGACTCAGTAAACGTTGTAGATTATGCACCTGCAAATCAAAATGAAGA
ATTTCAAGTACAACAAACGGTAGGTTATTCTTATGGTGGAGCTATTAATATCTCTAACGGCTTATCAGGTG

GAGGTAATGGTTCAAAATCTTTTTCAGAGACAATTAACTATAAACAAGCAAGCTATAGAACTAGCTTAGA
TAAAAGAACTAATTTCAAAAAAATTGGTTGGGATGTTGAAGCACATAAAATTATGAATAATGGTTGGGGA
CCATATGGCAGAGATAGTTATCATTCAACTTATGGTAATGAAATGTTTTTAGGCTCAAGACAAAGCAACTT
AAATGCTGGACAAAACTTCTTGGAATATCACAAAATGCCAGTGTTATCCAGAGGTAACTTCAATCCAGAA
TTTATTGGTGTCCTATCTCGAAAACAAAACGCTGCAAAAAAATCAAAAATTACTGTTACTTATCAAAGAGA
AATGGATAGATATACAAACTTTTGGAATCAACTTCACTGGATAGGTAATAATTATAAAGATGAAAATAGA
GCAACTCATACATCAATTTATGAAGTTGATTGGGAAAATCATACAGTTAAATTAATAGATACTCAATCTAA
GGAAAAAAATCCTATGAGCTAAGGTACC

[0171] The mutants, which were selected based on structural analysis described above, included five single, two double and one triple mutants of LukS-PV as well as four single and one triple mutants of LukF-PV (Table 1). The mutant proteins along with the His-tagged wild-type subunits were produced in *E.coli* strain XL1-Blue [*recA1 endA1 gyrA96 thi-1 hsdR17 supE44 relA1 lac* [F′ *proAB lacI*q*Z*Δ*M15* Tn*10* (Tetr)] and purified on a HisTrap™ HP column (GE Healthcare Cat#17-5248-02) used according to the manufacturer's instructions. All proteins were quality controlled by SDS-PAGE (Sodium Dodecyl Sulfate-Polyacrylamide Gel Electrophoresis) using common techniques and western blotting with respective antibodies (LukS-PV: V5184 rabbit polyclonal Ab (Genscript), LukF-PV: 1A11 mA (IBT)).

[0172] SDS-PAGE and Western blot analysis of LukS-PV Mut9, LukF-PV Mut1 and LukF-PV triple mutant (K102A/D121A/E147A) are shown in **Figure 7A-C**.

Example 3: Attenuation of LukS-PV and LukF-PV Mutants

[0173] Each of the LukS-PV and LukF-PV mutants were tested in a neutrophil toxicity assay in combination with the wild-type LukF-PV, or LukS-PV, respectively. Using a 96-well round bottom tissue culture plate, the wild-type or mutant LukS-PV or LukF-PV proteins were semi-log diluted in duplicates down the plate in assay media (RPMI, 2% FBS, 5mM glutamine) followed by addition of 5 x 10^5 DMSO induced HL-60 cells. HL-60 cells were differentiated into neutrophils by treatment with DMSO. The suspension was gently tapped and plates incubated for 48 hours at 37^0C with 5% CO_2 and 95% humidity. To determine cellular viability, 20 μL of 2mg/mL diluted XTT (Sigma-Aldrich, St. Louis, MO) was added to each well, incubated for 6 hours at 37^0C with 5% CO_2 and 95% humidity, centrifuged and supernatant transferred to an ELISA plate and read to 470nm.

The percent (%) viability was determined as follows: % Viability = (OD value of Experimental Sample Well / OD value of HL-60 cells without PVL Toxin) x 100. The data are presented as % cell survival in **Figures 3 and 4**.

[0174] Mutant LukS-PV data showed that while each of the single mutants or double mutants slightly reduced the toxicity of LukS-PV in complex with the wild-type LukF-PV, a triple mutant combining the mutations T28F, K97A, and S209A led to nearly complete attenuation. In the presence of the triple mutant combined with the wild-type LukF-PV, over 90% of cells remained viable (**Figure 3**).

[0175] Mutant LukF-PV proteins were tested in a neutrophil toxicity assay as described above, in combination with the wild-type LukS-PV or LukS-PV triple mutant (T28F, K97A, and S209A). As shown in **Figure 4**, each of the single mutations reduced the toxicity of LukF-PV when combined with the wild-type LukS-PV. Of the three LukF-PV mutants tested, the K102A mutant showed the highest degree of attenuation with complete loss of toxicity at 300 ng/ml and about 50% reduced toxicity at 3000 ng/ml. When combined with the LukS-PV triple mutant all three LukF-PV mutants (LukF K102A, LukF D121A and LukF E147A) showed complete inactivation.

Example 4: Polyclonal antibodies to PVL protect mice from lethal challenge with community acquired *S. aureus* strain USA300 (LAC)

[0176] The ability of anti-PVL polyclonal antibodies to protect against bacteremia caused by *S. aureus* USA300 in mice was tested. For this study polyclonal antibodies were generated in rabbits by immunizing with His-tagged protein containing the wild-type sequence of LukS-PV presented by SEQ ID NO: 6 and an N-terminal 6xHis tag. Polyclonal antibodies (total IgG) were purified from hyperimmune serum over a protein G column. Furthermore, specific anti-LukS-PV antibodies were purified from total IgG using AminoLink® Plus Immobilization Kit (Thermoscientific). The Kit included reagents, column and buffers needed to make the affinity column packed with beads. Beads coupled with LukS-PV protein and affinity purification of polyclonal anti-LukS-PV antibody was carried out according to the manufacturer's protocol. Furthermore, to test the ability of anti-LukS-PV antibodies to synergize with anti-α-hemolysin antibodies (Hla), combinations of anti-LukS-PV and anti-Hla polyclonal antibodies were examined. A model as disclosed in Fattom *et al.*, *Infect Immun* 64, 1659-1665, 1996, in which

BALB/c mice were challenged via intraperitoneal route with *S. aureus* mixed with Hog-Mucin was applied. Mice were pre-treated with the indicated antibodies 24 hour prior to challenge. Naïve mouse IgG was used as control. After challenge with $5x10^4$ USA300 and 3% Hog-Mucin (Sigma-Aldrich, St. Louis, MO), mice were monitored for morbidity and mortality for 5 days. As shown in **Table 3**, all mice treated with naïve mouse IgG succumbed to death within 16-20 hours post challenge. In contrast, 3 out of 5 mice who received 50 ug of purified anti-LukS-PV and 2 out of 5 mice who received 2 mg of anti-Hla total IgG survived suggesting that each component contributes to protection. When 2 mg of anti-Hla IgG was combined with 50 or 25 μg of purified anti LukS-PV antibodies, 100% survival was observed. Lower dose of purified anti-LukS-PV (12.5μg) when added to anti-Hla lead to 80% survival which was higher than the survival achieved by either component alone. These data suggest that vaccination with a combination of LukS-PV or Hla vaccines may lead to additive or synergistic protective effect against *S. aureus* bacteremia.

Table 3: Protection against USA300 bacteremia by antibodies to LukS-PV and Hla

Group#	N	Anti-LukS (affinity Purified)	Anti-Hla (Total IgG)	Naïve mouse IgG	% Survival				
					16h	20h	36h	48h	120h
1	5	50 ug	2 mg	0	100%	100%	100%	100%	100%
2	5	25 ug	2 mg	0	100%	100%	100%	100%	100%
3	5	12.5 ug	2 mg	0	80%	80%	80%	80%	80%
4	5	50 ug	0	0	100%	60%	60%	60%	60%
5	5	0	2 mg	0	60%	40%	40%	40%	40%
6	5	0	0	2 mg	60%	0%	0%	0%	0%

Example 5: Sequence identity for staphylococcal two component pore-forming toxins

[0177] The sequence identity between LukS, LukM, LukM, LukE, and HIgA/S was compared. *S. aureus* γ-hemolysin (Hlg), leukocidin (Luk) and PVL are related two-component pore-forming toxins (Kaneko *et al.,* Biosci Biotechnol Biochem, 2004. 68(5): p. 981-1003).

[0178] LukS-PV has high sequence identity with LukS, LukM, LukE, and HIgA/C ranging from 65% to 81% as shown in **Figure 5**. All three sites mutagenized in the attenuated triple mutant LukS-PV vaccine candidate tested herein were shown to be conserved throughout

the family (shown in box with * in **Figure 5**). Similarly, LukF-PV was shown to be highly homologous to LukF, LukD, LukDv, and HlgB, and the sites mutated in the LukS-PV vaccines tested herein were conserved. Consistent with this homology, it was shown that LukS-PV polyclonal antibodies inhibited cytotoxic activity towards PMNs in the supernatants of not only PVL-positive strains (USA300&400) but also in PVL deficient strains such as Newman and 8325-4 (**Figure 6**). These data showed that antibodies elicited against PVL subunits showed broader reactivity and neutralized non-PVL leukocidins.

Example 6: *In vitro* structural and functional characterization of mutant proteins

[0179] Functional activity of LukS-PV and LukF-PV mutants disclosed herein was tested in a cytotoxicity assay using HL-60 cells differentiated to neutrophils (Romero-Steiner *et al.*, Clin Diagn Lab Immunol, 1997. 4(4): p. 415-22). To ensure the structural integrity of the mutants, these proteins along with wild-type counterparts were analyzed by circular dichroism (CD) spectrometry. Furthermore, the thermal stability of the proteins was determined using Differential Scanning Fluorimetry (DSF).

[0180] *Analysis of cytotoxicity:* Cellular cytotoxicity was tested using a combination of each mutant subunit with the wild-type form of the other subunit using HL-60 cells (ATCC, Catalog Number CCL-240) differentiated *in vitro* into neutrophils (Romero-Steiner *et al.*). The HL-60 cells were propagated in RPMI/15% FBS and 1.6% dimethylsulfoxide (DMSO) for 6 days. The differentiated neutrophil-like cells were harvested and transferred to 96 well plates for PVL toxicity assay at a final density of $5x10^5$ cells/well. Each PVL subunit (mutant or wild-type) was used at 200 ng/ml. Cells were incubated for 48 hours at 37°C and cellular viability was evaluated after 16 hours of further incubation with 100 μg/ml of XTT (Sigma-Aldrich) and colorimetric measurement at OD470 nm. Percent viability of the cells was then calculated in comparison to the wells without toxin.

[0181] As shown in **Figure 8A**, single mutants of LukS-PV did not have a significant impact on toxicity of PVL when the mutant was combined with wild-type LukF, and double mutants slightly reduced the PVL toxicity. However, the triple mutant LukS-PV_T28F/K97A/S209A (denoted as Mut9) was completely attenuated despite combining with wild-type LukF (**Figure 8A**). All three single mutants of LukF caused a right shift in dose response curve with the highest attenuation achieved with LukF_K102A (denoted as Mut1) (**Figure 8B**). When this mutant was combined with LukS Mut9 no toxicity was

observed (**Figure 8B**). Low toxicity was observed with LukF mut1 when combined with wild-type LukS toward high concentration. A triple LukF mutant (K102A/D121A/E147A) was constructed and tested. As shown in **Figure 8C**, the triple LukF mutant was completely attenuated when combined with wild-type LukS and also with LukS mut9.

[0182] *Thermal Stability analysis:* Thermal stability of LukS-PV and LukF-PV mutant proteins was assessed by Thermofluor (Differential Scanning Fluorimetry) using Sypro Orange as the external fluorescent probe, which binds to hydrophobic residues detecting their exposure during protein unfolding. When heated above critical temperature (>70°C for LukS and LukF-PV), proteins tend to unfold. This results in increased fluorescence, but if unfolding leads to aggregation the result is a decreased fourescence. This increase and decrease of the fluorescent signal is a means to monitor protein unfolding, calculate the melting temperatures, and compare the thermal stabilities of different proteins under different experimental conditions (Ericsson *et al.*, Anal Biochem, 2006. 357(2): p. 289-98; He *et al.*, J Pharm Sci, 2010. 99(4): p. 1707-20). The results are shown in **Figure 9**.

[0183] **Figure 9A** shows the changes in fluorescent signal of the proteins during thermal unfolding in the presence of dye while **Figure 9B** shows the plot of the fraction of unfolded protein based on fitting each protein melting curve using two-state equations as described in Devi *et al.*, Biochemistry, 2006. 45(6): p. 1599-607. Wild-type and mutant proteins of both subunits showed very low background fluorescence when properly folded at 25°C and retain intensity until 55°C showing that the proteins were stable. Melting above 55°C caused an increase in the fluorescent signal, which was due to protein unfolding. This steep increase also supported a highly co-operative unfolding process. LukS-PV wild-type curve was slightly shifted to the right indicating its higher stability. The maximum fluorescence intensity was observed at 75°C for the LukS-PV wild-type while it was at 70°C for other mutants. When heated above these temperatures, the fluorescent intensity dropped down for all the proteins indicating an aggregation event was taking place. Therefore, intensity values only up to 75°C were considered for creating the fraction unfolded protein plot (**Figure 9B**). Apparent Tm values from Boltzmann Sigmoid fitting of the data showed that the Tm for all the tested mutants ranged from 62.6 to 63.6, which was similar to wild-type LukS (64.8) and wild-type LukF

(62.9) and suggested that that the mutations did not affect the thermal stability of the proteins.

Example 7: Immunogenicity study in mice using different clinically relevant adjuvants

[0184] *Immunogenicity and adjuvant studies:* An immunogenicity study was performed in mice using different clinically relevant adjuvants including two forms of alum-based adjuvants, Alhydrogel ($Al(OH)_3$) and aluminum phosphate ($AlPO_4$), as well as two novel adjuvants currently in clinical trials IDC-1001 (also known as GLA-SE; glucopyranosyl lipid adjuvant stable emulsion) (Coler *et al.*, PLoS One, 2010. **5**(10): p. e13677; Coler *et al.*, PLoS One, 2011. **6**(1): p. e16333) and CpG (Mullen *et al.*, PLoS One, 2008. **3**(8): p. e2940).

[0185] Groups of 5 female BALB/c mice were vaccinated intramuscularly (IM) three times with 5 μg of LukS-PV T28F/K97A/S209A (LukS-Mut9) with each of the adjuvants at 2 week intervals. As controls, the wild-type (wt) LukS-PV as well as an irrelevant antigen (STEBVax; staph enterotoxin B vaccine) were combined with Alhydrogel. Mice were bled on days 21 and 35. All tested adjuvants induced robust total antibody response over one log higher than without adjuvant (**Figure 10A**). Neutralizing antibody titer was determined using HL-60 derived neutrophils as described above. As shown in **Figure 10B**, the highest neutralizing titer was achieved after three vaccinations using the alum-based adjuvants and IDC-1001. The antibody response to LukS-Mut9 was compared to the response to wild-type LukS-PV, and the results supported the conservation of immunological epitopes in the mutant.

Example 8: Efficacy of PVL vaccine candidates in murine pneumonia and intraperitoneal sepsis models

[0186] Efficacy studies were performed in murine pneumonia and intraperitoneal sepsis models. Studies were performed to evaluate the efficacy of PVL vaccine candidates alone and in combination with a subunit vaccine for α-hemolysin, AT-62 (Adhikari et al., PLoS One, 2012. **7**(6): p. e38567). Initially, passive immunization studies were preformed with lethality and bacterial burden as endpoints using the bacteremia model in mice. Thereafter, proof of concept active immunization studies in both bacteremia/sepsis as well as pneumonia models were performed.

[0187] *Description of animal models:* In the mouse pneumonia model, female BALB/c mice were anesthetized with isoflurane and inoculated intranasally (IN) with a lethal dose (~$2x10^8$) of USA300 in 50µl PBS and placed into the cages in a prone position and monitored for morbidity (weight, hunched posture, labored breathing, ruffled fur, impaired mobility) and mortality 4 times a day within the first 48 hours and then once a day until termination of the study. In the bacteremia model, female BALB/c mice were challenged via intra-peritoneal (IP) injection with USA300 in 3% mucin solution as previously described in Fattom *et al.*, Infect Immun, 1996. 64(5): p. 1659-65. Briefly, lypholized hog mucin type III was solubilized to 6% in PBS, sterilized by autoclaving and rapidly cooled on ice. PBS washed, overnight grown bacteria were suspended in PBS at 2 x 10^5 CFU/ml. Bacteria and mucin solution were mixed to achieve the intended challenge dose (see **Table 4** below) in 0.5ml of 3% hog mucin. Mice were monitored for morbidity and mortality twice a day for 7-14 days. Mice were 6 weeks of age for active and 10 weeks for passive immunogenicity studies. To determine bacterial dissemination to organs, mice were euthanized at 12h after challenge and blood and organs (liver, combined kidneys, lungs and spleen) were aseptically removed, homogenized and taken up in of 500 µl PBS. Blood samples and organ homogenates were streaked in different dilutions on BHI agar plates and CFU was enumerated after ON incubation at 37°C.

[0188] *Passive immunization studies:* The efficacy of rabbit polyclonal antibodies to LukS-PV (LukS-IgG) and Hla (AT62-IgG) alone and in combination was explored in the bacteremia model. Groups of 5 mice were injected IP with different doses of the antibodies, challenged 24 hours later, and monitored for 7 days. As shown in **Table 4** (Exp.1), as low as 0.25 mg of LukS-IgG provided full protection. In contrast, 4 mg of AT62-IgG was needed to provide 100% protection with partial efficacy at 2.5 mg (see **Table 4 (**Exp. 2)).

Table 4: Efficacy of passive immunization with rabbit polyclonal antibodies against LukS and Alpha toxin in USA300 bacteremia model

Exp. 1	Survivor/Total
4 mg LukS-IgG	5/5
1 mg LukS-IgG	5/5
0.25 mg LukS-IgG	5/5

4 mg naïve IgG	0/5
Exp. 2	Survivor/Total
5 mg AT62-IgG	5/5
2.5 mg AT62-IgG	2/5
1.25 mg AT62-IgG	1/5
0.62 mg AT62-IgG	0/5
5 mg naïve IgG	1/5

[0189] Next, the affinity purified LukS-IgG was combined with a suboptimal dose (2 mg) of AT62-IgG. As shown in **Table 5**, 50μg of affinity purified LukS-IgG or 2 mg of AT62-IgG provided partial protection while the combination of the two antibodies at these doses fully protected mice. Full protection was also observed with 2 mg of AT62-IgG and 25 μg of affinity purified LukS-IgG, and 4 out of 5 mice survived with 12.5 μg LukS antibody in the combination with 2 mg of AT62-IgG.

Table 5: Combination passive immunization study of rabbit pAb against LukS and Alpha toxin in USA300 bacteremia model

AT62-IgG	Affinity Pur. LukS-IgG	Naïve IgG	Survivor Total
2 mg	-	-	2/5
-	50 ug	2 mg	3/5
2 mg	50 ug	-	5/5
2 mg	25 ug	-	5/5
2 mg	12.5 ug	-	4/5
-	-	2 mg	0/5

[0190] In a set of similar studies, the synergistic effect of pretreatment (24 hours before challenge) with AT62-IgG and LukS-IgG on bacterial dissemination determined 12 hours after USA 300 challenge was tested. As shown in **Figure 11**, the two antibodies strongly synergized the reduction of bacterial burden in blood and organs. These data strongly supported that antibodies to LukS and alpha toxin act synergistically in protecting from lethal bacteremia and sepsis.

[0191] The efficacy of LukS-PV mut9 and LukF-PV mut1 in combination with alpha toxin vaccine AT-62 was tested in BALB/c mice. Groups of 10 mice were immunized three times IM with 10μg of each vaccine or BSA (as control) individually or in double or triple combinations at two weeks intervals with $AlPO_4$ in a 1:8 ratio. For the bacteremia/sepsis model, mice were challenged IP on day 42 with 1xLD90 of USA300 ($5x10^4$ CFU) in 3% mucin and monitored for 7 days. As shown in **Figure 12A**, the S and F mutants provided 60% and 40% protection, respectively, and the combination of the two mutant subunits increased protection to 80%, which was similar to AT-62 alone. Full protection was observed when the three antigens were combined together. A similar study was performed in a pneumonia model with a high challenge dose ($2x10^8$ CFU) of USA300. While none of the individual components provided significant protection, a combination of the two leukocidins with AT-62 led to 50% protection (P=0.0021) **(Figure 12B)**.

Example 9: Cross-reactive and cross-neutralizing antibody generated by LukS-PV mut9 *in vivo*

[0192] An immunogenicity assay was carried out by immunizing the LukS-PV mutant 9 (LukS-PV T28F/K97A/S209A) in a group of 4 mice. Serum samples were collected after the fourth immunization and the antibody titer against wild-type LukS-PV **(Figure 13A),** HlgC **(Figure 13B)** and HlgB **(Figure 13C)** were determined. These results clearly show the presence of cross reactive antibodies for both HlgB and C induced by immunization with LukS-PV mut9. Based on HL-60 cell based neutralization assay, polyclonal anti-LukS-PV mut9 antibody was shown to neutralize both PVL (wild-type LukS-PV + LukF-PV) and Gamma hemolysin (wild type HlgB + HlgC) leukotoxins **(Figure 13D)**. These experiments further confirmed the induction of cross protective anti-leukotoxin antibodies by immunization with LukS-PV mut9 and supporting the broad spectrum application of this mutant vaccine.

Example 10: Leukocidin oligomerization and inhibition of oligomerization by antibodies to LukS-PV

[0193] Oligomerization of the leukocidin components is a required step for cytotoxicity of these toxins. In studies described herein, it was explored whether (i) mutations in LukS-PV or LukF-PV interfere with homologous and/or heterologous oligomerization of the

leukocidin components, and (ii) whether antibodies to LukS inhibit homologous and/or heterologous oligomerization. An oligomerization assay for Leukocidin components (PVL and gamma hemolysins) was performed using a 2-methyl-2,4-pentanediol (MPD) based assay as described in Yamashita *et al.*, Proc Natl Acad Sci U S A, 2011. 108(42): p. 17314-9. Briefly, equal amounts of both components were incubated together in the presence of 40% MPD for 24 hours at room temperature. Samples were run in a SDS PAGE without boiling and gels were stained with Gel Code Blue™ reagent. For the inhibition of PVL oligomerization, LukS-PV was pre-incubated with rabbit anti-LukS-PV polyclonal antibodies (pAbs) at decreasing concentration for 30 minutes. An equal amount of LukF-PV was added to the mix and incubated at room temperature in the presence of 40% MPD for 24 hours. Samples were analyzed in a SDS PAGE without boiling and gels were stained with Gel Code Blue™ reagent.

[0194] As shown in **Figure 14A (Lane 2)**, wild-type (wt) forms of LukS-PV and LukF-PV formed an oligomeric band of >160 kd. A similar oligomeric band was seen with LukF-PV mutant 1 in combination with wild-type LukS-PV (**Figure 14A, Lane 3**). Cross oligomerization between wild-type LukS-PV and gamma hemolysin component B was shown (**Figure 14A, Lane 4**). However, LukS-PV mutant 9 did not oligomerize with either wild-type LukF-PV or with LukF-PV mutant 1 (**Figure 14A, Lanes 5 and 6**), which is consistent with the attenuated toxicity observed for LukS-PV mutant 9. This mutant also did not oligomerize with wild-type gamma hemolysin B subunit (**Figure 14A, Lane 7**), further confirming its safety to use as a vaccine candidate. **Figure 14B**, shows the inhibition of oligomerization of wild-type LukS-PV/LukF-PV with rabbit polyclonal anti-LukS antibody in a dose dependent manner. **Figure 14C,** showed that rabbit polyclonal anti-LukS antibody was also able to cross inhibit the heterologous oligomerization of LukS-PV + hlgB.

[0195] The present disclosure is not to be limited in scope by the specific embodiments described which are intended as single illustrations of individual aspects of the disclosure, and any compositions or methods which are functionally equivalent are within the scope of this disclosure. Indeed, various modifications of the disclosure in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

THE EMBODIMENTS OF THE INVENTION FOR WHICH AN EXCLUSIVE PROPERTY OR PRIVILEGE IS CLAIMED ARE DEFINED AS FOLLOWS:

1. An isolated mutant staphylococcal leukocidin subunit polypeptide having reduced toxicity relative to a corresponding wild-type leukocidin subunit, wherein the corresponding wild-type leukocidin subunit is a Panton-Valentine leukocidin (PVL) LukS-PV and the mutant staphylococcal leukocidin subunit polypeptide comprises: an amino acid substitution at a position corresponding to T28 of SEQ ID NO: 6, wherein the threonine corresponding to T28 of SEQ ID NO: 6 is substituted with phenylalanine; an amino acid substitution at a position corresponding to K97 of SEQ ID NO: 6, wherein the lysine corresponding to K97 of SEQ ID NO: 6 is substituted with alanine; and an amino acid substitution at a position corresponding to S209 of SEQ ID NO: 6, wherein the serine corresponding to S209 of SEQ ID NO: 6 is substituted with alanine, or wherein the corresponding wild-type leukocidin subunit is a PVL LukF-PV and the mutant staphylococcal subunit polypeptide comprises an amino acid substitution at a position corresponding to K102 of SEQ ID NO: 17, wherein the lysine corresponding to K102 of SEQ ID NO: 17 is substituted with alanine.

2. The mutant leukocidin subunit of claim 1, wherein the corresponding wild-type leukocidin subunit is a LukS-PV comprising the amino acid sequence SEQ ID NO: 5, SEQ ID NO: 6, or SEQ ID NO: 15.

3. The mutant leukocidin subunit of claim 1 comprising the amino acid of SEQ ID NO: 14.

4. The mutant leukocidin subunit polypeptide of claim 1, wherein the corresponding wild-type leukocidin subunit is a LukF-PV comprising the amino acid sequence of SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, or SEQ ID NO: 27.

5. The mutant leukocidin subunit of claim 1 or 4, which further comprises an amino acid substitution at a position corresponding to D121 of SEQ ID NO: 17, wherein the aspartate corresponding to position D121 of SEQ ID NO: 17 is substituted with alanine.

6. The mutant leukocidin subunit of any one of claims 1, 4, and 5, which further comprises an amino acid substitution at a position corresponding to E147 of SEQ ID NO: 17, wherein the glutamate corresponding to position E147 of SEQ ID NO: 17 is substituted with alanine.

7. The mutant leukocidin subunit of claim 1 or claim 4, wherein the mutant LukF-PV subunit comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 18 and SEQ ID NO: 136.

8. The mutant leukocidin subunit of claim 7 comprising the amino acid sequence of SEQ ID NO: 18.

9. The mutant leukocidin subunit of claim 7 comprising the amino acid sequence of SEQ ID NO: 136.

10. The mutant leukocidin subunit of any one of claims 1 to 9, which is less toxic in a neutrophil toxicity assay compared to the corresponding wild-type leukocidin subunit.

11. The mutant leukocidin subunit of any one of claims 1 to 10, which comprises a calculated molecular energy between 600 kcal/mol and 7500 kcal/mol in complex with a wild-type Panton-Valentine leukocidin (PVL) LukF-PV subunit.

12. The mutant leukocidin subunit of claim 11, which comprises a calculated molecular energy between 900 kcal/mol and 3900 kcal/mol in complex with the wild-type Panton-Valentine leukocidin (PVL) LukF-PV.

13. The mutant leukocidin subunit of claim 12, which comprises a calculated molecular energy between 2000 kcal/mol and 3650 kcal/mol in complex with the wild-type Panton-Valentine leukocidin (PVL) LukF-PV.

14. The mutant leukocidin subunit of claim 11, which comprises a calculated molecular energy between 900 kcal/mol and 1500 kcal/mol in complex with a wild-type Panton-Valentine leukocidin (PVL) LukS-PV.

15. A polypeptide complex comprising the LukS-PV mutant leukocidin subunit of any one of claims 1 to 3 or the LukF-PV mutant leukocidin subunit of any one of claims 1, and 4 to 9, or a combination thereof, and an additional staphylococcal leukocidin subunit polypeptide.

16. The mutant leukocidin subunit of any one of claims 1 to 14 further comprising a heterologous amino acid sequence, wherein the heterologous amino acid sequence encodes a peptide selected from the group consisting of a His-tag, a ubiquitin tag, a NusA tag, a chitin binding domain, a B-tag (6 amino acid tag from bluetongue (BT) viruses: Gln-Tyr-Pro-Ala-Leu-Thr or QYPALT), a HSB-tag, green fluorescent protein (GFP), a calmodulin binding protein (CBP), a galactose-binding protein, a maltose binding protein (MBP), cellulose binding domains (CBD's), an avidin/streptavidin/*Strep*tag, trpE, chloramphenicol acetyltransferase, *lacZ*(β-Galactosidase), a FLAG™ peptide, an S-tag, a T7-tag, a fragment of any of said heterologous peptides, and a combination of two or more of said heterologous peptides, or wherein the heterologous amino acid sequence encodes an immunogen, a T-cell epitope, a B-cell epitope, a fragment of any of said heterologous peptides, and a combination of two or more of said heterologous peptides.

17. The mutant leukocidin subunit of any one of claims 1 to 14, which does not oligomerize with a wild-type leukocidin component.

18. The mutant leukocidin subunit of claim 17, wherein the wild-type leukocidin component is selected from the group consisting of a LukS-PV subunit, a LukF-PV subunit, a LukE subunit, a LukD subunit, a Gamma hemolysin A, a Gamma hemolysin B, a Gamma hemolysin C, or any combination thereof.

19. An isolated polynucleotide comprising a nucleic acid which encodes the mutant leukocidin subunit of any one of claims 1 to 14.

20. The polynucleotide of claim 19, further comprising a heterologous nucleic acid, wherein said heterologous nucleic acid comprises a promoter operably associated with the nucleic acid encoding the polypeptide.

21. A vector comprising the polynucleotide of claim 19 or 20.

22. The vector of claim 21, which is a plasmid.

23. A host cell comprising the vector of claim 21 or claim 22.

24. The host cell of claim 23, which is a bacterium, an insect cell, a mammalian cell, yeast or a plant cell.

25. The host cell of claim 24, wherein the bacterium is *Escherichia coli.*

26. A method of producing a mutant staphylococcal leukocidin subunit polypeptide, comprising culturing the host cell of any one of claims 23 to 25, and recovering the polypeptide.

27. A pharmaceutical composition comprising the mutant leukocidin subunit of any one of claims 1 to 14 or the polypeptide complex of claim 15 and a carrier.

28. The pharmaceutical composition of claim 27, further comprising an adjuvant.

29. The pharmaceutical composition of claim 27 or 28, further comprising an additional staphylococcal antigen, wherein the additional staphylococcal antigen is an alpha-hemolysin subunit polypeptide.

30. The pharmaceutical composition of claim 27 for inducing a host immune response in a subject against a *Staphylococcus aureus* strain, wherein the immune response is selected from the group consisting of an innate response, a humoral response, an antibody response, a T cell response, and a combination of two or more of said immune responses.

31. The pharmaceutical composition of claim 30, wherein the immune response is an antibody response.

32. The pharmaceutical composition of any one of claims 30 and 31, wherein the immune response results in neutralization of a wild-type staphylococcal leukocidin toxin.

33. The pharmaceutical composition of claim 27 for preventing or treating a Staphylococcal disease or infection in a subject.

34. The pharmaceutical composition of claim 33, wherein the infection is a localized or systemic infection of skin, soft tissue, blood, or an organ, or is auto-immune in nature.

35. The pharmaceutical composition of claim 33, wherein the disease is a respiratory disease.

36. The pharmaceutical composition of claim 35, wherein the respiratory disease is pneumonia.

37. The pharmaceutical composition of claim 34, wherein the infection is a systemic infection of blood.

38. The pharmaceutical composition of any one of claims 30 to 37, wherein the subject is a vertebrate.

39. The pharmaceutical composition of claim 38, wherein the vertebrate is a mammal.

40. The pharmaceutical composition of claim 39, wherein the mammal is a human.

41. The pharmaceutical composition of any one of claims 27 to 40, wherein the composition is for administration via intramuscular injection, intradermal injection, intraperitoneal injection, subcutaneous injection, intravenous injection, oral administration, mucosal administration, intranasal administration, or pulmonary administration.

42. A method of producing a vaccine against *S. aureus* infection comprising combining the isolated mutant leukocidin subunit of any one of claims 1 to 14, or polypeptide complex of claim 15, with an adjuvant.

43. The method of claim 42, further comprising combining the mutant leukocidin subunit or polypeptide complex with an additional staphylococcal antigen, wherein the additional staphylococcal antigen is an alpha-hemolysin subunit polypeptide.

44. Use of the mutant leukocidin subunit of any one of claims 1 to 14 or the polypeptide complex of claim 15 in the manufacture of a pharmaceutical composition for inducing a host immune response in a subject against a *Staphylococcus aureus* strain, wherein the immune response is selected from the group consisting of an innate response, a humoral response, an antibody response, a T cell response, and a combination of two or more of said immune responses.

45. Use of the pharmaceutical composition of any one of claims 27 to 29 for inducing a host immune response in a subject against a *Staphylococcus aureus* strain, wherein the immune response is selected from the group consisting of an innate response, a

humoral response, an antibody response, a T cell response, and a combination of two or more of said immune responses.

46. The use according to claim 44 or 45, wherein the immune response is an antibody response.

47. The use according to any one of claims 44 to 46, wherein the immune response results in neutralization of a wild-type staphylococcal leukocidin toxin.

48. Use of the mutant leukocidin subunit of any one of claims 1 to 14 or the polypeptide complex of claim 15 in the manufacture of a pharmaceutical composition for preventing or treating a Staphylococcal disease or infection in a subject.

49. Use of the pharmaceutical composition of any one of claims 27 to 29 for preventing or treating a Staphylococcal disease or infection in a subject.

50. The use according to claim 48 or 49, wherein the infection is a localized or systemic infection of skin, soft tissue, blood, or an organ, or is auto-immune in nature.

51. The use according to claim 48 or 49, wherein the disease is a respiratory disease.

52. The use according to claim 51, wherein the respiratory disease is pneumonia.

53. The use according to claim 50, wherein the infection is a systemic infection of blood.

54. The use according to any one of claims 44 to 53, wherein the subject is a vertebrate.

55. The use according to claim 54, wherein the vertebrate is a mammal.

56. The use according to claim 55, wherein the mammal is a human.

57. The use according to any one of claims 44 to 56, wherein the composition is for administration via intramuscular injection, intradermal injection, intraperitoneal injection, subcutaneous injection, intravenous injection, oral administration, mucosal administration, intranasal administration, or pulmonary administration.

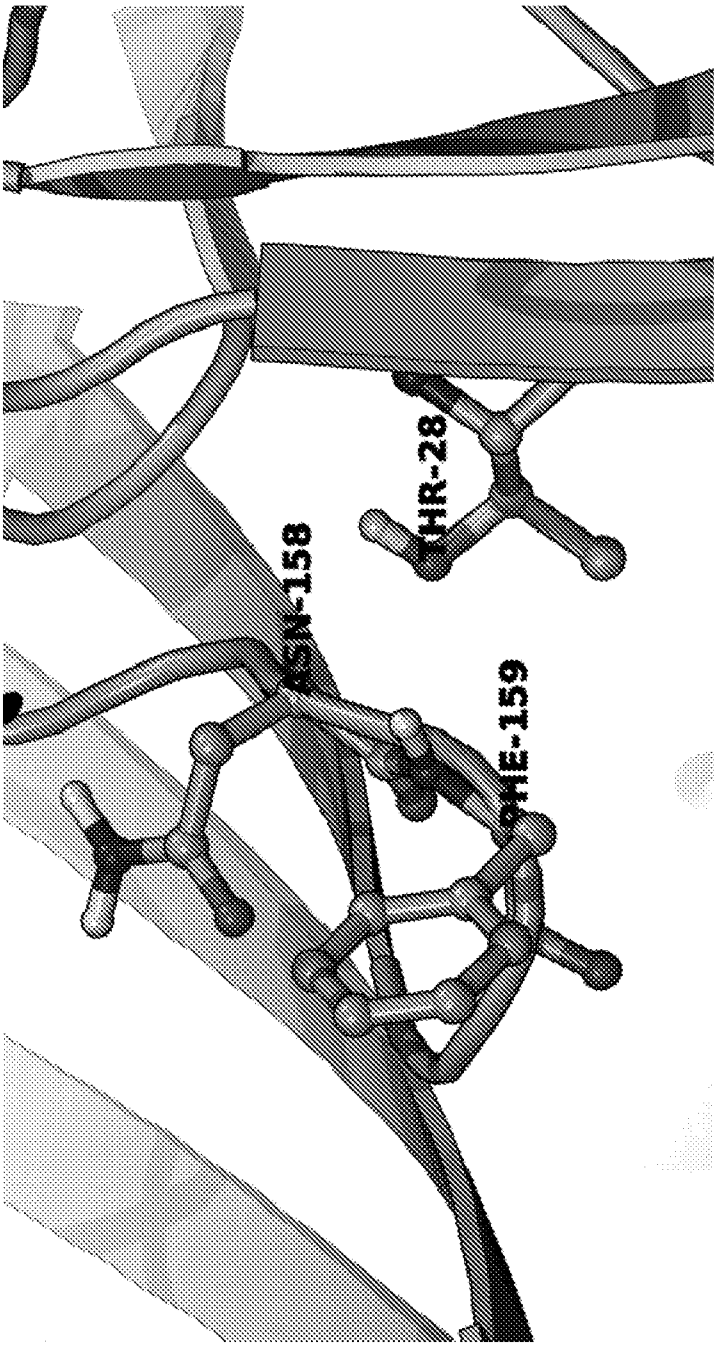


FIG. 1

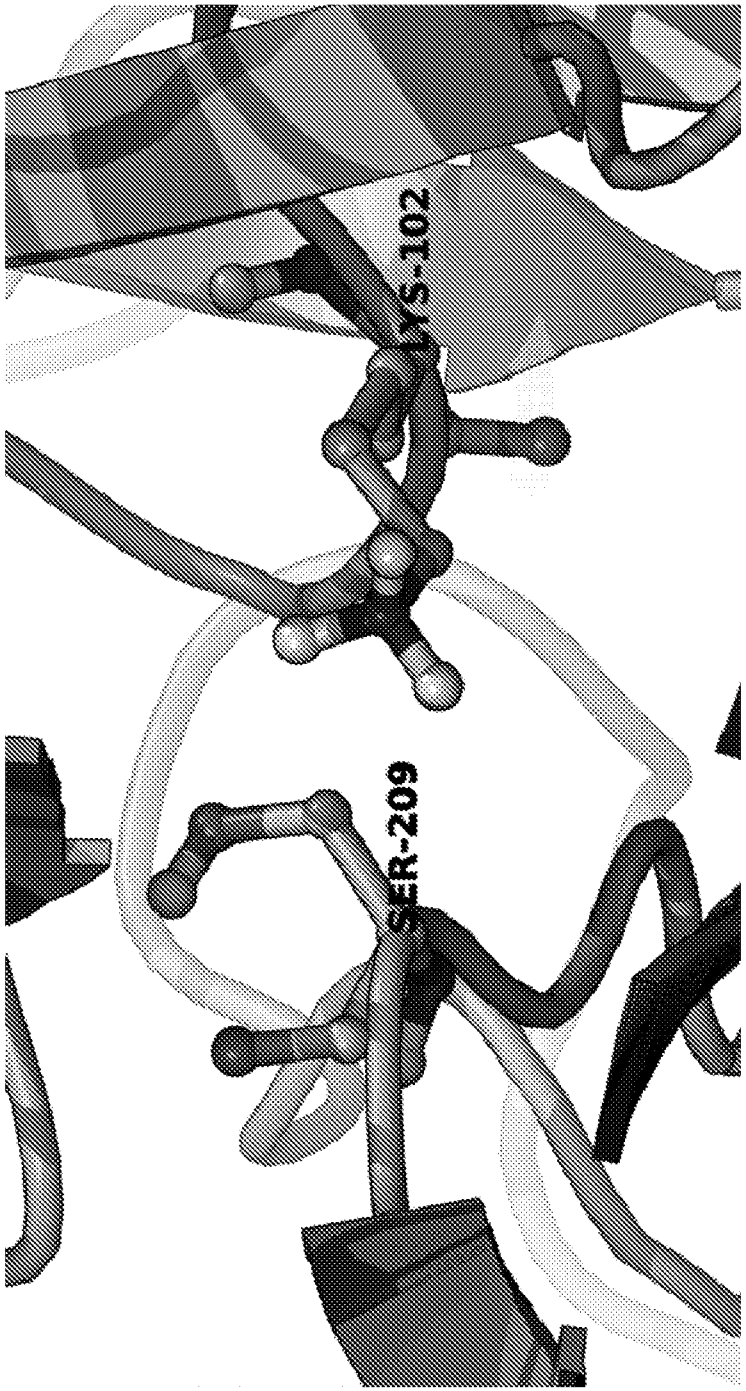


FIG. 2

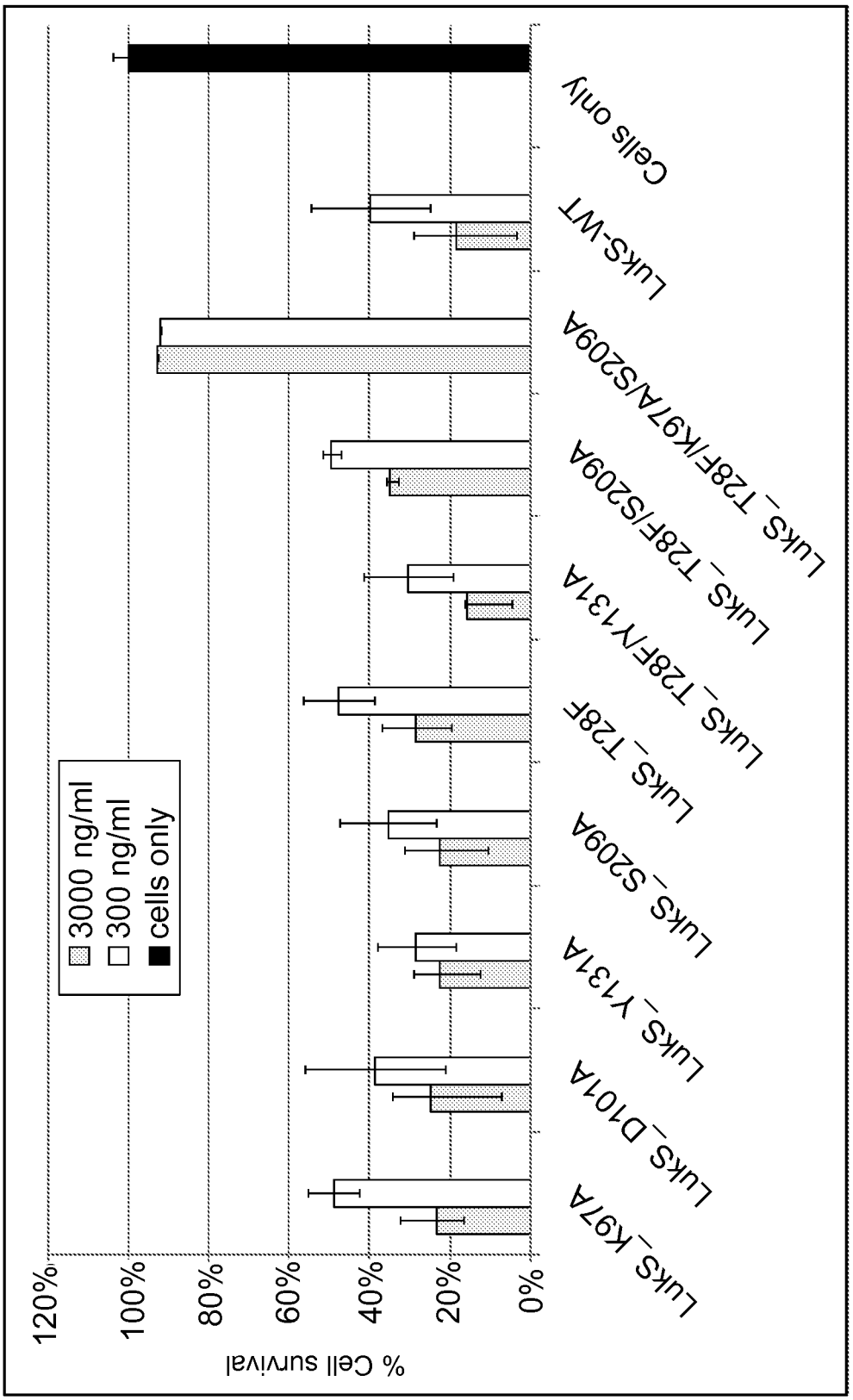

% Cell survival
120%
100%
80%
60%
40%
20%
0%
3000 ng/ml
300 ng/ml
cells only
LukS_K97A
LukS_D101A
LukS_Y131A
LukS_S209A
LukS_T28F
LukS_T28F/Y131A
LukS_T28F/S209A
LukS_T28F/K97A/S209A
LukS-WT
Cells only

FIG. 3

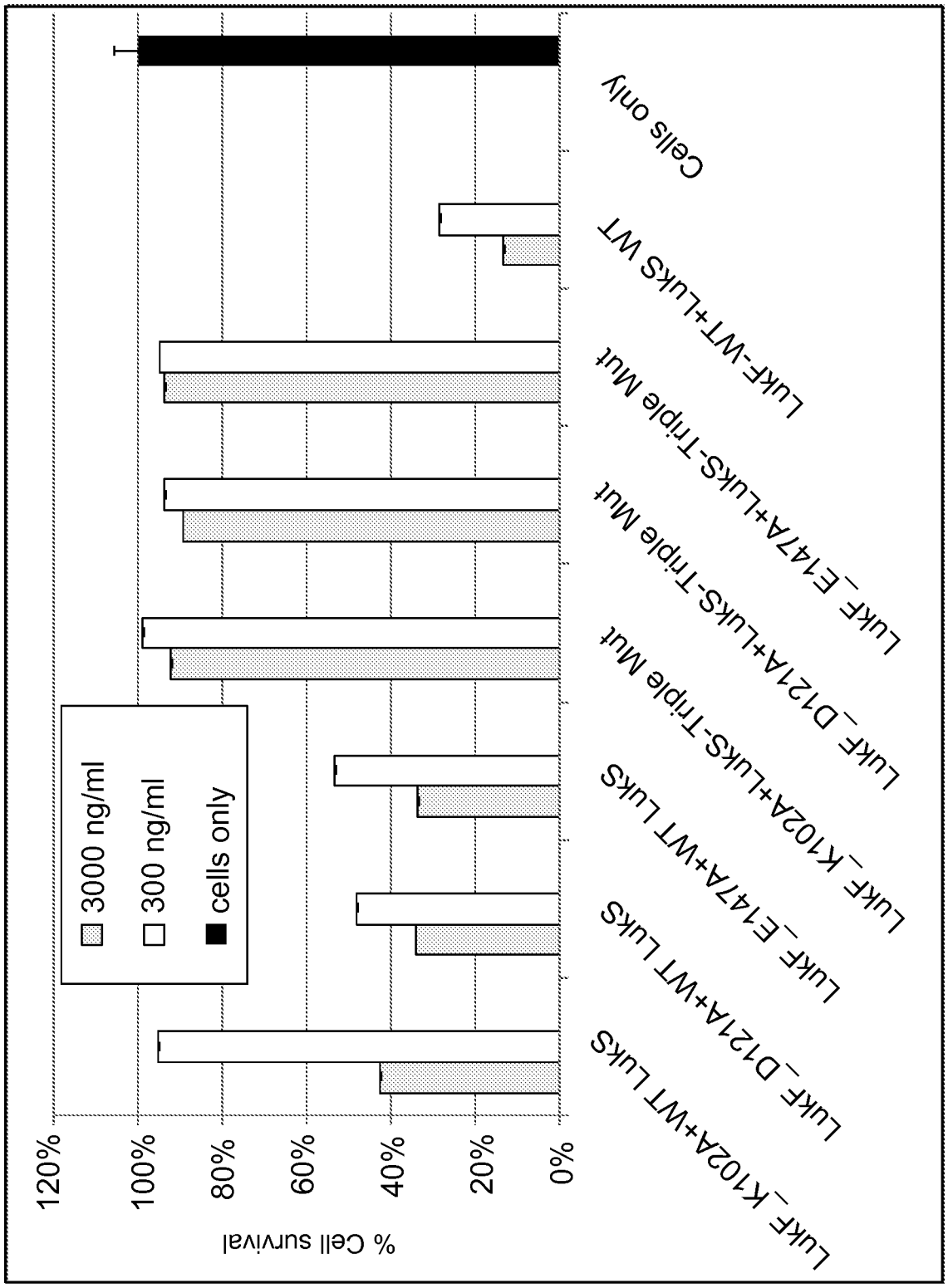

% Cell survival
120%
100%
80%
60%
40%
20%
0%
3000 ng/ml
300 ng/ml
cells only
Cells only
LukF-WT+LukS WT
LukF_E147A+LukS-Triple Mut
LukF_D214A+LukS-Triple Mut
LukF_K102A+LukS-Triple Mut
LukF_E147A+WT LukS
LukF_D214A+WT LukS
LukF_K102A+WT LukS

FIG. 4

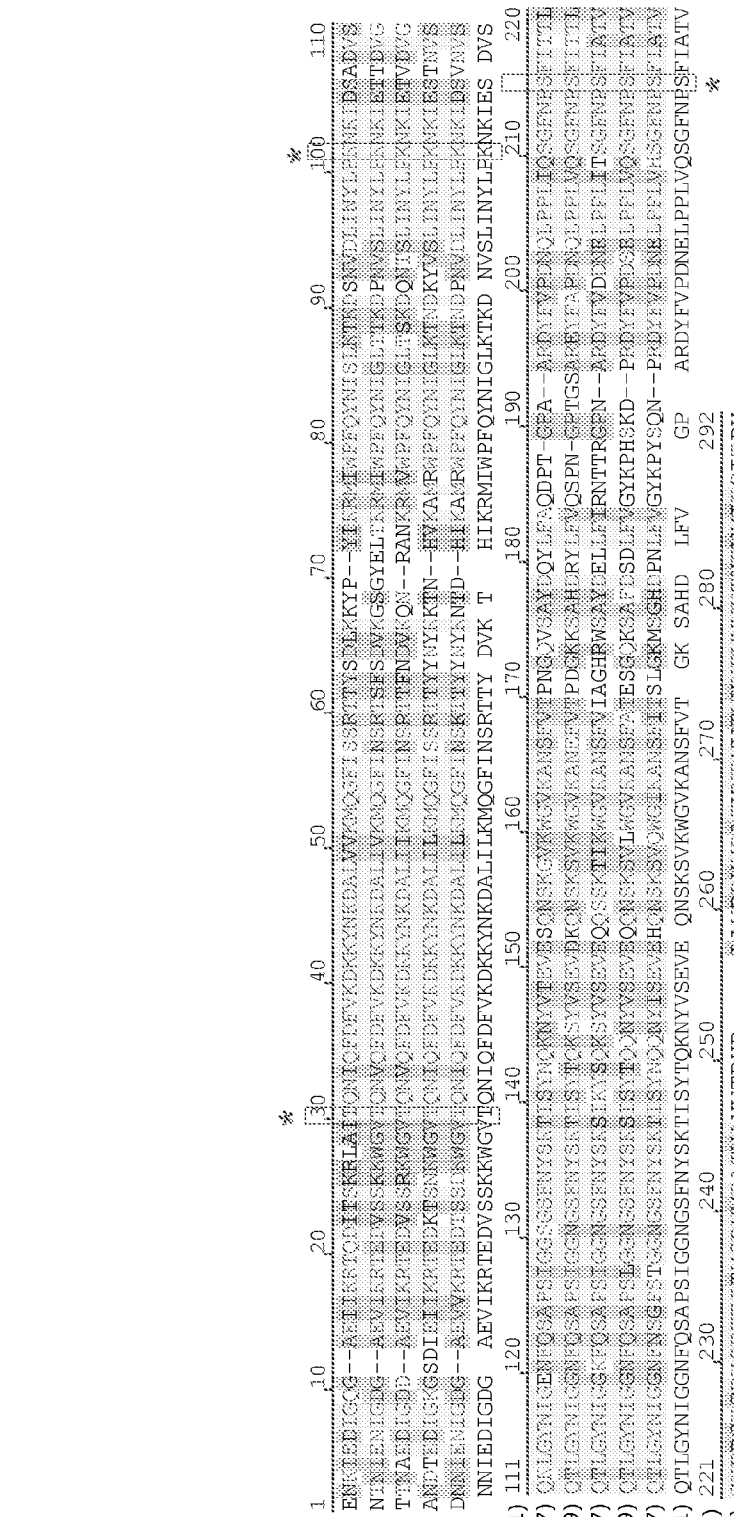


FIG. 5

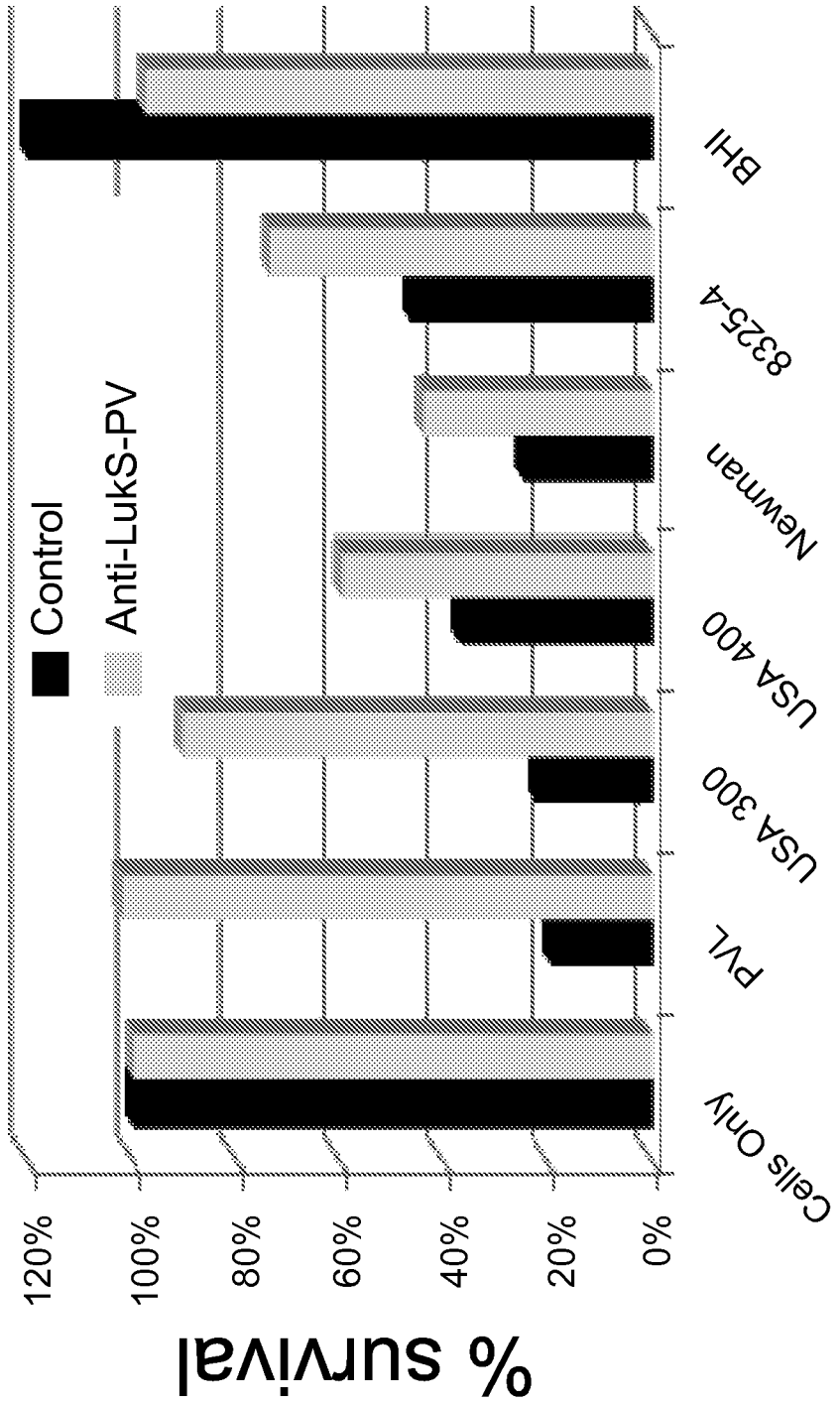

% survival
120%
100%
80%
60%
40%
20%
0%
Control
Anti-LukS-PV
Cells Only
PVL
USA 300
USA 400
Newman
8325-4
BHI

FIG. 6

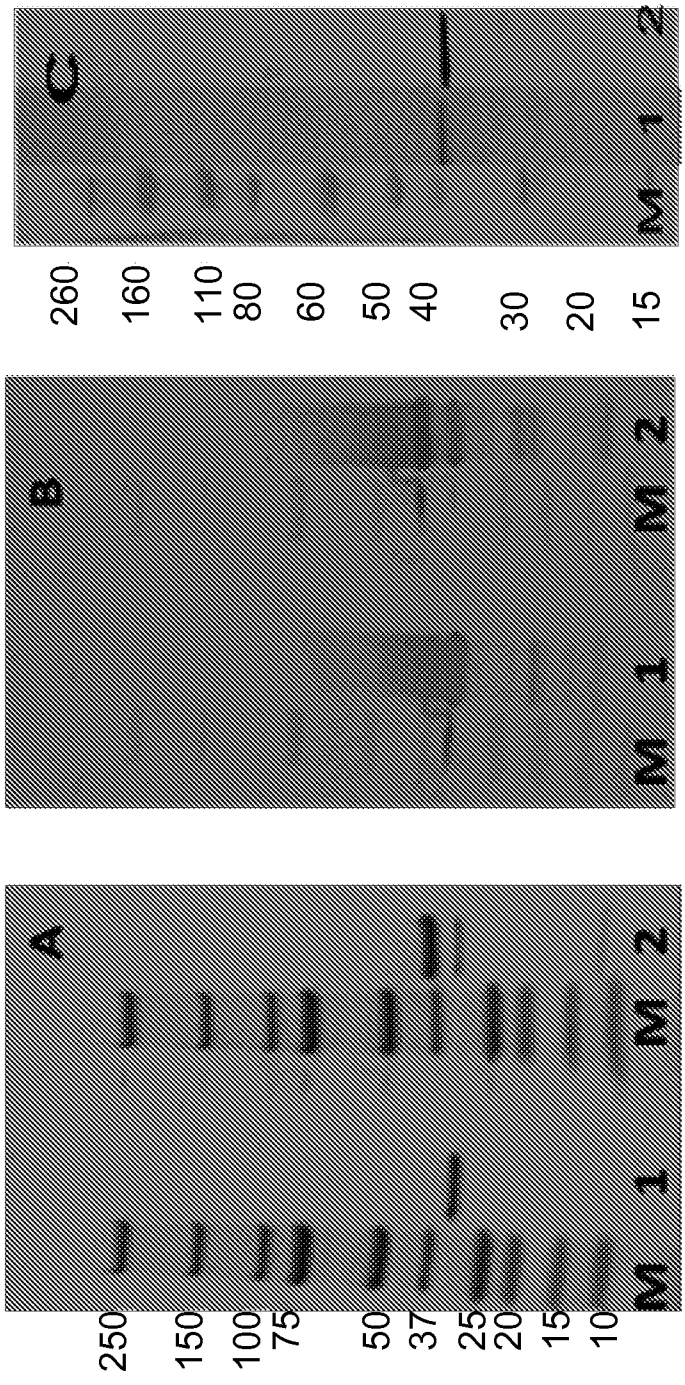

A
M 1 M 2
250
150
100
75
50
37
25
20
15
10
B
M 1 M 2
C
M 1 2
260
160
110
80
60
50
40
30
20
15

FIG. 7

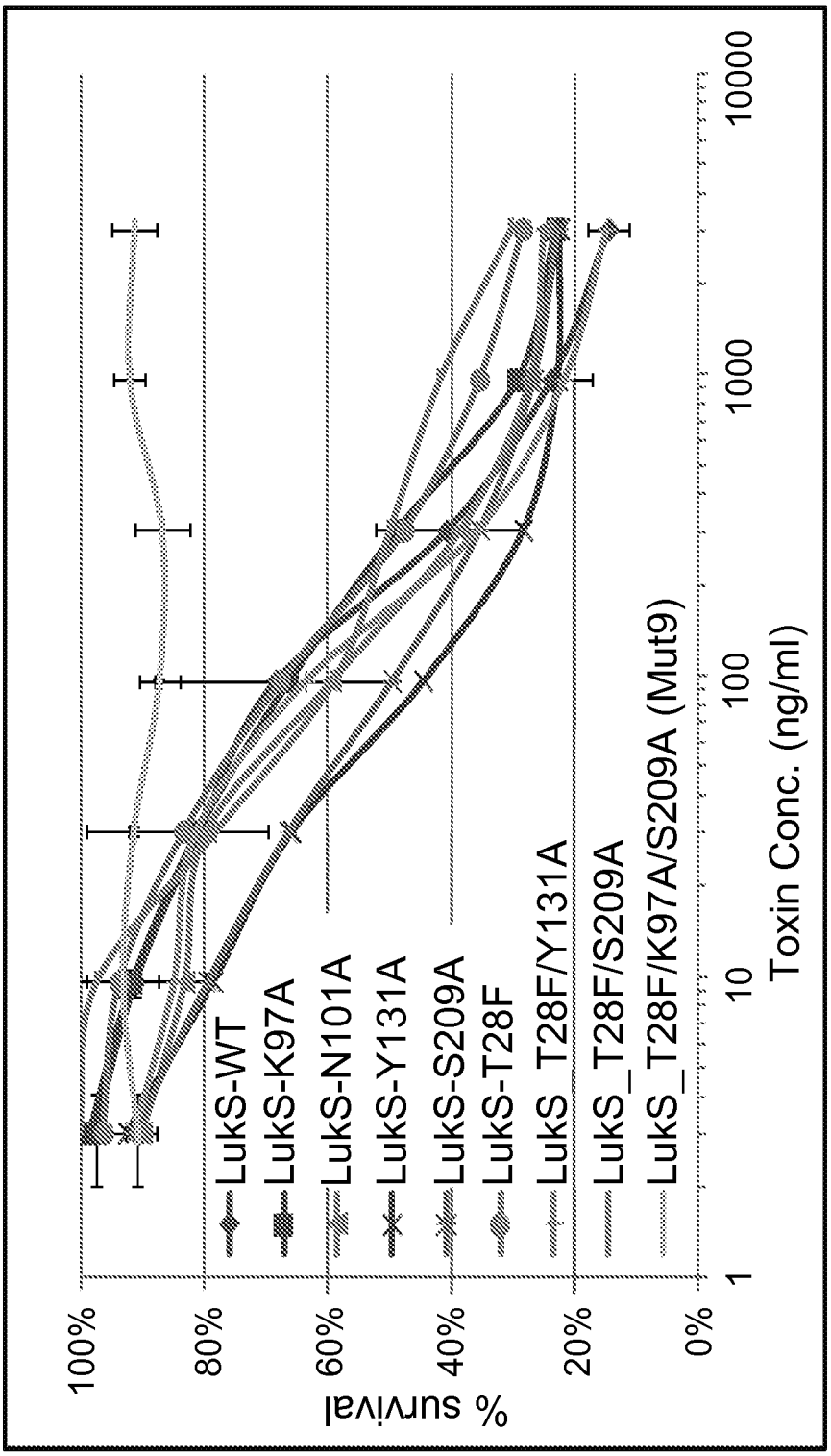

100%
80%
60%
40%
20%
0%
% survival
1
10
100
1000
10000
Toxin Conc. (ng/ml)
LukS-WT
LukS-K97A
LukS-N101A
LukS-Y131A
LukS-S209A
LukS-T28F
LukS_T28F/Y131A
LukS_T28F/S209A
LukS_T28F/K97A/S209A (Mut9)

FIG. 8A

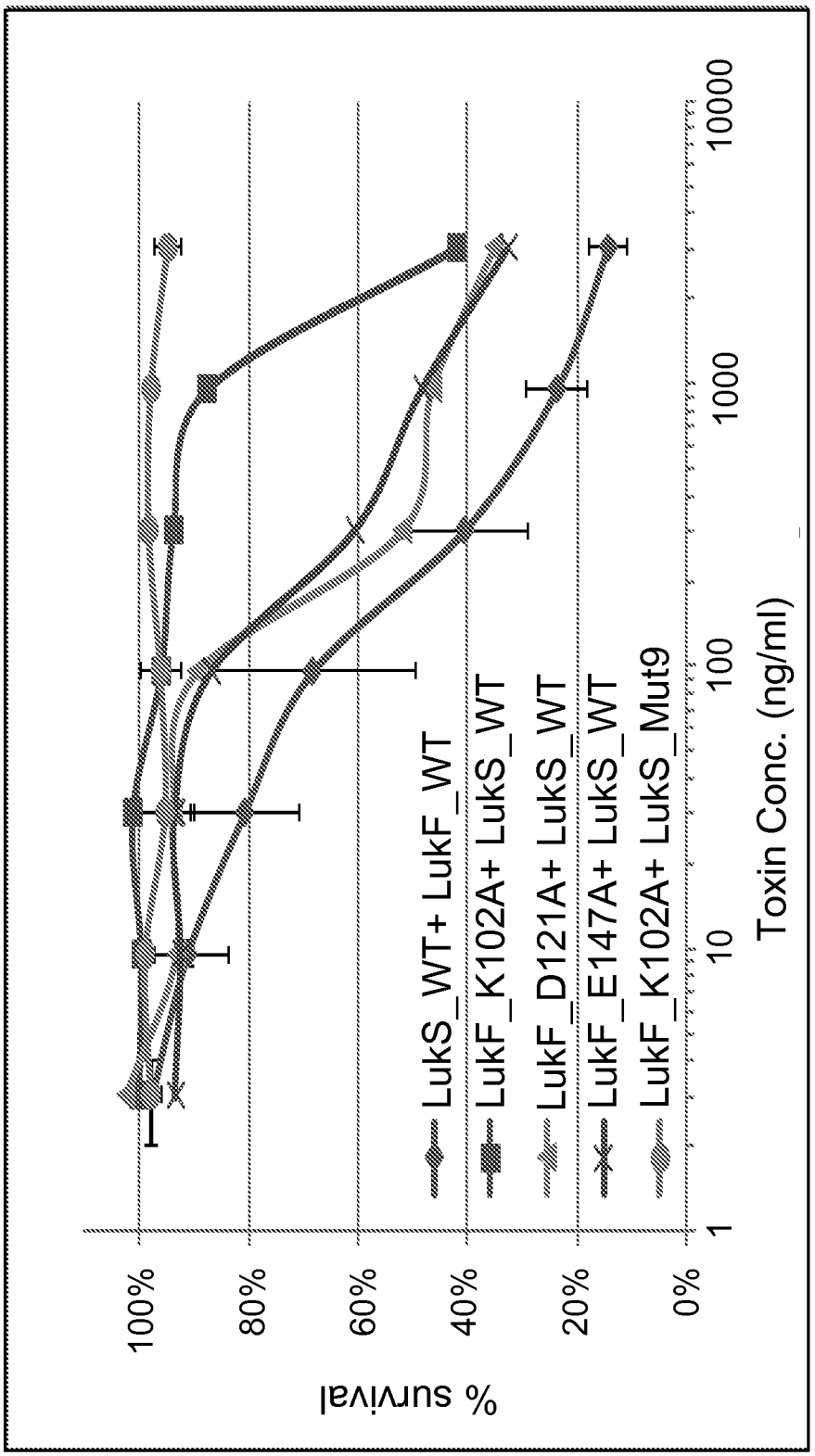

% survival
100%
80%
60%
40%
20%
0%
1
10
100
1000
10000
Toxin Conc. (ng/ml)
LukS_WT+ LukF_WT
LukF_K102A+ LukS_WT
LukF_D121A+ LukS_WT
LukF_E147A+ LukS_WT
LukF_K102A+ LukS_Mut9

FIG. 8B

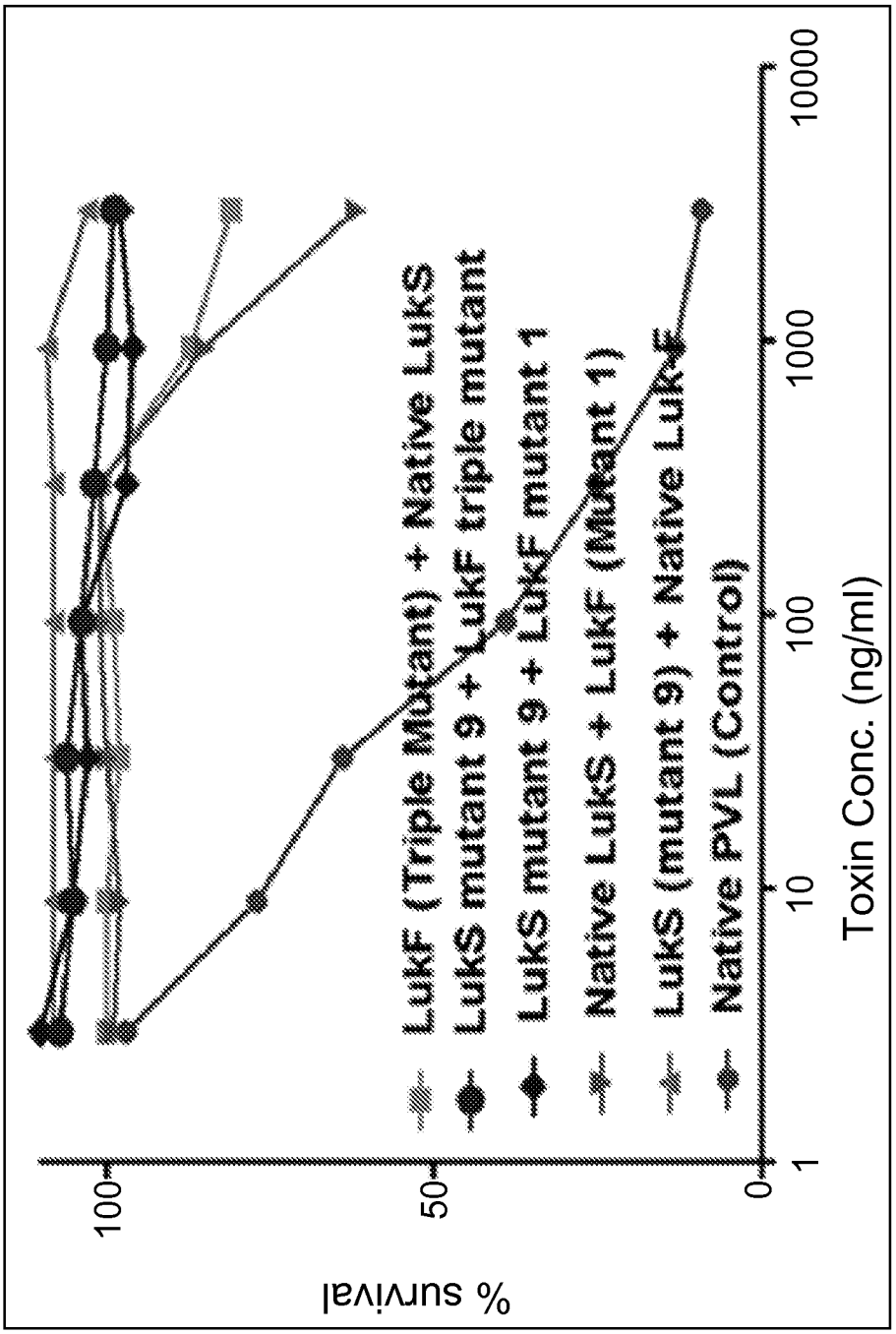

% survival
100
50
0
1
10
100
1000
10000
Toxin Conc. (ng/ml)
LukF (Triple Mutant) + Native LukS
LukS mutant 9 + LukF triple mutant
LukS mutant 9 + LukF mutant 1
Native LukS + LukF (Mutant 1)
LukS (mutant 9) + Native LukF
Native PVL (Control)

FIG. 8C

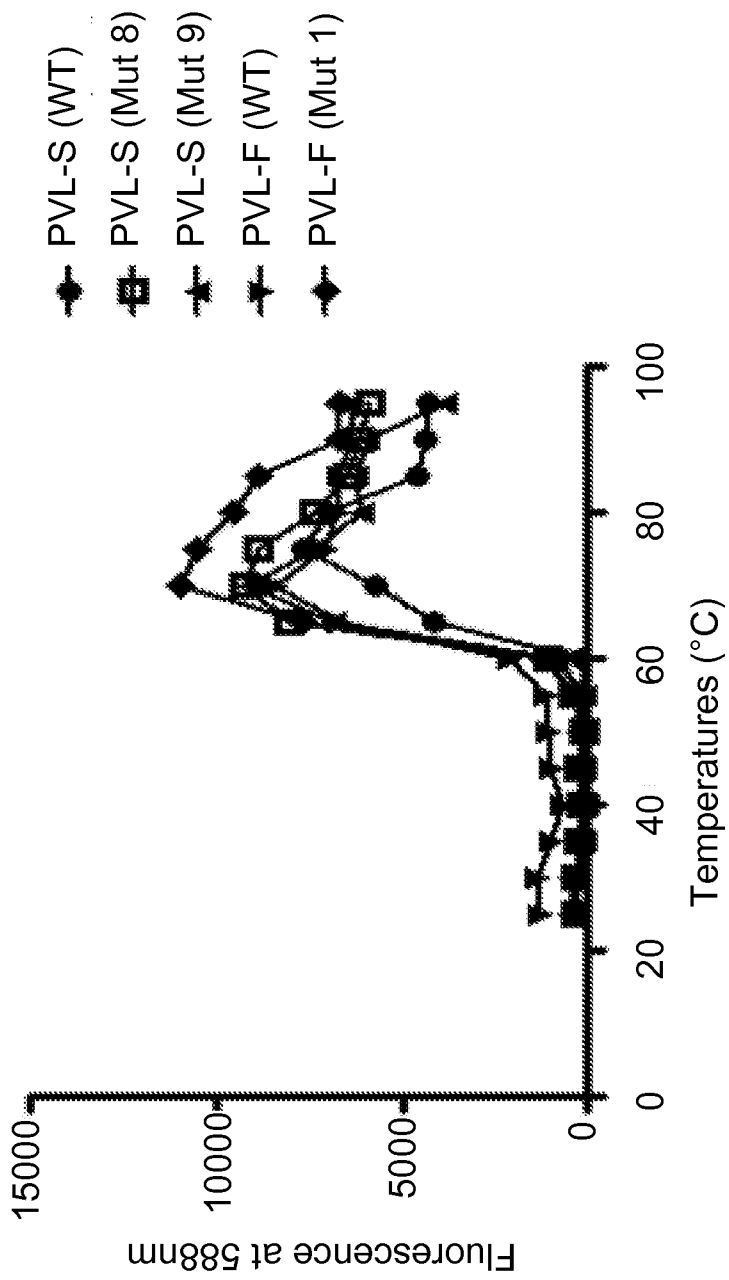

PVL-S (WT)
PVL-S (Mut 8)
PVL-S (Mut 9)
PVL-F (WT)
PVL-F (Mut 1)
Fluorescence at 588nm
15000
10000
5000
0
0
20
40
60
80
100
Temperatures (°C)

FIG. 9A

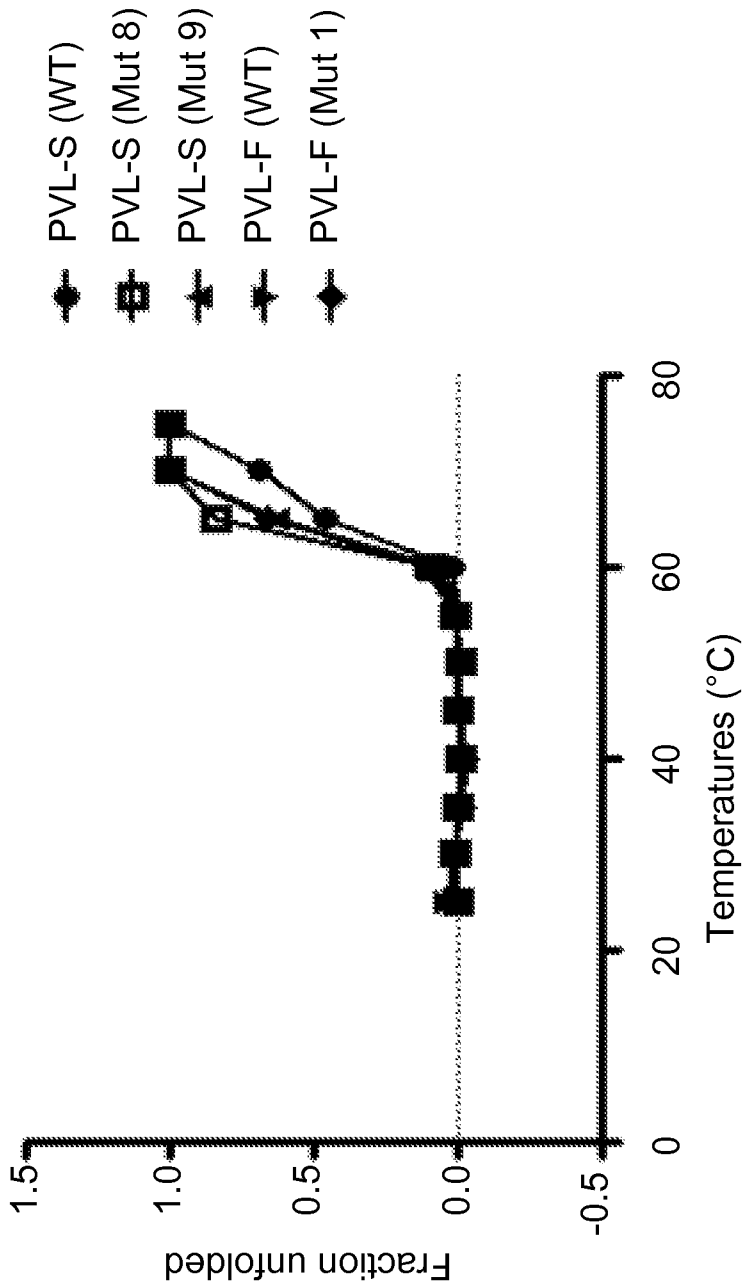

PVL-S (WT)
PVL-S (Mut 8)
PVL-S (Mut 9)
PVL-F (WT)
PVL-F (Mut 1)
Fraction unfolded
1.5
1.0
0.5
0.0
-0.5
0
20
40
60
80
Temperatures (°C)

FIG. 9B

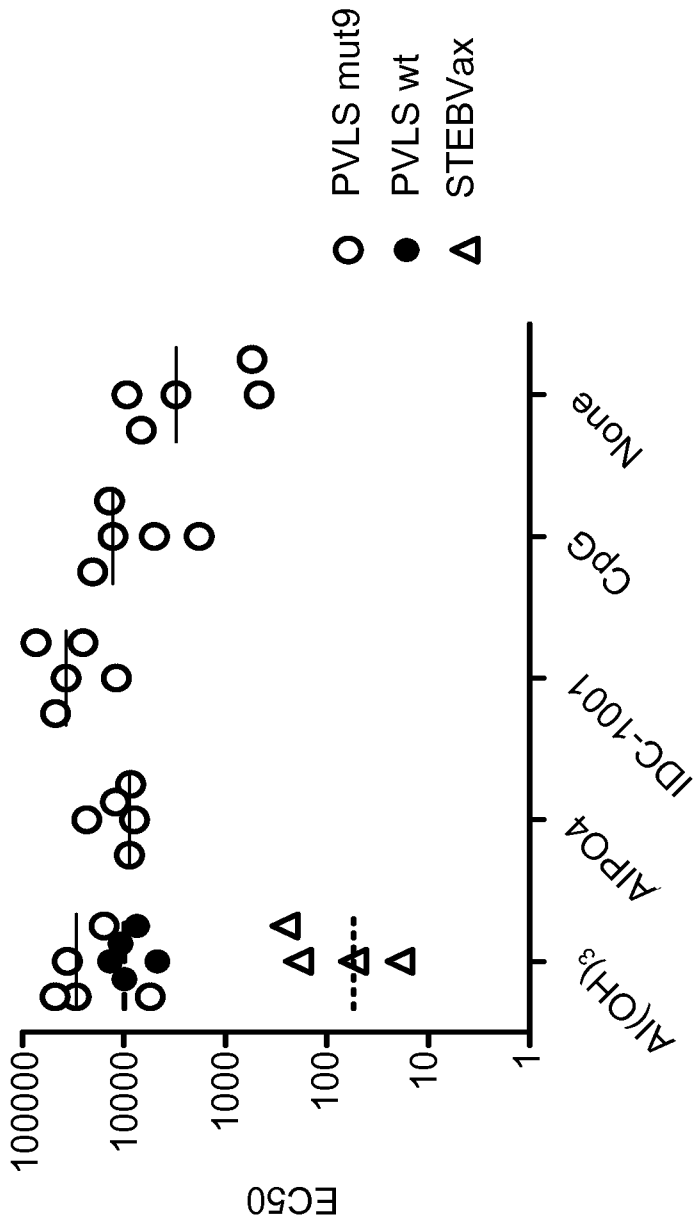

PVLS mut9
PVLS wt
STEBVax
EC50
100000
10000
1000
100
10
1
Al(OH)3
AlPO4
IDC-1001
CpG
None

FIG. 10A

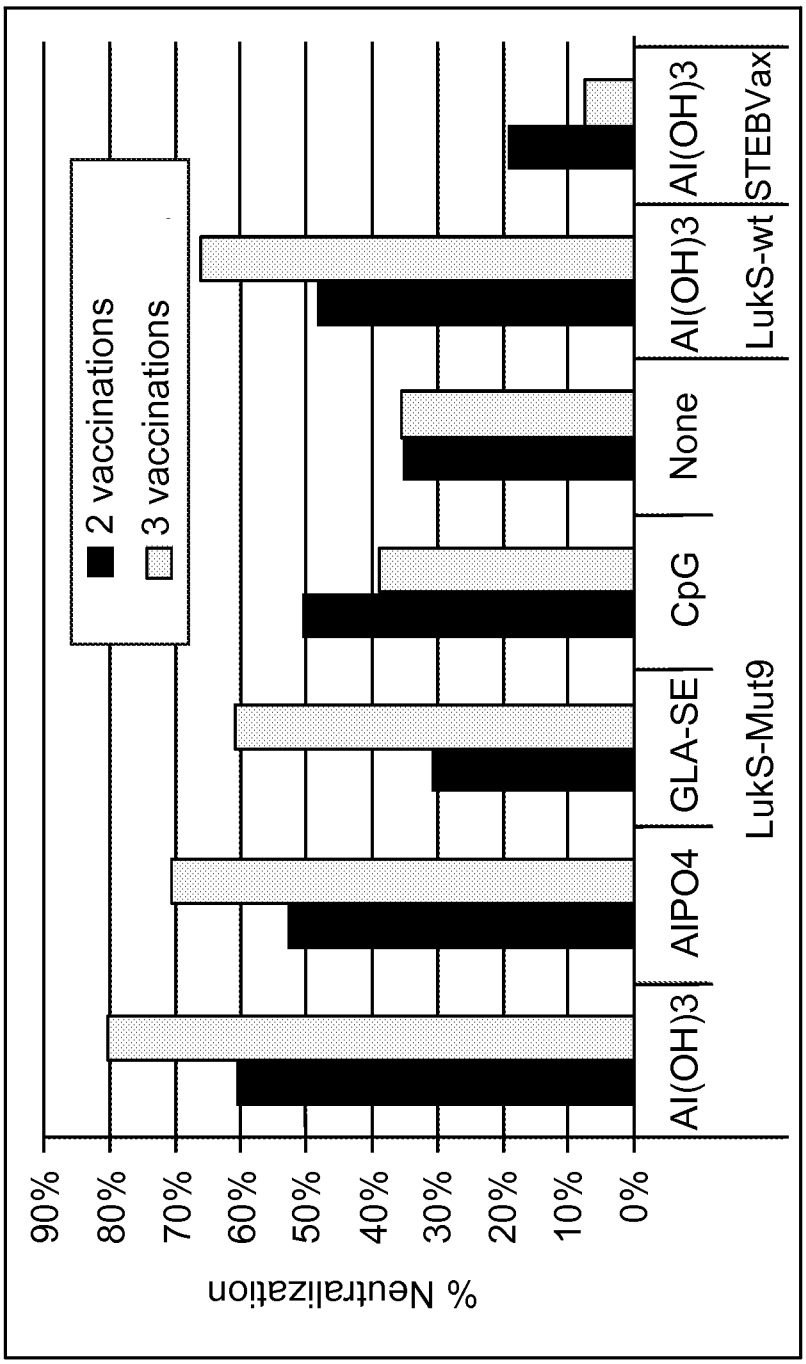
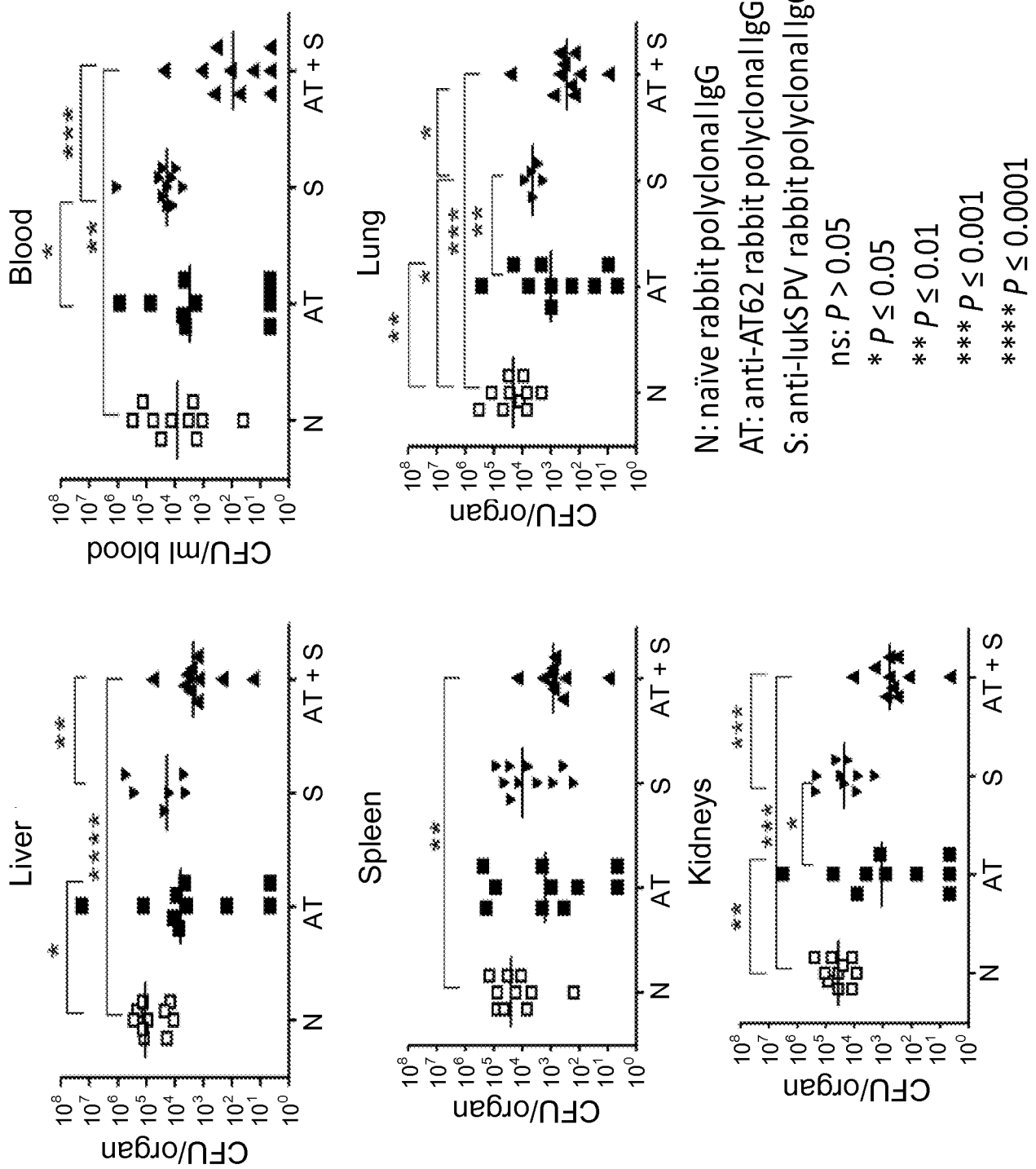

% Neutralization
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
2 vaccinations
3 vaccinations
Al(OH)3
AlPO4
GLA-SE
CpG
None
Al(OH)3
Al(OH)3
LukS-Mut9
LukS-wt
STEBVax

FIG. 10B


Blood
CFU/ml blood
Liver
CFU/organ
Lung
CFU/organ
Spleen
CFU/organ
Kidneys
CFU/organ
N
AT
S
AT + S
N: naïve rabbit polyclonal IgG
AT: anti-AT62 rabbit polyclonal IgG
S: anti-lukSPV rabbit polyclonal IgG
ns: P > 0.05
* P ≤ 0.05
** P ≤ 0.01
*** P ≤ 0.001
**** P ≤ 0.0001

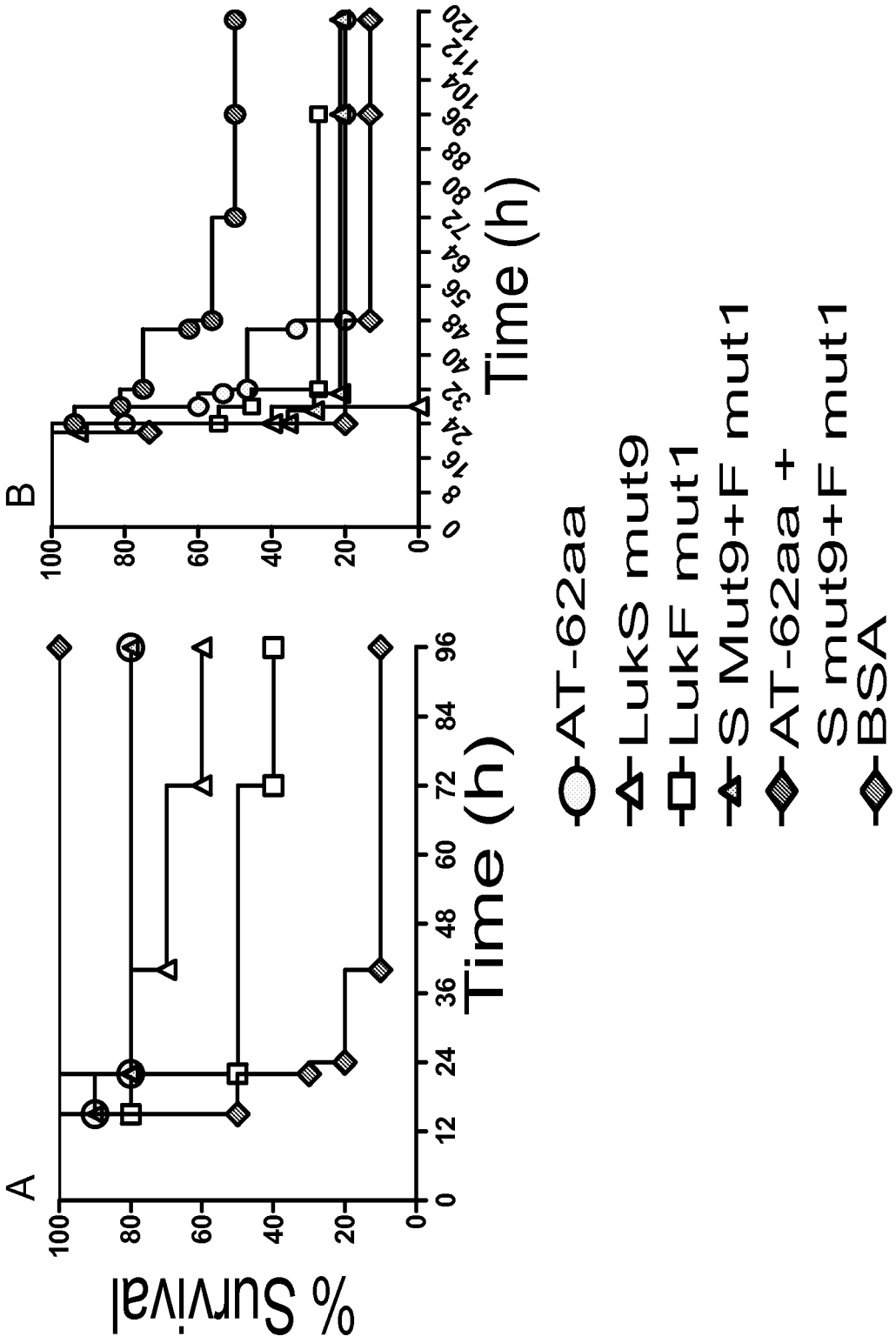

A
B
% Survival
Time (h)
Time (h)
0
12
24
36
48
60
72
84
96
0
6
16
24
32
40
48
56
64
72
80
88
96
104
112
120
0
20
40
60
80
100
AT-62aa
LukS mut9
LukF mut1
S Mut9+F mut1
AT-62aa +
S mut9+F mut1
BSA

FIG. 12

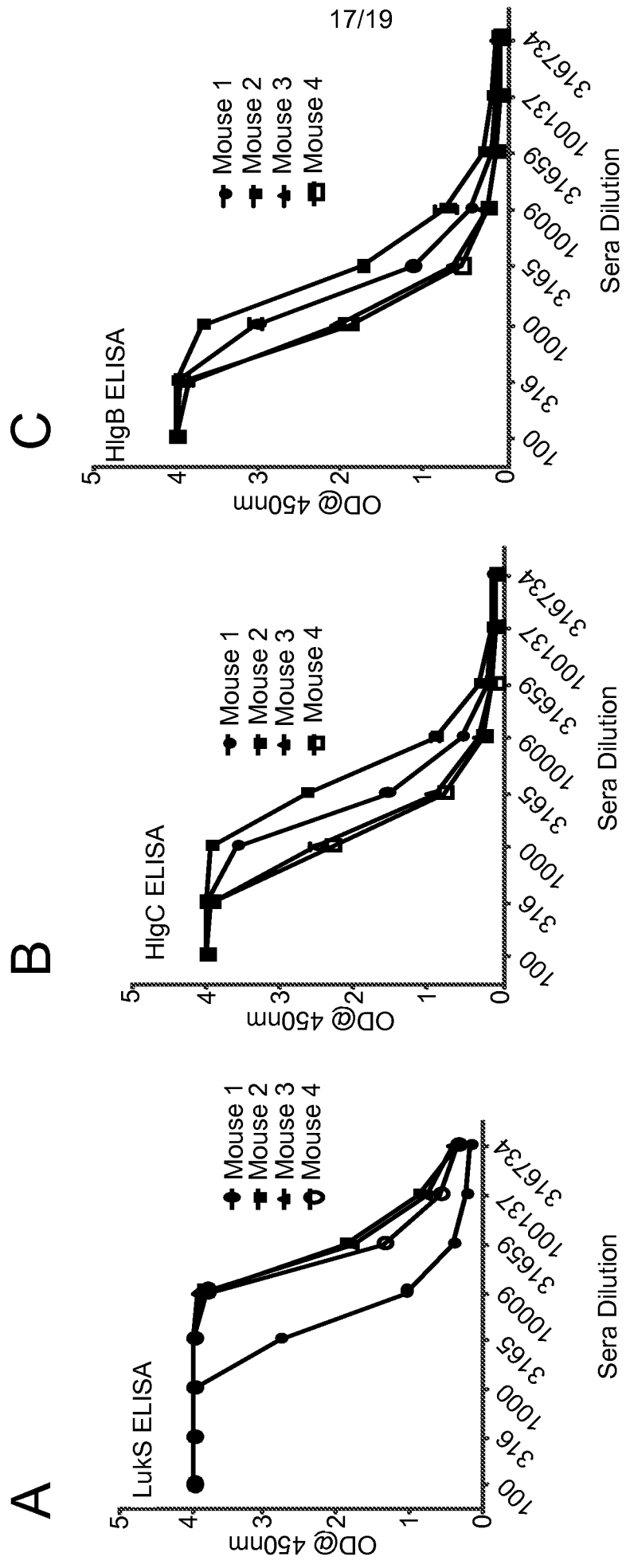

A
LukS ELISA
OD@ 450nm
Sera Dilution
Mouse 1
Mouse 2
Mouse 3
Mouse 4
B
HlgC ELISA
OD@ 450nm
Sera Dilution
Mouse 1
Mouse 2
Mouse 3
Mouse 4
C
HlgB ELISA
OD@ 450nm
Sera Dilution
Mouse 1
Mouse 2
Mouse 3
Mouse 4

FIG. 13

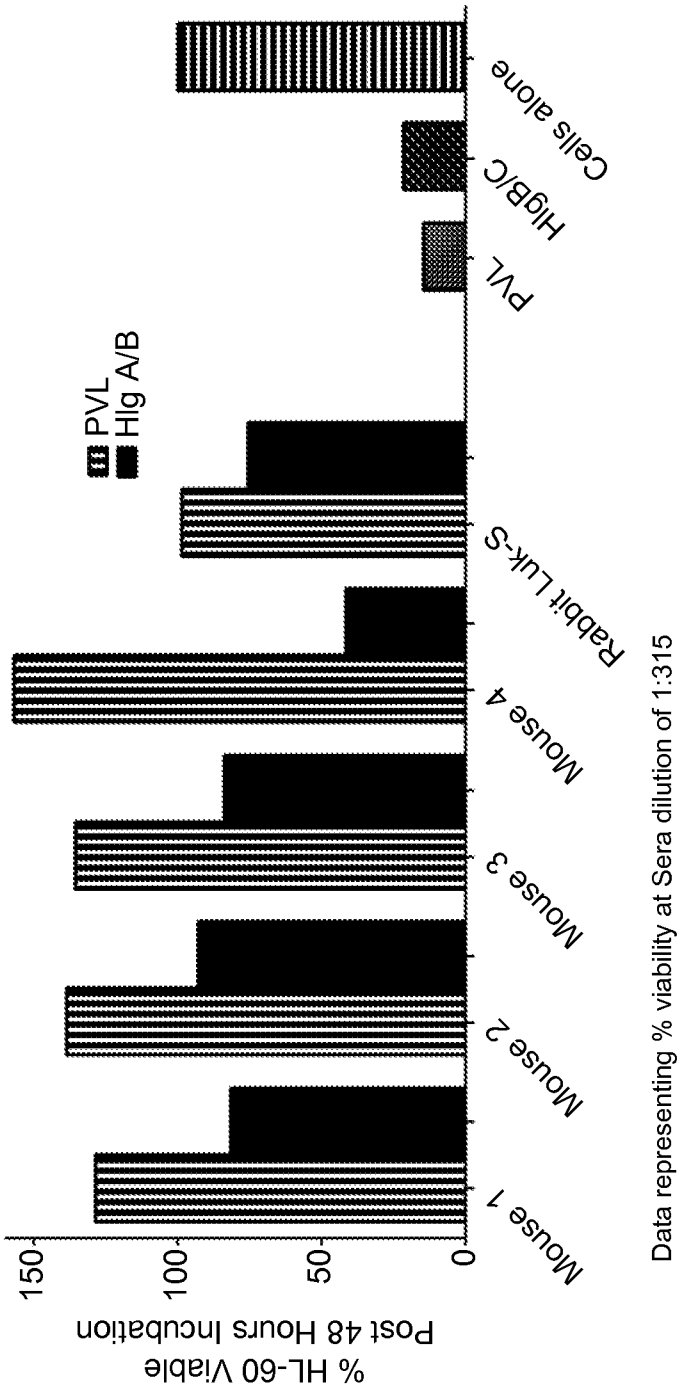

% HL-60 Viable
Post 48 Hours Incubation
150
100
50
0
PVL
Hlg A/B
Mouse 1
Mouse 2
Mouse 3
Mouse 4
Rabbit Luk-S
PVL
HlgB/C
Cells alone
Data representing % viability at Sera dilution of 1:315

FIG. 13D

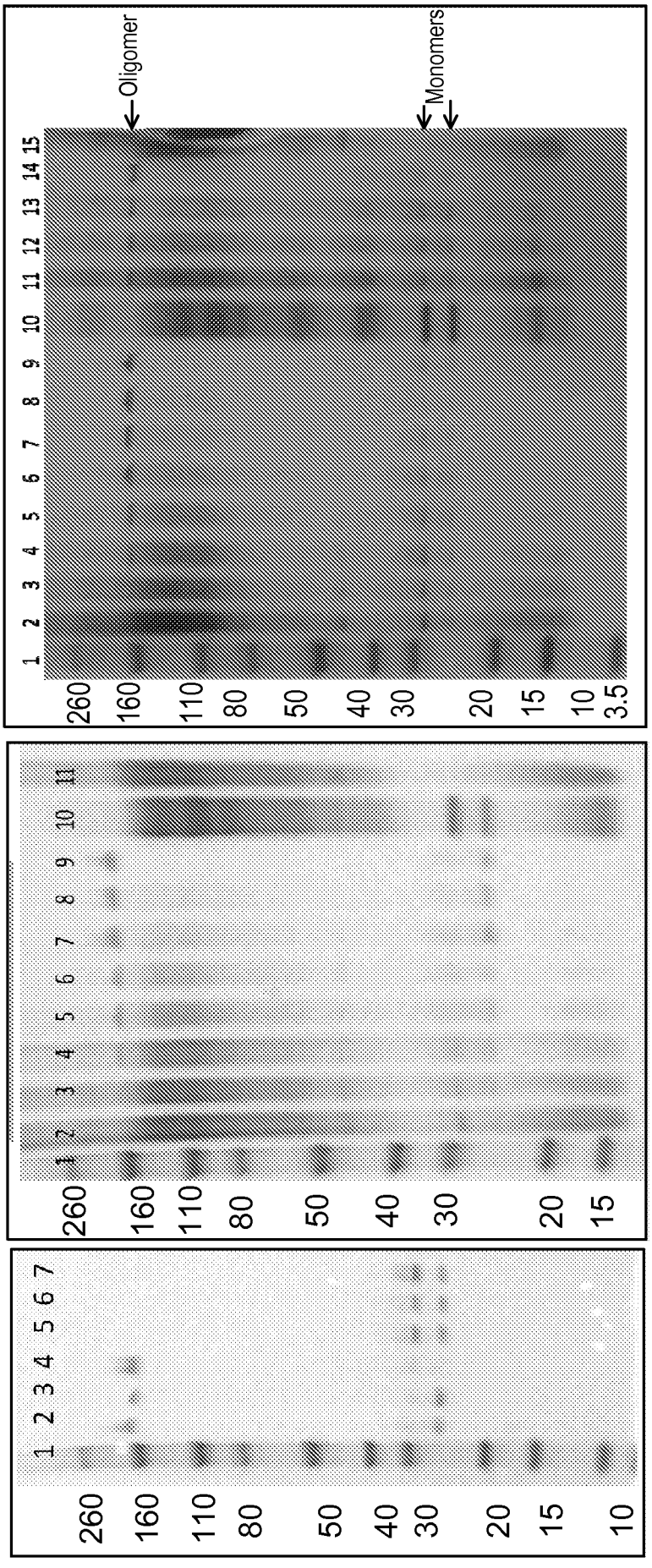


FIG. 14