



US008017133B2

(12) **United States Patent**
Patti et al.

(10) **Patent No.:** **US 8,017,133 B2**
(45) **Date of Patent:** ***Sep. 13, 2011**

(54) **MULTICOMPONENT VACCINES**
(75) Inventors: **Joseph M. Patti**, Cumming, GA (US);
Timothy J. Foster, Dublin (IE);
Magnus Hook, Houston, TX (US)

(73) Assignees: **Inhibitex**, Alpharetta, GA (US); **The Provost Fellows and Scholars of the College of the Holy and Undivided Trinity of Queen Elizabeth Near Dublin**, Dublin (IE); **The Texas A & M University System**, College Station, TX (US)

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 0 days.
This patent is subject to a terminal disclaimer.

(21) Appl. No.: **12/710,790**

(22) Filed: **Feb. 23, 2010**

(65) **Prior Publication Data**
US 2010/0150956 A1 Jun. 17, 2010

Related U.S. Application Data
(62) Division of application No. 10/795,267, filed on Mar. 9, 2004, now Pat. No. 7,666,438, which is a division of application No. 09/386,959, filed on Aug. 31, 1999, now Pat. No. 6,703,025.

(60) Provisional application No. 60/098,439, filed on Aug. 31, 1998.

(51) **Int. Cl.**
A61K 39/085 (2006.01)

(52) **U.S. Cl.** **424/243.1**; 424/192.1; 424/193.1; 424/197.11; 536/123.1

(58) **Field of Classification Search** None
See application file for complete search history.

(56) **References Cited**
U.S. PATENT DOCUMENTS
6,008,341 A * 12/1999 Foster et al. 536/23.7

OTHER PUBLICATIONS
McDevitt et al (Mol.Microbiol. 11: 237-248. 1994).*
Fattom et al (Infect. Immun. Jul. 1990. 58(7): 2367-2374).*
Fattom et al (Infect. Immun. May 1996, 64(5): 1659-1665).*
* cited by examiner

Primary Examiner — Jennifer Graser
(74) *Attorney, Agent, or Firm* — B. Aaron Schulman, Esq.; Terry L. Wright, Esq.; Stites & Harbison PLLC

(57) **ABSTRACT**
Multicomponent vaccines are provided which aid in the prevention and treatment of staphylococcal infections and which include certain selected combinations of bacterial binding proteins or fragments thereof, or antibodies to those proteins or fragments. By careful selection of the proteins, fragments, or antibodies, a vaccine is provided that imparts protection against a broad spectrum of *Staphylococcus* and other bacterial strains and against proteins that are expressed at different stages of the logarithmic growth curve. In one embodiment of the invention, a composition is provided that includes a fibrinogen binding domain of a fibrinogen binding protein and a bacterial component such as a capsular polysaccharide, and both active and passive vaccines based on these components are also provided, along with methods of treating infection using these compositions and vaccines.

7 Claims, 12 Drawing Sheets

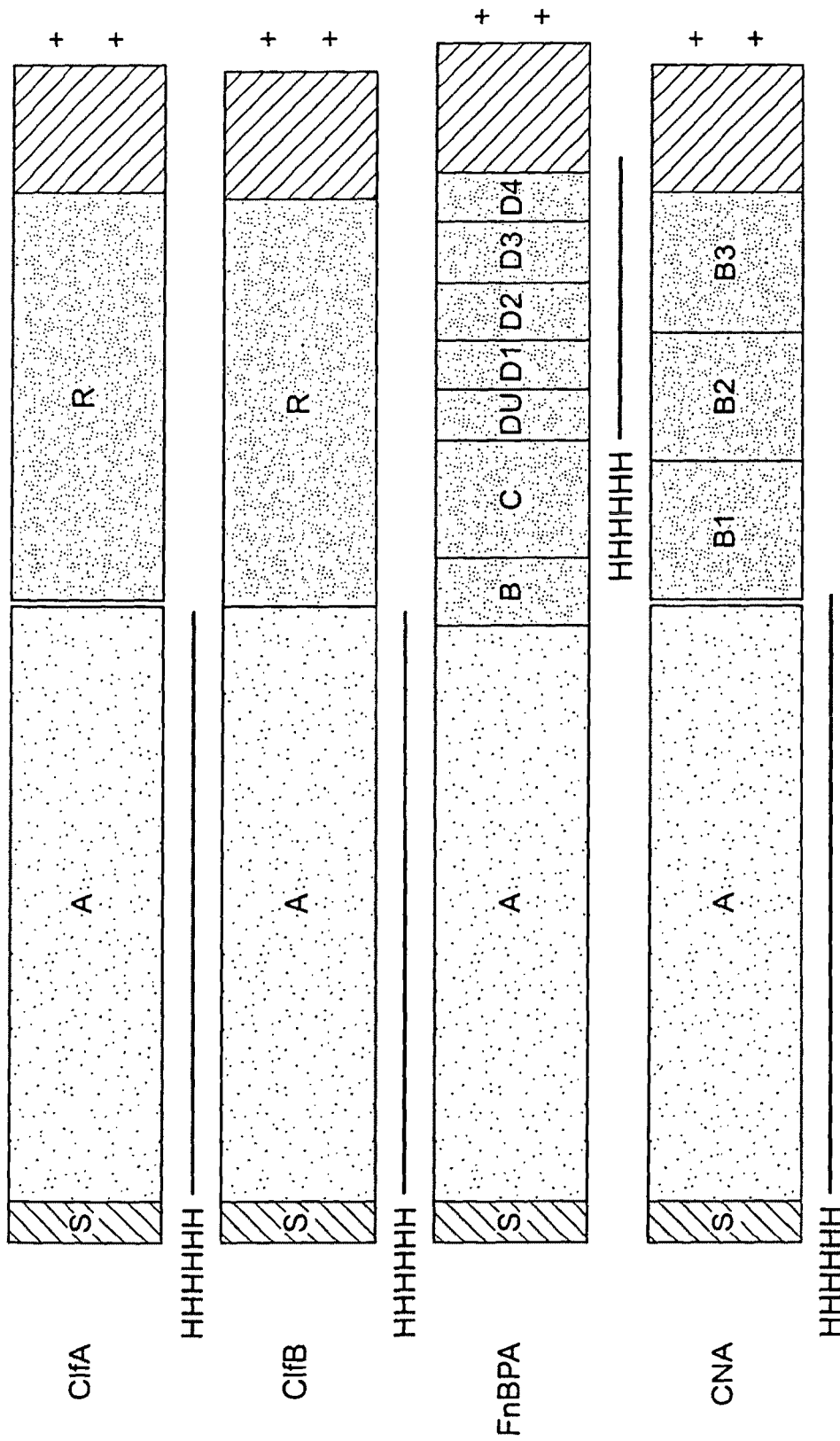


FIG. 1

IMMUNE RESPONSE IN MSCRAMM VACCINATED RHESUS MONKEYS

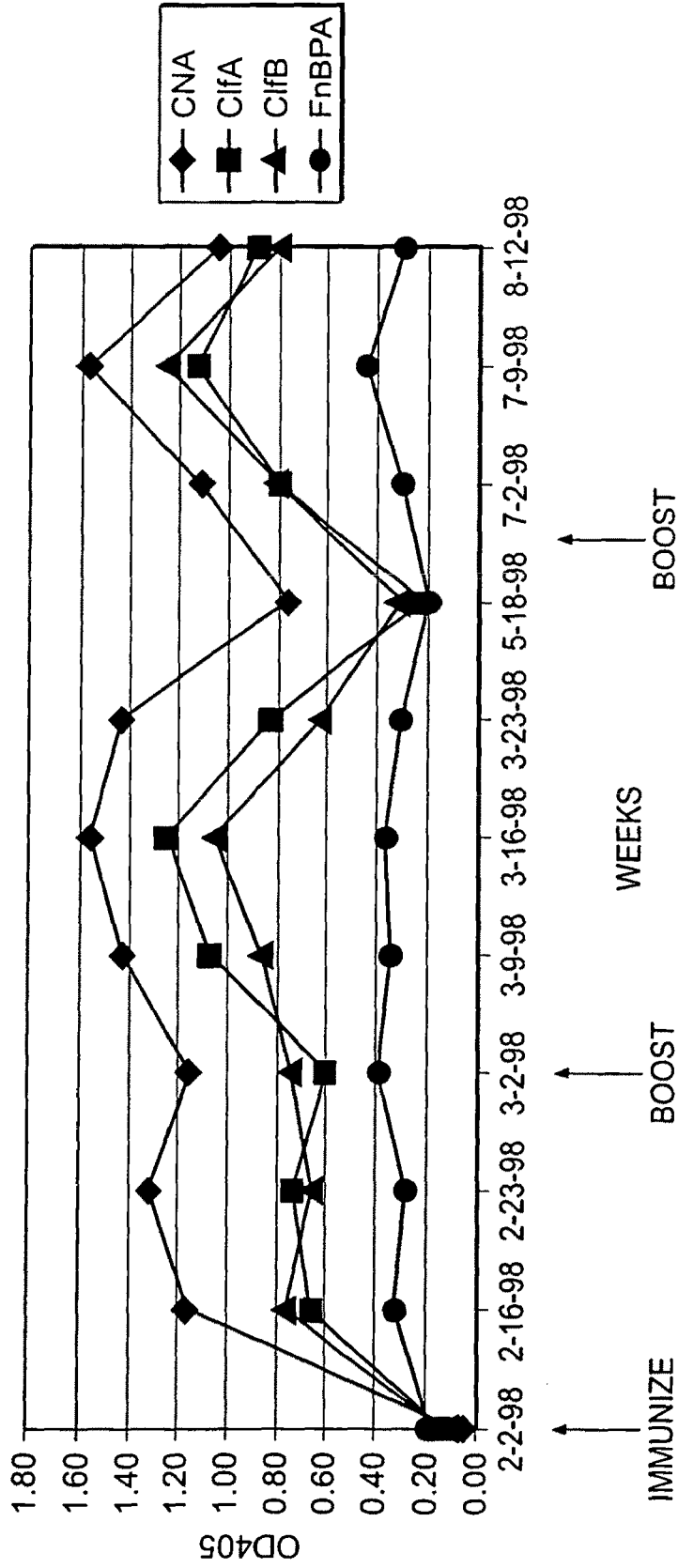


FIG. 2

CODING SEQUENCE FOR SdrF - INCLUDES FLANKING SEQUENCES

tattggataaattatgcttataaagtatttacataaaaatgtaaatgcaatttacaagta
Y W I N Y A Y K V F T - K C K C N L Q V
aatattcaaattatcttctgtaaaatatttattttaactggaggtatagtatgaaaaag
N I Q I I S L - N I Y F N W R Y S M K K
agaagacaaggaccaattaacaagagagtggttttctatccaacaaggtaacaagtac
R R Q G P I N K R V D F L S N K V N K Y
tcgattaggaagttcacagtaggtacagcttcaatactcgtgggtgctacgttaatgttt
S I R K F T V G T A S I L V G A T L M F
ggtgccgcagacaatgaggctaaagcggctgaagacaatcaattagaatcagcttcaaaa
G A A D N E A K A A E D N Q L E S A S K
gaagaacagaaaggtagtcgtgataatgaaaactcaaaacttaatcaagtcgatttagac
E E Q K G S R D N E N S K L N Q V D L D
aacggatcacatagttctgagaaaacaacaatgtaaacaatgcaactgaagtaaaaaaa
N G S H S S E K T T N V N N A T E V K K
gttgaagcaccaacgacaagtgacgtatctaagcctaagctaataagcagtagtgacg
V E A P T T S D V S K P K A N E A V V T
aatgagtcaactaaacaaaacaacagaagcaccaactgttaatgaggaatcaatagct
N E S T K P K T T E A P T V N E E S I A
gaaacacccaaaacctcaactacacaacaagattcgactgagaagaataatccatcttta
E T P K T S T T Q Q D S T E K N N P S L
aaagataatttaaattcatcctcaacgacatctaaagaaagtaaaacagacgaacattct
K D N L N S S S T T S K E S K T D E H S
actaagcaagctcaaatgttactaataaatcaaatttagacacaaatgactctccaact
T K Q A Q M S T N K S N L D T N D S P T
caaagtgagaaaacttcatcacaagcaaataacgacagtacagataatcagtcagcacct
Q S E K T S S Q A N N D S T D N Q S A P
tctaaacaattagattcaaaccatcagaacaaaagtatataaaacaaaatttaatgat
S K Q L D S K P S E Q K V Y K T K F N D
gaacctactcaagatggtgaacacacgacaactaaattaaacaccttctgtttcaaca
E P T Q D V E H T T T K L K T P S V S T
gatagttcagtcfaatgataagcaagattacacacgaagtgctgtagctagtttaggtggt
D S S V N D K Q D Y T R S A V A S L G V
gattctaataagaaacagaagcaattacaaatgcagtttagagacaatttagatttaaaagct
D S N E T E A I T N A V R D N L D L K A
gcatctagagaacaaatcaatgaagcaatcattgctgaagcactaaaaaaagacttttct
A S R E Q I N E A I I A E A L K K D F S

FIG. 3

aaccctgattatggtgtcgatacgccattagctcctaaacagatctcaatcaaaaaattca
N P D Y G V D T P L A L N R S Q S K N S
ccacataagagtgcaggtccacgcatgaatttaatgagtttagctgctgagcctaataagt
P H K S A S P R M N L M S L A A E P N S
ggtaaaaatgtgaatgataaagttaaaatcaciaaccctacgctttcacttaataagagt
G K N V N D K V K I T N P T L S L N K S
aataatcacgctaataacgtaatatggccaacaagtaacgaacaatttaatttaaagca
N N H A N N V I W P T S N E Q F N L K A
aattatgaattagatgacagcataaaagagggagatacttttactattaagtatggtcag
N Y E L D D S I K E G D T F T I K Y G Q
tatattagaccgggtggtttagaacttctgcaataaaaactcaactacgtagtaaggat
Y I R P G G L E L P A I K T Q L R S K D
ggctctattgtagctaattggtgtatatgataaaactacaaaacgacgacttatacattt
G S I V A N G V Y D K T T N T T T Y T F
actaactatggtgatcaatatcaaaaatattacaggtagttttgatttaattgacgacgct
T N Y V D Q Y Q N I T G S F D L I A T P
aagagggaaacagcaattaaggataatcagaattatcctatggaagtgacgattgctaac
K R E T A I K D N Q N Y P M E V T I A N
gaagtagtcaaaaaagacttcattgtggattatggtaataaaaaggacaatacaactaca
E V V K K D F I V D Y G N K K D N T T T
gcagcggtagcaaatgtggataatgtaataataaacataacgaagttgtttatctaac
A A V A N V D N V N N K H N E V V Y L N
caaaataacaaaaccctaaatgctaaatatttctcaacagtaaaaaatggtgaattt
Q N N Q N P K Y A K Y F S T V K N G E F
ataccaggtgaagtgaagtttacgaagtgacggataccaatgcatggttagatagcttc
I P G E V K V Y E V T D T N A M V D S F
aatcctgatttaaatagttctaatgtaaaagatgtgacaagtcaatttgcacctaaagta
N P D L N S S N V K D V T S Q F A P K V
agtgcagatggtactagagttgatatcaattttgctagaagtatggcaaatggtaaaaag
S A D G T R V D I N F A R S M A N G K K
tatattgtaactcaagcagtgagaccaacgggaactggaaatgtttataccgaatattgg
Y I V T Q A V R P T G T G N V Y T E Y W
ttaacaagagatggtactaccaatacaaatgatttttaccgtggaacgaagtctacaacg
L T R D G T T N T N D F Y R G T K S T T
gtgacttatctcaatggttcttcaacagcacaggggataatcctacatatagtctaggt
V T Y L N G S S T A Q G D N P T Y S L G
gactatgtatggttagataaaaataaaaacgggtgttcaagatgatgatgagaaaggttta
D Y V W L D K N K N G V Q D D D E K G L

FIG. 3 (CONT'D 1)

gcaggtgtttatgttactcttaaagacagtaacaatagagaattacaacgtgtaactact
A G V Y V T L K D S N N R E L Q R V T T
gatcaatctggacattatcaatcttgataattacaaaatggaacgtacacagtcgagttt
D Q S G H Y Q F D N L Q N G T Y T V E F
gcgattcctgataattatacgccatctcccgcaaataattctacaaatgatgcaatagat
A I P D N Y T P S P A N N S T N D A I D
tcagatggtgaacgtgatggtacacgtaaagtagttggtgccaaggaacaattaataat
S D G E R D G T R K V V V A K G T I N N
gctgataatgactgtagatactggcttttatttaactcctaaatacaatgtcggagat
A D N M T V D T G F Y L T P K Y N V G D
tatgtatgggaagatacaaaataaagatggtatccaagatgacaatgaaaaggaatttct
Y V W E D T N K D G I Q D D N E K G I S
ggtgttaaagtaacgttaaaaaataaaaaatggagatactattggcacaacgacaacagat
G V K V T L K N K N G D T I G T T T T D
tcaaatggtaaatatgaattcacaggttagagaacggggattacacaatagaatcttgag
S N G K Y E F T G L E N G D Y T I E F E
acgccggaaggctacacaccgactaaacaaaactcgggaagtgacgaaggtaaagattca
T P E G Y T P T K Q N S G S D E G K D S
aacggtacgaaaacaacagtcacagtcacagatgcagataataaaacaatagactcaggt
N G T K T T V T V K D A D N K T I D S G
ttctacaagccaacatataacttaggtgactatgtatgggaagatacaaaataaagatggt
F Y K P T Y N L G D Y V W E D T N K D G
attcaagacgacagtgaaaaagggatttctggggtaaagtgacgttaaaagataaaaaat
I Q D D S E K G I S G V K V T L K D K N
ggaaatgccattgggacaacgacaacagacgcaagtggtcattatcaatctaaaggatta
G N A I G T T T T D A S G H Y Q F K G L
gaaaatggaagctacacagttgagtttgagacaccatcaggttatacaccgacaaaagcg
E N G S Y T V E F E T P S G Y T P T K A
aattcaggtcaagatataactgtagattccaacggtataacaacaacaggtatcattaac
N S G Q D I T V D S N G I T T T G I I N
ggagctgataatctcacaattgatagtggtttctacaaaacaccaaataatagtgctgga
G A D N L T I D S G F Y K T P K Y S V G
gattatgtatgggaagatacaaaataaagatggtatccaagatgacaatgaaaaggaatt
D Y V W E D T N K D G I Q D D N E K G I
tctggtgttaaagtaacgttaaggatgaaaaggaatataattagcactacaacaact
S G V K V T L K D E K G N I I S T T T T
gatgaaaatgggaagtatcaatcttgataatcttagatagtggttaattacattatctttt
D E N G K Y Q F D N L D S G N Y I I H F

FIG. 3 (CONT'D 2)

gagaaaccggaaggcatgactcaaactacagcaaattctggaaatgatgatgaaaagat
E K P E G M T Q T T A N S G N D D E K D
gctgatggggaagatggtcgtgttacgattactgatcatgatgactttagtatagataat
A D G E D V R V T I T D H D D F S I D N
ggttatthtgacgatgattcagacagtgactcagacgcagatagtgattcagactcagac
G Y F D D D S D S D S D A D S D S D S D
agtgactcggacgcagacagcgattctgacgcagacagtgactcagacgcagatagtgat
S D S D A D S D S D A D S D S D A D S D
tctgactcagacagcgactcagacgcagatagtgattccgattcagacagcgactcggat
S D S D S D S D A D S D S D S D S D S D
tcagatagtgattcggatgcagacagcgactcggattctgacagtgattctgacgcagac
S D S D S D A D S D S D S D S D S D A D
agtgactcagattcagacagtgactcggattcagacagcgattcggattccgattcagac
S D S D S D S D S D S D S D S D S D S D
agtgactcggattcagacagtgactcagactccgacagtgattccgattcagatagcgac
S D S D S D S D S D S D S D S D S D S D
tccgacgcagatagtgattcggacgcagacagtgactcagattcagacagtgattcggac
S D A D S D S D A D S D S D S D S D S D
gcagacagtgactcggactcagatagtgattcagatgcagacagcgattcagactcagat
A D S D S D S D S D S D A D S D S D S D
agcgactcggattcagacagcgactccgacgcagacagcgactcggattcagatagtgat
S D S D S D S D S D A D S D S D S D S D
tctgactcagacagtgactcagattccgatagtgattcggattcagatagtgattccgac
S D S D S D S D S D S D S D S D S D S D
gcagacagcgattcggattccgatagcgattcagactcagacagcgattcagattcagac
A D S D S D S D S D S D S D S D S D S D
agcgactcagattcagatagtgattccgacgcagacagcgatgcagacagcgactcagac
S D S D S D S D S D A D S D A D S D S D
gcagacagtgattcagatgcagacagcgattctgactcagatagtgactcagacgcagat
A D S D S D A D S D S D S D S D S D A D
agtgattccgattccgatagcgattcagattctgatagtgactcagactcagacagtgac
S D S D S D S D S D S D S D S D S D S D
tcagattccgatagcgactcggattcagatagtgattccgacgcagacagtgactcagac
S D S D S D S D S D S D S D S D S D S D
tcagatagtgactcggattccgatagtgattccgacgcagacagcgattctgactcagat
S D S D S D S D S D S D A D S D S D S D
agtgactcagacgcagatagtgattccgattccgatagcgattcggatgcagacagcgac
S D S D A D S D S D S D S D S D A D S D

FIG. 3 (CONT'D 3)

tccgattcagatagtgattccgacgcagacagtgactcagactcagatagtgactcggat
S D S D S D S D A D S D S D S D S D S D
tccgatagtgattccgacgcagacagcgattccgattccgatagcgattcagactccgac
S D S D S D A D S D S D S D S D S D S D
agcgattcagattcagacagcgactcagattccgatagtgattccgattcagacagtgac
S D S D S D S D S D S D S D S D S D S D S D
tccgattccgatagtgactcagactcagacagtgactcagattcagatagcgactcagat
S D S D S D S D S D S D S D S D S D S D S D
tcagacagtgattccggactcagatagtgactccgattcagacagtgattccggattccgat
S D S D S D S D S D S D S D S D S D S D S D
agcgattccggattccgatagtgactccggattcagacagtgattccggactcagacagcgac
S D S D S D S D S D S D S D S D S D S D S D
tccgattcagatagtgattccgactcagacagcgattccggattccgatagtgactcggat
S D S D S D S D S D S D S D S D S D S D S D
tcagacagtgattccggactcagacagcgactccgattcagatagtgattccgacgcagac
S D S D S D S D S D S D S D S D S D S D A D
agcgactccgattcagatagtgattccggacgcagacagcgattccgatagtgactcggat
S D S D S D S D S D A D S D S D S D S D
tcagacagtgattccggactcagacagcgattccgattcagacagtgactccggactcagat
S D S D S D S D S D S D S D S D S D S D S D
agcgactccgattcagacagtgactccggactcagatagtgactccgattcagacagcgac
S D S D S D S D S D S D S D S D S D S D S D
tccgattctgataaaaaatgcaaaagataaattacctgatacaggagcaaatgaagatcat
S D S D K N A K D K L P D T G A N E D H
gattctaaaggcacattacttggacttttatttgcaggtttaggagcattattattagga
D S K G T L L G T L F A G L G A L L L G
agacgtcgtaaaaaagataataaagaaaaatagcactattgattcattcataagttattt
R R R K K D N K E K * H Y - F I H K L F
caagccaggtctatatggcctggtttgaaatcatattaaattgaaaggagaaaaagatga
Q A R S I W P G L K S Y - I E R R K R -
gtatgg
V W

FIG. 3 (CONT'D 4)

SdrG coding and flanking sequences.

atattgcaaaaaagacttatataactatattgtattttactctagaaacgatttttacttgaa
I A K K T Y I L Y C I L L - K R F L L E
aattacattgaaatagtcaaagataaggagtttttatgatttaaaaaaaaaataatttacta
N Y I E I V K D K E F L - L K K N N L L
actaaaaagaacctatagcaataaatccaataaatatgcaattagaaaattcacagta
T K K K P I A N K S N K Y A I R K F T V
ggtacagcgtctatttgaataggtgcagcattattgtttggttaggtcataatgaggcc
G T A S I V I G A A L L F G L G H N E A
aaagctgaggagaatacagtacaagacgttaaagattcgaatatggatgatgaattatca
K A E E N T V Q D V K D S N M D D E L S
gatagcaatgatcagtcagtaatgaagaaaagaatgatgtaataataatagtcagtc
D S N D Q S S N E E K N D V I N N S Q S
ataaacaccgatgatgataaccaataaaaaagaagaacgaatagcaacgatgccata
I N T D D D N Q I K K E E T N S N D A I
gaaaatcgctctaaagatataacacagtcacaacaaatgtagatgaaaacgaagcaaca
E N R S K D I T Q S T T N V D E N E A T
ttttacaaaagaccctcaagataatactcagcttaaagaagaagtggtaaaagaacc
F L Q K T P Q D N T Q L K E E V V K E P
tcatcagtcgaatcctcaaattcatcaatggatactgcccaacaaccatctcatacaaca
S S V E S S N S S M D T A Q Q P S H T T
ataaatagtgaagcatctattcaacaagtgataatgaagaaaattcccgcgtatcagat
I N S E A S I Q T S D N E E N S R V S D
tttgtaactctaaaataatagagagtaacactgaatccaataaagaagagaatactata
F A N S K I I E S N T E S N K E E N T I
gagcaacctaacaagtaagagaagattcaataacaagtcaaccgtctagctataaaaat
E Q P N K V R E D S I T S Q P S S Y K N
atagatgaaaaaatttcaaatacaagatgagttattaaatttaccataaatgaatatgaa
I D E K I S N Q D E L L N L P I N E Y E
aataaggtttagaccgttatctacaacatctgcccaaccatcgagtaagcgtgtaaccgta
N K V R P L S T T S A Q P S S K R V T V
aatcaattagcggcagaacaaggttcgaatgtaatcatttaattaagttactgatcaa
N Q L A A E Q G S N V N H L I K V T D Q
agtattactgaaggatgatgatagtgatggtattattaaagcacatgatgctgaaaac
S I T E G Y D D S D G I I K A H D A E N
ttaatctatgatgtaacttttgaagtagatgataaggtgaaatctggtgatacgatgaca
L I Y D V T F E V D D K V K S G D T M T

FIG. 4

gtgaatatagataagaatacagttccatcagatttaaccgatagtttgcaataccaaaa
V N I D K N T V P S D L T D S F A I P K
ataaaagataattctggagaaatcatcgctacaggtacttatgacaacacaaataaacia
I K D N S G E I I A T G T Y D N T N K Q
attacctacacttttacagattatgtagataaatatgaaaatattaagcgcaccttaa
I T Y T F T D Y V D K Y E N I K A H L K
ttaacatcatacattgataaatcaaaggttccaaataataacactaagtttagatgtagaa
L T S Y I D K S K V P N N N T K L D V E
tataagacggccctttcatcagtaataaaacaattacggttgaatatcaaaaacctaac
Y K T A L S S V N K T I T V E Y Q K P N
gaaaatcggactgctaaccttcaaagtatgttcacaaacatagatacgaaaaaccataca
E N R T A N L Q S M F T N I D T K N H T
gttgagcaaacgatttatattaacctctctcgttattcagccaaagaaacaaatgtaaat
V E Q T I Y I N P L R Y S A K E T N V N
atttcagggaatggcgatgaaggttcaacaattatcgacgatagtacaatcattaaagtt
I S G N G D E G S T I I D D S T I I K V
tataaggttgagataatcaaaatttaccagatagtaacagaatttatgattacagtgaa
Y K V G D N Q N L P D S N R I Y D Y S E
tatgaagatgtcaciaatgatgattatgcccaattaggaataataatgacgtgaatatt
Y E D V T N D D Y A Q L G N N N D V N I
aattttggtaatatagattcaccatatattattaaagttattagtaaatatgacccta
N F G N I D S P Y I I K V I S K Y D P N
aaggacgattacacgacgatacagcaactgtgacaatgcaaacgactataaatgagtat
K D D Y T T I Q Q T V T M Q T T I N E Y
actggtgagtttagaacagcatcctatgataatacaattgctttctctacaagttcaggt
T G E F R T A S Y D N T I A F S T S S G
caaggacaaggtgacttgccctctgaaaaaacttataaaatcggagattacgtatgggaa
Q G Q G D L P P E K T Y K I G D Y V W E
gatgtagataaagatggattcaaaatacaaatgataatgaaaaaccgcttagtaatgta
D V D K D G I Q N T N D N E K P L S N V
ttggtaactttgacgtatcctgatggaacttcaaaatcagtcagaacagatgaagagggg
L V T L T Y P D G T S K S V R T D E E G
aaatatcaatttgatgggttaaaaaacggattgacttataaaattacattcgaacaccg
K Y Q F D G L K N G L T Y K I T F E T P
gaaggatatacggcagcgttaaacattcaggaacaaatcctgcactagactcagaaggc
E G Y T P T L K H S G T N P A L D S E G
aattctgtatgggtaactattaacggacaagacgatatgactattgatageggatttat
N S V W V T I N G Q D D M T I D S G F Y

FIG. 4 (CONT'D 1)

caaacacctaaatagcttagggaactatgtatgggtatgacactaataaagatggtatt
Q T P K Y S L G N Y V W Y D T N K D G I
caaggtgatgatgaaaaaggaatctctggagtaaaagtgacgttaaagatgaaaacgga
Q G D D E K G I S G V K V T L K D E N G
aatatcattagtagacaacaacaactgatgaaaatggaaagtatcaatttgataatttaaat
N I I S T T T T D E N G K Y Q F D N L N
agtggtaattatattgttcattttgataaaccttcaggtatgactcaaacaacaacagat
S G N Y I V H F D K P S G M T Q T T T D
tctggatgatgatgacgaacaggatgctgatggggaagaagtccatgtaacaattactgat
S G D D D E Q D A D G E E V H V T I T D
catgatgacttttagtatagataacggatactatgatgacgactcagattcagatagtgat
H D D F S I D N G Y Y D D D S D S D S D
tcagactcagatagcgcgactcagactccgatagcgattccgactcagacagcgactca
S D S D S D D S D S D S D S D S D S D S
gattccgatagtgattcagattcagacagtgactcagactcagatagtgattcagattca
D S D S D S D S D S D S D S D S D S D S
gacagcgattccgactcagacagtgactcaggattagacaatagctcagataagaataca
D S D S D S D S D S G L D N S S D K N T
aaagataaattaccggatacaggagctaataagaatcatgattctaaaggcacattactt
K D K L P D T G A N E D H D S K G T L L
ggagctttatattgcaggtttaggagcgttattattaggggaagcgtcgcaaaaatagaaaa
G A L F A G L G A L L L G K R R K N R K
aataaaaattaaattattcaaatgaaattagtgaagaagcagatacgacatttgaaatag
N K N * I I Q M K L V K E A D T T F E -
aaagtatatttagtccaacaaatataaggtggtg
K V Y L V Q Q I - G V

FIG. 4 (CONT'D 2)

SdrH coding region

atgaaaaagttaaacttaaacattcatttatgcttacgggctttgctttcatggtaact
M K K F N I K H S F M L T G F A F M V T
acatcattattcagtcaccaagcacatgctgaaggtaatcatcctattgacattaat
T S L F S H Q A H A E G N H P I D I N F
tctaaagatcaaattgataaaaatacagctaagagcaatattatcaatcgagtgaatgac
S K D Q I D R N T A K S N I I N R V N D
actagtcgcacaggaattagtagtaattcggataatgatttagatacagatatcgtttca
T S R T G I S M N S D N D L D T D I V S
aatagtgactcagaaaatgacacatatttagatagtgattcagattcagacagtgactca
N S D S E N D T Y L D S D S D S D S D S
gattcagatagtgactcagattcagatagtgactcagattcagatagtgactcagattca
D S D S D S D S D S D S D S D S D S D S D S
gacagtgattcagactcagatagtgactcagattcagacagtgattcagactcagatagt
D S D S D S D S D S D S D S D S D S D S D S
gattcagattcagacagtgattcagattcagacagtgactcagactcagacagtgattca
D S D S D S D S D S D S D S D S D S D S D S
gattcagatagtgattcagattcagatagtgattcagattcagatagtgattcagattca
D S D S D S D S D S D S D S D S D S D S D S
gacagtgactcagactcagacagtgattcagattcagatagtgattcagactcagatagt
D S D S D S D S D S D S D S D S D S D S D S
gactcagattcagatagtgattcagactctggtacaagttcaggtaagggttcacatacc
D S D S D S D S D S G T S S G K G S H T
ggaaaaaacctggtaacctaaaggaaatacaaatagaccttctcaagacatacgaat
G K K P G N P K G N T N R P S Q R H T N
caaccccaaaggcctaaatacaatcaacaaatcaaaacaatataaacaatataaaccat
Q P Q R P K Y N Q T N Q N N I N N I N H
aatattaatcatacacgtactagtgagatggtgctttaaactcaacaaaatatt
N I N H T R T S G D G A P F K R Q Q N I
attaattctaattcaggtcatagaaatcaaaataataaatcaatttatatggaacaaa
I N S N S G H R N Q N N I N Q F I W N K
aatggcttttttaaatctcaaaataataccgaacatagaatgaatagtagcgataatacc
N G F F K S Q N N T E H R M N S S D N T
aattcattaattagcagattcagacaattagccacgggtgcttataagtacaatccgttt
N S L I S R F R Q L A T G A Y K Y N P F
ttgattaatcaagtaaaaaatttgaatcaattagatggaaaggtgacagatagtgacatt
L I N Q V K N L N Q L D G K V T D S D I

FIG. 5

tatagcttgtttagaaagcaatcatttagaggaaatgaatatttaaattcattacaaaa
Y S L F R K Q S F R G N E Y L N S L Q K
gggacaagctatttcagatttcaatattttaatccacttaattctagtaaatactatgaa
G T S Y F R F Q Y F N P L N S S K Y Y E
aatttagatgatcagggttttagctttaattacaggagaaatcggctcaatgccagaactt
N L D D Q V L A L I T G E I G S M P E L
aaaaaacctacggataaagaagataaaaaatcatagcgcttcaaaaaccatagtgcagat
K K P T D K E D K N H S A F K N H S A D
gagataacaacaataatgatggacactccaaagattatgataagaaaaagaaaatacat
E I T T N N D G H S K D Y D K K K K I H
cgaagtcttttatcgttaagtattgcaataattggaatttttctaggagtcactggacta
R S L L S L S I A I I G I F L G V T G L
tatatctttagaagaaaaagtaa
Y I F R R K K *

FIG. 5 (CONT'D)

1

MULTICOMPONENT VACCINES

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a divisional application of application Ser. No. 10/795,267, filed Mar. 9, 2004, now U.S. Pat. No. 7,666,438, issued Feb. 23, 2010, which is a divisional application of application Ser. No.: 09/386,959, filed Aug. 31, 1999, now U.S. Pat. No. 6,703,025, issued Mar. 9, 2004, which claims benefit of U.S. Provisional Application No. 60/098,439, filed Aug. 31, 1998, all of said applications incorporated herein by reference.

The present invention was made in part from work supported by grant no. 97-35204-5046 from the United States Department of Agriculture. The U.S. government has certain rights in this invention.

The invention is in the field of biological products for the treatment and diagnosis of bacterial infections.

The invention is in the field of biological products for the treatment and diagnosis of bacterial infections.

BACKGROUND OF THE INVENTION

Staphylococci are Gram-positive spherical cells, usually arranged in grape-like irregular clusters. Some are members of the normal flora of the skin and mucous membranes of humans, others cause suppuration, abscess formation, a variety of pyogenic infections, and even fatal septicemia. Pathogenic staphylococci often hemolyze blood, coagulate plasma, and produce a variety of extracellular enzymes and toxins. The most common type of food poisoning is caused by a heat-stable staphylococci enterotoxin.

The genus *Staphylococcus* has at least 30 species. The three main species of clinical importance are *Staphylococcus aureus*, *Staphylococcus epidermidis*, and *Staphylococcus saprophyticus*. *Staphylococcus aureus* is coagulase-positive, which differentiates it from the other species. *S. aureus* is a major pathogen for humans. Almost every person has some type of *S. aureus* infection during a lifetime, ranging in severity from food poisoning or minor skin infections to severe life-threatening infections. The coagulase-negative staphylococci are normal human flora which sometimes cause infection, often associated with implanted devices, especially in very young, old and immunocompromised patients. Approximately 75% of the infections caused by coagulase-negative staphylococci are due to *S. epidermidis*. Infections due to *Staphylococcus warneri*, *Staphylococcus hominis*, and other species are less common. *S. saprophyticus* is a relatively common cause of urinary tract infections in young women. The staphylococci produce catalase, which differentiates them from the streptococci.

S. aureus colonization of the articular cartilage, of which collagen is a major component, within the joint space appears to be an important factor contributing to the development of septic arthritis. Hematogenously acquired bacterial arthritis remains a serious medical problem. This rapidly progressive and highly destructive joint disease is difficult to eradicate. Typically, less than 50% of the infected patients fail to recover without serious joint damage. *S. aureus* is the predominant pathogen isolated from adult patients with hematogenous and secondary osteomyelitis.

In hospitalized patients, *Staphylococcus* bacteria such as *S. aureus* are a major cause of infection. Initial localized infections of wounds or indwelling medical devices can lead to more serious invasive infections such as septicemia, osteomyelitis, mastitis and endocarditis. In infections associated

2

with medical devices, plastic and metal surfaces become coated with host plasma and matrix proteins such as fibrinogen and fibronectin shortly after implantation. The ability of *S. aureus* and other staphylococcal bacteria to adhere to these proteins is essential to the initiation of infection. Vascular grafts, intravenous catheters, artificial heart valves, and cardiac assist devices are thrombogenic and prone to bacterial colonization. Of the staphylococcal bacteria, *S. aureus* is generally the most damaging pathogen of such infections.

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. 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 it appears to be only a matter of time before vancomycin will become ineffective as well.

There is a strong and rapidly growing need for therapeutics to treat infections from staphylococci such as *S. aureus* which are effective against antibiotic resistant strains of the bacteria. The U.S. National Institutes for Health has recently indicated that this goal is now a national priority.

Bacterial adherence to host tissue occurs when specific microbial surface adhesins termed MSCRAMMs (Microbial Surface Components Recognizing Adhesive Matrix Molecules) specifically recognize and bind to extracellular matrix (ECM) components, such as fibronectin, fibrinogen, collagen, and elastin. Many pathogenic bacteria have been shown to specifically recognize and bind to various components of the ECM in an interaction which appears to represent a host tissue colonization mechanism. This adherence involves a group of bacterial proteins termed MSCRAMMs (Patti, J., et al., *Ann Rev Microbiol*, 48:585-617, 1994; Patti, J. and Hook, M., *Curr Opin Cell Biol.*, 6:752-758, 1994).

MSCRAMMs on the bacterial cell surface and ligands within the host tissue interact in a lock and key fashion resulting in the adherence of bacteria to the host. Adhesion is often required for bacterial survival and helps bacteria evade host defense mechanisms and antibiotic challenges. Once the bacteria have successfully adhered and colonized host tissues, their physiology is dramatically altered and damaging components such as toxins and enzymes are secreted. Moreover, the adherent bacteria often produce a biofilm and quickly become resistant to the killing effect of most antibiotics.

A bacterium can express MSCRAMMs that recognize a variety of matrix proteins. Ligand-binding sites in MSCRAMMs appear to be defined by relatively short contiguous stretches of amino acid sequences (motifs). Because a similar motif can be found in several different species of bacteria, it appears as though these functional motifs are subjected to interspecies transfer (Patti and Hook, *Curr Opin Cell Biol*, 6:752-758, 1994). In addition, a single MSCRAMM can sometimes bind several ECM ligands.

Vaccination Studies

Historically, studies on bacterial adherence have focused primarily on Gram-negative bacteria, which express a wide

variety of fimbrial adhesive proteins (designated adhesins) on their cell surface (Falkow, S., *Cell*, 65:1099-1102, 1991). These adhesins recognize specific glycoconjugates exposed on the surface of host cells (particularly epithelial layers). Employing the lectin-like structures in attachment allows the microorganism to efficiently colonize the epithelial surfaces. This provides the bacteria an excellent location for replication and also the opportunity to disseminate to neighboring host tissues. It has been demonstrated that immunization with pilus adhesins can elicit protection against microbial challenge, such as in *Hemophilus influenza* induced otitis media in a chinchilla model (Sirakova et al., *Infect Immun*, 62(5):2002-2020, 1994), *Moraxella bovis* in experimentally induced infectious bovine keratoconjunctivitis (Lepper et al., *Vet Microbiol*, 45(2-3):129-138, 1995), and *E. coli* induced diarrhea in rabbits (McQueen et al., *Vaccine*, 11:201-206, 1993). In most cases, immunization with adhesins leads to the production of immune antibodies that prevent infection by inhibiting bacterial attachment and colonization, as well as enhancing bacterial opsonophagocytosis and antibody-dependent complement-mediated killing.

The use of molecules that mediate the adhesion of pathogenic microbes to host tissue components as vaccine components is emerging as an important step in the development of future vaccines. Because bacterial adherence is the critical first step in the development of most infections, it is an attractive target for the development of novel vaccines. An increased understanding of the interactions between MSCRAMMs and host tissue components at the molecular level coupled with new techniques in recombinant DNA technology have laid the foundation for a new generation of subunit vaccines. Entire or specific domains of MSCRAMMs, either in their native or site-specifically altered forms, can now be produced. Moreover, the ability to mix and match MSCRAMMs from different microorganisms creates the possibility of designing a single vaccine that will protect against multiple bacteria.

Recent clinical trials with a new subunit vaccine against whooping cough, consisting of the purified Bordetella pertussis MSCRAMMs filamentous hemagglutinin and pertactin, in addition to an inactivated pertussis toxin, are a prime example of the success of this type of approach. Several versions of the new acellular vaccine were shown to be safe and more efficacious than the old vaccine that contained whole bacterial cells (Greco et al., *N Eng J Med*, 334:341-348, 1996; Gustaffson et al., *N Eng J Med*, 334:349-355, 1996).

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 antibody titers and human immunity.

Over the past several decades live, heat-killed, and formalin fixed preparations of *S. aureus* cells have been tested as vaccines to prevent staphylococcal infections. A multicenter clinical trial was designed to study the effects of a commercial vaccine, consisting of a *staphylococcus* toxoid and whole killed staphylococci, on the incidence of peritonitis, exit site infection, and *S. aureus* nasal carriage among continuous peritoneal dialysis patients (Poole-Warren et al., *Clin Nephrol.*, 35:198-206, 1991). Although immunization with the vaccine elicited an increase in the level of specific antibodies to *S. aureus*, the incidence of peritonitis was unaffected. Simi-

larly, immunization of rabbits with whole cells of *S. aureus* could not prevent or modify any stage in the development of experimental endocarditis, reduce the incidence of renal abscess, or lower the bacterial load in infected kidneys (Greenberg, D. P., et al., *Infect Immun*, 55:3030-3034, 1987).

Currently there is no FDA approved vaccine for the prevention of *S. aureus* infections. However, a *S. aureus* vaccine (StaphVAX), based on capsular polysaccharide, is currently being developed by NABI (North American Biologicals Inc.). This vaccine consists of type 5 or type 8 capsular polysaccharides conjugated to *Pseudomonas aeruginosa* exotoxin A (rEPA). The vaccine is designed to induce type-specific opsonic antibodies and enhance opsonophagocytosis (Karakawa et al., *Infect Immun*, 56:1090-1095, 1988). Using a refined lethal challenge mouse model (Fattom et al., *Infect Immun*, 61:1023-1032, 1993) it has been shown that intraperitoneal infusion of type 5 capsular polysaccharide specific IgG reduces the mortality of mice inoculated intraperitoneally with *S. aureus*. The type 5 capsular polysaccharide-rEPA vaccine has also been used to vaccinate seventeen patients with end-stage renal disease (Welch et al., *J Amer Soc Nephrol*, 7(2):247-253, 1996). Geometric mean (GM) IgG antibody levels to the type 5 conjugate increased between 13 and 17-fold after the first immunization, however no additional increases could be detected after additional injections. Interestingly, the GM IgM levels of the vaccinated patients were significantly lower than control individuals. Supported by the animal studies, the vaccine has recently completed a Phase II trial in continuous ambulatory peritoneal dialysis patients. The clinical trial showed the vaccine to be safe but ineffective in preventing staphylococcal infections (NABI SEC FORM 10-K405, Dec. 31, 1995). Two possible explanations for the inability of StaphVAX to prevent infections related to peritoneal dialysis in vaccinated patients are that the immunogenicity of the vaccine was too low due to suboptimal vaccine dosing or that antibodies in the bloodstream are unable to affect infection in certain anatomic areas, such as the peritoneum.

Gram-positive bacteria related sepsis is on the increase. In fact between one-third and one-half of all cases of sepsis are caused by Gram-positive bacteria, particularly *S. aureus* and *S. epidermidis*. In the United States, it can be estimated that over 200,000 patients will develop Gram-positive related sepsis this year.

Using a mouse model (Bremen et al., *Infect Immun*, 59(8):2615-2623, 1991), it has been clearly demonstrated that active immunization with M55 domain of the Col-binding MSCRAMM can protect mice against sepsis induced death. Mice were immunized subcutaneously with either M55 or a control antigen (bovine serum albumin) and then challenged intravenously with *S. aureus*. Eighty-three percent (35/42) of the mice immunized with M55 survived compared to only 27% of the BSA immunized mice (12/45). This a compilation of 3 separate studies.

Schennings, et al., demonstrated that immunization with fibronectin binding protein from *S. aureus* protects against experimental endocarditis in rats (*Micro Pathog*, 15:227-236, 1993). Rats were immunized with a fusion protein (gal-FnBP) encompassing beta-galactosidase and the domains of fibronectin binding protein from *S. aureus* responsible for binding to fibronectin. Antibodies against fusion protein gal-FnBP were shown to block the binding of *S. aureus* to immobilized fibronectin in vitro. Endocarditis in immunized and non-immunized control rats was induced by catheterization via the right carotid artery, resulting in damaged aortic heart valves which became covered by fibrinogen and fibronectin. The catheterized rats were then infected intravenously with

1×10^5 cells of *S. aureus*. The number of bacteria associated with aortic valves was determined 11/2 days after the challenge infection and a significant difference in bacterial numbers between immunized and non-immunized groups was then observed.

A mouse mastitis model was used by Mamo, et al., (*Vaccine*, 12:988-992, 1994) to study the effect of vaccination with fibrinogen binding proteins (especially FnBP-A) and collagen binding protein from *S. aureus* against challenge infection with *S. aureus*. The mice vaccinated with fibrinogen binding proteins showed reduced rates of mastitis compared with controls. Gross examination of challenged mammary glands of mice showed that the glands of mice immunized with fibrinogen binding proteins developed mild intramammary infection or had no pathological changes compared with glands from control mice. A significantly reduced number of bacteria could be recovered in the glands from mice immunized with fibrinogen binding proteins as compared with controls. Mamo then found that vaccination with FnBP-A combined with staphylococcal alpha toxoid did not improve the protection (Mamo, et al., *Vaccine*, 12:988-992, 1994). Next, Mamo, et al., immunized mice with only collagen binding protein, which did not induce protection against the challenge infection with *S. aureus*.

Whole killed staphylococci were included in a vaccine study in humans undergoing peritoneal dialysis (Poole-Warren et al., *Clin. Nephrol.*, 35:198-206, 1991). In this clinical trial, a commercially available vaccine of alpha-hemolysin toxoid combined with a suspension of whole killed bacteria) was administered intramuscularly ten times over 12 months, with control patients receiving saline injections. Vaccination elicited significant increases in the levels of antibodies to *S. aureus* cells in the peritoneal fluid and to alpha-hemolysin in the serum. However, immunization did not reduce the incidences of peritonitis, catheter-related infections or nasal colonization among vaccine recipients. The lack of protective efficacy in this trial were attributed to a suboptimal vaccine formulation.

Secreted proteins have been explored as components of subcellular vaccines. The alpha toxin is among the most potent staphylococcal exotoxins; it has cytolytic activity, induces tissue necrosis and kills laboratory animals. Immunization with formaldehyde-detoxified alpha toxin does not protect animals from systemic or localized infections, although it may reduce the clinical severity of the infections (Ekstedt, R. D., in *The Staphylococci*, 385-418, 1972).

One study has evaluated the protective efficacy of antibodies to the *S. aureus* microcapsule in an experimental model of staphylococcal infection (Nemeth, J. and Lee, J. C., *Infect. Immun.* 63:375-380, 1995). Rats were actively immunized with killed, microencapsulated bacteria or passively immunized with high-titer rabbit antiserum specific for the capsular polysaccharide. Control animals were injected with saline or passively immunized with normal rabbit serum. Protection against catheter-induced endocarditis resulting from intravenous challenge with the same strain was then evaluated. Despite having elevated levels of anticapsular antibodies, the immunized animals were susceptible to staphylococcal endocarditis and immunized and control animals had similar numbers of bacteria in the blood.

As described in the Detailed Description of the Invention hereinbelow, a number of patents and patent applications describe the gene sequences for fibronectin, fibrinogen, collagen, elastin, and MHC II analogous type binding proteins. These patents and patent applications are incorporated by reference in their entirety. These documents teach that the proteins, fragments, or antibodies immunoreactive with those

proteins or fragments can be used in vaccinations for the treatment of *S. aureus* infections. PCT/US97/087210 discloses the vaccination of mice with a combination of a collagen binding protein (M55 fragment), a fibronectin binding peptide (formulin treated FnBP-A (D1-D3)) and a fibrinogen binding peptide (ClfA).

The lack of adequate protection against staphylococcal infection that has been seen to date from the vaccines described above is likely the result of the failure to generate the proper immune response, perhaps along with improper immunization scheduling or an improper immunization route. Additional factors that also contribute to the poor performance of past vaccines can be reflected in the fact that staphylococcal bacteria such as *S. aureus* have been observed to temporally regulate the expression of most of its virulence factors via regulatory genes loci agr and sar. For example, *S. aureus* contains two genes that encode cell surface fibrinogen binding proteins, ClfA and ClfB. Interestingly, ClfA is predominantly expressed in early exponential growth, while ClfB is expressed later in the growth phase. Accordingly, the antigens that the invading organism presents to the host in vivo may not be the same as those used in the vaccine. In addition, not every *S. aureus* antigen is expressed on every isolate. For example, only about 50% of *S. aureus* clinical isolates express the gene cna, which encodes for the collagen binding MSCRAMM. To generate an effective immunotherapeutic against *S. aureus*, the vaccine must be multi-component and contain antigens that span the growth cycle as well as include antigens that are expressed by a majority of *S. aureus* isolates.

Despite the advances in the art of compositions for the treatment of infections from staphylococcal bacteria such as *S. aureus*, there remains a need to provide a more effective product, and preferably one that exhibits a broad spectrum immunization against staphylococcal bacteria of various strains, and to particular proteins which may be expressed at different stages of the bacterial growth phase.

Therefore, it is an object of the invention to provide a new therapeutic composition for immunization against infections from staphylococcal bacteria such as *S. aureus* and *S. epidermidis*.

It is another object of the present invention to provide a vaccine that will provide protection against mastitis, arthritis, endocarditis, septicemia, and osteomyelitis, furunculosis, cellulitis, pyemia, pneumonia, pyoderma, suppuration of wounds, food poisoning, bladder infections and other infectious diseases.

It is another object of the present invention to provide a therapeutic composition that immunizes against staphylococcal infection, enhances the amount of intracellular killing of staphylococcal bacteria, and increases the rate of phagocytosis of staphylococcal bacteria.

It is still another object of the present invention to provide a composition that will further protect the host by neutralizing exotoxins.

SUMMARY OF THE INVENTION

It has been discovered that the treatment of staphylococcal infections can be significantly enhanced by immunization with certain selected combinations of bacterial binding proteins or fragments thereof, or antibodies to those proteins or fragments. The proteins or fragments can be used in active vaccines, and the antibodies in passive vaccines. Alternatively, the combinations can be used to select donor blood pools for the preparation of purified blood products for passive immunization. By careful selection of the proteins, frag-

ments, or antibodies, a vaccine is provided that imparts protection against a broad spectrum of *Staphylococcus* bacterial strains and against proteins that are expressed at different stages of the logarithmic growth curve.

The vaccine and products described herein respond to the urgent need of the medical community for a substitute for small molecule antibiotics, which are rapidly losing effectiveness. The vaccines are a significant improvement over the prior art, which while generally teaching the use of MSCRAMMs to impart immunization, did not teach which combinations of the large number of known MSCRAMMs should be used to impart superior protection.

In one embodiment of the invention, a composition is provided that includes at least a collagen binding protein or peptide (or an appropriate site directed mutated sequence thereof) such as CNA, or a protein or fragment with sufficiently high homology thereto, in combination with a fibrinogen binding protein, preferably Clumping factor A ("ClfA") or Clumping factor B ("ClfB"), or a useful fragment thereof or a protein or fragment with sufficiently high homology thereto.

In another embodiment of the invention, a composition is provided that includes at least a fibronectin binding protein or peptide (or an appropriate site directed mutated sequence thereof), or a protein or fragment with sufficiently high homology thereto, in combination with the fibrinogen binding protein, preferably A or B (ClfA or ClfB, respectively), or a useful fragment thereof or a protein or fragment with sufficiently high homology thereto.

In a third embodiment, a composition is provided that includes at least the fibrinogen binding protein A (ClfA) and the fibrinogen binding protein B (ClfB), or useful fragments thereof or a protein or fragment with sufficiently high homology thereto.

In a fourth embodiment, a composition is provided that includes at least a fibronectin binding protein or peptide (or an appropriate site directed mutated sequence thereof), or a protein or fragment with sufficiently high homology thereto, in combination with (i) the fibrinogen binding protein A and B (ClfA and ClfB), or a useful fragment thereof or a protein or fragment with sufficiently high homology thereto; and (ii) a collagen binding protein or useful fragment thereof.

In an additional embodiment, a composition is provided that includes the components of the prior embodiments in combination with an elastin binding protein or peptide or a protein or fragment with sufficiently high homology thereto.

In another embodiment, a composition is provided that includes the components of the prior embodiments in combination with a MHC II analogous protein or peptide or a protein or fragment with sufficiently high homology thereto.

In another embodiment, a composition is provided that includes the components of any of the prior combinations in combination with a bacterial component to increase the rate of phagocytosis of the staphylococcal bacteria. In a one such embodiment, the bacterial component comprises a capsular polysaccharide, such as capsular polysaccharide type 5 or type 8.

In an additional embodiment, a composition is provided that includes any of the prior combinations in combination with the extracellular matrix-binding proteins SdrC, SdrD, SdrE or a consensus or variable sequence amino acid motif, or useful fragments thereof or proteins or fragments with sufficiently high homology thereto.

In an additional embodiment, a composition is provided that includes any of the prior combinations in combination with the extracellular matrix-binding proteins SdrF, SdrG, or SdrH, or a consensus or variable sequence amino acid motif,

or useful fragments thereof or proteins or fragments with sufficiently high homology thereto. This embodiment is particularly effective in developing vaccines that can be useful with regard to both coagulase-positive and coagulase-negative staphylococcal bacteria.

In another embodiment, a composition is provided that includes at least the extracellular matrix-binding proteins SdrC, SdrD and SdrE or useful fragments thereof, such as the consensus or variable sequence amino acid motif, or a protein or fragment with sufficiently high homology thereto.

Alternatively, compositions are provided that include monoclonal or polyclonal antibodies which are immunoreactive to the selected combination of described components. These compositions can be used in vaccinations to treat patients infected with *Staphylococcus* infections.

In other embodiments of the invention, the combinations of proteins, fragments or antibodies as described are used in diagnostic kits.

As described below, proteins and peptides to be used in the composition which bind to fibronectin, fibrinogen, collagen, and elastin are known. Alternatively, one can identify new fibronectin, fibrinogen, collagen, and elastin binding proteins, or the epitopes thereof for use in the composition. Methods of identifying a peptide of a binding domain of a binding protein that binds to the ligand of choice are known. For example, one can contact a candidate protein or peptide with the ligand under conditions effective to allow binding of the ligand to the binding domain of a binding protein, and identify a positive candidate peptide that binds to the ligand.

Antibodies that bind to the binding domains of the composition proteins or peptides can be generated by administering to an animal a pharmaceutical composition comprising an immunologically effective amount of the combination of proteins or peptides, even though the peptide does not specifically bind to the ECM.

The combination of the isolated, recombinant or synthetic MSCRAMM proteins, or active fragments thereof or fusion proteins thereof, are also useful as scientific research tools to identify staphylococcal binding sites on the host ECM molecules, thereby promoting an understanding of the mechanisms of bacterial pathology and the development of antibacterial therapies. Furthermore, the isolated, recombinant or synthetic proteins, or antigenic portions thereof (including epitope-bearing fragments), or fusion proteins thereof can be administered to animals as immunogens or antigens, alone or in combination with an adjuvant, for the production of antisera reactive with MSCRAMM proteins. In addition, the proteins can be used to screen antisera for hyperimmune patients from whom can be derived antibodies having a very high affinity for the proteins. Antibodies isolated from the antisera are useful for the specific detection of staphylococcal bacteria or binding proteins, as research tools, or as therapeutic treatments against staphylococcal infection.

The proteins, or active fragments thereof, and antibodies to the proteins are useful for the treatment of infections from staphylococcal infections from bacteria such as *S. aureus* as described above; for the development of anti-*Staphylococcus* vaccines for active or passive immunization; and, when administered as pharmaceutical composition to a wound or used to coat medical devices or polymeric biomaterials in vitro and in vivo, both the proteins and the antibodies are useful as blocking agents to prevent or inhibit the binding of staphylococcal bacteria to the wound site or biomaterials.

Preferably, animal derived antibody is modified so that it is less immunogenic in the patient to whom it is administered. For example, if the patient is a human, the antibody may be "humanized" by transplanting the complementarily determin-

ing regions of the hybridoma-derived antibody into a human monoclonal antibody as described by Jones et al., (*Nature* 321:522-525 (1986)) or Tempest et al. (*Biotechnology* 9:266-273 (1991)).

Kits are also provided that are useful as a diagnostic agent for the detection of staphylococcal infections. According to yet another embodiment, anti-MSCRAMM antibodies as well as the MSCRAMM polypeptides of this invention, are useful as diagnostic agents for detecting infection by staphylococcal bacteria, because the polypeptides are capable of binding to antibody molecules produced in animals, including humans that are infected with staphylococcal bacteria such as *S. aureus*, and the antibodies are capable of binding to particular staphylococcal bacteria or antigens thereof.

Diagnostic agents may be included in a kit which can also include instructions for use and other appropriate reagents. The kit can also contain a means to evaluate the product of the assay, for example, a color chart, or numerical reference chart. The polypeptide or antibody may be labeled with a detection means that allows for the detection of the MSCRAMM polypeptide when it is bound to an antibody, or for the detection of the anti-MSCRAMM polypeptide antibody when it is bound to *Staphylococcus* bacteria.

The detection means may be a fluorescent labeling agent such as fluorescein isocyanate (FIC), fluorescein isothiocyanate (FITC), and the like, an enzyme, such as horseradish peroxidase (HRP), glucose oxidase or the like, a radioactive element such as ^{125}I or ^{51}Cr that produces gamma ray emissions, or a radioactive element that emits positrons which produce gamma rays upon encounters with electrons present in the test solution, such as ^{11}C , ^{15}O , or ^{13}N . The linking of the detection means is well known in the art. For instance, monoclonal anti-MSCRAMM polypeptide antibody molecules produced by a hybridoma can be metabolically labeled by incorporation of radioisotope-containing amino acids in the culture medium, or polypeptides may be conjugated or coupled to a detection means through activated functional groups.

The diagnostic kits of the present invention may be used to detect the presence of a quantity of *Staphylococcus* bacteria or anti-*Staphylococcus* antibodies in a body fluid sample such as serum, plasma or urine. Thus, in preferred embodiments, an MSCRAMM polypeptide or anti-MSCRAMM polypeptide antibody composition of the present invention is bound to a solid support typically by adsorption from an aqueous medium. Useful solid matrices are well known in the art, and include crosslinked dextran; agarose; polystyrene; polyvinylchloride; cross-linked polyacrylamide; nitrocellulose or nylon-based materials; tubes, plates or the wells of microtiter plates. The polypeptides or antibodies of the present invention may be used as diagnostic agents in solution form or as a substantially dry powder, e.g., in lyophilized form.

BRIEF DESCRIPTION OF THE DRAWING FIGURES

FIG. 1 is a schematic representation of the peptides used in illustrative vaccine, MSCRAMM IV. This drawing illustrates the essential features of the collagen binding MSCRAMM CNA, fibrinogen binding MSCRAMM ClfA, fibrinogen binding MSCRAMM ClfB and fibronectin binding MSCRAMM FnBPA proteins. The MSCRAMMs are shown with regions denoted that were expressed as recombinant proteins and used to generate antibodies in rabbits immunized with MSCRAMM IV. All proteins were designed with an amino terminal histidine tag to facilitate purification by metal chelating chromatography.

FIG. 2 is a time course graph of the immune response in MSCRAMM vaccinated Rhesus Monkeys as shown by changes in antibody titers against the MSCRAMMs CNA, ClfA, ClfB and FnBPA, respectively. The titers were analyzed by ELISA and measured as changes in absorbance (quantified at 405 nm) during each week over the course of a six-month period of treatment following the original immunization with the antigen.

FIG. 3 shows the nucleic acid sequence coding for the sdrF gene from *S. epidermidis* (SEQ. ID NO. 1) and the amino acid sequence coded thereby (SEQ. ID NOS. 2-6).

FIG. 4 shows the nucleic acid sequence coding for the sdrG gene from *S. epidermidis* (SEQ. ID NO. 7) and the amino acid sequence coded thereby (SEQ. ID NOS. 8-12).

FIG. 5 shows the nucleic acid sequence coding for the sdrH gene (SEQ. ID NO. 13) from *S. epidermidis* and the amino acid sequence coded thereby (SEQ. ID NO. 14).

DETAILED DESCRIPTION OF THE INVENTION

Compositions suitable for use as vaccines are provided that include at least:

(i) A collagen binding protein, peptide or domain (or an appropriate site directed mutated sequence thereof) such as CNA, or a protein, fragment or domain with sufficiently high homology thereto, in combination with a fibrinogen binding protein, preferably Clumping factor A ("ClfA") or Clumping factor B ("ClfB"), or a useful fragment thereof or a protein or fragment with sufficiently high homology thereto;

(ii) a fibronectin binding protein or peptide (or an appropriate site directed mutated sequence thereof), or a protein or fragment with sufficiently high homology thereto, in combination with the fibrinogen binding proteins A and B (ClfA and ClfB), or useful fragments thereof or proteins or fragments with sufficiently high homology thereto; or

(iii) the fibrinogen binding protein A (ClfA) and the fibrinogen binding protein B (ClfB), or useful fragments thereof or a protein or fragment with sufficiently high homology thereto; or

(iv) fibronectin binding protein or peptide (or an appropriate site directed mutated sequence thereof), or a protein or fragment with sufficiently high homology thereto, in combination with the fibrinogen binding protein A and B (ClfA and ClfB), or a useful fragment thereof or a protein or fragment with sufficiently high homology thereto; and a collagen binding protein or useful fragment thereof, or a protein or fragment with sufficiently high homology thereto;

(v) components of any of the above embodiments in combination with an elastin binding protein or peptide or a protein or fragment with sufficiently high homology thereto; or

(vi) components of any of the above embodiments in combination with a MHC II analogous type binding protein or peptide, protein or fragment with sufficiently high homology thereto; or

(vii) components of any of the above embodiments in combination with a bacterial component to increase the rate of phagocytosis of a staphylococcal bacteria such as *S. aureus*; or

(viii) components of any of the above embodiments in combination with the extracellular matrix-binding proteins SdrC, SdrD or SdrE, or useful fragments thereof, such as a consensus or variable sequence amino acid motif, or proteins or fragments with sufficiently high homology thereto; or

(ix) components of any of the above embodiments in combination with the extracellular matrix-binding proteins SdrF, SdrG or SdrH, or useful fragments thereof, such as a consensus or variable sequence amino acid motif, or proteins

or fragments with sufficiently high homology thereto, such that a vaccine created from said components will also be useful to immunize a patient against infection from coagulase-negative bacteria such as *S. epidermidis* as well as coagulase positive bacteria such as *S. aureus*; or

(ix) the extracellular matrix-binding proteins SdrC, SdrD and SdrE or useful fragments thereof, such as a consensus or variable sequence amino acid motif, or a protein or fragment with sufficiently high homology thereto.

Isolated protein fragments from wild-type or naturally occurring variants or synthetic or recombinant peptides corresponding to wild-type, naturally occurring variants or introduced mutations that do not correspond to a naturally occurring binding domain of a binding protein can be used in these embodiments.

The isolated peptides should be of a sufficient length to allow for the generation of an antibody that binds both to the isolated peptide and the binding domain, and blocks the binding of the binding protein to its ligand. In certain aspects, peptides comprising at least about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 22, about 24, about 25, about 30, about 35, about 40, about 45 or about 50 contiguous amino acids are preferred. In other preferred aspects of the invention, the isolated peptide comprises at least about 6 contiguous amino acids from the wild type sequence of the binding domain.

In one aspect of the invention, the isolated peptide or antibody compositions are used to generate an immunological response in an animal. In this aspect, the compositions preferably further comprise an adjuvant. Many adjuvants are known for use in vaccinations and are readily adapted to this composition. The isolated peptide or protein composition is preferably dispersed in a pharmaceutically acceptable excipient.

The isolated peptide can be linked to a selected amino acid sequence to make a fusion protein. As a nonlimiting example, a fusion protein can be made that comprises at least a first peptide of a binding domain of a binding protein operatively linked to a selected amino acid sequence. In one embodiment, if the peptide is a fibronectin binding domain, the first peptide does not specifically bind to fibronectin. In preferred aspects, the first peptide is linked to a selected carrier molecule or amino acid sequence, including, but not limited to, keyhole limpet hemocyanin (KLH) and bovine serum albumin (BSA).

Immunological compositions, including vaccine, and other pharmaceutical compositions containing the selected MSCRAMM proteins or the DNA encoding such MSCRAMM proteins are included within the scope of the present invention. The combination of binding proteins, or active or antigenic fragments thereof, or fusion proteins thereof can be formulated and packaged, alone or in combination with other antigens, using methods and materials known to those skilled in the art for vaccines. The immunological response may be used therapeutically or prophylactically and may provide antibody immunity or cellular immunity such as that produced by T lymphocytes such as cytotoxic T lymphocytes or CD4+ T lymphocytes.

Vaccines can be prepared for use in both active and passive immunizations. Preferably the antigenic material is extensively dialyzed to remove undesired small molecular weight molecules and/or lyophilized for more ready formulation into a desired vehicle.

I. Definitions

The terms FnBP-A protein, FnBP-B protein, ClfA protein, ClfB protein, SdrC protein, SdrD protein, SdrE protein, SdrF

protein, SdrG protein, SdrH protein, CNA protein, EbpS protein and MHCII protein are defined herein to include FnBP-A, FnBP-B, ClfA, ClfB, SdrC, SdrD, SdrE, SdrF, SdrG, SdrH, CNA, EbpS and MHCII subdomains, respectively, active or antigenic fragments of FnBP-A, FnBP-B, ClfA, ClfB, SdrC, SdrD, SdrE, SdrF, SdrG, SdrH, CNA, EbpS and MHCII proteins, and proteins or fragments that have sufficiently high homology therewith. Active fragments of FnBP-A, FnBP-B, ClfA, CHB, SdrC, SdrD, SdrE, SdrF, SdrG, SdrH, CNA, EbpS and MHCII proteins are defined herein as peptides or polypeptides capable of blocking the binding of *Staphylococcus* bacteria to host ECM. Antigenic fragments of FnBP-A, FnBP-B, ClfA, ClfB, SdrC, SdrD, SdrE, SdrF, SdrG, SdrH, CNA, EbpS and MHCII proteins are defined herein as peptides or polypeptides capable of producing an immunological response.

The term "adhesin" as used herein includes naturally occurring and synthetic or recombinant proteins and peptides which can bind to extracellular matrix proteins and/or mediate adherence to host cells.

The term "amino acid" as used herein includes naturally occurring and synthetic amino acids and includes, but is not limited to, alanine, valine, leucine, isoleucine, proline, phenylalanine, tryptophan, methionine, glycine, serine, threonine, cysteine, tyrosine, asparagine, glutamate, aspartic acid, glutamic acid, lysine, arginine, and histidine.

An "antibody" is any immunoglobulin, including antibodies and fragments thereof, that binds a specific epitope. The term as used herein includes monoclonal antibodies, polyclonal, chimeric, single chain, bispecific, simianized, and humanized-antibodies as well as Fab fragments, including the products of an Fab immunoglobulin expression library.

The phrase "antibody molecule" in its various grammatical forms as used herein contemplates both an intact immunoglobulin molecule and an immunologically active portion of an immunoglobulin molecule.

As used herein, an "antigenically functional equivalent" protein or peptide is one that incorporates an epitope that is immunologically cross-reactive with one or more epitopes either derived from any of the particular MSCRAMM proteins disclosed (e.g., FnB-B, FnB-A, FnBP-B and FnBP-A) or derived from any of the particular bacterial components disclosed (e.g., teichoic acids, alpha toxin and capsular polysaccharide type 5). Antigenically functional equivalents, or epitopic sequences, may be first designed or predicted and then tested, or may simply be directly tested for cross-reactivity.

As used herein, "pg" means picogram, "ng" means nanogram, "ug" or "µg" mean microgram, "mg" means milligram, "ul" or "µl" mean microliter, "ml" means milliliter, "l" means liter.

A "cell line" is a clone of a primary cell that is capable of stable growth in vitro for many generations.

A "clone" is a population of cells derived from a single cell or common ancestor by mitosis.

A DNA "coding sequence" is a double-stranded DNA sequence which is transcribed and translated into a polypeptide in vivo when placed under the control of appropriate regulatory sequences. The boundaries of the sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxyl) terminus. A coding sequence can include, but is not limited to, prokaryotic sequences, cDNA from eukaryotic MBNA, genetic DNA sequences from eukaryotic (e.g., mammalian) DNA, and even synthetic DNA sequences. A polyadenylation signal and transcription termination sequence will usually be located 3' to the coding sequence. "DNA molecule" refers to the poly-

meric form of deoxyribonucleotides (adenine, guanine, thymine, or cytosine) in its either single stranded form, or a double-stranded helix. This term refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this term includes double-stranded DNA found, inter alia, in linear DNA molecules (e.g. restriction fragments), viruses, plasmids, and chromosomes. In discussing the structure of particular double-stranded DNA molecules, sequences may be described herein according to the normal convention of giving only the sequence in the 5' to 3' direction along the nontranscribed strand of DNA (i.e., the strand having a sequence homologous to the mRNA. Transcriptional and translational control sequences are "DNA regulatory sequences", such as promoters, enhancers, polyadenylation signals, terminators, and the like, that provide for the expression of a coding sequence in a host cell.

An "expression control sequence" is a DNA sequence that controls and regulates the transcription and translation of another DNA sequence. A coding sequence is "under the control" of transcriptional and translational control sequences in a cell when RNA polymerase transcribes the coding sequence into mRNA, which is then translated into the protein encoded by the coding sequence.

As used herein, the term "extracellular matrix proteins," or ECM, refers to four general families of macromolecules, collagens, structural glycoproteins, proteoglycans and elastins, including fibronectin, and fibrinogen, that provide support and modulate cellular behavior.

"Immunologically effective amounts" are those amounts capable of stimulating a B cell and/or T cell response.

As used herein, the term "in vivo vaccine" refers to immunization of animals with proteins so as to elicit a humoral and cellular response that protects against later exposure to the pathogen.

The term "ligand" is used to include molecules, including those within host tissues, to which pathogenic bacteria attach.

The term "MHC II antigens" as used herein refers to cell-surface molecules that are responsible for rapid graft rejection and are required for antigen presentation to T-cells.

The phrase "monoclonal antibody" in its various grammatical forms refers to an antibody having only one species of antibody combining site capable of immunoreacting with a particular antigen.

The term "oligonucleotide," as used herein is defined as a molecule comprised of two or more nucleotides, preferably more than three. Its exact size will depend upon many factors which, in turn, depend upon the ultimate function and use of the oligonucleotide.

As used herein, the phrase "pharmaceutically acceptable" refers to molecular entities and compositions that are physiologically tolerable and do not typically produce an unacceptable allergic or similar untoward reaction when administered to a human.

The term "primer" as used herein refers to an oligonucleotide, whether occurring naturally as in a purified restriction digest or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product, which is complementary to a nucleic acid strand, is induced, i.e., in the presence of nucleotides and an inducing agent such as a DNA polymerase and at a suitable temperature and pH. The primer may be either single-stranded or double-stranded and must be sufficiently long to prime the synthesis of the desired extension product in the presence of the inducing agent. The exact length of the primer will depend upon many factors, including temperature, source of primer and use of the

method. For example, for diagnostic applications, depending on the complexity of the target sequence, the oligonucleotide primer typically contains 15-25 or more nucleotides, although it may contain fewer nucleotides.

The primers herein are selected to be substantially complementary to different strands of a particular target DNA sequence. This means that the primers must be sufficiently complementary to hybridize with their respective strands. Therefore, the primer sequence need not reflect the exact sequence of the template. For example, a noncomplementary nucleotide fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being complementary to the strand. Alternatively, noncomplementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence of the strand to hybridize therewith and thereby form the template for the synthesis of the extension product.

A "promoter sequence" is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bounded at its 3' terminus by the transcription initiation site and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence will be found a transcription initiation site (conveniently defined by mapping with nuclease Si), as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase. Eukaryotic promoters will often, but not always, contain "TATA" boxes and "CAT" boxes. Prokaryotic promoters contain Shine-Dalgarno sequences in addition to the -10 and -35 consensus sequences.

A "replicon" is a genetic element (e.g., plasmid, chromosome, virus) that functions as an autonomous unit of DNA replication in vivo; i.e., capable of replication under its own control.

As used herein, the terms "restriction endonucleases" and "restriction enzymes" refer to bacterial enzymes, each of which cut double-stranded DNA at or near a specific palindromic nucleotide sequence.

A "signal sequence" can be included before the coding sequence. This sequence encodes a signal peptide, N-terminal to the polypeptide, that communicates to the host cell to direct the polypeptide to the cell surface or secrete the polypeptide into the media, and this signal peptide is clipped off by the host cell before the protein leaves the cell. Signal sequences can be found associated with a variety of proteins native to prokaryotes and eukaryotes.

As used herein, the term "site directed mutagen" refers to a compound that can increase the rate at which mutations occur at a certain site within the DNA molecule.

A cell has been "transformed" by exogenous or heterologous DNA when such DNA has been introduced inside the cell. The transforming DNA may or may not be integrated (covalently linked) into chromosomal DNA making up the genome of the cell. In prokaryotes, yeast, and mammalian cells for example, the transforming DNA may be maintained on an episomal element such as a plasmid. With respect to eukaryotic cells, a stably transformed cell is one in which the transforming DNA has become integrated into a chromosome so that it is inherited by daughter cells through chromosome replication. This stability is demonstrated by the ability of the eukaryotic cell to establish cell lines or clones comprised of a population of daughter cells containing the transforming DNA.

A "vector" is a replicon, such as plasmid, phage or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment.

The term "wound" is used herein to mean the epithelial cellular layer, and other surface structures over tissue, damaged by mechanical, chemical or other influence.

By "immunologically effective amount" is meant an amount of a peptide composition that is capable of generating an immune response in the recipient animal. This includes both the generation of an antibody response (B cell response), and/or the stimulation of a cytotoxic immune response (T cell response). The generation of such an immune response will have utility in both the production of useful bioreagents, e.g., CTLs and, more particularly, reactive antibodies, for use in diagnostic embodiments, and will also have utility in various prophylactic or therapeutic embodiments.

The selected combinations of bacterial binding proteins or fragments thereof in the composition used include those binding to fibronectin, fibrinogen, collagen, and elastin. Any such protein, peptide, fragment thereof, or sequence substantially homologous thereto can be used in this invention. Illustrative examples are provided below. In addition, bacterial binding proteins or fragments to MHC II analogous

II. Fibronectin-Binding Mscramms

Fibronectin (Fn) is a 440-kDa glycoprotein found in the ECM and body fluids of animals. The primary biological function of fibronectin appears to be related to its ability to serve as a substrate for the adhesion of cells expressing the appropriate integrins. Several bacterial species have been shown to bind fibronectin specifically and to adhere to a fibronectin-containing substratum. Most *S. aureus* isolates bind Fn, but do so in varying extents, which reflects variations in the number of MSCRAMM molecules expressed on the bacterial cell surface. The interaction between Fn and *S. aureus* is highly specific (Kuusela, P., *Nature*, 276:718-20, 1978). Fn binding is mediated by two surface exposed proteins with molecular weights of 110 kDa, named FnBP-A and FnBP-B. The primary Fn binding site consists of a motif of 35-40 amino acids, repeated three to five times. The genes for these have been cloned and sequenced (Jonsson, K., et al., *Eur. J. Biochem.*, 202:1041-1048, 1991).

WO-A-85/05553 discloses bacterial cell surface proteins having fibronectin, fibrinogen, collagen, and or laminin binding ability.

U.S. Pat. Nos. 5,320,951 and 5,571,514 to Hook, et al., discloses the fibronectin binding protein A (fnbA) gene sequence, and products and methods based on this sequence.

U.S. Pat. No. 5,175,096 to Hook et al., discloses the gene sequence of fnbB, a hybrid DNA molecule (fnbB) and biological products and methods based on this sequence.

U.S. Pat. No. 5,652,217 discloses an isolated and purified protein having binding activity that is encoded by a hybrid DNA molecule from *S. aureus* of defined sequence.

U.S. Pat. No. 5,440,014 discloses a fibronectin binding peptide within the D3 homology unit of a fibronectin binding protein of *S. aureus* which can be used for vaccination of ruminants against mastitis caused by staphylococcal infections, for treatment of wounds, for blocking protein receptors, for immunization of other animals, or for use in a diagnostic assay.

U.S. Pat. No. 5,189,015 discloses a method for the prophylactic treatment of the colonization of a *S. aureus* bacterial strain having the ability to bind to fibronectin in a mammal that includes administering to the mammal in need of treatment a prophylactically therapeutically active amount of a

protein having fibronectin binding properties, to prevent the generation of infections caused by a *S. aureus* bacterial strain having the ability to bind fibronectin, wherein the protein has a molecular weight of 87 kDa to 165 kDa.

U.S. Pat. No. 5,416,021 discloses a fibronectin binding protein encoding DNA from *Streptococcus dysgalactiae*, along with a plasmid that includes DNA encoding for fibronectin binding protein from *S. dysgalactiae* contained in *E. coli*, DNA encoding a fibronectin binding protein from *S. dysgalactiae* and an *E. coli* microorganism transformed by DNA encoding a fibronectin binding protein from *S. dysgalactiae*.

It has been observed that antibodies to wild type fibronectin binding protein do not substantially inhibit the ability of *S. aureus* to bind to fibronectin, and thus do not exhibit a significant therapeutic effect, in vivo. PCT/US98/01222 discloses antibodies that block the binding of fibronectin to fibronectin binding proteins. The antibodies were raised against a site-directed mutated sequence of fibronectin binding protein that does not bind to fibronectin. It was identified that there is a rapid complexation of fibronectin with fibronectin binding proteins and fragments in vivo. Peptide epitopes that do not bind to fibronectin, even though based on a fibronectin binding domain of a fibronectin binding protein, do not form a complex with fibronectin in vivo. This allows antibodies to be made against the uncomplexed peptide epitope, which inhibit or block the binding of fibronectin to fibronectin binding proteins.

III. Collagen-Binding Mscramms

Collagen is the major constituent of cartilage. Collagen (Cn) binding proteins are commonly expressed by staphylococcal strains. The Cn binding MSCRAMM of *S. aureus* adheres to cartilage in a process that constitutes an important part of the pathogenic mechanism in staphylococcal infections. (Switalski, et al. *Mol. Micro.* 7(1), 99-107, 1993) Cn binding by *S. aureus* is found to play a role in at least, but not only, arthritis and septicemia. CNAs with molecular weights of 133, 110 and 87 kDa (Patti, J., et al., *J. Biol. Chem.*, 267:4766-4772, 1992) have been identified. Strains expressing CNAs with different molecular weights do not differ in their Cn binding ability (Switalski, L. M., et al., *Mol. Microbiol.*, 7:99-107, 1993).

Staphylococcal strains recovered from the joints of patients diagnosed with septic arthritis or osteomyelitis almost invariably express a CBP, whereas significantly fewer isolates obtained from wound infections express this adhesin (Switalski et al., *Mol. Microbiol.*, 7:99-107, 1993). Similarly, *S. aureus* strains isolated from the bones of patients with osteomyelitis often have an MSCRAMM recognizing the bone-specific protein, bone sialoprotein (BSP) (Ryden et al., *Lancet*, 11:515-518, 1987). *S. aureus* colonization of the articular cartilage within the joint space appears to be an important factor contributing to the development of septic arthritis.

PCT WO 92/07002 discloses a hybrid DNA molecule which includes a nucleotide sequence from *S. aureus* coding for a protein or polypeptide having collagen binding activity and a plasmid or phage comprising the nucleotide sequence. Also disclosed are an *E. coli* strain expressing the collagen binding protein, a microorganism transformed by the recombinant DNA, the method for producing a collagen binding protein or polypeptide, and the protein sequence of the collagen binding protein or polypeptide.

The cloning, sequencing, and expression of a gene *cna*, encoding a *S. aureus* CBP has been reported (Patti, J., et al., *J.*

Biol. Chem., 267:4766-4772, 1992). The *cna* gene encodes an 133-kDa adhesin that contains structural features characteristic of surface proteins isolated from Gram-positive bacteria.

Recently, the ligand-binding site has been localized within the N-terminal half of the CBP (Patti, J. et al., *Biochemistry*, 32:11428-11435, 1993). By analyzing the Col binding activity of recombinant proteins corresponding to different segments of the MSCRAMM, a 168-amino-acid long protein fragment (corresponding to amino acid residues 151-318) that had appreciable Col binding activity was identified. Short truncations of this protein in the N or C terminus resulted in a loss of ligand binding activity but also resulted in conformational changes in the protein as indicated by circular dichroism spectroscopy.

Patti et al. (*J of Biol Chem.*, 270, 12005-12011, 1995) disclose a collagen binding epitope in the *S. aureus* adhesin encoded by the *cna* gene. In their study, the authors synthesized peptides derived from the sequence of the said protein and used them to produce antibodies. Some of these antibodies inhibit the binding of the protein to collagen.

PCT/US97/08210 discloses that certain identified epitopes of the collagen binding protein (M55, M33, and M17) can be used to generate protective antibodies. The application also discloses the crystal structure of the CBP which provides critical information necessary for identifying compositions which interfere with, or block completely, the binding of Col to CBPS. The ligand-binding site in the *S. aureus* CBP and a 25-amino-acid peptide was characterized that directly inhibits the binding of *S. aureus* to 125 I-labeled type II Col.

IV. Fibrinogen-Binding Mscramms

Fibrin is the major component of blood clots, and fibrinogen/fibrin is one of the major plasma proteins deposited on implanted biomaterials. Considerable evidence exists to suggest that bacterial adherence to fibrinogen/fibrin is important in the initiation of device-related infection. For example, as shown by Vaudaux et al., *S. aureus* adheres to in vitro plastic that has been coated with fibrinogen in a dose-dependent manner (*J. Infect. Dis.* 160:865-875 (1989)). In addition, in a model that mimics a blood clot or damage to a heart valve, Herrmann et al. demonstrated that *S. aureus* binds avidly via a fibrinogen bridge to platelets adhering to surfaces (*J. Infect. Dis.* 167: 312-322 (1993)). *S. aureus* can adhere directly to fibrinogen in blood clots formed in vitro, and can adhere to cultured endothelial cells via fibrinogen deposited from plasma acting as a bridge (Moreillon et al., *Infect. Immun.* 63:4738-4743 (1995); Cheung et al., *J. Clin. Invest.* 87:2236-2245 (1991)). As shown by Vaudaux et al. and Moreillon et al., mutants defective in the fibrinogen-binding protein clumping factor (ClfA) exhibit reduced adherence to fibrinogen in vitro, to explanted catheters, to blood clots, and to damaged heart valves in the rat model for endocarditis (Vaudaux et al., *Infect. Immun.* 63:585-590 (1995); Moreillon et al., *Infect. Immun.* 63: 4738-4743 (1995)).

An adhesin for fibrinogen, often referred to as "clumping factor," is located on the surface of *S. aureus* cells. The interaction between bacteria and fibrinogen in solution results in the instantaneous clumping of bacterial cells. The binding site on fibrinogen is located in the C-terminus of the gamma chain of the dimeric fibrinogen glycoprotein. The affinity is very high and clumping occurs in low concentrations of fibrinogen. Scientists have recently shown that clumping factor also promotes adherence to solid phase fibrinogen, to blood clots, and to damaged heart valves (McDevitt et al., *Mol. Microbiol.*

11: 237-248 (1994); Vaudaux et al., *Infect. Immun.* 63:585-590 (1995); Moreillon et al., *Wect. Immun.* 63: 4738-4743 (1995)).

Two genes in *S. aureus* have been found that code for two Fg binding proteins, ClfA and ClfB. The gene, *clfA*, was cloned and sequenced and found to code for a polypeptide of 92 kDa. ClfA binds the gamma chain of fibrinogen, and ClfB binds the alpha and beta chains (Eidhin, et al., *Mol Micro*, awaiting publication, 1998). ClfB is a cell wall associated protein with a predicted molecular weight of 88 kDa and an apparent molecular weight of 124 kDa that binds both soluble and immobilized fibrinogen and acts as a clumping factor.

The gene for a clumping factor protein, designated ClfA, was cloned, sequenced and analyzed in detail at the molecular level (McDevitt et al., *Mol. Microbiol.* 11: 237-248 (1994); McDevitt et al., *Mol. Microbiol.* 16:895-907 (1995)). The predicted protein is composed of 933 amino acids. A signal sequence of 39 residues occurs at the N-terminus followed by a 520 residue region (region A), which contains the fibrinogen binding domain. A 308 residue region (region R), composed of 154 repeats of the dipeptide serine-aspartate, follows. The R region sequence is encoded by the 18 basepair repeat GAY TCN GAY TCN GAY AGY in which Y equals pyrimidines and N equals any base. The C-terminus of ClfA has features present in many surface proteins of gram-positive bacteria such as an LPDTG motif, which is responsible for anchoring the protein to the cell wall, a membrane anchor, and positive charged residues at the extreme C-terminus.

The platelet integrin alpha IIbβ3 recognizes the C-terminus of the gamma chain of fibrinogen. This is a crucial event in the initiation of blood clotting during coagulation. ClfA and alpha IIbβ3 appear to recognize precisely the same sites on fibrinogen gamma chain because ClfA can block platelet aggregation, and a peptide corresponding to the C-terminus of the gamma chain (198-411) can block both the integrin and ClfA interacting with fibrinogen (McDevitt et al., *Eur. Biochem.* 247:416-424 (1997)). The fibrinogen binding site of alpha IIbβ3 is close to, or overlaps, a Ca²⁺ binding determinant referred to as an "EF hand". ClfA region A carries several EF hand-like motifs. A concentration of Ca²⁺ in the range of 3-5 mM blocks these ClfA-fibrinogen interactions and changes the secondary structure of the ClfA protein. Mutations affecting the ClfA EF hand reduce or prevent interactions with fibrinogen. Ca²⁺ and the fibrinogen gamma chain seem to bind to the same, or to overlapping, sites in ClfA region A.

The alpha chain of the leukocyte integrin, alpha MB2, has an insertion of 200 amino acids (A or I domain) which is responsible for ligand binding activities. A novel metal ion-dependent adhesion site (MIDAS) motif in the I domain is required for ligand binding. Among the ligands recognized is fibrinogen. The binding site on fibrinogen is in the gamma chain (residues 190-202). It was recently reported that *Candida albicans* has a surface protein, alpha Intlp, having properties reminiscent of eukaryotic integrins. The surface protein has amino acid sequence homology with the I domain of MB2, including the MIDAS motif. Furthermore, Intlp binds to fibrinogen.

ClfA region A also exhibits some degree of sequence homology with alpha Intlp. Examination of the ClfA region A sequence has revealed a potential MIDAS motif. Mutations in putative cation coordinating residues in the DxSxS portion of the MIDAS motif in ClfA results in a significant reduction in fibrinogen binding. A peptide corresponding to the gamma-chain binding site for alpha Mβ2 (190-202) has been shown by O'Connell et al. to inhibit ClfA-fibrinogen interactions (O'Connell, *J. Biol. Chem.*, in press, 1998). Thus it appears

that ClfA can bind to the gamma-chain of fibrinogen at two separate sites. The ligand binding sites on ClfA are similar to those employed by eukaryotic integrins and involve divalent cation binding EF-hand and MIDAS motifs.

Also known is the fibrinogen binding protein, ClfB. Used herein are the protein as well as antibodies to the protein and diagnostic kits that include the protein or its antibodies. ClfB has a predicted molecular weight of approximately 88 kDa and an apparent molecular weight of approximately 124 kDa. ClfB is a cell-wall associated protein and binds both soluble and immobilized fibrinogen. In addition, ClfB binds both the alpha and beta chains of fibrinogen and acts as a clumping factor.

Proteins related to the fibrinogen-binding ClfA and ClfB have been found, which bind to the extracellular matrix. The SdrC, SdrD and SdrE proteins are related in primary sequence and structural organization to the ClfA and ClfB proteins, and are also localized on the cell surface. With the A region of these proteins localized on the cell surface, the proteins can interact with the proteins in plasma, the extracellular matrix or with molecules on the surface of host cells. SdrC can bind to the extracellular matrix proteins, for example, vitronectin. SdrE also binds to the extracellular matrix, for example, SdrE binds bone sialoprotein (BSP).

It has been discovered that in the A region of SdrC, SdrD, SdrE, ClfA, and ClfB, there is highly conserved amino acid sequence that can be used to derive a consensus TYTFT-DYVD motif. The motif can be used in multicomponent vaccines to impart broad spectrum immunity to bacterial infections, and also can be used to produce monoclonal or polyclonal antibodies that impart broad spectrum passive immunity. In an alternative embodiment, any combination of the variable sequence motif derived from the Sdr and Clf protein families, (T/I) (Y/F) (T/V) (F) (T) (D/N) (Y) (V) (D/N), can be used to impart immunity or to induce protective antibodies.

V. Elastin-Binding Mscramms

The primary role of elastin is to confer the property of reversible elasticity to tissues and organs (Rosenbloom, J., et al., *FASEB J.*, 7:1208-1218, 1993). Elastin expression is highest in the lung, skin and blood vessels, but the protein is widely expressed in mammalian hosts for *S. aureus*. *S. aureus* binding to elastin was found to be rapid, reversible, of high affinity and ligand specific. Furthermore, a 25 kDa cell surface elastin binding protein (EbpS) was isolated and proposed to mediate *S. aureus* binding to elastin-rich host ECM. EbpS binds to a region in the N-terminal 30 kDa fragment of elastin.

PCT/US97/03106 discloses the gene sequences for an elastin binding protein. DNA sequence data disclosed indicates that the ebps open reading frame consists of 606 bp, and encodes a novel polypeptide of 202 amino acids. EbpS protein has a predicted molecular mass of 23,345 daltons and pI of 4.9. EbpS was expressed in *E. coli* as a fusion protein with polyhistidine residues attached to the N-terminus. A polyclonal antibody raised against recombinant EbpS interacted specifically with the 25 kDa cell surface EbpS and inhibited staphylococcal elastin binding. Furthermore, recombinant EbpS bound specifically to immobilized elastin and inhibited binding of *Staphylococcus aureus* to elastin. A degradation product of recombinant EbpS lacking the first 59 amino acids of the molecule and a C-terminal fragment of CNBr-cleaved recombinant EbpS, however, did not interact with elastin. These results strongly suggest that EbpS is the cell surface molecule mediating binding of *Staphylococcus aureus* to elastin. The finding that some constructs of recombinant

EbpS do not interact with elastin suggests that the elastin binding site in EbpS is contained in the first 59 amino acids of the molecule.

Several independent criteria indicate that EbpS is the surface protein mediating cellular elastin binding. First, rEbpS binds specifically to immobilized elastin and inhibits binding of *S. aureus* cells to elastin in a dose dependent manner. These results establish that EbpS is an elastin binding protein that is functionally active in a soluble form. Second, an antibody raised against rEbpS recognizes a 25 kDa protein expressed on the cell surface of *S. aureus* cells. In addition to the size similarity and antibody reactivity, further evidence that this 25 kDa protein is cell surface EbpS is provided by the experiment showing that binding of the 25 kDa protein to immobilized anti-rEbpS IgG is inhibited in the presence of excess unlabeled rEbpS. Finally, Fab fragments prepared from the anti-rEbpS antibody, but not from its pre-immune control, inhibit binding of *S. aureus* to elastin. This result suggests that the topology of surface EbpS is such that the elastin binding site is accessible to interact with ligands (i.e. elastin and the anti-rEbpS Fab fragment) and not embedded in the cell wall or membrane domains. The composite data demonstrate that EbpS is the cell surface protein responsible for binding *S. aureus* to elastin.

The present and previous findings suggest the existence of a functionally active 40 kDa intracellular precursor form of EbpS that requires processing at the C terminus prior to surface expression. This notion is based on the following observations: i) there exists an intracellular 40 kDa elastin binding protein that is never detected during cell surface labeling experiments, ii) the 25 kDa EbpS and the 40 kDa elastin binding protein have an identical N-terminal sequence, and iii) a single gene exists for EbpS. Because the size of the ebps open reading frame is not sufficient to encode a 40 kDa protein, at first the inventors disregarded this hypothesis. However, their studies with rEbpS demonstrated that although the actual size of the recombinant protein is 26 kDa, it migrates aberrantly as a 45 kDa protein in SDS-30 PAGE. This finding suggests that full length native EbpS, with a predicted size of 23 kDa, may be migrating in SDS-PAGE as the 40 kDa intracellular precursor, and that the 25 kDa surface form of EbpS is actually a smaller form of the molecule processed at the C-terminus. Although EbpS lacks an N-terminal signal peptide and other known sorting and anchoring signals, this proposed intracellular processing event may explain some questions regarding how EbpS is targeted to the cell surface. In fact, C-terminal signal peptides have been identified in several bacterial proteins (Fath, M. J. and Kolter, R., *Microbiol. Rev.*, 57:995-1017, 1993) and alternative means of anchoring proteins to the cells surface have been reported in gram positive bacteria (Yother, J. and White, J. M., *J. Bacteriol.*, 176:2976-2985, 1994).

Using overlapping EbpS fragments and recombinant constructs, the elastin binding site in EbpS was mapped to the amino terminal domain of the molecule (PCT/US97/03106). Overlapping synthetic peptides spanning amino acids 14-34 were then used to better define the binding domain. Among these, peptides corresponding to residues 14-23 and 18-34 specifically inhibited elastin binding by more than 95%. Common to all active synthetic peptides and proteolytic and recombinant fragments of EbpS is the hexameric sequence ¹⁸Thr-Asn-Ser-His-Gln-Asp²³. Further evidence that this sequence is important for elastin binding was the loss of activity when Asp²³ was substituted with Asn in the synthetic peptide corresponding to residues 18-34. However, the synthetic hexamer TNSHQD by itself did not inhibit staphylococcal binding to elastin. These findings indicate that

although the presence of the TNSHQD sequence is essential for EbpS activity, flanking amino acids in the N- or C-terminal direction and the carboxyl side chain of Asp²³ are required for elastin recognition.

VI. MHC II-ANALOGOUS PROTEINS, (MAP)

In addition to fibrinogen, fibronectin, collagen and elastin, *S. aureus* strains associate with other adhesive eukaryotic proteins, many of which belong to the family of adhesive matrix proteins, such as vitronectin. (Chatwal et al., *Infect. Immun.*, 55:1878-1883, 1987). U.S. Pat. No. 5,648,240 discloses a DNA segment comprising a gene encoding a *S. aureus* broad spectrum adhesin that has a molecular weight of about 70 kDa. The adhesin is capable of binding fibronectin or vitronectin and includes a MHC II mimicking unit of about 30 amino acids. Further analyses of the binding specificities of this protein reveal that it functionally resembles an MHC II antigen in that it binds synthetic peptides. Thus, in addition to mediating bacterial adhesion to ECM proteins, it may play a role in staphylococcal infections by suppressing the immune system of the host. The patent further claims a recombinant vector that includes the specified DNA sequence, a recombinant host cell transformed with the vector, and DNA which hybridizes with the DNA of specified sequence. Also disclosed is a composition that includes a protein or polypeptide encoded by the specified DNA sequence and a method of inducing an immune response in an animal that includes administering an immunogenic composition that includes the encoded protein or polypeptide. A method of making a MHC II antigen protein analog comprising the steps of inserting the specified DNA sequence in a suitable expression vector and culturing a host cell transformed with the vector under conditions to produce the MHC II antigen protein analog is additionally claimed in the patent.

VII. Sdr Proteins From Staphylococcus Epidermidis

Staphylococcus epidermidis, a coagulase-negative bacterium, is a common inhabitant of human skin and a frequent cause of foreign-body infections. Pathogenesis is facilitated by the ability of the organism to first adhere to, and subsequently to form biofilms on, indwelling medical devices such as artificial valves, orthopedic devices, and intravenous and peritoneal dialysis catheters. Device-related infections may jeopardize the success of medical treatment and significantly increase patient mortality. Accordingly, the ability to develop vaccines that can control or prevent outbreaks of *S. epidermidis* infection is of great importance, as is the development of multicomponent vaccines that can prevent or treat infection from a broad spectrum of bacteria, including both coagulase-positive and coagulase negative bacteria at the same time.

Three Sdr (serine-aspartate (SD) repeat region) proteins that are expressed by *S. epidermidis* have been designated as SdrF, SdrG and SdrH, and the amino acid sequences of these proteins and their nucleic acid sequences are shown in FIGS. 3-5, respectively. In addition, a more complete description of these proteins is provided in a co-pending U.S. patent application of Foster et al. which is based on U.S. provisional application Ser. Nos. 60/098,443 and 60/117,119. These applications are incorporated herein by reference.

In accordance with the present invention, a composition useful as a vaccine is provided that includes the components of any of the above embodiments in combination with an SdrF, SdrG or an SdrH protein. In addition, antibodies to these proteins can be raised using conventional means, and anti-

bodies to the SdrF, SdrG or an SdrH proteins can be employed in any of the above combinations which employ antibodies to the other adhesins discussed herein. The compositions and vaccines which include an SDR protein such as SdrF, SdrG or SdrH can thus be used to treat a broad spectrum of bacterial infections, including those arising both from coagulase-positive and coagulase-negative bacteria.

VIII. Bacterial Components

In an embodiment of the invention, a composition is provided that includes the components of any of the above embodiments in combination with a bacterial component, preferably capsular polysaccharides type 5 or type 8, to increase the rate of opsonization and phagocytosis of *S. aureus*.

Staphylococci contain antigenic polysaccharides, such as capsular polysaccharide types 5 and 8, and proteins as well as other substances important in cell wall structure. Peptidoglycan, a polysaccharide polymer containing linked subunits, provides the rigid exoskeleton of the cell wall. Peptidoglycan is destroyed by strong acids or exposure to lysozyme. It is important in the pathogenesis of infection. It elicits production of interleukin-1 (endogenous pyrogen) and opsonic antibodies by monocytes. It can be a chemoattractant for polymorphonuclear leukocytes, have endotoxin-like activity, produce a localized Shwartzman phenomenon, and activate complement.

Teichoic acids, lipoteichoic acid for example, which are polymers of glycerol or ribitol phosphate, are linked to the peptidoglycan and can be antigenic. Antiteichoic antibodies detectable by gel diffusion may be found in patients with active endocarditis due to *S. aureus*.

Protein A is a cell wall component of many *S. aureus* strains that binds to the Fc portion of IgG molecules except IgG3. The Fab portion of IgG bound to protein A is free to combine with a specific antigen. Protein A has become an important reagent in immunology and diagnostic laboratory technology; for example, protein A with attached IgG molecules directed against a specific bacterial antigen will agglutinate bacteria that have that antigen ("coagglutination").

Some *S. aureus* strains have capsules, which inhibit phagocytosis by polymorphonuclear leukocytes unless specific antibodies are present. Most strains of *S. aureus* have coagulase, or clumping factor, on the cell wall surface; coagulase binds nonenzymatically to fibrinogen, yielding aggregation of the bacteria.

Staphylococci can produce disease both through their ability to multiply and spread widely in tissues and through their production of many extracellular substances. Some of these substances are enzymes; others are considered to be toxins, though they may function as enzymes. Many of the toxins are under the genetic control of plasmids; some may be under both chromosomal and extrachromosomal control; and for others the mechanism of genetic control is not well defined.

A. Catalase: Staphylococci produce catalase, which converts hydrogen peroxide into water and oxygen. The catalase test differentiates the staphylococci, which are positive, from the streptococci, which are negative.

B. Coagulase: *S. aureus* produces coagulase, an enzyme-like protein that clots oxalated or citrated plasma in the presence of a factor contained in many sera. The serum factor reacts with coagulase to generate both esterase and clotting activities, in a manner similar to the activation of prothrombin to thrombin. The action of coagulase circumvents the normal plasma clotting cascade. Coagulase may deposit fibrin on the surface of staphylococci, perhaps altering

their ingestion by phagocytic cells or their destruction within such cells. Coagulase production is considered synonymous with invasive pathogenic potential. However, coagulase-negative bacteria such as *S. epidermidis* also pose a threat for serious infection as well.

- C. Other Enzymes: Other enzymes produced by staphylococci include a hyaluronidase, or spreading factor; a staphylokinase resulting in fibrinolysis but acting much more slowly than streptokinase; proteinases; lipases; and β -lactamase.
- D. Exotoxins: These include several toxins that are lethal for animals on injection, cause necrosis in skin, and contain soluble hemolysins which can be separated by electrophoresis. The alpha toxin (hemolysin) is a heterogeneous protein that can lyse erythrocytes and damage platelets and is probably identical with the lethal and dermonecrotic factors of exotoxin. Alpha toxin also has a powerful action on vascular smooth muscle. Beta toxin degrades sphingomyelin and is toxic for many kinds of cells, including human red blood cells. These toxins and two others, the gamma and delta toxins; are antigenically distinct and bear no relationship to streptococcal lysins. Exotoxin treated with formalin gives a non-poisonous but antigenic toxoid, but this is not clinically useful.
- E. Leukocidin: This toxin of *S. aureus* can kill exposed white blood cells of many animals. Its role in pathogenic staphylococci may not kill white blood cells and may be phagocytosed as effectively as nonpathogenic varieties. However, they are capable of very active intra-cellular multiplication, whereas the nonpathogenic organisms tend to die inside the cell. Antibodies to leukocidin may play a role in resistance to recurrent staphylococcal infections.
- F. Exfoliative Toxin: This toxin of *S. aureus* includes at least two proteins that yield the generalized desquamation of the staphylococcal scaled skin syndrome. Specific antibodies protect against the exfoliative action of the toxin.
- G. Toxic Shock Syndrome Toxin. Most *S. aureus* strains isolated from patients with toxic shock syndrome produce a toxin called toxic shock syndrome toxin-1 (TSST-1), which is the same as enterotoxin F and pyrogenic exotoxin C. TSST-1 is the prototypical superantigen which promotes the protean manifestations of the toxic shock syndrome. In humans, the toxin is associated with fever, shock, and multisystem involvement, including a desquamative skin rash. In rabbits, TSST-1 produces fever, enhanced susceptibility to the effects of bacterial lipopolysaccharides, and other biologic effects similar to toxic shock syndrome, but the skin rash and desquamation do not occur.
- H. Enterotoxins: There are at least six (A-F) soluble toxins produced by nearly 50% of *S. aureus* strains. Like TSST-1, the enterotoxins are superantigens that bind to MHC class II molecules, yielding T cell stimulation. The enterotoxins are heat-stable (they resist boiling for 30 minutes) and are resistant to the action of gut enzymes. An important cause of food poisoning, enterotoxins are produced when *S. aureus* grows in carbohydrate and protein foods. The gene for enterotoxin production may be on the chromosome, but a plasmid may carry a protein that regulates active toxin production. Ingestion of 25 μ g of enterotoxin B by humans or monkeys results in vomiting and diarrhea. The emetic effect of enterotoxin is probably the result of central nervous system stimulation (vomiting center) after the toxin acts on neural receptors in the gut. Enterotoxins can be assayed by precipitin tests (gel diffusion).

There are also many other antigenic proteins produced by Staphylococcal organisms. These include the MSCRAMMs

mentioned above, as well as: bone sialoprotein binding protein, clusterin binding protein, heparin sulfate binding protein, thrombospondin binding protein, transferrin binding protein and vitronectin binding protein. *S. aureus* further expresses virulence factors such as phosphatidyl phospholipase, and toxin expression regulators such as Rap protein.

IX. Proteins and peptides with substantial homology or Equivalent function to those described herein

The disclosed compositions can include, as desired, full sequence proteins, peptides, protein or peptide fragments, isolated epitopes, fusion proteins, or any alternative which binds to the target ECM, whether in the form of a wild type, a site-directed mutant, or a sequence which is substantially homologous thereto.

Two DNA sequences are "substantially homologous" when at least about 70%, (preferably at least about 80%, and most preferably at least about 90 or 95%) of the nucleotides match over the defined length of the DNA sequences. Sequences that are substantially homologous can be identified by comparing the sequences using standard software available in sequence data banks, or in a Southern hybridization experiment under, for example, stringent conditions as defined for that particular system. Defining appropriate hybridization conditions is within the skill of the art. See, e.g., Maniatis et al., *Molecular Cloning: A Laboratory Manual*, 1982; *DNA Cloning*, Vols. I & II, supra; *Nucleic Acid Hybridization*, [R. D. Hames & S. J. Higgins eds. (1985)].

When used in conjunction with amino acid sequences, the term "substantially similar" means an amino acid sequence which is not identical to published sequences, but which produces a protein having the same functionality and activities, either because one amino acid is replaced with another similar amino acid, or because the change (whether it be substitution, deletion or insertion) does not substantially effect the active site of the protein. Two amino acid sequences are "substantially homologous" when at least about 70%, (preferably at least about 80%, and most preferably at least about 90% or 95%) of the amino acids match over the defined length of the sequences.

It should also be understood that each of the MSCRAMM polypeptides of this invention may be part of a larger protein. For example, a ClfA polypeptide of this invention may be fused at its N-terminus or C-terminus to a CHB polypeptide, or to a non-fibrinogen binding polypeptide or combinations thereof. Polypeptides which may be useful for this purpose include polypeptides derived any of the MSCRAMM proteins, and serotypic variants of any of the above. Non-MSCRAMM polypeptides which may be useful for this purpose include any of the bacterial components described above.

Modification and changes may be made in the structure of the peptides of the present invention and DNA segments which encode them and still obtain a functional molecule that encodes a protein or peptide with desirable characteristics. The following is a discussion based upon changing the amino acids of a protein to create an equivalent, or even an improved, second generation molecule. The amino acid changes may be achieved by changing the codons of the DNA sequence, according to Table 1. It should be understood by one skilled in the art that the codons specified in Table 1 are for RNA sequences. The corresponding codons for DNA have a T substituted for U. In keeping with standard nomenclature (*J. Biol. Chem.*, 243:3552-3559, 1969), abbreviations for amino acid residues are further shown in Table I.

For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence, and, of course, its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus contemplated by the inventors that various changes may be made in the peptide sequences of the disclosed compositions, or corresponding DNA sequences which encode said peptides without appreciable loss of their biological utility or activity.

TABLE I

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

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, *J Mol Biol*, 157(1):105-132, 1982, incorporate herein by reference). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like. Each amino acid has been assigned a hydropathic index on the basis of their hydrophobicity and charge characteristics (Kyte and Doolittle, supra 1982), these are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, i.e., still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are within ± 2 is preferred, those which are within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U.S. Pat. No. 4,554,101, incorporated herein by reference, states that the greatest local average hydrophi-

licity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein.

As detailed in U.S. Pat. No. 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+1.0); aspartate (+3.0 \pm 1); glutamate (+3.0 \pm 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5 \pm 1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5); tryptophan (-3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ± 2 is preferred, those which are within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

As outlined above, amino acid substitutions are generally therefore based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions which take various of the foregoing characteristics into consideration are well known to those of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

The polypeptides of the present invention can be chemically synthesized. The synthetic polypeptides are prepared using the well known techniques of solid phase, liquid phase, or peptide condensation techniques, or any combination thereof, can include natural and unnatural amino acids. Amino acids used for peptide synthesis may be standard Boc (N^{α} -amino protected N^{α} -t-butyloxycarbonyl) amino acid resin with the standard deprotecting, neutralization, coupling and wash protocols of the original solid phase procedure of Merrifield [*J. Am. Chem. Soc.*, 85:2149-2154 (1963)], or the base-labile N^{α} -amino protected 9-fluorenylmethoxycarbonyl (Fmoc) amino acids first described by Carpino and Han [*J. Org. Chem.*, 37:3403-3409 (1972)]. Both Fmoc and Boc N^{α} -amino protected amino acids can be obtained from Fluka, Bachem, Advanced Chemtech, Sigma, Cambridge Research Biochemical, Bachem, or Peninsula Labs or other chemical companies familiar to those who practice this art. In addition, the method of the invention can be used with other N^{α} -protecting groups that are familiar to those skilled in this art. Solid phase peptide synthesis may be accomplished by techniques familiar to those in the art and provided, for example, in Stewart and Young, 1984, *Solid Phase Synthesis*, Second Edition, Pierce Chemical Co., Rockford, Ill.; Fields et al., *Int. J. Pept. Protein es.* 35:161-214 (1990), or using automated synthesizers, such as sold by ABS. Thus, polypeptides of the invention may comprise D-amino acids, a combination of D- and L-amino acids, and various "designer" amino acids (e.g., 13-methyl amino acids, Ca-methyl amino acids, and Na-methyl amino acids, etc.) to convey special properties. Synthetic amino acids include ornithine for lysine, fluoro-phenylalanine for phenylalanine, and norleucine for leucine or isoleucine. Additionally, by assigning specific amino acids at specific coupling steps, α -helices, β turns, β sheets, β -turns, and cyclic peptides can be generated.

In a further embodiment, subunits of peptides that confer useful chemical and structural properties will be chosen. For example, peptides comprising D-amino acids will be resistant to L-amino acid-specific proteases in vivo. In addition, the present invention envisions preparing peptides that have more

well defined structural properties, and the use of peptidomimetics, and peptidomimetic bonds, such as ester bonds, to prepare peptides with novel properties. In another embodiment, a peptide may be generated that incorporates a reduced peptide bond, i.e., $R_1-CH_2-NH-R_2$, where R_1 and R_2 are amino acid residues or sequences. A reduced peptide bond may be introduced as a dipeptide subunit. Such a molecule would be resistant to peptide bond hydrolysis, e.g., protease activity. Such peptides would provide ligands with unique function and activity, such as extended half-lives in vivo due to resistance to metabolic breakdown, or protease activity. Furthermore, it is well known that in certain systems constrained peptides show enhanced functional activity (Hruby, *Life Sciences*, 31:189-199 (1982)); (Hruby et al., *Biochem J*, 268:249-262 (1990)).

The following non-classical amino acids may be incorporated in the peptide in order to introduce particular conformational motifs: 1,2,3,4-tetrahydroisoquinoline-3-carboxylate (Kazmierski et al., *J. Am. Chem. Soc.*, 113:2275-2283, 1991); (2S,3S)-methyl-phenylalanine, (2S,3R)-methyl-phenylalanine, (2R,3S)-methyl-phenylalanine and (2R,3R)-methyl-phenylalanine (Kazmierski and Hruby, *Tetrahedron Lett.*, 1991); 2-aminotetrahydro-naphthalene-2-carboxylic acid (Landis, *Ph.D. Thesis, University of Arizona*, 1989); hydroxy-1,2,3,4-tetrahydroisoquinoline-3-carboxylate (Miyake et al., *J. Takeda Res. Labs.*, 43:53-76, 1989); β -carboline (D and L) (Kazmierski, Ph.D. Thesis, University of Arizona 1988); HIC (histidine isoquinoline carboxylic acid) (Zechel et al., *Int. J. Pep. Protein Res.*, 43, 1991); and MC (histidine cyclic urea) (Dharanipragada).

The following amino acid analogs and peptidomimetics may be incorporated into a peptide to induce or favor specific secondary structures: LL-Acp (LL-3-amino-2-propenidone-6-carboxylic acid), a β -turn inducing dipeptide analog (Kemp et al., *J. Org. Chem.*, 50:5834-5838 (1985)); β -sheet inducing analogs [Kemp et al., *Tetrahedron Lett.*, 29:5081-5082 (1988)]; β -turn inducing analogs (Kemp et al., *Tetrahedron Lett.*, 29:5057-5060 (1988)); alpha-helix inducing analogs [Kemp et al., *Tetrahedron Lett.*, 29:4935-4938 (1988)]; β -3-turn inducing analogs [Kemp et al., *J. Org. Chem.*, 54:109:115 (1989)]; and analogs provided by the following references: Nagai and Sato, *Tetrahedron Lett.*, 26:647-650 (1985); DiMaio et al., *J. Chem. Soc. Perkin Trans.*, p. 1687 (1989); also a Gly-Ala turn analog (Kahn et al., *Tetrahedron Lett.*, 30:2317, 1989); amide bond isostere (Jones et al., *Tetrahedron Lett.*, 29:3853-3856, 1989); tetrazole (Zabrocki et al., *J. Am. Chem. Soc.*, 110:5875-5880, 1988); DTC (Samanen et al., *Int. J. Protein Pep. Res.*, 35:501:509, 1990); and analogs taught in Olson et al., (*J. Am. Chem. Sci.*, 112:323-333, 1990) and Garvey et al. (*J. Org. Chem.*, 56:436, 1990). Conformationally restricted mimetics of beta turns and beta bulges, and peptides containing them, are described in U.S. Pat. No. 5,440,013, issued Aug. 8, 1995 to Kahn.

X. Uses For Mscramm And Antibody Compositions

The protein compositions disclosed herein can be used for the treatment of wounds, for blocking protein receptors or for immunization (vaccination). In the latter case, the body creates specific antibodies, which can protect against invasion by bacterial strains comprising such a cell surface protein, and whereby the antibodies block the adherence of the bacterial strains to a damaged tissue.

The protein composition can be dispersed in a sterile, isotonic saline solution, optionally with the addition of a pharmaceutically acceptable dispersing agent. Different types of adjuvants can further be used to sustain the release in the

tissue, and thus expose the peptide for a longer time to the immune defense system of a body.

The proteins, nucleic acid molecules or antibodies are useful for interfering with the initial physical interaction between a pathogen and mammalian host responsible for infection, such as the adhesion of bacteria, particularly gram positive bacteria, to mammalian extracellular matrix proteins on indwelling devices or to extracellular matrix proteins in wounds; to block protein-mediated mammalian cell invasion; to block bacterial adhesion between mammalian extracellular matrix proteins and bacterial proteins that mediate tissue damage; and, to block the normal progression of pathogenesis in infections initiated other than by the implantation of indwelling devices or surgical techniques. Medical devices or polymeric biomaterials to be coated with the antibodies, proteins and active fragments described herein include, but are not limited to, staples, sutures, replacement heart valves, cardiac assist devices, hard and soft contact lenses, intraocular lens implants (anterior chamber, posterior chamber or phasic), other implants such as corneal inlays, kerato-prostheses, vascular stents, epikeratophalia devices, glaucoma shunts, retinal staples, scleral buckles, dental prostheses, thyroplastic devices, laryngoplastic devices, vascular grafts, soft and hard tissue prostheses including, but not limited to, pumps, electrical devices including stimulators and recorders, auditory prostheses, pacemakers, artificial larynx, dental implants, mammary implants, penile implants, cranio/facial tendons, artificial joints, tendons, ligaments, menisci, and disks, artificial bones, artificial organs including artificial pancreas, artificial hearts, artificial limbs, and heart valves; stents, wires, guide wires, intravenous and central venous catheters, laser and balloon angioplasty devices, vascular and heart devices (tubes, catheters, balloons), ventricular assists, blood dialysis components, blood oxygenators, urethral/ureteral/urinary devices (Foley catheters, stents, tubes and balloons), airway catheters (endotracheal and tracheostomy tubes and cuffs), enteral feeding tubes (including nasogastric, intragastric and jejunal tubes), wound drainage tubes, tubes used to drain the body cavities such as the pleural, peritoneal, cranial, and pericardial cavities, blood bags, test tubes, blood collection tubes, vacutainers, syringes, needles, pipettes, pipette tips, and blood tubing.

The term "coated" or "coating", as used herein, means to apply the protein, antibody, or active fragment to a surface of the device, preferably an outer surface that would be exposed to *S. aureus* infection. The surface of the device need not be entirely covered by the protein, antibody or active fragment.

XI. Preparation Of Proteins, Dna, And Antibodies

The skilled reader can employ conventional molecular biology, microbiology, and recombinant DNA techniques to prepare the proteins, peptides, and antibody compositions described herein. Such techniques are explained fully in the literature. See, e.g., Sambrook et al, *Molecular Cloning: A Laboratory Manual* (1989); *Current Protocols in Molecular Biology* Volumes I-III (Ausubel, R. @-I ed., 1994); *Cell Biology: A Laboratory Handbook* Volumes I-III (J. E. Celis, ed., 1994); *Current Protocols in Immunology* Volumes I-III (Coligan, J. E., ed., 1994); *Oligonucleotide Synthesis* (M. J. Gait ed. 1984); *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins eds., 1985); *Transcription And Translation* (B. D. Hames & S. J. Higgins, eds., 1984); *Animal Cell Culture* [R. I. Freshney, ed. 1, (1986); *Immobilized Cells And Enzymes* [IRL Press, (1986)]; B. Perbal, *A Practical Guide To Molecular Cloning* (1984).

Reference to antibodies throughout the specification includes whole polyclonal and monoclonal antibodies, and parts thereof, either alone or conjugated with other moieties. Antibody parts include Fab and F(ab)₂ fragments and single chain antibodies. The antibodies may be made in vivo in suitable laboratory animals or in vitro using recombinant DNA techniques. An antibody can be a polyclonal or a monoclonal antibody. In a preferred embodiment, an antibody is a polyclonal antibody. Means for preparing and characterizing antibodies are well known in the art (See, e.g., Harlow and Lane, *Antibodies: a Laboratory Manual*, Cold Spring Harbor, N.Y., 1988).

Briefly, a polyclonal antibody is prepared by immunizing an animal with an immunogen comprising a polypeptide of the present invention and collecting antisera from that immunized animal. A wide range of animal species can be used for the production of antisera. Typically an animal used for production of anti-antisera is a rabbit, a mouse, a rat, a hamster or a guinea pig. Because of the relatively large blood volume of rabbits, a rabbit is a preferred choice for production of polyclonal antibodies.

Antibodies, both polyclonal and monoclonal, specific for MSCRAMM epitopes may be prepared using conventional immunization techniques, as will be generally known to those of skill in the art. A composition containing antigenic epitopes of particular binding MSCRAMMs (either synthetic peptides, site-specifically mutated, or truncated peptides) can be used to immunize one or more experimental animals, such as a rabbit or mouse, which will then proceed to produce specific antibodies against epitope-containing MSCRAMM peptides.

Polyclonal antisera may be obtained, after allowing time for antibody generation, simply by bleeding the animal and preparing serum samples from the whole blood.

The amount of immunogen composition used in the production of polyclonal antibodies varies upon the nature of the immunogen, as well as the animal used for immunization. A variety of routes can be used to administer the immunogen (subcutaneous, intramuscular, intradermal, intravenous and intraperitoneal). The production of polyclonal antibodies may be monitored by sampling blood of the immunized animal at various points following immunization. A second, booster injection, also may be given. The process of boosting and titering is repeated until a suitable titer is achieved. When a desired level of immunogenicity is obtained, the immunized animal can be bled and the serum isolated and stored.

One of the important features provided by the present invention is a polyclonal sera that is relatively homogenous with respect to the specificity of the antibodies therein. Typically, polyclonal antisera is derived from a variety of different "clones," i.e., B-cells of different lineage. Monoclonal antibodies, by contrast, are defined as coming from antibody-producing cells with a common B-cell ancestor, hence their "mono" clonality.

When peptides are used as antigens to raise polyclonal sera, one expects considerably less variation in the clonal nature of the sera than if a whole antigen were employed. Unfortunately, if incomplete fragments of an epitope are presented, the peptide may very well assume multiple (and probably non-native) conformations. As a result, even short peptides can produce polyclonal antisera with relatively plural specificities and, unfortunately, an antisera that does not react or reacts poorly with the native molecule.

Polyclonal antisera according to the present invention is produced against peptides that are predicted to comprise whole, intact epitopes. It is believed that these epitopes are, therefore, more stable in an immunologic sense and thus

express a more consistent immunologic target for the immune system. Under this model, the number of potential B-cell clones that will respond to this peptide is considerably smaller and, hence, the homogeneity of the resulting sera will be higher. In various embodiments, the present invention provides for polyclonal antisera where the clonality, i.e., the percentage of clone reacting with the same molecular determinant, is at least 80%. Even higher clonality—90%, 95% or greater—is contemplated.

To obtain monoclonal antibodies, one also initially immunizes an experimental animal, often preferably a mouse, with an MSCRAMM-derived epitope-containing composition. One then, after a period of time sufficient to allow antibody generation, obtains a population of spleen or lymph cells from the animal. The spleen or lymph cells are then fused with cell lines, such as human or mouse myeloma strains, to produce antibody-secreting hybridomas. These hybridomas may be isolated to obtain individual clones which can then be screened for production of antibody to the desired peptide. Following immunization, spleen cells are removed and fused, using a standard fusion protocol with plasmacytoma cells to produce hybridomas secreting monoclonal antibodies against MSCRAMM-derived epitopes. Hybridomas which produce monoclonal antibodies to the selected antigens are identified using standard techniques, such as ELISA and Western blot methods. Hybridoma clones can then be cultured in liquid media and the culture supernatants unified to provide the MSCRAMM-derived epitope-specific monoclonal antibodies.

Immortal antibody-producing cell lines can also be created by techniques other than fusion, such as direct transformation of B lymphocytes with oncogenic DNA, or transfection with Epstein-Barr virus. See, e.g., M. Schreier et al., *Hybridoma Techniques* (1980); Hammerling et al., *Monoclonal Antibodies And T-cell Hybridomas* (1981); Kennett et al., *Monoclonal Antibodies* (1980); see also U.S. Pat. Nos. 4,341,761; 4,399,121; 4,427,783; 4,444,887; 4,451,570; 4,466,917; 4,472,500; 4,491,632; 4,493,890.

It is proposed that the monoclonal antibodies of the present invention will find useful application in standard immunochemical procedures, such as ELISA and Western blot methods, as well as other procedures which may utilize antibody specific to the MSCRAMM epitopes.

Additionally, it is proposed that monoclonal antibodies specific to the particular MSCRAMM-derived peptides may be utilized in other useful applications. For example, their use in immunoabsorbent protocols may be useful in purifying native or recombinant peptide species or synthetic or natural variants thereof.

In general, both poly- and monoclonal antibodies against these peptides may be used in a variety of embodiments. For example, they may be employed in antibody cloning protocols to obtain cDNAs or genes encoding the peptides discussed herein or related proteins. They may also be used in inhibition studies to analyze the effects of MSCRAMM-derived peptides in cells or animals. Anti-MSCRAMM epitope antibodies will also be useful in immunolocalization studies to analyze the distribution of MSCRAMMs during various cellular events, for example, to determine the cellular or tissue-specific distribution of the MSCRAMM peptides under different physiological conditions. A particularly useful application of such antibodies is in purifying native or recombinant MSCRAMMs, for example, using an antibody affinity column. The operation of all such immunological techniques will be known to those of skill in the art in light of the present disclosure.

Techniques for the production of single chain antibodies are known to those skilled in the art and described in U.S. Pat. No. 4,946,778 and can be used to produce single chain antibodies to the proteins described herein. Phage display technology may be used to select antibody genes having binding, activities for MSCRAMMs, or antigenic portions thereof, from PCR-amplified v genes of lymphocytes from humans screened for having antibodies to MSCRAMMs or naive libraries. Bispecific antibodies have two antigen binding domains wherein each domain is directed against a different epitope.

The antibody may be labeled directly with a detectable label for identification and quantification of a staphylococcal bacterium such as *S. aureus*. Labels for use in immunoassays are generally known to those skilled in the art and include enzymes, radioisotopes, and fluorescent, luminescent and chromogenic substances including colored particles such as colloidal gold and latex beads. Suitable immunoassays include enzyme-linked immunosorbent assays (ELISA).

Alternatively, the antibody may be labeled indirectly by reaction with labeled substances that have an affinity for immunoglobulin, such as protein A or G or second antibodies. The antibody may be conjugated with a second substance and detected with a labeled third substance having an affinity for the second substance conjugated to the antibody. For example, the antibody may be conjugated to biotin and the antibody-biotin conjugate detected using labeled avidin or streptavidin. Similarly, the antibody may be conjugated to a hapten and the antibody-hapten conjugate detected using labeled anti-hapten antibody. These and other methods of labeling antibodies and assay conjugates are well known to those skilled in the art. Antibodies to the binding proteins may also be used in production facilities or laboratories to isolate additional quantities of the protein, such as by affinity chromatography.

In general, the preparation of bispecific antibodies is also well known in the art, as exemplified by Glennie et al. (*J Immunol*, 139:2367-2375, 1987). Bispecific antibodies have been employed clinically, for example, to treat cancer patients (Bauer et al, *Vox Sang*, 61:156-157, 1991). One method for the preparation of bispecific antibodies involves the separate preparation of antibodies having specificity for different epitopes of one or more fibronectin binding domains from one or more fibronectin binding protein(s).

While numerous methods are known in the art for the preparation of bispecific antibodies, the Glennie et al., (1987 supra) method involves the preparation of peptic F(ab'Y)2 fragments from the two chosen antibodies, followed by reduction of each to provide separate Fab'YSH fragments. The SH groups on one of the two partners to be coupled are then alkylated with a cross-linking reagent such as o-phenylenedimaleimide to provide free maleimide groups on one partner. This partner may then be conjugated to the other by means of a thioether linkage, to give the desired F(ab'Y)2 heteroconjugate.

Due to ease of preparation, high yield and reproducibility, the Glennie et al., (1987 supra) method is often preferred for the preparation of bispecific antibodies, however, there are numerous other approaches that can be employed and that are envisioned by the inventors. For example, other techniques are known wherein cross-linking with SPDP or protein A is carried out, or a specific construct is prepared (Titus et al, *J Immunol*, 138:4018-4022, 1987; Tutt et al, *Eur J Immunol*, 21:1351-1358, 1991).

Another method for producing bispecific antibodies is by the fusion of two hybridomas to form a quadroma (Flavell et al, *Br. J. Cancer*, 64(2):274-280, 1991; Pimm et al, *J. Cancer*

Res Clin Oncol, 118:367-370, 1992; French et al, *Cancer Res*, 51:2358-2361, 1991; Embleton et al., *Br. J. Cancer*, 63(5): 670-674, 1991). As used herein, the term "quadroma" is used to describe the productive fusion of two B cell hybridomas. Using now standard techniques, two antibody producing hybridomas are fused to give daughter cells, and those cells that have maintained the expression of both sets of clonotype immunoglobulin genes are then selected.

A preferred method of generating a quadroma involves the selection of an enzyme deficient mutant of at least one of the parental hybridomas. This first mutant hybridoma cell line is then fused to cells of a second hybridoma that had been lethally exposed, e.g., to iodoacetamide, precluding its continued survival. Cell fusion allows for the rescue of the first hybridoma by acquiring the gene for its enzyme deficiency from the lethally treated hybridoma, and the rescue of the second hybridoma through fusion to the first hybridoma. Preferred, but not required, is the fusion of immunoglobulins of the same isotype, but of a different subclass. A mixed subclass antibody permits the use if an alternative assay for the isolation of a preferred quadroma.

In more detail, one method of quadroma development and screening involves obtaining a hybridoma line that secretes the first chosen mAb and making this deficient for the essential metabolic enzyme, hypoxanthine-guanine phosphoribosyltransferase (HGPRT). To obtain deficient mutants of the hybridoma, cells are grown in the presence of increasing concentrations of 8-azaguanine (1×10^7 M to 1×10^{-5} M). The mutants are subcloned by limiting dilution and tested for their hypoxanthine/aminopterin/thymidine (HAT) sensitivity. The culture medium may consist of, for example, DMEM supplemented with 10% FCS, 2 mM L-Glutamine and 1 mM penicillin-streptomycin.

A complementary hybridoma cell line that produces the second desired MAb is used to generate the quadromas by standard cell fusion techniques (Galfre et al, *Methods Enzymol*, 73:1-46, 1981), or by using the protocol described by Clark et al (*Int J Cancer*, 2:15-17, 1988). Briefly, 4.5×10^7 HAT-sensitive first cells are mixed with $2.8 \times$ phosphate buffered saline) for 30 in minutes on ice before fusion. Cell fusion is induced using polyethylene glycol (PEG) and the cells are plated out in 96 well microculture plates. Quadromas are selected using Hat-containing medium. Bispecific antibody-containing cultures are identified using, for example, a solid phase isotype-specific ELISA and isotype-specific immunofluorescence staining.

In one identification embodiment to identify the bispecific antibody, the wells of microliter plates (Falcon, Becton Dickinson Labware) are coated with a reagent that specifically interacts with one of the parent hybridoma antibodies and that lacks cross-reactivity with both antibodies. The plates are washed, blocked, and the supernatants (SNs) to be tested are added to each well. Plates are incubated at room temperature for 2 hours, the supernatants discarded, the plates washed, and diluted alkaline phosphatase-anti-antibody conjugate added for 2 hours at room temperature. The plates are washed and a phosphatase substrate, e.g., p-Nitrophenyl phosphate (Sigma, St. Louis) is added to each well. Plates are incubated, 3N NaOH is added to each well to stop the reaction, and the OD410 values determined using an ELISA reader.

In another identification embodiment, microliter plates pre-treated with poly-L-lysine are used to bind one of the target cells to each well, the cells are then fixed, e.g. using 1% glutaraldehyde, and the bispecific antibodies are tested for their ability to bind to the intact cell. In addition, FACS, immunofluorescence staining, idiotype specific antibodies, antigen binding competition assays, and other methods com-

mon in the art of antibody characterization may be used in conjunction with the present invention to identify preferred quadromas.

Following the isolation of the quadroma, the bispecific antibodies are purified away from other cell products. This may be accomplished by a variety of protein isolation Procedures, known to those skilled in the art of immunoglobulin purification. Means for preparing and characterizing antibodies are well known in the art (See, e.g., *Antibodies: A Laboratory Manual*, 1988).

For example, supernatants from selected quadromas are passed over protein A or protein G sepharose columns to bind IgG (depending on the isotype). The bound antibodies are then eluted with, e.g. a pH 5.0 citrate buffer. The elute fractions containing the BsAbs, are dialyzed against an isotonic buffer. Alternatively, the eluate is also passed over an anti-immunoglobulin-sepharose column. The BsAb is then eluted with 3.5 M magnesium chloride. BsAbs purified in this way are then tested for binding activity by, e.g., an isotype-specific ELISA and immunofluorescence staining assay of the target cells, as described above.

Purified BsAbs and parental antibodies may also be characterized and isolated by SDS PAGE electrophoresis, followed by staining with silver or Coomassie. This is possible when one of the parental antibodies has a higher molecular weight than the other, wherein the band of the BsAbs migrates midway between that of the two parental antibodies. Reduction of the samples verifies the presence of heavy chains with two different apparent molecular weights.

Furthermore, recombinant technology is now available for the preparation of antibodies in general, allowing the preparation of recombinant antibody genes encoding an antibody having the desired dual specificity (Van Duk et al., *Int J. Cancer*, 43:344-349, 1989). Thus, after selecting the monoclonal antibodies having the most preferred binding characteristics, the respective genes for these antibodies can be isolated, e.g., by immunological screening of a phage expression library (Oi and Morrison, 1986; *Winter and Milstein*, 1991). Then, through rearrangement of Fab coding domains, the appropriate chimeric construct can be readily obtained.

Humanized monoclonal antibodies are antibodies of animal origin that have been modified using genetic engineering techniques to replace constant region and/or variable region framework sequences with human sequences, while retaining the original antigen specificity.

Such antibodies are commonly derived from rodent antibodies with specificity against human antigens. Such antibodies are generally useful for in vivo therapeutic applications. This strategy reduces the host response to the foreign antibody and allows selection of the human effector functions.

The techniques for producing humanized immunoglobulins are well known to those of skill in the art. For example U.S. Pat. No. 5,693,762 discloses methods for producing, and compositions of, humanized immunoglobulins having one or more complementarily determining regions (CDR's). When combined into an intact antibody, the humanized immunoglobulins are substantially non-immunogenic in humans and retain substantially the same affinity as the donor immunoglobulin to the antigen, such as a protein or other compound containing an epitope.

Other U.S. patents, each incorporated herein by reference, that teach the production of antibodies useful in the present invention include U.S. Pat. No. 5,565,332, which describes the production of chimeric antibodies using a combinatorial approach; U.S. Pat. No. 4,816,567 which describes recombi-

nant immunoglobulin preparations and U.S. Pat. No. 4,867,973 which describes antibody-therapeutic agent conjugates.

U.S. Pat. No. 5,565,332 describes methods for the production of antibodies, or antibody fragments, which have the same binding specificity as a parent antibody but which have increased human characteristics. Humanized antibodies may be obtained by chain shuffling, perhaps using phage display technology, in as much as such methods will be useful in the present invention the entire text of U.S. Pat. No. 5,565,332 is incorporated herein by reference.

Using the peptide antigens described herein, the present invention also provides methods of generating an immune response, which methods generally comprise administering to an animal, a pharmaceutically-acceptable composition comprising an immunologically effective amount of an MSCRAMM-derived peptide composition. Preferred animals include mammals, and particularly humans. Other preferred animals include murines, bovines, equines, porcines, canines, and felines. The composition may include partially or significantly purified MSCRAMM-derived peptide epitopes, obtained from natural or recombinant sources, which proteins or peptides may be obtainable naturally or either chemically synthesized, or alternatively produced in vitro from recombinant host cells expressing DNA segments encoding such epitopes. Smaller peptides that include reactive epitopes, such as those between about 30 and about 100 amino acids in length will often be preferred. The antigenic proteins or peptides may also be combined with other agents, such as other staphylococcal or streptococcal peptide or nucleic acid compositions, if desired. The composition may also include staphylococcal produced bacterial components such as those discussed above, obtained from natural or recombinant sources, which proteins may be obtainable naturally or either chemically synthesized, or alternatively produced in vitro from recombinant host cells expressing DNA segments encoding such peptides.

Immunoformulations of this invention, whether intended for vaccination, treatment, or for the generation of antibodies useful in the detection of staphylococci and streptococci, or prevention of bacterial adhesion to ECM components such as fibronectin, collagen, elastin, fibrinogen or vitronectin may comprise site-specifically mutated, truncated, or synthetically-derived antigenic peptide fragments from these proteins. As such, antigenic functional equivalents of the proteins and peptides described herein also fall within the scope of the present invention.

Further means contemplated by the inventors for generating an immune response in an animal includes administering to the animal, or human subject, a pharmaceutically-acceptable composition comprising an immunologically effective amount of a nucleic acid composition encoding a peptide epitope, or an immunologically effective amount of an attenuated live organism that includes and expresses such a nucleic acid composition.

The amount of expressible DNA or transcribed RNA to be introduced into a vaccine recipient will have a very broad dosage range and may depend on the strength of the transcriptional and translational promoters used. In addition, the magnitude of the immune response may depend on the level of protein expression and on the immunogenicity of the expressed gene product. In general, effective dose ranges of about 1 ng to 5 mg, 100 ng to 2.5 mg, 1 µg to 750 µg, and preferably about 10 µg to 300 µg of DNA is administered directly into muscle tissue. Subcutaneous injection, intradermal introduction, impression through the skin, and other modes of administration such as intraperitoneal, intravenous, or inhalation delivery are also suitable. It is also contemplated

that booster vaccinations may be provided. Following vaccination with an MSCRAMM polynucleotide immunogen, boosting with MSCRAMM protein immunogens such as the M55 gene product is also contemplated.

The polynucleotide may be "naked", that is, unassociated with any proteins, adjuvants or other agents which affect the recipients' immune system. In this case, it is desirable for the polynucleotide to be in a physiologically acceptable solution, such as, but not limited to, sterile saline or sterile buffered saline. Alternatively, the DNA may be associated with liposomes, such as lecithin liposomes or other liposomes known in the art, as a DNA-liposome mixture, or the DNA may be associated with an adjuvant known in the art to boost immune responses, such as a protein or other carrier. Agents which assist in the cellular uptake of DNA, such as, but not limited to, calcium ions, may also be used. These agents are generally referred to herein as transfection facilitating reagents and pharmaceutically acceptable carriers. Techniques for coating microprojectiles coated with polynucleotide are known in the art and are also useful in connection with this invention. For DNA intended for human use it may be useful to have the final DNA product in a pharmaceutically acceptable carrier or buffer solution. Pharmaceutically acceptable carriers or buffer solutions are known in the art and include those described in a variety of texts such as Remington's Pharmaceutical Sciences.

In another embodiment, the invention is a polynucleotide which comprises contiguous nucleic acid sequences capable of being expressed to produce a gene product upon introduction of said polynucleotide into eukaryotic tissues *in vivo*. The encoded gene product preferably either acts as an immunostimulant or as an antigen capable of generating an immune response. Thus, the nucleic acid sequences in this embodiment encode an MSCRAMM immunogenic epitope, and optionally a cytokine or a T-cell costimulatory element, such as a member of the B7 family of proteins.

There are several advantages of immunization with a gene rather than its gene product. The first is the relative simplicity with which native or nearly native antigen can be presented to the immune system. Mammalian proteins expressed recombinantly in bacteria, yeast, or even mammalian cells often require extensive treatment to insure appropriate antigenicity. A second advantage of DNA immunization is the potential for the immunogen to enter the MHC class I pathway and evoke a cytotoxic T cell response. Immunization of mice with DNA encoding the influenza A nucleoprotein (NP) elicited a CD8⁺ response to NP that protected mice against challenge with heterologous strains of flu. (Montgomery, D. L. et al., *Cell Mol Biol*, 43(3):285-292, 1997; Ulmer, J. et al., *Vaccine*, 15(8):792-794, 1997)

Cell-mediated immunity is important in controlling infection. Since DNA immunization can evoke both humoral and cell-mediated immune responses, its greatest advantage may be that it provides a relatively simple method to survey a large number of *S. aureus* genes for their vaccine potential.

Immunization by DNA injection also allows the ready assembly of multicomponent subunit vaccines. Simultaneous immunization with multiple influenza genes has recently been reported. (Donnelly, J. et al., *Vaccines*, 55-59, 1994). The inclusion in a *S. aureus* vaccine of genes whose products activate varied and multiple responses from the immune system may also provide thorough protection from subsequent challenge.

Further provided is a composition comprising an isolated nucleic acid segment that encodes a peptide of a binding domain of a binding protein, wherein the peptide does or does not specifically bind to its ligand. It is also contemplated that

attenuated organisms may be engineered to express recombinant MSCRAMM gene products and themselves be delivery vehicles for the invention. Particularly preferred are attenuated bacterial species such as *Mycobacterium*, and in particular *M. bovis*, *M. smegmatis*, or BCG. Alternatively, pox-, polio-, adeno-, or other viruses, and bacteria such as *Salmonella*, *Shigella*, *Listeria*, *Streptococcus* species may also be used in conjunction with the methods and compositions disclosed herein.

The naked DNA technology, often referred to as genetic immunization, has been shown to be suitable for protection against infectious organisms. Such DNA segments could be used in a variety of forms including naked DNA and plasmid DNA, and may administered to the subject in a variety of ways including parenteral, mucosal, and so-called microprojectile-based "gene-gun" inoculations. The use of nucleic acid compositions of the present invention in such immunization techniques is thus proposed to be useful as a vaccination strategy against at least streptococcal and staphylococcal infection.

It is recognized by those skilled in the art that an optimal dosing schedule of a DNA vaccination regimen may include as many as five to six, but preferably three to five, or even more preferably one to three administrations of the immunizing entity given at intervals of as few as two to four weeks, to as long as five to ten years, or occasionally at even longer intervals.

Particular aspects of the invention concern the use of plasmid vectors for the cloning and expression of recombinant peptides, and particular peptide epitopes comprising either native, or site-specifically mutated binding site epitopes. The generation of recombinant vectors, transformation of host cells, and expression of recombinant proteins is well-known to those of skill in the art. Prokaryotic hosts are preferred for expression of the peptide compositions of the present invention. An example of a preferred prokaryotic host is *E. coli*, and in particular, *E. coli* strains ATCC 69791, BL21(DE3), JM101, RRI, LE392, B, ⁷⁷⁶(ATCC 31537), and W3110 (F, λ , prototrophic, ATCC 273325). Alternatively, other *Enterobacteriaceae* species such as *Salmonella typhimurium* and *Serratia marcescens*, or even other Gram-negative hosts including various *Pseudomonas* species may be used in the recombinant expression of the genetic constructs discussed herein. Additional hosts may include well known eukaryotic and prokaryotic hosts, such as strains of *Bacillus*, *Streptomyces*, fungi such as yeasts, and animal cells, such as CHO, R1.1, B-W and L-M cells, African Green Monkey kidney cells (e.g., COS 1, COS 7, BSC1, BSC40, and BMT10), insect cells (e.g., Sf9), and human cells and plant cells in tissue culture.

A wide variety of host/expression vector combinations may be employed in expressing the DNA. Useful expression vectors, for example, may consist of segments of chromosomal, non-chromosomal and synthetic DNA sequences. Suitable vectors include derivatives of SV40 and known bacterial plasmids. e.g., *E. coli* plasmids col E1, pCR1, pBR322, pMB9 and their derivatives, plasmids such as RP4; phage DNAs, e.g., the numerous derivatives of phage λ , e.g., NM989, and other phage DNA, e.g., M13 and filamentous single stranded phage DNA; yeast plasmids such as the 2 μ plasmid or derivatives thereof; vectors useful in eukaryotic cells, such as vectors useful in insect or mammalian cells; vectors derived from combinations of plasmids and phage DNAs, such as plasmids that have been modified to employ phage DNA or other expression control sequences; and the like.

As is well known in the art, DNA sequences may be expressed by operatively linking them to an expression control sequence in an appropriate expression vector and employing that expression vector to transform an appropriate unicellular host. Such operative linking of a DNA sequence of this invention to an expression control sequence, of course, includes, if not already part of the DNA sequence, the provision of an initiation codon, ATG, in the correct reading frame upstream of the DNA sequence.

Any of a wide variety of expression control sequences—sequences that control the expression of a DNA sequence operatively linked to it—may be used in these vectors to express the DNA sequences of this invention. Such useful expression control sequences include, for example, the early or late promoters of SV40, CMV, vaccinia, polyoma or adenovirus, the lac system, the trp system, the TAC system, the TRC system, the LTR system, the major operator and promoter regions of phage λ , the control regions of fd coat protein, the promoter for 3-phospho-glycerate kinase or other glycolytic enzymes, the promoters of acid phosphatase (e.g., Pho5), the promoters of the yeast α -mating factors, and other sequences known to control the expression of genes of prokaryotic or eukaryotic cells or their viruses, and various combinations thereof.

It will be understood that not all vectors, expression control sequences and hosts will function equally well to express the DNA sequences of this invention. Neither will all hosts function equally well with the same expression system. However, one skilled in the art will be able to select the proper vectors, expression control sequences, and hosts without undue experimentation to accomplish the desired expression without departing from the scope of this invention. For example, in selecting a vector, the host must be considered because the vector must function in it. The vector's copy number, the ability to control that copy number, and the expression of any other proteins encoded by the vector, such as antibiotic markers, will also be considered.

In selecting an expression control sequence, a variety of factors will normally be considered. These include, for example, the relative strength of the system, its controllability, and its compatibility with the particular DNA sequence or gene to be expressed, particularly with regard to potential secondary structures. Suitable unicellular hosts will be selected by consideration of, e.g., their compatibility with the chosen vector, their secretion characteristics, their ability to fold proteins correctly, and their fermentation requirements, as well as the toxicity to the host of the product encoded by the DNA sequences to be expressed, and the ease of purification of the expression products. Considering these and other factors a person skilled in the art will be able to construct a variety of vector/expression control sequence/host combinations that will express the DNA sequences encoding the components of this invention on fermentation or in large scale animal culture.

In certain embodiments, it is also contemplated that the nucleic acid segments discussed herein will be used to transect appropriate host cells. Technology for introduction of DNA into cells is well-known to those of skill in the art. Four general methods for delivering a nucleic segment into cells have been described: (1) chemical methods (Graham and VanDerEb, *Virology*, 54 (2):536-539, 1973); physical methods such as microinjection (Capecchi, *Cell*, 22(2):479-488, 1980), electroporation (Wong and Neuman, *Biochim Biophys Res Commun*, 107(2):584-587, 1982; Fromm et al., *Proc Natl Acad Sci USA*, 82(17):5824-5828, 1985) and the gene gun (Yang et al., *Proc Natl Acad Sci USA*, 87:4144-4148, 1990); (3) viral vectors (Eglitis and Anderson, *Bio-*

techniques, 6(7):608-614, 1988); and (4) receptor-mediated mechanisms (Wagner, et al., *Proc Natl Acad Sci USA*, 89(13):6099-6103, 1992).

DNA sequences encoding MSCRAMM can be prepared synthetically or cloned. The DNA sequence can be designed with the appropriate codons for the MSCRAMM amino acid sequence. In general, one will select preferred codons for the intended host if the sequence will be used for expression. The complete sequence is assembled from overlapping oligonucleotides prepared by standard methods and assembled into a complete coding sequence. See, e.g., Edge, *Nature*, 292:756 (1981); Nambair et al., *Science*, 223:1299 (1984); Jay et al., *J. Biol. Chem.*, 259:6311 (1984).

Synthetic DNA sequences allow convenient construction of genes which will express MSCRAMM analogs. Alternatively, DNA encoding analogs can be made by site-directed mutagenesis of native MSCRAMM genes or cDNAs, and analogs can be made directly using conventional polypeptide synthesis. A general method for site-specific incorporation of unnatural amino acids into proteins is described in Noren et al., *Science*. 244:182-188 (April 1989). This method may be used to create analogs with unnatural amino acids.

XII. Antisense Oligonucleotides And Ribozymes

The present invention extends to the preparation of antisense oligonucleotides and ribozymes that may be used to interfere with the expression of the MRCR AMM at the translational level. This approach utilizes antisense nucleic acid and ribozymes to block translation of a specific mRNA, either by masking the mRNA with an antisense nucleic acid or cleaving it with a ribozyme.

Antisense nucleic acids are DNA or RNA molecules that are complementary to at least a portion of a specific mRNA molecule. In the cell, they hybridize to that specific mRNA, forming a double stranded molecule. The cell does not translate an mRNA in this double-stranded form. Therefore, antisense nucleic acids interfere with the expression of mRNA into protein. Oligomers of about fifteen nucleotides and molecules that hybridize to the AUG initiation codon will be particularly efficient, since they are easy to synthesize and are likely to pose fewer problems than larger molecules when introducing them into MSCRAMM-producing cells. Antisense methods have been used to inhibit the expression of many genes in vitro (Marcus-Sekura, 1988; Hambor et al., 1988).

Ribozymes are RNA molecules possessing the ability to specifically cleave other single stranded RNA molecules in a manner somewhat analogous to DNA restriction endonucleases. Ribozymes were discovered from the observation that certain mRNAs have the ability to excise their own introns. By modifying the nucleotide sequence of these RNAs, researchers have been able to engineer molecules that recognize specific nucleotide sequences in an RNA molecule and cleave it (Cech, 1988). Because they are sequence-specific, only mRNAs with particular sequences are inactivated.

Investigators have identified two types of ribozymes, *Tetrahymena*-type and "hammerhead"-type. (Hasselhoff and Gerlach, *Nature*, 334(6183):585-591, 1988) *Tetrahymena*-type ribozymes recognize four-base sequences, while "hammerhead"-type recognizes eleven- to eighteen-base sequences. The longer the recognition sequence, the more likely it is to occur exclusively in the target mRNA species. Therefore, hammerhead-type ribozymes are preferable to *Tetrahymena*-type ribozymes for inactivating a specific mRNA species, and eighteen base recognition sequences are preferable to shorter recognition sequences.

The DNA sequences described herein may thus be used to prepare antisense molecules against, and ribozymes that cleave mRNAs for MSCRAMM and their ligands.

XIII. Pharmaceutical Compositions

A pharmaceutical composition is provided that comprises the binding proteins, the peptides, the antibodies, or the nucleic acids as described above optionally in combination with bacterial components, in a pharmaceutically acceptable excipient, in an effective amount to treat *S. aureus* infection. The compositions are typically used in the preparation of an immunization formulation that optionally includes an adjuvant and other customary additives. The compositions can also comprise diagnostic kits as described herein.

Methods for preparing pharmaceutical compositions which contain polypeptides, analogs or active fragments as active ingredients are well understood in the art. Typically, such compositions are prepared as injectables, either as liquid solutions or suspensions, however, solid forms suitable for solution in, or suspension in, liquid prior to injection can also be prepared. The preparation can also be emulsified. The active therapeutic ingredient is often mixed with excipients which are pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like and combinations thereof. In addition if desired, the composition can contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents which enhance the effectiveness of the active ingredient.

A polypeptide, analog or active fragment can be formulated into the therapeutic composition as neutralized pharmaceutically acceptable salt forms. Pharmaceutically acceptable salts include the acid addition salts (formed with the free amino groups of the polypeptide or antibody molecule) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed from the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine and the like.

The therapeutic polypeptide-, analog- or active fragment-containing compositions are conventionally administered intravenously, as by injection of a unit dose, for example. The term "unit dose" when used in reference to a therapeutic composition of the present invention refers to physically discrete units suitable as unitary dosage for humans, each unit containing a predetermined quantity of active material calculated to produce the desired therapeutic effect in association with the required diluent; i.e., carrier, or vehicle.

The compositions are administered in a manner compatible with the dosage formulation, and in a therapeutically effective amount. The quantity to be administered depends on the subject to be treated, capacity of the subject's immune system to utilize the active ingredient, and degree of inhibition or neutralization of MSCRAMM binding capacity desired. Precise amounts of active ingredient required to be administered depend on the judgment of the practitioner and are peculiar to each individual. However, suitable dosages may range from about 0.1 to 20, preferably about 0.5 to about 10, and more preferably one to several, milligrams of active ingredient per kilogram body weight of individual per day and depend on the route of administration. Suitable regimes for initial administration and booster shots are also variable, but are typified by an initial administration followed by repeated doses at one or

more hour intervals by a subsequent injection or other administration. Alternatively, continuous intravenous infusion sufficient to maintain concentrations of ten nanomolar to ten micromolar in the blood are contemplated.

5 The therapeutic compositions may further include an effective amount of the MSCRAMM/MSCRAMM antagonist or analog thereof, and one or more of the following active ingredients: an antibiotic, a steroid.

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

25 The preparation of such compositions that are essentially free from endotoxin can be achieved by following the published methodology, for example, U.S. Pat. No. 4,271,147 (incorporated herein by reference) discloses methods for the preparation of *Neisseria meningitidis* membrane proteins for use in vaccines.

The immunological compositions, such as vaccines, and other pharmaceutical compositions can be used alone or in combination with other blocking agents to protect against human and animal infections caused by staphylococcal bacteria such as *S. aureus*. In particular, the compositions can be used to protect humans against endocarditis or to protect humans or ruminants against mastitis caused by staphylococcal infections. The vaccine can also be used to protect canine and equine animals against similar staphylococcal infections.

40 To enhance immunogenicity, the proteins may be conjugated to a carrier molecule. Suitable immunogenic carriers include proteins, polypeptides or peptides such as albumin, hemocyanin, thyroglobulin and derivatives thereof, particularly bovine serum albumin (BSA) and keyhole limpet hemocyanin (KLH), polysaccharides, carbohydrates, polymers, and solid phases. Other protein derived or non-protein derived substances are known to those skilled in the art. An immunogenic carrier typically has a molecular weight of at least 1,000 daltons, preferably greater than 10,000 daltons. Carrier molecules often contain a reactive group to facilitate covalent conjugation to the hapten. The carboxylic acid group or amine group of amino acids or the sugar groups of glycoproteins are often used in this manner. Carriers lacking such groups can often be reacted with an appropriate chemical to produce them. Preferably, an immune response is produced when the immunogen is injected into animals such as mice, rabbits, rats, goats, sheep, guinea pigs, chickens, and other animals, most preferably mice and rabbits. Alternatively, a multiple antigenic peptide comprising multiple copies of the protein or polypeptide, or an antigenically or immunologically equivalent polypeptide may be sufficiently antigenic to improve immunogenicity without the use of a carrier.

55 The MSCRAMM protein or proteins may be administered with an adjuvant in an amount effective to enhance the immunogenic response against the conjugate. At this time, the only adjuvant widely used in humans has been alum (aluminum phosphate or aluminum hydroxide). Saponin and its purified

component Quil A, Freund's complete adjuvant and other adjuvants used in research and veterinary applications have toxicities which limit their potential use in human vaccines. However, chemically defined preparations such as muramyl dipeptide, monophosphoryl lipid A, phospholipid conjugates such as those described by Goodman-Snitkoff et al. (*J. Immunol.* 147:410-415, 1991) and incorporated by reference herein, encapsulation of the conjugate within a proteoliposome as described by Miller et al., (*J. Exp. Med.* 176:1739-1744, 1992) and incorporated by reference herein, and encapsulation of the protein in lipid vesicles such as Novasome™ lipid vesicles (Micro Vesicular Systems, Inc., Nashua, N.H.) may also be useful.

In certain embodiments, the inventors contemplate the use of liposomes and/or nanocapsules for the introduction of particular peptides or nucleic acid segments into host cells. In particular, the malonyltyrosyl and phosphotyrosyl peptides of the present invention may be formulated for delivery in solution with DMSO or encapsulated in liposomes.

Such formulations may be preferred for the introduction of pharmaceutically acceptable formulations of the nucleic acids, peptides, and/or antibodies disclosed herein. The formation and use of liposomes is generally known to those of skill in the art (see for example, Couvreur et al, *FEBS Lett*, 84:323-326, 1977; and *Crit. Rev Ther Drug Carrier Syst*, 5:1-20, 1988 which describes the use of liposomes and nanocapsules in the targeted antibiotic therapy of intracellular bacterial infections and diseases). Recently, liposomes were developed with improved serum stability and circulation half-times (Gabizon and Papahadjopoulos, *Proc Natl Acad Sci USA*, 85:6949-6953, 1988; Allen and Choun, *FEBS Lett*, 223:42-46, 1987).

Liposomes have been used successfully with a number of cell types that are normally resistant to transfection by other procedures including T cell suspensions, primary hepatocyte cultures and PC 12 cells (Muller et al., *DNA Cell Biol*, 9(3): 221-229, 1990). In addition, liposomes are free of the DNA length constraints that are typical of viral-based delivery systems. Liposomes have been used effectively to introduce genes, drugs, radiotherapeutic agents, enzymes, viruses, transcription factors and allosteric effectors into a variety of cultured cell lines and animals. In addition, several successful clinical trials examining the effectiveness of liposome-mediated drug delivery have been completed (Lopez-Berestein et al, *Cancer Drug Review*, 2(3):183-189, 1985; Sculier et al, *Eur J Cancer Clin Oncol*, 24(3):527-538, 1988). Furthermore, several studies suggest that the use of liposomes is not associated with autoimmune responses, toxicity or gonadal localization after systemic delivery (Mori and Fukatsu, *Epilepsia*, 33(6):994-1000, 1992).

Liposomes are formed from phospholipids that are dispersed in an aqueous medium and spontaneously form multilamellar concentric bilayer vesicles (also termed multilamellar vesicles (MLVs)). MLVs generally have diameters of from 25 nm to 4 micron. Sonication of MLVs results in the formation of small unilamellar vesicles (SUVS) with diameters in the range of 200 to 500 Å, containing an aqueous solution in the core.

Liposomes bear many resemblances to cellular membranes and are contemplated for use in connection with the present invention as carriers for the peptide compositions. They are widely suitable, as both water- and lipid-soluble substances can be entrapped, i.e., in the aqueous spaces and within the bilayer itself, respectively. It is possible that the drug-bearing liposomes may even be employed for site-specific delivery of active agents by selectively modifying the liposomal formulation.

In addition to the teachings of Couvreur et al. (*FEBS Lett*, 84:323-326, 1977; and *Crit. Rev Ther Drug Carrier Syst*, 5:1-20, 1988), the following information may be utilized in generating liposomal formulations. Phospholipids can form a variety of structures other than liposomes when dispersed in water, depending on the molar ratio of lipid to water. At low ratios the liposome is the preferred structure. The physical characteristics of liposomes depend on pH, ionic strength and the presence of divalent cations. Liposomes can show low permeability to ionic and polar substances, but at elevated temperatures undergo a phase transition which markedly alters their permeability. The phase transition involves a change from a closely packed, ordered structure, known as the gel state, to a loosely packed, less-ordered structure, known as the fluid state. This occurs at a characteristic phase-transition temperature and results in an increase in permeability to ions, sugars and drugs.

In addition to temperature, exposure to proteins can alter the permeability of liposomes. Certain soluble proteins such as cytochrome C bind, deform and penetrate the bilayer, thereby causing changes in permeability. Cholesterol inhibits this penetration of proteins, apparently by packing the phospholipids more tightly. It is contemplated that the most useful liposome formations for antibiotic and inhibitor delivery will contain cholesterol.

The ability to trap solutes varies between different types of liposomes. For example, MLVs are moderately efficient at trapping solutes, but SUVs are extremely inefficient. SUVs offer the advantage of homogeneity and reproducibility in size distribution, however, and a compromise between size and trapping efficiency is offered by large unilamellar vesicles (LUVs). These are prepared by ether evaporation and are three to four times more efficient at solute entrapment than MLVs.

In addition to liposome characteristics, an important determinant in entrapping compounds is the physicochemical properties of the compound itself. Polar compounds are trapped in the aqueous spaces and nonpolar compounds bind to the lipid bilayer of the vesicle. Polar compounds are released through permeation or when the bilayer is broken, but nonpolar compounds remain affiliated with the bilayer unless it is disrupted by temperature or exposure to lipoproteins. Both types show maximum efflux rates at the phase transition temperature.

Liposomes interact with cells via four different mechanisms: Endocytosis by phagocytic cells of the reticuloendothelial system such as macrophages and neutrophils; adsorption to the cell surface, either by nonspecific weak hydrophobic or electrostatic forces, or by specific interactions with cell-surface components; fusion with the plasma cell membrane by insertion of the lipid bilayer of the liposome into the plasma membrane, with simultaneous release of liposomal contents into the cytoplasm; and by transfer of liposomal lipids to cellular or subcellular membranes, or vice versa, without any association of the liposome contents. It often is difficult to determine which mechanism is operative and more than one may operate at the same time.

The fate and disposition of intravenously injected liposomes depends on their physical properties, such as size, fluidity and surface charge. They may persist in tissues for hours or days, depending on their composition, and half lives in the blood range from minutes to several hours. Larger liposomes, such as MLVs and LUVS, are taken up rapidly by phagocytic cells of the reticuloendothelial system, but physiology of the circulatory system restrains the exit of such large species at most sites. They can exit only in places where large openings or pores exist in the capillary endothelium, such as

the sinusoids of the liver or spleen. Thus, these organs are the predominate site of uptake. On the other hand, SUVs show a broader tissue distribution but still are sequestered highly in the liver and spleen. In general, this in vivo behavior limits the potential targeting of liposomes to only those organs and tissues accessible to their large size. These include the blood, liver, spleen, bone marrow and lymphoid organs.

Targeting is generally not a limitation in terms of the present invention. However, should specific targeting be desired, methods are available for this to be accomplished. Antibodies may be used to bind to the liposome surface and to direct the antibody and its drug contents to specific antigenic receptors located on a particular cell-type surface. Carbohydrate determinants (glycoprotein or glycolipid cell-surface components that play a role in cell-cell recognition, interaction and adhesion) may also be used as recognition sites as they have potential in directing liposomes to particular cell types. Mostly, it is contemplated that intravenous injection of liposomal preparations would be used, but other routes of administration are also conceivable.

Alternatively, the invention provides for pharmaceutically-acceptable nanocapsule formulations of the peptides of the present invention. Nanocapsules can generally entrap compounds in a stable and reproducible way (Henry-Michelland et al, *Int J. Pharm.*, 35:121-127, 1987). To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1 micron) should be designed using polymers able to be degraded in vivo. Biodegradable poly-alkyl-cyanoacrylate nanoparticles that meet these requirements are contemplated for use in the present invention, and such particles may be easily made, as described by Couvreur et al, (supra, 1977 and 1988).

Suitable methods of administration include, but are not limited to, topical, oral, anal, vaginal, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal and intradermal administration.

For topical administration, the composition is formulated in the form of an ointment, cream, gel, lotion, drops (such as eye drops and ear drops), or solution (such as mouthwash). Wound or surgical dressings, sutures and aerosols may be impregnated with the composition. The composition may contain conventional additives, such as preservatives, solvents to promote penetration, and emollients. Topical formulations may also contain conventional carriers such as cream or ointment bases, ethanol, or oleyl alcohol.

In a preferred embodiment, a vaccine is packaged in a single dosage for immunization by parenteral (i.e., intramuscular, intradermal or subcutaneous) administration or nasopharyngeal (i.e., intranasal) administration. The vaccine is most preferably injected intramuscularly into the deltoid muscle. The vaccine is preferably combined with a pharmaceutically acceptable carrier to facilitate administration. The carrier is usually water or a buffered saline, with or without a preservative. The vaccine may be lyophilized for resuspension at the time of administration or in solution.

The carrier to which the protein may be conjugated may also be a polymeric delayed release system. Synthetic polymers are particularly useful in the formulation of a vaccine to effect the controlled release of antigens. For example, the polymerization of methyl methacrylate into spheres having diameters less than one micron has been reported by Kreuter, J., *Microcapsules And Nanoparticles In Medicine And Pharmacology*, M. Donbrow (Ed). CRC Press, p. 125-148.

Microencapsulation of the protein will also give a controlled release. A number of factors contribute to the selection of a particular polymer for microencapsulation. The reproducibility of polymer synthesis and the microencapsulation

process, the cost of the microencapsulation materials and process, the toxicological profile, the requirements for variable release kinetics and the physicochemical compatibility of the polymer and the antigens are all factors that must be considered. Examples of useful polymers are polycarbonates, polyesters, polyurethanes, polyorthoesters polyamides, poly (d,l-lactide-co-glycolide) (PLGA) and other biodegradable polymers. The use of PLGA for the controlled release of antigen is reviewed by Eldridge, J. H., et al. *Current Topics In Microbiology And Immunology*, 146:59-66 (1989).

The preferred dose for human administration is from 0.01 mg/kg to 10 mg/kg, preferably approximately 1 mg/kg. Based on this range, equivalent dosages for heavier body weights can be determined. The dose should be adjusted to suit the individual to whom the composition is administered and will vary with age, weight and metabolism of the individual. The vaccine may additionally contain stabilizers such as thimerosal (ethyl(2-mercaptobenzoate-S) mercury sodium salt) (Sigma Chemical Company, St. Louis, Mo.) or physiologically acceptable preservatives.

It will be readily apparent to one skilled in the art that various substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention.

XIV. Kits

This invention also includes a kit comprising anti-MSCRAMM antibody or an MSCRAIVIM antigen for the detection and diagnosis of infections caused or exacerbated by *Staphylococcus* bacteria such as *S. aureus* or *S. epidermidis*. The preferred kit contains sufficient antibody to bind substantially all of the antigen in the sample in about ten minutes or less, or sufficient antigen to bind antibodies for MSCRAMMs. The antibody or antigen can be immobilized on a solid support, and can be labeled with a detectable agent, as described above. The kit optionally contains a means for detecting the detectable agent. If the antibody or antigen is labeled with a fluorochrome or radioactive label, no means for detecting the agent will typically be provided, as the user will be expected to have the appropriate spectrophotometer, scintillation counter, or microscope. If the detectable agent is an enzyme, a means for detecting the detectable agent can be supplied with the kit, and would typically include a substrate for the enzyme in sufficient quantity to detect all of the antigen-antibody complex. One preferred means for detecting a detectable agent is a substrate that is converted by an enzyme into a colored product. A common example is the use of the enzyme horseradish peroxidase with 2,2'-azino-di-[3-ethylbenzothiazoline sulfonate] (ABTS).

The kit can optionally contain a lysing agent that lyses cells present in the sample of body fluid. Suitable lysing agents include surfactants such as Tween-80, Nonidet P40, and Triton X-100. Preferably, the lysing agent is immobilized onto the solid support along with the antibody.

The kit can also contain a buffer solution for washing the substrate between steps. The buffer solution is typically a physiological solution such as a phosphate buffer, physiological saline, citrate buffer, or Tris buffer.

The kit can optionally include different concentrations of a preformed antigen to calibrate the assay. The kit can additionally contain a visual or numeric representation of amounts of antigen in a calibrated standard assay for reference purposes. For example, if an assay is used that produces a colored product, a sheet can be included that provides a depiction of increasing intensities associated with differing amounts of antigen.

45

The kit can optionally include two antibodies in the detection system. The first antibody which is present in small amounts is specific for the antigen being assayed for. The second antibody provided in higher amounts is used to detect the first antibody. For example, a rabbit antibody can be used to detect the LOOH/amine antigen, and then an anti-rabbit IgG antibody can be used to detect the bound rabbit antibody. Goat antibodies and anti-antibodies are also commonly used.

As one nonlimiting example, a kit for the detection of the lipid peroxidation state of a patient is provided that includes a rabbit antibody specific for desired antibody, anti-rabbit IgG antibody in sufficient amounts to detect the bound first antibody, an enzyme conjugated to the second antibody and a substrate for the enzyme which changes color on exposure to the enzyme. In addition, a kit may be prepared using one or more MSCRAMM antigens such as the M55 domain of the collagen binding protein and the ClfA fibrinogen binding protein, and this kit will enable the detection of samples with antibodies to collagen binding and fibrinogen binding MSCRAMMs.

EXAMPLES

The following examples are included to demonstrate preferred embodiments of the present invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples which follow represent techniques discovered by the inventors to function well in the practice of the invention, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

Example 1

Preparation of Prototype Four Component MSCRAMM Vaccine

A series of recombinant proteins, representing domains from the collagen, Fn, and Fbg-binding MSCRAMMs (FIG. 1), were overexpressed in *E. coli* and affinity purified by metal chelating chromatography as previously described (see, e.g., Joh et al., *Biochemistry*, 33 (20):6086-6092, 1994; Patti et al., *J. Biol. Chem.* 270, 12005-12011, 1995; McDevitt et al., *Mol. Micro.* 11 (2):237-248, 1994; Ni Eidhin et al., *Infect. Immun. Submitted*, 1998). Used were the following: amino acids contained in the recombinant collagen-binding MSCRAMM expressed from *cna* (M55, such as disclosed in co-pending U.S. patent application Ser. No. 08/856,253, incorporated herein by reference); amino acids contained in the recombinant fibrinogen-binding MSCRAMM expressed from *clfA* (pCF40, such as disclosed in U.S. patent application Ser. No. 08/293,728, incorporated herein by reference); amino acids contained in the recombinant fibrinogen-binding MSCRAMM expressed from *clfB* (Region A, such as disclosed in U.S. application Ser. No. 09/200,650, incorporated herein by reference); and amino acids contained in the recombinant fibronectin-binding MSCRAMM (DUD4, such as those disclosed in co-pending U.S. application Ser. No. 09/010,317, incorporated herein by reference). The recombinant FN-binding MSCRAMM protein DUD4 was treated with formalin (5% formalin overnight, 4° C.) prior to combining it with the M55, Region A from ClfA, and Region A from ClfB.

46

Example 2

Example of Growing *E. coli* Strains for Production of Recombinant Proteins

Overnight cultures of *E. coli* JM101 or TOP 3 cells (Stratagene) harboring the recombinant plasmids were diluted 1:50 in 1 L of Luria Broth (Gibco BRL) containing 50 mg/mL ampicillin. *E. coli* cells were grown until the culture reached an OD₆₀₀ of 0.5-0.8. Expression of the recombinant proteins was induced by adding IPTG to a final concentration of 0.2 mM. After a three hour induction period, cells were collected by centrifugation, resuspended in 15 mL of Buffer A (5 mM imidazole, 0.5 M NaCl, 20 mM Tris-HCl, pH 7.9) and lysed by passage through a French press twice at 20,000 lb./in². Cell debris was removed by centrifugation at 50,000×g for 10 min and the supernatant was passed through a 0.45 μm filter.

Example 3

Purification of HIS₆ Containing Recombinant Proteins Expressed from pQE-30 (Qiagen®; Qiagen Inc., Chatsworth, Calif.) or PV-4 Based Recombinant Plasmids

The recombinant proteins were purified by immobilized metal chelate chromatography, using a column of iminodiacetic acid/Sepharose® 6B Fast Flow (Sigma, St. Louis, Mo.) charged with Ni²⁺; (Porath et al. 1975; Hochuli et al. 1988). The HIS₆ tagged proteins were purified by immobilized metal chelate affinity chromatography. More specifically, a column containing iminodiacetic acid Sepharose® 6B FF, connected to a FPLC® system (Pharmacia), was charged with 150 mM Ni⁺⁺ and equilibrated with buffer A (5 mM imidazole, 0.5 M NaCl, 20 mM Tris, pH 7.9). After equilibration, the bacterial supernatant was applied to the column and the column was washed with 10 bed volumes of buffer A. Subsequently, the column was eluted with buffer B (200 mM imidazole, 0.5 M NaCl, 20 mM Tris, pH 7.9). The eluate was monitored for protein by the absorbance at 280 nm and peak fractions were analyzed by SDS-PAGE. Endotoxin was removed from the purified recombinant proteins by detergent extraction with 1% Triton X-114 followed by metal chelate affinity chromatography and passage through a polymyxin B-sepharose column. The level of endotoxin was quantitated using a chromogenic *Limulus Amebocyte* Lysate (BioWhittaker, Walkersville, Md.) assay.

Example 4

Immunization of Animals with Four Component MSCRAMM Vaccine—MSCRAMM IV Rhesus Monkeys

100 μg of M55 (1 EU/mg), ClfA (2.5 EU/mg), ClfB (<1.0 EU/mg), and DUD4 (<10 EU/mg) were mixed together to form the MSCRAMM IV vaccine. The cocktail was mixed with TiterMax™ Gold (CytRX, Norcross, Ga.) in a 1:1 ratio. Two female rhesus monkeys, ID#495Z & 664U (~9.4 kg), were vaccinated intramuscularly (IM) in the hind quadriceps with 200 μl of the vaccine. Twenty-eight days later the two monkeys were boosted IM with 200 μl of the same vaccine formulation. Two additional female monkeys, ID#215W & 203U (~8.0 kg), were immunized with the MSCRAMM IV that was compounded in a 1:1 ratio with aluminum hydroxide

47

(2% Alhydrogel; Superfos, Denmark). Twenty-eight days later the two monkeys were boosted IM with 200 μ l of the same vaccine formulation.

The clinical regimen followed is described below.

Day 0	15 ml pre-immunization plasma sample, complete blood chemistry
Day 1	Vaccinate IM hind quadriceps with 0.2 ml MSCRAMM IV (100 μ g), injection site exam, temperature recorded
Day 7	Liver panel, temperature recorded, injection site exam
Day 14	15 ml plasma sample
Day 21	15 ml plasma sample
Day 28	Complete blood chemistry, temperature recorded 15 ml plasma sample, boost with IM injection of 0.2 ml MSCRAMM IV (100 μ g)
Day 30	Liver panel, temperature recorded, injection site exam
Day 35	Liver panel, temperature recorded, injection site, 15 ml plasma sample
Day 42	15 ml plasma sample
Day 49	15 ml plasma sample
Day 106	15 ml plasma sample

All 4 animals seroconverted following the initial immunization. Antibody levels >3 times above background could be detected by ELISA 106 days after the primary vaccination. The four animals received another booster immunization in the 21st week of the study. Each animal was given a booster of four subcutaneous injections of 125 μ l of the vaccine for a total booster of 600 μ l of the vaccine. Antibody levels at least 3 times above background, and as much as 15 times above background, could be detected by ELISA 189 days after the primary vaccination. See FIG. 2. No adverse injection site reactions were detected by direct observation by veterinarians. In addition, liver enzyme profiles, CBC, and hematology profiles were within the normal range for rhesus monkeys.

Example 5

Analysis of Plasma Samples from the Vaccinated Monkeys were Analyzed by ELISA

Immulon-2 microtiter plates (Dynex Technologies, Chantilly, Va.) were coated overnight at 4° C. with 10 μ g/ml (50 μ l) of the collagen binding MSCRAMM (M55), fibrinogen binding MSCRAMM (clfA; pCF₄₄), fibrinogen binding MSCRAMM (ClfB; Region A), and the fibronectin binding MSCRAMM (DUD4). Fifty microliters of the diluted plasma samples were added to the MSCRAMM coated wells and incubated for 1 hr at room temperature. Wash buffer consisting of PBS containing 0.05% vol/vol Tween-20, a blocking solution of 1% wt/vol BSA, 0.05% Tween-20 in PBS, and antibody dilution buffer consisting of PBS containing 0.1% BSA, 0.05% Tween-20. Incubation with primary and secondary antibodies was for 60 min at 25° C. The secondary antibody was alkaline phosphatase-conjugated goat anti-monkey immunoglobulin G, (Rockland, Gilbertsville, Pa.), diluted 3500-fold in antibody dilution buffer. ELISA plates were developed for 30 min at 37° C. with 1 mg/ml p-nitrophenyl phosphate (Sigma) in 1 M diethanolamine, 0.5 mM MgCl₂, pH 9.8, and quantified at 405 nm on a Perkin Elmer HTS 7000 Bio-Assay reader. Each plasma sample was diluted 100-fold in phosphate buffered saline, containing 0.05% Tween 20, 0.1% BSA, pH 7.4. ELISA data are shown in FIG. 2.

Example 6

Inhibition Assays

Methicillin resistant *S. aureus* strain 601 (Smeltzer, M. S., *Gene*. 196:249-159, 1997) was cultured under constant rota-

48

tion for 15 h at 37° C. in BHI broth. A 1:100 dilution of the overnight culture was made into BHI and the bacteria were grown at 37° C. until mid exponential phase. The bacteria were harvested by centrifugation, washed three times in sterile PBS, pH 7.4, and then resuspended in a carbonate buffer (50 mM NaHCO₃, pH 8.5). The bacteria were mixed with 1 mg/ml FITC (Sigma; F-7250) in 50 mM NaHCO₃, pH 8.5 and incubated end-over-end in the dark for 1 hr at 25° C. The FITC labeling reaction was stopped by centrifugation of the bacterial cells and removing the supernatant containing the unreacted FITC. The labeled bacteria were washed three times in PBS to remove unincorporated FITC, resuspended in PBS, adjusted to $\sim 1 \times 10^8$ cfu/ml and stored at $\pm 20^\circ$ C. in PBS, pH 7.4.

Example 7

Purification of IgG from Immunized Monkeys

IgG was purified from the monkey plasma by affinity chromatography on PROSEP®-A high capacity resin (Bioprocessing Inc., Princeton, N.J.). Briefly, the plasma was thawed and passed through 0.45 μ filter. The plasma was applied to a benchtop column containing PROSEP®-A high capacity resin. The unbound material was removed by washing the column extensively with PBS. The IgG was eluted from the column with 0.1 M sodium citrate, pH 3.0. The pH of eluted IgG was immediately neutralized to pH 6.8-7.4 by the addition of 1M Tris, pH 9.0. The IgG was then dialyzed into PBS, pH 7.4, concentrated and filter sterilized. The concentration of the purified IgG was determined by absorbance at 280 nm.

Example 8

Competitive Inhibition ELISA

Costar 96 well black plates were coated overnight at 4° C. or at room temperature for 2 hr with a 10 μ g/ml solution of matrix components consisting of bovine collagen, human fibrinogen, and bovine fibronectin in PBS, pH 7.4. The matrix protein coated plates were washed three times with PBS, 0.05% Tween 20 and then blocked with PBS, 1% BSA. The blocked plates were washed three times with PBS, 0.05% Tween 20. A 500 μ l aliquot of FITC-labeled *S. aureus* cells were mixed with an increasing amount of purified monkey IgG in PBS, 0.05% Tween 20, 0.1% BSA. The labeled cells and IgG were mixed on an end-over-end shaker for 1 hr at 25° C. Fifty μ l of the labeled cells/IgG mixture was added to each well on the microtiter plate and incubated at 25° C. on a rocker platform. The wells were washed three times with PBS, 0.05% Tween 20. The amount of bacteria bound to the immobilized matrix proteins was determined on a Perkin Elmer HTS 7000 Bio-Assay reader with the excitation filter set at 485 nm and the emission filter set at 535 nm.

Example 9

Animal Model of Sepsis

Using a mouse model of sepsis (Bremell, T. A., et al., *Infect. Immun.* 62 (7):2976-2985, 1992) we have demonstrated that passive immunization with IgG purified from rhesus monkeys immunized with the MSCRAMM IV can protect mice against sepsis induced death. Naive male NMRI mice 5-8 weeks old were passively immunized i.p. on day -1 with 20 mg of either purified IgG from rhesus monkeys immunized with MSCRAMM IV (n=12), or IgG from non-

immunized rhesus monkeys (n=13). On day 0, the mice were challenged i.v. with 2.4×10^7 CFU/mouse *S. aureus* strain LS-1. Mortality and weight change was monitored over the next 3 days. Three days after the inoculation 3/13 mice (13%) were dead in the control group, compared to 0/12 mice (0%) in the control group. Mortality in control group at day 13 was 53.8% (7/13) compared to only 16.2% (2/12) for the MSCRAMM IV passively immunized group. The control mice exhibited a significant decrease in their body weight compared to MSCRAMM IV IgG passively immunized mice ($28.0 \pm 2.5\%$ vs $21.3 \pm 3.1\%$; $p < 0.01$).

Example 10

Multicomponent Vaccines Containing M55
(Collagen-Binding MSCRAMM) and ClfA
(Fibrinogen-Binding MSCRAMM)

Sixty female Swiss Webster mice received a total of 50 μ g of either ovalbumin, M55 (collagen-binding MSCRAMM) or a combination of M55 and ClfA (fibrinogen-binding MSCRAMM) proteins via a subcutaneous injection. The primary injection was prepared by emulsifying the antigens in Freund's Complete Adjuvant. The mice received a second injection of 25 μ g total protein in Freund's Incomplete Adjuvant 14 days after the primary injection. A final injection of 25 μ g total protein in PBS was given 28 days after the primary injection. Post bleed samples from all mice were obtained two

weeks after the final injection to determine antibody titers against the different MSCRAMM proteins. The mice were then challenged (42 days after primary injection) via a single intravenous injection with 1.2×10^8 CFU of *S. aureus* 601. At day 5 post-challenge, the mice were sacrificed and their kidneys harvested. The kidneys were then homogenized and plated on blood agar plates. The plates were incubated at 37° C. overnight and the bacterial load in the kidneys was determined by colony counts. The results of the experiment showed a two log difference in bacterial load between the ovalbumin group (7.03 ± 0.93 log CFU/g) and the M55/ClfA group (4.83 ± 3.04 log CFU/g, $p = 0.006$). A difference in bacterial load was also observed in the M55 group (5.86 ± 3.42 log CFU/g, $p = 0.003$) when compared to the ovalbumin group.

As shown in the above specification and examples, immunological compositions, including vaccines, and other pharmaceutical compositions containing the MSCRAMM proteins are included within the scope of the present invention. One or more of the binding proteins, or active or antigenic fragments thereof, or fusion proteins thereof can be formulated and packaged, alone or in combination with other antigens, using methods and materials known to those skilled in the art for vaccines. The immunological response may be used therapeutically or prophylactically and may provide antibody immunity or cellular immunity such as that produced by T lymphocytes such as cytotoxic T lymphocytes or CD4+ T lymphocytes.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 22

<210> SEQ ID NO 1

<211> LENGTH: 5406

<212> TYPE: DNA

<213> ORGANISM: Staphylococcus epidermidis

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(5406)

<400> SEQUENCE: 1

tat tgg ata aat	tat gct tat	aaa gta ttt	aca taa	aaa tgt	aaa tgc	48
Tyr Trp Ile Asn	Tyr Ala Tyr	Lys Val Phe Thr	Lys Cys	Lys Cys	Lys Cys	
1	5	10	15	15	15	
aat tta caa gta	aat att caa	att att tcc	ttg taa	aat att	tat ttt	96
Asn Leu Gln Val	Asn Ile Gln	Ile Ile Ser Leu	Asn Ile Tyr	Phe		
20	25	30	30			
aac tgg agg	tat agt atg	aaa aag	aga aga	caa gga	cca att	144
Asn Trp Arg Tyr	Ser Met Lys	Lys Arg Arg	Gln Gly	Pro Ile	Asn Lys	
35	40	45	45	45	45	
aga gtg gat	ttt cta tcc	aac aag	gta aac	aag tac	tcg att	192
Arg Val Asp Phe	Leu Ser Asn	Lys Val Asn	Lys Tyr	Ser Ile	Arg Lys	
50	55	60	60	60	60	
ttc aca gta	ggt aca gct	tca ata	ctc gtg	ggt gct	acg tta	240
Phe Thr Val Gly	Thr Ala Ser	Ile Leu Val	Gly Ala	Thr Leu	Met Phe	
65	70	75	75	80	80	
ggt gcc gca gac	aat gag gct	aaa gcg	gct gaa	gac aat	caa tta	288
Gly Ala Ala Asp	Asn Glu Ala	Lys Ala Ala	Glu Asp	Asn Gln	Leu Glu	
85	90	90	95	95	95	
tca gct tca	aaa gaa gaa	cag aaa	ggt agt	cgt gat	aat gaa	336
Ser Ala Ser Lys	Glu Glu Gln	Lys Gly Ser	Arg Asp	Asn Glu	Asn Ser	
100	105	110	110	110	110	
aaa ctt	aat caa gtc	gat tta gac	aac gga	tca cat	agt tct	384

-continued

Lys	Leu	Asn	Gln	Val	Asp	Leu	Asp	Asn	Gly	Ser	His	Ser	Ser	Glu	Lys	
		115					120					125				
aca	aca	aat	gta	aac	aat	gca	act	gaa	gta	aaa	aaa	ggt	gaa	gca	cca	432
Thr	Thr	Asn	Val	Asn	Asn	Ala	Thr	Glu	Val	Lys	Lys	Val	Glu	Ala	Pro	
	130					135					140					
acg	aca	agt	gac	gta	tct	aag	cct	aaa	gct	aat	gaa	gca	gta	gtg	acg	480
Thr	Thr	Ser	Asp	Val	Ser	Lys	Pro	Lys	Ala	Asn	Glu	Ala	Val	Val	Thr	
	145				150					155				160		
aat	gag	tca	act	aaa	cca	aaa	aca	aca	gaa	gca	cca	act	ggt	aat	gag	528
Asn	Glu	Ser	Thr	Lys	Pro	Lys	Thr	Thr	Glu	Ala	Pro	Thr	Val	Asn	Glu	
			165					170						175		
gaa	tca	ata	gct	gaa	aca	ccc	aaa	acc	tca	act	aca	caa	caa	gat	tcg	576
Glu	Ser	Ile	Ala	Glu	Thr	Pro	Lys	Thr	Ser	Thr	Thr	Gln	Gln	Asp	Ser	
		180						185						190		
act	gag	aag	aat	aat	cca	tct	tta	aaa	gat	aat	tta	aat	tca	tcc	tca	624
Thr	Glu	Lys	Asn	Asn	Pro	Ser	Leu	Lys	Asp	Asn	Leu	Asn	Ser	Ser	Ser	
	195						200						205			
acg	aca	tct	aaa	gaa	agt	aaa	aca	gac	gaa	cat	tct	act	aag	caa	gct	672
Thr	Thr	Ser	Lys	Glu	Ser	Lys	Thr	Asp	Glu	His	Ser	Thr	Lys	Gln	Ala	
	210					215					220					
caa	atg	tct	act	aat	aaa	tca	aat	tta	gac	aca	aat	gac	tct	cca	act	720
Gln	Met	Ser	Thr	Asn	Lys	Ser	Asn	Leu	Asp	Thr	Asn	Asp	Ser	Pro	Thr	
	225				230					235				240		
caa	agt	gag	aaa	act	tca	tca	caa	gca	aat	aac	gac	agt	aca	gat	aat	768
Gln	Ser	Glu	Lys	Thr	Ser	Ser	Gln	Ala	Asn	Asn	Asp	Ser	Thr	Asp	Asn	
			245					250						255		
cag	tca	gca	cct	tct	aaa	caa	tta	gat	tca	aaa	cca	tca	gaa	caa	aaa	816
Gln	Ser	Ala	Pro	Ser	Lys	Gln	Leu	Asp	Ser	Lys	Pro	Ser	Glu	Gln	Lys	
			260					265					270			
gta	tat	aaa	aca	aaa	ttt	aat	gat	gaa	cct	act	caa	gat	ggt	gaa	cac	864
Val	Tyr	Lys	Thr	Lys	Phe	Asn	Asp	Glu	Pro	Thr	Gln	Asp	Val	Glu	His	
	275					280							285			
acg	aca	act	aaa	tta	aaa	aca	cct	tct	ggt	tca	aca	gat	agt	tca	gtc	912
Thr	Thr	Thr	Lys	Leu	Lys	Thr	Pro	Ser	Val	Ser	Thr	Asp	Ser	Ser	Val	
	290					295					300					
aat	gat	aag	caa	gat	tac	aca	cga	agt	gct	gta	gct	agt	tta	ggt	ggt	960
Asn	Asp	Lys	Gln	Asp	Tyr	Thr	Arg	Ser	Ala	Val	Ala	Ser	Leu	Gly	Val	
	305				310				315					320		
gat	tct	aat	gaa	aca	gaa	gca	att	aca	aat	gca	ggt	aga	gac	aat	tta	1008
Asp	Ser	Asn	Glu	Thr	Glu	Ala	Ile	Thr	Asn	Ala	Val	Arg	Asp	Asn	Leu	
			325					330						335		
gat	tta	aaa	gct	gca	tct	aga	gaa	caa	atc	aat	gaa	gca	atc	att	gct	1056
Asp	Leu	Lys	Ala	Ala	Ser	Arg	Glu	Gln	Ile	Asn	Glu	Ala	Ile	Ile	Ala	
			340					345						350		
gaa	gca	cta	aaa	aaa	gac	ttt	tct	aac	cct	gat	tat	ggt	gtc	gat	acg	1104
Glu	Ala	Leu	Lys	Lys	Asp	Phe	Ser	Asn	Pro	Asp	Tyr	Gly	Val	Asp	Thr	
		355				360							365			
cca	tta	gct	cta	aac	aga	tct	caa	tca	aaa	aat	tca	cca	cat	aag	agt	1152
Pro	Leu	Ala	Leu	Asn	Arg	Ser	Gln	Ser	Lys	Asn	Ser	Pro	His	Lys	Ser	
	370					375					380					
gca	agt	cca	cgc	atg	aat	tta	atg	agt	tta	gct	gct	gag	cct	aat	agt	1200
Ala	Ser	Pro	Arg	Met	Asn	Leu	Met	Ser	Leu	Ala	Ala	Glu	Pro	Asn	Ser	
	385				390					395				400		
ggt	aaa	aat	gtg	aat	gat	aaa	ggt	aaa	atc	aca	aac	cct	acg	ctt	tca	1248
Gly	Lys	Asn	Val	Asn	Asp	Lys	Val	Lys	Ile	Thr	Asn	Pro	Thr	Leu	Ser	
			405						410					415		
ctt	aat	aag	agt	aat	aat	cac	gct	aat	aac	gta	ata	tggt	cca	aca	agt	1296
Leu	Asn	Lys	Ser	Asn	Asn	His	Ala	Asn	Asn	Val	Ile	Trp	Pro	Thr	Ser	
			420				425						430			
aac	gaa	caa	ttt	aat	tta	aaa	gca	aat	tat	gaa	tta	gat	gac	agc	ata	1344

-continued

Asn	Glu	Gln	Phe	Asn	Leu	Lys	Ala	Asn	Tyr	Glu	Leu	Asp	Asp	Ser	Ile		
		435					440					445					
aaa	gag	gga	gat	act	ttt	act	att	aag	tat	ggt	cag	tat	att	aga	ccg	1392	
Lys	Glu	Gly	Asp	Thr	Phe	Thr	Ile	Lys	Tyr	Gly	Gln	Tyr	Ile	Arg	Pro		
	450				455					460							
ggt	ggt	tta	gaa	ctt	cct	gca	ata	aaa	act	caa	cta	cg	agt	aag	gat	1440	
Gly	Gly	Leu	Glu	Leu	Pro	Ala	Ile	Lys	Thr	Gln	Leu	Arg	Ser	Lys	Asp		
465				470						475					480		
ggc	tct	att	gta	gct	aat	ggg	gta	tat	gat	aaa	act	aca	aat	acg	acg	1488	
Gly	Ser	Ile	Val	Ala	Asn	Gly	Val	Tyr	Asp	Lys	Thr	Thr	Asn	Thr	Thr		
			485					490						495			
act	tat	aca	ttt	act	aac	tat	ggt	gat	caa	tat	caa	aat	att	aca	ggt	1536	
Thr	Tyr	Thr	Phe	Thr	Asn	Tyr	Val	Asp	Gln	Tyr	Gln	Asn	Ile	Thr	Gly		
			500				505						510				
agt	ttt	gat	tta	att	gcg	acg	cct	aag	agg	gaa	aca	gca	att	aag	gat	1584	
Ser	Phe	Asp	Leu	Ile	Ala	Thr	Pro	Lys	Arg	Glu	Thr	Ala	Ile	Lys	Asp		
	515						520					525					
aat	cag	aat	tat	cct	atg	gaa	gtg	acg	att	gct	aac	gaa	gta	gtc	aaa	1632	
Asn	Gln	Asn	Tyr	Pro	Met	Glu	Val	Thr	Ile	Ala	Asn	Glu	Val	Val	Lys		
	530					535					540						
aaa	gac	ttc	att	gtg	gat	tat	ggg	aat	aaa	aag	gac	aat	aca	act	aca	1680	
Lys	Asp	Phe	Ile	Val	Asp	Tyr	Gly	Asn	Lys	Lys	Asp	Asn	Thr	Thr	Thr		
	545			550					555					560			
gca	gcg	gta	gca	aat	gtg	gat	aat	gta	aat	aat	aaa	cat	aac	gaa	gtt	1728	
Ala	Ala	Val	Ala	Asn	Val	Asp	Asn	Val	Asn	Asn	Lys	His	Asn	Glu	Val		
				565				570						575			
gtt	tat	cta	aac	caa	aat	aac	caa	aac	cct	aaa	tat	gct	aaa	tat	ttc	1776	
Val	Tyr	Leu	Asn	Gln	Asn	Asn	Gln	Asn	Pro	Lys	Tyr	Ala	Lys	Tyr	Phe		
			580				585						590				
tca	aca	gta	aaa	aat	ggg	gaa	ttt	ata	cca	ggg	gaa	gtg	aaa	gtt	tac	1824	
Ser	Thr	Val	Lys	Asn	Gly	Glu	Phe	Ile	Pro	Gly	Glu	Val	Lys	Val	Tyr		
		595				600						605					
gaa	gtg	acg	gat	acc	aat	gcg	atg	gta	gat	agc	ttc	aat	cct	gat	tta	1872	
Glu	Val	Thr	Asp	Thr	Asn	Ala	Met	Val	Asp	Ser	Phe	Asn	Pro	Asp	Leu		
	610				615						620						
aat	agt	tct	aat	gta	aaa	gat	gtg	aca	agt	caa	ttt	gca	cct	aaa	gta	1920	
Asn	Ser	Ser	Asn	Val	Lys	Asp	Val	Thr	Ser	Gln	Phe	Ala	Pro	Lys	Val		
	625			630					635					640			
agt	gca	gat	ggg	act	aga	ggt	gat	atc	aat	ttt	gct	aga	agt	atg	gca	1968	
Ser	Ala	Asp	Gly	Thr	Arg	Val	Asp	Ile	Asn	Phe	Ala	Arg	Ser	Met	Ala		
			645					650						655			
aat	ggg	aaa	aag	tat	att	gta	act	caa	gca	gtg	aga	cca	acg	gga	act	2016	
Asn	Gly	Lys	Lys	Tyr	Ile	Val	Thr	Gln	Ala	Val	Arg	Pro	Thr	Gly	Thr		
			660					665					670				
gga	aat	ggt	tat	acc	gaa	tat	tgg	tta	aca	aga	gat	ggg	act	acc	aat	2064	
Gly	Asn	Val	Tyr	Thr	Glu	Tyr	Trp	Leu	Thr	Arg	Asp	Gly	Thr	Thr	Asn		
		675					680					685					
aca	aat	gat	ttt	tac	cg	gga	acg	aag	tct	aca	acg	gtg	act	tat	ctc	2112	
Thr	Asn	Asp	Phe	Tyr	Arg	Gly	Thr	Lys	Ser	Thr	Thr	Val	Thr	Tyr	Leu		
	690					695					700						
aat	ggg	tct	tca	aca	gca	cag	ggg	gat	aat	cct	aca	tat	agt	cta	ggt	2160	
Asn	Gly	Ser	Ser	Thr	Ala	Gln	Gly	Asp	Asn	Pro	Thr	Tyr	Ser	Leu	Gly		
	705				710					715				720			
gac	tat	gta	tgg	tta	gat	aaa	aat	aaa	aac	ggg	ggt	caa	gat	gat	gat	2208	
Asp	Tyr	Val	Trp	Leu	Asp	Lys	Asn	Lys	Asn	Gly	Val	Gln	Asp	Asp	Asp		
			725					730					735				
gag	aaa	ggg	tta	gca	ggg	ggt	tat	ggt	act	ctt	aaa	gac	agt	aac	aat	2256	
Glu	Lys	Gly	Leu	Ala	Gly	Val	Tyr	Val	Thr	Leu	Lys	Asp	Ser	Asn	Asn		
			740					745					750				
aga	gaa	tta	caa	cg	gta	act	act	gat	caa	tct	gga	cat	tat	caa	ttt	2304	

-continued

Arg	Glu	Leu	Gln	Arg	Val	Thr	Thr	Asp	Gln	Ser	Gly	His	Tyr	Gln	Phe			
		755						760					765					
gat	aat	tta	caa	aat	gga	acg	tac	aca	gtc	gag	ttt	gcg	att	cct	gat			2352
Asp	Asn	Leu	Gln	Asn	Gly	Thr	Tyr	Thr	Val	Glu	Phe	Ala	Ile	Pro	Asp			
	770				775					780								
aat	tat	acg	cca	tct	ccc	gca	aat	aat	tct	aca	aat	gat	gca	ata	gat			2400
Asn	Tyr	Thr	Pro	Ser	Pro	Ala	Asn	Asn	Ser	Thr	Asn	Asp	Ala	Ile	Asp			
	785				790					795					800			
tca	gat	ggg	gaa	cgt	gat	ggg	aca	cgt	aaa	gta	ggt	ggt	gcc	aaa	gga			2448
Ser	Asp	Gly	Glu	Arg	Asp	Gly	Thr	Arg	Lys	Val	Val	Val	Ala	Lys	Gly			
				805					810					815				
aca	att	aat	aat	gct	gat	aat	atg	act	gta	gat	act	ggc	ttt	tat	tta			2496
Thr	Ile	Asn	Asn	Ala	Asp	Asn	Met	Thr	Val	Asp	Thr	Gly	Phe	Tyr	Leu			
				820				825					830					
act	cct	aaa	tac	aat	gtc	gga	gat	tat	gta	tgg	gaa	gat	aca	aat	aaa			2544
Thr	Pro	Lys	Tyr	Asn	Val	Gly	Asp	Tyr	Val	Trp	Glu	Asp	Thr	Asn	Lys			
		835				840							845					
gat	ggg	atc	caa	gat	gac	aat	gaa	aaa	gga	att	tct	ggg	ggt	aaa	gta			2592
Asp	Gly	Ile	Gln	Asp	Asp	Asn	Glu	Lys	Gly	Ile	Ser	Gly	Val	Lys	Val			
	850					855							860					
acg	tta	aaa	aat	aaa	aat	gga	gat	act	att	ggc	aca	acg	aca	aca	gat			2640
Thr	Leu	Lys	Asn	Lys	Asn	Gly	Asp	Thr	Ile	Gly	Thr	Thr	Thr	Thr	Asp			
	865				870					875					880			
tca	aat	ggg	aaa	tat	gaa	ttc	aca	ggg	tta	gag	aac	ggg	gat	tac	aca			2688
Ser	Asn	Gly	Lys	Tyr	Glu	Phe	Thr	Gly	Leu	Glu	Asn	Gly	Asp	Tyr	Thr			
				885					890					895				
ata	gaa	ttt	gag	acg	ccg	gaa	ggc	tac	aca	ccg	act	aaa	caa	aac	tcg			2736
Ile	Glu	Phe	Glu	Thr	Pro	Glu	Gly	Tyr	Thr	Pro	Thr	Lys	Gln	Asn	Ser			
			900					905					910					
gga	agt	gac	gaa	ggg	aaa	gat	tca	aac	ggg	acg	aaa	aca	aca	gtc	aca			2784
Gly	Ser	Asp	Glu	Gly	Lys	Asp	Ser	Asn	Gly	Thr	Lys	Thr	Thr	Val	Thr			
		915				920							925					
gtc	aaa	gat	gca	gat	aat	aaa	aca	ata	gac	tca	ggg	ttc	tac	aag	cca			2832
Val	Lys	Asp	Ala	Asp	Asn	Lys	Thr	Ile	Asp	Ser	Gly	Phe	Tyr	Lys	Pro			
	930				935							940						
aca	tat	aac	tta	ggg	gac	tat	gta	tgg	gaa	gat	aca	aat	aaa	gat	ggg			2880
Thr	Tyr	Asn	Leu	Gly	Asp	Tyr	Val	Trp	Glu	Asp	Thr	Asn	Lys	Asp	Gly			
	945				950					955				960				
att	caa	gac	gac	agt	gaa	aaa	ggg	att	tct	ggg	ggt	aaa	gtg	acg	tta			2928
Ile	Gln	Asp	Asp	Ser	Glu	Lys	Gly	Ile	Ser	Gly	Val	Lys	Val	Thr	Leu			
			965					970						975				
aaa	gat	aaa	aat	gga	aat	gcc	att	ggg	aca	acg	aca	aca	gac	gca	agt			2976
Lys	Asp	Lys	Asn	Gly	Asn	Ala	Ile	Gly	Thr	Thr	Thr	Thr	Asp	Ala	Ser			
			980					985					990					
ggg	cat	tat	caa	ttt	aaa	gga	tta	gaa	aat	gga	agc	tac	aca	ggt	gag			3024
Gly	His	Tyr	Gln	Phe	Lys	Gly	Leu	Glu	Asn	Gly	Ser	Tyr	Thr	Val	Glu			
		995					1000						1005					
ttt	gag	aca	cca	tca	ggg	tat	aca	ccg	aca	aaa	gcg	aat	tca	ggg	caa			3072
Phe	Glu	Thr	Pro	Ser	Gly	Tyr	Thr	Pro	Thr	Lys	Ala	Asn	Ser	Gly	Gln			
	1010					1015						1020						
gat	ata	act	gta	gat	tcc	aac	ggg	ata	aca	aca	aca	ggg	atc	att	aac			3120
Asp	Ile	Thr	Val	Asp	Ser	Asn	Gly	Ile	Thr	Thr	Thr	Gly	Ile	Ile	Asn			
	1025				1030						1035				1040			
gga	gct	gat	aat	ctc	aca	att	gat	agt	ggg	ttc	tac	aaa	aca	cca	aaa			3168
Gly	Ala	Asp	Asn	Leu	Thr	Ile	Asp	Ser	Gly	Phe	Tyr	Lys	Thr	Pro	Lys			
				1045					1050					1055				
tat	agt	gtc	gga	gat	tat	gta	tgg	gaa	gat	aca	aat	aaa	gat	ggg	atc			3216
Tyr	Ser	Val	Gly	Asp	Tyr	Val	Trp	Glu	Asp	Thr	Asn	Lys	Asp	Gly	Ile			
			1060					1065					1070					
caa	gat	gac	aat	gaa	aag	gga	att	tct	ggg	ggt	aaa	gta	acg	tta	aag			3264

-continued

Gln	Asp	Asp	Asn	Glu	Lys	Gly	Ile	Ser	Gly	Val	Lys	Val	Thr	Leu	Lys	
		1075					1080					1085				
gat	gaa	aaa	gga	aat	ata	att	agc	act	aca	aca	act	gat	gaa	aat	ggg	3312
Asp	Glu	Lys	Gly	Asn	Ile	Ile	Ser	Thr	Thr	Thr	Thr	Asp	Glu	Asn	Gly	
	1090					1095					1100					
aag	tat	caa	ttt	gat	aat	tta	gat	agt	ggt	aat	tac	att	att	cat	ttt	3360
Lys	Tyr	Gln	Phe	Asp	Asn	Leu	Asp	Ser	Gly	Asn	Tyr	Ile	Ile	His	Phe	
	1105				1110					1115					1120	
gag	aaa	ccg	gaa	ggc	atg	act	caa	act	aca	gca	aat	tct	gga	aat	gat	3408
Glu	Lys	Pro	Glu	Met	Thr	Gln	Thr	Thr	Ala	Asn	Ser	Gly	Asn	Asp		
				1125					1130					1135		
gat	gaa	aaa	gat	gct	gat	ggg	gaa	gat	gtt	cgt	gtt	acg	att	act	gat	3456
Asp	Glu	Lys	Asp	Ala	Asp	Gly	Glu	Asp	Val	Arg	Val	Thr	Ile	Thr	Asp	
			1140					1145					1150			
cat	gat	gac	ttt	agt	ata	gat	aat	ggt	tat	ttt	gac	gat	gat	tca	gac	3504
His	Asp	Asp	Phe	Ser	Ile	Asp	Asn	Gly	Tyr	Phe	Asp	Asp	Asp	Ser	Asp	
	1155					1160					1165					
agt	gac	tca	gac	gca	gat	agt	gat	tca	gac	tca	gac	agt	gac	tcg	gac	3552
Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	
	1170					1175					1180					
gca	gac	agc	gat	tct	gac	gca	gac	agt	gac	tca	gac	gca	gat	agt	gat	3600
Ala	Asp	Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp	
	1185				1190					1195					1200	
tct	gac	tca	gac	agc	gac	tca	gac	gca	gat	agt	gat	tcc	gat	tca	gac	3648
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp	Ser	Asp	
				1205					1210					1215		
agc	gac	tcg	gat	tca	gat	agt	gat	tcg	gat	gca	gac	agc	gac	tcg	gat	3696
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp	
			1220					1225						1230		
tct	gac	agt	gat	tct	gac	gca	gac	agt	gac	tca	gat	tca	gac	agt	gac	3744
Ser	Asp	Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	
			1235					1240						1245		
tcg	gat	tca	gac	agc	gat	tcg	gat	tcc	gat	tca	gac	agt	gac	tcg	gat	3792
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	
	1250					1255						1260				
tca	gac	agt	gac	tca	gac	tcc	gac	agt	gat	tcc	gat	tca	gat	agc	gac	3840
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	
	1265				1270					1275					1280	
tcc	gac	gca	gat	agt	gat	tcg	gac	gca	gac	agt	gac	tca	gat	tca	gac	3888
Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp	Ser	Asp	
			1285						1290					1295		
agt	gat	tcg	gac	gca	gac	agt	gac	tcg	gac	tca	gat	agt	gat	tca	gat	3936
Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	
			1300					1305						1310		
gca	gac	agc	gat	tca	gac	tca	gat	agc	gac	tcg	gat	tca	gac	agc	gac	3984
Ala	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	
	1315						1320							1325		
tcc	gac	gca	gac	agc	gac	tcg	gat	tca	gat	agt	gat	tct	gac	tca	gac	4032
Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	
	1330						1335					1340				
agt	gac	tca	gat	tcc	gat	agt	gat	tcg	gat	tca	gat	agt	gat	tcc	gac	4080
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	
	1345				1350					1355					1360	
gca	gac	agc	gat	tcg	gat	tcc	gat	agc	gat	tca	gac	tca	gac	agc	gat	4128
Ala	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	
			1365						1370					1375		
tca	gat	tca	gac	agc	gac	tca	gat	tca	gat	agt	gat	tcc	gac	gca	gac	4176
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ala	Asp	
			1380						1385					1390		
agc	gat	gca	gac	agc	gac	tca	gac	gca	gac	agt	gat	tca	gat	gca	gac	4224

-continued

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Lys Asn Ala Lys
 1715 1720 1725

gat aaa tta cct gat aca gga gca aat gaa gat cat gat tct aaa ggc 5232
 Asp Lys Leu Pro Asp Thr Gly Ala Asn Glu Asp His Asp Ser Lys Gly
 1730 1735 1740

aca tta ctt gga act tta ttt gca ggt tta gga gca tta tta tta gga 5280
 Thr Leu Leu Gly Thr Leu Phe Ala Gly Leu Gly Ala Leu Leu Leu Gly
 1745 1750 1755

aga cgt cgt aaa aaa gat aat aaa gaa aaa tag cac tat tga ttc att 5328
 Arg Arg Arg Lys Lys Asp Asn Lys Glu Lys His Tyr Phe Ile
 1765 1770 1775

cat aag tta ttt caa gcc agg tct ata tgg cct ggt ttg aaa tca tat 5376
 His Lys Leu Phe Gln Ala Arg Ser Ile Trp Pro Gly Leu Lys Ser Tyr
 1780 1785 1790

taa att gaa agg aga aaa aga tga gta tgg 5406
 Ile Glu Arg Arg Lys Arg Val Trp
 1795 1800

<210> SEQ ID NO 2
 <211> LENGTH: 11
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus epidermidis

<400> SEQUENCE: 2

Tyr Trp Ile Asn Tyr Ala Tyr Lys Val Phe Thr
 1 5 10

<210> SEQ ID NO 3
 <211> LENGTH: 15
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus epidermidis

<400> SEQUENCE: 3

Lys Cys Lys Cys Asn Leu Gln Val Asn Ile Gln Ile Ile Ser Leu
 1 5 10 15

<210> SEQ ID NO 4
 <211> LENGTH: 1742
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus epidermidis

<400> SEQUENCE: 4

Asn Ile Tyr Phe Asn Trp Arg Tyr Ser Met Lys Lys Arg Arg Gln Gly
 1 5 10 15

Pro Ile Asn Lys Arg Val Asp Phe Leu Ser Asn Lys Val Asn Lys Tyr
 20 25 30

Ser Ile Arg Lys Phe Thr Val Gly Thr Ala Ser Ile Leu Val Gly Ala
 35 40 45

Thr Leu Met Phe Gly Ala Ala Asp Asn Glu Ala Lys Ala Ala Glu Asp
 50 55 60

Asn Gln Leu Glu Ser Ala Ser Lys Glu Glu Gln Lys Gly Ser Arg Asp
 65 70 75 80

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

Ser Ser Glu Lys Thr Thr Asn Val Asn Asn Ala Thr Glu Val Lys Lys
 100 105 110

Val Glu Ala Pro Thr Thr Ser Asp Val Ser Lys Pro Lys Ala Asn Glu
 115 120 125

Ala Val Val Thr Asn Glu Ser Thr Lys Pro Lys Thr Thr Glu Ala Pro
 130 135 140

-continued

Thr	Val	Asn	Glu	Glu	Ser	Ile	Ala	Glu	Thr	Pro	Lys	Thr	Ser	Thr	Thr
145					150					155					160
Gln	Gln	Asp	Ser	Thr	Glu	Lys	Asn	Asn	Pro	Ser	Leu	Lys	Asp	Asn	Leu
				165					170					175	
Asn	Ser	Ser	Ser	Thr	Thr	Ser	Lys	Glu	Ser	Lys	Thr	Asp	Glu	His	Ser
				180				185					190		
Thr	Lys	Gln	Ala	Gln	Met	Ser	Thr	Asn	Lys	Ser	Asn	Leu	Asp	Thr	Asn
		195					200					205			
Asp	Ser	Pro	Thr	Gln	Ser	Glu	Lys	Thr	Ser	Ser	Gln	Ala	Asn	Asn	Asp
	210					215					220				
Ser	Thr	Asp	Asn	Gln	Ser	Ala	Pro	Ser	Lys	Gln	Leu	Asp	Ser	Lys	Pro
225				230						235					240
Ser	Glu	Gln	Lys	Val	Tyr	Lys	Thr	Lys	Phe	Asn	Asp	Glu	Pro	Thr	Gln
				245					250						255
Asp	Val	Glu	His	Thr	Thr	Thr	Lys	Leu	Lys	Thr	Pro	Ser	Val	Ser	Thr
			260					265					270		
Asp	Ser	Ser	Val	Asn	Asp	Lys	Gln	Asp	Tyr	Thr	Arg	Ser	Ala	Val	Ala
			275				280					285			
Ser	Leu	Gly	Val	Asp	Ser	Asn	Glu	Thr	Glu	Ala	Ile	Thr	Asn	Ala	Val
	290					295					300				
Arg	Asp	Asn	Leu	Asp	Leu	Lys	Ala	Ala	Ser	Arg	Glu	Gln	Ile	Asn	Glu
305				310						315					320
Ala	Ile	Ile	Ala	Glu	Ala	Leu	Lys	Lys	Asp	Phe	Ser	Asn	Pro	Asp	Tyr
				325					330						335
Gly	Val	Asp	Thr	Pro	Leu	Ala	Leu	Asn	Arg	Ser	Gln	Ser	Lys	Asn	Ser
			340					345					350		
Pro	His	Lys	Ser	Ala	Ser	Pro	Arg	Met	Asn	Leu	Met	Ser	Leu	Ala	Ala
			355				360					365			
Glu	Pro	Asn	Ser	Gly	Lys	Asn	Val	Asn	Asp	Lys	Val	Lys	Ile	Thr	Asn
	370					375					380				
Pro	Thr	Leu	Ser	Leu	Asn	Lys	Ser	Asn	Asn	His	Ala	Asn	Asn	Val	Ile
385				390						395					400
Trp	Pro	Thr	Ser	Asn	Glu	Gln	Phe	Asn	Leu	Lys	Ala	Asn	Tyr	Glu	Leu
				405					410						415
Asp	Asp	Ser	Ile	Lys	Glu	Gly	Asp	Thr	Phe	Thr	Ile	Lys	Tyr	Gly	Gln
			420					425					430		
Tyr	Ile	Arg	Pro	Gly	Gly	Leu	Glu	Leu	Pro	Ala	Ile	Lys	Thr	Gln	Leu
		435					440						445		
Arg	Ser	Lys	Asp	Gly	Ser	Ile	Val	Ala	Asn	Gly	Val	Tyr	Asp	Lys	Thr
	450					455					460				
Thr	Asn	Thr	Thr	Thr	Tyr	Thr	Phe	Thr	Asn	Tyr	Val	Asp	Gln	Tyr	Gln
465					470					475					480
Asn	Ile	Thr	Gly	Ser	Phe	Asp	Leu	Ile	Ala	Thr	Pro	Lys	Arg	Glu	Thr
				485					490						495
Ala	Ile	Lys	Asp	Asn	Gln	Asn	Tyr	Pro	Met	Glu	Val	Thr	Ile	Ala	Asn
			500					505					510		
Glu	Val	Val	Lys	Lys	Asp	Phe	Ile	Val	Asp	Tyr	Gly	Asn	Lys	Lys	Asp
		515					520					525			
Asn	Thr	Thr	Thr	Ala	Ala	Val	Ala	Asn	Val	Asp	Asn	Val	Asn	Asn	Lys
	530					535					540				
His	Asn	Glu	Val	Val	Tyr	Leu	Asn	Gln	Asn	Asn	Gln	Asn	Pro	Lys	Tyr
545					550					555					560
Ala	Lys	Tyr	Phe	Ser	Thr	Val	Lys	Asn	Gly	Glu	Phe	Ile	Pro	Gly	Glu
				565					570						575

-continued

Val Lys Val Tyr Glu Val Thr Asp Thr Asn Ala Met Val Asp Ser Phe
 580 585 590

Asn Pro Asp Leu Asn Ser Ser Asn Val Lys Asp Val Thr Ser Gln Phe
 595 600 605

Ala Pro Lys Val Ser Ala Asp Gly Thr Arg Val Asp Ile Asn Phe Ala
 610 615 620

Arg Ser Met Ala Asn Gly Lys Lys Tyr Ile Val Thr Gln Ala Val Arg
 625 630 635 640

Pro Thr Gly Thr Gly Asn Val Tyr Thr Glu Tyr Trp Leu Thr Arg Asp
 645 650 655

Gly Thr Thr Asn Thr Asn Asp Phe Tyr Arg Gly Thr Lys Ser Thr Thr
 660 665 670

Val Thr Tyr Leu Asn Gly Ser Ser Thr Ala Gln Gly Asp Asn Pro Thr
 675 680 685

Tyr Ser Leu Gly Asp Tyr Val Trp Leu Asp Lys Asn Lys Asn Gly Val
 690 695 700

Gln Asp Asp Asp Glu Lys Gly Leu Ala Gly Val Tyr Val Thr Leu Lys
 705 710 715 720

Asp Ser Asn Asn Arg Glu Leu Gln Arg Val Thr Thr Asp Gln Ser Gly
 725 730 735

His Tyr Gln Phe Asp Asn Leu Gln Asn Gly Thr Tyr Thr Val Glu Phe
 740 745 750

Ala Ile Pro Asp Asn Tyr Thr Pro Ser Pro Ala Asn Asn Ser Thr Asn
 755 760 765

Asp Ala Ile Asp Ser Asp Gly Glu Arg Asp Gly Thr Arg Lys Val Val
 770 775 780

Val Ala Lys Gly Thr Ile Asn Asn Ala Asp Asn Met Thr Val Asp Thr
 785 790 795 800

Gly Phe Tyr Leu Thr Pro Lys Tyr Asn Val Gly Asp Tyr Val Trp Glu
 805 810 815

Asp Thr Asn Lys Asp Gly Ile Gln Asp Asp Asn Glu Lys Gly Ile Ser
 820 825 830

Gly Val Lys Val Thr Leu Lys Asn Lys Asn Gly Asp Thr Ile Gly Thr
 835 840 845

Thr Thr Thr Asp Ser Asn Gly Lys Tyr Glu Phe Thr Gly Leu Glu Asn
 850 855 860

Gly Asp Tyr Thr Ile Glu Phe Glu Thr Pro Glu Gly Tyr Thr Pro Thr
 865 870 875 880

Lys Gln Asn Ser Gly Ser Asp Glu Gly Lys Asp Ser Asn Gly Thr Lys
 885 890 895

Thr Thr Val Thr Val Lys Asp Ala Asp Asn Lys Thr Ile Asp Ser Gly
 900 905 910

Phe Tyr Lys Pro Thr Tyr Asn Leu Gly Asp Tyr Val Trp Glu Asp Thr
 915 920 925

Asn Lys Asp Gly Ile Gln Asp Asp Ser Glu Lys Gly Ile Ser Gly Val
 930 935 940

Lys Val Thr Leu Lys Asp Lys Asn Gly Asn Ala Ile Gly Thr Thr Thr
 945 950 955 960

Thr Asp Ala Ser Gly His Tyr Gln Phe Lys Gly Leu Glu Asn Gly Ser
 965 970 975

Tyr Thr Val Glu Phe Glu Thr Pro Ser Gly Tyr Thr Pro Thr Lys Ala
 980 985 990

Asn Ser Gly Gln Asp Ile Thr Val Asp Ser Asn Gly Ile Thr Thr Thr

-continued

995				1000				1005							
Gly	Ile	Ile	Asn	Gly	Ala	Asp	Asn	Leu	Thr	Ile	Asp	Ser	Gly	Phe	Tyr
1010						1015					1020				
Lys	Thr	Pro	Lys	Tyr	Ser	Val	Gly	Asp	Tyr	Val	Trp	Glu	Asp	Thr	Asn
1025				1030						1035					1040
Lys	Asp	Gly	Ile	Gln	Asp	Asp	Asn	Glu	Lys	Gly	Ile	Ser	Gly	Val	Lys
				1045					1050					1055	
Val	Thr	Leu	Lys	Asp	Glu	Lys	Gly	Asn	Ile	Ile	Ser	Thr	Thr	Thr	Thr
				1060				1065					1070		
Asp	Glu	Asn	Gly	Lys	Tyr	Gln	Phe	Asp	Asn	Leu	Asp	Ser	Gly	Asn	Tyr
				1075				1080				1085			
Ile	Ile	His	Phe	Glu	Lys	Pro	Glu	Gly	Met	Thr	Gln	Thr	Thr	Ala	Asn
1090					1095						1100				
Ser	Gly	Asn	Asp	Asp	Glu	Lys	Asp	Ala	Asp	Gly	Glu	Asp	Val	Arg	Val
1105				1110						1115					1120
Thr	Ile	Thr	Asp	His	Asp	Asp	Phe	Ser	Ile	Asp	Asn	Gly	Tyr	Phe	Asp
				1125					1130					1135	
Asp	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp	Ser	Asp
				1140				1145					1150		
Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp
				1155			1160				1165				
Ala	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp
1170					1175						1180				
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ala	Asp
1185				1190					1195					1200	
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp	Ser	Asp
				1205					1210					1215	
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp
				1220				1225					1230		
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp
				1235			1240				1245				
Ser	Asp	Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp
1250					1255						1260				
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp	Ser	Asp
1265				1270					1275						1280
Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp
				1285					1290					1295	
Ser	Asp	Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp
				1300				1305					1310		
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp
				1315			1320				1325				
Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp
1330					1335						1340				
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp
1345				1350					1355						1360
Ser	Asp	Ala	Asp	Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp	Ala	Asp	Ser	Asp
				1365					1370					1375	
Ser	Asp	Ala	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ala	Asp
				1380				1385					1390		
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp
				1395			1400				1405				
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp
1410					1415						1420				

-continued

Ser Asp Ala Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 1425 1430 1435 1440
 Ser Asp Ser Asp Ala Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 1445 1450 1455
 Ala Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ala Asp Ser Asp
 1460 1465 1470
 Ser Asp Ser Asp Ser Asp Ser Asp Ala Asp Ser Asp Ser Asp Ser Asp
 1475 1480 1485
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ala Asp Ser Asp Ser Asp
 1490 1495 1500
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 1505 1510 1515 1520
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 1525 1530 1535
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 1540 1545 1550
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 1555 1560 1565
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 1570 1575 1580
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 1585 1590 1595 1600
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 1605 1610 1615
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ala Asp
 1620 1625 1630
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ala Asp Ser Asp Ser Asp
 1635 1640 1645
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 1650 1655 1660
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 1665 1670 1675 1680
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 1685 1690 1695
 Lys Asn Ala Lys Asp Lys Leu Pro Asp Thr Gly Ala Asn Glu Asp His
 1700 1705 1710
 Asp Ser Lys Gly Thr Leu Leu Gly Thr Leu Phe Ala Gly Leu Gly Ala
 1715 1720 1725
 Leu Leu Leu Gly Arg Arg Arg Lys Lys Asp Asn Lys Glu Lys
 1730 1735 1740

<210> SEQ ID NO 5
 <211> LENGTH: 18
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus epidermidis

<400> SEQUENCE: 5

Phe Ile His Lys Leu Phe Gln Ala Arg Ser Ile Trp Pro Gly Leu Lys
 1 5 10 15

Ser Tyr

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

<400> SEQUENCE: 6

-continued

Ile Glu Arg Arg Lys Arg
1 5

<210> SEQ ID NO 7
<211> LENGTH: 2976
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus epidermidis
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (3)..(2975)

<400> SEQUENCE: 7

at att gca aaa aag act tat ata cta tat tgt att tta ctc tag aaa Ile Ala Lys Lys Thr Tyr Ile Leu Tyr Cys Ile Leu Leu Lys 1 5 10 15	47
cga ttt tta ctt gaa aat tac att gaa ata gtc aaa gat aag gag ttt Arg Phe Leu Leu Glu Asn Tyr Ile Glu Ile Val Lys Asp Lys Glu Phe 20 25 30	95
tta tga tta aaa aat aat tta cta act aaa aag aaa cct ata gca Leu Leu Lys Lys Asn Asn Leu Leu Thr Lys Lys Lys Pro Ile Ala 35 40 45	143
aat aaa tcc aat aaa tat gca att aga aaa ttc aca gta ggt aca gcg Asn Lys Ser Asn Lys Tyr Ala Ile Arg Lys Phe Thr Val Gly Thr Ala 50 55 60	191
tct att gta ata ggt gca gca tta ttg ttt ggt tta ggt cat aat gag Ser Ile Val Ile Gly Ala Ala Leu Leu Phe Gly Leu Gly His Asn Glu 65 70 75	239
gcc aaa gct gag gag aat aca gta caa gac gtt aaa gat tcg aat atg Ala Lys Ala Glu Glu Asn Thr Val Gln Asp Val Lys Asp Ser Asn Met 80 85 90 95	287
gat gat gaa tta tca gat agc aat gat cag tcc agt aat gaa gaa aag Asp Asp Glu Leu Ser Asp Ser Asn Asp Gln Ser Ser Asn Glu Glu Lys 100 105 110	335
aat gat gta atc aat aat agt cag tca ata aac acc gat gat gat aac Asn Asp Val Ile Asn Asn Ser Gln Ser Ile Asn Thr Asp Asp Asp Asn 115 120 125	383
caa ata aaa aag gaa gaa acg aat agc aac gat gcc ata gaa aat cgc Gln Ile Lys Lys Glu Glu Thr Asn Ser Asn Asp Ala Ile Glu Asn Arg 130 135 140	431
tct aaa gat ata aca cag tca aca aca aat gta gat gaa aac gaa gca Ser Lys Asp Ile Thr Gln Ser Thr Thr Asn Val Asp Glu Asn Glu Ala 145 150 155	479
aca ttt tta caa aag acc cct caa gat aat act cag ctt aaa gaa gaa Thr Phe Leu Gln Lys Thr Pro Gln Asp Asn Thr Gln Leu Lys Glu Glu 160 165 170 175	527
gtg gta aaa gaa ccc tca tca gtc gaa tcc tca aat tca tca atg gat Val Val Lys Glu Pro Ser Ser Val Glu Ser Ser Asn Ser Ser Met Asp 180 185 190	575
act gcc caa caa cca tct cat aca aca ata aat agt gaa gca tct att Thr Ala Gln Gln Pro Ser His Thr Thr Ile Asn Ser Glu Ala Ser Ile 195 200 205	623
caa aca agt gat aat gaa gaa aat tcc cgc gta tca gat ttt gct aac Gln Thr Ser Asp Asn Glu Glu Asn Ser Arg Val Ser Asp Phe Ala Asn 210 215 220	671
tct aaa ata ata gag agt aac act gaa tcc aat aaa gaa gag aat act Ser Lys Ile Ile Glu Ser Asn Thr Glu Ser Asn Lys Glu Glu Asn Thr 225 230 235	719
ata gag caa cct aac aaa gta aga gaa gat tca ata aca agt caa ccg Ile Glu Gln Pro Asn Lys Val Arg Glu Asp Ser Ile Thr Ser Gln Pro 240 245 250 255	767
tct agc tat aaa aat ata gat gaa aaa att tca aat caa gat gag tta	815

-continued

Ser	Ser	Tyr	Lys	Asn	Ile	Asp	Glu	Lys	Ile	Ser	Asn	Gln	Asp	Glu	Leu		
				260					265					270			
tta	aat	tta	cca	ata	aat	gaa	tat	gaa	aat	aag	gtt	aga	ccg	tta	tct		863
Leu	Asn	Leu	Pro	Ile	Asn	Glu	Tyr	Glu	Asn	Lys	Val	Arg	Pro	Leu	Ser		
		275						280					285				
aca	aca	tct	gcc	caa	cca	tcg	agt	aag	cgt	gta	acc	gta	aat	caa	tta		911
Thr	Thr	Ser	Ala	Gln	Pro	Ser	Ser	Lys	Arg	Val	Thr	Val	Asn	Gln	Leu		
		290						295					300				
gcg	gca	gaa	caa	ggt	tcg	aat	gtt	aat	cat	tta	att	aaa	gtt	act	gat		959
Ala	Ala	Glu	Gln	Gly	Ser	Asn	Val	Asn	His	Leu	Ile	Lys	Val	Thr	Asp		
		305				310						315					
caa	agt	att	act	gaa	gga	tat	gat	gat	agt	gat	ggt	att	att	aaa	gca		1007
Gln	Ser	Ile	Thr	Glu	Gly	Tyr	Asp	Asp	Ser	Asp	Gly	Ile	Ile	Lys	Ala		
		320			325					330					335		
cat	gat	gct	gaa	aac	tta	atc	tat	gat	gta	act	ttt	gaa	gta	gat	gat		1055
His	Asp	Ala	Glu	Asn	Leu	Ile	Tyr	Asp	Val	Thr	Phe	Glu	Val	Asp	Asp		
				340						345					350		
aag	gtg	aaa	tct	ggt	gat	acg	atg	aca	gtg	aat	ata	gat	aag	aat	aca		1103
Lys	Val	Lys	Ser	Gly	Asp	Thr	Met	Thr	Val	Asn	Ile	Asp	Lys	Asn	Thr		
			355					360						365			
gtt	cca	tca	gat	tta	acc	gat	agt	ttt	gca	ata	cca	aaa	ata	aaa	gat		1151
Val	Pro	Ser	Asp	Leu	Thr	Asp	Ser	Phe	Ala	Ile	Pro	Lys	Ile	Lys	Asp		
			370					375					380				
aat	tct	gga	gaa	atc	atc	gct	aca	ggt	act	tat	gac	aac	aca	aat	aaa		1199
Asn	Ser	Gly	Glu	Ile	Ile	Ala	Thr	Gly	Thr	Tyr	Asp	Asn	Thr	Asn	Lys		
			385			390						395					
caa	att	acc	tac	act	ttt	aca	gat	tat	gta	gat	aaa	tat	gaa	aat	att		1247
Gln	Ile	Thr	Tyr	Thr	Phe	Thr	Asp	Tyr	Val	Asp	Lys	Tyr	Glu	Asn	Ile		
			400			405				410					415		
aaa	gcg	cac	ctt	aaa	tta	aca	tca	tac	att	gat	aaa	tca	aag	gtt	cca		1295
Lys	Ala	His	Leu	Lys	Leu	Thr	Ser	Tyr	Ile	Asp	Lys	Ser	Lys	Val	Pro		
				420					425						430		
aat	aat	aac	act	aag	tta	gat	gta	gaa	tat	aag	acg	gcc	ctt	tca	tca		1343
Asn	Asn	Asn	Thr	Lys	Leu	Asp	Val	Glu	Tyr	Lys	Thr	Ala	Leu	Ser	Ser		
				435					440					445			
gta	aat	aaa	aca	att	acg	gtt	gaa	tat	caa	aaa	cct	aac	gaa	aat	cgg		1391
Val	Asn	Lys	Thr	Ile	Thr	Val	Glu	Tyr	Gln	Lys	Pro	Asn	Glu	Asn	Arg		
			450					455					460				
act	gct	aac	ctt	caa	agt	atg	ttc	aca	aac	ata	gat	acg	aaa	aac	cat		1439
Thr	Ala	Asn	Leu	Gln	Ser	Met	Phe	Thr	Asn	Ile	Asp	Thr	Lys	Asn	His		
			465			470							475				
aca	gtt	gag	caa	acg	att	tat	att	aac	cct	ctt	cgt	tat	tca	gcc	aaa		1487
Thr	Val	Glu	Gln	Thr	Ile	Tyr	Ile	Asn	Pro	Leu	Arg	Tyr	Ser	Ala	Lys		
					485					490					495		
gaa	aca	aat	gta	aat	att	tca	ggg	aat	ggc	gat	gaa	ggt	tca	aca	att		1535
Glu	Thr	Asn	Val	Asn	Ile	Ser	Gly	Asn	Gly	Asp	Glu	Gly	Ser	Thr	Ile		
				500					505						510		
atc	gac	gat	agt	aca	atc	att	aaa	gtt	tat	aag	gtt	gga	gat	aat	caa		1583
Ile	Asp	Asp	Ser	Thr	Ile	Ile	Lys	Val	Tyr	Lys	Val	Gly	Asp	Asn	Gln		
			515					520						525			
aat	tta	cca	gat	agt	aac	aga	att	tat	gat	tac	agt	gaa	tat	gaa	gat		1631
Asn	Leu	Pro	Asp	Ser	Asn	Arg	Ile	Tyr	Asp	Tyr	Ser	Glu	Tyr	Glu	Asp		
				530				535						540			
gtc	aca	aat	gat	gat	tat	gcc	caa	tta	gga	aat	aat	aat	gac	gtg	aat		1679
Val	Thr	Asn	Asp	Asp	Tyr	Gcc	Ala	Gln	Leu	Gly	Asn	Asn	Asn	Asp	Val	Asn	
				545				550					555				
att	aat	ttt	ggt	aat	ata	gat	tca	cca	tat	att	att	aaa	gtt	att	agt		1727
Ile	Asn	Phe	Gly	Asn	Ile	Asp	Ser	Pro	Tyr	Ile	Ile	Lys	Val	Ile	Ser		
				560		565				570					575		
aaa	tat	gac	cct	aat	aag	gac	gat	tac	acg	acg	ata	cag	caa	act	gtg		1775

-continued

Lys	Tyr	Asp	Pro	Asn	Lys	Asp	Asp	Tyr	Thr	Thr	Ile	Gln	Gln	Thr	Val	
				580					585						590	
aca	atg	caa	acg	act	ata	aat	gag	tat	act	ggt	gag	ttt	aga	aca	gca	1823
Thr	Met	Gln	Thr	Thr	Ile	Asn	Glu	Tyr	Thr	Gly	Glu	Phe	Arg	Thr	Ala	
			595					600					605			
tcc	tat	gat	aat	aca	att	gct	ttc	tct	aca	agt	tca	ggt	caa	gga	caa	1871
Ser	Tyr	Asp	Asn	Thr	Ile	Ala	Phe	Ser	Thr	Ser	Ser	Gly	Gln	Gly	Gln	
		610						615					620			
ggt	gac	ttg	cct	cct	gaa	aaa	act	tat	aaa	atc	gga	gat	tac	gta	tgg	1919
Gly	Asp	Leu	Pro	Pro	Glu	Lys	Thr	Tyr	Lys	Ile	Gly	Asp	Tyr	Val	Trp	
	625					630					635					
gaa	gat	gta	gat	aaa	gat	ggt	att	caa	aat	aca	aat	gat	aat	gaa	aaa	1967
Glu	Asp	Val	Asp	Lys	Asp	Gly	Ile	Gln	Asn	Thr	Asn	Asp	Asn	Glu	Lys	
	640				645					650					655	
ccg	ctt	agt	aat	gta	ttg	gta	act	ttg	acg	tat	cct	gat	gga	act	tca	2015
Pro	Leu	Ser	Asn	Val	Leu	Val	Thr	Leu	Thr	Tyr	Pro	Asp	Gly	Thr	Ser	
				660					665					670		
aaa	tca	gtc	aga	aca	gat	gaa	gag	ggg	aaa	tat	caa	ttt	gat	ggg	tta	2063
Lys	Ser	Val	Arg	Thr	Asp	Glu	Glu	Gly	Lys	Tyr	Gln	Phe	Asp	Gly	Leu	
			675					680					685			
aaa	aac	gga	ttg	act	tat	aaa	att	aca	ttc	gaa	aca	ccg	gaa	gga	tat	2111
Lys	Asn	Gly	Leu	Thr	Tyr	Lys	Ile	Thr	Phe	Glu	Thr	Pro	Glu	Gly	Tyr	
		690					695					700				
acg	ccg	acg	ctt	aaa	cat	tca	gga	aca	aat	cct	gca	cta	gac	tca	gaa	2159
Thr	Pro	Thr	Leu	Lys	His	Ser	Gly	Thr	Asn	Pro	Ala	Leu	Asp	Ser	Glu	
		705				710					715					
ggc	aat	tct	gta	tgg	gta	act	att	aac	gga	caa	gac	gat	atg	act	att	2207
Gly	Asn	Ser	Val	Trp	Val	Thr	Ile	Asn	Gly	Gln	Asp	Asp	Met	Thr	Ile	
	720				725					730				735		
gat	agc	gga	ttt	tat	caa	aca	cct	aaa	tat	agc	tta	ggg	aac	tat	gta	2255
Asp	Ser	Gly	Phe	Tyr	Gln	Thr	Pro	Lys	Tyr	Ser	Leu	Gly	Asn	Tyr	Val	
			740					745						750		
tgg	tat	gac	act	aat	aaa	gat	ggt	att	caa	ggt	gat	gat	gaa	aaa	gga	2303
Trp	Tyr	Asp	Thr	Asn	Lys	Asp	Gly	Ile	Gln	Gly	Asp	Asp	Glu	Lys	Gly	
			755					760						765		
atc	tct	gga	gta	aaa	gtg	acg	tta	aaa	gat	gaa	aac	gga	aat	atc	att	2351
Ile	Ser	Gly	Val	Lys	Val	Thr	Leu	Lys	Asp	Glu	Asn	Gly	Asn	Ile	Ile	
		770						775					780			
agt	aca	aca	aca	act	gat	gaa	aat	gga	aag	tat	caa	ttt	gat	aat	tta	2399
Ser	Thr	Thr	Thr	Thr	Asp	Glu	Asn	Gly	Lys	Tyr	Gln	Phe	Asp	Asn	Leu	
		785				790					795					
aat	agt	ggt	aat	tat	att	gtt	cat	ttt	gat	aaa	cct	tca	ggt	atg	act	2447
Asn	Ser	Gly	Asn	Tyr	Ile	Val	His	Phe	Asp	Lys	Pro	Ser	Gly	Met	Thr	
		800				805				810					815	
caa	aca	aca	aca	gat	tct	ggt	gat	gat	gac	gaa	cag	gat	gct	gat	ggg	2495
Gln	Thr	Thr	Thr	Asp	Ser	Gly	Asp	Asp	Asp	Glu	Gln	Asp	Ala	Asp	Gly	
				820					825					830		
gaa	gaa	gtc	cat	gta	aca	att	act	gat	cat	gat	gac	ttt	agt	ata	gat	2543
Glu	Glu	Val	His	Val	Thr	Ile	Thr	Asp	His	Asp	Asp	Phe	Ser	Ile	Asp	
			835					840					845			
aac	gga	tac	tat	gat	gac	gac	tca	gat	tca	gat	agt	gat	tca	gac	tca	2591
Asn	Gly	Tyr	Tyr	Asp	Asp	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	
		850						855					860			
gat	agc	gac	gac	tca	gac	tcc	gat	agc	gat	tcc	gac	tca	gac	agc	gac	2639
Asp	Ser	Asp	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	
		865				870						875				
tca	gat	tcc	gat	agt	gat	tca	gat	tca	gac	agt	gac	tca	gac	tca	gat	2687
Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	
		880			885					890					895	
agt	gat	tca	gat	tca	gac	agc	gat	tcc	gac	tca	gac	agt	gac	tca	gga	2735

-continued

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Gly	
	900 905 910
tta gac aat agc tca gat aag aat aca aaa gat aaa tta ccg gat aca	2783
Leu Asp Asn Ser Ser Asp Lys Asn Thr Lys Asp Lys Leu Pro Asp Thr	
	915 920 925
gga gct aat gaa gat cat gat tct aaa ggc aca tta ctt gga gct tta	2831
Gly Ala Asn Glu Asp His Asp Ser Lys Gly Thr Leu Leu Gly Ala Leu	
	930 935 940
ttt gca ggt tta gga gcg tta tta tta ggg aag cgt cgc aaa aat aga	2879
Phe Ala Gly Leu Gly Ala Leu Leu Leu Gly Lys Arg Arg Lys Asn Arg	
	945 950 955
aaa aat aaa aat taa att att caa atg aaa tta gtg aaa gaa gca gat	2927
Lys Asn Lys Asn Ile Ile Gln Met Lys Leu Val Lys Glu Ala Asp	
	960 965 970 975
acg aca ttt gaa tag aaa gta tat tta gtc caa caa ata taa ggt gtt g	2976
Thr Thr Phe Glu Lys Val Tyr Leu Val Gln Gln Ile Gly Val	
	980 985 990

<210> SEQ ID NO 8
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus epidermidis

<400> SEQUENCE: 8

Ile Ala Lys Lys Thr Tyr Ile Leu Tyr Cys Ile Leu Leu
 1 5 10

<210> SEQ ID NO 9
 <211> LENGTH: 18
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus epidermidis

<400> SEQUENCE: 9

Lys Arg Phe Leu Leu Glu Asn Tyr Ile Glu Ile Val Lys Asp Lys Glu
 1 5 10 15

Phe Leu

<210> SEQ ID NO 10
 <211> LENGTH: 930
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus epidermidis

<400> SEQUENCE: 10

Leu Lys Lys Asn Asn Leu Leu Thr Lys Lys Lys Pro Ile Ala Asn Lys
 1 5 10 15

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

Val Ile Gly Ala Ala Leu Leu Phe Gly Leu Gly His Asn Glu Ala Lys
 35 40 45

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

Glu Leu Ser Asp Ser Asn Asp Gln Ser Ser Asn Glu Glu Lys Asn Asp
 65 70 75 80

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

Lys Lys Glu Glu Thr Asn Ser Asn Asp Ala Ile Glu Asn Arg Ser Lys
 100 105 110

Asp Ile Thr Gln Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr Phe
 115 120 125

Leu Gln Lys Thr Pro Gln Asp Asn Thr Gln Leu Lys Glu Glu Val Val

-continued

130				135				140							
Lys	Glu	Pro	Ser	Ser	Val	Glu	Ser	Ser	Asn	Ser	Ser	Met	Asp	Thr	Ala
145				150				155							160
Gln	Gln	Pro	Ser	His	Thr	Thr	Ile	Asn	Ser	Glu	Ala	Ser	Ile	Gln	Thr
				165				170						175	
Ser	Asp	Asn	Glu	Asn	Ser	Arg	Val	Ser	Asp	Phe	Ala	Asn	Ser	Lys	
			180				185					190			
Ile	Ile	Glu	Ser	Asn	Thr	Glu	Ser	Asn	Lys	Glu	Glu	Asn	Thr	Ile	Glu
		195					200					205			
Gln	Pro	Asn	Lys	Val	Arg	Glu	Asp	Ser	Ile	Thr	Ser	Gln	Pro	Ser	Ser
		210				215					220				
Tyr	Lys	Asn	Ile	Asp	Glu	Lys	Ile	Ser	Asn	Gln	Asp	Glu	Leu	Leu	Asn
225				230				235							240
Leu	Pro	Ile	Asn	Glu	Tyr	Glu	Asn	Lys	Val	Arg	Pro	Leu	Ser	Thr	Thr
			245					250						255	
Ser	Ala	Gln	Pro	Ser	Ser	Lys	Arg	Val	Thr	Val	Asn	Gln	Leu	Ala	Ala
			260				265					270			
Glu	Gln	Gly	Ser	Asn	Val	Asn	His	Leu	Ile	Lys	Val	Thr	Asp	Gln	Ser
		275					280					285			
Ile	Thr	Glu	Gly	Tyr	Asp	Asp	Ser	Asp	Gly	Ile	Ile	Lys	Ala	His	Asp
		290			295						300				
Ala	Glu	Asn	Leu	Ile	Tyr	Asp	Val	Thr	Phe	Glu	Val	Asp	Asp	Lys	Val
305				310						315					320
Lys	Ser	Gly	Asp	Thr	Met	Thr	Val	Asn	Ile	Asp	Lys	Asn	Thr	Val	Pro
			325					330						335	
Ser	Asp	Leu	Thr	Asp	Ser	Phe	Ala	Ile	Pro	Lys	Ile	Lys	Asp	Asn	Ser
		340					345					350			
Gly	Glu	Ile	Ile	Ala	Thr	Gly	Thr	Tyr	Asp	Asn	Thr	Asn	Lys	Gln	Ile
		355					360					365			
Thr	Tyr	Thr	Phe	Thr	Asp	Tyr	Val	Asp	Lys	Tyr	Glu	Asn	Ile	Lys	Ala
		370				375					380				
His	Leu	Lys	Leu	Thr	Ser	Tyr	Ile	Asp	Lys	Ser	Lys	Val	Pro	Asn	Asn
385				390				395							400
Asn	Thr	Lys	Leu	Asp	Val	Glu	Tyr	Lys	Thr	Ala	Leu	Ser	Ser	Val	Asn
			405					410						415	
Lys	Thr	Ile	Thr	Val	Glu	Tyr	Gln	Lys	Pro	Asn	Glu	Asn	Arg	Thr	Ala
		420					425					430			
Asn	Leu	Gln	Ser	Met	Phe	Thr	Asn	Ile	Asp	Thr	Lys	Asn	His	Thr	Val
		435					440					445			
Glu	Gln	Thr	Ile	Tyr	Ile	Asn	Pro	Leu	Arg	Tyr	Ser	Ala	Lys	Glu	Thr
		450				455					460				
Asn	Val	Asn	Ile	Ser	Gly	Asn	Gly	Asp	Glu	Gly	Ser	Thr	Ile	Ile	Asp
465				470				475							480
Asp	Ser	Thr	Ile	Ile	Lys	Val	Tyr	Lys	Val	Gly	Asp	Asn	Gln	Asn	Leu
			485					490						495	
Pro	Asp	Ser	Asn	Arg	Ile	Tyr	Asp	Tyr	Ser	Glu	Tyr	Glu	Asp	Val	Thr
			500					505				510			
Asn	Asp	Asp	Tyr	Ala	Gln	Leu	Gly	Asn	Asn	Asn	Asp	Val	Asn	Ile	Asn
		515					520					525			
Phe	Gly	Asn	Ile	Asp	Ser	Pro	Tyr	Ile	Ile	Lys	Val	Ile	Ser	Lys	Tyr
	530					535					540				
Asp	Pro	Asn	Lys	Asp	Asp	Tyr	Thr	Thr	Ile	Gln	Gln	Thr	Val	Thr	Met
545				550						555					560

-continued

Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr Ala Ser Tyr
 565 570 575
 Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly Gln Gly Asp
 580 585 590
 Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val Trp Glu Asp
 595 600 605
 Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu Lys Pro Leu
 610 615 620
 Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr Ser Lys Ser
 625 630 635 640
 Val Arg Thr Asp Glu Glu Gly Lys Tyr Gln Phe Asp Gly Leu Lys Asn
 645 650 655
 Gly Leu Thr Tyr Lys Ile Thr Phe Glu Thr Pro Glu Gly Tyr Thr Pro
 660 665 670
 Thr Leu Lys His Ser Gly Thr Asn Pro Ala Leu Asp Ser Glu Gly Asn
 675 680 685
 Ser Val Trp Val Thr Ile Asn Gly Gln Asp Asp Met Thr Ile Asp Ser
 690 695 700
 Gly Phe Tyr Gln Thr Pro Lys Tyr Ser Leu Gly Asn Tyr Val Trp Tyr
 705 710 715 720
 Asp Thr Asn Lys Asp Gly Ile Gln Gly Asp Asp Glu Lys Gly Ile Ser
 725 730 735
 Gly Val Lys Val Thr Leu Lys Asp Glu Asn Gly Asn Ile Ile Ser Thr
 740 745 750
 Thr Thr Thr Asp Glu Asn Gly Lys Tyr Gln Phe Asp Asn Leu Asn Ser
 755 760 765
 Gly Asn Tyr Ile Val His Phe Asp Lys Pro Ser Gly Met Thr Gln Thr
 770 775 780
 Thr Thr Asp Ser Gly Asp Asp Asp Glu Gln Asp Ala Asp Gly Glu Glu
 785 790 795 800
 Val His Val Thr Ile Thr Asp His Asp Asp Phe Ser Ile Asp Asn Gly
 805 810 815
 Tyr Tyr Asp Asp Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 820 825 830
 Asp Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 835 840 845
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 850 855 860
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Gly Leu Asp
 865 870 875 880
 Asn Ser Ser Asp Lys Asn Thr Lys Asp Lys Leu Pro Asp Thr Gly Ala
 885 890 895
 Asn Glu Asp His Asp Ser Lys Gly Thr Leu Leu Gly Ala Leu Phe Ala
 900 905 910
 Gly Leu Gly Ala Leu Leu Leu Gly Lys Arg Arg Lys Asn Arg Lys Asn
 915 920 925
 Lys Asn
 930

<210> SEQ ID NO 11

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Staphylococcus epidermidis

<400> SEQUENCE: 11

-continued

Ile Ile Gln Met Lys Leu Val Lys Glu Ala Asp Thr Thr Phe Glu
1 5 10 15

<210> SEQ ID NO 12
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus epidermidis

<400> SEQUENCE: 12

Lys Val Tyr Leu Val Gln Gln Ile
1 5

<210> SEQ ID NO 13
<211> LENGTH: 1464
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus epidermidis
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1464)

<400> SEQUENCE: 13

atg aaa aag ttt aac att aaa cat tca ttt atg ctt acg ggc ttt gct 48
Met Lys Lys Phe Asn Ile Lys His Ser Phe Met Leu Thr Gly Phe Ala
1 5 10 15

ttc atg gta act aca tca tta ttc agt cac caa gca cat gct gaa ggt 96
Phe Met Val Thr Ser Leu Phe Ser His Gln Ala His Ala Glu Gly
20 25 30

aat cat cct att gac att aat ttt tct aaa gat caa att gat aga aat 144
Asn His Pro Ile Asp Ile Asn Phe Ser Lys Asp Gln Ile Asp Arg Asn
35 40 45

aca gct aag agc aat att atc aat cga gtg aat gac act agt cgc aca 192
Thr Ala Lys Ser Asn Ile Ile Asn Arg Val Asn Asp Thr Ser Arg Thr
50 55 60

gga att agt atg aat tcg gat aat gat tta gat aca gat atc gtt tca 240
Gly Ile Ser Met Asn Ser Asp Asn Asp Leu Asp Thr Asp Ile Val Ser
65 70 75 80

aat agt gac tca gaa aat gac aca tat tta gat agt gat tca gat tca 288
Asn Ser Asp Ser Glu Asn Asp Thr Tyr Leu Asp Ser Asp Ser Asp Ser
85 90 95

gac agt gac tca gat tca gat agt gac tca gat tca gat agt gac tca 336
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
100 105 110

gat tca gat agt gac tca gat tca gac agt gat tca gac tca gat agt 384
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
115 120 125

gac tca gat tca gac agt gat tca gac tca gat agt gat tca gat tca 432
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
130 135 140

gac agt gat tca gat tca gac agt gac tca gac tca gac agt gat tca 480
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
145 150 155 160

gat tca gat agt gat tca gat tca gat agt gat tca gat tca gat agt 528
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
165 170 175

gat tca gat tca gac agt gac tca gac tca gac agt gat tca gat tca 576
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
180 185 190

gat agt gat tca gac tca gat agt gac tca gat tca gat agt gat tca 624
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
195 200 205

gac tct ggt aca agt tca ggt aag ggt tca cat acc gga aaa aaa cct 672
Asp Ser Gly Thr Ser Ser Gly Lys Gly Ser His Thr Gly Lys Lys Pro
210 215 220

-continued

```

ggt aac cct aaa gga aat aca aat aga cct tct caa aga cat acg aat      720
Gly Asn Pro Lys Gly Asn Thr Asn Arg Pro Ser Gln Arg His Thr Asn
225                230                235                240

caa ccc caa agg cct aaa tac aat caa aca aat caa aac aat ata aac      768
Gln Pro Gln Arg Pro Lys Tyr Asn Gln Thr Asn Gln Asn Asn Ile Asn
                245                250                255

aat ata aac cat aat att aat cat aca cgt act agt gga gat ggt gcg      816
Asn Ile Asn His Asn Ile Asn His Thr Arg Thr Ser Gly Asp Gly Ala
                260                265                270

cct ttt aaa cgt caa caa aat att att aat tct aat tca ggt cat aga      864
Pro Phe Lys Arg Gln Gln Asn Ile Ile Asn Ser Asn Ser Gly His Arg
275                280                285

aat caa aat aat ata aat caa ttt ata tgg aac aaa aat ggc ttt ttt      912
Asn Gln Asn Asn Ile Asn Gln Phe Ile Trp Asn Lys Asn Gly Phe Phe
290                295                300

aaa tct caa aat aat acc gaa cat aga atg aat agt agc gat aat acc      960
Lys Ser Gln Asn Asn Thr Glu His Arg Met Asn Ser Ser Asp Asn Thr
305                310                315                320

aat tca tta att agc aga ttc aga caa tta gcc acg ggt gct tat aag      1008
Asn Ser Leu Ile Ser Arg Phe Arg Gln Leu Ala Thr Gly Ala Tyr Lys
325                330                335

tac aat ccg ttt ttg att aat caa gta aaa aat ttg aat caa tta gat      1056
Tyr Asn Pro Phe Leu Ile Asn Gln Val Lys Asn Leu Asn Gln Leu Asp
340                345                350

gga aag gtg aca gat agt gac att tat agc ttg ttt aga aag caa tca      1104
Gly Lys Val Thr Asp Ser Asp Ile Tyr Ser Leu Phe Arg Lys Gln Ser
355                360                365

ttt aga gga aat gaa tat tta aat tca tta caa aaa ggg aca agc tat      1152
Phe Arg Gly Asn Glu Tyr Leu Asn Ser Leu Gln Lys Gly Thr Ser Tyr
370                375                380

ttc aga ttt caa tat ttt aat cca ctt aat tct agt aaa tac tat gaa      1200
Phe Arg Phe Gln Tyr Phe Asn Pro Leu Asn Ser Ser Lys Tyr Tyr Glu
385                390                395                400

aat tta gat gat cag gtt tta gct tta att aca gga gaa atc ggc tca      1248
Asn Leu Asp Asp Gln Val Leu Ala Leu Ile Thr Gly Glu Ile Gly Ser
405                410                415

atg cca gaa ctt aaa aaa cct acg gat aaa gaa gat aaa aat cat agc      1296
Met Pro Glu Leu Lys Lys Pro Thr Asp Lys Glu Asp Lys Asn His Ser
420                425                430

gcc ttc aaa aac cat agt gca gat gag ata aca aca aat aat gat gga      1344
Ala Phe Lys Asn His Ser Ala Asp Glu Ile Thr Thr Asn Asn Asp Gly
435                440                445

cac tcc aaa gat tat gat aag aaa aag aaa ata cat cga agt ctt tta      1392
His Ser Lys Asp Tyr Asp Lys Lys Lys Lys Ile His Arg Ser Leu Leu
450                455                460

tcg tta agt att gca ata att gga att ttt cta gga gtc act gga cta      1440
Ser Leu Ser Ile Ala Ile Ile Gly Ile Phe Leu Gly Val Thr Gly Leu
465                470                475

tat atc ttt aga aga aaa aag taa
Tyr Ile Phe Arg Arg Lys Lys
485

```

```

<210> SEQ ID NO 14
<211> LENGTH: 487
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus epidermidis

```

<400> SEQUENCE: 14

```

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

```


-continued

Phe	Met	Val	Thr	Thr	Ser	Leu	Phe	Ser	His	Gln	Ala	His	Ala	Glu	Gly
			20					25					30		
Asn	His	Pro	Ile	Asp	Ile	Asn	Phe	Ser	Lys	Asp	Gln	Ile	Asp	Arg	Asn
		35					40					45			
Thr	Ala	Lys	Ser	Asn	Ile	Ile	Asn	Arg	Val	Asn	Asp	Thr	Ser	Arg	Thr
	50					55					60				
Gly	Ile	Ser	Met	Asn	Ser	Asp	Asn	Asp	Leu	Asp	Thr	Asp	Ile	Val	Ser
65					70					75					80
Asn	Ser	Asp	Ser	Glu	Asn	Asp	Thr	Tyr	Leu	Asp	Ser	Asp	Ser	Asp	Ser
				85					90						95
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
			100					105					110		
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
			115					120				125			
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
			130					135				140			
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
145					150					155					160
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
				165					170						175
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
			180					185					190		
Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
			195					200					205		
Asp	Ser	Gly	Thr	Ser	Ser	Gly	Lys	Gly	Ser	His	Thr	Gly	Lys	Lys	Pro
	210					215						220			
Gly	Asn	Pro	Lys	Gly	Asn	Thr	Asn	Arg	Pro	Ser	Gln	Arg	His	Thr	Asn
225					230					235					240
Gln	Pro	Gln	Arg	Pro	Lys	Tyr	Asn	Gln	Thr	Asn	Gln	Asn	Asn	Ile	Asn
				245						250					255
Asn	Ile	Asn	His	Asn	Ile	Asn	His	Thr	Arg	Thr	Ser	Gly	Asp	Gly	Ala
			260					265						270	
Pro	Phe	Lys	Arg	Gln	Gln	Asn	Ile	Ile	Asn	Ser	Asn	Ser	Gly	His	Arg
		275						280					285		
Asn	Gln	Asn	Asn	Ile	Asn	Gln	Phe	Ile	Trp	Asn	Lys	Asn	Gly	Phe	Phe
	290					295					300				
Lys	Ser	Gln	Asn	Asn	Thr	Glu	His	Arg	Met	Asn	Ser	Ser	Asp	Asn	Thr
305					310					315					320
Asn	Ser	Leu	Ile	Ser	Arg	Phe	Arg	Gln	Leu	Ala	Thr	Gly	Ala	Tyr	Lys
				325					330						335
Tyr	Asn	Pro	Phe	Leu	Ile	Asn	Gln	Val	Lys	Asn	Leu	Asn	Gln	Leu	Asp
			340						345					350	
Gly	Lys	Val	Thr	Asp	Ser	Asp	Ile	Tyr	Ser	Leu	Phe	Arg	Lys	Gln	Ser
		355						360					365		
Phe	Arg	Gly	Asn	Glu	Tyr	Leu	Asn	Ser	Leu	Gln	Lys	Gly	Thr	Ser	Tyr
	370					375						380			
Phe	Arg	Phe	Gln	Tyr	Phe	Asn	Pro	Leu	Asn	Ser	Ser	Lys	Tyr	Tyr	Glu
385					390					395					400
Asn	Leu	Asp	Asp	Gln	Val	Leu	Ala	Leu	Ile	Thr	Gly	Glu	Ile	Gly	Ser
				405						410					415
Met	Pro	Glu	Leu	Lys	Lys	Pro	Thr	Asp	Lys	Glu	Asp	Lys	Asn	His	Ser
			420						425					430	
Ala	Phe	Lys	Asn	His	Ser	Ala	Asp	Glu	Ile	Thr	Thr	Asn	Asn	Asp	Gly
		435						440							445

-continued

His Ser Lys Asp Tyr Asp Lys Lys Lys Lys Ile His Arg Ser Leu Leu
 450 455 460

Ser Leu Ser Ile Ala Ile Ile Gly Ile Phe Leu Gly Val Thr Gly Leu
 465 470 475 480

Tyr Ile Phe Arg Arg Lys Lys
 485

<210> SEQ ID NO 15
 <211> LENGTH: 18
 <212> TYPE: DNA
 <213> ORGANISM: Staphylococcus aureus
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (6) and (12)
 <223> OTHER INFORMATION: n = (a or c or g or t)

<400> SEQUENCE: 15

gaytcngayt cngayagy

18

<210> SEQ ID NO 16
 <211> LENGTH: 5
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 16

Leu Pro Asp Thr Gly
 1 5

<210> SEQ ID NO 17
 <211> LENGTH: 9
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 17

Thr Tyr Thr Phe Thr Asp Tyr Val Asp
 1 5

<210> SEQ ID NO 18
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 18

Thr Asn Ser His Gln Asp
 1 5

<210> SEQ ID NO 19
 <211> LENGTH: 3498
 <212> TYPE: DNA
 <213> ORGANISM: Staphylococcus aureus
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (301)..(3099)

<400> SEQUENCE: 19

ggtaccataa attacacatc tgcttttgaa aaaatatgat ttcaagctag gattacatta 60

ggtagagttc atattaataa taaaaaatgt ttgcaatcaa atcgtaagtt gtcgtttgta 120

attcttaaaa tagcaataaa taaaatgttt gttagtaaag tattattgtg gataataaaa 180

tatcgataca aattaattgc tataatgcaa ttttagtgta taattccatt aacagagatt 240

aaatatact taaagggtat atagttaata taaaatgact ttttaaaaag agggaataaa 300

atg aat atg aag aaa aaa gaa aaa cac gca att cgg aaa aaa tcg att 348
 Met Asn Met Lys Lys Lys Glu Lys His Ala Ile Arg Lys Lys Ser Ile

-continued

1	5	10	15	
ggc gtg gct tca gtg ctt gta ggt acg tta atc ggt ttt gga cta ctc				396
Gly Val Ala Ser Val Leu Val Gly Thr Leu Ile Gly Phe Gly Leu Leu	20	25	30	
agc agt aaa gaa gca gat gca agt gaa aat agt gtt acg caa tct gat				444
Ser Ser Lys Glu Ala Asp Ala Ser Glu Asn Ser Val Thr Gln Ser Asp	35	40	45	
agc gca agt aac gaa agc aaa agt aat gat tca agt agc gtt agt gct				492
Ser Ala Ser Asn Glu Ser Lys Ser Asn Asp Ser Ser Ser Val Ser Ala	50	55	60	
gca cct aaa aca gac gac aca aac gtg agt gat act aaa aca tcg tca				540
Ala Pro Lys Thr Asp Asp Thr Asn Val Ser Asp Thr Lys Thr Ser Ser	65	70	75	80
aac act aat aat ggc gaa acg agt gtg gcg caa aat cca gca caa cag				588
Asn Thr Asn Asn Gly Glu Thr Ser Val Ala Gln Asn Pro Ala Gln Gln	85	90	95	
gaa acg aca caa tca tca tca aca aat gca act acg gaa gaa acg ccg				636
Glu Thr Thr Gln Ser Ser Ser Thr Asn Ala Thr Thr Glu Glu Thr Pro	100	105	110	
gta act ggt gaa gct act act acg aca acg aat caa gct aat aca ccg				684
Val Thr Gly Glu Ala Thr Thr Thr Thr Asn Gln Ala Asn Thr Pro	115	120	125	
gca aca act caa tca agc aat aca aat gcg gag gaa tta gtg aat caa				732
Ala Thr Thr Gln Ser Ser Asn Thr Asn Ala Glu Glu Leu Val Asn Gln	130	135	140	
aca agt aat gaa acg act ttt aat gat act aat aca gta tca tct gta				780
Thr Ser Asn Glu Thr Thr Phe Asn Asp Thr Asn Thr Val Ser Ser Val	145	150	155	160
aat tca cct caa aat tct aca aat gcg gaa aat gtt tca aca acg caa				828
Asn Ser Pro Gln Asn Ser Thr Asn Ala Glu Asn Val Ser Thr Thr Gln	165	170	175	
gat act tca act gaa gca aca cct tca aac aat gaa tca gct cca cag				876
Asp Thr Ser Thr Glu Ala Thr Pro Ser Asn Asn Glu Ser Ala Pro Gln	180	185	190	
agt aca gat gca agt aat aaa gat gta gtt aat caa gcg gtt aat aca				924
Ser Thr Asp Ala Ser Asn Lys Asp Val Val Asn Gln Ala Val Asn Thr	195	200	205	
agt gcg cct aga atg aga gca ttt agt tta gcg gca gta gct gca gat				972
Ser Ala Pro Arg Met Arg Ala Phe Ser Leu Ala Ala Val Ala Ala Asp	210	215	220	
gca ccg gca gct ggc aca gat att acg aat cag ttg acg aat gtg aca				1020
Ala Pro Ala Ala Gly Thr Asp Ile Thr Asn Gln Leu Thr Asn Val Thr	225	230	235	240
gtt ggt att gac tct ggt acg act gtg tat ccg cac caa gca ggt tat				1068
Val Gly Ile Asp Ser Gly Thr Thr Val Tyr Pro His Gln Ala Gly Tyr	245	250	255	
gtc aaa ctg aat tat ggt ttt tca gtg cct aat tct gct gtt aaa ggt				1116
Val Lys Leu Asn Tyr Gly Phe Ser Val Pro Asn Ser Ala Val Lys Gly	260	265	270	
gac aca ttc aaa ata act gta cct aaa gaa tta aac tta aat ggt gta				1164
Asp Thr Phe Lys Ile Thr Val Pro Lys Glu Leu Asn Leu Asn Gly Val	275	280	285	
act tca act gct aaa gtg cca cca att atg gct gga gat caa gta ttg				1212
Thr Ser Thr Ala Lys Val Pro Pro Ile Met Ala Gly Asp Gln Val Leu	290	295	300	
gca aat ggt gta atc gat agt gat ggt aat gtt att tat aca ttt aca				1260
Ala Asn Gly Val Ile Asp Ser Asp Gly Asn Val Ile Tyr Thr Phe Thr	305	310	315	320
gac tat gta aat act aaa gat gat gta aaa gca act ttg acc atg ccc				1308
Asp Tyr Val Asn Thr Lys Asp Asp Val Lys Ala Thr Leu Thr Met Pro				

-continued

645		650		655				
tca gat	tca gat	agc gat	tca gat	tca gat	agc gat	tca gat	tcc gac	2316
Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	
	660		665		670			
agt gat	tcc gac	tca gac	agc gat	tct gac	tcc gac	agt gat	tcc gac	2364
Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	
	675		680		685			
tca gac	agc gat	tca gat	tcc gac	agt gat	tcc gac	tca gat	agc gat	2412
Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	
	690		695		700			
tcc gac	tca gat	agc gac	tca gat	tca gac	agc gat	tca gat	tca gac	2460
Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	
705		710		715		720		
agc gat	tca gat	tca gat	agc gat	tca gat	tcc gac	agt gac	tca gat	2508
Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	
	725		730		735			
tcc gac	agt gac	tcg gat	tca gat	agc gat	tca gat	tcc gac	agt gac	2556
Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	
	740		745		750			
tca gat	tcc gac	agt gac	tca gac	tca gac	agt gat	tcg gat	tca gac	2604
Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Ala	
	755		760		765			
agt gat	tcg gat	tca gat	agt gat	tcc gac	tcc gac	agt gac	tcg gat	2652
Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	
770		775		780				
tca gat	agc gac	tca gac	tcg gat	agc gac	tcg gat	tca gat	agc gat	2700
Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	
785		790		795		800		
tcg gac	tca gat	agc gat	tca gaa	tca gac	agc gat	tca gaa	tca gac	2748
Ser Asp	Ser Asp	Ser Asp	Ser Glu	Ser Asp	Ser Asp	Ser Glu	Ser Asp	
	805		810		815			
agc gat	tca gat	tca gac	agc gac	tca gac	agt gac	tca gat	tca gat	2796
Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	Ser Asp	
	820		825		830			
agt gac	tcg gat	tca gac	agt gat	tca gac	tca ggt	agt gac	tcc gat	2844
Ser Asp	Ser Asp	Ser Ala	Ser Asp	Ser Asp	Ser Gly	Ser Asp	Ser Asp	
	835		840		845			
tca tca	agt gat	tcc gac	tca gaa	agt gat	tca aat	agc gat	tcc gag	2892
Ser Ser	Ser Asp	Ser Asp	Ser Glu	Ser Asp	Ser Asn	Ser Asp	Ser Glu	
850		855		860				
tca ggt	tct aac	aat aat	gta gtt	ccg cct	aat tca	cct aaa	aat ggt	2940
Ser Gly	Ser Asn	Asn Asn	Val Val	Pro Pro	Asn Ser	Pro Lys	Asn Gly	
865		870		875		880		
act aat	gct tct	aat aaa	aat gag	gct aaa	gat agt	aaa gaa	cca tta	2988
Thr Asn	Ala Ser	Asn Lys	Asn Glu	Ala Lys	Asp Ser	Lys Glu	Pro Leu	
	885		890		895			
cca gat	aca ggt	tct gaa	gat gaa	gca aat	acg tca	cta att	tgg gga	3036
Pro Asp	Thr Gly	Ser Glu	Asp Glu	Ala Asn	Thr Ser	Leu Ile	Trp Gly	
	900		905		910			
tta tta	gca tca	ata ggt	tca tta	cta ctt	ttc aga	aga aaa	aaa gaa	3084
Leu Leu	Ala Ser	Ile Gly	Ser Leu	Leu Leu	Phe Arg	Arg Lys	Lys Glu	
	915		920		925			
aat aaa	gat aag	aaa taagtaataa	tgatattaaa	ttaatcatat	gattcatgaa			3139
Asn Lys	Asp Lys	Lys Lys						
930								
gaagccacct	taaaagggtgc	ttcttttact	tggattttcc	aaatatattg	tttgaatata			3199
attaataatt	aattcatcaa	cagttaatta	ttttaaaag	gtagatgtta	tataatttgg			3259
cttgccgaaa	aaatagggtg	taaggtaggt	tgtaattag	ggaaaattaa	ggagaaaata			3319

-continued

```

cagttgaaaa ataaattgct agttttatca ttgggagcat tatgtgtatc acaaatttgg 3379
gaaagtaatc gtgcgagtgct agtgggttct ggggagaaga atccatatgt atctgagtcg 3439
ttgaaactga ctaataataa aaataaatct agaacagtag aagagtataa gaaaagctt 3498

```

```

<210> SEQ ID NO 20
<211> LENGTH: 933
<212> TYPE: PRT
<213> ORGANISM: Staphylococcus aureus

```

```

<400> SEQUENCE: 20

```

```

Met Asn Met Lys Lys Lys Glu Lys His Ala Ile Arg Lys Lys Ser Ile
 1                               10 15
Gly Val Ala Ser Val Leu Val Gly Thr Leu Ile Gly Phe Gly Leu Leu
 20 25 30
Ser Ser Lys Glu Ala Asp Ala Ser Glu Asn Ser Val Thr Gln Ser Asp
 35 40 45
Ser Ala Ser Asn Glu Ser Lys Ser Asn Asp Ser Ser Val Ser Ala
 50 55 60
Ala Pro Lys Thr Asp Asp Thr Asn Val Ser Asp Thr Lys Thr Ser Ser
 65 70 75 80
Asn Thr Asn Asn Gly Glu Thr Ser Val Ala Gln Asn Pro Ala Gln Gln
 85 90 95
Glu Thr Thr Gln Ser Ser Ser Thr Asn Ala Thr Thr Glu Glu Thr Pro
 100 105 110
Val Thr Gly Glu Ala Thr Thr Thr Thr Asn Gln Ala Asn Thr Pro
 115 120 125
Ala Thr Thr Gln Ser Ser Asn Thr Asn Ala Glu Glu Leu Val Asn Gln
 130 135 140
Thr Ser Asn Glu Thr Thr Phe Asn Asp Thr Asn Thr Val Ser Ser Val
 145 150 155 160
Asn Ser Pro Gln Asn Ser Thr Asn Ala Glu Asn Val Ser Thr Thr Gln
 165 170 175
Asp Thr Ser Thr Glu Ala Thr Pro Ser Asn Asn Glu Ser Ala Pro Gln
 180 185 190
Ser Thr Asp Ala Ser Asn Lys Asp Val Val Asn Gln Ala Val Asn Thr
 195 200 205
Ser Ala Pro Arg Met Arg Ala Phe Ser Leu Ala Ala Val Ala Ala Asp
 210 215 220
Ala Pro Ala Ala Gly Thr Asp Ile Thr Asn Gln Leu Thr Asn Val Thr
 225 230 235 240
Val Gly Ile Asp Ser Gly Thr Thr Val Tyr Pro His Gln Ala Gly Tyr
 245 250 255
Val Lys Leu Asn Tyr Gly Phe Ser Val Pro Asn Ser Ala Val Lys Gly
 260 265 270
Asp Thr Phe Lys Ile Thr Val Pro Lys Glu Leu Asn Leu Asn Gly Val
 275 280 285
Thr Ser Thr Ala Lys Val Pro Pro Ile Met Ala Gly Asp Gln Val Leu
 290 295 300
Ala Asn Gly Val Ile Asp Ser Asp Gly Asn Val Ile Tyr Thr Phe Thr
 305 310 315 320
Asp Tyr Val Asn Thr Lys Asp Asp Val Lys Ala Thr Leu Thr Met Pro
 325 330 335
Ala Tyr Ile Asp Pro Glu Asn Val Lys Lys Thr Gly Asn Val Thr Leu
 340 345 350

```

-continued

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

-continued

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 785 790 795 800
 Ser Asp Ser Asp Ser Asp Ser Glu Ser Asp Ser Asp Ser Glu Ser Asp
 805 810 815
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 820 825 830
 Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Gly Ser Asp Ser Asp
 835 840 845
 Ser Ser Ser Asp Ser Asp Ser Glu Ser Asp Ser Asn Ser Asp Ser Glu
 850 855 860
 Ser Gly Ser Asn Asn Asn Val Val Pro Pro Asn Ser Pro Lys Asn Gly
 865 870 875 880
 Thr Asn Ala Ser Asn Lys Asn Glu Ala Lys Asp Ser Lys Glu Pro Leu
 885 890 895
 Pro Asp Thr Gly Ser Glu Asp Glu Ala Asn Thr Ser Leu Ile Trp Gly
 900 905 910
 Leu Leu Ala Ser Ile Gly Ser Leu Leu Leu Phe Arg Arg Lys Lys Glu
 915 920 925
 Asn Lys Asp Lys Lys
 930

<210> SEQ ID NO 21
 <211> LENGTH: 918
 <212> TYPE: PRT
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 21

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

-continued

Thr Ala Ser Asn Phe Lys Leu Glu Lys Thr Thr Phe Asp Pro Asn Gln
 225 230 235 240
 Ser Gly Asn Thr Phe Met Ala Ala Asn Phe Thr Val Thr Asp Lys Val
 245 250 255
 Lys Ser Gly Asp Tyr Phe Thr Ala Lys Leu Pro Asp Ser Leu Thr Gly
 260 265 270
 Asn Gly Asp Val Asp Tyr Ser Asn Ser Asn Asn Thr Met Pro Ile Ala
 275 280 285
 Asp Ile Lys Ser Thr Asn Gly Asp Val Val Ala Lys Ala Thr Tyr Asp
 290 295 300
 Ile Leu Thr Lys Thr Tyr Thr Phe Val Phe Thr Asp Tyr Val Asn Asn
 305 310 315 320
 Lys Glu Asn Ile Asn Gly Gln Phe Ser Leu Pro Leu Phe Thr Asp Arg
 325 330 335
 Ala Lys Ala Pro Lys Ser Gly Thr Tyr Asp Ala Asn Ile Asn Ile Ala
 340 345 350
 Asp Glu Met Phe Asn Asn Lys Ile Thr Tyr Asn Tyr Ser Ser Pro Ile
 355 360 365
 Ala Gly Ile Asp Lys Pro Asn Gly Ala Asn Ile Ser Ser Gln Ile Ile
 370 375 380
 Gly Val Asp Thr Ala Ser Gly Gln Asn Thr Tyr Lys Gln Thr Val Phe
 385 390 395 400
 Val Asn Pro Lys Gln Arg Val Leu Gly Asn Thr Trp Val Tyr Ile Lys
 405 410 415
 Gly Tyr Gln Asp Lys Ile Glu Glu Ser Ser Gly Lys Val Ser Ala Thr
 420 425 430
 Asp Thr Lys Leu Arg Ile Phe Glu Val Asn Asp Thr Ser Lys Leu Ser
 435 440 445
 Asp Ser Tyr Tyr Ala Asp Pro Asn Asp Ser Asn Leu Lys Glu Val Thr
 450 455 460
 Asp Gln Phe Lys Asn Arg Ile Tyr Tyr Glu His Pro Asn Val Ala Ser
 465 470 475 480
 Ile Lys Phe Gly Asp Ile Thr Lys Thr Tyr Val Val Leu Val Glu Gly
 485 490 495
 His Tyr Asp Asn Thr Gly Lys Asn Leu Lys Thr Gln Val Ile Gln Glu
 500 505 510
 Asn Val Asp Pro Val Thr Asn Arg Asp Tyr Ser Ile Phe Gly Trp Asn
 515 520 525
 Asn Glu Asn Val Val Arg Tyr Gly Gly Gly Ser Ala Asp Gly Asp Ser
 530 535 540
 Ala Val Asn Pro Lys Asp Pro Thr Pro Gly Pro Pro Val Asp Pro Glu
 545 550 555 560
 Pro Ser Pro Asp Pro Glu Pro Glu Pro Thr Pro Asp Pro Glu Pro Ser
 565 570 575
 Pro Asp Pro Glu Pro Glu Pro Ser Pro Asp Pro Asp Pro Asp Ser Asp
 580 585 590
 Ser Asp Ser Asp Ser Gly Ser Asp Ser Asp Ser Gly Ser Asp Ser Asp
 595 600 605
 Ser Glu Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp
 610 615 620
 Ser Asp Ser Glu Ser Asp Ser Asp Ser Glu Ser Asp Ser Asp Ser Asp
 625 630 635 640
 Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp

-continued

	645		650		655
Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Glu Ser Asp	660		665		670
Ser Asp Ser Glu Ser Asp Ser Glu Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp	675		680		685
Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp	690		695		700
Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp	705		710		715
Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp	725		730		735
Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp	740		745		750
Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp	755		760		765
Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp	770		775		780
Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp	785		790		795
Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp	805		810		815
Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp	820		825		830
Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Arg Val Thr	835		840		845
Pro Pro Asn Asn Glu Gln Lys Ala Pro Ser Asn Pro Lys Gly Glu Val	850		855		860
Asn His Ser Asn Lys Val Ser Lys Gln His Lys Thr Asp Ala Leu Pro	865		870		875
Glu Thr Gly Asp Lys Ser Glu Asn Thr Asn Ala Thr Leu Phe Gly Ala	885		890		895
Met Met Ala Leu Leu Gly Ser Leu Leu Leu Phe Arg Lys Arg Lys Gln	900		905		910
Asp His Lys Glu Lys Ala	915				

<210> SEQ ID NO 22
 <211> LENGTH: 2969
 <212> TYPE: DNA
 <213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 22

tagaaattga aatggagtaa tatttttgaa aaaaagaatt gattatttgt cgaataagca	60
gaataagtat tcgattagac gttttacagt aggtaccaca tcagtaatag taggggcaac	120
tatactatattt gggataggca atcatcaagc acaagcttca gaacaatcga acgataacaac	180
gcaatccttcg aaaataatg caagtcgaga ttccgaaaaa aacaatatga tagaaacacc	240
tcaattaaat acaacggcta atgatacatc tgatattagt gcaaacacaa acagtgcgaa	300
tgtagatagc acaacaaaac caatgtctac acaaacgagc aataaccacta caacagagcc	360
agcttcaaca aatgaaacac ctcaaccgac ggcaatataa aatcaagcaa ctgctgcaaa	420
aatgcaagat caaactgttc ctcaagaagg aaattctcaa gtagataata aaacaacgaa	480
tgatgctaata agcatagcaa caaacagtga gcttaaaaaa tctcaaacat tagatttacc	540
acaatcatca ccacaaaaga tttccaatgc gcaaggaact agtaaacc aa gtgttagaac	600

-continued

gagagctgta	cgtagttag	ctgttctga	accggtagta	aatgctgctg	atgctaaagg	660
tacaaatgta	aatgataaag	ttacggcaag	taatttcaag	ttagaaaaga	ctacatttga	720
ccctaatcaa	agtggttaaca	catttatggc	ggcaaat	acagtgcag	ataaagtga	780
atcaggggat	tattttacag	cgaagttacc	agatagtta	actggtaatg	gagacgtgga	840
ttatttcaat	tcaataata	cgatgccaat	tcgacagatt	aaaagtcga	atggcgtgt	900
tgtagctaaa	gcaacatatg	atatcttgac	taagacgtat	acatttgtct	ttacagatta	960
tgtaaataat	aaagaaaata	ttaacggaca	attttcatta	cctttattta	cagaccgagc	1020
aaaggcacct	aatcaggaa	catatgatgc	gaatattaat	attgctgatg	aaatgtttaa	1080
taataaaatt	acttataact	atagttgcc	aattgcagga	attgataaac	caaatggcgc	1140
gaacatttct	tctcaaat	ttgggttaga	tacagcttca	ggcacaaca	catacaagca	1200
aacagtattt	gttaacccta	agcaacgagt	ttaggtaat	acgtgggtgt	atattaag	1260
ctaccaagat	aaaatcgaag	aaagtgcgg	taaagtaagt	gctacagata	caaaactgag	1320
aatttttgaa	gtgaatgata	catctaaatt	atcagatagc	tactatgcag	atccaaatga	1380
ctctaacctt	aaagaagtaa	cagaccaatt	taaaaataga	atctattatg	agcatccaaa	1440
tgtagctagt	attaaatttg	gtgatattac	taaaacatat	gtagtattag	tagaagggca	1500
ttacgacaat	acaggtaaga	acttaaaaac	tcaggttatt	caagaaatg	ttgatcctgt	1560
aacaaataga	gactacagta	ttttcggttg	gaataatgag	aatgttgtag	gttatgggtg	1620
tggaaagtct	gatggtgatt	cagcagtaaa	tccgaaagac	ccaactccag	ggccgccggt	1680
tgaccagaa	ccaagtccag	accagaacc	agaaccaacg	ccagatccag	aaccaagtcc	1740
agaccagaa	ccggaaccaa	gccagacc	ggatccgat	tcggattcag	acagtgactc	1800
aggctcagac	agcagctcag	gttcagatag	cgactcagaa	tcagatagcg	attcggattc	1860
agacagtgat	tcagattcag	acagcgactc	agaatcagat	agcgattcag	aatcagatag	1920
cgactcagat	tcagatagcg	attcagattc	agatagcgat	tcagattcag	atagcgattc	1980
ggattcagac	agtgattcag	attcagacag	cgactcagaa	tcagatagcg	actcagaatc	2040
agatagttag	tcagattcag	acagtgactc	ggactcagac	agtgattcag	actcagatag	2100
cgattcagac	tcagatagcg	attcagattc	agacagcgac	tcagattcag	acagcgactc	2160
agactcagat	agcagctcag	actcagacag	cgactcagat	tcagatagcg	attcagactc	2220
agacagcgac	tcagactcag	acagcgactc	agactcagat	agcagctcag	attcagatag	2280
cgattcagac	tcagacagcg	actcagattc	agatagcgat	tcggactcag	acagcgattc	2340
agattcagac	agcagctcag	actcggatag	cgattcagat	tcagatagcg	attcggattc	2400
agacagtgat	tcagattcag	acagcgactc	agactcggat	agcagctcag	actcagacag	2460
cgattcagac	tcagatagcg	actcagactc	ggatagcgac	tcggattcag	atagcgactc	2520
agactcagat	agtgactccg	attcaagagt	tacaccacca	aataatgaac	agaaagcacc	2580
atcaaatcct	aaagggtgaag	taaaccattc	taataaggt	tcaaaacaac	acaaaactga	2640
tgcctttacca	gaaacaggag	ataagagcga	aaacacaaat	gcaactttat	ttgggtgcaat	2700
gatggcatta	ttaggatcat	tactattggt	tagaaaacgc	aagcaagatc	ataaagaaaa	2760
agcgtaaata	cttttttagg	ccgaatacat	ttgtattcgg	ttttttggt	gaaaatgatt	2820
ttaaagttaa	ttgattaagc	gtaaaatggt	gataaagtag	aattagaaag	gggtcatgac	2880

-continued

```

gtatggctta tatttcatta aactatcatt caccaacaat tggatgcat caaaatttga 2940
cagtcatttt accggaagaa cgagaattc 2969

```

What is claimed is:

1. A method of generating an immune response, comprising administering to a host an immunologically effective amount of the A domain of an isolated clumping factor A protein (ClfA) from *Staphylococcus aureus* and an isolated *Staphylococcus aureus* capsular polysaccharide selected from the group consisting of type 5, type 8 and a combination thereof.

2. The method of claim 1 wherein the *S. aureus* capsular polysaccharide can induce antibodies that can promote bacterial phagocytosis.

3. The method of claim 1 wherein the *S. aureus* capsular polysaccharide comprises type 8.

4. The method of claim 1, wherein the *S. aureus* capsular polysaccharide is conjugated to a carrier.

5. A method of generating an immune response, comprising administering to a host an immunologically effective amount of the A domain of an isolated clumping factor A protein (ClfA) from *Staphylococcus aureus* and an isolated *Staphylococcus aureus* capsular polysaccharide type 8.

6. The method of claim 5 wherein the *S. aureus* capsular polysaccharide can induce antibodies that can promote bacterial phagocytosis.

7. An immunogenic composition comprising an immunologically effective amount of the A domain of an isolated clumping factor A protein (ClfA) from *Staphylococcus aureus* and an isolated *Staphylococcus aureus* capsular polysaccharide selected from the group consisting of type 5, type 8, and a combination thereof.

* * * * *