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(71) Applicant(s)
Geneohm Sciences, Inc.

(72) Inventor(s)
Jean, Veronique;Courjal, Frank;Savoye, Chantal;Guillot, Melanie

(74) Agent / Attorney
Davies Collison Cave, Level 15 1 Nicholson Street, MELBOURNE, VIC, 3000

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(71) Applicant *(for all designated States except US)*: **GENEOHM SCIENCES, INC.** [US/US]; 6146 Nancy Ridge Drive, San Diego, CA 92121 (US).

(72) Inventors: **JEAN, Veronique**; 34 Chemin De La Cime, Lac Beauport, Québec, G3B1T (CA). **GUILLOT, Melanie**; 3915 Archambault, Quebec City, QUèbec G1P3S1 (CA). **COURJAL, Frank**; 4689 Rue Mary Cormier, Quebec City, Québec G1Y3M7 (CA). **SAVOYE, Chantal**; 350 rue Gingras, Ap 411, Quebec City, Québec G1X4C4 (CA).

(74) Agent: **MALLON, Joseph, J.**; Knobbe Martens Olson & Bear, LLP, 2040 Main Street, Fourteenth Floor, Irvine, CA 92614 (US).

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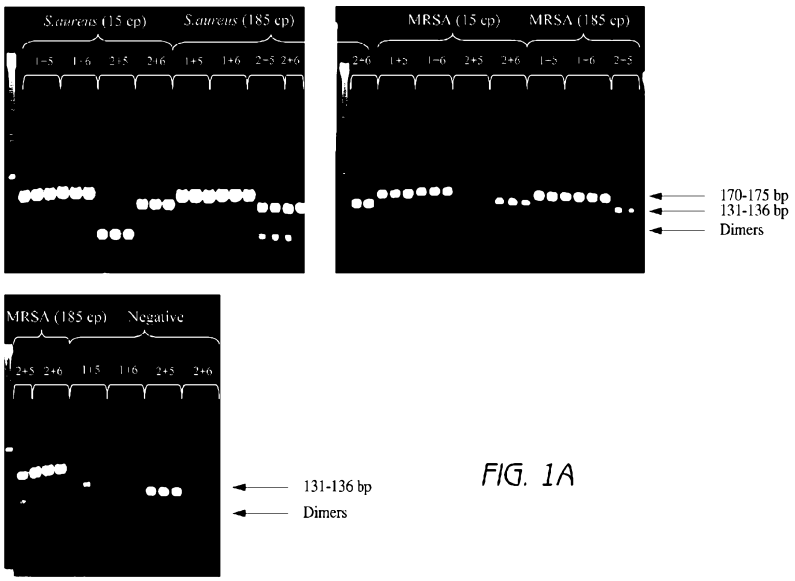

FIG. 1A

(57) Abstract: Aspects of the present invention relate to methods and compositions for the detection and/or quantification of S. aureus from a sample, as well as methods and compositions useful for the detection and/or quantification of S. *aureus* and MRSA in a single assay. Embodiments include nucleic acids that hybridize to S.*aureus*-specific *nuc* sequences and MREJ sequences.

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DETECTION OF *STAPHYLOCOCCUS AUREUS* AND IDENTIFICATION OF METHICILLIN-RESISTANT *STAPHYLOCOCCUS AUREUS*

RELATED APPLICATIONS

[0001] The present application claims priority to U.S. Provisional Application Serial No. 60/870,823, filed on December 19, 2006, by Jean et al. entitled "DETECTION OF STAPHYLOCOCCUS AUREUS AND IDENTIFICATION OF METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS," which is hereby expressly incorporated by reference in its entirety.

SEQUENCE LISTING

[0002] The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing is provided as a file entitled GENOM.072A.TXT, created November 29, 2007, which is 124 KB in size. The information in the electronic format of the Sequence Listing is incorporated herein by reference in its entirety.

BACKGROUND OF THE INVENTION

[0003] Members of the genus *Staphylococcus* are major human pathogens, causing a wide variety of hospital and community acquired infections worldwide. The coagulase-positive species *Staphylococcus aureus* is well documented as a human opportunistic pathogen (Murray et al. Eds, 2003, Manual of Clinical Microbiology, 8th Ed., ASM Press, Washington, D.C.). Nosocomial infections caused by *S. aureus* are a major cause of morbidity and mortality. Some of the most common infections caused by *S. aureus* involve the skin, and they include furuncles or boils, cellulitis, impetigo, and postoperative wound infections at various sites. Some of the more serious infections produced by *S. aureus* are bacteremia, pneumonia, osteomyelitis, acute endocarditis, myocarditis, pericarditis, cerebritis, meningitis, scalded skin syndrome, and various abcesses. Food poisoning mediated by staphylococcal enterotoxins is another important syndrome associated with *S. aureus*. Toxic shock syndrome, a community-acquired disease, has also been attributed to infection or colonization with toxigenic *S. aureus*.

[0004] Coagulase-negative *Staphylococci* had been regarded as harmless skin commensals prior to the 1970s, however, they are now recognized as important causes of

human infections (Kloos, et al. (2004) Clin. Microbiol. Rev. 7:117-140). In addition to being among the most frequently isolated bacteria in clinical microbiology laboratories, coagulase-negative *Staphylococci* serve as reservoirs of antimicrobial resistance determinants (Bastos, et al. (1999) Eur. J. Clin. Microbiol. Infect. Dis. 18:393-398). As such, it is important to characterize and distinguish *S. aureus* strains from other, coagulase-negative *Staphylococci*.

[0005] *S. aureus* strains produce an extracellular thermostable nuclease (thermostable TNase) with a frequency similar to that at which they produce coagulase. The sequence of the gene encoding TNase, *nuc*, was first disclosed in 1985 (Kovacevi et al. (1985), *J. Bact.* 162:521-528). TNase is a 17kDa protein that degrades both RNA and DNA at temperatures up to 100°C. TNase activity is not specific for *S. aureus*, however, *S. aureus* species-specific sequences exist. See, e.g., Brackstad, et al. (1992), J. Clin. Microbiol. 30:1654-1660; Zhang, et al. (2004), J. Clin. Microbiol. 42:4947-4955; Chesneau, et al. (1993) Mol. Cell. Probes 7:301-310, Wilson, et al. (1991) Appl. Environ. Microbiol. 57:1793-1798; Poulsen et al., (2003) J. Antimicrob. Chemo. 51:419-421, Costa et al., (2005), Diag. Microbiol. and Infect. Dis, 51: 13-17, Shittu et al., (2006), Diagn Microbiol Infect Dis. 2006 Jul 17. To date, none of the *S. aureus*-specific *nuc* sequences have been proven to be clinically useful by way of a large specificity study. Therefore, there exists a need for oligonucleotides that have been proven to be both highly specific and sensitive, which are useful in rapid detection and identification of *S. aureus* from clinical samples.

[0006] Both *S. aureus* and coagulase-negative *Staphylococci* have a remarkable ability to accumulate additional antibiotic resistant determinants, resulting in the formation of multidrug-resistant strains. This resistance limits therapeutic options for treatment and substantially increases patient morbidity and mortality. Methicillin-resistant *S. aureus* (MRSA) emerged in the 1980s as a major clinical and epidemiologic problem in hospitals (Oliveira et al., (2002) Lancet Infect Dis. 2:180-189). MRSA are resistant to all β-lactams including penicillins, cephalosporins, carbapenems, and monobactams, which are the most commonly used antibiotics to cure *S. aureus* infections. MRSA infections can only be treated with more toxic and more costly antibiotics, which are normally used as the last line of defense. Since MRSA can spread easily from patient to patient via personnel, hospitals over the world are confronted with the problem to control MRSA.

[0007] Methicillin resistance in *S. aureus* is unique in that it is due to acquisition of DNA from other coagulase-negative staphylococci (CNS), coding for a surnumerary β-lactam-resistant penicillin-binding protein (PBP), which takes over the biosynthetic functions of the normal PBPs when the cell is exposed to β-lactam antibiotics. *S. aureus* normally contains four PBPs, of which PBPs 1, 2 and 3 are essential. The low–affinity PBP in MRSA, termed PBP 2a (or PBP2'), is encoded by the choromosomal *mecA* gene and functions as a β-lactam -resistant transpeptidase. The *mecA* gene is absent from methicillin-sensitive *S. aureus* but is widely distributed among other species of staphylococci and is highly conserved (Ubukata et al., (1990) Antimicrob. Agents Chemother. 34:170-172).

[0008] Nucleotide sequence determination of the DNA region surrounding the *mecA* gene from *S. aureus* strain N315 (isolated in Japan in 1982), led to the discovery that the *mecA* gene is carried by a novel genetic element, designated staphylococcal cassette chromosome *mec* (SCC*mec*), which is inserted into the chromosome. SCC*mec* is a mobile genetic element characterized by the presence of terminal inverted and direct repeats, a set of site-specific recombinase genes (*ccrA* and *ccrB*), and the *mecA* gene complex (Ito et al., (1999) Antimicrob. Agents Chemother. 43:1449-1458; Katayama et al., (2000) Antimicrob. Agents Chemother. 44:1549-1555). SCC*mec* is precisely excised from the chromosome of *S. aureus* strain N315 and integrates into a specific *S. aureus* chromosomal site in the same orientation through recombinases encoded by the *ccrA* and *ccrB* genes. Cloning and sequence analysis of the DNA surrounding the *mecA* gene from MRSA strains NCTC 10442 (the first MRSA strain isolated in England in 1961) and 85/2082 (a strain from New Zealand isolated in 1985) led to the discovery of two novel genetic elements that shared similar structural features of SCC*mec*. The three SCC*mec* have been designated type I (NCTC 10442), type II (N315) and type III (85/2082) based on the year of isolation of the strains (Ito et al., (2001) Antimicrob. Agents Chemother. 45:1323-1336). Hiramatsu et al. have found that the SCC*mec* DNAs are integrated at a specific site in the chromosome of methicillin-sensitive *S. aureus* (MSSA). The nucleotide sequence of the regions surrounding the left and right boundaries of SCC*mec* DNA (i.e. *att*L and *att*R, respectively), as well as those of the regions around the SCC*mec* DNA integration site (i.e. *attBscc* which is the bacterial chromosome attachment site for SCC*mec* DNA), were analyzed. Sequence analysis of the *att*L, *att*R and *attBscc* sites

revealed that *attBscc* is located at the 3' end of a novel open reading frame (ORF), *orfX*. *orfX* encodes a putative 159-amino acid polypeptide that exhibits sequence homology with some previously identified polypeptides of unknown function (Ito et al., (1999) Antimicrob. Agents Chemother. 43:1449-1458). Two new types of SCC*mec*, designated type IV and type V were recently described (Ma et al., (2002) Antimicrob. Agents Chemother. 46:1147-1152, Ito et al., (2004) Antimicrob Agents Chemother. 48:2637-2651, Oliveira et al., (2001) Microb. Drug Resist. 7:349-360). Oliveira et al. also recently reported the existence of SCC*mec* type VI. Oliveira et al., (2006), Antimicrob Agents Chemother. 50:3457-3459. The sequence of the right extremity of some *Staphylococcus* strains classified as SCC*mec* type IV has been determined. *See,* Ma et al., (2002) Antimicrob. Agents Chemother. 46:1147-1152; Ito et al., (2001) Antimicrob. Agents Chemother. 45:1323-1336; Oliveira et al., (2001) Microb. Drug Resist. 7:349-360. Sequences from *S. aureus* strains CA05 and 8/6-3P, classified as SCC*mec* type IV, were nearly identical over 2000 nucleotides to that of type II SCC*mec* of *S. aureus* strain N315 (Ma et al., (2002) Antimicrob. Agents Chemother. 46:1147-1152; Ito et al., (2001) Antimicrob. Agents Chemother. 45:1323-1336).

[0009] Methods to detect and identify MRSA based on the detection of the *mecA* gene and *S. aureus*-specific chromosomal sequences have been described. *See,* Schuenck et al., Res. Microbiol., (2006), in press, Shittu et al., (2006), Diagn Microbiol Infect Dis. Jul 17, Grisold et al., (2006), Methods Mol. Biol.345 : 79-89, Costa et al., (2005), Diag. Microbiol. and Infect. Dis, 51: 13-17, Mc Donald et al., (2005), J. Clin. Microbiol., 43: 6147-6149, Zhang et al., (2005), J. Clin. Microbiol. 43: 5026-5033, Hagen et al. (2005), Int J Med Microbiol. 295:77-86, Maes, et al. (2002) J. Clin. Microbiol. 40:1514-1517, Saito et al., (1995) J. Clin. Microbiol. 33:2498-2500; Ubukata et al., (1992) J. Clin. Microbiol. 30:1728-1733; Murakami et al., (1991) J. Clin. Microbiol. 29:2240-2244; Hiramatsu et al., (1992) Microbiol. Immunol. 36:445-453). Furthermore, Levi and Towner (2003), J. Clin. Microbiol., 41:3890-3892 and Poulsen et al. (2003), J Antimicrob Chemother., 51:419-421 describe detection of methicillin resistance in coagulase-negative Staphylococci and in *S. aureus* using the EVIGENE™ MRSA Detection kit.

[0010] However, because the *mecA* gene is widely distributed in both *S. aureus* and coagulase-negative staphylococci, each of the methods described above are incapable of

discriminating between samples containing both methicillin-sensitive *S. aureus* ("MSSA") and methicillin-resistant coagulase-negative staphylococci, and samples that contain only MRSA or that have both methicillin-sensitive *S. aureus* and MRSA.

[0011] To address this problem, Hiramatsu et al. developed a PCR-based assay specific for MRSA that utilizes primers that hybridize to the right extremities of DNA of SCC*mec* types I-III in combination with primers specific to the *S. aureus* chromosome, which corresponds to the nucleotide sequence on the right side of the SCC*mec* integration site. (US patent 6,156,507, hereinafter the "'507 patent"). More recently, Zhang et al., (2005), J. Clin. Microbiol. 43: 5026-5033, described a multiplex assay for subtyping SCCmec types I to V MRSA. Nucleotide sequences surrounding the SCC*mec* integration site in other staphylococcal species (e.g., *S. epidermidis* and *S. haemolyticus*) are different from those found in *S. aureus*, therefore multiplex PCR assays that utilize oligonucleotides that hybridize to the right extremities of SCC*mec* and the *S. aureus* chromosome have the advantage of being specific for the detection of MRSA.

[0012] The PCR assay described in the '507 patent also led to the development of "MREP typing" (*mec* right extremity polymorphism) of SCC*mec* DNA (Ito et al., (2001) Antimicrob. Agents Chemother. 45:1323-1336; Hiramatsu et al., (1996) J. Infect. Chemother. 2:117-129). The MREP typing method takes advantage of the fact that the nucleotide sequences of the three MREP types differ at the right extremity of SCC*mec* DNAs adjacent to the integration site among the three types of SCC*mec*. Compared to type I, type III has a unique nucleotide sequence while type II has an insertion of 102 nucleotides to the right terminus of SCC*mec*. The MREP typing method described by Hiramatsu et al. uses the following nomenclature: SCC*mec* type I is MREP type i, SCC*mec* type II is MREP type ii, and SCCmec type III is MREP type iii. Hiramatsu later revised this nomenclature in view of the publication of the sequences of the genomes of strains N315 and Mu50, since the sequences revealed that SCC*mec* elements are located downstream of *orfX*. Consequently, MREP can now be referred to as MLEP (*mec* left extremity polymorphism) (Chongtrakool et al., (2006), Antimicrob. Agents Chemother. 50:1001-1012).

[0013] Recently, Chongtrakool et al. proposed replacing the SCC*mec* nomenclature with new nomenclature. Chongtrakool et al., (2006), Antimicrob. Agents

Chemother. 50:1001-1012. Chongtrakool et al.'s proposed nomenclature is based on the structure of SCC*mec* elements and has three features. The first feature is a description of the SCC type and is defined by *ccr* type and *mec* class. The second feature is the description of the J regions (junkyard regions), which are part of the SCC*mec* element, located between and around the *mec* and *ccr* complexes. The third feature is the enumeration which allows the numbering of *ccr* type and J regions according to their time of identification.

[0014] As stated above, SCC*mec* types II and IV have the same nucleotide sequence to the right extremity. Consequently, the MREP (or MLEP according to recent revision) typing method described above cannot differentiate the SCC*mec* type IV described by Hiramatsu et al. (Ma et al., (2002) Antimicrob. Agents Chemother. 46:1147-1152) from SCC*mec* type II).

[0015] We recently described DNA sequences and regions in MRSA named MREJ. PCT Application No. PCT/CA02/00824. The phrase MREJ refers to the *mec* right extremity junction « mec right extremity junction ». MREJ's are approximately 1 kilobase (kb) in length and include sequences from the SCC*mec* right extremity as well as bacterial chromosomal DNA to the right of the SCC*mec* integration site. Importantly, MREJ sequences provide advantages over MREP/MLEP sequences in classifying MRSA in that MREJ/MLEJ sequences enable the differentiation between strains classified as SCC*mec* type II and SCC*mec* type IV. As discussed in PCT Application No. PCT/CA02/00824, the strains that Hiramatsu classified as MREP types i-iii fall under MREJ types i-iii according to the MREJ typing system. We recently identified novel MREJ types iv-xx, and developed nucleic acid assays with improved ubiquity capable of detection and identification of MRSA of MREJ types i-xx. (Huletsky et al., 2004, J Clin. Microbiol. 42:1875-1884, International Patent Application PCT/CA02/00824, U.S. Patent Application No. 11/248,438). Based on the revision of MREP to MLEP, one can understand that previously called MREJ types could now be reclassified as MLEJ (*mec* left extremity junction). The skilled artisan will appreciate that any *S.aureus* and MRSA classification system is contemplated in the methods disclosed herein, as sequences can specifically detect *S. aureus* and identify those which are resistant to methicillin.

[0016] Maes et al. describe a PCR assay to discriminate *S. aureus* from coagulase negative Staphylococci and to determine methicillin resistance in blood cultures (Maes, et al. (2002) J. Clin. Microbiol. 40:1514-1517). The assay described in Maes et al. cannot distinguish MRSA from methicillin-resistant coagulase-negative Staphylococci.

[0017] Poulsen et al. describe detection of methicillin resistance in coagulase-negative Staphylococci and in *S. aureus* using the EVIGENE™ MRSA Detection kit. The assay described in Poulsen et al. cannot discriminate between a sample that has both methicillin-sensitive *S. aureus* and methicillin-resistant coagulase-negative staphylococci, and a sample that contains only MRSA or that has both methicillin-sensitive *S. aureus* and MRSA.

[0018] Accordingly, there remains a need for a rapid assay to detect and identify both MRSA and methicillin-sensitive *S. aureus* in the same reaction and to be able to distinguish *S. aureus* from coagulase-negative *Staphylococci* in the same reaction.

SUMMARY OF THE INVENTION

[0019] Disclosed herein are methods and compositions for specifically detecting the presence of a *Staphylococcus aureus* (*S. aureus*) strain and detecting the presence of a methicillin-resistant *S. aureus* (MRSA) strain from a clinical sample in a single assay. Also provided herein are methods and compositions for the specific detection of *S. aureus* from a sample.

[0020] Some embodiments relate to methods of detecting *S. aureus* and identifying the presence of MRSA from a sample that includes nucleic acids. In some embodiments, the sample can be contacted with at least one primer and or probe of at least 10 nucleotides that anneals under stringent conditions a *S. aureus*-specific sequence of the *nuc* gene, and at least one primer and/or probe specific for a MRSA strain. *S aureus* strains are rendered methicillin-resistant due to the presence of an SCC*mec* cassette containing a *mecA* gene that is inserted in bacterial nucleic acids. The insertion of the SCC*mec* cassette can generate a polymorphic right extremity junction (MREJ). The MRSA-specific primer(s) and/or probe(s) can anneal under stringent conditions to polymorphic MREJ nucleic acids, including, for example, MREJ types i to xx. *S. aureus*-specific and MRSA-specific primers anneal under conditions of, for example, 4mM $MgCl_2$, 100 mM Tris (pH 8.3), 10 mM KCl,

and 5 mM $(NH_4)_2SO_4$ at 59°C. The presence and/or amount of annealed probe(s), or amplification products produced through annealing of the primers to the nucleic acids, can be used as an indication of the presence and/or amount of *S. aureus* (MSSA and MRSA) and MRSA in the sample.

[0021] The at least one primer specific for a *S. aureus* strain can anneal under stringent conditions to the **SEQ ID NO: 200,** the complement thereof or any sequence which differs from **SEQ ID NO: 200** by 1 to 20 nucleotides.

[0022] In some embodiments, the at least one primer and/or probe that anneals under stringent conditions to the *S.aureus* specific *nuc* sequence hybridizes under stringent conditions to one of the following **SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11,** or **12** or the complement thereof. Preferably, the at least one primer and/or probe that anneals under stringent conditions to the *S.aureus* specific *nuc* sequence comprises, consists essentially of, or consists of one of the following **SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11,** or **12.**

[0023] In preferred embodiments, the *S.aureus*-specific primer(s) and/or probe(s) are at least 10 nucleotides in length, and anneal under stringent conditions to the nucleic acid of any one of **SEQ ID NOs: 1 to 12** or the complement thereof.

[0024] In still more preferred embodiments, the sample is also contacted with a probe that anneals under stringent conditions to the nucleic acid of any one of **SEQ ID NOs: 9, 10, 11,** or **12**, or the complement thereof. In some embodiments, the probe is a molecular beacon probe. Preferably, the probe comprises, consists essentially of, or consists of the sequence of **SEQ ID NOs: 9, 10, 11,** or **12.**

[0025] In some embodiments, the method also includes adding internal control DNA to the sample, and at least one primer and/or probe that anneals under stringent conditions to the internal control DNA. For example, in some embodiments, the Internal Control can be a linearized 4.23 kb plasmid purified from *E. coli*. The internal control can be used to monitor the presence of inhibitory substances coming from a specimen.

[0026] The at least one primer specific for an MRSA strain can anneal under stringent conditions to the MREJ sequences of types i to xx, as defined in any one of **SEQ ID NOs: 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60,**

61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, and **88,** the complement thereof or any sequence which differs from SEQ ID NOs 14 to 88 by 1 to 20 nucleotides.

[0027] In preferred embodiments, *S. aureus*-specific and MRSA-specific primers and/or probes are chosen to anneal to the sample nucleic acids under the same annealing conditions. In more preferred embodiments, the primer(s) and/or probe(s) are placed altogether in the same physical enclosure.

[0028] In preferred embodiments, the MRSA-specific primer(s) and/or probe(s) are at least 10 nucleotides in length, and anneal under stringent conditions to the nucleic acid of any one of **SEQ ID NOs: 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 15, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 201** (types i- ix) **182, 183, 184, 195, 186, 187, 188, 189, 190, 191, 193, 194, 195, 196, 197, 198** (types x-xx) or **199** or the complement thereof. Preferably, the MRSA-specific primer(s) and/or probe(s) comprise, consist essentially of, or consist of the nucleic acid of any one of **SEQ ID NOs: 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 15, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 201** (types i- ix) **182, 183, 184, 195, 186, 187, 188, 189, 190, 191, 193, 194, 195, 196, 197,** (types xi-xx) or **199.** In some embodiments, MRSA-specific primers also include an oligonucleotide that hybridizes under stringent condition to *orf22* of the *S. aureus* chromosome, wherein the primer can be used in an amplifciatin reaction with **SEQ ID NO: 197** to detect MREJ type x. In more preferred embodiments, the MRSA-specific primer(s) and/or probe(s) anneal under stringent conditions to the nucleic acid of any one of **SEQ ID NOs: 99, 199, 144, 150, 155,** and **163** or the complement thereof, such as a primer and/or probe that comprises, consists essentially of, or consists of the nucleic acid of

any one of **SEQ ID NOs: 99, 199, 144, 150, 155,** and **163**. In still more preferred embodiments, the sample is also contacted with a probe that anneals under stringent conditions to the nucleic acid of any one of **SEQ ID NOs: 126, 128, 130** and **131,** or the complement thereof. In some embodiments, the probe is a molecular beacon probe. Preferably, the probe comprises, consists essentially of, or consists of the nucleic acid of any one of **SEQ ID NOs: 126, 128, 130** and **131.**

[0029] In some embodiments, the sample and primer(s) and/or probe(s) described above are used in an amplification reaction, such as a PCR, LCR, NABSA, 3SR, SDA, bDNA, TMA, CPT, SPA, NDSA, rolling circle amplification, anchored-strand displacement amplification, solid-phase (immobilized) rolling circle amplification, or Q beta replicase amplification reaction.

[0030] Other aspects relate to the specific detection of an *S. aureus* strain in a sample that includes nucleic acids. At least one primer and/or probe that is specific for the *nuc* gene of *S. aureus* is provided. The primers and/or probe(s) include a nucleic acid that can anneal to at least 11 consecutive nucleotides of any one of the nucleic acids of **SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11,** or **12**, or the complement thereof, under stringent conditions, such as 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM $MgCl_2$ at 59°C; or 4mM $MgCl_2$, 100 mM Tris (pH 8.3), 10 mM KCl, and 5 mM $(NH_4)_2SO_4$ at 59°C. The primer(s) and/or probe(s) are allowed to anneal to the nucleic acids of the sample. Annealed primer(s) and/or probe(s) indicate the presence of an *S. aureus* strain in the sample. The annealed primer(s) and/or probe(s) can be detected, and the presence and/or amount of annealed probe(s), the amount of an amplification product produced through annealing of the primers to the nucleic acids, indicates the presence and/or amount of *S. aureus* present in the sample.

[0031] In some embodiments, the sample and primer(s) and/or probe(s) described above are used in an amplification reaction, such as a PCR, LCR, NABSA, 3SR, SDA, bDNA, TMA, CPT, SPA, NDSA, rolling circle amplification, anchored-strand displacement amplification, solid-phase (immobilized) rolling circle amplification, or Q beta replicase amplification reaction.

[0032] In preferred embodiments, a primer pair including a first primer that anneals under stringent conditions to **SEQ ID NO:1** or the complement thereof (such as a primer that comprises, consists essentially of, or consists of **SEQ ID NO: 1**), and a second primer that anneals under stringent conditions to **SEQ ID NO: 6** (such as a primer that comprises, consists essentially of, or consists of **SEQ ID NO: 6**), or the complement thereof, is allowed to anneal to the nucleic acids of the sample. In more preferred embodiments, a probe that anneals under stringent conditions to **SEQ ID NO:9** or **10** (such as a probe that comprises, consists essentially of, or consists of **SEQ ID NO: 9** or **10**), or the complement thereof**,** is also provided.

[0033] In other preferred embodiments, a primer pair including a first primer that anneals under stringent conditions to **SEQ ID NO: 3** (such as a primer that comprises, consists essentially of, or consists of **SEQ ID NO: 3**)or the complement thereof, and a second primer that anneals under stringent conditions to **SEQ ID NO: 8** (such as a primer that comprises, consists essentially of, or consists of **SEQ ID NO: 8**)or the complement thereof, is allowed to anneal to the nucleic acids of the sample. In more preferred embodiments, a probe that anneals under stringent conditions to **SEQ ID NO: 11** or **12**, (such as a primer that comprises, consists essentially of, or consists of **SEQ ID NO: 11** or **12**)or the complement thereof, is also provided.

[0034] In still other preferred embodiments, the sample is contacted with at least one primer pair, that includes a first primer and a second primer that anneal under stringent conditions to the nucleic acid sequence of at least one of the following pairs:

[0035] **SEQ ID NOs: 1** and **5;**

[0036] **SEQ ID NOs: 1** and **6;**

[0037] **SEQ ID NOs: 2** and **5;**

[0038] **SEQ ID NOs: 2** and **6;**

[0039] **SEQ ID NOs: 3** and 7

[0040] **SEQ ID NOs: 3** and **8;**

[0041] **SEQ ID NOs: 4** and **7;** and

[0042] **SEQ ID NOs: 4** and **8,** or the complements thereof.

[0043] For example, in preferred embodiments, the sample is contacted with at least one primer pair that includes a first primer and a second primer that comprise, consist essentially of, or consist of the nucleic acid sequence of at least one of the following pairs:

[0044] **SEQ ID NOs: 1** and **5;**

[0045] **SEQ ID NOs: 1** and **6;**

[0046] **SEQ ID NOs: 2** and **5;**

[0047] **SEQ ID NOs: 2** and **6;**

[0048] **SEQ ID NOs: 3** and 7

[0049] **SEQ ID NOs: 3** and **8;**

[0050] **SEQ ID NOs: 4** and **7;** and

[0051] **SEQ ID NOs: 4** and **8.**

[0052] In preferred embodiments, the sample is also contacted with at least one primer pair including a first primer and a second primer that anneal under stringent conditions to the nucleic acid sequence of at least one of the following pairs:

[0053] **SEQ ID NOs: 99** and **199;**

[0054] **SEQ ID NOs: 99** and **144;**

[0055] **SEQ ID NOs: 99** and **150;**

[0056] **SEQ ID NOs: 99** and **155;** and

[0057] **SEQ ID NOs: 99** and **163**, or the complement thereof.

[0058] For example, in some embodiments, the sample is contacted with at least one primer pair including a first primer and a second primer that comprise, consist essentially of, or consist of at least one of the following pairs:

[0059] **SEQ ID NOs: 99** and **199;**

[0060] **SEQ ID NOs: 99** and **144;**

[0061] **SEQ ID NOs: 99** and **150;**

[0062] **SEQ ID NOs: 99** and **155;** and

[0063] **SEQ ID NOs: 99** and **163**.

[0064] In preferred embodiments, the sample is contacted with a plurality of primer pairs, wherein the primers anneal under stringent conditions to the nucleic acid sequences of

[0065] **SEQ ID NOs: 1** and **6**

[0066] **SEQ ID NOs: 99** and **199;**

[0067] **SEQ ID NOs: 99** and **144;**

[0068] **SEQ ID NOs: 99** and **150;**

[0069] **SEQ ID NOs: 99** and **155;** and

[0070] **SEQ ID NOs: 99** and **163,** or the complements thereof, such as primer pairs that comprise, consist essentially of, or consist of the nucleic acid sequences of:

[0071] **SEQ ID NOs: 1** and **6**

[0072] **SEQ ID NOs: 99** and **199;**

[0073] **SEQ ID NOs: 99** and **144;**

[0074] **SEQ ID NOs: 99** and **150;**

[0075] **SEQ ID NOs: 99** and **155;** and

[0076] **SEQ ID NOs: 99** and **163**.

[0077] In other preferred embodiments, the sample is contacted with a plurality of primer pairs, wherein the primers anneal under stringent conditions to the nucleic acid sequences of

[0078] **SEQ ID NOs: 3** and **8**

[0079] **SEQ ID NOs: 99** and **199;**

[0080] **SEQ ID NOs: 99** and **144;**

[0081] **SEQ ID NOs: 99** and **150;**

[0082] **SEQ ID NOs: 99** and **155;** and

[0083] **SEQ ID NOs: 99** and **163,** or the complements thereof, such as primer pairs that comprise, consist essentially of, or consist of the nucleic acid sequences of:

[0084] **SEQ ID NOs: 3** and **8**

[0085] **SEQ ID NOs: 99** and **199;**

[0086] **SEQ ID NOs: 99** and **144;**

[0087] **SEQ ID NOs: 99** and **150;**

[0088] **SEQ ID NOs: 99** and **155;** and

[0089] **SEQ ID NOs: 99** and **163**.

[0090] Preferably, the sample is also contacted with at least one probe that anneals under stringent conditions to the nucleic acid sequence of any one of **SEQ ID NOs: 9, 10, 11, 12, 126, 128, 130 and 131** or the complement thereof, such as a probe that comprises, consists essentially of, or consists of the nucleic acid sequence of any one of **SEQ ID NOs: 9, 10, 11, 12, 126, 128, 130 and 131**.

[0091] Other aspects relate to oligonucleotides useful for the specific detection of *S. aureus*. Some embodiments provide oligonucleotides which anneal under stringent conditions with at least 11 consecutive nucleotides of the nucleic acid sequence of one of the following **SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12**, such as nucleic acids that comprise, consist essentially of, or consist of one of **SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12**.

[0091a] In a preferred embodiment, the invention relates to a method of specifically detecting the presence of a *Staphylococcus aureus* (*S. aureus*) strain and identifying a methicillin-resistant *S. aureus* strain from a sample in a single assay, comprising:

simultaneously contacting said clinical sample with

at least one primer pair that is capable of amplifying a sequence from a *nuc* gene *S. aureus* when an *S. aureus* strain is present in the clinical sample to produce a *nuc* amplicon, said primer pair comprising a first and a second *nuc* primer, said first and second *nuc* primers being between 11 and 45 nucleotides in length and being capable of annealing under PCR conditions to opposite strands of *S. aureus* chromosomal DNA within the *nuc* gene; and

at least one primer pair that is capable of amplifying a polymorphic *mec* right extremity junction (MREJ) sequence of a methicillin resistant *S. aureus* (MRSA) strain when an MRSA strain is present in the clinical sample to produce an MREJ amplicon, said MREJ sequence comprising polymorphic sequences from the right extremity of an *SCCmec* cassette inserted into the *S. aureus* chromosome and *S. aureus* chromosomal DNA, said first and second MREJ primers being between 11 and 45 nucleotides in length and being capable of annealing under PCR conditions to opposite strands of MRSA chromosomal DNA, to create an amplification mixture,

wherein said PCR conditions comprise 4mM $MgCl_2$, 100mM Tris (pH 8.3), 10mM KCl, 5mM $(NH_4)_2SO_4$, 0.15 mg/mL BSA, 4% trehalose at 59°C

subjecting the amplification mixture to an amplification protocol to enable amplification of both *nuc* and MREJ sequences, thereby producing an amplified sample; and

detecting the presence and/or amount of *nuc* amplicons and MREJ amplicons in the amplified sample as an indication of the presence and or amount of *S. aureus* and MRSA, respectively, present in the sample.

[0092] Yet other aspects relate to kits when used for detecting the presence of an *S. aureus* strain in a sample that includes nucleic acids. The kit can include at least one oligonucleotide that anneals under stringent conditions to one of the following **SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12**, or the complement thereof. For example, the kit can include at least one oligonucleotide that comprises, consists essentially of, or consists of **SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12**. In preferred embodiments, the kit also includes at least one probe, wherein the probe can anneal to the nucleic acid sequence of **SEQ ID NO: 9, 10, 11 or 12**, or the complement thereof, under stringent conditions. In preferred embodiments, the probe can comprise, consist essentially of, or consist of **SEQ ID NO: 9, 10, 11 or 12**.

[0093] In preferred embodiments, the kit also includes at least one primer specific for an MRSA strain. *S aureus* strains are rendered methicillin-resistant due to the presence of an SCC*mec* insert containing a *mecA* gene that is inserted in bacterial nucleic acids. The insertion of the SCC*mec* insert can generate a polymorphic right extremity junction (MREJ). The MRSA-specific primer(s) and/or probe(s) can anneal under stringent conditions to polymorphic MREJ nucleic acids, including, for example, MREJ types i to xx.

[0094] In preferred embodiments, the kit includes at least one MRSA-specific oligonucleotide that anneals under stringent conditions to one of the following **SEQ ID NOs: 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57,**

58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, and **88**, or the complement thereof. For example, in some embodiments, a kit can contain at least one MRSA-specific oligonucleotide that is at least 10 nucleotides in length, and anneals under stringent conditions to the nucleic acid sequence of any one of the following **SEQ ID NOs: 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 15, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 201** (types i- ix) **182, 183, 184, 195, 186, 187, 188, 189, 190, 191, 193, 194, 195, 196, 197,** (types xi-xx) or **199** or the complement thereof. In some embodiments, the MRSA-specific oligonucleotides can also include an oligonucleotide that hybridizes under stringent conditions to *orf22* of the *S. aureus* chromosome, wherein the oligonucleotide can be used in an amplification reaction with **SEQ ID NO: 197** to detect MREJ type x. Preferably, the MRSA-specific oligonucleotide can comprise, consist essentially of, or consist of any one of the following **SEQ ID NOs: 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 15, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 201** (types i- ix) **182, 183, 184, 195, 186, 187, 188, 189, 190, 191, 193, 194, 195, 196, 197,** (types xi-xx) or **199.**

[0095] In some embodiments, the kit contains a plurality of oligonucleotides that anneal under stringent conditions to **SEQ ID NOs: 1, 6, 99, 144, 150, 155,** and **163.** For example, in preferred embodiments, the kit can contain a plurality of oligonucleotides that comprise, consist essentially of, or consist of **SEQ ID NOs: 1, 6, 99, 144, 150, 155,** and **163**. In some embodiments, the kit contains a plurality of oligonucleotides that anneal under stringent conditions to **SEQ ID NOs: 3, 8, 99, 144, 150, 155,** and **163**, such as a plurality of oligonucleotides that comprise, consist essentially of, or consist of **SEQ ID NOs: 3, 8, 99, 144, 150, 155,** and **163.** Preferably, the kit also includes at least one probe that anneals under

stringent conditions to the following **SEQ ID NOs: 9, 10, 11, 12, 126, 128, 130 or 131**, such as at least one probe that comprises, consists essentially of, or consists of **SEQ ID NOs: 9, 10, 11, 12, 126, 128, 130 or 131**.

[0095a] In a preferred embodiment, the invention provides a kit for specifically detecting the presence of a *Staphylococcus aureus* (*S. aureus*) strain and identifying a methicillin-resistant *S. aureus* strain from a sample in a single assay, comprising:

at least one primer pair that is capable of amplifying a sequence from a *nuc* gene *S. aureus* when an *S. aureus* strain is present in the clinical sample to produce a *nuc* amplicon, said primer pair comprising a first and a second *nuc* primer, said first and second *nuc* primers being between 11 and 45 nucleotides in length and being capable of annealing under PCR conditions to opposite strands of *S. aureus* chromosomal DNA within the *nuc* gene; and

at least one primer pair that is capable of amplifying a polymorphic *mec* right extremity junction (MREJ) sequence of a methicillin resistant *S. aureus* (MRSA) strain when an MRSA strain is present in the clinical sample to produce an MREJ amplicon, said MREJ sequence comprising polymorphic sequences from the right extremity of an *SCCmec* cassette inserted into the *S. aureus* chromosome and *S. aureus* chromosomal DNA, said first and second MREJ primers being between 11 and 45 nucleotides in length and being capable of annealing under PCR conditions to opposite strands of MRSA chromosomal DNA, to create an amplification mixture,

wherein said PCR conditions comprise 4mM $MgCl_2$, 100mM Tris (pH 8.3), 10mM KCl, 5mM $(NH_4)_2SO_4$, 0.15 mg/mL BSA, 4% trehalose at 59°C.

BRIEF DESCRIPTION OF THE DRAWINGS

[0096] **Figures IA** and **IB** show photographs of agarose gels showing the products of PCR amplification reactions. The number of copies and source of template DNA are indicated (15 cp = 15 copies; 185 cp = 185 copies) (*S. aureus* = MSSA strain ATCC 25923; MRSA = MRSA strain ATCC 43300). Arrows indicate the PCR product sizes and primer dimers.

[0097] **Figures 2A** and **2B** show a graphical depiction of PCR amplification curves measured from reactions containing molecular beacon probes. Reactions contained

0, 2.5, 5, 10, 15, or 20 copies of MSSA (Figure 2A) or MRSA (Figure 2B) template DNA, as well as 3000 copies of internal control DNA. Molecular beacon probes were added to each reaction and the fluorescence of the reactions was measured. FAM labeled probes hybridize to MRSA-specific sequences, TET-labeled probes hybridize to internal control DNA sequences, and Texas-Red-labeled probes hybridize to *S. aureus*-specific *nuc* sequences.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

[0098] Methods and compositions disclosed herein relate to detection and/or quantification of *S. aureus* in a sample, and also relate to detection and/or quantification of a *Staphylococcus aureus* (*S. aureus*) strain and identification a methicillin-resistant *S. aureus* strain from a sample in a single assay. The embodiments disclosed herein are useful for detection and/or quantification of *S. aureus* and MRSA from any type of sample, such as any clinical sample, any environmental sample, any microbial culture, any microbial colony, any tissue, and any cell line.

[0099] Staphylococci are Gram-positive cocci. *S. aureus* can be distinguished from other clinically relevant species of *Staphylococcus* by a positive result on the basis of their ability to clot blood plasma (the coagulase reaction) and their ability to form clumps in the presence of fibrinogen. *S. aureus*, as some other staphylococci has the ability to produce a thermostable nuclease (TNase), Becker et al., (2005), Diagn Microbiol Infect Dis., 51:237-

244, Brakstad et al, (1995), APMIS, 103:219-224, Chesneau, et al. (1993) Mol. Cell. Probes 7:301-310. Nevertheless, some nucleotide sequences in the gene encoding the nuclease are specific of *S. aureus* strains (Costa et al., (2005), Diag. Microbiol. and Infect. Dis, 51: 13-17, Mc Donald et al., (2005), J. Clin. Microbiol., 43: 6147-6149, Zhang, et al. (2004), J. Clin. Microbiol. 42:4947-4955; Maes, et al. (2002) J. Clin. Microbiol. 40:1514-1517),

Methods of Detecting *S. aureus* or *S. aureus* and *MRSA*

[0100] Some embodiments relate to methods of specifically detecting *S. aureus* in a sample. Disclosed herein are novel primers and/or probes **(***e.g.,* **SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11,** and **12)** that anneal to *S. aureus*-specific sequences of the *nuc* gene, exemplified by **SEQ ID NO: 200**, which are useful to distinguish *S. aureus* from other Staphylococci, as well as other TNase-producing species of bacteria. In some embodiments, at least one primer and/or probe that anneals under stringent conditions to **SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11,** or **12**, or the complement thereof is provided. For example, in some embodiments, the at least one primer and/or probe can comprise, consist essentially of, or consist of **SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11,** or **12**. The at least one primer is allowed to anneal to the nucleic acids of the sample, e.g., under standard PCR conditions or stringent conditions. The presence and/or amount of annealed probe(s) and/or the amount of an amplification product produced through annealing of the primers to the nucleic acids, is detected, thereby indicating the presence and/or amount of *S. aureus* present in the sample.

[0101] The term "consisting essentially of," when used in reference to nucleic acid can refer to the specified nucleic acid sequences, and can include any additional nucleotide that does not materially affect the basic and novel characteristics of the specified sequence. The term "consisting essentially of" also can refer to variants that are substantially similar to, and differ from a reference sequence in an inconsequential way as judged by examination of the sequence. For example, nucleic acid sequences encoding the same amino acid sequence are substantially similar despite differences in degenerate positions or modest differences in length or composition of any non-coding regions.

Primers and/or Probes and nucleotides

[0102] As used herein, the terms "primer" and "probe" are not limited to oligonucleotides or nucleic acids, but rather encompass molecules that are analogs of nucleotides, as well as nucleotides. Nucleotides and polynucleotides, as used herein shall be generic to polydeoxyribonucleotides (containing 2-deoxy-D-ribose), to polyribonucleotides (containing D-ribose), to any other type of polynucleotide which is an N- or C-glycoside of a purine or pyrimidine base, and to other polymers containing nonnucleotidic backbones, for example, polyamide (e.g., peptide nucleic acids (PNAs)) and polymorpholino (commercially available from the Anti-Virals, Inc., Corvallis, Oreg., as NEUGENE™ polymers), and other synthetic sequence-specific nucleic acid polymers providing that the polymers contain nucleobases in a configuration which allows for base pairing and base stacking, such as is found in DNA and RNA.

[0103] The terms nucleotide and polynucleotide include, for example, 3'-deoxy-2',5'-DNA, oligodeoxyribonucleotide N3'→P5' phosphoramidates, 2'-O-alkyl-substituted RNA, double- and single-stranded DNA, as well as double- and single-stranded RNA, DNA:RNA hybrids, and hybrids between PNAs and DNA or RNA. The terms also include known types of modifications, for example, labels which are known in the art, methylation, "caps," substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoramidates, carbamates, etc.), with negatively charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.), and with positively charged linkages (e.g., aminoalklyphosphoramidates, aminoalkylphosphotriesters), those containing pendant moieties, such as, for example, proteins (including nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), those with intercalators (e.g., acridine, psoralen, etc.), those containing chelators (e.g., metals, radioactive metals, boron, oxidative metals, etc.), those containing alkylators, those with modified linkages (e.g., alpha anomeric nucleic acids, etc.), as well as unmodified forms of the polynucleotide or oligonucleotide.

[0104] It will be appreciated that, as used herein, the terms "nucleoside" and "nucleotide" will include those moieties which contain not only the known purine and pyrimidine bases, but also other heterocyclic bases which have been modified. Such

modifications include methylated purines or pyrimidines, acylated purines or pyrimidines, or other heterocycles. Modified nucleosides or nucleotides will also include modifications on the sugar moiety, e.g., wherein one or more of the hydroxyl groups are replaced with a halogen, an aliphatic group, or are functionalized as ethers, amines, or the like. Other modifications to nucleotides or polynucleotides involve rearranging, appending, substituting for, or otherwise altering functional groups on the purine or pyrimidine base which form hydrogen bonds to a respective complementary pyrimidine or purine. The resultant modified nucleotide or polynucleotide may form a base pair with other such modified nucleotidic units but not with A, T, C, G or U. For example, guanosine (2-amino-6-oxy-9-beta.-D-ribofuranosyl-purine) may be modified to form isoguanosine (2-oxy-6-amino-9-.beta.-D-ribofuranosyl-purine). Such modification results in a nucleoside base which will no longer effectively form a standard base pair with cytosine. However, modification of cytosine (1-.beta.-D-ribofuranosyl-2-oxy-4-amino-pyrimidine) to form isocytosine (1-.beta.-D-ribofuranosyl-2-amino-4-oxy-pyrimidine) results in a modified nucleotide which will not effectively base pair with guanosine but will form a base pair with isoguanosine. Isocytosine is available from Sigma Chemical Co. (St. Louis, Mo.); isocytidine may be prepared by the method described by Switzer et al. (1993) Biochemistry 32:10489-10496 and references cited therein; 2'-deoxy-5-methyl-isocytidine may be prepared by the method of Tor et al. (1993) J. Am. Chem. Soc. 115:4461-4467 and references cited therein; and isoguanine nucleotides may be prepared using the method described by Switzer et al. (1993), supra, and Mantsch et al. (1993) Biochem. 14:5593-5601, or by the method described U.S. Pat. No. 5,780,610 to Collins et al. The non-natural base pairs referred to as κ and π., may be synthesized by the method described in Piccirilli et al. (1990) Nature 343:33-37 for the synthesis of 2,6-diaminopyrimidine and its complement (1-methylpyrazolo[4,3]-pyrimidine-5,7-(4H,6H)-dione. Other such modified nucleotidic units which form unique base pairs have been described in Leach et al. (1992) J. Am. Chem. Soc. 114:3675-3683 and Switzer et al., supra, or will be apparent to those of ordinary skill in the art.

[0105] Primers and/or probes are preferably between 10 and 45 nucleotides in length. For example, the primers and or probes can be at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41,

42, 43, 44, 45, or more nucleotides in length. Primers and/or probes can be provided in any suitable form, included bound to a solid support, liquid, and lyophilized, for example.

Annealing and Specific Binding

[0106] Binding or annealing of the primers and/or probes to target nucleic acid sequences is accomplished through hybridization. It will be appreciated by one skilled in the art that specific hybridization is achieved by selecting sequences which are at least substantially complementary to the target or reference nucleic acid sequence. This includes base-pairing of the oligonucleotide target nucleic acid sequence over the entire length of the oligonucleotide sequence. Such sequences can be referred to as "fully complementary" with respect to each other. Where an oligonucleotide is referred to as "substantially complementary" with respect to a nucleic acid sequence herein, the two sequences can be fully complementary, or they may form mismatches upon hybridization, but retain the ability to hybridize under stringent conditions or standard PCR conditions as discussed below.

[0107] A positive correlation exists between probe length and both the efficiency and accuracy with which a probe will anneal to a target sequence. In particular, longer sequences have a higher melting temperature (T_m) than do shorter ones, and are less likely to be repeated within a given target sequence, thereby minimizing promiscuous hybridization.

[0108] As used herein, "T_m" and "melting temperature" are interchangeable terms which refer to the temperature at which 50% of a population of double-stranded polynucleotide molecules becomes dissociated into single strands. Formulae for calculating the T_m of polynucleotides are well known in the art. For example, the T_m may be calculated by the following equation: T_m =69.3+0.41 x.(G+C)%-6- 50/L, wherein L is the length of the probe in nucleotides. The T_m of a hybrid polynucleotide may also be estimated using a formula adopted from hybridization assays in 1 M salt, and commonly used for calculating T_m for PCR primers: [(number of A+T) x 2°C +(number of G+C) x 4°C]. *See*, *e.g.*, C. R. Newton et al. PCR, 2nd Ed., Springer-Verlag (New York: 1997), p. 24. Other more sophisticated computations exist in the art, which take structural as well as sequence characteristics into account for the calculation of T_m. A calculated T_m is merely an estimate; the optimum temperature is commonly determined empirically.

[0109] Primer or probe sequences with a high G+C content or that comprise palindromic sequences tend to self-hybridize, as do their intended target sites, since unimolecular, rather than bimolecular, hybridization kinetics are generally favored in solution. However, it is also important to design a probe that contains sufficient numbers of G:C nucleotide pairings since each G:C pair is bound by three hydrogen bonds, rather than the two that are found when A and T (or A and U) bases pair to bind the target sequence, and therefore forms a tighter, stronger bond. Preferred G+C content is about 50%.

[0110] Hybridization temperature varies inversely with probe annealing efficiency, as does the concentration of organic solvents, *e.g.*, formamide, which might be included in a hybridization mixture, while increases in salt concentration facilitate binding. Under stringent annealing conditions, longer hybridization probes, or synthesis primers, hybridize more efficiently than do shorter ones, which are sufficient under more permissive conditions. Preferably, stringent hybridization is performed in a suitable buffer under conditions that allow the reference or target nucleic acid sequence to hybridize to the probes. Stringent hybridization conditions can vary (for example from salt concentrations of less than about 1 M, more usually less than about 500 mM and preferably less than about 200 mM) and hybridization temperatures can range (for example, from as low as 0°C to greater than 22°C, greater than about 30°C and (most often) in excess of about 37°C depending upon the lengths and/or the nucleic acid composition of the probes. Stringent hybridization temperatures for PCR range from 40 and 75°C, preferably between 45 and 70°C, depending on lengths and compositions of primers. Longer fragments may require higher hybridization temperatures for specific hybridization. As several factors affect the stringency of hybridization, the combination of parameters is more important than the absolute measure of a single factor. Accordingly, by way of example, the term "stringent hybridization conditions" may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M

NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 μg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995). For example, the term "stringent conditions" encompasses standard PCR conditions, as described below.

[0111] For a review of PCR technology, including standard PCR conditions, applied to clinical microbiology, see DNA Methods in Clinical Microbiology, Singleton P., published by Dordrecht ; Boston: Kluwer Academic, (2000) Molecular Cloning to Genetic Engineering White, B.A. Ed. in Methods in Molecular Biology 67: Humana Press, Totowa (1997) and "PCR Methods and Applications", from 1991 to 1995 (Cold Spring Harbor Laboratory Press). Non-limiting examples of "PCR conditions" include the conditions disclosed in the references cited herein, and also in the examples below, such as, for example, 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM $MgCl_2$, with an annealing temperature of 72°C; or 4mM $MgCl_2$, 100mM Tris, pH 8.3, 10mM KCl, 5mM $(NH_4)_2SO_4$, 0.15mg BSA, 4% Trehalose, with an annealing temperature of 59°C, or 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM $MgCl_2$, with an annealing temperature of 55°C.

[0112] As used herein, when used to describe primers and/or probes, the terms "specific" or "species-specific" refer to primers and/or probes which hybridize or anneal under stringent conditions and/or standard PCR conditions to nucleic acids of a specified species or type (e.g. *S. aureus* or MRSA), and which do not substantially anneal or hybridize under the same conditions to unrelated nucleic acids, such as nucleic acids other than the specified species or MREJ type.

[0113] In a preferred embodiment, the probes or primers described herein hybridize under stringent conditions to target sequences (*e.g.*, *S. aureus* specific *nuc* sequences or MREJ sequences). In other preferred embodiments, the primers or probes described herein exhibit 100% complementarity over at least 10 to 45 nucleotides in length. For example, the primers and or probes exhibit complementarity over at least 10, 11, 12, 13,

14, 15, 16,17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, or more nucleotides to the target sequence. In some embodiments, the primers or probes exhibit 100% complementarity to the target sequence over 10 to 45 consecutive nucleotides in all but at least 1 position (*e.g.*, the primer and/or probe contains a mismatch), 2 positions, 3 positions, 4 positions, 5 positions, 6 positions, 7 positions or more.

[0114] Probes or primers that include sequences that can hybridize as described herein and that also include a portion that does not hybridize to the target sequence (*e.g.,* a tag or a marker), are also contemplated. For example, in some embodiments, the primer and/or probe can contain a detectable moiety, such as a fluorescent moiety, or any other detectable marker, such as those described below. In some embodiments, the primer and/or probe may contain nucleic acid or other molecular components that facilitate subsequent manipulations, such as polymerization reactions, or enzymatic reactions such as digestion with restriction endonucleases, and the like, or that couple the primer and/or probe to a solid support.

Amplification and Detection

[0115] In the methods described herein, detection of annealed primers and/or probes can be direct or indirect. For example, probes can be annealed to the sample being tested, and detected directly. On the other hand, primers can be annealed to the sample being tested, followed by an amplification step. The amplified products can be detected directly, or through detection of probes that anneal to the amplification products.

[0116] In preferred embodiments, an amplification and/or detection step follows the annealing step. In other preferred embodiments, detection occurs during the annealing step. Any type of nucleic acid amplification technology can be used in the methods described herein. Non-limiting examples of amplification reactions that can be used in the methods described herein include but are not restricted to: polymerase chain reaction (PCR) (*See,* PCR PROTOCOLS, A GUIDE TO METHODS AND APPLICATIONS, ed. Innis, Academic Press, N.Y. (1990) and PCR STRATEGIES (1995), ed. Innis, Academic Press, Inc., N.Y. (Innis)), ligase chain reaction (LCR) (*See,* Wu (1989) *Genomics* 4:560; Landegren (1988) *Science* 241:1077; Barringer (1990) *Gene* 89:117), nucleic acid sequence-based amplification

(NASBA), self-sustained sequence replication (3SR) (*See,* Guatelli (1990) *Proc. Natl. Acad. Sci. USA*, 87:1874), strand displacement amplification (SDA), branched DNA signal amplification bDNA, transcription-mediated amplification (TMA)(*See,* Kwoh (1989) *Proc. Natl. Acad. Sci. USA* 86:1173), cycling probe technology (CPT), nested PCR, multiplex PCR, solid phase amplification (SPA), nuclease dependent signal amplification (NDSA), rolling circle amplification technology (RCA), Anchored strand displacement amplification, solid-phase (immobilized) rolling circle amplification, Q Beta replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario). These and other techniques are also described in Berger (1987) *Methods Enzymol.* 152:307-316; Sambrook, Ausubel, Mullis (1987) U.S. Pat. Nos. 4,683,195 and 4,683,202; Amheim (1990) *C&EN* 36-47; Lomell *J. Clin. Chem.*, 35:1826 (1989); Van Brunt, *Biotechnology*, 8:291-294 (1990); Wu (1989) *Gene* 4:560; Sooknanan (1995) *Biotechnology* 13:563-564.

[0117] In preferred embodiments, PCR is used to amplify nucleic acids in the sample. During DNA amplification by PCR, two oligonucleotide primers binding respectively to each strand of the heat-denatured target DNA from the microbial genome, are used to amplify exponentially *in vitro* the target DNA. Successive thermal cycles allow denaturation of the DNA, annealing of the primers and synthesis of new targets at each cycle. (Persing *et al*, (1993), Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.).

[0118] The skilled artisan will appreciate that standard amplification protocols may be modified to improve nucleic acid amplification efficiency, including modifications to the reaction mixture. (Ralser et al., (2006), Biochem Biophys Res Commun., 347:747-51, Kang et al., (2005), J Biochem Biophys Methods. (2005), 64:147-51, Chakrabarti and Schutt, (2002), Biotechniques, **32**:866-874; Al-Soud and Radstrom, (2000), J. Clin. Microbiol., **38**:4463-4470; Al-Soud and Radstrom, 1998, Appl. Environ. Microbiol., **64**:3748-3753; Wilson, 1997, Appl. Environ. Microbiol., **63**:3741-3751). Such modifications of the amplification reaction mixture include but are not limited to the use of various polymerases or the addition of nucleic acid amplification facilitators such as betaine, BSA, sulfoxides, protein gp32, detergents, cations, and tetramethylamonium chloride.

[0119] Detection of amplified nucleic acids may include any real-time or post-amplification technologies known to those skilled in the art. Classically, the detection of PCR amplification products is performed by standard ethidium bromide-stained agarose gel electrophoresis, however, the skilled artisan will readily appreciate that other methods for the detection of specific amplification products, which may be faster and more practical for routine diagnosis, may be used, such as those described in co-pending patent application WO01/23604 A2. Amplicon detection may also be performed by solid support or liquid hybridization using species-specific internal DNA probes hybridizing to an amplification product. Such probes may be generated from any sequence from the MREJ or *nuc* nucleic acid sequences provided herein, and designed to specifically hybridize to DNA amplification products produced utilizing the methods disclosed herein. Alternatively, amplicons can be characterized by sequencing. See, e.g., co-pending patent application WO01/23604 A2 for examples of detection and sequencing methods.

[0120] Other non-limiting examples of nucleic acid detection technologies that can be used in the embodiments disclosed herein include, but are not limited to the use of fluorescence resonance energy transfer (FRET)-based methods such as adjacent hybridization of probes (including probe-probe and probe-primer methods) (*See,* J. R. Lakowicz, "Principles of Fluorescence Spectroscopy," Kluwer Academic/Plenum Publishers, New York, 1999)., TaqMan probe technology (*See,* European Patent EP 0 543 942), molecular beacon probe technology (*See,* Tyagi et al., (1996) *Nat. Biotech.* 14:303–308.), Scorpion probe technology (*See*, Thewell (2000), *Nucl. Acids Res.* 28:3752), nanoparticle probe technology (*See,* Elghanian, et al. (1997) *Science* 277:1078-1081.) and Amplifluor probe technology (*See,* U.S. Pat. No's: 5,866,366; 6,090,592; 6,117,635; and 6,117,986).

[0121] In preferred embodiments, molecular beacons are used for detection of the target nucleic acids. Molecular beacons are single stranded oligonucleotides that, unless bound to target, exist in a hairpin conformation. The 5' end of the oligonucleotide contains a fluorescent dye. A quencher dye is attached to the 3' end of the oligonucleotide. When the beacon is not bound to target, the hairpin structure positions the fluorophore and quencher in close proximity, such that no fluorescence can be observed. Once the beacon hybridizes with target, however, the hairpin structure is disrupted, thereby separating the fluorophore and

quencher and enabling detection of fluorescence. (*See,* Kramer FR., 1996, Nat Biotechnol **3**:303-8.). Other detection methods include target gene nucleic acids detection via immunological methods, solid phase hybridization methods on filters, chips or any other solid support. In these systems, the hybridization can be monitored by any suitable method known to those skilled in the art, including fluorescence, chemiluminescence, potentiometry, mass spectrometry, plasmon resonance, polarimetry, colorimetry, flow cytometry or scanometry. Nucleotide sequencing, including sequencing by dideoxy termination or sequencing by hybridization (e.g. sequencing using a DNA chip) represents another method to detect and characterize target nucleic acids, such as *nuc* or MREJ nucleic acid sequences.

Methods

[0122] In preferred embodiments, methods to detect a *S. aureus* strain in a sample include the step of providing a primer pair, with a first and a second primer. The first and the second primer can anneal under stringent conditions to at least one of **SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11,** or **12**, or the complements thereof, such as primers that comprise, consist essentially of, or consist of **SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11,** or **12**. In preferred embodiments, the primer pairs comprise first and second primers that anneal under stringent conditions to **SEQ ID NOs: 1** and **5; SEQ ID NOs: 1** and **6; SEQ ID NOs: 2** and **5, SEQ ID NOs: 2** and **6; SEQ ID NOs: 3** and **7; SEQ ID NOs: 3** and **8; SEQ ID NOs: 4** and **7;** or **SEQ ID NOs: 4** and **8,** or the complements thereof. For example, in preferred embodiments, the primer pairs can comprise, consist essentially of, **SEQ ID NOs: 1** and **5; SEQ ID NOs: 1** and **6; SEQ ID NOs: 2** and **5, SEQ ID NOs: 2** and **6; SEQ ID NOs: 3** and **7; SEQ ID NOs: 3** and **8; SEQ ID NOs: 4** and **7;** or **SEQ ID NOs: 4** and **8.** The sample can be contacted with and allowed to anneal to the primer pair. Preferably, an amplification reaction (*e.g.*, PCR) is performed with the annealed primer pair to amplify *S. aureus*-specific *nuc* sequences using the techniques described herein. Amplification products can then be detected using any of the methods described herein.

[0123] In some embodiments, the primer pair includes a first primer that anneals under stringent conditions to **SEQ ID NO: 1** or the complement thereof, and a second primer that anneals under stringent conditions to **SEQ ID NO: 6**, or the complement thereof, such as a primer pair that comprises, consists essentially of, or consists of **SEQ ID NO: 1** and **SEQ**

ID NO: 6. In some embodiments, the primer pair is used to amplify *nuc* sequences present in the sample. Optionally, a probe that anneals under stringent conditions to **SEQ ID NO: 9** or **10** or the complement thereof is also provided, for example, a probe that comprises, consists essentially of, or consist of **SEQ ID NO: 9** or **10**. In some embodiments, the probe is a molecular beacon probe, and the resulting amplification product can be detected by the probe.

[0124] In other preferred embodiments, a first primer that anneals under stringent conditions to **SEQ ID NO: 3** or the complement thereof and a second primer that anneals under stringent conditions to **SEQ ID NO: 8**, or the complement thereof, are provided, such as a primer pair that comprises, consists essentially of, or consists of **SEQ ID NO: 3** and **SEQ ID NO: 8**. In some embodiments, the primer pair is used to amplify *nuc* sequences present in the sample. Optionally, a probe that anneals under stringent conditions to **SEQ ID NO: 11** or **12** or the complement thereof is also provided for example, a probe that comprises, consists essentially of, or consist of **SEQ ID NO: 11** or **12**. In some embodiments, the probe is a molecular beacon probe.

[0125] Other aspects of the invention relate to methods and compositions for detecting the presence of *S. aureus* strains and identifying MRSA strains from a sample in a single assay or reaction. The term "single assay" or "single reaction" is intended to refer to the situation in which steps to detect *S. aureus* and steps to detect MRSA are performed simultaneously, or at substantially the same time, for example in the same physical enclosure. The skilled artisan will appreciate, however, that steps to detect *S. aureus* and steps to detect MRSA can also be performed sequentially. In preferred embodiments, *S. aureus* and MRSA are simultaneously detected, for example in a multiplex PCR reaction.

[0126] Some embodiments involve the steps of contacting the sample with at least one primer and/or probe that anneals under stringent conditions to a species-specific sequence of the *nuc* gene of *S. aureus*, and contacting the sample with at least one primer and/or probe that anneals under stringent conditions to a sequence that is specific to MREJ sequences of MRSA strains.

[0127] The MRSA-specific primer(s) and/or probe(s) can anneal under stringent conditions to polymorphic MREJ nucleic acids, including, for example, MREJ types i to xx. The phrase MREJ refers to the *mec* right extremity junction « mec right extremity junction ».

MREJ's are approximately 1 kilobase (kb) in length and include sequences from the SCC*mec* right extremity as well as bacterial chromosomal DNA to the right of the SCC*mec* integration site (*See,* Huletsky et al., (2004) *J.Clin. Microbiol.,* 42:1875–1884). Based on the determination of the whole-genome sequences of strain N315 and Mu50, the nomenclature was recently reviewed because SCC*mec* elements are located downstream (and not upstream) of *orfX*. Consequently, MREP (M*ec* Right Extremity Polymorphism) is also referred to as MLEP (M*ec* Left Extremity Polymorphism). By a similar token, MREJ types can be referred to as MLEJ (mec left extremity junction). (Chongtrakool et al., (2006), Antimicrob. Agents Chemother. 50:1001-1012). Nevertheless, any equivalent way to classify *S. aureus* and namely MRSA strains will be under the scope of this patent, since sequences will be able to specifically detect *S. aureus* and to identify those which are resistant to methicillin.

[0128] Non-limiting examples MREJ type i to xx sequences are listed in **SEQ ID NOs: 14-88**. Accordingly, in some embodiments, in addition to at least one *S. aureus*-specific *nuc* primer and/or probe, (*e.g.*, an oligonucleotide that hybridizes under stringent conditions to one of the following **SEQ ID NO: 200**, the complement thereof or any sequence which differs from **SEQ ID NO: 200** by 1 to 20 nucleotides, at least one primer and/or probe that specifically anneals under stringent conditions to at least one MREJ sequence of MREJ types i-xx (*e.g.*, **SEQ ID NOs: 14-88**) or the complement thereof is provided. Exemplary primers and probes and combinations of primers and probes useful for the detection of MRSA of MREJ types i-xx are found in, for example, International Patent Application PCT/CA02/00824, and in U.S. Patent Application No. 11/248,438, hereby expressly incorporated by reference in their entireties. For example, in some embodiments, the at least one MRSA-specific primer and/or probe provided in the method is at least 10 nucleotides in length, and can hybridize under stringent conditions to one of the following **SEQ ID NOs: 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 15, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 201** (MREJ types i- ix) **182, 183, 184, 195, 186, 187, 188, 189, 190, 191, 193, 194, 195, 196,**

197, (MREJ types xi-xx) or **199,** or the complement thereof. For example, the MRSA-specific primers can comprise, consist essentially of, or consist of one of the following **SEQ ID NOs: 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 15, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 201** (MREJ types i- ix) **182, 183, 184, 195, 186, 187, 188, 189, 190, 191, 193, 194, 195, 196, 197,** (MREJ types xi-xx) or **199.** *nuc*-specific primers and/or probes (*e.g.*, comprising an oligonucleotide that hybridizes under stringent conditions to one of the following **SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11,** or **12** or the complement thereof, such as oligonucleotides that comprise, consist essentially of, or consist of one of the following **SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11,** or **12**) and MRSA (*i.e.*, MREJ)-specific primers and/or probes (*e.g.*, comprising an oligonucleotide that hybridizes under stringent conditions to **SEQ ID NOs: 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 15, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 201** (types i- ix) **182, 183, 184, 195, 186, 187, 188, 189, 190, 191, 193, 194, 195, 196, 197,** (types xi-xx) or **199,** or the complement thereof) are annealed to the nucleic acids of the sample, and the presence of annealed primers and/or probes, or amplification products produced therefrom, is detected, indicating the presence and/or amount of *S. aureus* as well as MRSA. For example, in some embodiments, the sample is contacted with at least one primer pair comprising oligonucleotides that hybridize under stringent conditions to **SEQ ID NOs: 92** and **82; 92** and **83; 92** and **84; 104** and **86; 104** and **87; 104** and **88; 99** and **89; 99** and **199** (for the detection of MREJ type i); **SEQ ID NOs: 92** and **82; 92** and **129; 92** and **130; 93** and **83;** and **92** and **84; 99 and 89; 99** and **199** (for the detection of MREJ type ii); **SEQ ID NOs: 92** and **136; 92** and **137; 92** and **138; 99** and **202; 99** and **144** (for the detection of MREJ type iii); **SEQ ID NOs: 92** and **141; 99** and

105; 99 and **150** (for the detection of MREJ type iv); **SEQ ID NOs: 92** and **146; 99** and **196; 99** and **155** (for the detection of MREJ type v); **SEQ ID NOs: 92** and **152; 99** and **161;** (for the detection of MREJ type vi); **SEQ ID NOs: 92** and **153; 92** and **154; 99** and **162; 99** and **163** (for the detection of MREJ type vii); **SEQ ID NOs: 92** and **162; 92** and **163; 99** and **170** (for the detection of MREJ type viii); **SEQ ID NOs: 92** and **168; 99** and **177** (for the detection of MREJ type ix); **SEQ ID NOs: 197** and an oligonucleotide that hybridizes under stringent conditions to *orf22* (for the detection of MREJ type x); **SEQ ID NOs: 189** and **106; 189** and **99; 189** and **190; 189** and **109** (for the detection of MREJ type xi); **SEQ ID NOs: 194** and **106; 194** and **99; 104** and **191; 194** and **109** (for the detection of MREJ type xii); **SEQ ID NOs: 177** and **106; 177** and **99; 177** and **190;** and **177** and **109** (for the detection of MREJ type xiii); **SEQ ID NOs: 177** and **106; 177** and **99; 177** and **193; 177** and **109** (for the detection of MREJ type xiv); **SEQ ID NOs: 184** and **106; 108** and **99; 184** and **191; 184** and **191** (for the detection of MREJ type xv); **SEQ ID NOs: 89** and **109** (for the detection of MREJ type xvi); **SEQ ID NOs: 185** and **106; 185** and **99; 185** and **191; 185** and **109** (for the detection of MREJ type xvii); **SEQ ID NOs: 186** and **106; 186** and **99; 186** and **193; 186** and **109** (for the detection of MREJ type xviii); **SEQ ID NOs: 187** and **106; 107** and **99; 187** and **913; 187** and **109** (for the detection of MREJ type xix); **SEQ ID NOs: 188** and **106; 188** and **99; 188** and **913;** and **188** and **109** (for the detection of MREJ type xx), or the complement thereof.

[0129] The most clinically relevant MRSA strains have MREJ types i, ii, iii, iv, v, and vii. Accordingly, preferred methods and compositions relate to the detection of *S. aureus* and MRSA of MREJ types i-v and vii in a sample. At least one *S. aureus*-specific *nuc*-specific primer and/or probe is provided, and primers and/or probes useful for the specific detection of MREJ types i, ii, iii, iv, v and vii are provided. For example, in some embodiments, primers and/or probes that hybridize under stringent conditions to each of the following SEQ ID NOs or the complements thereof are provided: **SEQ ID NOs: 99, 199, 144, 150, 155,** and **163,** such as primers and/or probes that comprise, consist essentially of, or consist of at least one of the following **SEQ ID NOs: 99, 199, 144, 150, 155,** and **163**. Optionally, at least one probe comprising an oligonucleotide that hybridizes under stringent conditions to **SEQ ID NOs: 126, 128, 130** and **131** or the complement thereof is provided, for the detection of MREJ

sequences of types i, ii, iii, iv, v and vii. For example, at least one primer and/or probe that comprises, consists essentially of, or consists of at least one of the following **SEQ ID NOs: 126, 128, 130** and **131,** is provided.

[0130] In other preferred embodiments, the at least one primer(s) and/or probe(s) that anneal to MREJ sequences comprises a pair of oligonucleotides that hybridize under stringent conditions to **SEQ ID NOs: 99** and **199** (for the detection of type i and type ii MREJ); **SEQ ID NOs: 99** and **144** (for the detection of type iii MREJ); **SEQ ID NOs: 99** and **150** (for the detection of type iv MREJ); **SEQ ID NOs: 99** and **155** (for the detection of type v MREJ); and **SEQ ID NOs: 99** and **163** (for the detection of type vii MREJ), or the complement thereof. Optionally oligonucleotides that hybridize under stringent conditions to each of **SEQ ID NOs: 99** and **199** (for the detection of type i and type ii MREJ); **SEQ ID NOs: 99** and **144** (for the detection of type iii MREJ); **SEQ ID NOs: 99** and **150** (for the detection of type iv MREJ); **SEQ ID NOs: 99** and **155** (for the detection of type v MREJ); and **SEQ ID NOs: 99** and **163** (for the detection of type vii MREJ) are provided. Optionally, the sample is also contacted with a probe comprising an oligonucleotide that hybridizes under stringent conditions to the nucleic acid of **SEQ ID NOs: 9, 10, 11, 12, 126, 128, 130 or 131,** for the detection of MREJ sequences, or **SEQ ID NOs: 9, 10, 11,** and **12** for the detection of *S. aureus nuc,* or the complements thereof.

[0131] In preferred embodiments, the *nuc*-specific primer(s) and/or probe(s) comprise at least one first primer pair that hybridizes under stringent conditions to the following oligonucleotide pairs or the complements thereof: **SEQ ID NOs: 1** and **5; SEQ ID NOs: 1** and **6; SEQ ID NOs: 2** and **5, SEQ ID NOs: 2** and **6; SEQ ID NOs: 3** and **7; SEQ ID NOs: 3** and **8; SEQ ID NOs: 4** and **7;** or **SEQ ID NOs: 4** and **8;** for the detection of *S. aureus* in a sample. For example, in some embodiments, the *nuc*-specific primer(s) and/or probe(s) comprise at least one first primer pair that comprises, consists essentially of, or consists of: **SEQ ID NOs: 1** and **5; SEQ ID NOs: 1** and **6; SEQ ID NOs: 2** and **5, SEQ ID NOs: 2** and **6; SEQ ID NOs: 3** and **7; SEQ ID NOs: 3** and **8; SEQ ID NOs: 4** and **7;** or **SEQ ID NOs: 4** and **8.** Optionally, in embodiments where the sample is contacted with a first primer pair comprising oligonucleotides that hybridize under stringent conditions to **SEQ ID NOs: 1** and **5,** or **1** and **6,** or the complements thereof, (*e.g.*, oligonucleotides that comprise,

consist essentially of, or consist of **SEQ ID NOs: 1** and **5,** or **SEQ ID NOs: 1** and **6**), the sample can also be contacted with a probe comprising an oligonucleotide that hybridizes under stringent conditions to **SEQ ID NO: 9** (*e.g.,* **SEQ ID NO: 10**) or the complement thereof. Optionally, in embodiments where the sample is contacted with a first primer pair comprising oligonucleotides that hybridize under stringent conditions to **SEQ ID NOs: 3** and **7,** or **SEQ ID NOs: 3** and **8**, or the complements thereof, (*e.g.*, oligonucleotides that comprise, consist essentially of, or consist of **SEQ ID NOs: 3** and **7,** or **SEQ ID NOs: 3** and **8**),the sample can also be contacted with a probe comprising an oligonucleotide that hybridizes under stringent conditions **SEQ ID NO: 11** (*e.g.,* **SEQ ID NO: 12**) or the complement thereof. Preferably, the first primer pair comprises oligonucleotides that hybridize under stringent conditions to **SEQ ID NOs: 1** and **6**; or **SEQ ID NOs: 3** and **8** or the complements thereof.

[0132] Optionally, the sample is also contacted with at least one probe comprising an oligonucleotide that hybridizes under stringent conditions to **SEQ ID NOs: 9, 10, 11, 12,** for the detection of *S. aureus nuc* sequences, or to **SEQ ID NOs: 126, 128, 130** or **131,** for the detection of MREJ sequences, or the complement thereof, *e.g.*, at least one probe that comprises, consists essentially of, or consists of **SEQ ID NOs: 9, 10, 11, 12, 126, 128, 130** or **131**.

[0133] The presence and/or amount of annealed probe(s) can be detected, or the amount of an amplification product produced through annealing of the primers to the nucleic acids can be detected, as an indication of the presence and/or amount of *S. aureus*, and as an indication of the presence and/or amount of MRSA.

Compositions and kits

[0134] Provided herein are also compositions and kits that comprise, consist essentially of, or consist of oligonucleotides described herein. Preferably, oligonucleotides are between 10 and 45 nucleotides in length. For example, oligonucleotides can be at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 31, 32, 33, 34, 35 or more nucleotides in length. As will be understood by those skilled in the art, the nucleic acids of the embodiments disclosed herein can be single-stranded (coding or antisense), or double-stranded, and may be a DNA (genomic, cDNA, or synthetic) or RNA molecule. Additional coding or non-coding sequences may, but need not, be present within a nucleic acid of the

embodiments disclosed herein, and a nucleic acid may, but need not, be linked to other molecules and/or support materials.

[0135] Accordingly, some embodiments comprise, consist essentially of, or consist of, at least one oligonucleotide of between about 10 to about 45 nucleotides, and preferably at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 31, 32, 33, 34, 35 nucleotides in length which hybridizes under stringent conditions with any of nucleic acids of the following sequences derived from *S. aureus nuc* sequences or the complements thereof: **SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11** or **12,** for example, oligonucleotides that comprise, consist essentially of, or consist of at least one of the following **SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11** or **12**. Preferred embodiments comprise, consist essentially of, or consist of a primer pair that hybridizes under stringent conditions with any of the pairs of the following **SEQ ID NOs: 1** and **5; SEQ ID NOs: 1** and **6; SEQ ID NOs: 2** and **5, SEQ ID NOs: 2** and **6; SEQ ID NOs: 3** and **7; SEQ ID NOs: 3** and **8; SEQ ID NOs: 4** and **7;** or **SEQ ID NOs: 4** and **8,** or the complements thereof, for example primer pairs that comprise, consist essentially of, or consist of the following **SEQ ID NOs: 1** and **5; SEQ ID NOs: 1** and **6; SEQ ID NOs: 2** and **5, SEQ ID NOs: 2** and **6; SEQ ID NOs: 3** and **7; SEQ ID NOs: 3** and **8; SEQ ID NOs: 4** and **7;** or **SEQ ID NOs: 4** and **8.** In some embodiments, at least one probe comprising an oligonucleotide that hybridizes under stringent conditions **SEQ ID NOs: 9** and **11** (*e.g.*, **SEQ ID NOs: 10** and **12**), or the complement thereof, is provided.

[0136] Other aspects relate to compositions useful for the detection of *S. aureus* and MRSA in a single reaction. Accordingly, some embodiments comprise, consist essentially of, or consist of, at least one primer and/or probe that is preferably between about 10 to about 45 nucleotides in length, such as an oligonucleotide that is at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 31, 32, 33, 34, 35 in length that hybridizes to an *S. aureus*-specific *nuc* sequence, and at least one primer and/or probe that hybridizes to at least one MREJ sequence of MREJ types i-xx. Some embodiments provide at least two primer pairs, wherein a first primer pair hybridizes under stringent conditions to *S. aureus*-specific *nuc* sequences (*e.g.,* **SEQ ID NOs: 1** and **5; SEQ ID NOs: 1** and **6; SEQ ID NOs: 2** and **5, SEQ ID NOs: 2** and **6; SEQ ID NOs: 3** and **7; SEQ ID NOs: 3** and **8; SEQ ID NOs: 4** and **7;** or **SEQ ID NOs: 4** and **8**) and a second primer pair hybridizes to MREJ sequences (*e.g.*,

SEQ ID NOs: 92 and **82; 92** and **83; 92** and **84; 104** and **86; 104** and **87; 104** and **88; 99** and **89; 99** and **199** (for the detection of MREJ type i); **SEQ ID NOs: 92** and **82; 92** and **129; 92** and **130; 93** and **83;** and **92** and **84; 99 and 89; 99** and **199** (for the detection of MREJ type ii); **SEQ ID NOs: 92** and **136; 92** and **137; 92** and **138; 99** and **202; 99** and **144** (for the detection of MREJ type iii); **SEQ ID NOs: 92** and **141; 99** and **105; 99** and **150** (for the detection of MREJ type iv); **SEQ ID NOs: 92** and **146; 99** and **196; 99** and **155** (for the detection of MREJ type v); **SEQ ID NOs: 92** and **152; 99** and **161;** (for the detection of MREJ type vi); **SEQ ID NOs: 92** and **153; 92** and **154; 99** and **162; 99** and **163** (for the detection of MREJ type vii); **SEQ ID NOs: 92** and **162; 92** and **163; 99** and **170** (for the detection of MREJ type viii); **SEQ ID NOs: 92** and **168; 99** and **177** (for the detection of MREJ type ix); **SEQ ID NOs: 197** and an oligonucleotide that hybridizes under stringent conditions to *orf22* (for the detection of MREJ type x); **SEQ ID NOs: 189** and **106; 189** and **99; 189** and **190; 189** and **109** (for the detection of MREJ type xi); **SEQ ID NOs: 194** and **106; 194** and **99; 104** and **191; 194** and **109** (for the detection of MREJ type xii); **SEQ ID NOs: 177** and **106; 177** and **99; 177** and **190;** and **177** and **109** (for the detection of MREJ type xiii); **SEQ ID NOs: 177** and **106; 177** and **99; 177** and **193; 177** and **109** (for the detection of MREJ type xiv); **SEQ ID NOs: 184** and **106; 108** and **99; 184** and **191; 184** and **191** (for the detection of MREJ type xv); **SEQ ID NOs: 89** and **109** (for the detection of MREJ type xvi); **SEQ ID NOs: 185** and **106; 185** and **99; 185** and **191; 185** and **109** (for the detection of MREJ type xvii); **SEQ ID NOs: 186** and **106; 186** and **99; 186** and **193; 186** and **109** (for the detection of MREJ type xviii); **SEQ ID NOs: 187** and **106; 107** and **99; 187** and **913; 187** and **109** (for the detection of MREJ type xix); **SEQ ID NOs: 188** and **106; 188** and **99; 188** and **913;** and **188** and **109** (for the detection of MREJ type xx)). In some embodiments, at least one probe(s) that can hybridize to amplification products produced by an *S. aureus*-specific *nuc* primer pair and/or MREJ-specific primer pair described herein is also provided (*e.g.*, **SEQ ID NOs: 9, 10, 11, 12, 126, 128, 130 or 131**).

[0137] Accordingly, some embodiments comprise, consist essentially of, or consist of primer pairs that hybridize under stringent conditions to the nucleic acid sequences of:

[0138] **SEQ ID NOs: 1** and **6**

[0139] **SEQ ID NOs: 99** and **199;**

[0140] **SEQ ID NOs: 99** and **144;**

[0141] **SEQ ID NOs: 99** and **150;**

[0142] **SEQ ID NOs: 99** and **155;** and

[0143] **SEQ ID NOs: 99** and **163,** or the complements thereof.

[0144] Other embodiments comprise, consist essentially of, or consist of a plurality of primer pairs, wherein the primers anneal under stringent conditions to the nucleic acid sequences of:

[0145] **SEQ ID NOs: 3** and **8;**

[0146] **SEQ ID NOs: 99** and **199;**

[0147] **SEQ ID NOs: 99** and **144;**

[0148] **SEQ ID NOs: 99** and **150;**

[0149] **SEQ ID NOs: 99** and **155;** and

[0150] **SEQ ID NOs: 99** and **163,** or the complements thereof.

[0151] Still other aspects relate to kits for the detection and/or quantification of *S. aureus*, or *S. aureus* and MRSA. In some embodiments, the kits comprise, consist essentially of, or consist of, at least one oligonucleotide of between about 10 to about 45 nucleotides in length, for example at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 31, 32, 33, 34, 35 nucleotides in length, which hybridizes under stringent conditions with any of nucleic acids of the following sequences derived from *S. aureus nuc* sequences or the complements thereof: **SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11** or **12**. Preferred embodiments provide kits that comprise, consist essentially of, or consist of a primer pair that hybridizes under stringent conditions with any of the pairs of the following **SEQ ID NOs: 1** and **5; SEQ ID NOs: 1** and **6; SEQ ID NOs: 2** and **5, SEQ ID NOs: 2** and **6; SEQ ID NOs: 3** and **7; SEQ ID NOs: 3** and **8; SEQ ID NOs: 4** and **7;** or **SEQ ID NOs: 4** and **8,** or the complements thereof**.** In some embodiments, the kit provides at least one probe comprising an oligonucleotide that hybridizes under stringent conditions **SEQ ID NOs: 9** and **11** (*e.g.*, **SEQ ID NOs: 10** and **12**), or the complement thereof**.**

[0152] Other embodiments provide kits useful for the detection of *S. aureus* and MRSA together. In some embodiments, the kits comprise, consist essentially of, or consist of, at least one primer and/or probe that is between about 10 to about 45 nucleotides in length,

for example, at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 31, 32, 33, 34, 35 nucleotides in length, that hybridizes to an *S. aureus*-specific *nuc* sequence, and at least one primer and/or probe that hybridizes to at least one MREJ sequence of MREJ types i-xx. Some embodiments provide kits, wherein the kits include at least two primer pairs. A first primer pair can hybridize under stringent conditions to *S. aureus*-specific *nuc* sequences (*e.g.*, primers that are at least 10 nucleotides in length and can hybridize under stringent conditions to **SEQ ID NOs: 1** and **5; SEQ ID NOs: 1** and **6; SEQ ID NOs: 2** and **5, SEQ ID NOs: 2** and **6; SEQ ID NOs: 3** and **7; SEQ ID NOs: 3** and **8; SEQ ID NOs: 4** and **7;** or **SEQ ID NOs: 4** and **8**, or the complement thereof) and a second primer pair can hybridize under stringent conditions to MREJ sequences (*e.g.*, primers that are at least 10 nucleotides in length and can hybridize under stringent conditions to **SEQ ID NOs: 92** and **82; 92** and **83; 92** and **84; 104** and **86; 104** and **87; 104** and **88; 99** and **89; 99** and **199** (for the detection of MREJ type i); **SEQ ID NOs: 92** and **82; 92** and **129; 92** and **130; 93** and **83;** and **92** and **84; 99 and 89; 99** and **199** (for the detection of MREJ type ii); **SEQ ID NOs: 92** and **136; 92** and **137; 92** and **138; 99** and **202; 99** and **144** (for the detection of MREJ type iii); **SEQ ID NOs: 92** and **141; 99** and **105; 99** and **150** (for the detection of MREJ type iv); **SEQ ID NOs: 92** and **146; 99** and **196; 99** and **155** (for the detection of MREJ type v); **SEQ ID NOs: 92** and **152; 99** and **161;** (for the detection of MREJ type vi); **SEQ ID NOs: 92** and **153; 92** and **154; 99** and **162; 99** and **163** (for the detection of MREJ type vii); **SEQ ID NOs: 92** and **162; 92** and **163; 99** and **170** (for the detection of MREJ type viii); **SEQ ID NOs: 92** and **168; 99** and **177** (for the detection of MREJ type ix); **SEQ ID NOs: 197** and an oligonucleotide that hybridizes under stringent conditions to *orf22* (for the detection of MREJ type x); **SEQ ID NOs: 189** and **106; 189** and **99; 189** and **190; 189** and **109** (for the detection of MREJ type xi); **SEQ ID NOs: 194** and **106; 194** and **99; 104** and **191; 194** and **109** (for the detection of MREJ type xii); **SEQ ID NOs: 177** and **106; 177** and **99; 177** and **190;** and **177** and **109** (for the detection of MREJ type xiii); **SEQ ID NOs: 177** and **106; 177** and **99; 177** and **193; 177** and **109** (for the detection of MREJ type xiv); **SEQ ID NOs: 184** and **106; 108** and **99; 184** and **191; 184** and **191** (for the detection of MREJ type xv); **SEQ ID NOs: 89** and **109** (for the detection of MREJ type xvi); **SEQ ID NOs: 185** and **106; 185** and **99; 185** and **191; 185** and **109** (for the detection of MREJ type xvii); **SEQ ID NOs: 186**

and **106; 186** and **99; 186** and **193; 186** and **109** (for the detection of MREJ type xviii); **SEQ ID NOs: 187** and **106; 107** and **99; 187** and **913; 187** and **109** (for the detection of MREJ type xix); **SEQ ID NOs: 188** and **106; 188** and **99; 188** and **913;** and **188** and **109** (for the detection of MREJ type xx) or the complements thereof). In some embodiments, the kits include at least one probe(s) that can hybridize under stringent conditions to amplification products produced by an *S. aureus*-specific *nuc* primer pair and/or MREJ-specific primer pair described herein is also provided (*e.g.*, a probe comprising an oligonucleotide that can hybridize under stringent conditions to **SEQ ID NOs: 9, 10, 11, 12, 126, 128, 130 or 131** or the complement thereof).

[0153] Accordingly, some embodiments provide kits that comprise, consist essentially of, or consist of primer pairs that hybridize under stringent conditions to the nucleic acid sequences of:

[0154] **SEQ ID NOs: 1** and **6**

[0155] **SEQ ID NOs: 99** and **199;**

[0156] **SEQ ID NOs: 99** and **144;**

[0157] **SEQ ID NOs: 99** and **150;**

[0158] **SEQ ID NOs: 99** and **155;** and

[0159] **SEQ ID NOs: 99** and **163,** or the complements thereof.

[0160] Other embodiments provide kits that comprise, consist essentially of, or consist of a plurality of primer pairs, wherein the primers anneal under stringent conditions to the nucleic acid sequences of:

[0161] **SEQ ID NOs: 3** and **8;**

[0162] **SEQ ID NOs: 99** and **199;**

[0163] **SEQ ID NOs: 99** and **144;**

[0164] **SEQ ID NOs: 99** and **150;**

[0165] **SEQ ID NOs: 99** and **155;** and

[0166] **SEQ ID NOs: 99** and **163,** or the complements thereof.

[0167] The diagnostic kits, primers and probes disclosed herein can be used to detect and/or identify *S. aureus*, as well as detect and/or identify both *S. aureus* and MRSA of MREJ types i to xx, in both *in vitro* and/or *in situ* applications. For example, it is

contemplated that the kits may be used in combination with any previously described primers/probes for detecting MRSA of MREJ types i to xx. It is also contemplated that the diagnostic kits, primers and probes disclosed herein can be used alone or in combination with any other assay suitable to detect and/or identify microorganisms, including but not limited to: any assay based on nucleic acids detection, any immunoassay, any enzymatic assay, any biochemical assay, any lysotypic assay, any serological assay, any differential culture medium, any enrichment culture medium, any selective culture medium, any specific assay medium, any identification culture medium, any enumeration culture medium, any cellular stain, any culture on specific cell lines, and any infectivity assay on animals.

[0168] Having generally described this invention, a further understanding can be obtained by reference to certain specific examples which are provided herein for purposes of illustration only, and are not intended to be limiting.

EXAMPLE 1

[0169] This example illustrates the utility of various primer pairs, chosen for optimized, specific detection of *S. aureus* from a sample using PCR. **SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8** were designed to anneal to *S. aureus*-specific regions of the *nuc* gene. PCR reaction mixtures included 0.5μM of each of the indicated primers, 0.2mM dNTPs (Roche), 2mM $MgCl_2$ (SIGMA), 1 unit FASTSTART™ Taq DNA polymerase (Roche), 50 mM Tris (EMD), 10 mM KCl (Laboratoire Mat), and 5mM $(NH_4)_2SO_4$ (SIGMA).

[0170] For each primer pair tested, three replicates containing varying amounts of chromosomal template DNA were run. One set of reactions included 15 copies of chromosomal template DNA from *S. aureus* strain ATCC 43300 (MRSA). Another set of reactions included 185 copies of ATCC 43300 template DNA. A negative control was also run, which did not have any added template DNA. Parallel sets of reactions were run with chromosomal template DNA from *S. aureus* strain ATCC 25923 (MSSA).

[0171] PCR reactions were performed using a SMARTCYCLER® QT-PCR machine (Cepheid). The cycling parameters were as follows: 95°C for 900min, followed by 45 cycles of 95°C for 5 sec, 59°C for 15 sec and 72°C for 20 sec. Amplified products were visualized on agarose gels (Figures 1A and 1B).

[0172] As shown in Figures 1A and 1B, the following primer pairs showed particularly good results in the specific amplification of DNA from both MSSA and MRSA *S. aureus* strains:

[0173] **SEQ ID NOs: 1** and **5**

[0174] **SEQ ID NOs: 1** and **6**

[0175] **SEQ ID NOs: 2** and **6**

[0176] **SEQ ID NOs: 4** and **7**

[0177] **SEQ ID NOs: 4** and **8**

[0178] **SEQ ID NOs: 3** and **7,** and

[0179] **SEQ ID NOs: 3** and **8**.

[0180] The primer pair **SEQ ID NOs: 2** and **5** was less sensitive, as indicated by the relative amount of amplification product produced, compared to other primer pairs.

EXAMPLE 2

[0181] The ability to detect *S. aureus* and to identify MRSA in a single reaction was tested. A multiplex PCR reaction was designed to include primers that anneal under standard PCR conditions to the *S. aureus* species-specific *orfX* sequence and a sequence of SCC*mec* right extremity junction (MREJ) of the most commonly clinically encountered MRSA types (*i.e.*, MRSA of MREJ types i, ii, iii, iv, v, vii). **SEQ ID NOs: 99, 199, 144, 150, 155** and **163** were used for the detection of MRSA of MREJ types i, ii, iii, iv, v, and vii. Primers that anneal to *S. aureus* specific regions of the *nuc* gene under the same conditions (**SEQ ID NOs: 3** and **8**) were used in the reaction for the detection of both MRSA and MSSA strains in the test reactions. Molecular beacon probes which are detectable on the SMARTCYCLER® apparatus at FAM, Texas Red and TET channels were designed for hybridization to amplification products of the MRSA specific reactions **(SEQ ID NOs: 126 and 130**), *nuc/S. aureus* specific reactions (**SEQ ID NO: 12**), and an internal control, respectively.

[0182] PCR reactions included 0.9μM **SEQ ID NO: 99**, 0.4μM **SEQ ID NO: 199**; 0.6μM **SEQ ID NO: 144**, 0.3μM **SEQ ID NO: 150**, 0.2μM **SEQ ID NO: 155**, 0.7μM **SEQ ID NO: 163**, 0.1μM **SEQ ID NO: 3**, 0.1μM **SEQ ID NO: 8**, 0.1μM **SEQ ID NO: 126**, 0.1μM **SEQ ID NO: 130**, 0.25μM **SEQ ID NO: 12**, 0.2μM control DNA, 0.3mM

dNTPs (Roche) 4mM $MgCl_2$ (SIGMA), 2.8 units FASTSTART® Taq DNA polymerase (Roche), 100mM Tris, pH 8.3 (EMD), 10mM KCl (Laboratoire Mat), 5mM $(NH4)_2SO_4$ (SIGMA), 0.15mg/mL BSA (SIGMA), 4% Trehalose (SIGMA), 3000 copies of internal control template DNA, 2780 copies of *S. epidermidis* chromosomal DNA, and either 0, 2.5, 5, 10, 15 or 20 copies MSSA chromosomal DNA (isolated from ATCC strain 25923) or 0, 2.5, 5, 10 or 20 copies of MRSA chromosomal DNA (isolated from ATCC strain 43300).

[0183] PRC reactions were performed in a SMARTCYCLER® instrument (Cepheid). Cycling parameters were as follows: 95°C for 900min, followed by 45 cycles of 95°C for 5 sec, 59°C for 15 sec and 72°C for 20 sec. The fluorescence was continuously measured at the appropriate wavelengths, and is graphically depicted in Figures 2A and 2B.

[0184] Figure 2A depicts the fluorescence readings of reactions containing MSSA template DNA. Under these reaction conditions, 2.5 copies of MSSA DNA were easily detected (Texas Red Channel), demonstrating the utility of **SEQ ID NOs: 3, 8** and **12** in multiplex PCR. As expected, positive signals are also present in the TET channel indicating that the internal control worked properly, and that no inhibitors were present in the reactions.

[0185] Figure 2B depicts the fluorescence readings of reactions containing MRSA template DNA. Under these reaction conditions, 2.5 copies of MRSA DNA were easily detected (FAM channel). This demonstrates the utility of **SEQ ID NOs: 99, 199, 150, 155, 144, 126,** and **130** in a multiplex PCR that can detect all *S. aureus* strains, including MRSA. As shown in the Texas-Red channel, the *nuc*-specific primers and probes (**SEQ ID NOs: 3, 8,** and **12**) detected 2.5 copies of DNA. Positive signals are also present in the TET channel, indicating that the internal control worked properly, and that no inhibitors were present in the reactions.

[0186] This example highlights the very high sensitivity obtainable with a PCR multiplex assay that amplifies MREJ sequences from MRSA and *nuc* sequences from *S. aureus* with an internal control.

EXAMPLE 3

[0187] The specificity of a multiplex PCR assay that amplifies MREJ sequences from MRSA and the *nuc* sequence from *S. aureus* was analyzed. Chromosomal DNA from

80 bacterial species other than *S. aureus* was used as template DNA in a multiplex PCR assay as described in Example 2. The strains tested are enumerated in Table 2.

[0188] 1ng of chromosomal DNA isolated from each species indicated in Table 1 was used in a separate reaction containing 0.9μM **SEQ ID NO: 99**, 0.4μM **SEQ ID NO: 199**; 0.6μM **SEQ ID NO: 144**, 0.3μM **SEQ ID NO: 150**, 0.2μM **SEQ ID NO: 155**, 0.7μM **SEQ ID NO: 163**, 0.1μM **SEQ ID NO: 3**, 0.1μM **SEQ ID NO: 8**, 0.1μM **SEQ ID NO: 126**, 0.1μM **SEQ ID NO: 131**, 0.25μM **SEQ ID NO: 11**, 0.2μM internal control DNA, 0.3mM dNTPs (Roche) 4mM $MgCl_2$ (SIGMA), 2.8 units FASTSTART® Taq DNA polymerase (Roche), 100mM Tris, pH 8.3 (EMD), 10mM KCl (Laboratoire Mat), 5mM $(NH_4)_2SO_4$ (SIGMA), 0.15mg/mL BSA (SIGMA), 4% Trehalose (SIGMA), 3000 copies of internal control template DNA, and 2780 copies of *S. epidermidis* DNA.

[0189] Each reaction was performed in triplicate. The reactions were allowed to proceed following the parameters set forth in Example 2. Table 2 summarizes the results of the reactions. No positive signal was observed in the FAM and Texas Red channels for the 80 different species tested. A positive signal was detected in the TET channel for each of the 80 different species tested, indicating that the reactions did not contain inhibitors. The algorithm of interpretation of results is summarized in Table 3.

Table 2

Species	Strain number	PCR results		
		MRSA (FAM)	IC (TET)	*S. aureus* (Texas Red)
Acinetobacter baumannii	ATCC 19606	-	+	-
Acinetobacter lwoffi	CDCF 3697	-	+	-
Actinomyces israelii	ATCC 12102	-	+	-
Actinomyces pyogenes	ATCC 19411	-	+	-
Bacillus cereus	ATCC 14579	-	+	-
Bacteroides fragilis	ATCC 25285	-	+	-
Bifidobacterium breve	ATCC 15700	-	+	-
Bordetella pertusis	ATCC 9797	-	+	-
Corynebacterium genitalium	LSPQ3583	-	+	-
Corynebacterium aquaticus	ATCC 14665	-	+	-
Corynebacterium bovis	ATCC 7715	-	+	-
Corynebacterium flavescens	ATCC 10340	-	+	-
Enterobacter cloacae	ATCC 13047	-	+	-

Species	Strain number	PCR results		
		MRSA (FAM)	IC (TET)	*S. aureus* (Texas Red)
Enterococcus faecalis	ATCC19433	-	+	-
Enterococcus faecium	ATCC 19434	-	+	-
Enterococcus flavescens	ATCC 49996	-	+	-
Enterrococcus gallinarum	ATCC 49573	-	+	-
Enterrococcus hirae	ATCC 8043	-	+	-
Escherichia coli	ATCC 23511	-	+	-
Helicobacter pylori	IDI-2019	-	+	-
Fusobacterium nucleatum subsp. Polymorphum	ATCC 10953	-	+	-
Gardnerella vaginalis	ATCC 14019	-	+	-
Haemophilus influenzae	ATCC 9006	-	+	-
Homo sapiens	2.16	-	+	-
Klebsiella pneumoniae	ATCC 13883	-	+	-
Lactobacillus crispatus	ATCC 33820	-	+	-
Listeria monocytogenes	L 374	-	+	-
Micrococcus luteus	ATCC 9341	-	+	-
Moraxella catarrhalis	ATCC 43628	-	+	-
Neisseria gonorrhoeae	ATCC 35201	-	+	-
Neisseria meningitides	ATCC 13077	-	+	-
Pasteurella aerogenes	ATCC 27883	-	+	-
Peptostreptococcus anaerobius	ATCC 27337	-	+	-
Peptostreptococcus asaccharolyticus	LSPQ 2639	-	+	-
Porphyromonas asaccharolytica	ATCC 25260	-	+	-
Prevotella melaninogenica	ATCC 25845	-	+	-
Propionibacterium acnes	ATCC 6919	-	+	-
Proteus mirabilis	ATCC 29906	-	+	-
Pseudomonas aeruginosa	ATCC 35554	-	+	-
Pseudomonas fluorescens	ATCC 13525	-	+	-
Salmonella typhimurium	ATCC 14028	-	+	-
Serratia marcescens	ATCC 13880	-	+	-
Shigella sonnei	ATCC 29930	-	+	-
Staphylococcus arlettae	CCRI-9265	-	+	-
Staphylococcus auricularis	R413	-	+	-
Staphylococcus capitis	CCRI-9572	-	+	-
Staphylococcus caprae	CCRI-9117	-	+	-
Staphylococcus carnosus	R714	-	+	-
Staphylococcus chromogenes	ATCC 43764	-	+	-
Staphylococcus cohnii subsp. Urealyticum	R570	-	+	-
Staphylococcus delphini	ATCC 49171	-	+	-

Species	Strain number	PCR results		
		MRSA (FAM)	IC (TET)	*S. aureus* (Texas Red)
Staphylococcus epidermidis	ATCC 35984	-	+	-
Staphylococcus equorum	ATCC 43958	-	+	-
Staphylococcus felis	ATCC 49168	-	+	-
Staphylococcus gallinarum	ATCC 35539	-	+	-
Staphylococcus haemolyticus	ATCC 29970	-	+	-
Staphylococcus hominis	CCRI-1347	-	+	-
Staphylococcus intermedius	ATCC 29663	-	+	-
Staphylococcus kloosii	ATCC 43959	-	+	-
Staphylococcus lentus	ATCC 29070	-	+	-
Staphylococcus lugdunensis	ATCC 43809	-	+	-
Staphylococcus pasteuri	ATCC 51129	-	+	-
Staphylococcus pulvereri	ATCC 51698	-	+	-
Staphylococcus saprophyticus	ATCC 15305	-	+	-
Staphylococcus sciuri	R573	-	+	-
Staphylococcus simulans	ATCC 27848	-	+	-
Staphylococcus warneri	ATCC 35985	-	+	-
Staphylococcus xylosus	LSPQ2517	-	+	-
Streptococcus agalactiae	ATCC 12973	-	+	-
Streptococcus anginosus	ATCC 33397	-	+	-
Streptococcus mitis	ATCC 49456	-	+	-
Streptococcus mutans	ATCC 25175	-	+	-
Streptococcus pneumoniae	ATCC 49619	-	+	-
Streptococcus pyogenes	ATCC 12384	-	+	-
Streptococcus salivarius	ATCC 7073	-	+	-
Streptococcus sanguinis	ATCC 10556	-	+	-
Streptococcus suis	ATCC 43765	-	+	-
Yersinia enterocolitica	ATCC 23715	-	+	-
Candida albicans	ATCC 10231	-	+	-
Candida glabrata	ATCC 66032	-	+	-

Table 3

FAM Assay Result Reported	Texas-Red Assay Result Reported	IC (TET) Result Reported	Interpretation of Result
Negative	Negative	PASS	No *S. aureus* DNA detected
Positive	Positive or Negative	N/A	MRSA DNA detected
Negative	Positive	N/A	*S. aureus* DNA detected, no MRSA DNA detected
Unresolved		Fail	Unresolved- inhibitory specimen or reagent

		failure

[0190] This example highlights the complete specificity reached with a PCR multiplex assay that amplifies MREJ sequences from MRSA and *nuc* sequence from *S. aureus* with an internal control.

EXAMPLE 4

[0191] The ability of a multiplex PCR assay that amplifies MREJ sequences from MRSA and *nuc* sequence from *S. aureus* to accurately detect *S. aureus* and identify MRSA directly from wound specimens was tested.

[0192] A multiplex PCR reaction was designed to include primers to amplify sequences specific to the MREJ regions of the most clinically relevant MRSA (*e.g.*, primers that anneal to *S. aureus* species-specific *orfX* sequences and SCC*mec* sequences), as well as primers that anneal to *S. aureus* specific regions of the *nuc* gene of all *S. aureus* strains (*e.g.*, MRSA and MSSA), under the same conditions. Briefly, **SEQ ID NOs: 99, 199, 144, 150, 155** and **163** were used for amplification of sequences of the MREJ region of various MRSA of MREJ types i, ii, iii, iv, v, and vii. Primers that anneal to *S. aureus* specific regions of the *nuc* gene under the same conditions (**SEQ ID NOs: 3 and 8**) were used in the reaction for the detection of both MRSA and MSSA strains in the test reactions. Molecular beacon probes which are detectable on the SMARTCYCLER® apparatus at FAM, Texas Red and Tet channels were designed for hybridization to amplification products of the MRSA specific reactions (**SEQ ID NOs: 126** and **130**), *nuc/S. aureus* specific reactions (**SEQ ID NO: 12**), and the internal control, respectively.

[0193] One hundred and three wound samples were collected on patients using Amies liquid swabs (Copan Diagnostics, Inc). Samples were cultured and subcultured on blood agar plates (Becton Dickinson). Based on their morphology, suspected *S. aureus* were identified with a coagulase test (Jorgenson, J. H., and W. E. Kloos. 1987. Staphylococcal Infections, in B. B. Wentworth (ed.), Diagnostic procedures for bacterial infections, 7th ed., American Public Health Association,Washington, D. C.) and in some cases with latex agglutination (Staphaurex, Remel Inc.) Methicillin resistance was determined using the VITEK™ bacterial identification system (bioMérieux, Durham, NC).

[0194] DNA was isolated from the isolates using the IDI™ lysis kit (GeneOhm Sciences, Inc.). A swab of the isolate was broken in 1mL of TE buffer (10mM Tris, 1mM EDTA, pH 8.0) and vortexed for 1min at high speed. 50µL of the cell suspensions were transferred to a lysis tube containing glass beads and vortexed for 5 minutes at high speed. The tubes were centrifuged at 13,000 rpms for 2min and heated at 95°C for 2 minutes. The tube was placed on ice until used in the reaction.

[0195] 3µL of the lysis reaction was added to a PCR mix that contained 0.9µM **SEQ ID NO: 99**, 0.4µM **SEQ ID NO: 199**, 0.6µM **SEQ ID NO: 144**, 0.3µM **SEQ ID NO: 150**, 0.2µM **SEQ ID NO: 155**, 0.7µM **SEQ ID NO: 163**, 0.1µM **SEQ ID NO: 3**, 0.1µM **SEQ ID NO: 8**, 0.1µM **SEQ ID NO: 126**, 0.1µM **SEQ ID NO: 130**, 0.25µM **SEQ ID NO:12**, 0.2µM internal control DNA, 0.3µM dNTPs (Roche), 4mM $MgCl_2$ (SIGMA), 2.8 units FASTSTART® Taq polymerase (Roche), 100mM Tris, pH 8.3 (EMD), 10mM KCl (LaboratoireMat), 5mM $(NH_4)_2SO_4$ (SIGMA), 0.15 mg/mL BSA (SIGMA) 4% trehalose (SIGMA), 3000 copies internal control DNA, and 2780 copies *S. epidermidis* chromosomal DNA.

[0196] PCR was carried out in a SMARTCYCLER® (Cepheid) using the same cycling parameters as described in Example 2. For each specimen, the cycle threshold (CT) in FAM, Texas-Red, and TET channels was determined using the SMARTCYCLER® software. Assay results were interpreted as indicated in Table 3:

[0197] The multiplex PCR assay above is designed such that any *S. aureus* strain produces a positive signal in the Texas-Red channel. The presence of a clinically relevant MRSA will produce a positive signal in the FAM channel. Accordingly, a negative result in the FAM channel combined with a positive result in the Texas-Red channel is indicative of the presence of MSSA.

[0198] In instances where a discordant result appeared between culture assays described above, and the multiplex PCR reaction, Tryptic Soy Broth was added to the TE buffer tube containing the swab, and incubated overnight, at 35°C. 50µL of the overnight culture was plated on blood agar plates and isolates were identified as MRSA, MSSA, or negative (no *S. aureus*).

[0199] The data collected are depicted in Tables 4A, 4B and 4C, below.

Table 4A

(A)		PCR				
		MRSA	MSSA	Negative	Total	Unresolved
Culture	MRSA	27 (32)*	0 (0)	0 (0)	27 (32)	1 (0)
	MSSA	2 (2)	18 (19)	1 (0)	21 (21)	1 (0)
	Negative	4 (0)	1 (1)	43 (45)	48 (46)	5 (4)
	Total	33 (34)	19 (20)	44 (45)	96 (99)	7 (4)

* before resolution of discordant results (after resolution of discordant results)

Table 4B

	before resolution	after resolution
MRSA sensitivity	100% (27/27)	100% (32/32)
MSSA sensitivity	85.7% (18/21)	90.5 % (19/21)
S.aureus sensitivity	97.9% (47/48)	100% (53/53)
Specificity	89.6% (43/48)	97.8% (45/46)
Unresolved	6.8% (7/103)	3.9% (4/103)

Table 4C

Specimen number	Culture result	PCR result			
		Status	MRSA (FAM CT)	IC (TET CT)	*S.aureus* (Texas Red CT)
1	MSSA	MSSA	0.0	0.0	23.5
2	NEGATIVE	Unresolved	0.0	37.5	0.0
3	MSSA	MSSA	0.0	0.0	30.5
4	NEGATIVE	NEGATIVE	0.0	37.8	0.0
5	NEGATIVE	NEGATIVE	0.0	37.3	0.0
6	MRSA	MRSA	25.0	0.0	24.5
7	MRSA	MRSA	36.0	0.0	0.0
8	MSSA	MRSA	30.7	0.0	33.0
9	MSSA	MSSA	0.0	0.0	23.8
10	NEGATIVE	NEGATIVE	0.0	37.3	0.0
11	MRSA	MRSA	27.8	0.0	27.5
12	NEGATIVE	NEGATIVE	0.0	37.1	0.0
13	NEGATIVE	NEGATIVE	0.0	37.1	0.0
14	MRSA	MRSA	25.6	0.0	25.0

Specimen number	Culture result	PCR result			
		Status	MRSA (FAM CT)	IC (TET CT)	*S.aureus* (Texas Red CT)
15	MSSA	MSSA	0.0	37.1	35.7
16	NEGATIVE	NEGATIVE	0.0	37.1	0.0
17	MRSA	MRSA	23.9	0.0	23.5
18	MRSA	MRSA	25.2	0.0	24.5
19	MSSA	MSSA	0.0	0.0	21.5
20	NEGATIVE	NEGATIVE	0.0	37.0	0.0
21	MSSA	MSSA	0.0	0.0	21.3
22	NEGATIVE	NEGATIVE	0.0	36.6	0.0
23	MRSA	MRSA	26.9	0.0	26.7
24	MRSA	MRSA	23.2	0.0	21.5
25	MSSA	MRSA	37.1	38.0	38.5
26	NEGATIVE	NEGATIVE	0.0	38.7	0.0
27	NEGATIVE	NEGATIVE	0.0	37.2	0.0
28	NEGATIVE	NEGATIVE	0.0	36.9	0.0
29	MRSA	MRSA	27.1	0.0	26.5
30	NEGATIVE	NEGATIVE	0.0	38.5	0.0
31	NEGATIVE	NEGATIVE	0.0	37.3	0.0
32	NEGATIVE	NEGATIVE	0.0	37.0	0.0
33	NEGATIVE	NEGATIVE	0.0	37.1	0.0
34	NEGATIVE	Unresolved	0.0	36.8	0.0
35	NEGATIVE	NEGATIVE	0.0	36.0	0.0
36	MRSA	MRSA	25.9	0.0	25.8
37	NEGATIVE	NEGATIVE	0.0	36.9	0.0
38	NEGATIVE	NEGATIVE	0.0	37.2	0.0
39	MSSA	MSSA	0.0	0.0	28.5
40	NEGATIVE	NEGATIVE	0.0	37.4	0.0
41	NEGATIVE	NEGATIVE	0.0	39.2	0.0
42	NEGATIVE	MSSA	0.0	0.0	34.7
43	NEGATIVE	NEGATIVE	0.0	36.9	0.0
44	NEGATIVE	NEGATIVE	0.0	37.3	0.0
45	NEGATIVE	NEGATIVE	0.0	38.5	0.0
46	NEGATIVE	NEGATIVE	0.0	37.5	0.0
47	NEGATIVE	NEGATIVE	0.0	36.7	0.0
48	MSSA	MSSA	0.0	36.0	34.9
49	MSSA	MSSA	0.0	0.0	29.0
50	NEGATIVE	NEGATIVE	0.0	37.7	0.0

Specimen number	Culture result	PCR result			
		Status	MRSA (FAM CT)	IC (TET CT)	*S.aureus* (Texas Red CT)
51	NEGATIVE	NEGATIVE	0.0	36.8	0.0
52	MRSA	MRSA	27.6	0.0	23.8
53	MSSA	MSSA	0.0	0.0	25.7
54	MSSA	MSSA	0.0	34.8	32.8
55	MRSA	MRSA	24.5	0.0	24.9
56	NEGATIVE	NEGATIVE	0.0	36.5	0.0
57	NEGATIVE	NEGATIVE	0.0	36.7	0.0
58	MRSA	MRSA	24.3	0.0	24.0
59	MRSA	MRSA	22.5	0.0	21.5
60	MRSA	MRSA	28.9	0.0	28.7
61	NEGATIVE	Unresolved	0.0	0.0	0.0
62	NEGATIVE	NEGATIVE	0.0	36.7	0.0
63	MRSA	MRSA	23.9	0.0	23.5
64	MSSA	MSSA	0.0	0.0	23.8
65	MRSA	MRSA	29.4	0.0	29.5
66	MRSA	MRSA	33.7	0.0	33.8
67	NEGATIVE	NEGATIVE	0.0	36.5	0.0
68	NEGATIVE	NEGATIVE	0.0	36.9	0.0
69	MRSA	MRSA	23.2	0.0	22.5
70	MRSA	MRSA	23.6	0.0	22.5
71	MRSA	MRSA	37.4	0.0	0.0
72	MSSA	MSSA	0.0	0.0	22.0
73	NEGATIVE	NEGATIVE	0.0	35.7	0.0
74	MRSA	MRSA	36.3	36.8	35.7
75	NEGATIVE	NEGATIVE	0.0	36.5	0.0
76	NEGATIVE	NEGATIVE	0.0	36.7	0.0
77	MRSA	MRSA	22.3	0.0	22.1
78	NEGATIVE	NEGATIVE	0.0	37.1	0.0
79	NEGATIVE	NEGATIVE	0.0	34.9	0.0
80	NEGATIVE	NEGATIVE	0.0	36.2	0.0
81	MRSA	MRSA	21.5	0.0	22.5
82	NEGATIVE	NEGATIVE	0.0	37.7	0.0
83	MSSA	MSSA	0.0	0.0	22.7
84	MSSA	MSSA	0.0	0.0	22.7
85	MRSA	MRSA	22.9	0.0	23.0
86	NEGATIVE	NEGATIVE	0.0	37.9	0.0

Specimen number	Culture result	PCR result			
		Status	MRSA (FAM CT)	IC (TET CT)	*S.aureus* (Texas Red CT)
87	MRSA	MRSA	32.3	0.0	33.7
88	MSSA	MSSA	0.0	0.0	30.0
89	MRSA	MRSA	21.3	0.0	21.5
90	NEGATIVE	NEGATIVE	0.0	37.4	0.0
91	NEGATIVE	NEGATIVE	0.0	39.2	0.0
92	MSSA	MSSA	0.0	0.0	31.2
93	MRSA	MRSA	31.9	0.0	32.0
94	NEGATIVE	Unresolved	0.0	0.0	0.0
95	MSSA	MSSA	0.0	0.0	25.1
96	NEGATIVE	NEGATIVE	0.0	36.8	0.0
97	MSSA	MSSA	0.0	37.5	41.7
98	MRSA	MRSA	32.5	0.0	32.9
99	NEGATIVE	NEGATIVE	0.0	37.2	0.0
100	MRSA	MRSA	28.8	0.0	29.5
101	MRSA	MRSA	23.2	0.0	0.0
102	NEGATIVE	NEGATIVE	0.0	36.6	0.0
103	MRSA	MRSA	35.2	35.7	36.0

[0200] As shown in Tables 4A and 4B, the multiplex assay is 100% sensitive for MRSA, indicating that every positive MRSA result achieved in the PCR assay corresponded to a positive result in the culture identification, both before and after resolution. The sensitivity of the PCR assay for *S. aureus* detection after resolution was 90.5%, with 19 of 21 of MSSA strains showing a positive result in the PCR assay. Importantly, however, the two strains that were incorrectly identified as not being MSSA are strains that were formerly MSSA but lost a portion of the SCC*mec* element and retained the junction near *orfX* to which the PCR amplification primers hybridize.

[0201] Table 4C shows the individual PCR and culture results for each of the 103 wound specimens following the resolution of discordant results. The shaded entries indicate that the results obtained in the culture test and in the PCR assay were in agreement. The column labeled (CT) indicates the PCR cycle in which a positive signal becomes detectable

over background noise. As shown in the table, four samples were not able to be resolved in the PCR assay, due to the presence of reaction inhibitors in the sample.

[0202] The results above demonstrate the high sensitivity and specificity of the multiplex PCR assay applied directly to wound specimens. Accordingly, the multiplex assay offers the first convenient, reliable, sensitive, and specific assay specific for both MRSA and MSSA.

[0203] The methods, compositions, and devices described herein are presently representative of preferred embodiments, they are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention and are defined by the scope of the disclosure. Accordingly, it will be apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention.

[0204] As used in the claims below and throughout this disclosure, by the phrase "consisting essentially of" is meant including any elements listed after the phrase, and limited to other elements that do not interfere with or contribute to the activity or action specified in the disclosure for the listed elements. Thus, the phrase "consisting essentially of" indicates that the listed elements are required or mandatory, but that other elements are optional and may or may not be present depending upon whether or not they affect the activity or action of the listed elements.

[0205] Numerous literature and patent references have been cited in the present patent application. Each and every reference that is cited in this patent application is hereby expressly incorporated by reference in its entirety.

[0206] The reference in this specification to any prior publication (or information derived from it), or to any matter which is known, is not, and should not be taken as an acknowledgment or admission or any form of suggestion that that prior publication (or information derived from it) or known matter forms part of the common general knowledge in the field of endeavour to which this specification relates.

[0207] Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group

of integers or steps but not the exclusion of any other integer or step or group of integers or steps.

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A method of specifically detecting the presence of a *Staphylococcus aureus* (*S. aureus*) strain and identifying a methicillin-resistant *S. aureus* strain from a sample in a single assay, comprising:

simultaneously contacting said clinical sample with

at least one primer pair that is capable of amplifying a sequence from a *nuc* gene *S. aureus* when an *S. aureus* strain is present in the clinical sample to produce a *nuc* amplicon, said primer pair comprising a first and a second *nuc* primer, said first and second *nuc* primers being between 11 and 45 nucleotides in length and being capable of annealing under PCR conditions to opposite strands of *S. aureus* chromosomal DNA within the *nuc* gene; and

at least one primer pair that is capable of amplifying a polymorphic *mec* right extremity junction (MREJ) sequence of a methicillin resistant *S. aureus* (MRSA) strain when an MRSA strain is present in the clinical sample to produce an MREJ amplicon, said MREJ sequence comprising polymorphic sequences from the right extremity of an *SCCmec* cassette inserted into the *S. aureus* chromosome and *S. aureus* chromosomal DNA, said first and second MREJ primers being between 11 and 45 nucleotides in length and being capable of annealing under PCR conditions to opposite strands of MRSA chromosomal DNA, to create an amplification mixture,

wherein said PCR conditions comprise 4mM $MgCl_2$, 100mM Tris (pH 8.3), 10mM KCl, 5mM $(NH_4)_2SO_4$, 0.15 mg/mL BSA, 4% trehalose at 59°C

subjecting the amplification mixture to an amplification protocol to enable amplification of both *nuc* and MREJ sequences, thereby producing an amplified sample; and

detecting the presence and/or amount of *nuc* amplicons and MREJ amplicons in the amplified sample as an indication of the presence and or amount of *S. aureus* and MRSA, respectively, present in the sample.

2. The method according to claim 1, wherein said assay further comprises:

providing an internal control nucleic acid sequence to said clinical sample, wherein said *nuc* primer pair and/or said MREJ primer pair produce an internal control amplicon under said amplification protocol.

3. The method according to claim 1 or claim 2, wherein said MREJ sequence is selected from the group consisting of an MREJ type i, type ii, type iii, type iv, type v, type vi, type vii, type viii, type ix, and type x sequence, or any combination thereof.

4. The method according to claim 3, wherein said MREJ sequence is a type i sequence, wherein SEQ ID NO: 14 comprises said MREJ type i sequence.

5. The method according to claim 3, wherein said MREJ sequence is a type ii sequence, wherein SEQ ID NO: 23 comprises said MREJ type ii sequence.

6. The method according to claim 3, wherein said MREJ sequence is a type iii sequence, wherein SEQ ID NO:43 comprises said MREJ type iii sequence.

7. The method according to claim 3, wherein said MREJ sequence is a type iv sequence, wherein SEQ ID NO: 59 comprises said MREJ type iv sequence.

8. The method according to claim 3, wherein said MREJ sequence is a type v sequence, wherein SEQ ID NO:65 comprises said MREJ type v sequence.

9. The method according to claim 3, wherein said MREJ sequence is a type vi sequence, wherein SEQ ID NO: 69 comprises said MREJ type vi sequence.

10. The method according to claim 3, wherein said MREJ sequence is a type vii sequence, wherein SEQ ID NO:70 comprises said MREJ type vii sequence.

11. The method according to any one of claims 1 to 10, wherein said detecting the presence and/or amount of *nuc* amplicons in the amplified sample comprises contacting

the amplified sample with a *nuc* probe that anneals under said PCR conditions to said *nuc* amplicon, wherein said *nuc* probe comprises a detectable moiety.

12. The method according to any one of claims 1 to 11, wherein said detecting the presence and/or amount of MREJ amplicons in the amplified sample comprises contacting the amplified sample with an MREJ probe that anneals under said PCR conditions to said MREJ amplicon, wherein said MREJ probe comprises a detectable moiety.

13. The method according to claim 3, wherein said MREJ sequence comprises type i, ii, iii, iv, v and vii MREJ sequences.

14. The method according to claim 13, wherein said at least one MREJ primer pairs anneal under said PCR conditions to the nucleic acid sequences selected from the group consisting of: 99 and 199; 99 and 201; 99 and 195; 99 and 155; and 99 and 163; or the complements thereof.

15. The method according to any one of claims 1 to 14, wherein said first and second *nuc* primers comprise oligonucleotides that anneal under said PCR conditions to at least 11 consecutive nucleotides of one of the sequences selected from the group consisting of SEQ ID NOs: 1-12, or the complement thereof.

16. The method according to claim 15, wherein said *nuc* primer pair comprises a first primer that anneals under said PCR conditions to SEQ ID NO: 1, or the complement thereof and a second primer that anneals under said PCR conditions to SEQ ID NO: 6 or the complement thereof.

17. The method according to claim 16, further comprising providing a probe that anneals under said PCR conditions to SEQ ID NO: 9 or 10, or the complement thereof.

18. The method according to any one of claims 1 to 14, wherein said *nuc* primer pair comprises a first primer that anneals under said PCR conditions to SEQ ID NO: 3 or the complement thereof, and a second primer that anneals under said PCR conditions to SEQ ID NO: 8 or the complement thereof.

19. The method according to claim 18, further comprising providing a probe that anneals under said PCR conditions to SEQ ID NO: 11 or 12, or the complement thereof.

20. The method according to claim 19, wherein said MREJ probe comprises an oligonucleotide that anneals under said PCR conditions to at least 11 consecutive nucleotides of SEQ ID NO:126, 128, 130, 131, and 204, or the complement thereof.

21. A kit that when used specifically detects the presence of a *Staphylococcus aureus* (*S. aureus*) strain and identifies a methicillin-resistant *S. aureus* strain from a sample in a single assay, comprising:

at least one primer pair that is capable of amplifying a sequence from a *nuc* gene *S. aureus* when an *S. aureus* strain is present in the clinical sample to produce a *nuc* amplicon, said primer pair comprising a first and a second *nuc* primer, said first and second *nuc* primers being between 11 and 45 nucleotides in length and being capable of annealing under PCR conditions to opposite strands of *S. aureus* chromosomal DNA within the *nuc* gene; and

at least one primer pair that is capable of amplifying a polymorphic *mec* right extremity junction (MREJ) sequence of a methicillin resistant *S. aureus* (MRSA) strain when an MRSA strain is present in the clinical sample to produce an MREJ amplicon, said MREJ sequence comprising polymorphic sequences from the right extremity of an *SCCmec* cassette inserted into the *S. aureus* chromosome and *S. aureus* chromosomal DNA, said first and second MREJ primers being between 11 and 45 nucleotides in length and being capable of annealing under PCR conditions to opposite strands of MRSA chromosomal DNA, to create an amplification mixture,

wherein said PCR conditions comprise 4mM $MgCl_2$, 100mM Tris (pH 8.3), 10mM KCl, 5mM $(NH_4)_2SO_4$, 0.15 mg/mL BSA, 4% trehalose at 59°C.

22. The kit according to claim 21, wherein said MREJ sequence is selected from the group consisting of an MREJ type i, type ii, type iii, type iv, type v, type vi, type vii, type viii, type ix, and type x sequence, or any combination thereof.

23. The kit according to claim 21 or claim 22, wherein said kit comprises a plurality of primer pairs that are collectively capable of amplifying a polymorphic *mec* right extremity junction (MREJ) sequences of MREJ type i, an MREJ type ii, MREJ type iii, MREJ type iv, MREJ type v, and MREJ type vii.

24. The kit according to any one of claims 21-23, wherein said detecting the presence and/or amount of *nuc* amplicons in the amplified sample comprises contacting the amplified sample with a *nuc* probe that anneals under said PCR conditions to said *nuc* amplicon, wherein said *nuc* probe comprises a detectable moiety.

25. The kit according to any one of claims 21-24, wherein said detecting the presence and/or amount of MREJ amplicons in the amplified sample comprises contacting the amplified sample with an MREJ probe that anneals under said PCR conditions to said MREJ amplicon, wherein said MREJ probe comprises a detectable moiety.

26. The method according to any one of claims 1 to 20 or a kit according to any one of claims 21 to 25 substantially as hereinbefore defined.

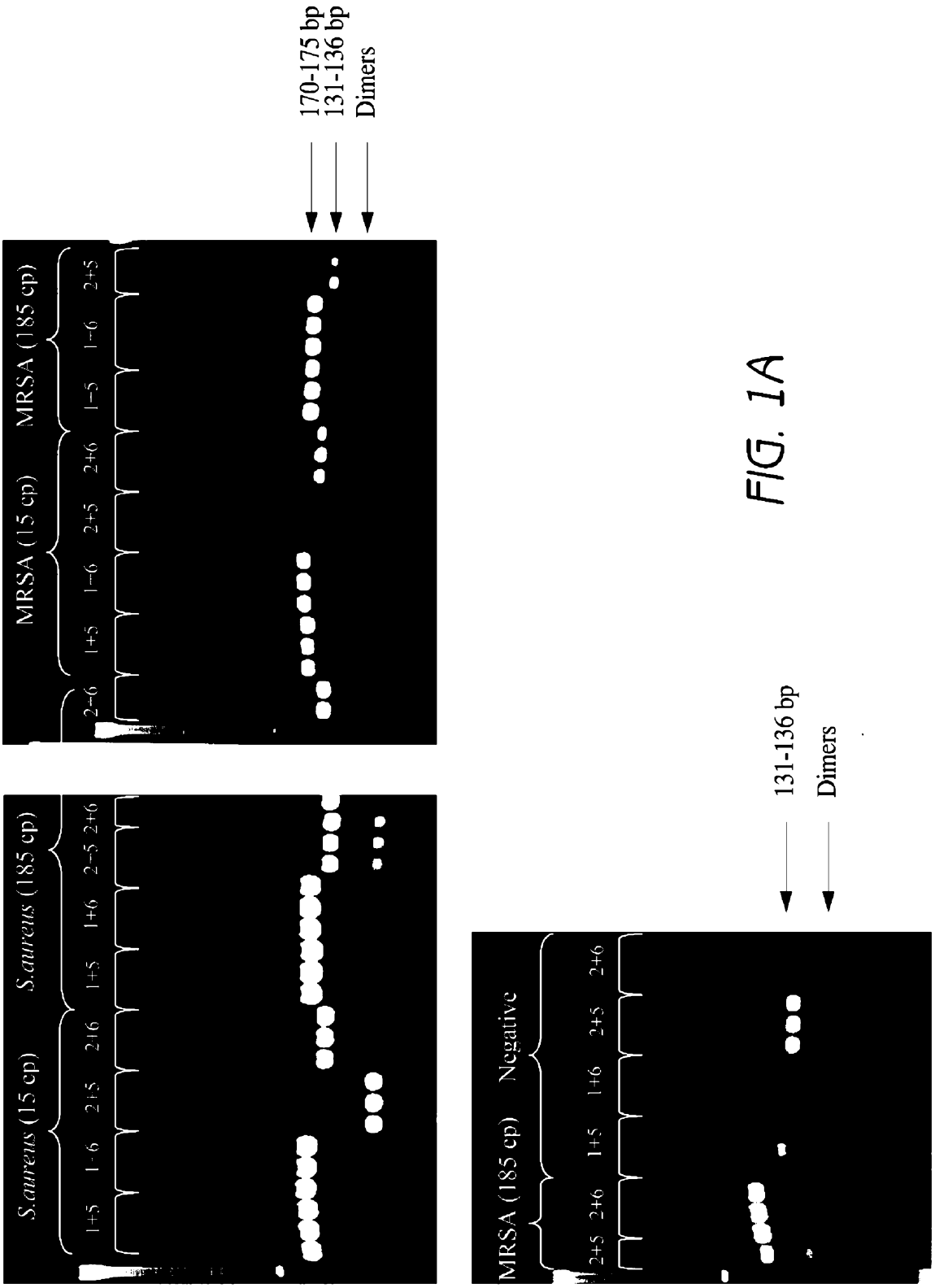

170-175 bp
131-136 bp
Dimers
MRSA (15 cp)
MRSA (185 cp)
2+6 1+5 1+6 2+5 2+6 1+5 1+6 2+5 2+6 1+5 1+6
S.aureus (15 cp)
S.aureus (185 cp)
1+5 1+6 2+5 2+6 1+5 1+6 2+5 2+6
131-136 bp
Dimers
MRSA (185 cp)
Negative
2+5 2+6 1+5 1+6 2+5 2+6

FIG. 1A

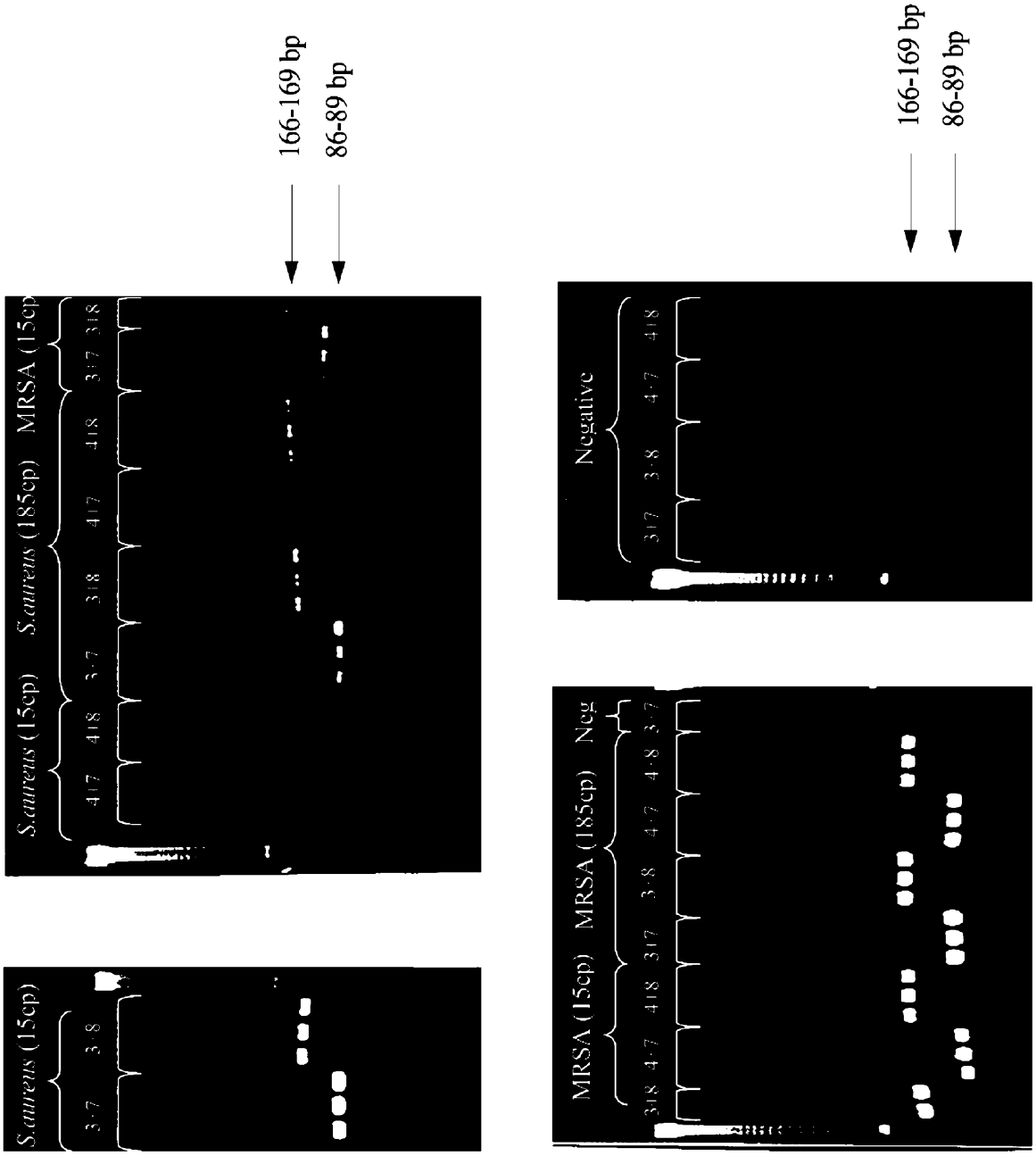
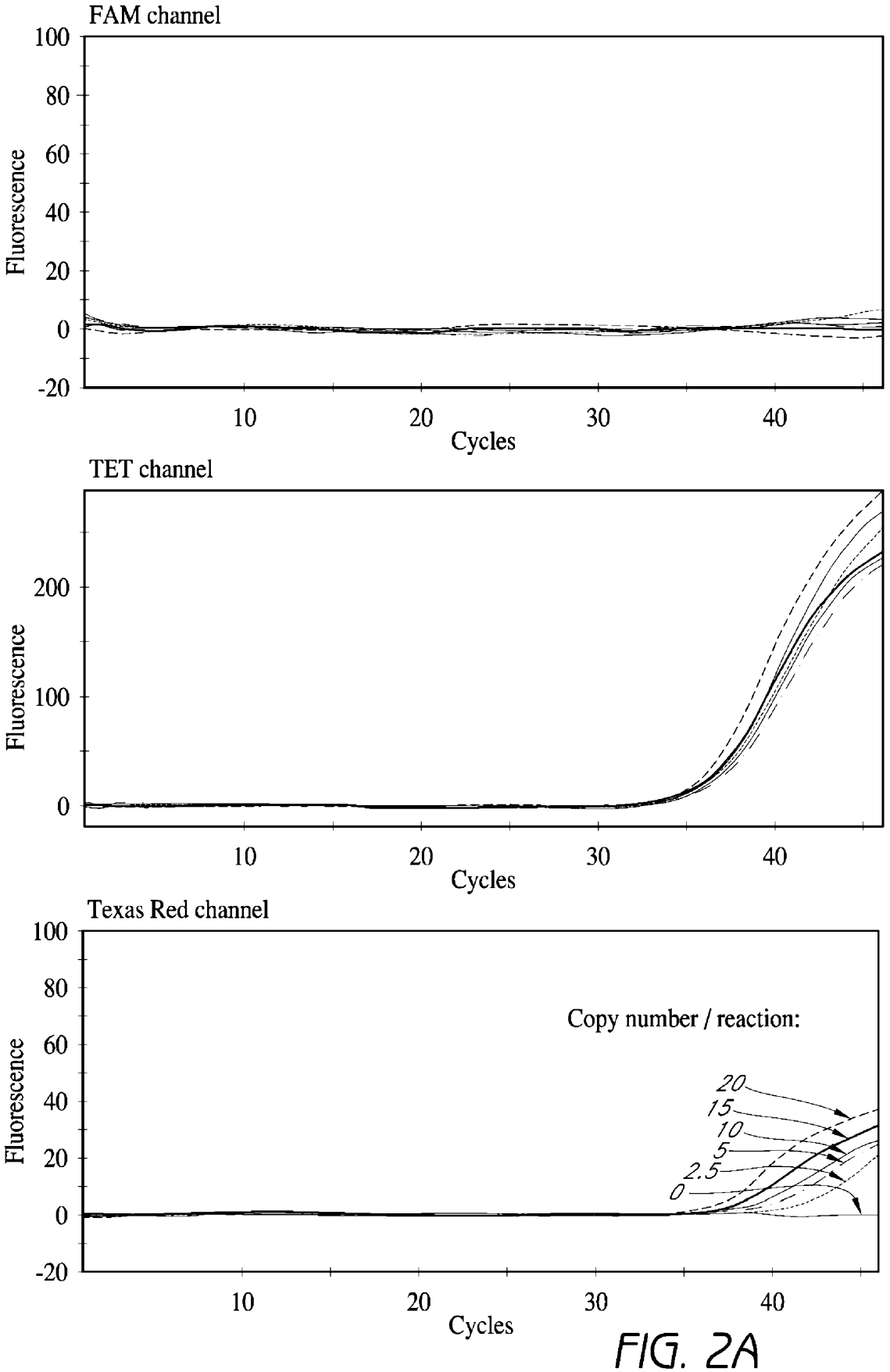

166-169 bp
86-89 bp
S.aureus (15cp) S.aureus (185cp) MRSA (15cp)
317 318 4·7 418 3·8 4·7 418 3·7 318
166-169 bp
86-89 bp
Negative
317 3·8 4·7 418
S.aureus (15cp)
3·7 3·8
MRSA (15cp) MRSA (185cp) Neg
318 4·7 418 317 3·8 4·7 4·8 3·7

FIG. 1B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Fluorescence
100
80
60
40
20
0
-20
10
20
30
40
Cycles
TET channel
Fluorescence
200
100
0
10
20
30
40
Cycles
Texas Red channel
Fluorescence
100
80
60
40
20
0
-20
Copy number / reaction:
20
15
10
5
2.5
0
10
20
30
40
Cycles

FIG. 2A

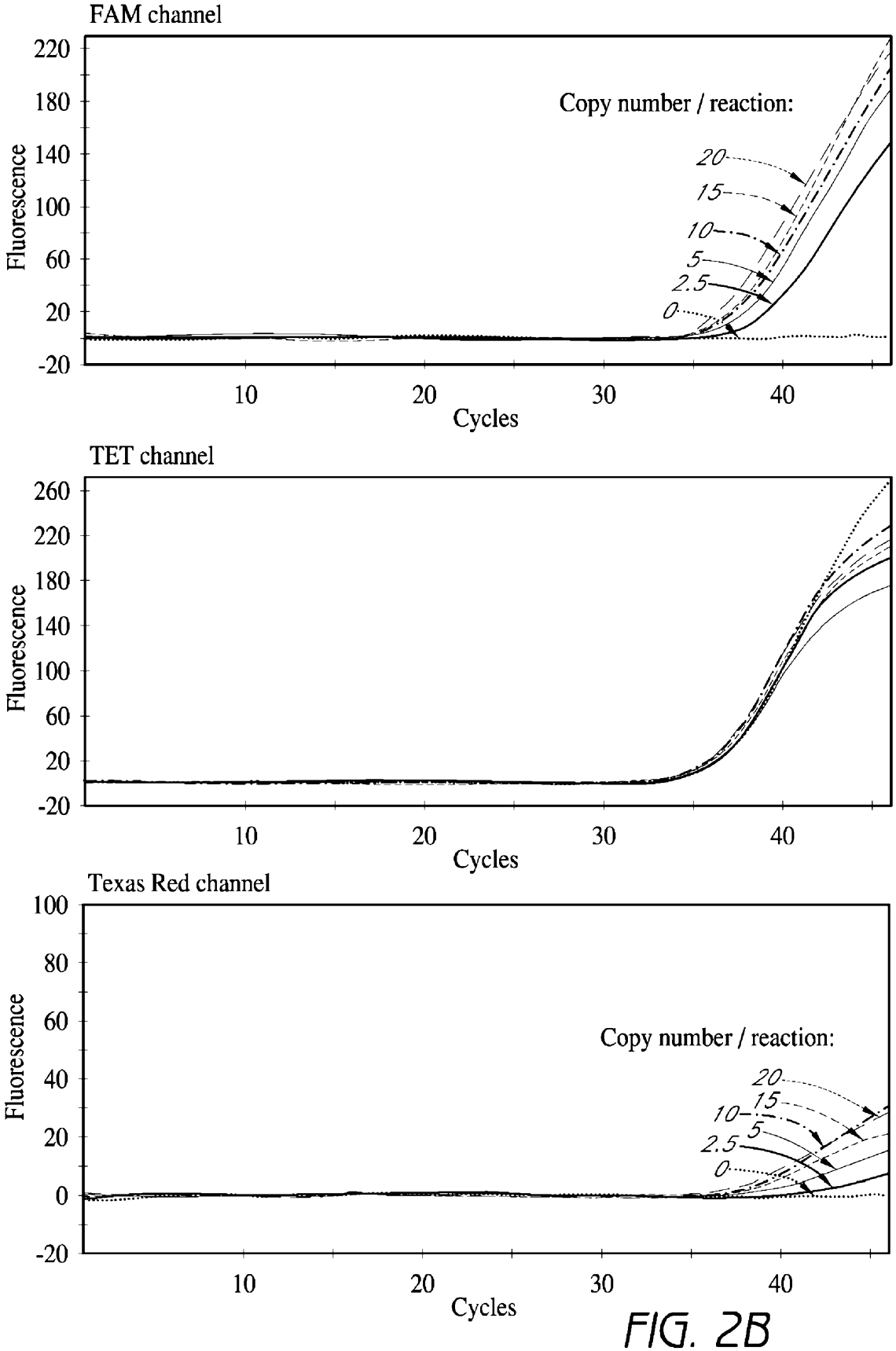
FAM channel
Fluorescence
220
180
140
100
60
20
-20
Copy number / reaction:
20
15
10
5
2.5
0
10
20
30
40
Cycles
TET channel
Fluorescence
260
220
180
140
100
60
20
-20
10
20
30
40
Cycles
Texas Red channel
Fluorescence
100
80
60
40
20
0
-20
Copy number / reaction:
20
15
10
5
2.5
0
10
20
30
40
Cycles

FIG. 2B

SEQUENCE LISTING

<110> GENEOHM SCIENCES, INC.
Veronique Jean
Melanie Guillot
Frank Courjal
Chantal Savoye

<120> DETECTION OF STAPHYLOCOCCUS AUREUS AND IDENTIFICATION OF METHICILLIN-RESISTANT STAPHYLOCOCCUS AUREUS

<130> GENOM.072VPC

<150> 60/870823
<151> 2006-12-19

<160> 205

<170> FastSEQ for Windows Version 4.0

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<220>
<223> Staphylococcus aureus

<400> 3
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<210> 5
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tttttgacat agttagcctc cgcagtcttt catttcaagt aaataatagc gaaatattct 240
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tttttgacat agttagcctc cgcagtcttt catttcaagt aaataatagc gaaatattct 240
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atattttata ataggaggga atttc 385

<210> 17
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<223> Staphylococcus aureus

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tttttgacat agttagcctc cgcagtcttt catttcaagt aaataatagc gaaatattct 240
ttatactgaa tacttatagt gaagcaaagt tctagctttg agaaaattct ttctgcaact 300
aaatatagta aattacggta aaatataaat aagtacatat tgaagaaaat gagacataat 360
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<210> 18
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<220>
<223> Staphylococcus aureus

<400> 18

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ttatactgaa tacttatagt gaagcaaagt tctagctttg agaaaattct ttctgcaact 300
aaatatagta aattacggta aaatataaat aagtacatat tgaagaaaat gagacataat 360
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<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

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aaaatgagac ataatatatt ttataatagg agggaatttc 340

<210> 20
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<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

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<213> Artificial Sequence

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<223> Staphylococcus aureus

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<223> Staphylococcus aureus

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caagcagtta aaagtgcata taaaagaaga taaatattca gttgtaggga aggttgctac 660
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tcttattata ccaatatttt ttgcagtttt tgatattttc ctgacattta 3050

<210> 24
<211> 960
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 24
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gtgaagcaaa gttctagctt tgagaaaatt ctttctgcaa ctaaatatag taaattacgg 420
taaaatataa ataagtacat attgaagaaa atgagacata atatatttta taataggagg 480
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gtgaagcaaa gttctagctt tgagaaaatt ctttctgcaa ctaaatatag taaattacgg 900
taaaatataa ataagtacat attgaagaaa atgagacata atatatttta taataggagg 960

<210> 25
<211> 480
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 25
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gtgtatagag catttaagat tatgcgtgga gaagcatatc ataaatgatg cggtttttc 180
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tccgcagtct ttcatttcaa gtaaataata gcgaaatatt ctttatactg aatacttata 360
gtgaagcaaa gttctagctt tgagaaaatt ctttctgcaa ctaaatatag taaattacgg 420
taaaatataa ataagtacat attgaagaaa atgagacata atatatttta taataggagg 480

<210> 26
<211> 458
<212> DNA
<213> Artificial Sequence

<220>

<223> Staphylococcus aureus

<400> 26
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gtgtacagag catttaagat tatgcgtgga gaagcatatc ataaatgatg cggtttttc 180
agccgcttca taaagggatt ttgaatgtat cagaacatat gaggtttatg tgaattgctg 240
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tccgcagtct ttcatttcaa gtaaataata gcgaaatatt ctttatactg aatacttata 360
gtgaagcaaa gttctagctt tgagaaaatt ctttctgcaa ctaaatatag taaattacgg 420
taaaatataa ataagtacat attgaagaaa atgagaca 458

<210> 27
<211> 3050
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 27
aatttggtaa acctcaaaag gtaattacag atcaggcacc ttcaacgaag gtagcaatgg 60
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ataacctcat tgagcaagat caccgtcata ttaaagtaag aaagacaagg tatcaaagta 180
tcaatacagc aaagaatact ttaaaaggta ttgaatgtat tcacgctcta tataaaaaga 240
accgcaggtc tcttcagatc tacggatttt cgccatgcca cgaaattagc atcatgctag 300
caagttaagc gaacactgac atgataaatt agtggttagc tatatttttt tactttgcaa 360
cagaaccgaa aataatctct tcaatttatt tttatatgaa tcctgtgact caatgattgt 420
aatatctaaa gatttcagtt catcatagac aatgttcttt tcaacatttt ttatagcaaa 480
ttgattaaat aaattctcta atttctcccg tttgatttca ctaccataga ttatattatc 540
attgatatag tcaatgaata atgacaaatt atcactcata acagtcccaa ccccttttatt 600
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cttaaatatc gacaaattaa aaaacaataa aattacttga atattattca taatatatta 720
acaactttat tatactgctc tttatatata aaatcattaa taattaaaca agccttaaaa 780
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<210> 28
<211> 1501
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 28
ttgcacaacc aattggtaaa gacaaagtga tggatccagc gaaacaacca gcgccaagta 60
aagttgtatt gttgccagcg catagaggaa ctgttagtag tggtagagaa ggttctgatc 120
gcgcattgga aggaactgct gtatcaagta agagcgggaa acaattggct agcatgtcag 180
cgcctaaagg tagcacacat gagaagcagt taccaaaaac tggaactgat caaagttcaa 240
gcccagcagc gatgtttgta ttagtagcag gtataggttt aattgcgact gtacgacgta 300
gaaaagctag ctaaaatata ttgaaaacaa tactactgta tttcttaaac aagaggtacg 360
gtagtgtttt tttatgaaaa aaagctataa ccgttgataa atatgggata taaaaacggg 420
gataagtaat aagacatcaa ggtatttatc cacagaaatg gggatagtta tccagaattg 480
tgtacaattt aaagagaaat acccacaatg cccacagagt tatccacaaa tacacaggtt 540
atacactaaa aattgggcat gaatgtcaga aaaatatcaa aaactgcaaa gaatattggt 600
ataataagag ggaacagtgt gaacaagtta ataacttgtg gataactgga aagttgataa 660
caatttggag gaccaaacga catgaaaatc accattttag ctgtagggaa actaaaagag 720
aaatattgga agcaagccat agcagaatat gaaaaacgtt taggcccata caccaagata 780
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c 1501

<210> 29
<211> 917
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 29
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cccaagggca aagcgacttt gtattcgtca ttggcggatc aaacggcctg cacaaggacg 120
tcttacaacg tagtaactac gcactatcat tcagcaaaat gacattccca catcaaatga 180
tgcgggttgt gttaattgag caagtgtata gagcatttaa gattatgcgt ggagaagcat 240
atcataaatg atgcggtttt ttcagccgct tcataaaggg attttgaatg tatcagaaca 300
tatgaggttt atgtgaattg ctgttatgtt tttaagaagc ttatcataag taatgaggtt 360
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attctttata ctgaatactt atagtgaagc aaagttctag ctttgagaaa attctttctg 480
caactaaata tagtaaatta cggtaaaata taaataagta catattgaag aaaatgagac 540
ataatatatt ttataatagg agggaatttc aaatgataga caactttatg caggtcctta 600
aattaattaa agagaaacgt accaataatg tagttaaaaa atctgattgg gataaaggtg 660
atctatataa aactttagtc catgataagt tacccaagca gttaaaagtg catataaaag 720
aagataaata ttcagttgta gggaaggttg ctactgggaa ctatagtaaa gttccttgga 780
tttcaatata tgatgagaat ataacaaaag aaacaaagga tggatattat ttggtatatc 840
tttttcatcc ggaaggagaa ggcatatact tatctttgaa tcaaggatgg tcaaagataa 900
gtgatatgtt tccgcgg 917

<210> 30
<211> 1132
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 30
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ttaggcccat acaccaagat agacatcata gaagttccag acgaaaaagc accagaaaat 120
atgagcgaca aagaaattga gcaagtaaaa gaaaaagaag gccaacgaat actagccaaa 180
atcaaaccac aatcaacagt cattacatta gaaatacaag gaaagatgct atcttccgaa 240
ggattggccc aagaattgaa ccaacgcatg acccaagggc aaagcgactt tgtattcgtc 300
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agagcattta agattatgcg tggagaagca tatcataaat gatgcggttt tttcagccgc 480
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gtctttcatt tcaagtaaat aatagcgaaa tattctttat actgaatact tatagtgaag 660
caaagttcta gctttgagaa aattctttct gcaactaaat atagtaaatt acggtaaaat 720
ataaataagt acatattgaa gaaaatgaga cataatatat tttataatag gagggaattt 780
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ttatctttga atcaaggatg gtcaaagata agtgatatgt ttccgcggga ta 1132

<210> 31
<211> 1133
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 31
agctgtaggg aaactaaaag agaaatattg gaagcaagcc atagcagaat atgaaaaacg 60
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aatcaaacca caatcaacag tcattacatt agaaatacaa ggaaagatgc tatcttccga 240
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cattggcgga tcaaacggcc tgcacaagga cgtcttacaa cgtagtaact acgcactatc 360
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agtctttcat ttcaagtaaa taatagcgaa atattcttta tactgaatac ttatagtgaa 660
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<210> 32
<211> 1087
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 32
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agaaattgag caagtaaaag aaaaagaagg ccaacgaata ctagccaaaa tcaaaccaca 180
atcaacagtc attacattag aaatacaagg aaagatgcta tcttccgaag gattggcaca 240
agaattgaac caacgcatga cccaagggca aagcgacttt gtattcgtca ttggcggatc 300
aaacggcctg cacaaggacg tcttacaacg tagtaactac gcactatcat tcagcaaaat 360
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ttatcataag taatgaggtt catgattttt gacatagtta gcctccgcag tctttcattt 600
caagtaaata atagcgaaat attctttata ctgaatactt atagtgaagc aaagttctag 660
ctttgagaaa attctttctg caactaaata tagtaaatta cggtaaaata taaataagta 720
catattgaag aaaatgagac ataatatatt ttataatagg agggaatttc aaatgataga 780
caactttatg caggtcctta aattaattaa agagaaacgt accaataatg tagttaaaaa 840
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<210> 33
<211> 903
<212> DNA
<213> Artificial Sequence

<220>

<223> Staphylococcus aureus

<400> 33
caaggaaaga tgctatcttc cgaaggattg gcccaagaat tgaaccaacg catgacccaa 60
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tttttgacat agttagcctc cgcagtcttt catttcaagt aaataatagc gaaatattct 420
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aaatatagta aattacggta aaatataaat aagtacatat tgaagaaaat gagacataat 540
atattttata ataggaggga atttcaaatg atagacaact ttatgcaggt ccttaaatta 600
attaaagaga aacgtaccaa taatgtagtt aaaaaatctg attgggataa aggtgatcta 660
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aaatattcag ttgtagggaa ggttgctact gggaactata gtaaagttcc ttggatttca 780
atatatgatg agaatataac aaaagaaaca aaggatggat attatttggt atatcttttt 840
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atg 903

<210> 34
<211> 1114
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 34
ggaaactaaa agagaaatat tggaagcaag ccatagcaga atatgaaaaa cgtttaggcc 60
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acaaagaaat tgagcaagta aaagaaaaag aaggccaacg aatactagcc aaaatcaaac 180
cacaatcaac agtcattaca ttagaaatac aaggaaagat gctatcttcc gaaggattgg 240
cccaagaatt gaaccaacgc atgacccaag ggcaaagcga ctttgtattc gtcattggcg 300
gatcaaacgg cctgcacaag gacgtcttac aacgtagtaa ctacgcacta tcattcagca 360
aaatgacatt cccacatcaa atgatgcggg ttgtgttaat tgagcaagtg tatagagcat 420
ttaagattat gcgtggagaa gcatatcata aatgatgcgg ttttttcagc cgcttcataa 480
agggattttg aatgtatcag aacatatgag gtttatgtga attgctgtta tgtttttaag 540
aagcttatca taagtaatga ggttcatgat ttttgacata gttagcctcc gcagtctttc 600
atttcaagta aataatagcg aaatattctt tatactgaat acttatagtg aagcaaagtt 660
ctagctttga gaaaattctt tctgcaacta aatatagtaa attacggtaa aatataaata 720
agtacatatt gaagaaaatg agacataata tattttataa taggagggaa tttcaaatga 780
tagacaactt tatgcaggtc cttaaattaa ttaaagagaa acgtaccaat aatgtagtta 840
aaaaatctga ttgggataaa ggtgatctat ataaaacttt agtccatgat aagttaccca 900
agcagttaaa agtgcatata aaagaagata aatattcagt tgtagggaag gttgctactg 960
ggaactatag taaagttcct tggatttcaa tatatgatga gaatataaca aaagaaacaa 1020
aggatggata ttatttggta tatcttttc atccggaagg agaaggcata tacttatctt 1080
tgaatcaagg atggtcaaag ataagtgata tgtt 1114

<210> 35
<211> 1121
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 35
ggaaactaaa agagaaatat tggaagcaag ccatagcaga atatgaaaaa cgtttaggcc 60
catacaccaa gatagacatc atagaagttc cagacgaaaa agcaccagaa aatatgagcg 120
acaaagaaat tgagcaagta aaagaaaaag aaggccaacg aatactagcc aaaatcaaac 180
cacaatccac agtcattaca ttagaaatac aaggaaagat gctatcttcc gaaggattgg 240
cccaagaatt gaaccaacgc atgacccaag ggcaaagcga ctttgtattc gtcattggcg 300
gatcaaacgg cctgcacaag gacgtcttac aacgcagtaa ctatgcacta tcatttagca 360
aaatgacatt cccacatcaa atgatgcggg ttgtgttaat tgaacaagtg tatagagcat 420
ttaagattat gcgtggagaa gcatatcata aatgatgcgg ttttttcagc cgcttcataa 480
agggattttg aatgtatcag aacatatgag gtttatgtga attgctgtta tgtttttaag 540
aagcttatca taagtaatga ggttcatgat ttttgacata gttagcctcc gcagtctttc 600
atttcaagta aataatagcg aaatattctt tatactgaat acttatagtg aagcaaagtt 660
ctagctttga gaaaattctt tctgcaacta aatatagtaa attacggtaa aatataaata 720
agtacatatt gaagaaaatg agacataata tattttataa taggagggaa tttcaaatga 780
tagacaactt tatgcaggtc cttaaattaa ttaaagagaa acgtaccaat aatgtagtta 840
aaaaatctga ttgggataaa ggtgatctat ataaaacttt agtccatgat aagttaccca 900
agcagttaaa agtgcatata aaagaagata aatattcagt tgtagggaag gttgctactg 960
ggaactatag taaagttcct tggatttcaa tatatgatga gaatataaca aaagaaacaa 1020
aggatggata ttatttggta tatcttttc atccggaagg agaaggcata tacttatctt 1080
tgaatcaagg atggtcaaag ataagtgata tgtttccgcg g 1121

<210> 36
<211> 1121
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 36
tagctgtagg gaaactaaaa gagaaatatt ggaagcaagc catagcagaa tatgaaaaac 60
gtttaggccc atacaccaag atagacatca tagaagttcc agacgaaaaa gcaccagaaa 120
atatgagcga caaagaaatt gagcaagtaa aagaaaaaga aggccaacga atactagcca 180
aaatcaaacc acaatccaca gtcattacat tagaaataca aggaaagatg ctatcttccg 240
aaggattggc ccaagaattg aaccaacgca tgacccaagg gcaaagcgac tttgtattcg 300
tcattggcgg atcaaacggc ctgcacaagg acgtcttaca acgcagtaac tatgcactat 360
catttagcaa aatgacattc ccacatcaaa tgatgcgggt tgtgttaatt gaacaagtgt 420
atagagcatt taagattatg cgtggagaag catatcataa atgatgcggt tttttcagcc 480
gcttcataaa gggattttga atgtatcaga acatatgagg tttatgtgaa ttgctgttat 540
gtttttaaga agcttatcat aagtaatgag gttcatgatt tttgacatag ttagcctccg 600
cagtctttca tttcaagtaa ataatagcga aatattcttt atactgaata cttatagtga 660
agcaaagttc tagctttgag aaaattcttt ctgcaactaa atatagtaaa ttacggtaaa 720
atataaataa gtacatattg aagaaaatga gacataatat attttataat aggagggaat 780
ttcaaatgat agacaacttt atgcaggtcc ttaaattaat taaagagaaa cgtaccaata 840
atgtagttaa aaaatctgat tgggataaag gtgatctata taaaacttta gtccatgata 900
agttacccaa gcagttaaaa gtgcatataa aagaagataa atattcagtt gtagggaagg 960
ttgctactgg gaactatagt aaagttcctt ggatttcaat atatgatgag aatataacaa 1020
aagaaacaaa ggatggatat tatttggtat atcttttca tccggaagga gaaggcatat 1080
acttatcttt gaatcaagga tggtcaaaga taagtgatat g 1121

<210> 37
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 37
ctgtagggaa actaaaagag aaatattgga agcaagccat agcagaatat gaaaaacgtt 60
taggcccata caccaagata gacatcatag aagttccaga cgaaaaagca ccagaaaata 120
tgagcgacaa agaaattgag caagtaaaag aaaaagaagg ccaacgaata ctagccaaaa 180
tcaaaccaca atccacagtc attacattag aaatacaagg aaagatgcta tcttccgaag 240
gattggccca agaattgaac caacgcatga cccaagggca aagcgacttt gtattcgtca 300
ttggcggatc aaacggcctg cacaaggacg tcttacaacg cagtaactat gcactatcat 360
ttagcaaaat gacattccca catcaaatga tgcgggttgt gttaattgaa caagtgtata 420
gagcatttaa gattatgcgt ggagaagcat atcataaatg atgcggtttt ttcagccgct 480
tcataaaggg attttgaatg tatcagaaca tatgaggttt atgtgaattg ctgttatgtt 540
tttaagaagc ttatcataag taatgaggtt catgattttt gacatagtta gcctccgcag 600
tctttcattt caagtaaata atagcgaaat attctttata ctgaatactt atagtgaagc 660
aaagttctag ctttgagaaa attctttctg caactaaata tagtaaatta cggtaaaata 720
taaataagta catattgaag aaaatgagac ataatatatt ttataatagg agggaatttc 780
aaatgataga caactttatg caggtcctta aattaattaa agagaaacgt accaataatg 840
tagttaaaaa atctgattgg gataaaggtg atctatataa aactttagtc catgataagt 900
tacccaagca gttaaaagtg catataaaag aagataaata ttcagttgta gggaaggttg 960
ctactgggaa ctatagtaaa gttccttgga tttcaatata tgatgagaat ataacaaaag 1020
aaacaaagga tggatattat ttggtatatc tttttcatcc ggaaggagaa ggcatatact 1080
tatctttgaa tcaaggatgg tcaaagataa gtgatatgtt tccgcgggat a 1131

<210> 38
<211> 896
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 38
cattagaaat acaaggaaag atgctatctt ccgaaggatt ggcccaagaa ttgaaccaac 60
gcatgaccca agggcaaagc gactttgtat tcgtcattgg cggatcaaac ggcctgcaca 120
aggacgtctt acaacgcagt aactatgcac tatcatttag caaaatgaca ttcccacatc 180
aaatgatgcg ggttgtgtta attgaacaag tgtatagagc atttaagatt atgcgtggag 240
aagcatatca taaatgatgc ggtttttca gccgcttcat aaagggattt tgaatgtatc 300
agaacatatg aggtttatgt gaattgctgt tatgttttta agaagcttat cataagtaat 360
gaggttcatg atttttgaca tagttagcct ccgcagtctt tcatttcaag taaataatag 420
cgaaatattc tttatactga atacttatag tgaagcaaag ttctagcttt gagaaaattc 480
tttctgcaac taaatatagt aaattacggt aaaatataaa taagtacata ttgaagaaaa 540
tgagacataa tatattttat aataggaggg aatttcaaat gatagacaac tttatgcagg 600
tccttaaatt aattaaagag aaacgtacca ataatgtagt taaaaaatct gattgggata 660
aaggtgatct atataaaact ttagtccatg ataagttacc caagcagtta aaagtgcata 720
taaaagaaga taaatattca gttgtaggga aggttgctac tgggaactat agtaaagttc 780
cttggatttc aatatatgat gagaatataa caaaagaaac aaaggatgga tattatttgg 840
tatatctttt tcatccggaa ggagaaggca tatacttatc tttgaatcaa ggatgg 896

<210> 39
<211> 1125
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 39
ggaaactaaa agagaaatat tggaagcaag ccatatcaga atatgaaaaa cgtttaggcc 60

catacaccaa gatagacatc atagaagttc cagacgaaaa agcaccagaa aatatgagcg 120
acaaagaaat cgagcaagta aaagaaaaag aaggccaacg aatactagcc aaaatcaaac 180
cacaatcaac agtcattaca ttagaaatac aaggaaagat gctatcttcc gaaggattgg 240
ctcaagaatt gaaccaacgc atgacccaag ggcaaagcga ctttgtattc gttattggcg 300
gatcaaacgg cctgcacaag gacgtcttac aacgcagtaa ctatgcacta tcattcagca 360
aaatgacatt tccacatcag atgatgcggg ttgtgttaat tgagcaagtg tatagagcat 420
ttaagattat gcgtggggaa gcatatcata aatgatgcgg ttttttcagc cgcttcataa 480
agggattttg aatgtatcag aacatatgag gtttatgtga attgctgtta tgtttttaag 540
aagcttatca taagtaatga ggttcatgat ttttgacata gttagcctcc gcagtctttc 600
atttcaagta aataatagcg aaatattctt tatactgaat acttatagtg aagcaaagtt 660
ctagctttga gaaaattctt tctgcaacta aatatagtaa attacggtaa aatataaata 720
agtacatatt gaagaaaatg agacataata tattttataa taggagggaa tttcaaatga 780
tagacaactt tatgcaggtc cttaaattaa ttaaagagaa acgtaccaat aatgtagtta 840
aaaaatctga ttgggataaa ggtgatctat ataaaacttt agtccatgat aagttaccca 900
agcagttaaa agtgcatata aaagaagata aatattcagt tgtagggaag gttgctactg 960
ggaactatag taaagttcct tggatttcaa tatatgatga gaatataaca aaagaaacaa 1020
aggatggata ttatttggta tatcttttc atccggaagg agaaggcata tacttatctt 1080
tgaatcaagg atggtcaaag ataagtgata tgtttccgcg ggata 1125

<210> 40
<211> 1125
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 40
ggaaactaaa agagaaatat tggaagcaag ccatagcaga atatgaaaaa cgtttaggcc 60
catacaccaa gatagacatc atagaagttc cagacgaaaa agcaccagaa aatatgagcg 120
acaaagaaat tgagcaagta aaagaaaaag aaggccaacg aatactagcc aaaatcaaac 180
cacaatcaac agtcattaca ttagaaatac aaggaaagat gctatcttcc gaaggattgg 240
cacaagaatt gaaccaacgc atgacccaag ggcaaagcga ctttgtattc gtcattggcg 300
gatcaaacgg cctgcacaag gacgtcttac aacgtagtaa ctacgcacta tcattcagca 360
aaatgacatt cccacatcaa atgatgcggg ttgtgttaat tgagcaagtg tatagagcgt 420
ttaagattat gcgtggagaa gcatatcata aatgatgcgg ttttttcagc cgcttcataa 480
agggattttg aatgtatcag aacatatgag gtttatgtga attgctgtta tgtttttaag 540
aagcttatca taagtaatga ggttcatgat ttttgacata gttagcctcc gcagtctttc 600
atttcaagta aataatagcg aaatattctt tatactgaat acttatagtg aagcaaagtt 660
ctagctttga gaaaattctt tctgcaacta aatatagtaa attacggtaa aatataaata 720
agtacatatt gaagaaaatg agacataata tattttataa taggagggaa tttcaaatga 780
tagacaactt tatgcaggtc cttaaattaa ttaaagagaa acgtaccaat aatgtagtta 840
aaaaatctga ttgggataaa ggtgatctat ataaaacttt agtccatgat aagttaccca 900
agcagttaaa agtgcatata aaagaagata aatattcagt tgtagggaag gttgctactg 960
ggaactatag taaagttcct tggatttcaa tatatgatga gaatataaca aaagaaacaa 1020
aggatggata ttatttggta tatcttttc atccggaagg agaaggcata tacttatctt 1080
tgaatcaagg atggtcaaag ataagtgata tgtttccgcg ggata 1125

<210> 41
<211> 926
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 41

tacattagaa atacaaggaa agatgctatc ttccgaagga ttggcccaag aattgaacca 60
acgcatgacc caagggcaaa gcgactttgt attcgtcatt ggcggatcaa acggcctgca 120
caaggacgtc ttacaacgca gtaactatgc actatcattt agcaaaatga cattcccaca 180
tcaaatgatg cgggttgtgt taattgaaca agtgtataga gcatttaaga ttatgcgtgg 240
agaagcatat cataaatgat gcggtttttt cagccgcttc ataaagggat tttgaatgta 300
tcagaacata tgaggtttat gtgaattgct gttatgtttt taagaagctt atcataagta 360
atgaggttca tgatttttga catagttagc ctccgcagtc tttcatttca agtaaataat 420
agcgaaatat tctttatact gaatacttat agtgaagcaa agttctagct ttgagaaaat 480
tctttctgca actaaatata gtaaattacg gtaaaatata aataagtaca tattgaagaa 540
aatgagacat aatatatttt ataataggag ggaatttcaa atgatagaca actttatgca 600
ggtccttaaa ttaattaaag agaaacgtac caataatgta gttaaaaaat ctgattggga 660
taaaggtgat ctatataaaa ctttagtcca tgataagtta cccaagcagt taaaagtgca 720
tataaaagaa gataaatatt cagttgtagg gaaggttgct actgggaact atagtaaagt 780
tccttggatt tcaatatatg atgagaatat aacaaaagaa acaaaggatg gatattattt 840
ggtatatctt tttcatccgg aaggagaagg catatactta tctttgaatc aaggatggtc 900
aaagataagt gatatgtttc cgcggg 926

<210> 42
<211> 928
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 42
tacattagaa atacaaggaa agatgctatc ttccgaagga ttggcccaag aattgaacca 60
acgcatgacc caagggcaaa gcgactttgt attcgtcatt ggcggatcaa acggcctgca 120
caaggacgtc ttacaacgca gtaactacgc actatcattc agcaaaatga cattcccaca 180
tcaaatgatg cgggttgtgt taattgaaca agtgtacaga gcatttaaga ttatgcgtgg 240
agaagcatat cataaatgat gcggtttttt cagccgcttc ataaagggat tttgaatgta 300
tcagaacata tgaggtttat gtgaattgct gttatgtttt taagaagctt atcataagta 360
atgaggttca tgatttttga catagttagc ctccgcagtc tttcatttca agtaaataat 420
agcgaaatat tctttatact gaatacttat agtgaagcaa agttctagct ttgagaaaat 480
tctttctgca actaaatata gtaaattacg gtaaaatata aataagtaca tattgaagaa 540
aatgagacat aatatatttt ataataggag ggaatttcaa atgatagaca actttatgca 600
ggtccttaaa ttaattaaag agaaacgtac caataatgta gttaaaaaat ctgattggga 660
taaaggtgat ctatataaaa ctttagtcca tgataagtta cccaagcagt taaaagtgca 720
tataaaagaa gataaatatt cagttgtagg gaaggttgct actgggaact atagtaaagt 780
tccttggatt tcaatatatg atgagaatat aacaaaagaa acaaaggatg gatattattt 840
ggtatatctt tttcatccgg aaggagaagg catatactta tctttgaatc aaggatggtc 900
aaagataagt gatatgtttc cgcgggat 928

<210> 43
<211> 479
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 43
ttcgtcattg gcggatcaaa cggcctgcac aaggacgtct tacaacgcag taactacgca 60
ctatcattca gcaaaatgac attcccacat caaatgatgc gggttgtgtt aattgaacaa 120
gtgtacagag catttaagat tatgcgtgga gaagcgtatc ataaataaaa ctaaaaatta 180
ggttgtgtat aatttaaaaa tttaatgaga tgtggaggaa ttacatatat gaaatattgg 240
attatacctt gcaatatcat acgatgttta tagagtgttt aataaaccat ttttcaacta 300

ttgatgatct agaatatata ataactgtac aaattatatt gattatggaa ctacaattaa 360
attaagaaat tgatgatgaa attttaaatt taaactaatg gaatcaagaa agaatgaaag 420
gaaatataca atgcctacga ttaataaaag gaagtttatt agattttgtg ttagaaaca 479

<210> 44
<211> 480
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 44
ttcgtcattg gcggatcaaa cggcctgcac aaggacgtct tacaacgcag taactacgca 60
ctatcattca gcaaaatgac attcccacat caaatgatgc gggttgtgtt aattgaacaa 120
gtgtacagag catttaagat tatgcgtgga gaagcgtatc ataaataaaa ctaaaaatta 180
ggttgtgtat aatttaaaaa tttaatgaga tgtggaggaa ttacatatat gaaatattgg 240
attatacctt gcaatatcat acgatgttta tagagtgttt aataaaccat ttttcaacta 300
ttgatgatct agaatatata ataactgtac aaattatatt gattatggaa ctacaattaa 360
attaagaaat tgatgatgaa attttaaatt taaactaatg gaatcaagaa agaatgaaag 420
gaaatataac atgcctacga ttaataaaag gaagtttatt agattttgtg ttagaaacag 480

<210> 45
<211> 480
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 45
ttcgtcattg gcggatcaaa cggcctgcac aaggacgtct tacaacgcag taactacgca 60
ctatcattca gcaaaatgac atccccacat caaatgatgc gggttgtgtt aattgaacaa 120
gtgtacagag catttaagat tatgcgtgga gaagcgtatc ataaataaaa ctaaaaatta 180
ggttgtgtat aatttaaaaa tttaatgaga tgtggaggaa ttacatatat gaaatattgg 240
attatacctt gcaatatcat acgatgttta tagagtgttt aataaaccat ttttcaacta 300
ttgatgatct agaatatata ataactgtac aaattatatt gattatggaa ctacaattaa 360
attaagaaat tgatgatgaa attttaaatt taaactaatg gaatcaagaa agaatgaaag 420
gaaatataca atgcctacga ttaataaaag gaagtttatt agatttgtgt tagaaacagt 480

<210> 46
<211> 480
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 46
ttcgtcattg gcggatcaaa cggcctgcac aaggacgtct tacaacgcag taactacgca 60
ctatcattca gcaaaatgac attcccacat caaatgatgc gggttgtgtt aattgaacaa 120
gtgtacagag catttaagat tatgcgtgga gaagcgtatc ataaataaaa ctaaaaatta 180
ggttgtgtat aatttaaaaa tttaatgaga tgtggaggaa ttacatatat gaaatattgg 240
attatacctt gcaatatcat acgatgttta tagagtgttt aataaaccat ttttcaacta 300
ttgatgatct agaatatata ataactgtac aaattatatt gattatggaa ctacaattaa 360

attaagaaat tgatgatgaa attttaaatt taaactaatg gaatcaagaa agaatgaaag 420
gaaatataca atgcctacga ttaataaaag gaagtttatt agattttgtg ttagaaacag 480

<210> 47
<211> 309
<212> DNA
<213> Unknown

<220>
<223> Staphylococcus aureus

<220>
<221> misc_feature
<222> 237
<223> n = a, t, c, or g

<400> 47
ggcggatcaa acggcctgca caaggacgtc ttacaacgca gtaactacgc actatcattc 60
agcaaaatga cattcccaca tcaaatgatg cgggttgtgt taattgaaca agtgtacaga 120
gcatttaaga ttatgcgtgg agaagcgtat cataaataaa actaaaaatt aggttgtgta 180
taatttaaaa atctaatgag atgtggagga attacatata tgaaatattg gattatncct 240
tgcaatatca tacgatgttt atagagtgtt taataaacca tttttcaact attgatgatc 300
tacaatata 309

<210> 48
<211> 471
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 48
ttggcggatc aaacggcctg cacaaggacg tcttacaacg cagtaactac gcactatcat 60
tcagcaaaat gacattccca catcaaatga tgcgggttgt gttaattgaa caagtgtaca 120
gagcatttaa gattatgcgt ggagaagcgt atcataaata aaactaaaaa ttaggttgtg 180
tataatttaa aaatttaatg agatgtggag gaattacata tatgaaatat tggattatac 240
cttgcaatat catacgatgt ttatagagtg tttaataaac cattttcaa ctattgatga 300
tctagaatat ataataactg tacaaattat attgattatg gaactacaat taaattaaga 360
aattgatgat gaaatttaa atttaaacta atggaatcaa gaaagaatga aaggaaatat 420
acaatgccta cgattaataa aaggaagttt attagatttt gtgttagaaa c 471

<210> 49
<211> 480
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 49
ttcgtcattg gcggatcaaa cggcctgcac aaggacgtct tacaacgcag taactacgca 60
ctatcattca gcaaaatgac attcccacat caaatgatgc gggttgtgtt aattgaacaa 120
gtgtacagag catttaagat tatgcgtgga gaagcgtatc ataaataaaa ctaaaaatta 180
ggttgtgtat aatttaaaaa tttaatgaga tgtggaggaa ttacatatat gaaatattgg 240
attatacctt gcaatatcat acgatgttta tagagtgttt aataaaccat ttttcaacta 300

ttgatgatct agaatatata ataactgtac aaattatatt gattatggaa ctacaattaa 360
attaagaaat tgatgatgaa attttaaatt taaactaatg gaatcaagaa agaatgaaag 420
gaaatataca atgcctacga ttaataaaag gaagtttatt agattttgtg ttagaaacag 480

<210> 50
<211> 480
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 50
ttcgtcattg gcggatcaaa cggcctgcac aaggacgtct tacaacgcag taactacgca 60
ctatcattca gcaaaatgac attcccacat caaatgatgc gggttgtgtt aattgaacaa 120
gtgtacagag catttaagat tatgcgtgga gaagcgtatc ataaataaaa ctaaaaatta 180
ggttgtgtat aatttaaaaa tttaatgaga tgtggaggaa ttacatatat gaaatattgg 240
attatacctt gcaatatcat acgatgttta tagagtgttt aataaaccat ttttcaacta 300
ttgatgatct agaatatata ataactgtac aaattatatt gattatggaa ctacaattaa 360
attaagaaat tgatgatgaa attttaaatt taaactaatg gaatcaagaa agaatgaaag 420
gaaatataca atgcctacga ttaataaaag gaagtttatt agattttgtg ttagaaacag 480

<210> 51
<211> 480
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 51
ttcgtcattg gcggatcaaa cggcctgcac aaggacgtct tacaacgcag taactacgca 60
ctatcattca gcaaaatgac attcccacat caaatgatgc gggttgtgtt aattgaacaa 120
gtgtacagag catttaagat tatgcgtgga gaagcgtatc ataaataaaa ctaaaaatta 180
ggttgtgtat aatttaaaaa tttaatgaga tgtggaggaa ttacatatat gaaatattgg 240
attatacctt gcaatatcat acgatgttta tagagtgttt aataaaccat ttttcaacta 300
ttgatgatct agaatatata ataactgtac aaattatatt gattatggaa ctacaattaa 360
attaagaaat tgatgatgaa attttaaatt taaactaatg gaatcaagaa agaatgaaag 420
gaaatataca atgcctacga ttaataaaag gaagtttatt agattttgtg ttagaaacag 480

<210> 52
<211> 478
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 52
ttcgtcattg gcggatcaaa cggcctgcac aaggacgtct tacaacgcag taactacgca 60
ctatcattca gcaaaatgac attcccacat caaatgatgc gggttgtgtt aattgaacaa 120
gtgtacagag catttaagat tatgcgtgga gaagcgtatc ataaataaaa ctaaaaatta 180
ggttgtgtat aatttaaaaa tttaatgaga tgtggaggaa ttacatatat gaaatattgg 240
attatacctt gcaatatcat acgatgttta tagagtgttt aataaaccat ttttcaacta 300

ttgatgatct agaatatata ataactgtac aaattatatt gattatggaa ctacaattaa 360
attaagaaat tgatgatgaa attttaaatt taaactaatg gaatcaagaa agaatgaaag 420
gaaatataca atgcctacga ttaataaaag gaagtttatt agattttgtg ttagaaac 478

<210> 53
<211> 479
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 53
ttcgtcattg gcggatcaaa cggcctgcac aaggacgtct tacaacgcag taactacgca 60
ctatcattca gcaaaatgac attcccacat caaatgatgc gggttgtgtt aattgaacaa 120
gtgtacagag catttaagat tatgcgtgga gaagcgtatc ataaataaaa ctaaaaatta 180
ggttgtgtat aatttaaaaa tttaatgaga tgtggaggaa ttacatatat gaaatattgg 240
attatacctt gcaatatcat acgatgttta tagagtgttt aataaaccat ttttcaacta 300
ttgatgatct agaatatata ataactgtac aaattatatt gattatggaa ctacaattaa 360
attaagaaat tgatgatgaa attttaaatt taaactaatg gaatcaagaa agaatgaaag 420
gaaatataca atgcctacga ttaataaaag gaagtttatt agattttgtg ttagaaaca 479

<210> 54
<211> 480
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<220>
<221> misc_feature
<222> 406
<223> n = a, t, c, or g

<400> 54
ttcgtcattg gcggatcaaa cggcctgcac aaggacgtct tacaacgcag taactacgca 60
ctatcattca gcaaaatgac attcccacat caaatgatgc gggttgtgtt aattgaacaa 120
gtgtacagag catttaagat tatgcgtgga gaagcgtatc ataaataaaa ctaaaaatta 180
ggttgtgtat aatttaaaaa tttaatgaga tgtggaggaa ttacatatat gaaatattgg 240
attatacctt gcaatatcat acgatgttta tagagtgttt aataaaccat ttttcaacta 300
ttgatgatct agaatatata ataactgtac aaattatatt gattatggaa ctacaattaa 360
attaagaaat tgatgatgaa attttaaatt taaactaatg gaatcncgaa agaatgaaag 420
gaaatataca atgcctacga ttaataaaag gaagtttatt agattttgtg ttagaaacag 480

<210> 55
<211> 480
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 55
ttcgtcattg gcggatcaaa cggcctgcac aaggacgtct tacaacgcag taactacgca 60
ctatcattca gcaaaatgac attcccacat caaatgatgc gggttgtgtt aattgaacaa 120

gtgtacagag catttaagat tatgcgtgga gaagcgtatc ataaataaaa ctaaaaatta 180
ggttgtgtat aatttaaaaa tttaatgaga tgtggaggaa ttacatatat gaaatattgg 240
attatacctt gcaatatcat acgatgttta tagagtgttt aataaaccat ttttcaacta 300
ttgatgatct agaatatata ataactgtac aaattatatt gattatggaa ctacaattaa 360
attaagaaat tgatgatgaa attttaaatt taaactaatg gaatcaagaa agaatgaaag 420
gaaatataca atgcctacga ttaataaaag gaagtttatt agattttgtg ttagaaacag 480

<210> 56
<211> 1256
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 56
ttcagaaaaa tgattaatgt gtttcaataa aatctctcct tctttgtgaa catattcatt 60
tttatactaa ttaatataat ttccaaaaaa gtttctgttt aaaagtgaaa aatattattt 120
accgtttgac ttaaatcttc aatatatagg tgtttatatg tatcattttg cgccaatttg 180
aataaacggg aatcaagtct gtttctgagt ttatttcaac tttcttatag taaacattgt 240
cttaatatga tgaacttcaa taaaactttc cctatgcccc ataaaatttt ctcaaaatca 300
aaaataacat accttacaac ttttaccgtc gatatcaatt gctcttttct taatttagga 360
ttgctttcaa attttgtact ataacgtgaa actacttttc cttctttata attaaaattt 420
actaattcac aatcattttt acttccattt acaaaaacat ccactgtttc taacacaaaa 480
tctaataaac ttccttttat taatcgtagg cattgtatat ttcctttcat tctttcttga 540
ttccattagt ttaaatttaa aatttcatcc atcaatttct taatttaatt gtagttccat 600
aatcaatata atttgtacag ttattatata ttctagatca tcaatagttg aaaaatggtt 660
tattaaacac tctataaaca tcgtatgata ttgcaaggta taatccaata tttcatatat 720
gtaattcctc cacatctcat taaattttta aattatacac aacctaattt ttagttttat 780
ttatgatacg cttctccacg cataatctta aatgctctgt acacttgttc aattaacaca 840
acccgcatca tttgatgtgg gaatgtcatt ttgctgaatg atagtgcgta gttactgcgt 900
tgtaagacgt ccttgtgcag gccgtttgat ccgccaatga cgaatacaaa gtcgctttgc 960
ccttgggtca tgcgttggtt caattcttgg gccaatcctt cggaagatag catctttcct 1020
tgtatttcta atgtaatgac tgttgattgt ggtttgattt tggctagtat tcgttggcct 1080
tctttttctt ttacttgctc aatttctttg tcgctcatat tttctggtgc tttttcgtct 1140
ggaacttcta tgatgtctat cttggtgtat gggcctaaac gtttttcata ttctgctatg 1200
gcttgcttcc aatatttctc ttttagtttc cctacagcta aaatggtgat tttcat 1256

<210> 57
<211> 679
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 57
ataagaggga acagtgtgaa caagttaata acttgtggat aactggaaag ttgataacaa 60
tttggaggac caaacgacat gaaaatcacc attttagctg tagggaaact aaaagagaaa 120
tattggaagc aagccatagc agaatatgaa aaacgtttag gcccatacac caagatagac 180
atcatagaag ttccagacga aaaagcacca gaaaatatga gcgacaaaga aattgagcaa 240
gtaaaagaaa aagaaggcca acgaatacta gccaaaatca aaccacaatc cacagtcatt 300
acattagaaa tacaaggaaa gatgctatct tccgaaggat tggcccaaga attgaaccaa 360
cgcatgaccc aagggcaaag cgactttgta ttcgtcattg gcggatcaaa cggcctgcac 420
aaggacgtct tacaacgcag taactatgca ctatcattta gcaaaatgac attcccacat 480
caaatgatgc gggttgtgtt aattgaacaa gtgtatagag catttaagat tatgcgtgga 540

gaggcttatc ataaataaaa ctaaaaatta gattgtgtat aatttaaaaa tttaatgaga 600
tgtggaggaa ttacatatat gaaatattgg agtatacctt gcaatatcat acgatgttta 660
tagagtgttt aataaacca 679

<210> 58
<211> 782
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 58
caatgcccac agagttatcc acaaatacac aggttataca ctaaaaattg ggcatgaatg 60
tcagaaaaat atcaaaaact gcaaagaata ttggtataat aagagggaac agtgtgaaca 120
agttaataac ttgtggataa ctggaaagtt gataacaatt tggaggacca aacgacatga 180
aaatcaccat tttagctgta gggaaactaa aagagaaata ttggaagcaa gccatagcag 240
aatatgaaaa acgtttaggc ccatacacca agatagacat catagaagtt ccagacgaaa 300
aagcaccaga aaatatgagc gacaaagaaa ttgagcaagt aaaagaaaaa gaaggccaac 360
gaatactagc caaaatcaaa ccacaatcaa cagtcattac attagaaata caaggaaaga 420
tgctatcttc cgaaggattg gcccaagaat tgaaccaacg catgacccaa gggcaaagcg 480
actttgtatt cgtcattggc ggatcaaacg gcctgcacaa ggacgtctta caacgcagta 540
actacgcact atcattcagc aaaatgacat tcccacatca aatgatgcgg gttgtgttaa 600
ttgaacaagt gtacagagca tttaagatta tgcgtggaga agcgtatcat aaataaaact 660
aaaaattagg ttgtgtataa tttaaaaatt taatgagatg tggaggaatt acatatatga 720
aatattggat tataccttgc aatatcatac gatgtttata gagtgtttaa taaaccattt 780
tt 782

<210> 59
<211> 1045
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 59
ccagtttttt gtttaatgaa caaggtaaat tacgagataa tatttgaaga aaacaataaa 60
gtagagatgg atttccatat cctctttagt agcggttttt atctgtaagg tttattaata 120
attaaataaa taggcgggat agttatatat agcttattaa tgaaagaata tgattattaa 180
tttagtatta tattttaata ttaaaaagaa gatatgaaat aattattcat accttccacc 240
ttacaataat tagttttcaa tcgaatatta agattattag tagtcttaaa agttaagact 300
tccttatatt aatgacctaa tttattattt gcctcatgaa ttatcttttt atttctttga 360
tatgtcccaa accacatcgt gatatacact acaataaata ttatgatgaa actaataata 420
ttctcaaagt tcagatggaa ccaacctgct agaatagcga gtgggaagaa taggattatc 480
atcaatataa agtgaactac agtctgtttt gttatactcc aatcggtatc tgtaaatatc 540
aaattaccat aagtaaacaa aattccaatc aatgcccata gtgctacaca tattagcata 600
ataaccgctt cattaaagtt ttcataataa attttaccca taaaagaatc tggatatagt 660
ggtacatatt tatcccttga aaaaaataag tgaagtaatg acagaaatca taagaccagt 720
gaacgcacct ttttgaacag cgtggaataa ttttttcata gtgagatgga ccattccatt 780
tgtttctaac ttcaagtgat caatgtaatt tagattgata atttctgatt ttgaaatacg 840
cacgaatatt gaaccgacaa gctcttcaat ttggtaaagt cgctgataaa gttttaaagc 900
tttattattc attgttatcg catacctgtt tatcttctac tatgaactgt gcaatttgtt 960
ctagatcaat tgggtaaaca tgatggttct gttgcaaagt aaaaaaatat agctaaccac 1020
taatttatca tgtcagtgtt cgctt 1045

<210> 60

<211> 1118
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 60
cagagcattt aagattatgc gtggagaagc gtaccacaaa tgatgcggtt ttttatccag 60
ttttttgttt aatgaacaag gtaaattacg agataatatt tgaagaaaac aataaagtag 120
agatggattt ccatatcctc tttagtagcg gtttttatct gtaaggttta ttaataatta 180
aataaatagg cgggatagtt atatatagct tattaatgaa agaatatgat tattaattta 240
gtattatatt ttaatattaa aaagaagata tgaaataatt attcatacct tccaccttac 300
aataattagt tttcaatcga atattaagat tattagtagt cttaaaagtt aagacttcct 360
tatattaatg acctaattta ttatttgcct catgaattat ctttttattt ctttgatatg 420
tcccaaacca catcgtgata tacactacaa taaatattat gatgaaacta ataatattct 480
caaagttcag atggaaccaa cctgctagaa tagcgagtgg gaagaatagg attatcatca 540
atataaagtg aactacagtc tgttttgtta tactccaatc ggtatctgta aatatcaaat 600
taccataagt aaacaaaatt ccaatcaatg cccatagtgc tacacatatt agcataataa 660
ccgcttcatt aaagttttca taataaattt tacccataaa agaatctgga tatagtagta 720
catatttatc ccttgaaaaa aataagtgaa gtaatgacag aaatcataag accagtgaac 780
gcacctttt gaacagcgtg gaataatttt ttcatagtga gatggaccat tccatttgtt 840
tctaacttca agtgatcaat gtaatttaga ttgataattt ctgattttga aatacgcacg 900
aatattgaac cgacaagctc ttcaatttgg taaagtcgct gataaagttt taaagcttta 960
ttattcattg ttatcgcata cctgtttatc ttctactatg aactgtgcaa tttgttctag 1020
atcaattggg taaacatgat ggttctgttg caaagtaaaa aaatatagct aaccactaat 1080
ttatcatgtc agtgttcgct taacttgcta gcatgatg 1118

<210> 61
<211> 1118
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 61
cagagcattt aagattatgc gtggagaagc gtaccacaaa tgatgcggtt ttttatccag 60
ttttttgttt aatgaacaag gtaaattacg agataatatt tgaagaaaac aataaagtag 120
agatggattt ccatatcctc tttagtagcg gtttttatct gtaaggttta ttaataatta 180
aataaatagg cgggatagtt atatatagct tattaatgaa agaatatgat tattaattta 240
gtattatatt ttaatattaa aaagaagata tgaaataatt attcatacct tccaccttac 300
aataattagt tttcaatcga atattaagat tattagtagt cttaaaagtt aagacttcct 360
tatattaatg acctaattta ttatttgcct catgaattat ctttttattt ctttgatatg 420
tcccaaacca catcgtgata tacactacaa taaatattat gatgaaacta ataatattct 480
caaagttcag atggaaccaa cctgctagaa tagcgagtgg gaagaatagg attatcatca 540
atataaagtg aactacagtc tgttttgtta tactccaatc ggtatctgta aatatcaaat 600
taccataagt aaacaaaatt ccaatcaatg cccatagtgc tacacatatt agcataataa 660
ccgcttcatt aaagttttca taataaattt tacccataaa agaatctgga tatagtagta 720
catatttatc ccttgaaaaa aataagtgaa gtaatgacag aaatcataag accagtgaac 780
gcacctttt gaacagcgtg gaataatttt ttcatagtga gatggaccat tccatttgtt 840
tctaacttca agtgatcaat gtaatttaga ttgataattt ctgattttga aatacgcacg 900
aatattgaac cgacaagctc ttcaatttgg taaagtcgct gataaagttt taaagcttta 960
ttattcattg ttatcgcata cctgtttatc ttctactatg aactgtgcaa tttgttctag 1020
atcaattggg taaacatgat ggttctgttg caaagtaaaa aaatatagct aaccactaat 1080
ttatcatgtc agtgttcgct taacttgcta gcatgatg 1118

<210> 62
<211> 1113
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 62
agcatttaag attatgcgtg gagaagcgta ccacaaatga tgcggttttt tatccagttt 60
tttgtttaat gaacaaggta aattacgaga taatatttga agaaaacaat aaagtagaga 120
tggatttcca tatcctcttt agtagcggtt tttatctgta aggtttatta ataattaaat 180
aaataggcgg gatagttata tatagcttat taatgaaaga atatgattat taatttagta 240
ttatatttta atattaaaaa gaagatatga aataattatt catacctttcc accttacaat 300
aattagtttt caatcgaata ttaagattat tagtagtctt aaaagttaag acttccttat 360
attaatgacc taatttatta tttgcctcat gaattatctt tttatttctt tgatatgtcc 420
caaaccacat cgtgatatac actacaataa atattatgat gaaactaata atattctcaa 480
agttcagatg gaaccaacct gctagaatag cgagtgggaa gaataggatt atcatcaata 540
taaagtgaac tacagtctgt tttgttatac tccaatcggt atctgtaaat atcaaattac 600
cataagtaaa caaaattcca atcaatgccc atagtgctac acatattagc ataataaccg 660
cttcattaaa gttttcataa taaattttac ccataaaaga atctggatat agtggtacat 720
atttatccct tgaaaaaaat aagtgaagta atgacagaaa tcataagacc agtgaacgca 780
ccttttgaa cagcgtggaa taatttttttc atagtgagat ggaccattcc atttgtttct 840
aacttcaagt gatcaatgta atttagattg ataatttctg attttgaaat acgcacgaat 900
attgaaccga caagctcttc aatttggtaa agtcgctgat aaagttttaa agctttatta 960
ttcattgtta tcgcatacct gtttatcttc tactatgaac tgtgcaattt gttctagatc 1020
aattgggtaa acatgatggt tctgttgcaa agtaaaaaaa tatagctaac cactaattta 1080
tcatgtcagt gttcgcttaa cttgctagca tga 1113

<210> 63
<211> 2153
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 63
ctgtagggaa actaaaagag aaatactgga agcaagccat agcagaatat gaaaaacgtt 60
taggcccata caccaagata gacatcatag aagttccaga cgaaaaagca ccagaaaata 120
tgagcgacaa agaaatcgag caagtaaaag aaaaagaagg ccaacgaata ctagccaaaa 180
tcaaaccaca atccacagtc attacattag aaatacaagg aaagatgcta tcttccgaag 240
gattggccca agaattgaac caacgcatga cccaagggca aagcgacttt gtattcgtca 300
ttggcggatc aaacggcctg cacaaggacg tcttacaacg cagtaactac gcactatcat 360
tcagcaaaat gacattccca catcaaatga tgcgggttgt gttaattgaa caagtgtaca 420
gagcatttaa gattatgcgt ggagaagcgt accacaaatg atgcggtttt ttatccagtt 480
ttttgtttaa tgaacaaggt aaattacgag ataatatttg aagaaaacaa taaagtagag 540
atggatttcc atatcctctt tagtagcggt ttttatctgt aaggtttatt aataattaaa 600
taaataggcg ggatagttat atatagctta ttaatgaaag aatatgatta ttaatttagt 660
attatatttt aatattaaaa agaagatatg aaataattat tcataccttc caccttacaa 720
taattagttt tcaatcgaat attaagatta ttagtagtct taaaagttaa gacttcctta 780
tattaatgac ctaatttatt atttgcctca tgaattatct ttttatttct ttgatatgtc 840
ccaaaccaca tcgtgatata cactacaata aatattatga tgaaactaat aatattctca 900
aagttcagat ggaaccaacc tgctagaata gcgagtggga agaataggat tatcatcaat 960
ataaagtgaa ctacagtctg ttttgttata ctccaatcgg tatctgtaaa tatcaaatta 1020
ccataagtaa acaaaattcc aatcaatgcc catagtgcta cacatattag cataataacc 1080
gcttcattaa agttttcata ataaatttta cccataaaag aatctggata tagtggtaca 1140

tatttatccc ttgaaaaaaa taagtgaagt aatgacagaa atcataagac cagtgaacgc 1200
acctttttga acagcgtgga ataatttttt catagtgaga tggaccattc catttgtttc 1260
taacttcaag tgatcaatgt aatttagatt gataatttct gattttgaaa tacgcacgaa 1320
tattgaaccg acaagctctt caatttggta aagtcgctga taaagtttta aagctttatt 1380
attcattgtt atcgcatacc tgtttatctt ctactatgaa ctgtgcaatt tgttctagat 1440
caattgggta aacatgatgg ttctgttgca aagtaaaaaa atatagctaa ccactaattt 1500
atcatgtcag tgttcgctta acttgctagc atgatgctaa tttcgtggca tggcgaaaat 1560
ccgtagatct gatgagacct gcggttcttt ttatatagag cgtaaataca ttcaatacct 1620
tttaaagtat tctttgctgt attgatactt tgataccttg tctttcttac tttaatatga 1680
cggtgatctt gctcaatgag gttattcaaa tatttcgatg tacaatgaca gtcaggttta 1740
agtttaaaag ctttaattac tttagccatt gctaccttcg ttgaaggtgc ctgatctgta 1800
attacctttt gaggtttacc aaattgttta atgagacgtt taataaacgc atatgctgaa 1860
tgattatctc gttgcttacg caaccaaata tctaatgtat gtccctctgc atcaatggca 1920
cgatataaat agctccattt tccttttatt ttgatgtacg tctcatcaat acgccatttg 1980
taataagctt ttttatgctt tttcttccaa atttgatata aaattggggc atattcttga 2040
acccaacggt agaccgttga atgatgaacg tttacaccac gtccccttaa tatttcagat 2100
atatcacgat aactcaatgc atatcttaga tagtagccaa cggctacagt gat 2153

<210> 64
<211> 2122
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 64
ggaaactaaa agagaaatat tggaagcaag ccatagcaga atatgaaaaa cgtttaggcc 60
catacaccaa gatagacatc atagaagttc cagacgaaaa agcaccagaa aatatgagcg 120
acaaagaaat tgagcaagta aaagaaaaag aaggccaacg aatactagcc aaaatcaaac 180
cacaatcaac agtcattaca ttagaaatac aaggaaagat gctatcttcc gaaggattgg 240
cccaagaatt gaaccaacgc atgacccaag ggcaaagcga ctttgtattc gtcattggcg 300
gatcaaacgg cctgcacaag gacgtcttac aacgcagtaa ctacgcacta tcattcagca 360
aaatgacatt cccacatcaa atgatgcggg ttgtgttaat tgaacaagtg tacagagcat 420
ttaagattat gcgtggagaa gcgtaccaca aatgatgcgg ttttttatcc agtttttgt 480
ttaatgaaca aggtaaatta cgagataata tttgaagaaa acaataaagt agagatggat 540
ttccatatcc tctttagtag cggtttttat ctgtaaggtt tattaataat taaataaata 600
ggcgggatag ttatatatag cttattaatg aaagaatatg attattaatt tagtattata 660
ttttaatatt aaaaagaaga tatgaaataa ttattcatac cttccacctt acaataatta 720
gttttcaatc gaatattaag attattagta gtcttaaaag ttaagacttc cttatattaa 780
tgacctaatt tattatttgc ctcatgaatt atctttttat ttctttgata tgtcccaaac 840
cacatcgtga tatacactac aataaatatt atgatgaaac taataatatt ctcaaagttc 900
agatggaacc aacctgctag aatagcgagt gggaagaata ggattatcat caatataaag 960
tgaactacag tctgttttgt tatactccaa tcggtatctg taaatatcaa attaccataa 1020
gtaaacaaaa ttccaatcaa tgcccatagt gctacacata ttagcataat aaccgcttca 1080
ttaaagtttt cataataaat tttacccata aaagaatctg gatatagtgg tacatattta 1140
tcccttgaaa aaaataagtg aagtaatgac agaaatcata agaccagtga acgcaccttt 1200
ttgaacagcg tggaataatt ttttcatagt gagatggacc attccatttg tttctaactt 1260
caagtgatca atgtaattta gattgataat ttctgatttt gaaatacgca cgaatattga 1320
accgacaagc tcttcaattt ggtaaagtcg ctgataaagt tttaaagctt tattattcat 1380
tgttatcgca tacctgttta tcttctacta tgaactgtgc aatttgttct agatcaattg 1440
ggtaaacatg atggttctgt tgcaaagtaa aaaaatatag ctaaccacta atttatcatg 1500
tcagtgttcg cttaacttgc tagcatgatg ctaatttcgt ggcatggcga aaatccgtag 1560
atctgatgag acctgcggtt ctttttatat agagcgtaaa tacattcaat acctttttaaa 1620
gtattctttg ctgtattgat actttgatac cttgtctttc ttactttaat atgacggtga 1680
tcttgctcaa tgaggttatt cagatatttc gatgtacaat gacagtcagg tttaagttta 1740
aaagctttaa ttactttagc cattgctacc ttcgttgaag gtgcctgatc tgtaattacc 1800

ttttgaggtt taccaaattg tttaatgaga cgtttgataa acgcatatgc tgaatgatta 1860
tctcgttgct tacgcaacca aatatctaat gtatgtccct ctgcatcaat ggcacgatat 1920
aaatagctcc attttccttt tattttgatg tacgtctcat caatacgcca tttgtaataa 1980
gctttttttat gctttttctt ccaaatttga tacaaaattg gggcatattc ttgaacccaa 2040
cggtagaccg ttgaatgatg aacgtttaca ccacgttccc ttaatatttc agatatatca 2100
cgataactca atgtatatct ta 2122

<210> 65
<211> 737
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 65
tttaagatta tgcgtggaga agcatatcat aaatgatgcg gttatttcag ccgtaatttt 60
ataatataaa gcagagttta ttaaatttta atgattactt tttattaaga attaattcta 120
gttgatatat tataatgtga aacacaaaat aataatttgt aattgttagt ttataggcat 180
ctgtatttgg aatttttttgt agactattta aaaaatagtg tatataagta ttgagttcat 240
gtattaactg tctttttttca tcgttcatca agtataagga tgtagagatt tgttggataa 300
tttcttcgga tgtttttaaa attatcatta aattagatgg tatctgatct tgagttttgt 360
ttttagtgta tgtatatttt aaaaaatttt tgattgttgt tatttgactc tcttttaatt 420
tgacaccctc atcaataaat gtgttaaata tatcttcatt tgtacttaaa tcatcaaaat 480
ttgccaacaa atatttgaac gtctctaaat cattatgttt gagttccgtt ttgctattcc 540
ataattccaa accatttggt agaaagccca agctgtgatt ttgatctccc catatagctg 600
aatttaaatc agtgagttga ttaatttttt caacacagaa atgtaatttt ggaatgagga 660
atcgaagttg ttcttctact tgctgtactt ttcttttgtt ttcaataaaa tttctacacc 720
atactgttat caaaccg 737

<210> 66
<211> 1592
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 66
aactaaaaga gaaatattgg aagcaagcca tagcagaata tgaaaaacgt ttaggcccat 60
acaccaagat agacatcata gaagttccag acgaaaaagc accagaaaat atgagtgaca 120
aagaaattga gcaagtaaaa gaaaaagaag gccaacgaat actagccaaa atcaaaccac 180
aatccacagt cattacatta gaaatacaag gaaagatgct atcttccgaa ggattggccc 240
aagaattgaa ccaacgcatg acccaagggc aaagcgactt tgttttcgtc attggcggat 300
caaacggcct gcacaaggac gtcttacaac gcagtaacta cgcactatca ttcagcaaaa 360
tgacattccc acatcaaatg atgcgggttg tgttaattga acaagtgtac agagcattta 420
agattatgcg aggagaagca tatcataaat gatgcggtta tttcagccgt aattttataa 480
tataaagcag agtttattaa attttaatga ttacttttta ttaagaatta attctagttg 540
atatattata atgtgaaaca caaaataata atttgtaatt gttagtttat aggcatctgt 600
atttggaatt ttttgtagac tatttaaaaa atagtgtata taagtattga gttcatgtat 660
taactgtctt ttttcatcgt tcatcaagta taaggatgta gagatttgtt ggataatttc 720
ttcggatgtt tttaaaatta tcattaaatt agatggtatc tgatcttgag ttttgttttt 780
agtgtatgta tattttaaaa aatttttgat tgttgttatt tgactctctt ttaatttgac 840
accctcatca ataaatgtgt taaatatatc ttcatttgta cttaaatcat caaaatttgc 900
caacaaatat ttgaacgtct ctaaatcatt atgtttgagt tccgttttgc tattccataa 960
ttccaaacca tttggtagaa agcccaagct gtgattttga tctccccata tagctgaatt 1020
taaatcagtg agttgattaa ttttttcaac acagaaatgt aattttggaa tgaggaatcg 1080

aagttgttct tctacttgct gtacttttct tttgttttca ataaaatttc tacaccatac 1140
tgttatcaaa ccgccaatta ttgtgcacaa tcctccaatg attgtagata aaattgacaa 1200
tatattacac acctttctta gaggtttatt aacatctatt tttgaattta aaattattac 1260
tttggtagcg ttataaccta tttaacagat tagagaaaaa ttgaatgatc gattgaagaa 1320
tttccaaaat accgtcccat atgcgttgaa ggagatttct attttcttct gtattcaaat 1380
ctttggcttt atcctttgct ttattcaata aatcatctga gtttttttca atatttttta 1440
atacatcttt ggcattttgt ttaaatactt taggatcgga agttagggca ttagagtttg 1500
ccacattaat catattatta ttaatcattt gaatttgatt atctgataat atctctgata 1560
acctacgctc atcgaggact ttattaacag tg 1592

<210> 67
<211> 730
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 67
agcatttaag attatgcgtg gagaagcata tcataaatga tgcggttatt tcagccgtaa 60
ttttataata taaagcagag tttattaaat tttaatgatt actttttatt aagaattaat 120
tctagttgat atattataat gtgaaacaca aaataataat ttgtaattgt tagtttatag 180
gcatctgtat ttggaatttt ttgtagacta tttaaaaaat agtgtatata agtattgagt 240
tcatgtatta actgtctttt ttcatcgttc atcaagtata aggatgtaga gatttgttgg 300
ataatttctt cggatgtttt taaaattatc attaaattag atggtatctg atcttgagtt 360
ttgtttttag tgtatgtata ttttaaaaaa tttttgattg ttgttatttg actctctttt 420
aatttgacac cctcatcaat aaatgtgtta aatatatctt catttgtact taaatcatca 480
aaatttgcca acaaatattt gaacgtctct aaatcattat gtttgagttc cgttttgcta 540
ttccataatt ccaaaccatt tggtagaaag cccaagctgt gattttgatc tccccatata 600
gctgaattta aatcagtgag ttgattaatt ttttcaacac agaaatgtaa ttttggaatg 660
aggaatcgaa gttgttcttc tacttgctgt acttttcttt tgttttcaat aaaatttcta 720
caccatactg 730

<210> 68
<211> 1696
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 68
aaagagaaat attggaagca agccatagca gaatatgaaa aacgtttagg cccatacacc 60
aagatagaca tcatagaagt tccagacgaa aaagcaccag aaaatatgag tgacaaagaa 120
attgagcaag taaaagaaaa agaaggccaa cgaatactag ccaaaatcaa accacaatcc 180
acagtcatta cattagaaat acaaggaaag atgctatctt ccgaaggatt ggcccaagaa 240
ttgaaccaac gcatgaccca agggcaaagc gactttgttt tcgtcattgg cggatcaaac 300
ggcctgcaca aggacgtctt acaacgcagt aactacgcac tatcattcag caaaatgaca 360
ttcccacatc aaatgatgcg ggttgtgtta attgaacaag tgtacagagc atttaagatt 420
atgcgaggag aagcatatca taaatgatgc ggttatttca gccgtaattt tataatataa 480
agcagagttt attaaatttt aatgattact ttttattaag aattaattct agttgatata 540
ttataatgtg aaacacaaaa taataatttg taattgttag tttataggca tctgtatttg 600
gaatttttg tagactattt aaaaaatagt gtatataagt attgagttca tgtattaact 660
gtctttttc atcgttcatc aagtataagg atgtagagat ttgttggata atttcttcgg 720
atgtttttaa aattatcatt aaattagatg gtatctgatc ttgagttttg tttttagtgt 780
atgtatattt taaaaaattt ttgattgttg ttatttgact ctcttttaat ttgacaccct 840
catcaataaa tgtgttaaat atatcttcat ttgtacttaa atcatcaaaa tttgccaaca 900

aatatttgaa cgtctctaaa tcattatgtt tgagttccgt tttgctattc cataattcca 960
aaccatttgg tagaaagccc aagctgtgat tttgatctcc ccatatagct gaatttaaat 1020
cagtgagttg attaattttt tcaacacaga aatgtaattt tggaatgagg aatcgaagtt 1080
gttcttctac ttgctgtact tttcttttgt tttcaataaa atttctacac catactgtta 1140
tcaaaccgcc aattattgtg cacaatcctc caatgattgt agataaaatt gacaatatat 1200
tacacacctt tcttagaggt ttattaacat ctatttttga atttaaaatt attactttgg 1260
tagcgttata acctatttaa cagattagag aaaaattgaa tgatcgattg aagaatttcc 1320
aaaataccgt cccatatgcg ttgaaggaga tttctatttt cttctgtatt caaatctttg 1380
gctttatcct ttgctttatt caataaatca tctgagtttt tttcaatatt ttttaataca 1440
tctttggcat tttgtttaaa tactttagga tcggaagtta gggcattaga gtttgccaca 1500
ttaatcatat tattattaat catttgaatt tgattatctg ataatatctc tgataaccta 1560
cgctcatcga ggactttatt aacagtgtct tcaacttgtt gttgtgtgat ttgtttatct 1620
tgattttgtt taatatctgc aagttgttct ttaatatctg ctatagaagc atttaaagct 1680
tcatctgaat acccat 1696

<210> 69
<211> 991
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 69
accattttag ctgtagggaa actaaaagag aaatactgga agcaagccat agcagaatat 60
gaaaaacgtt taggcccata caccaagata gacatcatag aagttccaga cgaaaaagca 120
ccagaaaata tgaactacaa agaaattgag caagtaaaag aaaaagaagg ccaacgaata 180
ctagccaaaa tcaaaccaca atcaacagtc attacattag aaatacaagg aaagatgcta 240
tcttccgaag gattggccca agaattgaac caacgcatga cccaagggca aagcgacttt 300
gtattcgtca ttggcggatc aaacggcctg cacaaggacg tcttacaacg cagtaactac 360
gcactatcat tcagcaaaat gacattccca catcaaatga tgcgggttgt gttaattgaa 420
caagtgtaca gagcatttaa gattatgcga ggagaagcgt atcataagtg atggtaaaaa 480
atatgagtaa gtagatgaag agtgaaaatc agattaatta ataataatgt atcaaattta 540
aataaagggg tttttaagta tgaatttaag aggtcatgaa aatagactta aatttcatgc 600
gaaatatgat gtgacaccta tatcacattt aaaattatta gaaggtcaaa agaaagacgg 660
tgaaggcggc atactgacag atagctatta ctgtttttca tacagcttaa aaggtaattc 720
taaaaaagtt ttaggtacgt ttaattgtgg ttatcatatt gctgaagatt tactaaaatt 780
atcaaatcaa gataaattac ctttatttaa cccgtttaaa gtaattaatg aaggtaatca 840
attgcagggc gtaacgaata aaggtaattt aaatattaat aggcaaagaa aacagtataa 900
tgaagtggct ttacagcttt caaatgctat taatttaatc ataatttgtt atgaggataa 960
tattaaagaa ccactttcaa cgataaaata c 991

<210> 70
<211> 1282
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 70
accattttag ctgtagggaa actaaaagag aaatattgga agcaagccat agcagaatat 60
gaaaaacgtt taggcccata caccaagata gacatcatag aagttccaga cgaaaaagca 120
ccagaaaata tgagcgacaa agaaattgag caagtaaaag aaaaagaagg ccaacgaata 180
ctagccaaaa tcaaaccaca atccacagtc attacattag aaatacaagg aaagatgcta 240
tcttccgaag gattggccca agaattgaac caacgcatga cccaagggca aagcgacttt 300
gtattcgtca ttggcggatc aaacggcctg cacaaggacg tcttacaacg cagtaactat 360

gcactatcat ttagcaaaat gacattccca catcaaatga tgcgggttgt gttaattgaa 420
caagtgtata gagcatttaa gattatgcgt ggagaagcgt accacaaata aaactaaaaa 480
atatgagaaa attattaaat tagctcaaat ctttgaagaa taaaaagtga atattaagtt 540
tgataattta ggtacaagta aagattaaga atttccatta tttaatacat ggtgtgtaaa 600
tcgacttctt tttgtattag atgtttgcag taagcgatgt aaagaagatg ctaataaata 660
tgtgaggaat gattacgata ctagataagc ggctaatgaa atttttaaa gtacatatat 720
agacatattt ttcatttagt aaaattttga atttcacttt gctaagacta gtgtctagaa 780
atttataatg atttattaac acctatttga aacttaagta taataaatga ttcggatttt 840
atttttaata aagacaaact tgaacgtagc aaagtagttt ttatgataaa taataagttt 900
taataatgtg acgcttttat ataagcacat tattatgaac aatgtgaatt gagcatctac 960
aattacatta ataaatatat aaatgatgat ttaaattcac atatatttat aatacacata 1020
ctatatgaaa gttttgatta tccgaataaa tgctaaaatt aataaaataa ttaaaggaat 1080
catacttatt atacgtatac gtttagctac tgaactactg gattcatttg gagattctag 1140
tagttctttt tcaatctcta aatctaaatc agttttgtaa taaccattaa ttcctaatct 1200
ttcatctagc tctgtacttt tttcatcatt tttatctttg ttgatatgtt ccattttctc 1260
gcctcttttt aatcaagtag aa 1282

<210> 71
<211> 1108
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 71
accattttag ctgtagggaa actaaaagag aaatattgga agcaagccat agcagaatat 60
gaaaaacgtt taggcccata caccaagata gacatcatag aagttccaga cgaaaaagca 120
ccagaaaata tgagcgacaa agaaattgag caagtaaaag aaaaagaagg ccaacgaata 180
ctagccaaaa tcaaaccaca atccacagtc attacattag aaatacaagg aaagatgcta 240
tcttccgaag gattggccca agaattgaac caacgcatga cccaagggca aagcgacttt 300
gtattcgtca ttggcggatc aaacggcctg cacaaggacg tcttacaacg cagtaactat 360
gcactatcat ttagcaaaat gacattccca catcaaatga tgcgggttgt gttaattgaa 420
caagtgtata gagcatttaa gattatgcgt ggagaagcgt accacaaata aaactaaaaa 480
atatgagaaa attattaaat tagctcaaat ctttgaagaa taaaaagtga atattaagtt 540
tgataattta ggtacaagta aagattaaga atttccatta tttaatacat ggtgtgtaaa 600
tcgacttctt tttgtattag atgtttgcag taagcgatgt aaagaagatg ctaataaata 660
tgtgaggaat gattacgata ctagataagc ggctaatgaa atttttaaa gtacatatat 720
agacatattt ttcatttagt aaaattttga atttcacttt gctaagacta gtgtctagaa 780
atttataatg atttattaac acctatttga aacttaagta taataaatga ttcggatttt 840
atttttaata aagacaaact tgaacgtagc aaagtagttt ttatgataaa taataagttt 900
taataatgtg acgcttttat ataagcacat tattatgaac aatgtgaatt gagcatctac 960
aattacatta ataaatatat aaatgatgat ttaaattcac atatatttat aatacacata 1020
ctatatgaaa gttttgatta tccgaataaa tgctaaaatt aataaaataa ttaaaggaat 1080
catacttatt atacgtatac gtttagct 1108

<210> 72
<211> 1530
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 72
ttagctgtag ggaaactaaa agagaaatat tggaagcaag ccatagcaga atatgaaaaa 60
cgtttaggcc catacaccaa gatagacatc atagaagttc cagacgaaaa agcaccagaa 120

aatatgagcg acaaagaaat tgagcaagta aaagaaaaag aaggccaacg aatactagcc 180
aaaatcaaac cacaatccac agtcattaca ttagaaatac aaggaaagat gctatcttcc 240
gaaggattgg cccaagaatt gaaccaacgc atgacccaag ggcaaagcga ctttgtattc 300
gtcattggcg gatcaaacgg cctgcacaag gacgtcttac aacgcagtaa ctatgcacta 360
tcatttagca aaatgacatt cccacatcaa atgatgcggg ttgtgttaat tgaacaagtg 420
tatagagcat ttaagattat gcgtggagaa gcatatcata aatgatgcgg ttttttcagc 480
cgcttcataa agggggggtga tcatatcgga acgtatgagg tttatgagaa ttgctgctat 540
gtttttatga agcgtatcat aaatgatgca gtttttgata atttttttctt tatcagagat 600
tttactaaaa atcccctcaa agtttgtttt tttcaacttc aactttgaag ggaataaata 660
aggaacttat ttatatttat cctttatctc attaatatct atttttttat taataatatt 720
ataaatatta aattctttag aaaagtcact atcactctta ttcttcatac taaacgttat 780
taatctaata atatcagcta ctatttcttt aaattctatt gcatcttctt ttttataagt 840
agcgcctgta tgaacaattt tatttctcat accatagtaa tctttcatat atttttttac 900
acaattttta atttcattag aattatccaa atctagatta tcaattgtct ttaataaatg 960
atcattaaca acattagcat acccacatcc aagcttcttt tttatctctt catcacttaa 1020
attttcatct aatttataat atctttctaa aaaatttgtg ataaaaactt ctaatgcagt 1080
ctgaatttgt acaattgcta aattatagtc agatttataa aaagaacgtt caccttttct 1140
catagccaaa acataaatat tgctaggatg attattgaaa atattataat ttttttaat 1200
atttaataaa tcacttttt tgatagatga atactgatct tcttctatct ttccaggcat 1260
gtcaatcatg aaaatactca tctcttttat atttccatct atagtatata ttatataata 1320
tggaatactt aatatatccc ctaatgatag ctggtatata ttatgatact gatatttaac 1380
gctaataatt ttaataagat tatttagaca attaaattgc ttattaaaaa ttttcgttag 1440
actattactt ttctttgatt ccctagaagt agaatttgat ttcaattttt taaactgatt 1500
gtgcttgatt attgaagtta tttcaacata 1530

<210> 73
<211> 1256
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 73
gctgtaggga aactaaaaga gaaatattgg aagcaagcca tagcagaata tgaaaaacgt 60
ttaggcccat acaccaagat agacatcata gaagttccag acgaaaaagc accagaaaat 120
atgagcgaca aagaaattga gcaagtaaaa gaaaaagaag gccaacgaat actagccaaa 180
attaaaccac aatccacagt cattacatta gaaatacaag gaaagatgct atcttccgaa 240
ggattggccc aagaattgaa ccaacgcatg acccaagggc aaagcgactt tgtattcgtc 300
attggcggat caaacggcct gcacaaggac gtcttacaac gcagtaacta cgcactatca 360
ttcagcaaaa tgacattccc acatcaaatg atgcgggttg tgttaattga gcaagtgtat 420
agagcattta agattatgcg tggagaagca tatcataaat gatgcggttt tttcagccgc 480
ttcataaagg gattttgaat gtatcagaac atatgaggtt tatgtgaatt gctgttatgt 540
ttttaagaag catatcataa gtgatgcggt ttttattaat tagttgctaa aaaatgaagt 600
atgcaatatt aattattatt aaattttgat atatttaaag aaagattaag tttagggtga 660
atgaatggct tatcaaagtg aatatgcatt agaaaatgaa gtacttcaac aacttgagga 720
attgaactat gaaagagtaa atatacataa tattaaatta gaaattaatg aatatctcaa 780
agaactagga gtgttgaaaa atgaataagc agacaaatac tccagaacta agatttccag 840
agtttgatga ggaatggaaa aaaaggaaat taggtgaagt agtaaattat aaaaatggtg 900
gttcatttga aagtttagtg aaaaaccatg gtgtatataa actcataact cttaaatctg 960
ttaatacaga aggaaagttg tgtaattctg gaaaatatat cgatgataaa tgtgttgaaa 1020
cattgtgtaa tgatacttta gtaatgatac tgagcgagca agcaccagga ctagttggaa 1080
tgactgcaat tatacctaat aataatgagt atgtactaaa tcaacgagta gcagcactag 1140
tgcctaaaca atttatagat agtcaatttc tatctaagtt aattaataga aaccagaaat 1200
atttcagtgt gagatctgct ggaacaaaag tgaaaaatat ttctaaagga catgta 1256

<210> 74

<211> 1032
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 74
accattttag ctgtagggaa actaaaagag aaatattgga agcaagccat agcagaatat 60
gaaaaacgtt taggcccata caccaagata gacatcatag aagttccaga cgaaaaagca 120
ccagaaaata tgagcgacaa agaaattgag caagtaaaag aaaaagaagg ccaacgaata 180
ctagccaaaa ttaaaccaca atccacagtc attacattag aaatacaagg aaagatgcta 240
tcttccgaag gattggccca agaattgaac caacgcatga cccaagggca aagcgacttt 300
gtattcgtca ttggcggatc aaacggcctg cacaaggacg tcttacaacg cagtaactac 360
gcactatcat tcagcaaaat gacattccca catcaaatga tgcgggttgt gttaattgag 420
caagtgtata gagcatttaa gattatgcgt ggagaagcat atcataagtg atgcggtttt 480
tattaattag ttgctaaaaa atgaagtatg caatattaat tattattaaa ttttgatata 540
tttaaagaaa gattaagttt agggtgaatg aatggcttat caaagtgaat atgcattaga 600
aaatgaagta cttcaacaac ttgaggaatt gaactatgaa agagtaaata tacataatat 660
taaattagaa attaatgaat atctcaaaga actaggagtg ttgaaaaatg aataagcaga 720
caaatactcc agaactaaga tttccagagt ttgatgagga atggaaaaaa aggaaattag 780
gtgaagtagt aaattataaa aatggtggtt catttgaaag tttagtgaaa aaccatggtg 840
tatataaact cataactctt aaatctgtta atacagaagg aaagttgtgt aattctggaa 900
aatatatcga tgataaatgt gttgaaacat tgtgtaatga tactttagta atgatactga 960
gcgagcaagc accaggacta gttggaatga ctgcaattat acctaataat aatgagtatg 1020
tactaaatca ac 1032

<210> 75
<211> 1116
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 75
accattttag ctgtagggaa actaaaagag aaatattgga agcaagccat agcagaatat 60
gaaaaacgtt taggcccata caccaagata gacatcatag aagttccaga cgaaaaagca 120
ccagaaaata tgagcgacaa agaaattgag caagtaaaag aaaaagaagg ccaacgaata 180
ctagccaaaa ttaaaccaca atccacagtc attacattag aaatacaagg aaagatgcta 240
tcttccgaag gattggccca agaattgaac caacgcatga cccaagggca aagcgacttt 300
gtattcgtca ttggcggatc aaacggcctg cacaaggacg tcttacaacg cagtaactac 360
gcactatcat tcagcaaaat gacattccca catcaaatga tgcgggttgt gttaattgag 420
caagtgtata gagcatttaa gattatgcgt ggagaagcat atcataaatg atgcggtttt 480
ttcagccgct tcataaaggg attttgaatg tatcagaaca tatgaggttt atgtgaattg 540
ctgttatgtt tttaagaagc atatcataaa tgatgcggtt ttttcagccg cttcataaag 600
ggattttgaa tgtatcagaa catatgaggt ttatgtgaat tgctgttatg tttttaagaa 660
gcatatcata agtgatgcgg tttttattaa ttagttgcta aaaaatgaag tatgcaatat 720
taattattat taaattttga tatatttaaa gaaagattaa gtttagggtg aatgaatggc 780
ttatcaaagt gaatatgcat tagaaaatga agtacttcaa caacttgagg aattgaacta 840
tgaaagagta aatatacata atattaaatt agaaattaat gaatatctca aagaactagg 900
agtgttgaaa aatgaataag cagacaaata ctccagaact aagatttcca gagtttgatg 960
aggaatggaa aaaaaggaaa ttaggtgaag tagtaaatta taaaaatggt ggttcatttg 1020
aaagtttagt gaaaaaccat ggtgtatata aactcataac tcttaaatct gttaatacag 1080
aaggaaagtt gtgtaattct ggaaaatata tcgatg 1116

<210> 76

<211> 1100
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 76
accattttag ctgtagggaa actaaaagag aaatattgga agcaagccat agcagaatat 60
gaaaaacgtt taggcccata caccaagata gacatcatag aagttccaga cgaaaaagca 120
ccagaaaata tgagcgacaa agaaattgag caagtaaaag aaaaagaagg ccaacgaata 180
ctagccaaaa ttaaaccaca atccacagtc attacattag aaatacaagg aaagatgcta 240
tcttccgaag gattggccca agaattgaac caacgcatga cccaagggca aagcgacttt 300
gtattcgtca ttggcggatc aaacggcctg cacaaggacg tcttacaacg cagtaactac 360
gcactatcat tcagcaaaat gacattccca catcaaatga tgcgggttgt gttaattgag 420
caagtgtata gagcatttaa gattatgcgt ggagaagcgt atcacaaata aaactaaaaa 480
ataagttgta tataacttat tttgaaattg gttaagtata taatatctcc aataaaatgt 540
agttaactta cgataatgct gaactatagc tttgtaaact aaaatgtaaa taattacaat 600
caaattgcaa caatatagtt caagaatgct acaatttgag gacagattga tagcattaat 660
ccctttaaaa tgaagctagg agataactta cattatgatt agtaaacaaa taaaggattt 720
acgaaagcaa cataattata ctcaagaaga gctagctgaa aaattaaata cttcaagaca 780
aacaatttct aaatgggaac aaggtatttc agaaccagac ttaattatgc ttatgcaatt 840
gtcacaatta ttttctgtta gtacagacta tctcattaca ggaagtgaca atattattaa 900
aaaagataat aaaagctatt atgaaatgaa tttttgggca tttatgtctg aaaaatggtg 960
ggtaattatt attatagtaa tcataatttg tggaacaata ggacaaattt tttcaaacta 1020
atgtaagtat ctctcaaata ttttgggagg ttttattatg aaaatcaaaa aattattaaa 1080
gacattatta attattttat 1100

<210> 77
<211> 1118
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 77
atgaaaatca ccattttagc tgtagggaaa ctaaaagaga aatattggaa gcaagccata 60
gcagaatatg aaaaacgttt aggcccatac accaagatag acatcataga agttccagac 120
gaaaaagcac cagaaaatat gagcgacaaa gaaattgagc aagtaaaaga aaaagaaggc 180
caacgaatac tagccaaaat caaaccacaa tcaacagtca ttacattaga aatacaagga 240
aagatgctat cttccgaagg attggcccaa gaattgaacc aacgcatgac ccaagggcaa 300
agcgactttg tattcgtcat tggcggatca aacggcctgc acaaggacgt cttacaacgc 360
agtaactacg cactatcatt cagcaaaatg acattcccac atcaaatgat gcgggttgtg 420
ttaattgaac aagtgtacag agcatttaag attatgcgtg gagaagcgta tcacaaataa 480
aactaaaaaa taagttgtat ataacttatt ttgaaattgg ttaagtatat agtatctcca 540
ataaaatgta gttaacttac gataatgctg aactatagct ttgtaaacta aaatgtaaat 600
aattacaatc aaattgcaac aatatagttc aagaatgcta caatttgagg acagattgat 660
agcattaatc cctttaaaat gaagctagga gataacttac attatgatta gtaaacaaat 720
aaaggattta cgaaagcaac ataattatac tcaagaagag ctagctgaaa aattaaatac 780
ttcaagacaa acaatttcta aatgggaaca aggtatttca gaaccagact taattatgct 840
tatgcaattg tcacaattat tttctgttag tacagactat ctcattacag gaagtgacaa 900
tattattaaa aaagataata aaagctatta tgaaatgaat ttttgggcat ttatgtctga 960
aaaatggtgg gtaattatta ttatagtaat cataatttgt ggaacaatag gacaaatttt 1020
ttcaaactaa tgtaagtatc tctcaaatat tttgggaggt tttattatga aaatcaaaaa 1080
attattaaag acattattaa ttattttatt atgttttg 1118

<210> 78
<211> 1168
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 78
atgaaaatca ccattttagc tgtagggaaa ctaaaagaga aatattggaa gcaagccata 60
gcagaatatg aaaaacgttt aggcccatac accaagatag acatcataga agttçcagac 120
gaaaaagcac cagaaaatat gagcgacaaa gaaattgagc aagtaaaaga aaaagaaggc 180
caacgaatac tagccaaaat caaaccacaa tcaacagtca ttacattaga aatacaagga 240
aagatgctat cttccgaagg attggcccaa gaattgaacc aacgcatgac ccaagggcaa 300
agcgactttg tattcgtcat tggcggatca aacggcctgc acaaggacgt cttacaacgc 360
agtaactacg cactatcatt cagcaaaatg acattcccac atcaaatgat gcgggttgtg 420
ttaattgaac aagtgtacag agcatttaag attatgcgtg gagaagcgta tcacaaataa 480
aactaaaaaa taagttgtat ataacttatt ttgaaattgg ttaagtatat agtatctcca 540
ataaaatgta gttaacttac gataatgctg aactatagct ttgtaaacta aaatgtaaat 600
aattacaatc aaattgcaac aatatagttc aagaatgcta caatttgagg acagattgat 660
agcattaatc cctttaaaat gaagctagga gataacttac attatgatta gtaaacaaat 720
aaaggattta cgaaagcaac ataattatac tcaagaagag ctagctgaaa aattaaatac 780
ttcaagacaa acaatttcta aatgggaaca aggtatttca gaaccagact taattatgct 840
tatgcaattg tcacaattat tttctgttag tacagactat ctcattacag gaagtgacaa 900
tattattaaa aaagataata aaagctatta tgaaatgaat ttttgggcat ttatgtctga 960
aaaatggtgg gtaattatta ttatagtaat cataatttgt ggaacaatag gacaaatttt 1020
ttcaaactaa tgtaagtatc tctcaaatat tttgggaggt tttattatga aaatcaaaaa 1080
attattaaag acattattaa ttattttatt atgttttgta ttgtctgtta ttgtgcaaaa 1140
tatttcaatg ctatggcata ttgtgagc 1168

<210> 79
<211> 1134
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 79
atgaaaatca ccattttagc tgtagggaaa ctaaaagaga aatattggaa gcaagccata 60
gcagaatatg aaaaacgttt aggcccatac accaagatag acatcataga agttccagac 120
gaaaaagcac cagaaaatat gagcgacaaa gaaattgagc aagtaaaaga aaaagaaggc 180
caacgaatac tagccaaaat caaaccacaa tccacagtca ttacattaga aatacaagga 240
aagatgctat cttccgaagg attggcccaa gaattgaacc aacgcatgac ccaagggcaa 300
agcgactttg tattcgtcat tggcggatca aacggcctgc acaaggacgt cttacaacgc 360
agtaactatg cactatcatt tagcaaaatg acattcccac atcaaatgat gcgggttgtg 420
ttaattgaac aagtgtatag agcatttaag attatgcgtg gagaggcgta tcataaataa 480
aactaaaaaa cggattgtgt ataatatatt ttaaatataa aaaggattga ttttatgtta 540
aataaattag aaaatgttag ttataaatca ttcgataatt acactagtga agatgatttg 600
actaaagtaa atatattttt tggaagaaat gggagtggaa aaagctcatt aagtgaatgg 660
ttaagaagac tagataatga aaaaagtgtt atctttaata ctggttactt aaaaaataat 720
attgaagaag ttgaagaaat agatggtgtg aatttggtta ttggagaaga atctataaat 780
catagtgacc aaattaagca tttaaatagc gctataaata gtttagaaaa ttttattact 840
cggaaaaata gtgaacttaa gcattcaaaa gaaagaattt acaataaaat gaatatcaga 900
ctaaatgaag ctagagaaag atttgaaata ggtagtaatg tggttaagca gaagaggaat 960
gctgacaaag atccagttaa tgctttttat agttggaaga aaaatgctaa cgatataatt 1020
caagagatga ctattgaatc tttagatgaa ttagaagaaa gaataacaag aaaagaagtc 1080

ttattaaata atataaaaac accaatttta gcttttgatt ataatgattt tagt 1134

<210> 80
<211> 818
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 80
aatattggaa gcaagccata gcagaatatg aaaaacgttt aggcccatac accaagatag 60
acatcataga agttccagac gaaaaagcac cagaaaatat gagcgacaaa gaaattgagc 120
aagtgtatag agcatttaag attatgcgtg gagaagcata tcataaatga tgcggttttt 180
tcagccgctt cataaaggga ttttgaatgt atcagaacat atgaggttta tgtgaattgc 240
tgttatgttt ttaagaagct tatcataagt aatgaggttc atgatttttg acatagttag 300
cctccgcagt ctttcatttc aagtaaataa tagcgaaata ttctttatac tgaatactta 360
tagtgaagca aagttctagc tttgagaaaa ttctttctgc aactaaatat agtaaattac 420
ggtaaaatat aaataagtac atattgaaga aaatgagaca taatatattt tataatagga 480
gggaatttca aatgatagac aactttatgc aggtccttaa attaattaaa gagaaacgta 540
ccaataatgt agttaaaaaa tctgattggg ataaaggtga tctatataaa actttagtcc 600
atgataagtt acccaagcag ttaaaagtgc atataaaaga agataaatat tcagttgtag 660
ggaaggttgc tactgggaac tatagtaaag ttccttggat ttcaatatat gatgagaata 720
taacaaaaga aacaaaggat ggatattatt tggtatatct ttttcatccg gaaggagaag 780
gcatatactt atcttgaatc aaggatggtc aaagataa 818

<210> 81
<211> 1090
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 81
atgaaaatca ccattttagc tgtagggaaa ctaaaagaga aatattggaa gcaagccata 60
gcagaatatg aaaaacgttt aggcccatac accaagatag acatcataga agttccagac 120
gaaaaagcac cagaaaatat gagcgacaaa gaaattgagc aagtaaaaga aaaagaaggc 180
caacgaatac tagccaaaat caaaccacaa tcaacagtca ttacattaga aatacaagga 240
aagatgctat cttccgaagg attggcccaa gaattgaacc aacgcatgac ccaagggcaa 300
agcgactttg tattcgtcat tggcggatca aacggcctgc acaaggacgt cttacaacgc 360
agtaactacg cactatcatt cagcaaaatg acattcccac atcaaatgat gcgggttgtg 420
ttaattgaac aagtgtacag agcatttaag attatgcgtg gagaagcata tcataagtga 480
tgcggttttt attaattagt tgctaaaaaa tgaagtatgc aatattaatt attattaaat 540
tttgatatat ttaaagaaag attaagttta gggtgaatga atggcttatc aaagtgaata 600
tgcattagaa aatgaagtac ttcaacaact tgaggaattg aactatgaaa gagtaaatat 660
acataatatt aaattagaaa ttaatgaata tctcaaagaa ctaggagtgt tgaaaaatga 720
ataagcagac aaatactcca gaactaagat ttccagagtt tgatgaggaa tggaaaaaaa 780
ggaaattagg tgaagtagta aattataaaa atggtggttc atttgaaagt ttagtgaaaa 840
accatggtgt atataaactc ataactctta aatctgttaa tacagaagga aagttgtgta 900
attctggaaa atatatcgat gataaatgtg ttgaaacatt gtgtaatgat actttagtaa 960
tgatactgag cgagcaagca ccaggactag ttggaatgac tgcaattata cctaataata 1020
atgagtatgt actaaatcaa cgagtagcag cactagtgcc taaacaattt atagatagtc 1080
aatttctatc 1090

<210> 82
<211> 1063

<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 82
atgaaaatca ccattttagc tgtagggaaa ctaaaagaga aatattggaa gcaagccata 60
gcagaatatg aaaaacgttt aggcccatac accaagatag acatcataga agttccagac 120
gaaaaagcac cagaaaatat gagcgacaaa gaaattgagc aagtaaaaga aaaagaaggc 180
caacgaatac tagccaaaat caaaccacaa tcaacagtca ttacattaga aatacaagga 240
aagatgctat cttccgaagg attggcccaa gaattgaacc aacgcatgac ccaagggcaa 300
agcgactttg tattcgtcat tggcggatca aacggcctgc acaaggacgt cttacaacgc 360
agtaactacg cactatcatt cagcaaaatg acattcccac atcaaatgat gcgggttgtg 420
ttaattgaac aagtgtacag agcatttaag attatgcgtg gagaagcata tcataagtga 480
tgcggttttt attaattagt tgctaaaaaa tgaagtatgc aatattaatt attattaaat 540
tttgatatat ttaaagaaag attaagttta gggtgaatga atggcttatc aaagtgaata 600
tgcattagaa aatgaagtac ttcaacaact tgaggaattg aactatgaaa gagtaaatat 660
acataatatt aaattagaaa ttaatgaata tctcaaagaa ctaggagtgt tgaaaaatga 720
ataagcagac aaatactcca gaactaagat ttccagagtt tgatgaggaa tggaaaaaaa 780
ggaaattagg tgaagtagta aattataaaa atggtggttc atttgaaagt ttagtgaaaa 840
accatggtgt atataaactc ataactctta aatctgttaa tacagaagga aagttgtgta 900
attctggaaa atatatcgat gataaatgtg ttgaaacatt gtgtaatgat actttagtaa 960
tgatactgag cgagcaagca ccaggactag ttggaatgac tgcaattata cctaataata 1020
atgagtatgt actaaatcaa cgagtagcag cactagtgcc taa 1063

<210> 83
<211> 756
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 83
tgacattccc acatcaaatg atgcgggttg tgttaattga gcaagtgtat agagcattta 60
agattatgcg tggagaagcg tatcacaaat aaaactaaaa aataggttgc gcataatata 120
attagaaagg aattagacat aaattaggag tccttcacag aatagcgaag gactcccatt 180
aaatatatta tggtgtaaag aaatcacaaa tcaatatata tacttaatac catatattaa 240
cttgtactat tataaagtac gacatcagta ttaggtatca ctttgaacac atgaatttca 300
ttatcacttt tattattcac aaaaaatttt ccaattctca attactgaat tatgtgtata 360
catgttgtta aaaattaata aaggatattt atgtttgttt aaagcatatc acaagtgatg 420
cggtttttta taaagattta cttgttagtg attttgataa aaatgcttaa tactatttca 480
ataatatgta tttaaaaatt agattaatag tatttaactt caaatggcct cgtataaact 540
catagcaaat taacgtaaat caatgaaata aaatgaaaac aatttcaaga atacattata 600
aacataaagt atacaaaaaa taaatgagcg tatttgttta aacgtataca ctcattttta 660
ttaaattaat ttattatatt ttacgattgt tatttatgaa attaacaaat tccatttttg 720
atagtgaaat taaaagcttt atcacttatt attgat 756

<210> 84
<211> 771
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 84
tgacattccc acatcaaatg atgcgggttg tgttaattga gcaagtgtat agagcattta 60
agattatgcg tggagaagcg tatcacaaat aaaactaaaa aataggttgc gcataatata 120
attagaaagg aattagacat aaattaggag tccttcacag aatagcgaag gactcccatt 180
aaatatatta tggtgtaaag aaatcacaaa tcaatatata tacttaatac catatattaa 240
cttgtactat tataaagtac gacatcagta ttaggtatca ctttgaacac atgaatttca 300
ttatcacttt tattattcac aaaaaatttt ccaattctca attactgaat tatgtgtata 360
catgttgtta aaaattaata aaggatattt atgtttgttt aaagcatatc acaagtgatg 420
cggtttttta taaagattta cttgttagtg attttgataa aaatgcttaa tactatttca 480
ataatatgta tttaaaaatt agattaatag tatttaactt caaatggcct cgtataaact 540
catagcaaat taacgtaaat caatgaaata aaatgaaaac aatttcaaga atacattata 600
aacataaagt atacaaaaaa taaatgagcg tatttgttta aacgtataca ctcattttta 660
ttaaattaat ttattatatt ttacgattgt tatttatgaa attaacaaat tccatttttg 720
atagtgaaat taaaagcttt atcacttatt attgataatt ttgactgcat c 771

<210> 85
<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 85
ttcagcaaaa tgacattccc acatcaaatg atgcgggttg tgttaattga acaagtgtac 60
agagcattta agattatgcg tggagaagcg tatcataagt agcggaggag ttttttacct 120
tgtgacttat cataaagtac gatgtttatg taagtgatta tcattattta agcaggtttt 180
tcaaattaaa taataacaag aataaaatgc acttagcgac attgaaattt attaatctag 240
taaactaata gatttataga aaattttatt tgcaagggga taattttgaa aagtagtatt 300
ttctatcttt ccataataca ttgtaattac aacggagggg atattgtgat gaagtgtata 360
gataaaacgt gggttagcta ttataaagaa ttagctgata agttaacaga ttatcaaaat 420
aaacgttatg aattaattag aaatagtgaa ggaagtatat aaaaaaacgg gaataaaatt 480
ccctacttta gcaagtgata atgtattgat ggacatagat ccttttacaa tatttgcatt 540
atttaataaa aattccatga gagaaactaa taaggtaaaa atattaacag aattagcttc 600
ggaattgaat attaagtcca aaattccgtc agtttttgac agtattccaa cagtcaataa 660
tctgaatgct acatattata a 681

<210> 86
<211> 1119
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 86
gacattccca catcaaatga tgcgggttgt gttaattgag caagtgtata gagcatttaa 60
gattatgcgt ggagaggcgt atcataagta aaactaaaaa attctgtatg aggagataat 120
aatttggagg gtgttaaatg gtggacatta aatccacgtt cattcaatat ataagatata 180
tcacgataat tgcgcatata acttaagtag tagctaacag ttgaaattag gccctatcaa 240
attggtttat atctaaaatg attaatatag aatgcttctt tttgtcctta ttaaattata 300
aaagtaactt tgcaatagaa acagttattt cataatcaac agtcattgac gtagctaagt 360
aatgataaat aatcataaat aaaattacag atattgacaa aaaatagtaa atataccaat 420
gaagtttcaa aagaacaatt ccaagaaatt gagaatgtaa ataataaggt caaagaattt 480
tattaagatt tgaaagagta tcaatcaaga aagatgtagt tttttaataa actatttgga 540
aaataattat cataatttaa aaactgacaa tttgcgagac tcataaaatg taataatgga 600
aatagatgta aaatataatt aaggggtgta atatgaagat taatatttat aaatctattt 660

ataattttca ggaaacaaat acaaattttt tagagaatct agaatcttta aatgatgaca 720
attatgaact gcttaatgat aaagaacttg ttagtgattc aaatgaatta aaattaatta 780
gtaaagttta tatacgtaaa aaagacaaaa aactattaga ttggcaatta ttaataaaga 840
atgtatacct agatactgaa gaagatgaca atttattttc agaatccggt catcattttg 900
atgcaatatt atttctcaaa gaagatacta cattacaaaa taatgtatat attatacctt 960
ttggacaagc atatcatgat ataaataatt tgattgatta tgacttcgga attgattttg 1020
cagaaagagc aatcaaaaat gaagacatag ttaataaaaa tgttaatttt tttcaacaaa 1080
acaggcttaa agagattgtt aattatagaa ggaatagtg 1119

<210> 87
<211> 1073
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 87
tattggaagc aagccatagc agaatatgaa aaacgtttag gcccatacac caagatagac 60
atcatagaag ttccagacga aaaagcacca gaaaatatga gcgacaaaga aattgagcaa 120
gtaaaagaaa aagaaggcca acgaatacta gccaaaatca aaccacaatc cacagtcatt 180
acattagaaa tacaaggaaa gatgctatct tccgaaggat tggcccaaga attgaaccaa 240
cgcatgaccc aagggcaaag cgactttgta ttcgtcattg gcggatcaaa cggcctgcac 300
aaggacgtct tacaacgcag taactatgca ctatcattta gcaaaatgac attcccacat 360
caaatgatgc gggttgtgtt aattgaacaa gtgtatagag catttaagat tatgcgtgga 420
gaggcgtatc ataagtgatg cttgttagaa tgatttttaa caatatgaaa tagctgtgga 480
agcttaaaca atttgtttat ctaagtactt atttaataat tgattgaact gtgattggca 540
ccaggctgtc tggtaaattg agaagttggg ttttggagcg tataaatgat agaattaata 600
taaaattcaa tttgaggagt aggagattat gtcgaatata aaaacaacac tagagacgtc 660
cgtaggacta gaaaaagaca acgataagct atttgattat ataactgaat tagagattca 720
aaacacgcct gaaaaccggg aagcaaaagt tgttattgaa gaaaggttac ataaagaata 780
taaatatgaa ttagatcaaa tgacaccaga gtatggaata caaaaaggca gtgttagaat 840
aggtcatgca gatgttgtaa tatttcatga ttctaaagat aaatctcaag agaatattaa 900
aataatagta gagtgtaaaa gaaagaatcg cagggatggt attgaacaat taaaaacata 960
tcttgcaggg tgtgagtctg cagaatacgg cgtttggttt aatggagaag atatagtata 1020
tataaaacga ttgaaaaaag caccacattg gaaaacagta tttaatatac cga 1073

<210> 88
<211> 595
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 88
atgaaaatca ccattttagc tgtagggaaa ctaaaagaga aatattggaa gcaagccata 60
gcagaatatg aaaaacgttt aggcccatac accaagatag acatcataga agttccagac 120
gaaaaagcac cagaaaatat gagtgacaaa gaaattgagc aagtaaaaga aaaagaaggc 180
caacgaatac tagccaaaat caaaccacaa tccacagtca ttacattaga aatacaagga 240
aagatgctat cttccgaagg attggcccaa gaattgaacc aacgcatgac ccaagggcaa 300
agcgactttg ttttcgtcat tggcggatca aacggcctgc acaaggacgt cttacaacgc 360
agtaactacg cactatcatt cagcaaaatg acattcccac atcaaatgat gcgggttgtg 420
ttaattgaac aagtgtacag agcatttaag attatgcgag gagaagcgta tcacaaataa 480
aactaaaaaa tagattgtgt ataatataaa aggagcggat ttatattaaa actttgaatt 540
caaaaattat tgaaagggaa gctaccttag aaattgaatc tatggcaact aatac 595

<210> 89
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 89
gtcaaaaatc atgaacctca ttacttatg 29

<210> 90
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 90
ctatgtcaaa aatcatgaac ctcattac 28

<210> 91
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 91
ggaggctaac tatgtcaaaa atc 23

<210> 92
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<220>
<221> misc_feature
<222> 27
<223> n = a, t, c, or g

<400> 92
tcatgaacct cattacttat gataagnt 28

<210> 93
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 93
gatagactaa ttatcttcat c 21

<210> 94
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 94
cagactgtgg acaaactgat t 21

<210> 95
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Staphylococcus aureus

<400> 95
tgagatcatc tacatcttta 20

<210> 96
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