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(54) **SPECIFIC AND UNIVERSAL PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN MICROBIOLOGY LABORATORIES**

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(57) **ABSTRACT**

The present invention relates to DNA-based methods for universal bacterial detection, for specific detection of the common bacterial pathogens *Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis, Streptococcus pneumoniae, Staphylococcus aureus, Staphylococcus epidermidis, Enterococcus faecalis, Staphylococcus saprophyticus, Streptococcus pyogenes, Haemophilus influenzae* and *Moraxella catarrhalis* as well as for specific detection of commonly encountered and clinically relevant bacterial antibiotic resistance genes directly from clinical specimens or, alternatively, from a bacterial colony. The above bacterial species can account for as much as 80% of bacterial pathogens isolated in routine microbiology laboratories.

The core of this invention consists primarily of the DNA sequences from all species-specific genomic DNA fragments selected by hybridization from genomic libraries or, alternatively, selected from data banks as well as any oligonucleotide sequences derived from these sequences which can be used as probes or amplification primers for PCR or any other nucleic acid amplification methods. This invention also includes DNA sequences from the selected clinically relevant antibiotic resistance genes.

With these methods, bacteria can be detected (universal primers and/or probes) and identified (species-specific primers and/or probes) directly from the clinical specimens or from an isolated bacterial colony. Bacteria are further evaluated for their putative susceptibility to antibiotics by resistance gene detection (antibiotic resistance gene specific primers and/or probes). Diagnostic kits for the detection of the presence, for the bacterial identification of the above-mentioned bacterial species and for the detection of antibiotic resistance genes are also claimed. These kits for the rapid (one hour or less) and accurate diagnosis of bacterial infections and antibiotic resistance will gradually replace conventional methods currently used in clinical microbiology laboratories for routine diagnosis. They should provide tools to clinicians to help prescribe promptly optimal treatments when necessary. Consequently, these tests should contribute to saving human lives, rationalizing treatment, reducing the development of antibiotic resistance and avoid unnecessary hospitalizations.

SPECIFIC AND UNIVERSAL PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN MICROBIOLOGY LABORATORIES

BACKGROUND OF THE INVENTION

[0001] Classical Identification of Bacteria

[0002] Bacteria are classically identified by their ability to utilize different substrates as a source of carbon and nitrogen through the use of biochemical tests such as the API20E™ system. Susceptibility testing of Gram negative bacilli has progressed to microdilution tests. Although the API and the microdilution systems are cost-effective, at least two days are required to obtain preliminary results due to the necessity of two successive overnight incubations to isolate and identify the bacteria from the specimen. Some faster detection methods with sophisticated and expensive apparatus have been developed. For example, the fastest identification system, the autoSCAN-Walk-Away system™ identifies both Gram negative and Gram positive from isolated bacterial colonies in 2 hours and susceptibility patterns to antibiotics in only 7 hours. However, this system has an unacceptable margin of error, especially with bacterial species other than *Enterobacteriaceae* (York et al., 1992. J. Clin. Microbiol. 30:2903-2910). Nevertheless, even this fastest method requires primary isolation of the bacteria as a pure culture, a process which takes at least 18 hours if there is a pure culture or 2 to 3 days if there is a mixed culture.

[0003] Urine Specimens

[0004] A large proportion (40-50%) of specimens received in routine diagnostic microbiology laboratories for bacterial identification are urine specimens (Pezzlo, 1988, Clin. Microbiol. Rev. 1:268-280). Urinary tract infections (UTI) are extremely common and affect up to 20% of women and account for extensive morbidity and increased mortality among hospitalized patients (Johnson and Stamm, 1989; Ann. Intern. Med. 111:906-917). UTI are usually of bacterial etiology and require antimicrobial therapy. The Gram negative bacillus *Escherichia coli* is by far the most prevalent urinary pathogen and accounts for 50 to 60% of UTI (Pezzlo, 1988, op. cit.). The prevalence for bacterial pathogens isolated from urine specimens observed recently at the "Centre Hospitalier de 1'Université Laval (CHUL)" is given in Tables 1 and 2.

[0005] Conventional pathogen identification in urine specimens. The search for pathogens in urine specimens is so preponderant in the routine microbiology laboratory that a myriad of tests have been developed. The gold standard is still the classical semi-quantitative plate culture method in which a calibrated loop of urine is streaked on plates and incubated for 18-24 hours. Colonies are then counted to determine the total number of colony forming units (CFU) per liter of urine. A bacterial UTI is normally associated with a bacterial count of $\geqq 10^7$ CFU/L in urine. However, infections with less than 10^7 CFU/L in urine are possible, particularly in patients with a high incidence of diseases or those catheterized (Stark and Maki, 1984, N. Engl. J. Med. 311:560-564). Importantly, close to 80% of urine specimens tested are considered negative ($<10^7$ CFU/L; Table 3).

[0006] Accurate and rapid urine screening methods for bacterial pathogens would allow a faster identification of negative results and a more efficient clinical investigation of the patient. Several rapid identification methods (Uriscreen™, UTIscreen™, Flash Track™ DNA probes and others) were recently compared to slower standard biochemical methods which are based on culture of the bacterial pathogens. Although much faster, these rapid tests showed low sensitivities and specificities as well as a high number of false negative and false positive results (Koening et al., 1992. J. Clin. Microbiol. 30:342-345; Pezzlo et al., 1992. J. Clin. Microbiol. 30:640-684).

[0007] Urine specimens found positive by culture are further characterized using standard biochemical tests to identify the bacterial pathogen and are also tested for susceptibility to antibiotics.

[0008] Any Clinical Specimens

[0009] As with urine specimen which was used here as an example, our probes and amplification primers are also applicable to any other clinical specimens. The DNA-based tests proposed in this invention are superior to standard methods currently used for routine diagnosis in terms of rapidity and accuracy. While a high percentage of urine specimens are negative, in many other clinical specimens more than 95% of cultures are negative (Table 4). These data further support the use of universal probes to screen out the negative clinical specimens. Clinical specimens from organisms other than humans (e.g. other primates, mammals, farm animals or live stocks) may also be used.

[0010] Towards the Development of Rapid DNA-Based Diagnostic Tests

[0011] A rapid diagnostic test should have a significant impact on the management of infections. For the identification of pathogens and antibiotic resistance genes in clinical samples, DNA probe and DNA amplification technologies offer several advantages over conventional methods. There is no need for subculturing, hence the organism can be detected directly in clinical samples thereby reducing the costs and time associated with isolation of pathogens. DNA-based technologies have proven to be extremely useful for specific applications in the clinical microbiology laboratory. For example, kits for the detection of fastidious organisms based on the use of hybridization probes or DNA amplification for the direct detection of pathogens in clinical specimens are commercially available (Persing et al, 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.).

[0012] The present invention is an advantageous alternative to the conventional culture identification methods used in hospital clinical microbiology laboratories and in private clinics for routine diagnosis. Besides being much faster, DNA-based diagnostic tests are more accurate than standard biochemical tests presently used for diagnosis because the bacterial genotype (e.g. DNA level) is more stable than the bacterial phenotype (e.g. biochemical properties). The originality of this invention is that genomic DNA fragments (size of at least 100 base pairs) specific for 12 species of commonly encountered bacterial pathogens were selected from genomic libraries or from data banks. Amplification primers or oligonucleotide probes (both less than 100 nucleotides in

length) which are both derived from the sequence of species-specific DNA fragments identified by hybridization from genomic libraries or from selected data bank sequences are used as a basis to develop diagnostic tests. Oligonucleotide primers and probes for the detection of commonly encountered and clinically important bacterial resistance genes are also included. For example, Annexes I and II present a list of suitable oligonucleotide probes and PCR primers which were all derived from the species-specific DNA fragments selected from genomic libraries or from data bank sequences. It is clear to the individual skilled in the art that oligonucleotide sequences appropriate for the specific detection of the above bacterial species other than those listed in Annexes 1 and 2 may be derived from the species-specific fragments or from the selected data bank sequences. For example, the oligonucleotides may be shorter or longer than the ones we have chosen and may be selected anywhere else in the identified species-specific sequences or selected data bank sequences. Alternatively, the oligonucleotides may be designed for use in amplification methods other than PCR. Consequently, the core of this invention is the identification of species-specific genomic DNA fragments from bacterial genomic DNA libraries and the selection of genomic DNA fragments from data bank sequences which are used as a source of species-specific and ubiquitous oligonucleotides. Although the selection of oligonucleotides suitable for diagnostic purposes from the sequence of the species-specific fragments or from the selected data bank sequences requires much effort it is quite possible for the individual skilled in the art to derive from our fragments or selected data bank sequences suitable oligonucleotides which are different from the ones we have selected and tested as examples (Annexes I and II).

[**0013**] Others have developed DNA-based tests for the detection and identification of some of the bacterial pathogens for which we have identified species-specific sequences (PCT patent application Serial No. WO 93/03186). However, their strategy was based on the amplification of the highly conserved 16S rRNA gene followed by hybridization with internal species-specific oligonucleotides. The strategy from this invention is much simpler and more rapid because it allows the direct amplification of species-specific targets using oligonucleotides derived from the species-specific bacterial genomic DNA fragments.

[**0014**] Since a high percentage of clinical specimens are negative, oligonucleotide primers and probes were selected from the highly conserved 16S or 23S rRNA genes to detect all bacterial pathogens possibly encountered in clinical specimens in order to determine whether a clinical specimen is infected or not. This strategy allows rapid screening out of the numerous negative clinical specimens submitted for bacteriological testing.

[**0015**] We are also developing other DNA-based tests, to be performed simultaneously with bacterial identification, to determine rapidly the putative bacterial susceptibility to antibiotics by targeting commonly encountered and clinically relevant bacterial resistance genes. Although the sequences from the selected antibiotic resistance genes are available and have been used to develop DNA-based tests for their detection (Ehrlich and Greenberg, 1994. PCR-based Diagnostics in Infectious Diseases, Blackwell Scientific Publications, Boston, Mass.; Persing et al, 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.), our approch is innovative as it represents major improvements over current "gold standard" diagnostic methods based on culture of the bacteria because it allows the rapid identification of the presence of a specific bacterial pathogen and evaluation of its susceptibility to antibiotics directly from the clinical specimens within one hour.

[**0016**] We believe that the rapid and simple diagnostic tests not based on cultivation of the bacteria that we are developing will gradually replace the slow conventional bacterial identification methods presently used in hospital clinical microbiology laboratories and in private clinics. In our opinion, these rapid DNA-based diagnostic tests for severe and common bacterial pathogens and antibiotic resistance will (i) save lives by optimizing treatment, (ii) diminish antibiotic resistance by reducing the use of broad spectrum antibiotics and (iii) decrease overall health costs by preventing or shortening hospitalizations.

SUMMARY OF THE INVENTION

[**0017**] In accordance with the present invention, there is provided sequence from genomic DNA fragments (size of at least 100 base pairs and all described in the sequence listing) selected either by hybridization from genomic libraries or from data banks and which are specific for the detection of commonly encountered bacterial pathogens (i.e. *Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis, Streptococcus pneumoniae, Staphylococcus aureus, Staphylococcus epidermidis, Enterococcus faecalis, Staphylococcus saprophyticus, Streptococcus pyogenes, Haemophilus influenzae* and *Moraxella catarrhalis*) in clinical specimens. These bacterial species are associated with approximately 90% of urinary tract infections and with a high percentage of other severe infections including septicemia, meningitis, pneumonia, intraabdominal infections, skin infections and many other severe respiratory tract infections. Overall, the above bacterial species may account for up to 80% of bacterial pathogens isolated in routine microbiology laboratories.

[**0018**] Synthetic oligonucleotides for hybridization (probes) or DNA amplification (primers) were derived from the above species-specific DNA fragments (ranging in sizes from 0.25 to 5.0 kilobase pairs (kbp)) or from selected data bank sequences (GenBank and EMBL). Bacterial species for which some of the oligonucleotide probes and amplification primers were derived from selected data bank sequences are *Escherichia coli, Enterococcus faecalis, Streptococcus pyogenes* and *Pseudomonas aeruginosa.* The person skilled in the art understands that the important innovation in this invention is the identification of the species-specific DNA fragments selected either from bacterial genomic libraries by hybridization or from data bank sequences. The selection of oligonucleotides from these fragments suitable for diagnostic purposes is also innovative. Specific and ubiquitous oligonucleotides different from the ones tested in the practice are considered as embodiments of the present invention.

[**0019**] The development of hybridization (with either fragment or oligonucleotide probes) or of DNA amplification protocols for the detection of pathogens from clinical specimens renders possible a very rapid bacterial identification. This will greatly reduce the time currently required for the identification of pathogens in the clinical laboratory

since these technologies can be applied for bacterial detection and identification directly from clinical specimens with minimum pretreatment of any biological specimens to release bacterial DNA. In addition to being 100% specific, probes and amplification primers allow identification of the bacterial species directly from clinical specimens or, alternatively, from an isolated colony. DNA amplification assays have the added advantages of being faster and more sensitive than hybridization assays, since they allow rapid and exponential in vitro replication of the target segment of DNA from the bacterial genome. Universal probes and amplification primers selected from the 16S or 23S rRNA genes highly conserved among bacteria, which permit the detection of any bacterial pathogens, will serve as a procedure to screen out the numerous negative clinical specimens received in diagnostic laboratories. The use of oligonucleotide probes or primers complementary to characterized bacterial genes encoding resistance to antibiotics to identify commonly encountered and clinically important resistance genes is also under the scope of this invention.

DETAILED DESCRIPTION OF THE INVENTION

[0020] Development of Species-Specific DNA Probes

[0021] DNA fragment probes were developed for the following bacterial species: *Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis, Streptococcus pneumoniae, Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus saprophyticus, Haemophilus influenzae* and *Moraxella catarrhalis*. (For *Enterococcus faecalis* and Streptococcus pyogenes, oligonucleotide sequences were exclusively derived from selected data bank sequences). These species-specific fragments were selected from bacterial genomic libraries by hybridization to DNA from a variety of Gram positive and Gram negative bacterial species (Table 5).

[0022] The chromosomal DNA from each bacterial species for which probes were seeked was isolated using standard methods. DNA was digested with a frequently cutting restriction enzyme such as Sau3AI and then ligated into the bacterial plasmid vector pGEM3Zf (Promega) linearized by appropriate restriction endonuclease digestion. Recombinant plasmids were then used to transform competent *E. coli* strain DH5α thereby yielding a genomic library. The plasmid content of the transformed bacterial cells was analyzed using standard methods. DNA fragments of target bacteria ranging in size from 0.25 to 5.0 kilobase pairs (kbp) were cut out from the vector by digestion of the recombinant plasmid with various restriction endonucleases. The insert was separated from the vector by agarose gel electrophoresis and purified in low melting point agarose gels. Each of the purified fragments of bacterial genomic DNA was then used as a probe for specificity tests.

[0023] For each given species, the gel-purified restriction fragments of unknown coding potential were labeled with the radioactive nucleotide α-^{32}P(dATP) which was incorporated into the DNA fragment by the random priming labeling reaction. Non-radioactive modified nucleotides could also be incorporated into the DNA by this method to serve as a label.

[0024] Each DNA fragment probe (i.e. a segment of bacterial genomic DNA of at least 100 bp in length cut out from clones randomly selected from the genomic library) was then tested for its specificity by hybridization to DNAs from a variety of bacterial species (Table 5). The double-stranded labeled DNA probe was heat-denatured to yield labeled single-stranded DNA which could then hybridize to any single-stranded target DNA fixed onto a solid support or in solution. The target DNAs consisted of total cellular DNA from an array of bacterial species found in clinical samples (Table 5). Each target DNA was released from the bacterial cells and denatured by conventional methods and then irreversibly fixed onto a solid support (e.g. nylon or nitrocellulose membranes) or free in solution. The fixed single-stranded target DNAs were then hybridized with the single-stranded probe. Pre-hybridization, hybridization and post-hybridization conditions were as follows: (i) Pre-hybridization; in 1 M NaCl+10% dextran sulfate+1% SDS (sodium dodecyl sulfate)+1 μg/ml salmon sperm DNA at 650° C. for 15 min. (ii) Hybridization; in fresh pre-hybridization solution containing the labeled probe at 650° C. overnight. (iii) Post-hybridization; washes twice in 3×SSC containing 1% SDS (1×SSC is 0.15M NaCl, 0.015M NaCitrate) and twice in 0.1×SSC containing 0.1% SDS; all washes were at 650° C. for 15 min. Autoradiography of washed filters allowed the detection of selectively hybridized probes. Hybridization of the probe to a specific target DNA indicated a high degree of similarity between the nucleotide sequence of these two DNAs. Species-specific DNA fragments selected from various bacterial genomic libraries ranging in size from 0.25 to 5.0 kbp were isolated for 10 common bacterial pathogens (Table 6) based on hybridization to chromosomal DNAs from a variety of bacteria performed as described above. All of the bacterial species tested (66 species listed in Table 5) were likely to be pathogens associated with common infections or potential contaminants which can be isolated from clinical specimens. A DNA fragment probe was considered specific only when it hybridized solely to the pathogen from which it was isolated. DNA fragment probes found to be specific were subsequently tested for their ubiquity (i.e. ubiquitous probes recognized most isolates of the target species) by hybridization to bacterial DNAs from approximately 10 to 80 clinical isolates of the species of interest (Table 6). The DNAs were denatured, fixed onto nylon membranes and hybridized as described above.

[0025] Sequencing of the Species-Specific Fragment Orobes

[0026] The nucleotide sequence of the totality or of a portion of the species-specific DNA fragments isolated (Table 6) was determined using the dideoxynucleotide termination sequencing method which was performed using Sequenase (USB Biochemicals) or T7 DNA polymerase (Pharmacia). These nucleotide sequences are shown in the sequence listing. Alternatively, sequences selected from data banks (GenBank and EMBL) were used as sources of oligonucleotides for diagnostic purposes for *Escherichia coli, Enterococcus faecalis, Streptococcus pyogenes* and *Pseudomonas aeruginosa*. For this strategy, an array of suitable oligonucleotide primers or probes derived from a variety of genomic DNA fragments (size of more than 100 bp) selected from data banks was tested for their specificity and ubiquity in PCR and hybridization assays as described later. It is important to note that the data bank sequences were selected based on their potential of being species-specific according to available sequence information. Only

data bank sequences from which species-specific oligonucleotides could be derived are included in this invention.

[0027] Oligonucleotide probes and amplification primers derived from species-specific fragments selected from the genomic libraries or from data bank sequences were synthesized using an automated DNA synthesizer (Millipore). Prior to synthesis, all oligonucleotides (probes for hybridization and primers for DNA amplification) were evaluated for their suitability for hybridization or DNA amplification by polymerase chain reaction (PCR) by computer analysis using standard programs (e.g. Genetics Computer Group (GCG) and Oligo™ 4.0 (National Biosciences)). The potential suitability of the PCR primer pairs was also evaluated prior to the synthesis by verifying the absence of unwanted features such as long stretches of one nucleotide, a high proportion of G or C residues at the 3' end and a 3'-terminal T residue (Persing et al, 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.).

[0028] Hybridization with Oligonucleotide Probes

[0029] In hybridization experiments, oligonucleotides (size less than 100 nucleotides) have some advantages over DNA fragment probes for the detection of bacteria such as ease of preparation in large quantities, consistency in results from batch to batch and chemical stability. Briefly, for the hybridizations, oligonucleotides were 5' end-labeled with the radionucleotide γ^{32}P(ATP) using T4 polynucleotide kinase (Pharmacia). The unincorporated radionucleotide was removed by passing the labeled single-stranded oligonucleotide through a Sephadex G50 column. Alternatively, oligonucleotides were labeled with biotin, either enzymatically at their 3' ends or incorporated directly during synthesis at their 5' ends, or with digoxigenin. It will be appreciated by the person skilled in the art that labeling means other than the three above labels may be used.

[0030] The target DNA was denatured, fixed onto a solid support and hybridized as previously described for the DNA fragment probes. Conditions for pre-hybridization and hybridization were as described earlier. Post-hybridization washing conditions were as follows: twice in 3×SSC containing 1% SDS, twice in 2×SSC containing 1% SDS and twice in 1×SSC containing 1% SDS (all of these washes were at 65° C. for 15 min), and a final wash in 0.1×SSC containing 1% SDS at 25° C. for 15 min. For probes labeled with radioactive labels the detection of hybrids was by autoradiography as described earlier. For non-radioactive labels detection may be calorimetric or by chemiluminescence.

[0031] The oligonucleotide probes may be derived from either strand of the duplex DNA. The probes may consist of the bases A, G, C, or T or analogs. The probes may be of any suitable length and may be selected anywhere within the species-specific genomic DNA fragments selected from the genomic libraries or from data bank sequences.

[0032] DNA Amplification

[0033] For DNA amplification by the widely used PCR (polymerase chain reaction) method, primer pairs were derived either from the sequenced species-specific DNA fragments or from data bank sequences or, alternatively, were shortened versions of oligonucleotide probes. Prior to synthesis, the potential primer pairs were analyzed by using the program oligo™ 4.0 (National Biosciences) to verify that they are likely candidates for PCR amplifications.

[0034] During DNA amplification by PCR, two oligonucleotide primers binding respectively to each strand of the denatured double-stranded target DNA from the bacterial genome are used to amplify exponentially in vitro the target DNA by successive thermal cycles allowing 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.). Briefly, the PCR protocols were as follows. Clinical specimens or bacterial colonies were added directly to the 50 μL PCR reaction mixtures containing 50 mM KCl, 10 mM Tris-HCl pH 8.3, 2.5 mM $MgCl_2$, 0.4 μM of each of the two primers, 200 μM of each of the four dNTPs and 1.25 Units of Taq DNA polymerase (Perkin Elmer). PCR reactions were then subjected to thermal cycling (3 min at 95° C. followed by 30 cycles of 1 second at 95° C. and 1 second at 55° C.) using a Perkin Elmer 480™ thermal cycler and subsequently analyzed by standard ethidium bromide-stained agarose gel electrophoresis. It is clear that other methods for the detection of specific amplification products, which may be faster and more practical for routine diagnosis, may be used. Such methods may be based on the detection of fluorescence after amplification (e.g. TaqMan™ system from Perkin Elmer or Amplisensor™ from Biotronics) or liquid hybridization with an oligonucleotide probe binding to internal sequences of the specific amplification product. These novel probes can be generated from our species-specific fragment probes. Methods based on the detection of fluorescence are particularly promising for utilization in routine diagnosis as they are, very rapid and quantitative and can be automated.

[0035] To assure PCR efficiency, glycerol or dimethyl sulfoxide (DMSO) or other related solvents, can be used to increase the sensitivity of the PCR and to overcome problems associated with the amplification of target with a high GC content or with strong secondary structures. The concentration ranges for glycerol and DMSO are 5-15% (v/v) and 3-10% (v\v), respectively. For the PCR reaction mixture, the concentration ranges for the amplification primers and the $MgCl_2$ are 0.1-1.0 μM and 1.5-3.5 mM, respectively. Modifications of the standard PCR protocol using external and nested primers (i.e. nested PCR) or using more than one primer pair (i.e. multiplex PCR) may also be used (Persing et al, 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). For more details about the PCR protocols and amplicon detection methods see examples 7 and 8.

[0036] The person skilled in the art of DNA amplification knows the existence of other rapid amplification procedures such as ligase chain reaction (LCR), transcription-based amplification systems (TAS), self-sustained sequence replication (3SR), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA) and branched DNA (bDNA) (Persing et al, 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). The scope of this invention is not limited to the use of amplification by PCR, but rather includes the use of any rapid nucleic acid amplification methods or any other procedures which may be used to increase rapidity and sensitivity of the

tests. Any oligonucleotides suitable for the amplification of nucleic acid by approaches other than PCR and derived from the species-specific fragments and from selected antibiotic resistance gene sequences included in this document are also under the scope of this invention.

[0037] Specificity and Ubiquity Tests for Oligonucleotide Probes and Primers

[0038] The specificity of oligonucleotide probes, derived either from the sequenced species-specific fragments or from data bank sequences, was tested by hybridization to DNAs from the array of bacterial species listed in Table 5 as previously described. Oligonucleotides found to be specific were subsequently tested for their ubiquity by hybridization to bacterial DNAs from approximately 80 isolates of the target species as described for fragment probes. Probes were considered ubiquitous when they hybridized specifically with the DNA from at least 80% of the isolates. Results for specificity and ubiquity tests with the oligonucleotide probes are summarized in Table 6. The specificity and ubiquity of the amplification primer pairs were tested directly from cultures (see example 7) of the same bacterial strains. For specificity and ubiquity tests, PCR assays were performed directly from bacterial colonies of approximately 80 isolates of the target species. Results are summarized in Table 7. All specific and ubiquitous oligonucleotide probes and amplification primers for each of the 12 bacterial species investigated are listed in Annexes I and II, respectively. Divergence in the sequenced DNA fragments can occur and, insofar as the divergence of these sequences or a part thereof does not affect the specificity of the probes or amplification primers, variant bacterial DNA is under the scope of this invention.

[0039] Universal Bacterial Detection

[0040] In the routine microbiology laboratory a high percentage of clinical specimens sent for bacterial identification is negative (Table 4). For example, over a 2 year period, around 80% of urine specimens received by the laboratory at the "Centre Hospitalier de 1' Université Laval (CHUL)" were negative (i.e. <10^7 CFU/L) (Table 3). Testing clinical samples with universal probes or universal amplification primers to detect the presence of bacteria prior to specific identification and screen out the numerous negative specimens is thus useful as it saves costs and may rapidly orient the clinical management of the patients. Several oligonucleotides and amplification primers were therefore synthesized from highly conserved portions of bacterial 16S or 23S ribosomal RNA gene sequences available in data banks (Annexes III and IV). In hybridization tests, a pool of seven oligonucleotides (Annex I; Table 6) hybridized strongly to DNA from all bacterial species listed in Table 5. This pool of universal probes labeled with radionucleotides or with any other modified nucleotides is consequently very useful for detection of bacteria in urine samples with a sensitivity range of $\geqq 10^7$ CFU/L. These probes can also be applied for bacterial detection in other clinical samples.

[0041] Amplification primers also derived from the sequence of highly conserved ribosomal RNA genes were used as an alternative strategy for universal bacterial detection directly from clinical specimens (Annex IV; Table 7). The DNA amplification strategy was developed to increase the sensitivity and the rapidity of the test. This amplification test was ubiquitous since it specifically amplified DNA from 23 different bacterial species encountered in clinical specimens.

[0042] Well-conserved bacterial genes other than ribosomal RNA genes could also be good candidates for universal bacterial detection directly from clinical specimens. Such genes may be associated with processes essential for bacterial survival (e.g. protein synthesis, DNA synthesis, cell division or DNA repair) and could therefore be highly conserved during evolution. We are working on these candidate genes to develop new rapid tests for the universal detection of bacteria directly from clinical specimens.

[0043] Antibiotic Resistance Genes

[0044] Antimicrobial resistance complicates treatment and often leads to therapeutic failures. Furthermore, overuse of antibiotics inevitably leads to the emergence of bacterial resistance. Our goal is to provide the clinicians, within one hour, the needed information to prescribe optimal treatments. Besides the rapid identification of negative clinical specimens with DNA-based tests for universal bacterial detection and the identification of the presence of a specific pathogen in the positive specimens with DNA-based tests for specific bacterial detection, the clinicians also need timely information about the ability of the bacterial pathogen to resist antibiotic treatments. We feel that the most efficient strategy to evaluate rapidly bacterial resistance to antimicrobials is to detect directly from the clinical specimens the most common and important antibiotic resistance genes (i.e. DNA-based tests for the detection of antibiotic resitance genes). Since the sequence from the most important and common bacterial antibiotic resistance genes are available from data banks, our strategy is to use the sequence from a portion or from the entire gene to design specific oligonucleotides which will be used as a basis for the development of rapid DNA-based tests. The sequence from the bacterial antibiotic resistance genes selected on the basis of their clinical relevance (i.e. high incidence and importance) is given in the sequence listing. Table 8 summarizes some characteristics of the selected antibiotic resistance genes.

EXAMPLES

[0045] The following examples are intended to be illustrative of the various methods and compounds of the invention.

Example 1

[0046] Isolation and cloning of fragments. Genomic DNAs from *Escherichia coli* strain ATCC 25922, *Klebsiella pneumoniae* strain CK2, *Pseudomonas aeruginosa* strain ATCC 27853, *Proteus mirabilis* strain ATCC 35657, *Streptococcus pneumoniae* strain ATCC 27336, *Staphylococcus aureus* strain ATCC 25923, *Staphylococcus epidermidis* strain ATCC 12228, *Staphylococcus saprophyticus* strain ATCC 15305, *Haemophilus influenzae* reference strain Rd and *Moraxella catarrhalis* strain ATCC 53879 were prepared using standard procedures. It is understood that the bacterial genomic DNA may have been isolated from strains other than the ones mentioned above. (For *Enterococcus faecalis* and *Streptococcus pyogenes* oligonucleotide sequences were derived exclusively from data banks). Each DNA was digested with a restriction enzyme which frequently cuts DNA such as Sau3AI. The resulting DNA fragments were ligated into a plasmid vector (pGEM3Zf) to create recombinant plasmids and transformed into compe-

tent *E. coli* cells (DH5α). It is understood that the vectors and corresponding competent cells should not be limited to the ones herein above specifically examplified. The objective of obtaining recombinant plasmids and transformed cells is to provide an easily reproducible source of DNA fragments useful as probes. Therefore, insofar as the inserted fragments are specific and selective for the target bacterial DNA, any recombinant plasmids and corresponding transformed host cells are under the scope of this invention. The plasmid content of the transformed bacterial cells was analyzed using standard methods. DNA fragments from target bacteria ranging in size from 0.25 to 5.0 kbp were cut out from the vector by digestion of the recombinant plasmid with various restriction endonucleases. The insert was separated from the vector by agarose gel electrophoresis and purified in a low melting point agarose gel. Each of the purified fragments was then used for specificity tests.

[0047] Labeling of DNA fragment probes. The label used was α^{32}P(dATP), a radioactive nucleotide which can be incorporated enzymatically into a double-stranded DNA molecule. The fragment of interest is first denatured by heating at 95° C. for 5 min, then a mixture of random primers is allowed to anneal to the strands of the fragments. These primers, once annealed, provide a starting point for synthesis of DNA. DNA polymerase, usually the Klenow fragment, is provided along with the four nucleotides, one of which is radioactive. When the reaction is terminated, the mixture of new DNA molecules is once again denatured to provide radioactive single-stranded DNA molecules (i.e. the probe). As mentioned earlier, other modified nucleotides may be used to label the probes.

[0048] Specificity and ubiquity tests for the DNA fragment probes. Species-specific DNA fragments ranging in size from 0.25 to 5.0 kbp were isolated for 10 common bacterial pathogens (Table 6) based on hybridization to chromosomal DNAs from a variety of bacteria. Samples of whole cell DNA for each bacterial strain listed in Table 5 were transferred onto a nylon membrane using a dot blot apparatus, washed and denatured before being irreversibly fixed. Hybridization conditions were as described earlier. A DNA fragment probe was considered specific only when it hybridized solely to the pathogen from which it was isolated. Labeled DNA fragments hybridizing specifically only to target bacterial species (i.e. specific) were then tested for their ubiquity by hybridization to DNAs from approximately 10 to 80 isolates of the species of interest as described earlier. The conditions for pre-hybridization, hybridization and post-hybridization washes were as described earlier. After autoradiography (or other detection means appropriate for the non-radioactive label used), the specificity of each individual probe can be determined. Each probe found to be specific (i.e. hybridizing only to the DNA from the bacterial species from which it was isolated) and ubiquitous (i.e. hybridizing to most isolates of the target species) was kept for further experimentations.

Example 2

[0049] Same as example 1 except that testing of the strains is by colony hybridization. The bacterial strains were inoculated onto a nylon membrane placed on nutrient agar. The membranes were incubated at 37° C. for two hours and then bacterial lysis and DNA denaturation were carried out according to standard procedures. DNA hybridization was performed as described earlier.

Example 3

[0050] Same as example 1 except that bacteria were detected directly from clinical samples. Any biological samples were loaded directly onto a dot blot apparatus and cells were lysed in situ for bacterial detection. Blood samples should be heparizined in order to avoid coagulation interfering with their convenient loading on a dot blot apparatus.

Example 4

[0051] Nucleotide sequencina of DNA fragments. The nucleotide sequence of the totality or a portion of each fragment found to be specific and ubiquitous (Example 1) was determined using the dideoxynucleotide termination sequencing method (Sanger et al., 1977, Proc. Natl. Acad. Sci. USA. 74:5463-5467). These DNA sequences are shown in the sequence listing. Oligonucleotide probes and amplification primers were selected from these nucleotide sequences, or alternatively, from selected data banks sequences and were then synthesized on an automated Biosearch synthesizer (Millipore™) using phosphoramidite chemistry.

[0052] Labeling of oliaonucleotides. Each oligonucleotide was 5' end-labeled with γ^{32}P-ATP by the T4 polynucleotide kinase (Pharmacia) as described earlier. The label could also be non-radioactive.

[0053] Specificity test for oligonucleotide probes. All labeled oligonucleotide probes were tested for their specificity by hybridization to DNAs from a variety of Gram positive and Gram negative bacterial species as described earlier. Species-specific probes were those hybridizing only to DNA from the bacterial species from which it was isolated. Oligonucleotide probes found to be specific were submitted to ubiquity tests as follows.

[0054] Ubiquity test for oligonucleotide probes. Specific oligonucleotide probes were then used in ubiquity tests with approximately 80 strains of the target species. Chromosomal DNAs from the isolates were transferred onto nylon membranes and hybridized with labeled oligonucleotide probes as described for specificity tests. The batteries of approximately 80 isolates constructed for each target species contain reference ATCC strains as well as a variety of clinical isolates obtained from various sources. Ubiquitous probes were those hybridizing to at least 80% of DNAs from the battery of clinical isolates of the target species. Examples of specific and ubiquitous oligonucleotide probes are listed in Annex 1.

Example 5

[0055] Same as example 4 except that a pool of specific oligonucleotide probes is used for bacterial identification (i) to increase sensitivity and assure 100% ubiquity or (ii) to identify simultaneously more than one bacterial species. Bacterial identification could be done from isolated colonies or directly from clinical specimens.

Example 6

[0056] PCR amplification. The technique of PCR was used to increase sensitivity and rapidity of the tests. The PCR primers used were often shorter derivatives of the extensive sets of oligonucleotides previously developed for

hybridization assays (Table 6). The sets of primers were tested in PCR assays performed directly from a bacterial colony or from a bacterial suspension (see Example 7) to determine their specificity and ubiquity (Table 7). Examples of specific and ubiquitous PCR primer pairs are listed in annex II.

[0057] Specificity and ubiquity tests for amplification primers. The specificity of all selected PCR primer pairs was tested against the battery of Gram negative and Gram positive bacteria used to test the oligonucleotide probes (Table 5). Primer pairs found specific for each species were then tested for their ubiquity to ensure that each set of primers could amplify at least 80% of DNAs from a battery of approximately 80 isolates of the target species. The batteries of isolates constructed for each species contain reference ATCC strains and various clinical isolates representative of the clinical diversity for each species.

[0058] Standard precautions to avoid false positive PCR results should be taken. Methods to inactivate PCR amplification products such as the inactivation by uracil-N-glycosylase may be used to control PCR carryover.

Example 7

[0059] Amplification directly from a bacterial colony or suspension. PCR assays were performed either directly from a bacterial colony or from a bacterial suspension, the latter being adjusted to a standard McFarland 0.5 (corresponds to 1.5×10^8 bacteria/mL). In the case of direct amplification from a colony, a portion of the colony was transferred directly to a 50 μL PCR reaction mixture (containing 50 mM KCl, 10 mM Tris pH 8.3, 2.5 mM $MgCl_2$, 0.4 μM of each of the two primers, 200 μM of each of the four dNTPs and 1.25 Unit of Taq DNA polymerase (Perkin Elmer)) using a plastic rod. For the bacterial suspension, 4 μL of the cell suspension was added to 46 μL of the same PCR reaction mixture. For both strategies, the reaction mixture was overlaid with 50 μL of mineral oil and PCR amplifications were carried out using an initial denaturation step of 3 min. at 95° C. followed by 30 cycles consisting of a 1 second denaturation step at 95° C. and of a 1 second annealing step at 55° C. in a Perkin Elmer 480™ thermal cycler. PCR amplification products were then analyzed by standard agarose gel (2%) electrophoresis. Amplification products were visualized in agarose gels containing 2.5 μg/mL of ethidium bromide under UV at 254 nm. The entire PCR assay can be completed in approximately one hour.

[0060] Alternatively, amplification from bacterial cultures was performed as described above but using a "hot start" protocol. In that case, an initial reaction mixture containing the target DNA, primers and dNTPs was heated at 85° C. prior to the addition of the other components of the PCR reaction mixture. The final concentration of all reagents was as described above. Subsequently, the PCR reactions were submitted to thermal cycling and analysis as described above.

Example 8

[0061] Amplification directly from clinical specimens. For amplification from urine specimens, 4 μL of undiluted or diluted (1:10) urine was added directly to 46 μL of the above PCR reaction mixture and amplified as described earlier.

[0062] To improve bacterial cell lysis and eliminate the PCR inhibitory effects of clinical specimens, samples were routinely diluted in lysis buffer containing detergent(s). Subsequently, the lysate was added directly to the PCR reaction mixture. Heat treatments of the lysates, prior to DNA amplification, using the thermocycler or a microwave oven could also be performed to increase the efficiency of cell lysis.

[0063] Our strategy is to develop rapid and simple protocols to eliminate PCR inhibitory effects of clinical specimens and lyse bacterial cells to perform DNA amplification directly from a variety of biological samples. PCR has the advantage of being compatible with crude DNA preparations. For example, blood, cerebrospinal fluid and sera may be used directly in PCR assays after a brief heat treatment. We intend to use such rapid and simple strategies to develop fast protocols for DNA amplification from a variety of clinical specimens.

Example 9

[0064] Detection of antibiotic resistance genes. The presence of specific antibiotic resistance genes which are frequently encountered and clinically relevant is identified using the PCR amplification or hybridization protocols described in previous sections. Specific oligonucleotides used as a basis for the DNA-based tests are selected from the antibiotic resistance gene sequences. These tests can be performed either directly from clinical specimens or from a bacterial colony and should complement diagnostic tests for specific bacterial identification.

Example 10

[0065] Same as examples 7 and 8 except that assays were performed by multiplex PCR (i.e. using several pairs of primers in a single PCR reaction) to (i) reach an ubiquity of 100% for the specific target pathogen or (ii) to detect simultaneously several species of bacterial pathogens.

[0066] For example, the detection of Escherichia coli requires three pairs of PCR primers to assure a ubiquity of 100%. Therefore, a multiplex PCR assay (using the "hot-start" protocol (Example 7)) with those three primer pairs was developed. This strategy was also used for the other bacterial pathogens for which more than one primer pair was required to reach an ubiquity of 100%.

[0067] Multiplex PCR assays could also be used to (i) detect simultaneously several bacterial species or, alternatively, (ii) to simultaneously identify the bacterial pathogen and detect specific antibiotic resistance genes either directly from a clinical specimen or from a bacterial colony.

[0068] For these applications, amplicon detection methods should be adapted to differentiate the various amplicons produced. Standard agarose gel electrophoresis could be used because it discriminates the amplicons based on their sizes. Another useful strategy for this purpose would be detection using a variety of fluorochromes emitting at different wavelengths which are each coupled with a specific oligonucleotide linked to a fluorescence quencher which is degraded during amplification to release the fluorochrome (e.g. TaqMan™, Perkin Elmer).

Example 11

[0069] Detection of amplification Products. The person skilled in the art will appreciate that alternatives other than

standard agarose gel electrophoresis (Example 7) may be used for the revelation of amplification products. Such methods may be based on the detection of fluorescence after amplification (e.g. Amplisensor™, Biotronics; TaqMan™) or other labels such as biotin (SHARP Signal™ system, Digene Diagnostics). These methods are quantitative and easily automated. One of the amplification primers or an internal oligonucleotide probe specific to the amplicon(s) derived from the species-specific fragment probes is coupled with the fluorochrome or with any other label. Methods based on the detection of fluorescence are particularly suitable for diagnostic tests since they are rapid and flexible as fluorochromes emitting different wavelengths are available (Perkin Elmer).

Example 12

[0070] Species-specific, universal and antibiotic resistance gene amplification primers can be used in other rapid amplification procedures such as the ligase chain reaction (LCR), transcription-based amplification systems (TAS), self-sustained sequence replication (3SR), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA) and branched DNA (bDNA) or any other methods to increase the sensitivity of the test. Amplifications can be performed from an isolated bacterial colony or directly from clinical specimens. The scope of this invention is therefore not limited to the use of PCR but rather includes the use of any procedures to specifically identify bacterial DNA and which may be used to increase rapidity and sensitivity of the tests.

Example 13

[0071] A test kit would contain sets of probes specific for each bacterium as well as a set of universal probes. The kit is provided in the form of test components, consisting of the set of universal probes labeled with non-radioactive labels as well as labeled specific probes for the detection of each bacterium of interest in specific clinical samples. The kit will also include test reagents necessary to perform the pre-hybridization, hybridization, washing steps and hybrid detection. Finally, test components for the detection of known antibiotic resistance genes (or derivatives therefrom) will be included. Of course, the kit will include standard samples to be used as negative and positive controls for each hybridization test.

[0072] Components to be included in the kits will be adapted to each specimen type and to detect pathogens commonly encountered in that type of specimen. Reagents for the universal detection of bacteria will also be included. Based on the sites of infection, the following kits for the specific detection of pathogens may be developed:

[0073] A kit for the universal detection of bacterial pathogens from most clinical specimens which contains sets of probes specific for highly conserved regions of the bacterial genomes.

[0074] A kit for the detection of bacterial pathogens retrieved from urine samples, which contains eight specific test components (sets of probes for the detection of *Escherichia coli, Enterococcus faecalis, Klebsiella pneumoniae, Proteus mirabilis, Pseudomonas aeruginosa, Staphylococcus saprophyticus, Staphylococcus aureus* and *Staphylococcus epidermidis*).

[0075] A kit for the detection of respiratory pathogens which contains seven specific test components (sets of probes for detecting *Streptococcus pneumoniae, Moraxella catarrhalis, Haemophilus influenzae, Klebsiella pneumoniae, Pseudomonas aeruginosa, Streptococcus pyogenes* and *Staphylococcus aureus*).

[0076] A kit for the detection of pathogens retrieved from blood samples, which contains eleven specific test components (sets of probes for the detection of *Streptococcus pneumoniae, Moraxella catarrhalis, Haemophilus influenzae, Proteus mirabilis, Klebsiella pneumoniae, Pseudomonas aeruginosa, Escherichia coli, Enterococcus faecalis, Staphylococcus aureus, Streptococcus pyogenes* and *Staphylococcus epidermidis*).

[0077] A kit for the detection of pathogens causing meningitis, which contains four specific test components (sets of probes for the detection of *Haemophilus influenzae, Streptococcus pneumoniae, Escherichia coli* and *Pseudomonas aeruginosa*).

[0078] A kit for the detection of clinically important antibiotic resistance genes which contains sets of probes for the specific detection of at least one of the 19 following genes associated with bacterial resistance : bla_{tem}, bla_{rob}, bla_{shv}, aadB, aacC1, aacC2, aacC3, aacA4, mecA, vanA, vanH, vanX, satA, aacA-aphD, vat, vga, msrA, sul and int.

[0079] Other kits adapted for the detection of pathogens from skin, abdominal wound or any other clinically relevant kits will be developed.

Example 14

[0080] Same as example 13 except that the test kits contain all reagents and controls to perform DNA amplification assays. Diagnostic kits will be adapted for amplification by PCR (or other amplification methods) performed directly either from clinical specimens or from a bacterial colony. Components required for universal bacterial detection, bacterial identification and antibiotic resistance genes detection will be included.

[0081] Amplification assays could be performed either in tubes or in microtitration plates having multiple wells. For assays in plates, the wells will be coated with the specific amplification primers and control DNAs and the detection of amplification products will be automated. Reagents and amplification primers for universal bacterial detection will be included in kits for tests performed directly from clinical specimens. Components required for bacterial identification and antibiotic resistance gene detection will be included in

kits for testing directly from colonies as well as in kits for testing directly from clinical specimens.

[0082] The kits will be adapted for use with each type of specimen as described in example 13 for hybridization-based diagnostic kits.

Example 15

[0083] It is understood that the use of the probes and amplification primers described in this invention for bacterial detection and identification is not limited to clinical microbiology applications. In fact, we feel that other sectors could also benefit from these new technologies. For example, these tests could be used by industries for quality control of food, water, pharmaceutical products or other products requiring microbiological control. These tests could also be applied to detect and identify bacteria in biological samples from organisms other than humans (e.g. other primates, mammals, farm animals and live stocks). These diagnostic tools could also be very useful for research purposes including clinical trials and epidemiological studies.

TABLE 1

Distribution of urinary isolates from positive urine samples (≧10^7 CFU/L) at the Centre Hospitalier de l'Université Laval (CHUL) for the 1992–1994 period.

	% of isolates			
Organisms	Nov 92 n = 267[a]	April 93 n = 265	July 93 n = 238	Jan 94 n = 281
Escherichia coli	53.2	51.7	53.8	54.1
Enterococcus faecalis	13.8	12.4	11.7	11.4
Klebsiella pneumoniae	6.4	6.4	5.5	5.3
Staphylococcus epidermidis	7.1	7.9	3.0	6.4
Proteus mirabilis	2.6	3.4	3.8	2.5
Pseudomonas aeruginosa	3.7	3.0	5.0	2.9
Staphylococcus saprophyticus	3.0	1.9	5.4	1.4
Others[b]	10.2	13.3	11.8	16.0

[a]n = total number of isolates for the indicated month.
[b]See table 2.

[0084]

TABLE 2

Distribution of uncommon[a] urinary isolates from positive urine samples (≧10^7 CFU/L) at the Centre Hospitalier de l'Université Laval (CHUL) for the 1992–1994 period.

	% of isolates			
Organisms[a]	Nov 92	April 93	July 93	Jan 94
Staphylococcus aureus	0.4	1.1	1.3	1.4
Staphylococcus spp.	2.2	4.9	1.7	6.0
Micrococcus spp.	0.0	0.0	0.4	0.7
Enterococcus faecium	0.4	0.4	1.3	1.4
Citrobacter spp.	1.4	0.8	0.4	0.7
Enterobacter spp.	1.5	1.1	1.3	1.4
Klebsiella oxytoca	1.1	1.5	2.5	1.8
Serratia spp.	0.8	0.0	0.5	0.0
Proteus spp.	0.4	0.4	0.0	1.1

TABLE 2-continued

Distribution of uncommon[a] urinary isolates from positive urine samples (≧10^7 CFU/L) at the Centre Hospitalier de l'Université Laval (CHUL) for the 1992–1994 period.

	% of isolates			
Organisms[a]	Nov 92	April 93	July 93	Jan 94
Morganella and Providencia	0.4	0.8	0.4	0.0
Hafnia alvei	0.8	0.0	0.0	0.0
NFB[b] (Stenotrophomonas, Acinetobacter)	0.0	0.4	1.3	1.1
Candida spp.	0.8	1.9	0.7	0.4

[a]Uncommon urinary isolates are those identified as "Others" in Table 1.
[b]NFB: non fermentative bacilli.

[0085]

TABLE 3

Distribution of positive[a] (bacterial count ≧10^7 CFU/L) and negative (bacterial count <10^7 CFU/L) urine specimens tested at the Centre Hospitalier de l'Université Laval (CHUL) for the 1992–1994 period.

	Number of isolates (%)			
Specimens	Nov 92	April 93	July 93	Jan 94
received:	1383(100)	1338(100)	1139(100)	1345(100)
positive:	267(19.3)	265(19.8)	238(20.9)	281(20.9)
negative:	1116(80.7)	1073(80.2)	901(79.1)	1064(79.1)

[a]Based on standard diagnostic methods, the minimal number of bacterial pathogens in urine samples to indicate an urinary tract infection is normally 10^7 CFU/L.

[0086]

TABLE 4

Distribution of positive and negative clinical specimens tested in the Microbiology Laboratory of the CHUL.

Clinical specimens[a]	No. of samples tested	% of positive specimens	% of negative specimens
Urine	17,981	19.4	80.6
Haemoculture/marrow	10,010	6.9	93.1
Sputum	1,266	68.4	31.6
Superficial pus	1,136	72.3	27.7
Cerebrospinal fluid	553	1.0	99.0
Synovial fluid-articular	523	2.7	97.3
Bronch./Trach./Amyg./Throat	502	56.6	43.4
Deep pus	473	56.8	43.2
Ears	289	47.1	52.9
Pleural and pericardial fluid	132	1.0	99.0
Peritonial fluid	101	28.6	71.4

[a]Specimens tested from February 1994 to January 1995.

[0087]

TABLE 5

Bacterial species (66) used for testing the specificity of DNA fragment probes, oligonucleotide probes and PCR primers.

Bacterial species Gram negative:	Number of strains tested	Bacterial species Gram positive:	Number of strains tested
Proteus mirabilis	5	*Streptococcus pneumoniae*	7
Klebsiella pneumoniae	5	*Streptococcus salivarius*	2
Pseudomonas aeruginosa	5	*Streptococcus viridans*	2
Escherichia coli	5	*Streptococcus pyogenes*	2
Moraxella catarrhalis	5	*Staphylococcus aureus*	2
Proteus vulgaris	2	*Staphylococcus epidermidis*	2
Morganella morganii	2	*Staphylococcus saprophyticus*	5
Enterobacter cloacae	2	Micrococcus species	2
Providencia stuartii	1	Corynebacterium species	2
Providencia species	1	*Streptococcus* groupe B	2
Enterobacter agglomerans	2	*Staphylococcus simulans*	2
Providencia rettgeri	2	*Staphylococcus ludgunensis*	1
Neisseria mucosa	1	*Staphylococcus capitis*	2
Providencia alcalifaciens	1	*Staphylococcus haemolyticus*	2
Providencia rustigianii	1	*Staphylococcus hominis*	2
Burkholderia cepacia	2	*Enterococcus faecalis*	2
Enterobacter aerogenes	2	*Enterococcus faecium*	1
Stenotrophomonas maltophilia	2	*Staphylococcus warneri*	1
Pseudomonas fluorescens	1	*Enterococcus durans*	1
Comamonas acidovorans	2	*Streptococcus bovis*	1
Pseudomonas putida	2	Diphteroids	2
Haemophilus influenzae	5	*Lactobacillus acidophilus*	1
Haemophilus parainfluenzae	2		
Bordetella pertussis	2		
Haemophilus parahaemolyticus	2		
Haemophilus haemolyticus	2		
Haemophilus aegyptius	1		
Kingella indologenes	1		
Moraxella atlantae	1		
Neisseria caviae	1		
Neisseria subflava	1		
Moraxella urethralis	1		
Shigella sonnei	1		
Shigella flexneri	1		
Klebsiella oxytoca	2		
Serratia marcescens	2		
Salmonella typhimurium	1		
Yersinia enterocolitica	1		
Acinetobacter calcoaceticus	1		
Acinetobacter lwoffi	1		
Haftnia alvei	2		
Citrobacter diversus	1		
Citrobacter freundii	1		
Salmonella species	1		

[0088]

TABLE 6

Species-specific DNA fragment and oligonucleotide probes for hybridization.

	Number of fragment probes[b]			Number of oligonucleotide probes		
Organisms[a]	Tested	Specific	Ubiquitous[c]	Synthesized	Specific	Ubiquitous[c]
E. coli[d]	—	—	—	20	12	9[f]
E. coli	14	2	2[e]	—	—	—
K. pneumoniae[d]	—	—	—	15	1	1
K. pneumoniae	33	3	3	18	12	8
P. mirabilis[d]	—	—	—	3	3	2
P. mirabilis	14	3	3[e]	15	8	7
P. aeruginosa[d]	—	—	—	26	13	9
P. aeruginosa	6	2	2[e]	6	0	0

TABLE 6-continued

Species-specific DNA fragment and oligonucleotide probes for hybridization.

Organisms[a]	Number of fragment probes[b] Tested	Specific	Ubiquitous[c]	Number of oligonucleotide probes Synthesized	Specific	Ubiquitous[c]
S. saprophyticus	7	4	4	20	9	7
H. influenzae[d]	—	—	—	16	2	2
H. influenzae	1	1	1	20	1	1
S. pneumoniae[d]	—	—	—	6	1	1
S. pneumoniae	19	2	2	4	1	1
M. catarrhalis	2	2	2	9	8	8
S. epidermidis	62	1	1	—	—	—
S. aureus	30	1	1	—	—	—
Universal probes[d]	—	—	—	7	—	7[g]

[a]No DNA fragment or oligonucleotide probes were tested for *E. faecalis* and *S. pyogenes*.
[b]Sizes of DNA fragments range from 0.25 to 5.0 kbp.
[c]A specific probe was considered ubiquitous when at least 80% of isolates of the target species (approximately 80 isolates) were recognized by each specific probe. When 2 or more probes are combined, 100% of the isolates are recognized.
[d]These sequences were selected from data banks.
[e]Ubiquity tested with approximately 10 isolates of the target species.
[f]A majority of probes (8/9) do not discriminate *E. coli* and *Shigella* spp.
[g]Ubiquity tests with a pool of the 7 probes detected all 66 bacterial species listed in Table 5.

[0089]

TABLE 7

PCR amplification for bacterial pathogens commonly encountered in urine, sputum, blood, cerebrospinal fluid and other specimens.

Organism	Primer pair[a] # (SEQ ID NO)	Amplicon size (bp)	Ubiquity[b]	DNA amplification from colonies[c]	from specimens[d]
E. coli	1[e] (55–56)	107	75/80	+	+
	2[e] (46–47)	297	77/80	+	+
	3 (42–43)	102	78/80	+	+
	4 (131–132)	134	73/80	+	+
	1 + 3 + 4	—	80/80	+	+
E.faecalis	1[e] (38–39)	200	71/80	+	+
	2[e] (40–41)	121	79/80	+	+
	1 + 2	—	80/80	+	+
K. pneumoniae	1 (67–68)	198	76/80	+	+
	2 (61–62)	143	67/80	+	+
	3[h] (135–136)	148	78/80	+	N.T.[i]
	4 (137–138)	116	69/80	+	N.T.
	1 + 2 + 3	—	80/80	+	N.T.
P. mirabilis	1 (74–75)	167	73/80	+	N.T.
	2 (133–134)	123	80/80	+	N.T.
P. aeruginosa	1[e] (83–84)	139	79/80	+	N.T.
	2[e] (85–86)	223	80/80	+	N.T.
S. saprophyticus	1 (98–99)	126	79/80	+	+
	2 (139–140)	190	80/80	+	N.T.
M. catarrhalis	1 (112–113)	157	79/80	+	N.T.
	2 (118–119)	118	80/80	+	N.T.
	3 (160–119)	137	80/80	+	N.T.
H. influenzae	1[e] (154–155)	217	80/80	+	N.T.
S. pneumoniae	1[e] (156–157)	134	80/80	+	N.T.
	2[e] (158–159)	197	74/80	+	N.T.
	3 (78–79)	175	67/80	+	N.T.
S. epidermidis	1 (147–148)	175	80/80	+	N.T.
	2 (145–146)	125	80/80	+	N.T.
S. aureus	1 (152–153)	108	80/80	+	N.T.
	2 (149–150)	151	80/80	+	N.T.
	3 (149–151)	176	80/80	+	N.T.
S. pyogenes[f]	1[e] (141–142)	213	80/80	+	N.T.
	2[e] (143–144)	157	24/24	+	N.T.
Universal	1[e] (126–127)	241	194/195[g]	+	+

See notes on next page

[0090] a All primer pairs are specific in PCR assays since no amplification was observed with DNA from 66 different species of both Gram positive and Gram negative bacteria other than the species of interest (Table 5).

[0091] b The ubiquity was normally tested on 80 strains of the species of interest. All retained primer pairs amplified at least 90% of the isolates. When combinations of primers were used, an ubiquity of 100% was reached.

[0092] c For all primer pairs and multiplex combinations, PCR amplifications directly performed from a bacterial colony were 100% species-specific.

[0093] d PCR assays performed directly from urine specimens.

[0094] e Primer pairs derived from data bank sequences. Primer pairs with no "e" are derived from our species-specific fragments.

[0095] f For S. pyogenes, primer pair #1 is specific for Group A Streptococci (GAS). Primer pair #2 is specific for the GAS-producing exotoxin A gene (SpeA).

[0096] g Ubiquity tested on 195 isolates from 23 species representative of bacterial pathogens commonly encountered in clinical specimens.

[0097] h Optimizations are in progress to eliminate non-specific amplification observed with some bacterial species other than the target species.

[0098] N.T.: not tested.

TABLE 8

Selected antibiotic resistance genes for diagnostic purposes.

Genes	Antibiotics	Bacteria[a]	SEQ ID NO
(bla_{tem}) TEM-1	β-lactams	Enterobacteriaceae, Pseudomonadaceae, Haemophilus, Neisseria	161
(bla_{rob}) ROB-1	β-lactams	Haemophilus, Pasteurella	162
(bla_{shv}) SHV-1	β-lactams	Klebsiella and other Enterobacteriaceae	163
aadB, aacC1, aacC2, aacC3, aacA4	Aminoglycosides	Enterobacteriaceae, Pseudomonadaceae	164, 165, 166 167, 168
mecA	β-lactams	Staphylococci	169
vanH, vanA, vanX	Vancomycin	Enterococci	170
satA	Macrolides	Enterococci	173
aacA-aphD	Aminoglycosides	Enterococci, Staphylococci	174
vat	Macrolides	Staphylococci	175
vga	Macrolides	Staphylococci	176
msrA	Erythromycin	Staphylococci	177
Int and Sul conserved sequences	β-lactams, trimethoprim, aminoglycosides, antiseptic, chloramphenicol	Enterobacteriaceae, Pseudomonadaceae	171, 172

[a]Bacteria having high incidence for the specified antibiotic resistance genes. The presence in other bacteria is not excluded.

[0099]

Annex I: Specific and ubiquitous oligonucleotides probes for hybridization

SEQ ID NO	Nucleotide Sequence	Originating DNA fragment SEQ ID NO	Originating DNA fragment Nucleotide position
	Bacterial species: *Escherichia coli*		
44	5'-CAC CCG CTT GCG TGG CAA GCT GCC C	5[a]	213–237
45	5'-CGT TTG TGG ATT CCA GTT CCA TCC G	5[a]	489–513
48	5'-TGA AGC ACT GGC CGA AAT GCT GCG T	6[a]	759–783
49	5'-GAT GTA CAG GAT TCG TTG AAG GCT T	6[a]	898–922
50	5'-TAG CGA AGG CGT AGC AGA AAC TAA C	7[a]	1264–1288
51	5'-GCA ACC CGA ACT CAA CGC CGG ATT T	7[a]	1227–1251
52	5'-ATA CAC AAG GGT CGC ATC TGC GGC C	7[a]	1313–1337

-continued

Annex I: Specific and ubiquitous oligonucleotides probes for hybridization

SEQ ID NO	Nucleotide Sequence	Originating DNA fragment SEQ ID NO	Originating DNA fragment Nucleotide position
53	5'-TGC GTA TGC ATT GCA GAC CTT GTG GC	7[a]	111-136
54	5'-GCT TTC ACT GGA TAT CGC GCT TGG G	7[a]	373-397
	Bacterial species: *Proteus mirabilis*		
70[b]	5'-TGG TTC ACT GAC TTT GCG ATG TTT C	12	23-47
71	5'-TCG AGG ATG GCA TGC ACT AGA AAA T	12	53-77
72[b]	5'-CGC TGA TTA GGT TTC GCT AAA ATC TTA TTA	12	80-109
73	5'-TTG ATC CTC ATT TTA TTA ATC ACA TGA CCA	12	174-203

[a]Sequences from data banks
[b]These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

[0100]

Annex I: Specific and ubiquitous oligonucleotides probes for hybridization

SEQ ID NO	Nucleotide Sequence	Originating DNA fragment SEQ ID NO	Originating DNA fragment Nucleotide position
	Bacterial species: *Proteus mirabilis*		
76	5'-CCG CCT TTA GCA TTA ATT GGT GTT TAT AGT	13	246-275
77	5'-CCT ATT GCA GAT ACC TTA AAT GTC TTG GGC	13	291-320
80[b]	5'-TTG AGT GAT GAT TTC ACT GAC TCC C	14	18-42
81	5'-GTG AGA CAG TGA TGG TGA GGA CAC A	15[a]	1185-1209
82	5'-TGG TTG TCA TGC TGT TTG TGT GAA AAT	15[a]	1224-1230
	Bacterial species: *Klebsiella pneumoniae*		
57	5'-GTG GTG TCG TTC AGG GGT TTC AC	8	45-67
58	5'-GCG ATA TTC ACA CCC TAC GCA GCC A	9	161-185
59[b]	5'-GTC GAA AAT GCC GGA AGA GGT ATA CG	9	203-228
60[b]	5'-ACT GAG CTG CAG ACC GGT AAA ACT CA	9	233-258
63[b]	5'-CGT GAT GGA TAT TCT TAA CGA AGG GC	10	250-275
64[b]	5'-ACC AAA CTG TTG AGC CGC CTG GA	10	201-223
65	5'-GTG ATC GCC CCT CAT CTG CTA CT	10	77-99
66	5'-CGC CCT TCG TTA AGA ATA TCC ATC AC	10	249-274
69	5'-CAG GAA GAT GCT GCA CCG GTT GTT G	11[a]	296-320

[a]Sequences from data banks
[b]These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

[0101]

Annex I: Specific and ubiquitous oligonucleotides probes for hybridization

SEQ ID NO	Nucleotide Sequence	Originating DNA fragment SEQ ID NO	Originating DNA fragment Nucleotide position
	Bacterial species: *Pseudomonas aeruginosa*		
87	5'-AAT GCG GCT GTA CCT CGG CGC TGG T	18[a]	2985–3009
88	5'-GGC GGA GGG CCA GTT GCA CCT GCC A	18[a]	2929–2953
89	5'-AGC CCT GCT CCT CGG CAG CCT CTG C	18[a]	2821–2845
90	5'-TGG CTT TTG CAA CCG CGT TCA GGT T	18[a]	1079–1103
91	5'-GCG CCC GCG AGG GCA TGC TTC GAT G	19[a]	705–729
92	5'-ACC TGG GCG CCA ACT ACA AGT TCT A	19[a]	668–692
93	5'-GGC TAC GCT GCC GGG CTG CAG GCC G	19[a]	505–529
94	5'-CCG ATC TAG ACC ATC GAG ATG GGC G	20[a]	1211–1235
95	5'-GAG CGC GGC TAT GTG TTC GTC GGC T	20[a]	2111–2135
	Bacterial species: *Streptococcus pneumoniae*		
120	5'-TCT GTG CTA GAG ACT GCC CCA TTT C	30	423–447
121	5'-CGA TGT CTT GAT TGA GCA GGG TTA T	31[a]	1198–1222

[a]Sequences from data banks
[b]These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

[0102]

Annex I: Specific and ubiquitous oligonucleotides probes for hybridization

SEQ ID NO	Nucleotide Sequence	Originating DNA fragment SEQ ID NO	Originating DNA fragment Nucleotide position
	Bacterial species: *Staphylococcus saprophyticus*		
96	5'-CGT TTT TAC CCT TAC CTT TTC GTA CTA CC	21	45–73
97[b]	5'-TCA GGC AGA GGT AGT ACG AAA AGG TAA GGG	21	53–82
100	5'-CAC CAA GTT TGA CAC GTG AAG ATT CAT	22	89–115
101[b]	5'-ATG AGT GAA GCG GAG TCA GAT TAT GTG CAG	23	105–134
102	5'-CGC TCA TTA CGT ACA GTG ACA ATC G	24	20–44
103	5'-CTG GTT AGC TTG ACT CTT AAC AAT CTT GTC	24	61–90
104[b]	5'-GAC GCG ATT GTC ACT GTA CGT AAT GAG CGA	24	19–48
	Bacterial species: *Moraxella catarrhalis*		
108	5'-GCC CCA AAA CAA TGA AAC ATA TGG T-3'	28	81–105
109	5'-CTG CAG ATT TTG GAA TCA TAT CGC C-3'	28	126–130
110	5'-TGG TTT GAC CAG TAT TTA ACG CCA T-3'	28	165–189

-continued

Annex I: Specific and ubiquitous oligonucleotides probes for hybridization

SEQ ID NO	Nucleotide Sequence	Originating DNA fragment SEQ ID NO	Nucleotide position
111	5'-CAA CGG CAC CTG ATG TAC CTT GTA C-3'	28	232–256
114	5'-TTA CAA CCT GCA CCA CAA GTC ATC A-3'	29	97–121
115	5'-GTA CAA ACA AGC CGT CAG CGA CTT A-3'	29	139–163
116	5'-CAA TCT GCG TGT GTG CGT TCA CT-3'	29	178–200
117	5'-GCT ACT TTG TCA GCT TTA GCC ATT CA-3'	29	287–312

[a]Sequences from data banks
[b]These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

[0103]

Annex I: Specific and ubiquitous oligonucleotides probes for hybridization

SEQ ID NO	Nucleotide sequence	Originating DNA fragment SEQ ID NO	Nucleotide position
Bacterial species: *Haemophilus influenzae*			
105[b]	5'-GCG TCA GAA AAA GTA GGC GAA ATG AAA G	25	138–165
106[b]	5'-AGC GGC TCT ATC TTG TAA TGA CAC A	26[a]	770–794
107[b]	5'-GAA ACG TGA ACT CCC CTC TAT ATA A	27[a]	5184–5208
	Universal probes[c]		
122[b]	5'-ATC CCA CCT TAG GCG GCT GGC TCC A	—	—
123	5'-ACG TCA AGT CAT CAT GGC CCT TAC GAG TAG G	—	—
124[b]	5'-GTG TGA CGG GCG GTG TGT ACA AGG C	—	—
125[b]	5'-GAG TTG CAG ACT CCA ATC CGG ACT ACG A	—	—
128[b]	5'-CCC TAT ACA TCA CCT TGC GGT TTA GCA GAG AG	—	—
129	5'-GGG GGG ACC ATC CTC CAA GGC TAA ATA C	—	—
130[b]	5'-CGT CCA CTT TCG TGT TTG CAG AGT GCT GTG TT	—	—

[a]Sequences from data banks
[b]These sequences are from the opposite DNA strand of the sequences given in the Sequence listing
[c]Universal probes were derived from 16S or 23S ribosomal RNA gene sequences not included in the Sequence listing

[0104]

Annex II: Specific and ubiquitous primers for DNA amplification			
		Originating DNA fragment	
SEQ ID NO	Nucleotide Sequence	SEQ ID NO	Nucleotide position
	Bacterial species: *Escherichia coli*		
42	5'-GCT TTC CAG CGT CAT ATT G	4	177–195
43[b]	5'-GAT CTC GAC AAA ATG GTG A	4	260–278
46	5'-TCA CCC GCT TGC GTG GC	5[a]	212–228
47[b]	5'-GGA ACT GGA ATC CAC AAA C	5[a]	490–508
55	5'-GCA ACC CGA ACT CAA CGC C	7[a]	1227–1245
56[b]	5'-GCA GAT GCG ACC CTT GTG T	7[a]	1315–1333
131	5'-CAG GAG TAC GGT GAT TTT TA	3	60–79
132[b]	5'-ATT TCT GGT TTG GTC ATA CA	3	174–193
	Bacterial species: *Enterococcus faecalis*		
38	5'-GCA ATA CAG GGA AAA ATG TC	1[a]	69–88
39[b]	5'-CTT CAT CAA ACA ATT AAC TC	1[a]	249–268
40	5'-GAA CAG AAG AAG CCA AAA AA	2[a]	569–588
41[b]	5'-GCA ATC CCA AAT AAT ACG GT	2[a]	670–689

[a]Sequences from data banks
[b] These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

[0105]

Annex II: Specific and ubiquitous primers for DNA amplification			
		Originating DNA fragment	
SEQ ID NO	Nucleotide Sequence	SEQ ID NO	Nucleotide position
	Bacterial species: *Klebsiella pneumoniae*		
61	5'-GAC AGT CAG TTC GTC AGC C	9	37–55
62[b]	5'-CGT AGG GTG TGA ATA TCG C	9	161–179
67	5'-TCG CCC CTC ATC TGC TAC T	10	81–99
68[b]	5'-GAT CGT GAT GGA TAT TCT T	10	260–278
135	5'-GCA GCG TGG TGT CGT TCA	8	40–57
136[b]	5'-AGC TGG CAA CGG CTG GTC	8	170–187
137	5'-ATT CAC ACC CTA CGC AGC CA	9	166–185
138[b]	5'-ATC CGG CAG CAT CTC TTT GT	9	262–281
	Bacterial species: *Proteus mirabilis*		
74	5'-GAA ACA TCG CAA AGT CAG T	12	23–41
75[b]	5'-ATA AAA TGA GGA TCA AGT TC	12	170–189

-continued

Annex II: Specific and ubiquitous primers for DNA amplification			
		Originating DNA fragment	
SEQ ID NO	Nucleotide Sequence	SEQ ID NO	Nucleotide position
133	5'-CGG GAG TCA GTG AAA TCA TC	14	17–36
134[b]	5'-CTA AAA TCG CCA CAC CTC TT	14	120–139

[a]Sequences from data banks
[b]These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

[0106]

Annex II: Specific and ubiquitous primers for DNA amplification			
		Originating DNA fragment	
SEQ ID NO	Nucleotide Sequence	SEQ ID NO	Nucleotide position
	Bacterial species: *Staphylococcus saprophyticus*		
98	5'-CGT TTT TAC CCT TAC CTT TTC GTA CT	21	45–70
99[b]	5'-ATC GAT CAT CAC ATT CCA TTT GTT TTT A	21	143–170
139	5'-CTG GTT AGC TTG ACT CTT AAC AAT C	24	61–85
140[b]	5'-TCT TAA CGA TAG AAT GGA GCA ACT G	24	226–250
	Bacterial species: *Pseudomonas aeruginosa*		
83	5'-CGA GCG GGT GGT GTT CAT C	16[a]	554–572
84[b]	5'-CAA GTC GTG GTG GGA GGG A	16[a]	674–692
85	5'-TCG CTG TTC ATC AAG ACC C	17[a]	1423–1441
86[b]	5'-CCG AGA ACC AGA CTT CAT C	17[a]	1627–1645
	Bacterial species: *Moraxella catarrhalis*		
112	5'-GGC ACC TGA TGT ACC TTG	28	235–252
113[b]	5'-AAC AGC TCA CAC GCA TT	28	375–391
118	5'-TGT TTT GAG CTT TTT ATT TTT TGA	29	41–64
119[b]	5'-CGC TGA CGG CTT GTT TGT ACC A	29	137–158
160	5'-GCT CAA ATC AGG GTC AGC	29	22–39
119[b]	5'-CGC TGA CGG CTT GTT TGT ACG A	29	137–158

[a]Sequences from data banks
[b]These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

[0107]

Annex II: Specific and ubiquitous primers for DNA amplification

SEQ ID NO	Nucleotide Sequence	Originating DNA fragment SEQ ID NO	Originating DNA fragment Nucleotide position
	Bacterial species: Staphylococcus epidermidis		
145	5'-ATC AAA AAG TTG GCG AAC CTT TTC A	36	21–45
146[b]	5'-CAA AAG AGC GTG GAG AAA AGT ATC A	36	121–145
147	5'-TCT CTT TTA ATT TCA TCT TCA ATT CCA TAG	36	448–477
148[b]	5'-AAA CAC AAT TAC AGT CTG GTT ATC CAT ATC	36	593–622
	Bacterial species: Staphylococcus aureus		
149[b]	5'-CTT CAT TTT ACG GTG ACT TCT TAG AAG ATT	37	409–438
150	5'-TCA ACT GTA GCT TCT TTA TCC ATA CGT TGA	37	288–317
149[b]	5'-CTT CAT TTT ACG GTG ACT TCT TAG AAG ATT	37	409–438
151	5'-ATA TTT TAG CTT TTC AGT TTC TAT ATC AAC	37	263–292
152	5'-AAT CTT TGT CGG TAC ACG ATA TTC TTC ACG	37	5–34
153[b]	5'-CGT AAT GAG ATT TCA GTA GAT AAT ACA ACA	37	83–112

[a]Sequences from data banks
[b]These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

[0108]

Annex II: Specific and ubiquitous primers for DNA amplification

SEQ ID NO	Nucleotide Sequence	Originating DNA fragment SEQ ID NO	Originating DNA fragment Nucleotide position
	Bacterial species: *Haemophilus influenzae*		
154	5'-TTT AAC GAT CCT TTT ACT CCT TTT G	27[a]	5074–5098
155[b]	5'-ACT GCT GTT GTA AAG AGG TTA AAA T	27[a]	5266–5290
	Bacterial species: *Streptococcus pneumoniae*		
78	5'-AGT AAA ATG AAA TAA GAA CAG GAC AG	34	164–189
79[b]	5'-AAA ACA GGA TAG GAG AAC GGG AAA A	34	314–338
156	5'-ATT TGG TGA CGG GTG ACT TT	31[a]	1401–1420
157[b]	5'-GCT GAG GAT TTG TTC TTC TT	31[a]	1515–1534
158	5'-GAG CGG TTT CTA TGA TTG TA	35[a]	1342–1361
159[b]	5'-ATC TTT CCT TTC TTG TTC TT	35[a]	1519–1538
	Bacterial species: *Streptococcus pyogenes*		
141	5'-TGA AAA TTC TTG TAA CAG GC	32[a]	286–305
142[b]	5'-GGC CAC CAG CTT GCC CAA TA	32[a]	479–498

-continued

Annex II: Specific and ubiquitous primers for DNA amplification			
		Originating DNA fragment	
SEQ ID NO	Nucleotide Sequence	SEQ ID NO	Nucleotide position
143	5'-ATA TTT TCT TTA TGA GGG TG	33[a]	966–985
144[b]	5'-ATC CTT AAA TAA AGT TGC CA	33[a]	1103–1122

[a]Sequences from data banks
[b]These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

[0109]

Annex II: Specific and ubiquitous primers for DNA amplification			
		Originating DNA fragment	
SEQ ID NO	Nucleotide Sequence	SEQ ID NO	Nucleotide position
	Universal primers[c]		
126	5'-GGA GGA AGG TGG GGA TGA CG	—	—
127[b]	5'-ATG GTG TGA CGG GCG GTG TG	—	—

[a] Sequences from data banks
[b] These sequences are from the opposite DNA strand of the sequences given in the Sequence listing
[c] Universal primers were derived from the 16S ribosomal RNA gene sequence not included in the Sequence listing

[0110]

Annex III Selection of Universal Probes by Alignment of the Sequences of Bacterial 16S and 23S Ribosomal RNA Genes.	
Reverse strand of SEQ ID NO: 122	**TGGAGCC AGCCGCCTA GGTGGGAT**
	1461 1510
Streptococcus salivarius	TGAGGTAACC TTT**TGGAGCC AGCCGCCTAA GGTGGGAT**AG ATGANNGGGG
Proteus vulgaris	TAGCTTAACC TTC**GGGAGGG CGCTTACCAC TTTGTGATT**C ATGACTGGGG
Pseudomonas aeruginosa	TAGTCTAACC GCA**AGGGGGA CGGTTACCAC GGAGTGATT**C ATGACTGGGG
Neisseria gonorrhoeae	TAGGGTAACC GCA**AGGAGTC CGCTTACCAC GGTATGCTT**C ATGACTGGGG
Streptococcus lactis	TTGCCTAACC GCA**AGGAGGG CGCTTCCTAA GGTAAGAC**CG ATGACNNGGG

[0111]

Annex III. Selection of universal probes by alignment of the sequences of bacterial 165 and 23S ribosomal RNA genes.	
SEQ ID NO: 123	ACGTCAAGTC ATCATGGC CCTTACGAGT AGG
	1251 1300
Haemophilus influenzae	GGTNGGGATG ACGTCAAGTC ..ATCATGGC CCTTACGAGT AGGGCTACAC

-continued

Annex III. Selection of universal probes by alignment of the sequences of bacterial 165 and 23S ribosomal RNA genes.	
Neisseria gonorrhoeae	GGTGGGGATG ACGTCAAGTC ..CTCATGGC CCTTATGACC AGGGCTTCAC
Pseudomonas cepacia	GGTNGGGATG ACGTCAAGTC ..CTCATGGC CCTTATGGGT AGGGCTTCAC
Serratia marcescens	GGTGGGGATG ACGTCAAGTC ..ATCATGGC CCTTACGAGT AGGGCTACAC
Escherichia coli	GGTGGGGATG ACGTCAAGTC ..ATCATGGC CCTTACGACC AGGGCTACAC
Proteus vulgaris	GGTGGGGATG ACGTTAAGTC GTATCATGGC CCTTACGAGT AGGGCTACAC
Pseudomonas aeruginosa	GGTGGGGATG ACGTCAAGTC ..ATCATGGC CCTTACGGCN AGGGCTACAC
Clostridium perfringens	GGTGGGGATG ACGTNNAATC ..ATCATGCC CNTTATGTGT AGGGCTACAC
Mycoplasma hominis	GGTGGGGATG ACGTCAAATC ..ATCATGCC TCTTACGAGT GGGGCCACAC
Helicobacter pylori	GGTGGGGACG ACGTCAAGTC ..ATCATGGC CCTTACGCCT AGGGCTACAC
Mycoplasma pneumoniae	GGAAGGGATG ACGTCAAATC ..ATCATGCC CCTTATGTCT AGGGCTGCAA

[0112]

Annex III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.	
Reverse of the probe SEQ ID NO: 124	GCCTTGTACA CACCGCCCGT CACAC
	1451 1490
Escherichia coli	ACGTTCCCGG GCCTTGTACA CACCGCCCGT CACACCATGG
Neisseria gonorrhoeae	ACGTTCCCNG NNCTTGTACA CACCGCCCGT CACACCATGG
Pseudomonas cepacia	ACGTTCCCGG GTCTTGTACA CACNGCCCGT CACACCATGG
Serratia marcescens	ACGTTCCCGG GCCTTGTACA CACCGCCCGT CACACCATGG
Proteus vulgaris	ACGTTCCCGG GCCTTGTACA CACCGCCCGT CACACCATGG
Haemophilus influenzae	ACGTTCCCGG GCNTTGTACA CACCGCCCGT CACACCATGG
Pseudomonas aeruginosa	ACGTTCCCGG GCCTTGTACA CACCGCCCGT CACACCATGG
Clostridium perfringens	ACGTTCCCNG GTCTTGTACA CACCGCNCGT CACACCATGA
Mycoplasma hominis	ACGTTCTCGG GTCTTGTACA CACCGCCCGT CACACCATGG
Helicobacter pylori	ACGTTCCCGG GTCTTGTACT CACCGCCCGT CACACCATGG
Mycoplasma pneumoniae	ACGTTCTCGG GTCTTGTACA CACCGCCCGT CAAACTATGA

[0113]

Annex III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.	
Reverse strand of SEQ ID NO 125:	TCG TAGTCCGGAT TGGAGTCTGC AACTC
	1361 1400
Escherichia coli	AAGTGCGTCG TAGTCCGGAT TGGAGTCTGC AACTCGACTC
Neisseria gonorrhoeae	AAACCGATCG TAGTCCGGAT TGCACTCTGC AACTCGAGTG

-continued

Annex III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.	
Pseudomonas cepacia	AAACCGATCG TAGTCCGGAT TGCACTCTGC AACTCGAGTG
Serratia marcescens	AAGTATGTCG TAGTCCGGAT TGGAGTCTGC AACTCGACTC
Proteus vulgaris	AAGTCTGTCG TAGTCCGGAT TGGAGTCTGC AACTCGACTC
Haemophilus influenzae	AAGTACGTCT AAGTCCGGAT TGGAGTCTGC AACTCGACTC
Pseudomonas aeruginosa	AAACCGATCG TAGTCCGGAT CGCAGTCTGC AACTCGACTG
Clostridium perfringens	AAACCAGTCT CAGTTCGGAT TGTAGGCTGA AACTCGCCTA
Mycoplasma hominis	AAGCCGATCT CAGTTCGGAT TGGAGTCTGC AATTCGACTC
Helicobacter pylori	ACACC..TCT CAGTTCGGAT TGTAGGCTGC AACTCGCCTG
Mycloplasma pneumoniae	AAGTTGGTCT CAGTTCGGAT TGAGGGCTGC AATTCGTCCT

[0114]

Annex III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.	
Reverse strand of SEQ ID NO: 128	CT CTCTGCTAAA CCGCAAGGTG ATGTATAGGG
	1991 2040
Lactobacillus lactis	AAACACAGCT CTCTGCTAAA CCGCAAGGTG ATGTATAGGG GGTGACGCCT
Escherichia coli	AAACACAGCA CTGTGCAAAC ACGAAAGTGG ACGTATACGG TGTGACGCCT
Pseudomonas aeruginosa	AAACACAGCA CTCTGCAAAC ACGAAAGTGG ACGTATAGGG TGTGACGCCT
Pseudomonas cepacia	AAACACAGCA CTCTGCAAAC ACGAAAGTGG ACGTATAGGG TGTGACGCCT
Bacillus stearothermophilus	AAACACAGGT CTCTGCGAAG TCGTAAGGCG ACGTATAGGG GCTGACACCT
Micrococcus luteus	AAACACAGGT CCATGCGAAG TCGTAAGACG ATGTATATGG ACTGACTCCT
SEQ ID NO: 129	GGGGGGACC ATCCTCCAAG GCTAAATAC
	481 530
Escherichia coli	TGTCTGAATA TGGGGGGACC ATCCTCCAAG GCTAAATACT CCTGACTGAC
Pseudomonas aeruginosa	TGTCTGAACA TGGGGGGACC ATCCTCCAAG GCTAAATACT ACTGACTGAC
Pseudomonas cepacia	TGTCTGAAGA TGGGGGGACC ATCCTCCAAG GCTAAATACT CGTGATCGAC
Lactobacillus lactis	AGTTTGAATC CGGGAGGACC ATCTCCCAAC CCTAAATACT CCTTAGTGAC
Micrococcus luteus	CGTGTGAATC TGCCAGGACC ACCTGGTAAG CCTGAATACT ACCTGTTGAC

[0115]

Annex III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.	
Reverse strand of SEQ ID NO: 130	AACACAGCA CTCTGCAAAC ACGAAAGTGG ACG
	1981 2030
Pseudomonas aeruginosa	TGTTTATTAA AAACACAGCA CTCTGCAAAC ACGAAAGTGG ACGTATAGGG

-continued

Annex III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.	
Escherichia coli	TGTTTATTAA AAACACAGCA CTGTGCAAAC ACGAAAGTGG ACGTATACGG
Pseudomonas cepacia	TGTTTAATAA AAACACAGCA CTCTGCAAAC ACGAAAGTGG ACGTATAGGG
Bacillus stearothermophilus	TGTTTATCAA AAACACAGGT CTCTGCGAAG TCGTAAGGCG ACGTATAGGG
Lactobacillus lactis	TGTTTATCAA AAACACAGCT CTCTGCTAAA CCACAAGGTG ATGTATAGGG
Micrococcus luteus	TGTTTATCAA AAACACAGGT CCATGCGAAG TCGTAAGACG ATGTATATGG

[0116]

Annex IV. Selection of the universal PCR primers by alignment of the bacterial 16S ribosomal RNA gene	
SEQ ID NO: 126	GGAGGAA GGTGGGGATG ACG
Reverse strand of SEQ ID NO: 127	CA CACCGCCCGT CACACCAT
	1241 1270......1461 1490
Escherichia coli	ACTGGAGGAA GGTGGGGATG ACGTCAAGTC......GCCTTGTACA CACCGCCCGT CACACCATGG
Neisseria gonorrhoeae	GCCGGAGGAA GGTGGGGATG ACGTCAAGTC......NNCTTGTACA CACCGCCCGT CACACCATGG
Pseudomonas cepacia	ACCGGAGGAA GGTNGGGATG ACGTCAAGTC......GTCTTGTACA CACNGCCCGT CACACCATGG
Seratia marcescens	ACTGGAGGAA GGTGGGGATG ACGTCAAGTC......GCCTTGTACA CACCGCCCGT CACACCATGG
Proteus vulgaris	ACCGGAGGAA GGTGGGGATG ACGTTAAGTC......GCCTTGTACA CACCGCCCGT CACACCATGG
Haemophilus influenzae	ACTGGAGGAA GGTNGGGATG ACGTCAAGTC......GCNTTGTACA CACCGCCCGT CACACCATGG
Legionella pneumophila	ACCGGAGGAA GGCGGGGATG ACGTCAAGTC......GCCTTGTACA CACCGCCCGT CACACCATGG
Pseudomonas aeruginos	ACCGGAGGAA GGTGGGGATG ACGTCAAGTC......GCCTTGTACA CACCGCCCGT CACACCATGG
Clostridium perfringens	CCAGGAGGAA GGTGGGGATG ACGTNNAATC......GTCTTGTACA CACCGCNCGT CACACCATGA
Mycoplasma hominis	CTGGGAGGAA GGTGGGGATG ACGTCAAATC......GTCTTGTACA CACCGCCCGT CACACCATGG
Helicobacter pylori	GGAGGAGGAA GGTGGGGACG ACGTCAAGTC......GTCTTGTACT CACCGCCCGT CACACCATGG
Mycoplasma pneumoniae	ATTGGAGGAA GGAAGGGATG ACGTCAAATC......GTCTTGTACA CACCGCCCGT CAAACTATGA

[0117]

SEQUENCE LISTING

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aattcaatcg gttgatgcaa tcggtgaaga aggagttaaa aaaattgttg cttctgataa    660
tccagaaact aaagatcttg tctttttagc tattgacaaa cgtgtaaata atgaagggca    720
attattttat aaagtcagag taacttcttc accaactggt gaccccgtat cattggttta    780
taaagtgaac gctacagatg gaacaattat ggaaaaacaa gatttaacgg aacatgtcgg    840
tagtgaagta acgttaaaaa actcttttca agtaacgttt aatgtaccag ttgaaaaaag    900
caatacggga attgctttac acggaacgga taacacaggg gtttaccatg cagtagttga    960
tggcaaaaat aattattcta ttattcaagc gccatcacta gcgacattaa atcagaatgc   1020
tattgacgcc tatacgcatg gaaaatttgt gaaaacatat tatgaagatc atttccaacg   1080
acacagtatt gatgatcgag ggatgcccat cttgtcagtt gttgatgaac aacatccaga   1140
tgcttatgac aatgcttttt gggatggaaa agcaatgcgt tatggtgaaa caagtacacc   1200
aacaggaaaa acgtatgctt cctctttaga tgtagttggt catgaaatga cacatggtgt   1260
gacggaacat actgccggtt tagaatattt aggacaatca ggtgccttga atgaatctta   1320
ttctgatttg atgggttata ttatttcggg tgcatctaat ccagaaattg gtgcggatac   1380
tcagagtgtt gaccgaaaaa caggtattcg aaatttacaa acgccaagta aacacggaca   1440
accagaaacc atggctcaat acgacgatcg agcacggtat aaaggaacgc cttattatga   1500
tcaaggcggt gttcattata acagtggaat tattaatcgg attggttaca ccattatcca   1560
gaacttaggc attgaaaaag cacagactat tttctacagc tcgttagtaa attacttaac   1620
acctaaagca caattcagtg atgctcgtga tgcgatgctt gctgctgcaa aagttcaata   1680
tggcgatgaa gcagcttcag tggtgtcagc agcctttaac tctgctggaa tcggagctaa   1740
agaagacatt caggtaaacc aaccaagtga atctgttctg gtcaatgaat gaaaaaaatt   1800
ccccaattaa ataaaaa                                                  1817
```

<210> SEQ ID NO 2
<211> LENGTH: 2275
<212> TYPE: DNA
<213> ORGANISM: Enterococcus faecalis

<400> SEQUENCE: 2

```
ggtaccaaag aaaaaaacga acgccacaac caacagcctc taaagcaaca cctgcttctg     60
aaattgaggg agatttagca aatgtcaatg agattctttt ggttcacgat gatcgtgtcg    120
ggtcagcaac gatgggaatg aaagtcttag aagaaatttt agataaagag aaaatttcaa    180
tgccgattcg aaaaattaat attaatgaat taactcaaca aacacaggct ttaattgtca    240
caaaagctga actaacggaa caagcacgta aaaaagcacc gaaagcgaca cacttatcag    300
```

-continued

```
taaaaagtta tggttaatcc ccaaaaatat gaaacagtgg gtttcgctct taaaagaaag    360
tgcctagaga ggaagaaaac aatggaaaat cttacgaata tttcaattga attaaatcaa    420
cagtttaata caaaagaaga agctattcgc ttttccggcc agaaactagt cgaggcaggc    480
tgtgttgagc ccgcttatat cgaagcaatg attgaaagag accaattgct atctgcccat    540
atggggaatt ttattgccat tcctcatgga acagaagaag ccaaaaaatt agtgaaaaaa    600
tcaggaatct gtgtagtgca agtcccagag ggcgttaatt ttggcaccga agaagatgaa    660
aaaattgcta ccgtattatt tgggattgcc ggagtcggtg aagaacattt gcaattagtc    720
caacaaattg cactttattg tagtgatatg gataacgtgg tgcaacttgc cgatgcatta    780
agtaaagaag aaataacaga aaatttagcc attgcttaaa ggagagaata agaatgaacg    840
cagtacattt tggagcagga aatattggac gcggctttat tggcgaaatt ttagctaaaa    900
cgggtttcat attaccgttt gtggatgtta atggaaacca tcatcaagcg ttaaaagaac    960
gtaaaagtta tacaattgaa ttggccgatg cctcacatca acaaattaac gttgaaaatg   1020
tgaccgggtt aaataacatg acagaaccag aaaaagtagt agaagcaatt gcggaagccg   1080
atttagtcac gacggcaatt ggtcctaata ttttaccaag aattgctgaa ttaattgctc   1140
aaggaattga tgcacgtgcc gaagcaaatt gtcaaaacgg cccgctggat attatcgctt   1200
gtgaaaatat gattggtggt tcaacctttt tagcagaaga agtggccata atatttgaaa   1260
aacccagctt atctgaacaa tggattggtt ttcctgatgc ggcagttgat cggattgttc   1320
cattacaaaa acataaagat ccactttttg ttcaagttga gcctttttgt gaatgggtca   1380
ttgatgatac caaccgaaaa gccaaagaga ttcagttaga aggcgtcatt acttgtcgat   1440
tagagccgta tattgaacga aaattattta gtgtaaccag tggccatgct acagttgcct   1500
atacaggggc gttgttaggc tatcaaacca ttgacgaagc gatgcaggac gccttagtgg   1560
tagcgcaact caaatcagtt ttgcaggaaa ccggtaaact tttagtggcc aaatggaatt   1620
ttgatgaaca agaacatgca gcctatattg aaaaaattat caaccgtttc caaaataaat   1680
atatttcaga tgctattaca cgtgtagcac ggacaccaat cagaaaatta ggtgcgcaag   1740
aacggtttat tcgaccaatc cgtgaattac aggaacgcaa tctagtgtcg gccgcattta   1800
tagcaatgat tggtattgtc tttaattatc atgatccaga agatgaacaa agccgtcaat   1860
tacaggaaat gcttgaccaa gaaagtgttg atacagtgga tcgctgaagt aacgggcatt   1920
gaagatccag aaacggttaa aaatattaaa caaaacgtag aactgctatg cgcgaccaca   1980
agtagcataa ttaacaaaat ccttctacca agatacttca catttcttaa ttaaagaaaa   2040
aacaaccgcg cctcacctga gccgaccccc aaaagttaga cctagaaatc taacttttgg   2100
aggttttttt gtatggcaaa atacagtttt gaaatttaaa cttaaacttg ttcatgacta   2160
cttatatggt caaggaggtc taaggtttct cgcaaagaag tatgggttta aagatagtct   2220
caaataagca aatggataaa tgcctataaa gaacttggtg aagaaggggg gatcc        2275
```

<210> SEQ ID NO 3
<211> LENGTH: 227
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 3

```
gatccgccat gggttgtttt ccgattgagg attttataga tggtttctgg cgacctgcac     60
```

-continued

```
aggagtacgg tgatttttaa ttattgcaat tgcacaagag tcagttctcc cccaaagaca    120

gcaccggtat caatataatg caggttgcca atatccacgc gatggcgcaa aggtgtatga    180

ccaaaccaga aatgatcggc cacctgcatc gccagttcgc gagtcgg                  227
```

<210> SEQ ID NO 4
<211> LENGTH: 278
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 4

```
gatctaaatc aaattaattg gttaaagata accacagcgg ggccgacata aactctgaca     60

agaagttaac aaccatataa cctgcacagg acgcgaacat gtcttctcat ccgtatgtca    120

cccagcaaaa taccccgctg gcggacgaca ccactctgat gtccactacc gatctcgctt    180

tccagcgtca tattggggcg cgctacgttg ggcgtgggc gtaattggtc aatcaggcgc     240

ggggtcagcg gataaacatt caccattttg tcgagatc                            278
```

<210> SEQ ID NO 5
<211> LENGTH: 1596
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 5

```
atggctgaca ttctgctgct cgataatatc gactctttta cgtacaacct ggcagatcag     60

ttgcgcagca atgggcataa cgtggtgatt taccgcaacc atataccggc gcaaacctta    120

attgaacgct tggcgaccat gagtaatccg gtgctgatgc tttctcctgg ccccggtgtg    180

ccgagcgaag ccggttgtat gccggaactc ctcacccgct tgcgtggcaa gctgcccatt    240

attggcattt gcctcggaca tcaggcgatt gtcgaagctt acgggggcta tgtcggtcag    300

gcgggcgaaa ttctccacgg taaagcctcc agcattgaac atgacggtca ggcgatgttt    360

gccggattaa caaacccgct gccggtggcg cgttatcact cgctggttgg cagtaacatt    420

ccggccggtt taaccatcaa cgcccatttt aatggcatgg tgatggcagt acgtcacgat    480

gcggatcgcg tttgtggatt ccagttccat ccggaatcca ttctcaccac ccagggcgct    540

cgcctgctgg aacaaacgct ggcctgggcg cagcataaac tagagccagc caacacgctg    600

caaccgattc tggaaaaact gtatcaggcg cagacgctta gccaacaaga aagccaccag    660

ctgttttcag cggtggtgcg tggcgagctg aagccggaac aactggcggc ggcgctggtg    720

agcatgaaaa ttcgcggtga gcacccgaac gagatcgccg gggcagcaac cgcgctactg    780

gaaaacgcag cgccgttccc gcgcccggat tatctgtttg ctgatatcgt cggtactggc    840

ggtgacggca gcaacagtat caatatttct accgccagtg cgtttgtcgc cgcggcctgt    900

gggctgaaag tggcgaaaca cggcaaccgt agcgtctcca gtaaatctgg ttcgtccgat    960

ctgctggcgg cgttcggtat taatcttgat atgaacgccg ataaatcgcg ccaggcgctg   1020

gatgagttag gtgtatgttt cctctttgcg ccgaagtatc acaccggatt ccgccacgcg   1080

atgccggttc gccagcaact gaaaacccgc accctgttca atgtgctggg gccattgatt   1140

aacccggcgc atccgccgct ggcgttaatt ggtgtttata gtccggaact ggtgctgccg   1200

attgccgaaa ccttgcgcgt gctggggtat caacgcgcgg cggtggtgca cagcggcggg   1260

atggatgaag tttcattaca cgcgccgaca atcgttgccg aactgcatga cggcgaaatt   1320
```

-continued

```
aaaagctatc agctcaccgc agaagacttt ggcctgacac cctaccacca ggagcaactg   1380

gcaggcggaa caccggaaga aaaccgtgac attttaacac gtttgttaca aggtaaaggc   1440

gacgccgccc atgaagcagc cgtcgctgcg aacgtcgcca tgttaatgcg cctgcatggc   1500

catgaagatc tgcaagccaa tgcgcaaacc gttcttgagg tactgcgcag tggttccgct   1560

tacgacagag tcaccgcact ggcggcacga gggtaa                             1596
```

<210> SEQ ID NO 6
<211> LENGTH: 2703
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 6

```
gacgacttag ttttgacgga atcagcatag ttaatcactt cactgtggaa aatgaggaaa     60

tattattttt tttgcgcttc gtaattaatg gttataaggt cggccagaaa cctttctaat    120

gcaagcgatg acgttttttt atgtgtctga atttgcactg tgtcacaatt ccaaatcttt    180

attaacaact cacctaaaac gacgctgatc cagcgtgaat actggtttcc cttatgttca    240

tcagattcat ttaagcaagg gtttcttctt cattcctgat gaaagtgcca tctaaaaaga    300

tgatcttaat aaatctatta agaatgagat ggagcacact ggatatttta cttatgaaac    360

tgtttcactc ctttacttaa tttatagagt taccttccgc tttttgaaaa tacgcaacgg    420

ccattttttg cacttagata cagattttct gcgctgtatt gcattgattt gatgctaatc    480

ctgtggtttg cactagcttt aagtggttga gatcacattt ccttgctcat ccccgcaact    540

cctccctgcc taatcccccg caggatgagg aaggtcaaca tcgagcctgg caaactagcg    600

ataacgttgt gttgaaaatc taagaaaagt ggaactccta tgtcacaacc tatttttaac    660

gataagcaat ttcaggaagc gctttcacgt cagtggcagc gttatggctt aaattctgcg    720

gctgaaatga ctcctcgcca gtggtggcta gcagtgagtg aagcactggc cgaaatgctg    780

cgtgctcagc cattcgccaa gccggtggcg aatcagcgac atgttaacta catctcaatg    840

gagtttttga ttggtcgcct gacgggcaac aacctgttga atctcggctg gtatcaggat    900

gtacaggatt cgttgaaggc ttatgacatc aatctgacgg acctgctgga agaagagatc    960

gacccggcgc tgggtaacgg tggtctggga cgtctggcgg cgtgcttcct cgactcaatg   1020

gcaactgtcg gtcagtctgc gacgggttac ggtctgaact atcaatatgg tttgttccgc   1080

cagtcttttg tcgatggcaa acaggttgaa gcgccggatg actggcatcg cagtaactac   1140

ccgtggttcc gccacaacga agcactggat gtgcaggtag ggattggcgg taaagtgacg   1200

aaagacggac gctgggagcc ggagtttacc attaccggtc aagcgtggga tctccccgtt   1260

gtcggctatc gtaatggcgt ggcgcagccg ctgcgtctgt ggcaggcgac gcacgcgcat   1320

ccgtttgatc tgactaaatt taacgacggt gatttcttgc gtgccgaaca gcagggcatc   1380

aatgcggaaa aactgaccaa agttctctat ccaaacgaca accatactgc cggtaaaaag   1440

ctgcgcctga tgcagcaata cttccagtgt gcctgttcgg tagcggatat tttgcgtcgc   1500

catcatctgg cggggcgtga actgcacgaa ctggcggatt actaagttat tcagctgaac   1560

gatacccacc caactatcgc gattccagaa ctgctgcgcg tgctgatcga tgagcaccag   1620

atgagctggg atgacgcttg ggccattacc agcaaaactt tcgcttacac caaccatacc   1680

ctgatgccag aagcgctgga acgctgggat gtgaaactgg tgaaaggctt actgccgcgc   1740
```

-continued

```
cacatgcaga ttattaacga aattaatact cgctttaaaa cgctggtaga gaaaacctgg   1800

ccgggcgatg aaaaagtgtg ggccaaactg gcggtggtgc acgacaaaca agtgcatatg   1860

gcgaacctgt gtgtggttgg cggtttcgcg gtgaacggtg ttgcggcgct gcactcggat   1920

ctggtggtga aagatctgtt cccggaatat caccagctat ggccgaacaa attccataac   1980

gtcaccaacg gtattacccc acgtcgctgg atcaaacagt gcaacccggc actggcggct   2040

ctgttggata aatcactgca aaaagagtgg gctaacgatc tcgatcagct gatcaatctg   2100

gttaaattgg ctgatgatgc gaaattccgt cagctttatc gcgtgatcaa gcaggcgaat   2160

aaagtccgtc tggcggagtt tgtgaaagtt cgtaccggta ttgacatcaa tccacaggcg   2220

attttcgata ttcagatcaa acgtttgcac gagtacaaac gccagcacct gaatctgctg   2280

cgtattctgg cgttgtacaa agaaattcgt gaaaacccgc aggctgatcg cgtaccgcgc   2340

gtcttcctct tcggcgcgaa agcggcaccg ggctactacc tggctaagaa tattatcttt   2400

gcgatcaaca aagtggctga cgtgatcaac aacgatccgc tggttggcga taagttgaag   2460

gtggtgttcc tgccggatta ttgcgtttcg gcggcggaaa aactgatccc ggcggcggat   2520

atctccgaac aaatttcgac tgcaggtaaa gaagcttccg gtaccggcaa tatgaaactg   2580

gcgctcaatg gtgcgcttac tgtcggtacg ctggatgggg cgaacgttga aatcgccgag   2640

aaagtcggtg aagaaaatat ctttattttt ggtcatacgg tcaaacaagt gaaggcaatc   2700

gac                                                                  2703
```

```
<210> SEQ ID NO 7
<211> LENGTH: 1391
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 7

agagaagcct gtcggcaccg tctggtttgc ttttgccact gcccgcggtg aaggcattac     60

ccggcgggat gcttcagcgg cgaccgtgat gcggtgcgtc gtcaggctac tgcgtatgca    120

ttgcagacct tgtggcaaca atttctacaa aacacttgat actgtatgag catacagtat    180

aattgcttca acagaacata ttgactatcc ggtattaccc ggcatgacag gagtaaaaat    240

ggctatcgac gaaaacaaac agaaagcgtt ggcggcagca ctgggccaga ttgagaaaca    300

atttggtaaa ggctccatca tgcgcctggg tgaagaccgt tccatggatg tggaaaccat    360

ctctaccggt tcgctttcac tggatatcgc gcttggggca ggtggtctgc cgatgggccg    420

tatcgtcgaa atctacggac cggaatcttc cggtaaaacc acgctgacgc tgcaggtgat    480

cgccgcagcg cagcgtgaag gtaaaacctg tgcgtttatc gatgctgaac acgcgctgga    540

cccaatctac gcacgtaaac tgggcgtcga tatcgacaac ctgctgtgct cccagccgga    600

caccggcgag caggcactgg aaatctgtga cgccctggcg cgttctggcg cagtagacgt    660

tatcgtcgtt gactccgtgg cggcactgac gccgaaagcg gaaatcgaag gcgaaatcgg    720

cgactctcac atgggccttg cggcacgtat gatgagccag gcgatgcgta agctggcggg    780

taacctgaag cagtccaaca cgctgctgat cttcatcaac cagatccgta tgaaaattgg    840

tgtgatgttc ggtaacccgg aaaccactac cggtggtaac gcgctgaaat tctacgcctc    900

tgttcgtctc gacatccgtc gtatcggcgc ggtgaaagag ggcgaaaacg tggtgggtag    960

cgaaacccgc gtgaaagtgg tgaagaacaa aatcgctgcg ccgtttaaac aggctgaatt   1020
```

-continued

```
ccagatcctc tacggcgaag gtatcaactt ctacggcgaa ctggttgacc tgggcgtaaa   1080

agagaagctg atcgagaaag caggcgcgtg gtacagctac aaaggtgaga agatcggtca   1140

gggtaaagcg aatgcgactg cctggctgaa agataacccg gaaaccgcga aagagatcga   1200

gaagaaagta cgtgagttgc tgctgagcaa cccgaactca acgccggatt tctctgtaga   1260

tgatagcgaa ggcgtagcag aaactaacga agatttttaa tcgtcttgtt tgatacacaa   1320

gggtcgcatc tgcggccctt ttgctttttt aagttgtaag gatatgccat gacagaatca   1380

acatcccgtc g                                                        1391
```

<210> SEQ ID NO 8
<211> LENGTH: 238
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 8

```
tcgccaggaa ggcggcattc ggctgggtca gagtgacctg cagcgtggtg tcgttcagcg     60

ctttcacccc caacgtctcg ggtccctttt gcccgagggc aatctcgcgg gcgttggcga    120

tatgcatatt gccagggtag ctcgcgtagg gggaggctgt tgccggcgag accagccgtt    180

gccagctcca gacgatatcc tgcgctgtaa tggccgtgcc gtcagaccag gtcagacc      238
```

<210> SEQ ID NO 9
<211> LENGTH: 385
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 9

```
cagcgtaatg cgccgcggca taacggcgcc actatcgaca gtcagttcgt cagcctgcag     60

cctgggctga atctgggacc atggcgcctg ccgaactaca gcacctatag ccacagcgat    120

aacaacagcc gctgggagtc ggtttactcc tatcttgccc gcgatattca caccctacgc    180

agccagctgg tggtcggtaa tacgtatacc tcttccggca ttttcgacag tttgagtttt    240

accggtctgc agctcagttc gacaaagaga tgctgccgga tagcctgcat gctttgcgcc    300

gacgattcga gggatcgcgc gcaccaccgc ggaggtctcg gtttatcaga atggttacag    360

catttataaa accaccgtcg ctacc                                          385
```

<210> SEQ ID NO 10
<211> LENGTH: 462
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 10

```
ctctatattc aggacgaaca tatctggacc tctggcgggg tcagttccgg ctttgatcgc     60

cctgcacccg cagcgggtga tcgcccctca tctgctactg cggcgctgca acaggcgacg    120

atcgatgacg ttattcctgg ccagcaaaca gcagaccaat taaggtctga tagtggctct    180

cttcctccgg cgcgcgacgg tccaggcggc tcaacagttt ggtgcatagc gctttgcggt    240

tgagatgacg cccttcgtta agaatatcca tcacgatctc cgtccatgga gagtagcgtt    300

tattccagaa tagggttttt caggatctca tggatctgcg cctgcttatc gctattttgt    360

aaccagatcg cataaagtgg acgggataac gtagcgctgt ccatgaccgt atgtaaccca    420

tgcttctctt tcgcccagcg agcaggtagc caacagcagc cg                       462
```

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<210> SEQ ID NO 11
<211> LENGTH: 730
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 11

gctgaccgct aaactgggtt acccgatcac tgacgatctg gacatctaca cccgtctggg 60

cggcatggtt tggcgcgctg actccaaagg caactacgct tcaaccggcg tttcccgtag 120

cgaacacgac actggcgttt ccccagtatt tgctggcggc gtagagtggg ctgttactcg 180

tgacatcgct acccgtctgg aataccagtg ggttaacaac atcggcgacg cgggcactgt 240

gggtacccgt cctgataacg gcatgctgag cctgggcgtt tcctaccgct tcggtcagga 300

agatgctgca ccggttgttg ctccggctcc ggctccggct ccggaagtgg ctaccaagca 360

cttcaccctg aagtctgacg ttctgttcaa cttcaacaaa gctaccctga aaccggaagg 420

tcagcaggct ctggatcagc tgtacactca gctgagcaac atggatccga aagacggttc 480

cgctgttgtt ctgggctaca ccgaccgcat cggttccgaa gcttacaacc agcagctgtc 540

tgagaaacgt gctcagtccg ttgttgacta cctggttgct aaaggcatcc cggctggcaa 600

aatctccgct cgcggcatgg gtgaatccaa cccggttact ggcaacacct gtgacaacgt 660

gaaagctcgc gctgccctga tcgattgcct ggctccggat cgtcgtgtag agatcgaagt 720

taaaggtatc 730

<210> SEQ ID NO 12
<211> LENGTH: 225
<212> TYPE: DNA
<213> ORGANISM: Proteus mirabilis

<400> SEQUENCE: 12

cgctactgtt taaatctcat ttgaaacatc gcaaagtcag tgaaccacat attcgaggat 60

ggcatgcact agaaaatatt aataagattt tagcgaaacc taatcagcgc aatatcgctt 120

aattatttta ggtatgttct cttctatcct acagtcacga ggcagtgtcg aacttgatcc 180

tcattttatt aatcacatga ccaatggtat aagcgtcgtc acata 225

<210> SEQ ID NO 13
<211> LENGTH: 402
<212> TYPE: DNA
<213> ORGANISM: Proteus mirabilis

<400> SEQUENCE: 13

acattttaaa taggaagcca cctgataaca tccccgcagt tggatcatca gatttatagc 60

ggcatttggt atccgctaga taaaagcagt ccaacgatcc cgccaattgt tagatgaaat 120

tggactattc tttttatttg ctccgcttta tcacagtggt tttcgctttg ccgcccctgt 180

gcgccaacag ctaagaacac gcacgctctt taatgtgtta ggcccattaa ttaatccagc 240

gcgttccgcc tttagcatta attggtgttt atagtcctga attattaatg cctattgcag 300

ataccttaaa tgtcttgggc tacaaacgtg cggcagtggt ccatagtggt ggaatggatg 360

aagtgtcatt acatgctccc acacaagtgg ctgagttaca ca 402

<210> SEQ ID NO 14
<211> LENGTH: 157
<212> TYPE: DNA

-continued

<213> ORGANISM: Proteus mirabilis

<400> SEQUENCE: 14

ctgaaacgca tttatgcggg agtcagtgaa atcatcactc aattttcacc cgatgtattt 60

tctgttgaac aagtctttat ggcaaaaaat gcagactcag cattaaaatt aggccaagca 120

agaggtgtgg cgattttagc ggcagtcaat aatgatc 157

<210> SEQ ID NO 15
<211> LENGTH: 1348
<212> TYPE: DNA
<213> ORGANISM: Proteus mirabilis

<400> SEQUENCE: 15

tttctcttta aaatcaattc ttaaagaaat tattaataat taacttgata ctgtatgatt 60

atacagtata atgagtttca acaagcaaaa tcatatacgt tttaatggta gtgacccatc 120

tttatgcttc actgcccaga gggagataac atggctattg atgaaaacaa acaaaaagca 180

ttggccgcag cacttggtca aattgaaaag caatttggta aaggttctat catgcgtctg 240

ggcgaagacc gttccatgaa cgtagaaact atctctacag gatctttatc attagacgtt 300

gctttaggtg caggtggatt gccacgtggc cgtattgttg aaatctatgg ccctgaatct 360

tctggtaaaa caaccttgac tctacaagtt attgcctctg ctcagcgtga aggaaaaatt 420

tgtgcattta ttgatgctga acatgcatta gacccaattt atgctcaaaa gctaggtgtc 480

gatatcgata atctactctg ctctcaacct gacacaggtg aacaagctct ggaaatttgt 540

gatgcattat ctcgctctgg tgcggtcgat gttattgtcg tggactccgt ggcagcatta 600

acaccaaaag ctgaaattga aggtgaaatt ggtgattcac acgttggttt agccgcacgt 660

atgatgagcc aagctatgcg taaactagcg ggtaacctta aaaactctaa tacactgctg 720

attttcatta accaaattcg tatgaaaatc ggtgttatgt ttggtaaccc agaaaccacg 780

accggtggta atgcgcttaa attctatgct tctgttcgtt tagacattcg tcgcattggc 840

tctgtcaaaa atggtgatga agtcattggt agtgagactc gcgttaaagt tgttaaaaat 900

aaagtggctg caccgtttaa acaagctgaa ttccaaatta tgtacggtga aggtattaat 960

acctatggcg aactgattga tttaggtgtt aaacataagt tagtagagaa agcaggtgct 1020

tggtatagct acaatggcga aaaaattggt caaggtaaag ctaacgcaac caattactta 1080

aaagaacatc ctgaaatgta caatgagtta aacactaaat tgcgtgaaat gttgttaaat 1140

catgctggtg aattcacaag tgctgcggat tttgcaggtg aagagtcaga cagtgatgct 1200

gacgacacaa aagagtaatt agctggttgt catgctgttt gtgtgaaaat agaccttaaa 1260

tcattggcta ttatcacgac agcatcccat agaataactt gtttgtataa attttattca 1320

gatggcaaag gaagccttaa aaaagctt 1348

<210> SEQ ID NO 16
<211> LENGTH: 2167
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 16

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ctacctggcg agcctggagc acgagcgggt tcgcttcgta cggcgctgag cgacagtcac 120

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aggagaggaa acggatggga tcgcaccagg agcggccgct gatcggcctg ctgttctccg    180
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agcaactgaa ccgcgagggc ggcgtcggcg gtcgcccgat cgaaacgctg tcccaggacc    300
ccggcggcga cccggaccgc tatcggctgt gcgccgagga cttcattcgc aaccgggggg    360
tacggttcct cgtgggctgc tacatgtcgc acacgcgcaa ggcggtgatg ccggtggtcg    420
agcgcgccga cgcgctgctc tgctacccga ccccctacga gggcttcgag tattcgccga    480
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acattccgct gtatccctcc gacgacgact tgcagcgcgc cgtcgagcgc atctaccagg    720
cgcgcgccga cgtggtcttc tccaccgtgg tgggcaccgg caccgccgag ctgtatcgcg    780
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tcccggagaa cgcgaccatc accgcctggg ccgaggcggc ctactggcag accttgttgc   1020
tcggccgcgc cgcgcaggcc gcaggcaact ggcgggtgga agacgtgcag cggcacctgt   1080
acgacatcga catcgacgcg ccacaggggc cggtccgggt ggagcgccag aacaaccaca   1140
gccgcctgtc ttcgcgcatc gcggaaatcg atgcgcgcgg cgtgttccag gtccgctggc   1200
agtcgcccga accgattcgc cccgaccctt atgtcgtcgt gcataacctc gacgactggt   1260
ccgccagcat gggcggggga ccgctcccat gagcgccaac tcgctgctcg gcagcctgcg   1320
cgagttgcag gtgctggtcc tcaacccgcc gggggaggtc agcgacgccc tggtcttgca   1380
gctgatccgc atcggttgtt cggtgcgcca gtgctggccg ccgccggaag ccttcgacgt   1440
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gctgctcgcc gccgggactc cgcgcactac cctggtggcg ctggtggagt acgaaagccc   1560
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tgcccaccgg gtgctgcctg tgctggtatc ggcgcggcgc atcagcgagg aaatggcgaa   1680
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ggccaaggtg ttgctgatgc agcgccatgg ctgggacgag cgcgaggcgc accagcacct   1800
gtcgcgggaa gcgatgaagc ggcgcgagcc gatcctgaag atcgctcagg agttgctggg   1860
aaacgagccg tccgcctgag cgatccgggc cgaccagaac aataacaaga ggggtatcgt   1920
catcatgctg ggactggttc tgctgtacgt tggcgcggtg ctgtttctca atgccgtctg   1980
gttgctgggc aagatcagcg gtcgggaggt ggcggtgatc aacttcctgg tcggcgtgct   2040
gagcgcctgc gtcgcgttct acctgatctt ttccgcagca gccgggcagg gctcgctgaa   2100
ggccggagcg ctgaccctgc tattcgcttt tacctatctg tgggtggccg ccaaccagtt   2160
cctcgag                                                             2167
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<210> SEQ ID NO 17
<211> LENGTH: 1872
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

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<400> SEQUENCE: 17

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tcgctgacgc tgctgggcct ggccaccgct cacgccaagg acgacatgaa agccgccgag     180
caataccagg gtgccgcttc cgccgtcgat cccgctcacg tggtgcgcac caacggcgct     240
cccgacatga gtgaaagcga gttcaacgag gccaagcaga tctacttcca acgctgcgcc     300
ggttgccacg gcgtcctgcg caagggcgcc accggcaagc cgctgacccc ggacatcacc     360
cagcaacgcg gccagcaata cctggaagcg ctgatcacct acggcacccc gctgggcatg     420
ccgaactggg gcagctccgg cgagctgagc aaggaacaga tcaccctgat ggccaagtac     480
atccagcaca ccccgccgca accgccggag tggggcatgc cggagatgcg cgaatcgtgg     540
aaggtgctgg tgaagccgga ggaccggccg aagaaacagc tcaacgacct cgacctgccc     600
aacctgttct cggtgaccct gcgcgacgcc gggcagatcg ccctggtcga cggcgacagc     660
aaaaagatcg tcaaggtcat cgataccggc tatgccgtgc atatctcgcg gatgtccgct     720
tccggccgct acctgctggt gatcggccgc gacgcgcgga tcgacatgat cgacctgtgg     780
gccaaggagc cgaccaaggt cgccgagatc aagatcggca tcgaggcgcg ctcggtggaa     840
agctccaagt tcaagggcta cgaggaccgc tacaccatcg ccggcgccta ctggccgccg     900
cagttcgcga tcatggacgg cgagaccctg gaaccgaagc agatcgtctc cacccgcggc     960
atgaccgtag acacccagac ctaccacccg gaaccgcgcg tggcggcgat catcgcctcc    1020
cacgagcacc ccgagttcat cgtcaacgtg aaggagaccg gcaaggtcct gctggtcaac    1080
tacaaggata tcgacaacct caccgtcacc agcatcggtg cggcgccgtt cctccacgac    1140
ggcggctggg acagcagcca ccgctacttc atgaccgccg ccaacaactc caacaaggtt    1200
gccgtgatcg actccaagga ccgtcgcctg tcggccctgg tcgacgtcgg caagaccccg    1260
cacccggggc gtggcgccaa cttcgtgcat cccaagtacg gcccggtgtg gagcaccagc    1320
cacctgggcg acggcagcat ctcgctgatc ggcaccgatc cgaagaacca tccgcagtac    1380
gcctggaaga aagtcgccga actacagggc cagggcggcg gctcgctgtt catcaagacc    1440
catccgaagt cctcgcacct ctacgtcgac accaccttca accccgacgc caggatcagc    1500
cagagcgtcg cggtgttcga cctgaagaac ctcgacgcca agtaccaggt gctgccgatc    1560
gccgaatggg ccgatctcgg cgaaggcgcc aagcgggtgg tgcagcccga gtacaacaag    1620
cgcggcgatg aagtctggtt ctcggtgtgg aacggcaaga acgacagctc cgcgctggtg    1680
gtggtggacg acaagaccct gaagctcaag gccgtggtca aggacccgcg gctgatcacc    1740
ccgaccggta agttcaacgt ctacaacacc cagcacgacg tgtactgaga cccgcgtgcg    1800
gggcacgccc cgcacgctcc cccctacgag gaaccgtgat gaaaccgtac gcactgcttt    1860
cgctgctcgc ca                                                        1872
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<210> SEQ ID NO 18
<211> LENGTH: 3451
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 18

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cgcctactaa agctcggctt attcatatgt atttatattc tttcaataga tcactcagcg    120
ctattttaag ttcaccctct gtaagttcac ctgggcgctc tttctttcct tcggtaaagc    180
tgtcggccag accaaacatt aaactcaagc atctcccaag cgatgcatca tcttgggcca    240
gcatccctga atcgcgcgtc ggacctccaa gtcttaaaaa attcttcgct gaaggttttc    300
ccatcaatcg atgaggctaa tagcttcttt gcaatatcta tcatttccat gctcacctta    360
aagcacctca tttttcatgt aaaaattgta ttgatccgtg ccagactcaa tcctccaccc    420
agaaacaaac atcccatcct ctccaatgat aacaacaata ttagtcctgg cattgtaatg    480
tacttttgag tttacttcgg agtggtaagt cccttttct acggttgcag gatcagcaag    540
gtgctcaaga attttatccc taaactctgc aagcgttcca ttgttggcgc ttttttcacc    600
cagcccaaaa tcatatttgt ggctatcaaa ttttttctgt agttgcctcc gtgtgaagat    660
accactatca agaggactac tgagcattac ataaacaggt ttgactccag aatccgccgg    720
gaaaatcacg atcagatcgt ttaggtccag tagcattccc ggataggact ccgggccggt    780
cttcaacggt gtgagggccg ctccctcata taccggcacc ggcttcggta tgaccggagt    840
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cggcgcttct gcgaccgtag agggaaccgt aacctcgtac agtcctgttg cggcgttata    960
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gcttttgcaa ccgcgttcag gtttacgctt gggggaagcc ccaatttagc ggcatccatg   1140
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agtaggtcag actggcaagc cacggccatc accgaggtgc tgaagccagg accgccagga   1260
cggcaatcgc atcggagatc gcttgagcaa gggatgcggc gcctgtgcga cctggatcag   1320
accccgctgc ggcggtggcg cacccgctgc cattggctgg catggcataa gtattggcag   1380
ccctgatcgc cgcttgacga gcgatttcct tgcgccttgc cgtttcggcg ttcagcttgt   1440
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tcttagcttc ctgtactcct gcattccagt accgacatac ggacttggtc ctggtgggac   2220
aaatggtgga gtaccgtagc ttgatcgagc aggaatatac tggattatgt cacgcccacc   2280
accctgcaca tgtgtaataa ccatcgaacc aggttcgtaa tcattgacag ccatagatcg   2340
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cccctacatt aatttgaaag tgtaatgtat tgagcgactc ccacctagag aaccctctcc   2400
cagtcaataa gccccaatgc atcggcaata cactgcaatc aacttcaata tcccgtgttt   2460
agatgatcca gaaggtgcgc tctctcgcct cttataatcg cgcctgcgtc aaacggtcat   2520
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ttaacgaact cccactttca aaattcatcc atgccgcccc ttcgcgagct tccggacaaa   2640
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gccgggctgc caccaccagg ccgagatgga cgccctgcat gtatcctccg atcggcaagc   3240
ctcccgttcg cacattcacc actctgcaat ccagttcata aatcccataa aagccctctt   3300
ccgctccccg ccagcctccc cgcatcccgc accctagacg ccccgccgct ctccgccggc   3360
tcgcccgaca agaaaaacca accgctcgat cagcctcatc cttcacccat cacaggagcc   3420
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<210> SEQ ID NO 19
<211> LENGTH: 744
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 19

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gagctgagca agaatgcctc gatcgaaggc ggctatcgtt acctgcgcac caacgccagc    600
accgagatga ccccgcatgg cggcaacaag ctgggctccc tggacctgca cagcagctcg    660
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<210> SEQ ID NO 20
<211> LENGTH: 2760
<212> TYPE: DNA

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<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 20

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accccgacat ggacgccaaa gccctgctcc tcggcagcct ctgcctggcc gccccattcg 180
ccgacgcggc gacgctcgac aatgctctct ccgcctgcct cgccgcccgg ctcggtgcac 240
cgcacacggc ggagggccag ttgcacctgc cactcaccct tgaggcccgg cgctccaccg 300
gcgaatgcgg ctgtacctcg gcgctggtgc gatatcggct gctggccagg ggcgccagcg 360
ccgacagcct cgtgcttcaa gagggctgct cgatagtcgc caggacacgc cgcgcacgct 420
gaccctggcg gcggacgccg gcttggcgag cggccgcgaa ctggtcgtca ccctgggttg 480
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cccgccgctc tccgccggct cgcccgacaa gaaaaaccaa ccgctcgatc agcctcatcc 720
ttcacccatc acaggagcca tcgcgatgca cctgataccc cattggatcc ccctggtcgc 780
cagcctcggc ctgctcgccg gcggctcgtc cgcgtccgcc gccgaggaag ccttcgacct 840
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cctgcacttt cccgagggcg gcagcctggc cgcgctgacc gcgcaccagg cttgccacct 1620
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gcaaagcatc gtcttcggcg gggtgcgcgc gcgcagccag gacctcgacg cgatctggcg   2220

cggtttctat atcgccggcg atccggcgct ggcctacggc tacgcccagg accaggaacc   2280

cgacgcacgc ggccggatcc gcaacggtgc cctgctgcgg gtctatgtgc cgcgctcgag   2340

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tccctcggcg atccccaccg acccgcgcaa cgtcggcggc gacctcgacc cgtccagcat   2580

ccccgacaag gaacaggcga tcagcgccct gccggactac gccagccagc ccggcaaacc   2640

gccgcgcgag gacctgaagt aactgccgcg accggccggc tcccttcgca ggagccggcc   2700

ttctcggggc ctggccatac atcaggtttt cctgatgcca gcccaatcga atatgaattc   2760
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<210> SEQ ID NO 21
<211> LENGTH: 172
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus saprophyticus

<400> SEQUENCE: 21

ttgatgaaat gcatcgatta ataaattttc atgtacgatt aaaacgtttt tacccttacc     60

ttttcgtact acctctgcct gaagttgacc acctttaaag tgattcgttg aaatccatta    120

tgctcattat taatacgatc tataaaaaca aatggaatgt gatgatcgat ga            172
```

```
<210> SEQ ID NO 22
<211> LENGTH: 155
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus saprophyticus

<400> SEQUENCE: 22

gttccattga ctctgtatca cctgttgtaa cgaacatcca tatgtcctga aactccaacc     60

acaggtttga ccacttccaa tttcagacca ccaagtttga cacgtgaaga ttcatcttct    120

aatatttcgg aattaatatc atattattta aatag                               155
```

```
<210> SEQ ID NO 23
<211> LENGTH: 145
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus saprophyticus

<400> SEQUENCE: 23

acatagaaaa actcaaaaga tttacttttt tcaaatggaa aataagggta cacacgatat     60

ttcccgtcat cttcagttac cggtacaaca tcctctttat taacctgcac ataatctgac    120

tccgcttcac tcatcaaact actaa                                          145
```

```
<210> SEQ ID NO 24
<211> LENGTH: 266
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus saprophyticus

<400> SEQUENCE: 24

tttcactgga attacatttc gctcattacg tacagtgaca atcgcgtcag atagtttctt     60

ctggttagct tgactcttaa caatcttgtc taaattttgt ttaattcttt gattcgtact    120

agaaatttta cttctaattc cttgtaattc ataacttgca ttatcatata aatcataagt    180
```

-continued

```
atcacatttt tgatgaatac tttgatataa atctgacaat acaggcagtt gctccattct    240

atcgttaaga atagggtaat taatag                                         266
```

<210> SEQ ID NO 25
<211> LENGTH: 845
<212> TYPE: DNA
<213> ORGANISM: Haemophilus influenzae

<400> SEQUENCE: 25

```
tgttaaattt ctttaacagg gattttgtta tttaaattaa acctattatt ttgtcgcttc     60

tttcactgca tctactgctt gagttgcttt ttctgaaacc gcctctttca tttcacttgc    120

tttttctgat gctgcttctt tcatttcgcc tactttttct gacgctgctt ctgttgctga    180

tttaattact tctttcgcat cttccacttt ctctgctact ttatttttca cgtctgtaga    240

aagctgctgt gctttttcct ttacttcagt cattgtatta gctgcagcat cttttgtttc    300

tgatgcgact gatgctacag tttgcttcgt atcctcaact ttttgttttg cttcttgctt    360

atcaaaacaa cctgtcacga ctaaagctga acctaaaacc aatgctaatg ttaatttttt    420

cattattttc tccatagaat aatttgattg ttacaaagcc ctattacttt gatgcagttt    480

agtttacggg aattttcata aaaagaaaaa cagtaatagt aaaactttac ctttctttaa    540

aaagattact ttataaaaaa acatctaaga tattgatttt taatagatta taaaaaacca    600

ataaaaattt tattttttgt aaaaaaaaag aatagtttat tttaaataaa ttacaggaga    660

tgcttgatgc atcaatattt ctgatttatt accatcccat aataattgag caatagttgc    720

aggataaaat gatattggat ttcgttttcc atacagttca gcaacaattt ctcccactaa    780

gggcaaatgg gaaacaatta atacagattt aacgccctcg tcttttagca cttctaaata    840

atcaa                                                                845
```

<210> SEQ ID NO 26
<211> LENGTH: 1598
<212> TYPE: DNA
<213> ORGANISM: Haemophilus influenzae

<400> SEQUENCE: 26

```
gaatagagtt gcactcaata gattcgggct ttataattgc ccagattttt atttataaca     60

aagggttcca aatgaaaaaa tttaatcaat ctctattagc aactgcaatg ttgttggctg    120

caggtggtgc aaatgcggca gcgtttcaat tggcggaagt ttctacttca ggtcttggtc    180

gtgcctatgc gggtgaagcg gcgattgcag ataatgcttc tgtcgtggca actaacccag    240

ctttgatgag tttatttaaa acggcacagt tttccacagg tggcgtttat attgattcta    300

gaattaatat gaatggtgat gtaacttctt atgctcagat aataacaaat cagattggaa    360

tgaaagcaat aaaggacggc tcagcttcac agcgtaatgt tgttcccggt gcttttgtgc    420

caaatcttta tttcgttgcg ccagtgaatg ataaattcgc gctgggtgct ggaatgaatg    480

tcaatttcgg tctaaaaagt gaatatgacg atagttatga tgctggtgta tttggtggaa    540

aaactgactt gagtgctatc aacttaaatt taagtggtgc ttatcgagta acagaaggtt    600

tgagcctagg tttaggggta aatgcggttt atgctaaagc ccaagttgaa cggaatgctg    660

gtcttattgc ggatagtgtt aaggataacc aaataacaag cgcactctca acacagcaag    720

aaccattcag agatcttaag aagtatttgc cctctaagga caaatctgtt gtgtcattac    780
```

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```
aagatagagc cgcttggggc tttggctgga atgcaggtgt aatgtatcaa tttaatgaag     840

ctaacagaat tggtttagcc tatcattcta aagtggacat tgattttgct gaccgcactg     900

ctactagttt agaagcaaat gtcatcaaag aaggtaaaaa aggtaattta acctttacat     960

tgccagatta cttagaactt tctggtttcc atcaattaac tgacaaactt gcagtgcatt    1020

atagttataa atataccat tggagtcgtt taacaaaatt acatgccagc ttcgaagatg    1080

gtaaaaaagc ttttgataaa gaattacaat acagtaataa ctctcgtgtt gcattagggg    1140

caagttataa tctttatgaa aaattgacct tacgtgcggg tattgcttac gatcaagcgg    1200

catctcgtca tcaccgtagt gctgcaattc cagataccga tcgcacttgg tatagtttag    1260

gtgcaaccta taaattcacg ccgaatttat ctgttgatct tggctatgct tacttaaaag    1320

gcaaaaaagt tcactttaaa gaagtaaaaa caataggtga caaacgtaca ttgacattga    1380

atacaactgc aaattatact tctcaagcac acgcaaatct ttacggtttg aatttaaatt    1440

atagtttcta atccgttaaa aaatttagca taataaagca caattccaca ctaagtgtgc    1500

ttttctttta taaaacaagg cgaaaaatga ccgcacttta ttacacttat taccccctcgc   1560

cagtcggacg gcttttgatt ttatctgacg gcgaaaca                            1598
```

<210> SEQ ID NO 27
<211> LENGTH: 9100
<212> TYPE: DNA
<213> ORGANISM: Haemophilus influenzae

<400> SEQUENCE: 27

```
gtcaaaaatt gcgtgcattc tagcgaaaaa atgggctttt gggaactgtg ggatttattt      60

aaaatcttag aaaatcttac cgcactttta agctataaag tgcggtgaaa tttagtggcg     120

tttataatgg agaattactc tggtgtaatc cattcgactg tccagcttcc agtaccttct     180

ggaactaatg tttttgtgag ataaggcaaa atttctttca tttgggtttc taatgtccaa     240

ggtggattaa ttaccaccat accgctcgca gtcattcctc gttgatcgct atctgggcga     300

acggcgagtt caatttttag aatttttcta attcccgttg cttctaaacc cttaaaaata     360

cgtttagttt gttggcgtaa tacaacagga taccaaatcg cataagtgcc agtggcaaaa     420

cgtttatagc cctcttcaat ggctttaaca acgagatcat aatcatcttt taattcataa     480

ggcggatcga tgagtactaa gcctcggcgt tcttttggcg gaagcgttgc tttgacttgt     540

tgaaagccat tgtcacattt tacggtgaca tttttgtcgt cgctaaaatt attgcgaaga     600

attggataat cgctaggatg aagctcggtc aatagtgcgc gatcttgtga gcgcaacaat     660

tccgcggcaa ttaatggaga acccgcgtaa taacgtagtt ctttgccacc ataattgagt     720

tttttgatca tttttacata acgagcaata tcttcgggta aatctgtttg atcccacagg     780

cgtccaatac cttctttata ttccccccgtt ttttctgatt catttgagga taaacgataa   840

cgccccacac cagagtgcgt atccaaataa aaaaagcctt tttctttgag tttaagattt     900

tccaaaatga gcattaaaac aatatgtttc aagacatcgg catgattgcc agcgtgaaat     960

gagtgatgat aactcagcat aatatattcc ttatatattc cttatttgtt taataacgaa    1020

ggcgagccaa ttgactcgcc cgattacaca ctaaagtgcg gtcattttta gaagagttct    1080

tgtggttgcg tcgctggcgt attgccttca ttatttaagc gttgctgtaa ctcagtagga    1140

acataataac cacgctcttg catttccgaa agataggtac gtgtcggttc tgttcccgca    1200
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ataaaatatt ctttgcgccc accgtttgga gaaagcaaac ctgtcaaagt atcaatgttt   1260
ttttccacaa tttttggcgg tagcgacaat ttacgttctg gcttatcact caaagccgtt   1320
ttcatataag tgatccaagc aggcattgct gtttttgctc ctgcttctcc acgcccaagt   1380
actcgtttgt tatcatcaaa cccgacataa gttgtggtta ctaagtttgc accaaatccc   1440
gcataccaag ccacttttga actgttggta gtacctgttt taccgcctat atcgctacgt   1500
ttaatgcttt gtgcaatacg ccagctggtg cctttccagt ctaaaccttg ttcgccataa   1560
attgccgtat ttaaggcact acgaatgaga aaagcaagtt cgccactaat gacacgtggc   1620
gcatattcta ttttcgacga agcatttttt gcagcagcca ttaaatcaat cgcatcttct   1680
ttaagtgcgg tcatatttga ttgtaattct ggcagttcag gcacagtttc aggttgttga   1740
tctaattctt cgccattggt gctgtcatct gttggtttta aggcattctc gcctaaagga   1800
atattggcaa agccgttgat tttgtctttg gtttcgccat aaattacagg tatatcatta   1860
cattcaatgc aagcaatttt agggtttgca ataaataagt ctttacccgt gttatcttga   1920
attttttcaa tgatataagg ttcaatgagg aagccaccat tatcaaacac cgcataagct   1980
cgcgccattt ctaatggtgt gaaagaggct gcgccaagtg ctaaggcttc actggcaaaa   2040
tattgatcac gtttaaaacc aaaacgttgt aaaaattctg ctgtgaaatc aatacctgcc   2100
gtttggatag cacgaatagc aattatattt ttggattgac ctaatcctac gcgtaaacgc   2160
atcgggccat cataacgatc aggcgagttt ttcggttgcc acattttttg tcccggtttt   2220
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gccgcgtaaa taaatggttt gatagaagaa cccacttgaa ctaaagactg tgtggctcga   2340
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gaattaagag aaactaatgc tgaatttgct gcgggaattt gtcctaattg ccattcccca   2460
ttagcacgct gatgaatcca aatttgctcg ccgactttca caggattgct tctgcctgtc   2520
caacgcattg cattggttga taaggtcatt ttttccccag aagcgagcaa tatatcagca   2580
ccgcctttta caattccaat cactgccgca ggaataaatg gctctgaatc aggtagtttg   2640
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gcgccaccgc gataaccgtg acgcatatcg taatcaatca agttattacg cacagctttt   2760
tgggcttcag cttggtcttt tgaaagtaca gtggtaaata ctttataacc actggtgtaa   2820
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gctcgaaatt caaattttgc gccgtgatag ctcgccacaa tcggctcttt caatgcagca   2940
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cgttcttctg aacgttttaa agaataaagc gggttcattg ttgaaggtgc tttaggtaaa   3060
ccagcaataa tcgccatttc cgataaggtc aattcattca atgatttacc gaaataggtt   3120
tgtgctgccg ctgcaacacc ataagaacga tagcctaaaa agattttgtt taaataaagc   3180
tctaatattt cttgtttgtt gagagtattt tcgatttcta ccgcaagcac ggcttcacga   3240
gctttacgaa taatggtttt ttctgaggtt aagaaaaagt tacgcgctaa ttgttgagta   3300
atcgtacttg cgccttgtga tgcaccgcca ttactcactg cgacaaacaa tgcacgggca   3360
atgccgatag ggtctaatcc gtgatgatcg taaaaacgac tgtcttccgt cgctaaaaat   3420
gcgtcaatta agcgttgtgg cacatcggct aatttcactg gaatacggcg ttgctcaccc   3480
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acttcgccaa ttaatttacc gtcagccgta taaatctgca ttggttgctg taattcaacg   3540
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gctactaaac ctaaaataca taaagttaat agggtgttta atattaattt tgcgatccgc   3660
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ttaccgcact ttacaaatcg gcattcatcg taagcagagt tattttgatt ttgtgtggtt   3840
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agcaagcatt cccgcccact taacttggtc gaaagtatta atgttgccac aagtgttaaa   4020
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agaagaattg tggtttgatt atcgttctac cccgttaaag caaggttttc gattagaggt   4140
tactgcaatt cgtaaaagta gcgctcaaac ttatttgcaa gattttcagc catttaatat   4200
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gtcgatgaat ttattgcctt ggcgtactta tcaacatcaa aagcgtttac gtcgtttagc   4620
tttttatatc gctttattta tcttgcttgc tattaattta atgttggctt ttagcaattt   4680
gattgaacaa cagaaacaaa atttgcaggc acagcaaaag tcgtttgaac aacttaatca   4740
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accttttcaa caaggagaac tgaataaatt taaacaagat gccaataact taagcttgga   4920
aggtaacgcg caagatcaaa cagaatttga actgattcat caatttttaa agaaacattt   4980
tcccaatgtg aaattaagtc aggttcaacc tgaacaagat acattgtttt ttcactttga   5040
tgtggaacaa ggggcggaaa aatgaaagct ttttttaacg atccttttac tccttttgga   5100
aaatggctaa gtcagccttt ttatgtgcac ggtttaacct ttttattgct attaagtgcg   5160
gtgatttttc gccccgtttt agattatata gaggggagtt cacgtttcca tgaaattgaa   5220
aatgagttag cggtgaaacg ttcagaattg ttgcatcaac agaaaatttt aacctcttta   5280
caacagcagt cggaaagtcg aaaactttct ccagaactgg ctgcacaaat tattcctttg   5340
aataaacaaa ttcaacgttt agctgcgcgt aacggtttat ctcagcattt acgttgggaa   5400
atggggcaaa agcctatttt gcatttacag cttacaggtc attttgaaaa aacgaagaca   5460
tttttatccg cacttttggc taattcgtca cagctttctg taagtcggtt gcaatttatg   5520
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ctttcgataa aacacagcgt aaccgttctc agtttgataa cgcacaaaca gtaatggagc   5700
aaacagaaat aatttcctca gatgtgccta ataatctatg cggagcggat gaaaatcgcc   5760
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aagcggctga aattcctttg aacgctttaa aattggtggg ggtagtgatt tctaaagata   5820
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acggcagtca atctggcaaa ggtcaggttg caggaaatct tacgacaaat gaaccgcact   6360
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ttgaacctct ttcgatattg attcagcgtt ttaaatttca aaatcaattt tggattgacc   7620
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aattgccaga ggcaatcatt ccagtgcctt tatatcattt tcgtcagtgg cgacggggtt   7740
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gtcgtcagaa tttaaaaaat gccttttctc ttgctgtttc gaaaaatgaa tttccttatc   7920
gtcgtgttgc gttggtggat gatgtgatta ctactggttc tacactcaat gaaatctcaa   7980
aattgttgcg aaaattaggt gtggaggaga ttcaagtgtg gggctggca cgagcttaat    8040
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ataaagcact ggaaaaaaaa gcgcgataag cgtattattc ccgatacttt ctctcaagta   8100

tttaggacat aattatggaa caagcaaccc agcaaatcgc tatttctgat gccgcacaag   8160

cgcattttcg aaaactttta gacacccaag aagaaggaac gcatattcgt attttcgcgg   8220

ttaatcctgg tacgcctaat gcggaatgtg gcgtatctta ttgccccccg aatgccgtgg   8280

aagaaagcga tattgaaatg aaatataata ctttttctgc atttattgat gaagtgagtt   8340

tgcctttctt agaagaagca gaaattgatt atgttaccga agagcttggt gcgcaactga   8400

ccttaaaagc accgaatgcc aaaatgcgta aggtggctga tgatgcgcca ttgattgaac   8460

gtgttgaata tgtaattcaa actcaaatta acccacagct tgcaaatcac ggtggacgta   8520

taaccttaat tgaaattact gaagatggtt acgcagtttt acaatttggt ggtggctgta   8580

acggttgttc aatggtggat gttacgttaa aagatggggt agaaaaacaa cttgttagct   8640

tattcccgaa tgaattaaaa ggtgcaaaag atataactga gcatcaacgt ggcgaacatt   8700

cttattatta gtgagttata aaagaagatt tataatgacc gcacttttga aagtgcggtt   8760

atttttatgg agaaaaaatg aaaatacttc aacaagatga ttttggttat tggttgctta   8820

cacaaggttc taatctgtat ttagtgaata atgaattgcc ttttggtatc gctaaagata   8880

ttgatttgga aggattgcag gcaatgcaaa ttggggaatg gaaaaattat ccgttgtggc   8940

ttgtggctga gcaagaaagt gatgaacgag aatatgtgag tttgagtaac ttgctttcac   9000

tgccagagga tgaattccat atattaagcc gaggtgtgga aattaatcat tttctgaaaa   9060

cccataaatt ctgtggaaag tgcggtcata aaacacaaca                         9100
```

<210> SEQ ID NO 28
<211> LENGTH: 525
<212> TYPE: DNA
<213> ORGANISM: Moraxella catarrhalis

<400> SEQUENCE: 28

```
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ctttcctgca gattttggaa tcatatcgcc atcagcacca gtatggtttg accagtattt    180

aacgccatag acatgtgtaa aaaaattaaa taacggtgca agcatgagac caacggcacc    240

tgatgtacct tgtacgatga cctcacctgc tgtggcaacc ataccaagtc cattgcctgt    300

gatatttttg cgaaaagaca aacttaccac acagaccaag ccgatgattg agatgacaaa    360

ataaaaccaa tccaaatgcg tgtgagctgt tgtggtccaa aatccagtaa atagtgcaat    420

aaatccgcaa acaaaccaaa gtagcaccca gcttgttgtc caatcttttt taccaaagcc    480

tgtgatgtta tctaaaatat caattttcat cagattttcc ctaat                    525
```

<210> SEQ ID NO 29
<211> LENGTH: 466
<212> TYPE: DNA
<213> ORGANISM: Moraxella catarrhalis

<400> SEQUENCE: 29

```
taatgataac cagtcaagca agctcaaatc agggtcagcc tgttttgagc tttttatttt     60

ttgatcatca tgcttaagat tcactctgcc attttttttac aacctgcacc acaagtcatc    120

atcgcatttg caaaaatggt acaaacaagc cgtcagcgac ttaaacaaaa aaaggctcaa    180
```

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```
tctgcgtgtg tgcgttcact tttacaaatc accatgcacc gctttgacat tgttggtgaa    240

tttcatgacc atgcacaccc ttattatatt aactcaaata aaatacgcta ctttgtcagc    300

tttagccatt cagataatca agtcgctctc atcatcagct taacaccttg tgccattgac    360

atagaagtta acgatattaa atacagtgtg gttgaacgat actttcatcc caatgaaatt    420

tatctactta ctcaatttag ctctactgat aggcaacagc ttatta                   466
```

<210> SEQ ID NO 30
<211> LENGTH: 631
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 30

```
gatctttgat tttcattgag tattactctc tcttgtcact tctttctatt ttaccataaa     60

gtccagcctt tgaagaactt ttactagaag acaaggggct tctgtctcta tttgccatct    120

taggcatcaa aaaagagggg tcatccctct ttacgaattc aatgctacta gggtatccaa    180

atactggttg ttgatgactg ccaaaatata ggtatctgct ttcaagaggt catctggtcc    240

aaattcaaca tccaatgggg aattttcctg ctctcggaaa cccaaaatat tcagattgta    300

tttgccacgg aggtctaatt tacttcagac tttgacctgc ccaagactga ggaattttca    360

tctccacgat agacacattt ttatccaact gaaagacatc aacactatta tgaaaagaat    420

ggtctgtgct agagactgcc ccatttcata ctctggcgag ataaccgagt cagctccaat    480

cttttctagc actttcttag cggtctgact tttgacctta gcaataacag tcggtacccc    540

caaactctta cagtgcataa ccgcaagcac actcgactcc agattttcac ctgtcgcgac    600

tacaacggta tcgcaggtat caatccctgc t                                   631
```

<210> SEQ ID NO 31
<211> LENGTH: 3754
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 31

```
ccaatatttt ggtcagcata gtgttctttt tcagtggtaa cagcttgcaa tacttgagca     60

gaaatggcag atttatcaag gaaaaagtta acgtaaggtc ctgttgcgac aactttttca    120

aaggcttggc tgttcatttt ttcagccagt tcagccgcaa tcatttgtgg tgctttacgt    180

tcgacttttg caagagaaaa agcagggaaa gcaatgtctc ccatttctga gtttttaggg    240

gtttccagta actttaaaat agcctcttgg tccaggctat caatgatgct agataattcg    300

ctagcaatca attcttttgt attcattaag agctcctttt tggacttttc tactatttta    360

tcacaatttt aaagaaagaa gaaaaaattt ttgaaatctc ctgttttttt ggtataatat    420

ggttataaat atagttataa atatagttat aaatatgcac gcaagaggat tttatgagaa    480

aaagagatcg tcatcagtta ataaaaaaaa tgattactga ggagaaatta agtacacaaa    540

aagaaattca agatcggttg gaggcgcaca atgtttgtgt gacgcagaca accttgtctc    600

gtgatttgcg cgaaatcggc ttgaccaagg tcaagaaaaa tgatatggtg tattatgtac    660

tagtaaatga gacagaaaag attgatttgg tggaattttt gtctcatcat ttagaaggtg    720

ttgcaagagc agagtttacc ttggtgcttc ataccaaatt gggagaagcc tctgttttgg    780

caaatattgt agatgtaaac aaggatgaat ggattttagg aacagttgct ggtgccaata    840
```

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```
ccttattggt tatttgtcga gatcagcacg ttgccaaact catggaagat cgtttgctag    900
atttgatgaa agataagtaa ggtcttggga gttgctctca agacttattt ttgaaaagga    960
gagacagaaa atggcgatag aaaagctatc acccggcatg caacagtatg tggatattaa   1020
aaagcaatat ccagatgctt ttttgctctt tcggatgggt gatttttatg aattatttta   1080
tgaggatgcg gtcaatgctg cgcagattct ggaaatttcc ttaacgagtc gcaacaagaa   1140
tgccgacaat ccgatcccta tggcgggtgt tccctatcat tctgcccaac agtatatcga   1200
tgtcttgatt gagcagggtt ataaggtggc tatcgcagag cagatggaag atcctaaaca   1260
agcagttggg gttgttaaac gagaggttgt tcaggtcatt acgccaggga cagtggtcga   1320
tagcagtaag ccggacagtc agaataattt tttggtttcc atagaccgcg aaggcaatca   1380
atttggccta gcttatatgg atttggtgac gggtgacttt tatgtgacag gtcttttgga   1440
tttcacgctg gtttgtgggg aaatccgtaa cctcaaggct cgagaagtgg tgttgggtta   1500
tgacttgtct gaggaagaag aacaaatcct cagccgccag atgaatctgg tactctctta   1560
tgaaaaagaa agctttgaag accttcattt attggatttg cgattggcaa cggtggagca   1620
aacggcatct agtaagctgc tccagtatgt tcatcggact cagatgaggg aattgaacca   1680
cctcaaacct gttatccgct acgaaattaa ggatttcttg cagatggatt atgcgaccaa   1740
ggctagtctg gatttggttg agaatgctcg ctcaggtaag aaacaaggca gtcttttctg   1800
gcttttggat gaaaccaaaa cggctatggg gatgcgtctc ttgcgttctt ggattcatcg   1860
ccccttgatt gataaggaac gaatcgtcca acgtcaagaa gtagtgcagg tctttctcga   1920
ccatttcttt gagcgtagtg acttgacaga cagtctcaag ggtgtttatg acattgagcg   1980
cttggctagt cgtgtttctt ttggcaaaac caatccaaag gatctcttgc agttggcgac   2040
taccttgtct agtgtgccac ggattcgtgc gattttagaa gggatggagc aacctactct   2100
agcctatctc atcgcacaac tggatgcaat ccctgagttg gagagtttga ttagcgcagc   2160
gattgctcct gaagctcctc atgtgattac agatgggga attatccgga ctggatttga   2220
tgagacttta gacaagtatc gttgcgttct cagagaaggg actagctgga ttgctgagat   2280
tgaggctaag gagcgagaaa actctggtat cagcacgctc aagattgact acaataaaaa   2340
ggatggctac tattttcatg tgaccaattc gcaactggga aatgtgccag cccacttttt   2400
ccgcaaggcg acgctgaaaa actcagaacg ctttggaacc gaagaattag cccgtatcga   2460
gggagatatg cttgaggcgc gtgagaagtc agccaacctc gaatacgaaa tatttatgcg   2520
cattcgtgaa gaggtcggca agtacatcca gcgtttacaa gctctagccc aaggaattgc   2580
gacggttgat gtcttacaga gtctggcggt tgtggctgaa acccagcatt tgattcgacc   2640
tgagtttggt gacgattcac aaattgatat ccggaaaggg cgccatgctg tcgttgaaaa   2700
ggttatgggg gctcagacct atattccaaa tacgattcag atggcagaag ataccagtat   2760
tcaattggtt acagggccaa acatgagtgg gaagtctacc tatatgcgtc agttagccat   2820
gacggcggtt atggcccagc tgggttccta tgttcctgct gaaagcgccc atttaccgat   2880
ttttgatgcg atttttaccc gtatcggagc agcagatgac ttggtttcgg gtcagtcaac   2940
ctttatggtg gagatgatgg aggccaataa tgccatttcg catgcgacca agaactctct   3000
cattctcttt gatgaattgg gacgtggaac tgcaacttat gacgggatgg ctcttgctca   3060
gtccatcatc gaatatatcc atgagcacat cggagctaag accctctttg cgacccacta   3120
```

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ccatgagttg actagtctgg agtctagttt acaacacttg gtcaatgtcc acgtggcaac   3180

tttggagcag gatgggcagg tcaccttcct tcacaagatt gaaccgggac cagctgataa   3240

atcctacggt atccatgttg ccaagattgc tggcttgcca gcagaccttt tagcaagggc   3300

ggataagatt ttgactcagc tagagaatca aggaacagag agtcctcctc ccatgagaca   3360

aactagtgct gtcactgaac agatttcact ctttgatagg gcagaagagc atcctatcct   3420

agcagaatta gctaaactgg atgtgtataa tatgacacct atgcaggtta tgaatgtctt   3480

agtagagtta aaacagaaac tataaaacca agactcacta gttaatctag ctgtatcaag   3540

gagacttctt tgacaattct ccactttttt gctagaataa catcacacaa acagaatgaa   3600

aagggctgac gcattgtcgc tccctttgt ctattttta aggagaaagt atgctgattc     3660

agaaaataaa aacctacaag tggcaggccc tgcttcgctc ctgatgacag gcttgatggt   3720

tgctagttca cttctgcaac cgcgttatct gcag                               3754
```

```
<210> SEQ ID NO 32
<211> LENGTH: 1337
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 32

aacaaaataa aagaacttac ctattttcca tccaaaatgt ttagcaatca tcatctgcaa     60

ggcaacgtat tgcatggcat tgatgtgatg agcaactaat atgtcattag aacgttgcgt    120

caaactagca tctaaataaa gatcgaaatg cagttatcaa aaatgcaagc tcctatcggc    180

ccttgtttta attattactc acattgcctt aatgtattta cttgcttatt attaactttt    240

ttgctaagtt agtagcgtca gttattcatt gaaaggacat tattatgaaa attcttgtaa    300

caggctttga tccctttggc ggcgaagcta ttaatcctgc ccttgaagct atcaagaaat    360

tgccagcaac cattcatgga gcagaaatca aatgtattga agttccaacg gtttttcaaa    420

aatctgccga tgtgctccag cagcatatcg aaagctttca acctgatgca gtcctttgta    480

ttgggcaagc tggtggccgg actggactaa cgccagaacg cgttgccatt aatcaagacg    540

atgctcgcat tcctgataac gaagggaatc agcctattga tacacctatt cgtgcagatg    600

gtaaagcagc ttatttttca accttgccaa tcaaagcgat ggttgctgcc attcatcagg    660

ctgggcttcc tgcttctgtt tctaatacag ctggtacctt tgtttgcaat catttgatgt    720

atcaagccct ttacttagtg gataaatatt gtccaaatgc caaagctggg tttatgcata    780

ttccctttat gatggaacag gttgttgata aacctaatac agctgccatg aacctcgatg    840

atattacaag aggaattgag gctgctattt ttgccattgt cgatttcaaa gatcgttccg    900

atttaaaacg tgtagggggc gctactcact gactgtgacg ctactaaacc tattttaaaa    960

aaacagagat atgaactaac tctgtttttt ttgtgctaaa aatgaaagac ctagggaaac   1020

ttttcatcgg tctttctcaa ttgtcatctt aatctaatac tacttctaac atcagcgggt   1080

atagtttgcc agtaattaag aaacgttgtt gatctaaatg agcaatccca ttcaaaacat   1140

taaggtcagg gtaatgggac ttatcaagat ttaaggcttt taacaaagga ctaatatcat   1200

aggtggctac cacctttcca gaatcaggtt ggagtttgac aatagtattg gtttgccaaa   1260

tattggcata gagataacca tctacatact ctaattcgtt aagcattgag atagggacac   1320

tttctatagc aactagt                                                  1337
```

-continued

<210> SEQ ID NO 33
<211> LENGTH: 1837
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 33

tcatgtttga cagcttatca tcgataagct tacttttcga atcaggtcta tccttgaaac 60

aggtgcaaca tagattaggg catggagatt taccagacaa ctatgaacgt atatactcac 120

atcacgcaat cggcaattga tgacattgga actaaattca atcaatttgt tactaacaag 180

caactagatt gacaactaat tctcaacaaa cgttaattta acaacattca agtaactccc 240

accagctcca tcaatgctta ccgtaagtaa tcataactta ctaaaacctt gttacatcaa 300

ggtttttttct ttttgtcttg ttcatgagtt accataactt tctatattat tgacaactaa 360

attgacaact cttcaattat ttttctgtct actcaaagtt ttcttcattt gatatagtct 420

aattccacca tcacttcttc cactctctct accgtcacaa cttcatcatc tctcactttt 480

tcgtgtggta acacataatc aaatatcttt ccgtttttac gcactatcgc tactgtgtca 540

cctaaaatat accccttatc aatcgcttct ttaaactcat ctatatataa catatttcat 600

cctcctacct atctattcgt aaaaagataa aaataactat tgtttttttt gttattttat 660

aataaaatta ttaatataag ttaatgtttt ttaaaaatat acaattttat tctatttata 720

gttagctatt ttttcattgt tagtaatatt ggtgaattgt aataaccttt ttaaatctag 780

aggagaaccc agatataaaa tggaggaata ttaatggaaa acaataaaaa agtattgaag 840

aaaatggtat tttttgtttt agtgacattt cttggactaa caatctcgca agaggtattt 900

gctcaacaag accccgatcc aagccaactt cacagatcta gtttagttaa aaaccttcaa 960

aatatatatt ttctttatga gggtgaccct gttactcacg agaatgtgaa atctgttgat 1020

caacttttat ctcacgattt aatatataat gtttcagggc caaattatga taaattaaaa 1080

actgaactta agaaccaaga gatggcaact ttatttaagg ataaaaacgt tgatatttat 1140

ggtgtagaat attaccatct ctgttattta tgtgaaaatg cagaaaggag tgcatgtatc 1200

tacggagggg taacaaatca tgaagggaat catttagaaa ttcctaaaaa gatagtcgtt 1260

aaagtatcaa tcgatggtat ccaaagccta tcatttgata ttgaaacaaa taaaaaaatg 1320

gtaactgctc aagaattaga ctataaagtt agaaaatatc ttacagataa taagcaacta 1380

tatactaatg gaccttctaa atatgaaact ggatatataa agttcatacc taagaataaa 1440

gaaagttttt ggtttgattt tttccctgaa ccagaattta ctcaatctaa atatcttatg 1500

atatataaag ataatgaaac gcttgactca aacacaagcc aaattgaagt ctacctaaca 1560

accaagtaac tttttgcttt tggcaacctt acctactgct ggatttagaa attttattgc 1620

aattctttta ttaatgtaaa aaccgctcat ttgatgagcg gttttgtctt atctaaagga 1680

gctttacctc ctaatgctgc aaaattttaa atgttggatt tttgtatttg tctattgtat 1740

ttgatgggta atcccatttt tcgacagaca tcgtcgtgcc acctctaaca ccaaaatcat 1800

agacaggagc ttgtagctta gcaactattt tatcgtc 1837

<210> SEQ ID NO 34
<211> LENGTH: 841
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pneumoniae

-continued

<400> SEQUENCE: 34

```
gatcaatatg tccaagaaac cacatgttcc taagacaaga gctaacagac tggccgtcaa     60
taatagtatt gttctttttt tcatcattac tccttaacta gtgtttaact gattaattag    120
ccagtaaata gtttatcttt atttacacta tctgttaaga tatagtaaaa tgaaataaga    180
acaggacagt caaatcgatt tctaacaatg ttttagaagt agaggtatac tattctaatt    240
tcaatctact atattttgca cattttcata aaaaaaatga gaactagaac tcacattctg    300
ctctcatttt tcgttttccc gttctcctat cctgttttta ggagttagaa aatgctgcta    360
cctttactta ctctccttta ataaagccaa tagtttttca gcttctgcca taatagtatt    420
gttgtcctgg gtgccaaata gtaaattatt ttttaatcct gtgagagtct ctttggcatt    480
ggacttgata attggattct ggatttttcc aagtaaatct tcagcctctc tcagttttct    540
taacctttca gtctcgacct gaggttcttc tgattcctct ggtgattctt ctggtgattc    600
ttcttctggt tcctctgttg gttttggaga ctctggtttc tcgctttgcg gtttctcttc    660
tcgaggggtt tcttcctcag gtttttctgt ctgaggtttc tcctcgtttg gtttttccgt    720
ttgattggta tcagcttgac cattttttgtt tctttgaaca tggtcgctag cgttaccaaa    780
accattatct gaatgcgacg ttcgtttgga tgttcgacat agtacttgac agtcgccaaa    840
a                                                                    841
```

<210> SEQ ID NO 35
<211> LENGTH: 4500
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 35

```
gatcaggaca gtcaaatcga tttctaacaa tgttttagaa gtagatgtgt actattctag     60
tttcaatcta ttatatttat agaatttttt gttgctagat ttgtcaaatt gcttaaaata    120
atttttttca gaaagcaaaa gccgatacct atcgagtagg gtagttcttg ctatcgtcag    180
gcttgtctgt aggtgttaac acttttcaaa aatctcttca aacaacgtca gctttgcctt    240
gccgtatata tgttactgac ttcgtcagtt ctatctgcca cctcaaaacg gtgttttgag    300
ctgacttcgt cagttctatc cacaacctca aaacagtgtt ttgagctgac ttcgtcagtt    360
ctatccacaa cctcaaaaca gtgttttgag ctgactttgt cagtcttatc tacaacctca    420
aaacagtgtt ttgagcatca tgcggctagc ttcttagttt gctctttgat tttcattgag    480
tataaaaaca gatgagtttc tgttttcttt ttatggacta taaatgttca gctgaaacta    540
ctttcaagga cattattata taaaagaatt ttttgaaact aaaatctact atattacact    600
atattgaaag cgttttaaaa atgaggtata ataaatttac taacacttat aaaaagtgat    660
agaatctatc tttatgtata tttaaagata gattgctgta aaaatagtag tagctatgcg    720
aaataacaga tagagagaag ggattgaagc ttagaaaagg ggaataatat gatatttaag    780
gcattcaaga caaaaaagca gagaaaaaga caagttgaac tacttttgac agttttttttc    840
gacagttttc tgattgattt atttcttcac ttatttggga ttgtcccctt taagctggat    900
aagattctga ttgtgagctt gattatattt cccattattt ctacaagtat ttatgcttat    960
gaaaagctat ttgaaaaagt gttcgataag gattgagcag gaagtatggt gtaaatagca   1020
taagctgatg tccatcattt gcttataaag agatatttta gtttaattgc agcggtgtcc   1080
```

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tggtagataa actagattgg caggagtctg attggagaaa ggagagggga aatttggcac   1140
caatttgaga tagtttgttt agttcatttt tgtcatttaa atgaactgta gtaaaagaaa   1200
gttaataaaa gacaaactaa gtgcattttc tggaataaat gtcttatttc agaaatcggg   1260
atatagatat agagaggaac agtatgaatc ggagtgttca agaacgtaag tgtcgttata   1320
gcattaggaa actatcggta ggagcggttt ctatgattgt aggagcagtg gtatttggaa   1380
cgtctcctgt tttagctcaa gaaggggcaa gtgagcaacc tctggcaaat gaaactcaac   1440
tttcgggggga gagctcaacc ctaactgata cagaaaagag ccagccttct tcagagactg   1500
aactttctgg caataagcaa gaacaagaaa ggaaagataa gcaagaagaa aaaattccaa   1560
gagattacta tgcacgagat ttggaaaatg tcgaaacagt gatagaaaaa gaagatgttg   1620
aaaccaatgc ttcaaatggt cagagagttg atttatcaag tgaactagat aaactaaaga   1680
aacttgaaaa cgcaacagtt cacatggagt ttaagccaga tgccaaggcc ccagcattct   1740
ataatctctt ttctgtgtca agtgctacta aaaaagatga gtacttcact atggcagttt   1800
acaataatac tgctactcta gaggggcgtg gttcggatgg gaaacagttt tacaataatt   1860
acaacgatgc acccttaaaa gttaaaccag gtcagtggaa ttctgtgact ttcacagttg   1920
aaaaaccgac agcagaacta cctaaaggcc gagtgcgcct ctacgtaaac ggggtattat   1980
ctcgaacaag tctgagatct ggcaatttca ttaaagatat gccagatgta acgcatgtgc   2040
aaatcggagc aaccaagcgt gccaacaata cggtttgggg gtcaaatcta cagattcgga   2100
atctcactgt gtataatcgt gctttaacac cagaagaggt acaaaaacgt agtcaacttt   2160
ttaaacgctc agatttagaa aaaaaactac ctgaaggagc ggctttaaca gagaaaacgg   2220
acatattcga aagcgggcgt aacggtaaac caaataaaga tggaatcaag agttatcgta   2280
ttccagcact tctcaagaca gataaaggaa ctttgatcgc aggtgcagat gaacgccgtc   2340
tccattcgag tgactggggt gatatcggta tggtcatcag acgtagtgaa gataatggta   2400
aaacttgggg tgaccgagta accattacca acttacgtga caatccaaaa gcttctgacc   2460
catcgatcgg ttcaccagtg aatatcgata tggtgttggt tcaagatcct gaaaccaaac   2520
gaatcttttc tatctatgac atgttcccag aagggaaggg aatctttgga atgtcttcac   2580
aaaaagaaga agcctacaaa aaaatcgatg gaaaaaccta tcaaatcctc tatcgtgaag   2640
gagaaaaggg agcttatacc attcgagaaa atggtactgt ctatacacca gatggtaagg   2700
cgacagacta tcgcgttgtt gtagatcctg ttaaaccagc ctatagcgac aagggggatc   2760
tatacaaggg taaccaatta ctaggcaata tctacttcac aacaaacaaa acttctccat   2820
ttagaattgc caaggatagc tatctatgga tgtcctacag tgatgacgac gggaagacat   2880
ggtcagcgcc tcaagatatt actccgatgg tcaaagccga ttggatgaaa ttcttgggtg   2940
taggtcctgg aacaggaatt gtacttcgga atgggcctca caagggacgg attttgatac   3000
cggtttatac gactaataat gtatctcact taaatggctc gcaatcttct cgtatcatct   3060
attcagatga tcatggaaaa acttggcatg ctggagaagc ggtcaacgat aaccgtcagg   3120
tagacggtca aaagatccac tcttctacga tgaacaatag acgtgcgcaa aatacagaat   3180
caacggtggt acaactaaac aatggagatg ttaaactctt tatgcgtggt ttgactggag   3240
atcttcaggt tgctacaagt aaagacggag gagtgacttg ggagaaggat atcaaacgtt   3300
atccacaggt taaagatgtc tatgttcaaa tgtctgctat ccatacgatg cacgaaggaa   3360
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aagaatacat catcctcagt aatgcaggtg gaccgaaacg tgaaaatggg atggtccact   3420
tggcacgtgt cgaagaaaat ggtgagttga cttggctcaa acacaatcca attcaaaaag   3480
gagagtttgc ctataattcg ctccaagaat taggaaatgg ggagtatggc atcttgtatg   3540
aacatactga aaaaggacaa aatgcctata ccctatcatt tagaaaattt aattgggact   3600
ttttgagcaa agatctgatt tctcctaccg aagcgaaagt gaagcgaact agagagatgg   3660
gcaaaggagt tattggcttg gagttcgact cagaagtatt ggtcaacaag gctccaaccc   3720
ttcaattggc aaatggtaaa acagcacgct tcatgaccca gtatgataca aaaaccctcc   3780
tatttacagt ggattcagag gatatgggtc aaaaagttac aggtttggca gaaggtgcaa   3840
ttgaaagtat gcataattta ccagtctctg tggcgggcac taagctttcg aatggaatga   3900
acggaagtga agctgctgtt catgaagtgc cagaatacac aggcccatta gggacatccg   3960
gcgaagagcc agctccaaca gtcgagaagc cagaatacac aggcccacta gggacatccg   4020
gcgaagagcc agccccgaca gtcgagaagc cagaatacac aggcccacta gggacagctg   4080
gtgaagaagc agctccaaca gtcgagaagc cagaatttac agggggagtt aatggtacag   4140
agccagctgt tcatgaaatc gcagagtata agggatctga ttcgcttgta actcttacta   4200
caaaagaaga ttatacttac aaagctcctc ttgctcagca ggcacttcct gaaacaggaa   4260
acaaggagag tgacctccta gcttcactag gactaacagc tttcttcctt ggtctgttta   4320
cgctagggaa aaagagagaa caataagaga agaattctaa acatttgatt ttgtaaaaat   4380
agaaggagat agcaggtttt caagcctgct atcttttttt gatgacattc aggctgatac   4440
gaaatcataa gaggtctgaa actactttca gagtagtctg ttctataaaa tatagtagat   4500
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<210> SEQ ID NO 36
<211> LENGTH: 705
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus epidermidis

<400> SEQUENCE: 36

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tcttgagatg tatagaattc aaaatattta ccatttgcat agtctgattg ctcaaagtct    120
tgatactttt ctccacgctc ttttgcaatt tccattgaac gttcgatgga ataatagttc    180
ataatcataa agaatatatt agcaaagtct tttgcttctt cagattcata gccaatttta    240
tttttagcta gataaccatg taagttcatt actcctagtc caacagaatg tagttcacta    300
ttcgcttttt ttacacctgg tgcattttga atatttgctt catcacttac aactgtaaga    360
gcatccatac ctgtgaacac agaatctctg aatttacctg attccataac attcactata    420
ttcaatgagc ctaagttaca tgaaatatct cttttaattt catcttcaat tccatagtcg    480
ttaattactg atgtctcttg taattggaaa atttcagtac ataaattact cattttaatt    540
tgcccaatat ttgaattcgc atgtactttg tttgcattat ctttaaacat aagatatgga    600
taaccagact gtaattgtgt ttgtgcaatc atatttaaca tttcacgtgc gtcttttttc    660
tttttatcga tttcgaaccc ggggtaccga attcctcgag tctag                    705
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<210> SEQ ID NO 37
<211> LENGTH: 442
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus aureus

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<400> SEQUENCE: 37

gatcaatctt tgtcggtaca cgatattctt cacgactaaa taaacgctca ttcgcgattt 60

tataaatgaa tgttgataac aatgttgtat tatctactga aatctcatta cgttgcatcg 120

gaaacattgt gttctgtatg taaaagccgt cttgataatc tttagtagta ccgaagctgg 180

tcatacgaga gttatatttt ccagccaaaa cgatattttt ataatcatta cgtgaaaaag 240

gtttcccttc attatcacac aaatatttta gcttttcagt ttctatatca actgtagctt 300

ctttatccat acgttgaata attgtacgat tctgacgcac catcttttgc acacctttaa 360

tgttatttgt tttaaaagca tgaataagtt tttcaacaca acgatgtgaa tcttctaaga 420

agtcaccgta aaatgaagga tc 442

<210> SEQ ID NO 38
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Enterococcus faecalis

<400> SEQUENCE: 38

gcaatacagg gaaaaatgtc 20

<210> SEQ ID NO 39
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Enterococcus faecalis

<400> SEQUENCE: 39

cttcatcaaa caattaactc 20

<210> SEQ ID NO 40
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Enterococcus faecalis

<400> SEQUENCE: 40

gaacagaaga agccaaaaaa 20

<210> SEQ ID NO 41
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Enterococcus faecalis

<400> SEQUENCE: 41

gcaatcccaa ataatacggt 20

<210> SEQ ID NO 42
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 42

gctttccagc gtcatattg 19

<210> SEQ ID NO 43
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 43

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gatctcgaca aaatggtga 19

<210> SEQ ID NO 44
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 44

cacccgcttg cgtggcaagc tgccc 25

<210> SEQ ID NO 45
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 45

cgtttgtgga ttccagttcc atccg 25

<210> SEQ ID NO 46
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 46

tcacccgctt gcgtggc 17

<210> SEQ ID NO 47
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 47

ggaactggaa tccacaaac 19

<210> SEQ ID NO 48
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 48

tgaagcactg gccgaaatgc tgcgt 25

<210> SEQ ID NO 49
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 49

gatgtacagg attcgttgaa ggctt 25

<210> SEQ ID NO 50
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 50

tagcgaaggc gtagcagaaa ctaac 25

<210> SEQ ID NO 51
<211> LENGTH: 25
<212> TYPE: DNA

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<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 51

gcaacccgaa ctcaacgccg gattt 25

<210> SEQ ID NO 52
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 52

atacacaagg gtcgcatctg cggcc 25

<210> SEQ ID NO 53
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 53

tgcgtatgca ttgcagacct tgtggc 26

<210> SEQ ID NO 54
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 54

gctttcactg gatatcgcgc ttggg 25

<210> SEQ ID NO 55
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 55

gcaacccgaa ctcaacgcc 19

<210> SEQ ID NO 56
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 56

gcagatgcga cccttgtgt 19

<210> SEQ ID NO 57
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 57

gtggtgtcgt tcagcgcttt cac 23

<210> SEQ ID NO 58
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 58

gcgatattca caccctacgc agcca 25

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<210> SEQ ID NO 59
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 59

gtcgaaaatg ccggaagagg tatacg 26

<210> SEQ ID NO 60
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 60

actgagctgc agaccggtaa aactca 26

<210> SEQ ID NO 61
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 61

gacagtcagt tcgtcagcc 19

<210> SEQ ID NO 62
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 62

cgtagggtgt gaatatcgc 19

<210> SEQ ID NO 63
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 63

cgtgatggat attcttaacg aagggc 26

<210> SEQ ID NO 64
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 64

accaaactgt tgagccgcct gga 23

<210> SEQ ID NO 65
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 65

gtgatcgccc ctcatctgct act 23

<210> SEQ ID NO 66
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

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<400> SEQUENCE: 66

cgcccttcgt taagaatatc catcac 26

<210> SEQ ID NO 67
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 67

tcgcccctca tctgctact 19

<210> SEQ ID NO 68
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 68

gatcgtgatg gatattctt 19

<210> SEQ ID NO 69
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 69

caggaagatg ctgcaccggt tgttg 25

<210> SEQ ID NO 70
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Proteus mirabilis

<400> SEQUENCE: 70

tggttcactg actttgcgat gtttc 25

<210> SEQ ID NO 71
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Proteus mirabilis

<400> SEQUENCE: 71

tcgaggatgg catgcactag aaaat 25

<210> SEQ ID NO 72
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Proteus mirabilis

<400> SEQUENCE: 72

cgctgattag gtttcgctaa aatcttatta 30

<210> SEQ ID NO 73
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Proteus mirabilis

<400> SEQUENCE: 73

ttgatcctca ttttattaat cacatgacca 30

<210> SEQ ID NO 74

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<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Proteus mirabilis

<400> SEQUENCE: 74

gaaacatcgc aaagtcagt 19

<210> SEQ ID NO 75
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Proteus mirabilis

<400> SEQUENCE: 75

ataaaatgag gatcaagttc 20

<210> SEQ ID NO 76
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Proteus mirabilis

<400> SEQUENCE: 76

ccgcctttag cattaattgg tgtttatagt 30

<210> SEQ ID NO 77
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Proteus mirabilis

<400> SEQUENCE: 77

cctattgcag ataccttaaa tgtcttgggc 30

<210> SEQ ID NO 78
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 78

agtaaaatga aataagaaca ggacag 26

<210> SEQ ID NO 79
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 79

aaaacaggat aggagaacgg gaaaa 25

<210> SEQ ID NO 80
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Proteus mirabilis

<400> SEQUENCE: 80

ttgagtgatg atttcactga ctccc 25

<210> SEQ ID NO 81
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Proteus mirabilis

<400> SEQUENCE: 81

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gtcagacagt gatgctgacg acaca 25

<210> SEQ ID NO 82
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Proteus mirabilis

<400> SEQUENCE: 82

tggttgtcat gctgtttgtg tgaaaat 27

<210> SEQ ID NO 83
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 83

cgagcgggtg gtgttcatc 19

<210> SEQ ID NO 84
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 84

caagtcgtcg tcggaggga 19

<210> SEQ ID NO 85
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 85

tcgctgttca tcaagaccc 19

<210> SEQ ID NO 86
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 86

ccgagaacca gacttcatc 19

<210> SEQ ID NO 87
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 87

aatgcggctg tacctcggcg ctggt 25

<210> SEQ ID NO 88
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 88

ggcggagggc cagttgcacc tgcca 25

<210> SEQ ID NO 89
<211> LENGTH: 25
<212> TYPE: DNA

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<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 89

agccctgctc ctcggcagcc tctgc 25

<210> SEQ ID NO 90
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 90

tggcttttgc aaccgcgttc aggtt 25

<210> SEQ ID NO 91
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 91

gcgcccgcga gggcatgctt cgatg 25

<210> SEQ ID NO 92
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 92

acctgggcgc caactacaag ttcta 25

<210> SEQ ID NO 93
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 93

ggctacgctg ccgggctgca ggccg 25

<210> SEQ ID NO 94
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 94

ccgatctaca ccatcgagat gggcg 25

<210> SEQ ID NO 95
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 95

gagcgcggct atgtgttcgt cggct 25

<210> SEQ ID NO 96
<211> LENGTH: 29
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus saprophyticus

<400> SEQUENCE: 96

cgtttttacc cttacctttt cgtactacc 29

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<210> SEQ ID NO 97
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus saprophyticus

<400> SEQUENCE: 97

tcaggcagag gtagtacgaa aaggtaaggg 30

<210> SEQ ID NO 98
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus saprophyticus

<400> SEQUENCE: 98

cgtttttacc cttacctttt cgtact 26

<210> SEQ ID NO 99
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus saprophyticus

<400> SEQUENCE: 99

atcgatcatc acattccatt tgttttta 28

<210> SEQ ID NO 100
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus saprophyticus

<400> SEQUENCE: 100

caccaagttt gacacgtgaa gattcat 27

<210> SEQ ID NO 101
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus saprophyticus

<400> SEQUENCE: 101

atgagtgaag cggagtcaga ttatgtgcag 30

<210> SEQ ID NO 102
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus saprophyticus

<400> SEQUENCE: 102

cgctcattac gtacagtgac aatcg 25

<210> SEQ ID NO 103
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus saprophyticus

<400> SEQUENCE: 103

ctggttagct tgactcttaa caatcttgtc 30

<210> SEQ ID NO 104
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus saprophyticus

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<400> SEQUENCE: 104

gacgcgattg tcactgtacg taatgagcga 30

<210> SEQ ID NO 105
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Haemophilus influenzae

<400> SEQUENCE: 105

gcgtcagaaa aagtaggcga aatgaaag 28

<210> SEQ ID NO 106
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Haemophilus influenzae

<400> SEQUENCE: 106

agcggctcta tcttgtaatg acaca 25

<210> SEQ ID NO 107
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Haemophilus influenzae

<400> SEQUENCE: 107

gaaacgtgaa ctcccctcta tataa 25

<210> SEQ ID NO 108
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Moraxella catarrhalis

<400> SEQUENCE: 108

gccccaaaac aatgaaacat atggt 25

<210> SEQ ID NO 109
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Moraxella catarrhalis

<400> SEQUENCE: 109

ctgcagattt tggaatcata tcgcc 25

<210> SEQ ID NO 110
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Moraxella catarrhalis

<400> SEQUENCE: 110

tggtttgacc agtatttaac gccat 25

<210> SEQ ID NO 111
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Moraxella catarrhalis

<400> SEQUENCE: 111

caacggcacc tgatgtacct tgtac 25

<210> SEQ ID NO 112

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<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Moraxella catarrhalis

<400> SEQUENCE: 112

ggcacctgat gtaccttg 18

<210> SEQ ID NO 113
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Moraxella catarrhalis

<400> SEQUENCE: 113

aacagctcac acgcatt 17

<210> SEQ ID NO 114
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Moraxella catarrhalis

<400> SEQUENCE: 114

ttacaacctg caccacaagt catca 25

<210> SEQ ID NO 115
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Moraxella catarrhalis

<400> SEQUENCE: 115

gtacaaacaa gccgtcagcg actta 25

<210> SEQ ID NO 116
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Moraxella catarrhalis

<400> SEQUENCE: 116

caatctgcgt gtgtgcgttc act 23

<210> SEQ ID NO 117
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Moraxella catarrhalis

<400> SEQUENCE: 117

gctactttgt cagctttagc cattca 26

<210> SEQ ID NO 118
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Moraxella catarrhalis

<400> SEQUENCE: 118

tgttttgagc tttttatttt ttga 24

<210> SEQ ID NO 119
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Moraxella catarrhalis

<400> SEQUENCE: 119

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cgctgacggc ttgtttgtac ca 22

<210> SEQ ID NO 120
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 120

tctgtgctag agactgcccc atttc 25

<210> SEQ ID NO 121
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 121

cgatgtcttg attgagcagg gttat 25

<210> SEQ ID NO 122
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
Oligonucleotide

<400> SEQUENCE: 122

atcccacctt aggcggctgg ctcca 25

<210> SEQ ID NO 123
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
Oligonucleotide

<400> SEQUENCE: 123

acgtcaagtc atcatggccc ttacgagtag g 31

<210> SEQ ID NO 124
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
Oligonucleotide

<400> SEQUENCE: 124

gtgtgacggg cggtgtgtac aaggc 25

<210> SEQ ID NO 125
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
Oligonucleotide

<400> SEQUENCE: 125

gagttgcaga ctccaatccg gactacga 28

<210> SEQ ID NO 126

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<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
Oligonucleotide

<400> SEQUENCE: 126

ggaggaaggt ggggatgacg 20

<210> SEQ ID NO 127
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
Oligonucleotide

<400> SEQUENCE: 127

atggtgtgac gggcggtgtg 20

<210> SEQ ID NO 128
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
Oligonucleotide

<400> SEQUENCE: 128

ccctatacat caccttgcgg tttagcagag ag 32

<210> SEQ ID NO 129
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
Oligonucleotide

<400> SEQUENCE: 129

ggggggacca tcctccaagg ctaaatac 28

<210> SEQ ID NO 130
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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Oligonucleotide

<400> SEQUENCE: 130

cgtccacttt cgtgtttgca gagtgctgtg tt 32

<210> SEQ ID NO 131
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 131

caggagtacg gtgattttta 20

<210> SEQ ID NO 132
<211> LENGTH: 20

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<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 132

atttctggtt tggtcataca 20

<210> SEQ ID NO 133
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Proteus mirabilis

<400> SEQUENCE: 133

cgggagtcag tgaaatcatc 20

<210> SEQ ID NO 134
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Proteus mirabilis

<400> SEQUENCE: 134

ctaaaatcgc cacacctctt 20

<210> SEQ ID NO 135
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 135

gcagcgtggt gtcgttca 18

<210> SEQ ID NO 136
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 136

agctggcaac ggctggtc 18

<210> SEQ ID NO 137
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 137

attcacaccc tacgcagcca 20

<210> SEQ ID NO 138
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 138

atccggcagc atctctttgt 20

<210> SEQ ID NO 139
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus saprophyticus

<400> SEQUENCE: 139

ctggttagct tgactcttaa caatc 25

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<210> SEQ ID NO 140
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus saprophyticus

<400> SEQUENCE: 140

tcttaacgat agaatggagc aactg 25

<210> SEQ ID NO 141
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 141

tgaaaattct tgtaacaggc 20

<210> SEQ ID NO 142
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 142

ggccaccagc ttgcccaata 20

<210> SEQ ID NO 143
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 143

atattttctt tatgagggtg 20

<210> SEQ ID NO 144
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 144

atccttaaat aaagttgcca 20

<210> SEQ ID NO 145
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus epidermidis

<400> SEQUENCE: 145

atcaaaaagt tggcgaacct tttca 25

<210> SEQ ID NO 146
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus epidermidis

<400> SEQUENCE: 146

caaaagagcg tggagaaaag tatca 25

<210> SEQ ID NO 147
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus epidermidis

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<400> SEQUENCE: 147

tctcttttaa tttcatcttc aattccatag 30

<210> SEQ ID NO 148
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus epidermidis

<400> SEQUENCE: 148

aaacacaatt acagtctggt tatccatatc 30

<210> SEQ ID NO 149
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 149

cttcatttta cggtgacttc ttagaagatt 30

<210> SEQ ID NO 150
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 150

tcaactgtag cttctttatc catacgttga 30

<210> SEQ ID NO 151
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 151

atattttagc ttttcagttt ctatatcaac 30

<210> SEQ ID NO 152
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 152

aatctttgtc ggtacacgat attcttcacg 30

<210> SEQ ID NO 153
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 153

cgtaatgaga tttcagtaga taatacaaca 30

<210> SEQ ID NO 154
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Haemophilus influenzae

<400> SEQUENCE: 154

tttaacgatc cttttactcc ttttg 25

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<210> SEQ ID NO 155
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Haemophilus influenzae

<400> SEQUENCE: 155

actgctgttg taaagaggtt aaaat 25

<210> SEQ ID NO 156
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 156

atttggtgac gggtgacttt 20

<210> SEQ ID NO 157
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 157

gctgaggatt tgttcttctt 20

<210> SEQ ID NO 158
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 158

gagcggtttc tatgattgta 20

<210> SEQ ID NO 159
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 159

atctttcctt tcttgttctt 20

<210> SEQ ID NO 160
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Moraxella catarrhalis

<400> SEQUENCE: 160

gctcaaatca gggtcagc 18

<210> SEQ ID NO 161
<211> LENGTH: 861
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 161

atgagtattc aacatttccg tgtcgccctt attccctttt ttgcggcatt ttgccttcct 60

gtttttgctc acccagaaac gctggtgaaa gtaaaagatg ctgaagatca gttgggtgca 120

cgagtgggtt acatcgaact ggatctcaac agcggtaaga tccttgagag ttttcgcccc 180

gaagaacgtt ttccaatgat gagcactttt aaagttctgc tatgtggcgc ggtattatcc 240

cgtgttgacg ccgggcaaga gcaactcggt cgccgcatac actattctca gaatgacttg 300

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gttgagtact caccagtcac agaaaagcat cttacggatg gcatgacagt aagagaatta    360

tgcagtgctg ccataaccat gagtgataac actgcggcca acttacttct gacaacgatc    420

ggaggaccga aggagctaac cgcttttttg cacaacatgg gggatcatgt aactcgcctt    480

gatcgttggg aaccggagct gaatgaagcc ataccaaacg acgagcgtga caccacgatg    540

cctgcagcaa tggcaacaac gttgcgcaaa ctattaactg gcgaactact tactctagct    600

tcccggcaac aattaataga ctggatggag gcggataaag ttgcaggacc acttctgcgc    660

tcggcccttc cggctggctg gtttattgct gataaatctg gagccggtga gcgtgggtct    720

cgcggtatca ttgcagcact ggggccagat ggtaagccct cccgtatcgt agttatctac    780

acgacgggga gtcaggcaac tatggatgaa cgaaatagac agatcgctga gataggtgcc    840

tcactgatta agcattggta a                                              861
```

<210> SEQ ID NO 162
<211> LENGTH: 918
<212> TYPE: DNA
<213> ORGANISM: Pasteurella haemolytica

<400> SEQUENCE: 162

```
atgttaaata agttaaaaat cggcacatta ttattgctga cattaacggc ttgttcgccc     60

aattctgttc attcggtaac gtctaatccg cagcctgcta gtgcgcctgt gcaacaatca    120

gccacacaag ccacctttca acagactttg gcgaatttgg aacagcagta tcaagcccga    180

attggcgttt atgtatggga tacagaaacg ggacattctt tgtcttatcg tgcagatgaa    240

cgctttgctt atgcgtccac tttcaaggcg ttgttggctg ggcggtgtt gcaatcgctg     300

cctgaaaaag atttaaatcg taccatttca tatagccaaa aagatttggt tagttattct    360

cccgaaaccc aaaaatacgt tggcaaaggc atgacgattg cccaattatg tgaagcagcc    420

gtgcggttta gcgacaacag cgcgaccaat ttgctgctca aagaattggg tggcgtggaa    480

caatatcaac gtattttgcg acaattaggc gataacgtaa cccataccaa tcggctagaa    540

cccgatttaa atcaagccaa acccaacgat attcgtgata cgagtacacc caaacaaatg    600

gcgatgaatt taaatgcgta tttattgggc aacacattaa ccgaatcgca aaaaacgatt    660

ttgtggaatt ggttggacaa taacgcaaca ggcaatccat tgattcgcgc tgctacgcca    720

acatcgtgga aagtgtacga taaaagcggg gcgggtaaat atggtgtacg caatgatatt    780

gcggtggttc gcataccaaa tcgcaaaccg attgtgatgg caatcatgag tacgcaattt    840

accgaagaag ccaaattcaa caataaatta gtagaagatg cagcaaagca agtatttcat    900

actttacagc tcaactaa                                                  918
```

<210> SEQ ID NO 163
<211> LENGTH: 864
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 163

```
atgcgttata ttcgcctgtg tattatctcc ctgttagcca ccctgccgct ggcggtacac     60

gccagcccgc agccgcttga gcaaattaaa ctaagcgaaa gccagctgtc gggccgcgta    120

ggcatgatag aaatggatct ggccagcggc cgcacgctga ccgcctggcg cgccgatgaa    180

cgctttccca tgatgagcac ctttaaagta gtgctctgcg gcgcagtgct ggcgcgggtg    240
```

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gatgccggtg acgaacagct ggagcgaaag atccactatc gccagcagga tctggtggac    300
tactcgccgg tcagcgaaaa acaccttgcc gacgcaatga cggtcggcga actctgcgcc    360
gccgccatta ccatgagcga taacagcgcc gccaatctgc tactggccac cgtcggcggc    420
cccgcaggat tgactgcctt tttgcgccag atcggcgaca acgtcacccg ccttgaccgc    480
tgggaaacgg aactgaatga ggcgcttccc ggcgacgccc gcgacaccac taccccggcc    540
agcatggccg cgaccctgcg caacgttggc ctgaccagcc agcgtctgag cgcccgttcg    600
caacggcagc tgctgcagtg gatggtggac gatcgggtcg ccggaccgtt gatccgctcc    660
gtgctgccgg cgggctggtt tatcgccgat aagaccggag ctggcgagcg gggtgcgcgc    720
gggattgtcg ccctgcttgg cccgaataac aaagcagagc gcattgtggt gatttatctg    780
cgggataccc cggcgagcat ggccgagcga aatcagcaaa tcgccgggat cggcaaggcg    840
ctgtacgagc actggcaacg ctaa                                           864
```

```
<210> SEQ ID NO 164
<211> LENGTH: 534
<212> TYPE: DNA
<213> ORGANISM: Klebsiella pneumoniae

<400> SEQUENCE: 164

atggacacaa cgcaggtcac attgatacac aaaattctag ctgcggcaga tgagcgaaat     60
ctgccgctct ggatcggtgg gggctgggcg atcgatgcac ggctagggcg tgtaacacgc    120
aagcacgatg atattgatct gacgtttccc ggcgagaggc gcggcgagct cgaggcaata    180
gttgaaatgc tcggcgggcg cgtcatggag gagttggact atggattctt agcggagatc    240
ggggatgagt tacttgactg cgaacctgct tggtgggcag acgaagcgta tgaaatcgcg    300
gaggctccgc agggctcgtg cccagaggcg gctgagggcg tcatcgccgg gcggccagtc    360
cgttgtaaca gctgggaggc gatcatctgg gattactttt actatgccga tgaagtacca    420
ccagtggact ggcctacaaa gcacatagag tcctacaggc tcgcatgcac ctcactcggg    480
gcggaaaagg ttgaggtctt gcgtgccgct ttcaggtcgc gatatgcggc ctaa          534
```

```
<210> SEQ ID NO 165
<211> LENGTH: 465
<212> TYPE: DNA
<213> ORGANISM: Unknown Organism
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown Organism:
      Enterobacteriaceae

<400> SEQUENCE: 165

atgggcatca ttcgcacatg taggctcggc cctgaccaag tcaaatccat gcgggctgct     60
cttgatcttt tcggtcgtga gttcggagac gtagccacct actcccaaca tcagccggac    120
tccgattacc tcgggaactt gctccgtagt aagacattca tcgcgcttgc tgccttcgac    180
caagaagcgg ttgttggcgc tctcgcggct tacgttctgc ccaggtttga gcagccgcgt    240
agtgagatct atatctatga tctcgcagtc tccggcgagc accggaggca gggcattgcc    300
accgcgctca tcaatctcct caagcatgag gccaacgcgc ttggtgctta tgtgatctac    360
gtgcaagcag attacggtga cgatcccgca gtggctctct atacaaagtt gggcatacgg    420
gaagaagtga tgcactttga tatcgaccca agtaccgcca cctaa                    465
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<210> SEQ ID NO 166
<211> LENGTH: 861
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 166

atgcatacgc ggaaggcaat aacggaggcg cttcaaaaac tcggagtcca aaccggtgac 60

ctattgatgg tgcatgcctc acttaaagcg attggtccgg tcgaaggagg agcggagacg 120

gtcgttgccg cgttacgctc cgcggttggg ccgactggca ctgtgatggg atacgcatcg 180

tgggaccgat caccctacga ggagactcgt aatggcgctc ggttggatga caaaacccgc 240

cgtacctggc cgccgttcga tcccgcaacg gccgggactt accgtgggtt cggcctgctg 300

aatcagtttc tggttcaagc cccggcgcg cggcgcagcg cgcaccccga tgcatcgatg 360

gtcgcggttg gtccactggc tgaaacgctg acggagcctc acaagctcgg tcacgccttg 420

ggggaagggt cgcccgtcga gcggttcgtt cgccttggcg ggaaggccct gctgttgggt 480

gcgccgctaa actccgttac cgcattgcac tacgccgagg cggttgccga tatccccaac 540

aaacggcggg tgacgtatga gatgccgatg cttggaagca acggcgaagt cgcctggaaa 600

acggcatcgg attacgattc aaacggcatt ctcgattgct ttgctatcga aggaaagccg 660

gatgcggtcg aaactatagc aaatgcttac gtgaagctcg gtcgccatcg agaaggtgtc 720

gtgggctttg ctcagtgcta cctgttcgac gcgcaggaca tcgtgacgtt cggcgtcacc 780

tatcttgaga agcatttcgg aaccactccg atcgtgccag cacacgaagt cgccgagtgc 840

tcttgcgagc cttcaggtta g 861

<210> SEQ ID NO 167
<211> LENGTH: 816
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 167

atgaccgatt tgaatatccc gcatacacac gcgcaccttg tagacgcatt tcaggcgctc 60

ggcatccgcg cggggcaggc gctcatgctg cacgcatccg ttaaagcagt gggcgcggtg 120

atgggcggcc ccaatgtgat cttgcaggcg ctcatggatg cgctcacgcc cgacggcacg 180

ctgatgatgt atgcgggatg gcaagacatc cccgacttta tcgactcgct gccggacgcg 240

ctcaaggccg tgtatcttga gcagcaccca ccctttgacc ccgccaccgc ccgcgccgtg 300

cgcgaaaaca gcgtgctagc ggaatttttg cgcacatggc cgtgcgtgca tcgcagcgca 360

aaccccgaag cctctatggt ggcggtaggc aggcaggccg ctttgctgac cgctaatcac 420

gcgctggatt atggctacgg agtcgagtcg ccgctggcta aactggtggc aatagaagga 480

tacgtgctga tgcttggcgc gccgctggat accatcacac tgctgcacca cgcggaatat 540

ctggccaaga tgcgccacaa gaacgtggtc cgctacccgt gcccgattct gcgggacggg 600

cgcaaagtgt gggtgaccgt tgaggactat gacaccggtg atccgcacga cgattatagt 660

tttgagcaaa tcgcgcgcga ttatgtggcg cagggcggcg gcacacgcgg caaagtcggt 720

gatgcggatg cttacctgtt cgccgcgcag gacctcacac ggtttgcggt gcagtggctt 780

gaatcacggt tcggtgactc agcgtcatac ggatag 816

<210> SEQ ID NO 168

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<211> LENGTH: 498
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 168

atgctctatg agtggctaaa tcgatctcat atcgtcgagt ggtggggcgg agaagaagca 60

cgcccgacac ttgctgacgt acaggaacag tacttgccaa gcgttttagc gcaagagtcc 120

gtcactccat acattgcaat gctgaatgga gagccgattg ggtatgccca gtcgtacgtt 180

gctcttggaa gcggggacgg atggtgggaa gaagaaaccg atccaggagt acgcggaata 240

gaccagttac tggcgaatgc atcacaactg ggcaaaggct tgggaaccaa gctggttcga 300

gctctggttg agttgctgtt caatgatccc gaggtcacca agatccaaac ggacccgtcg 360

ccgagcaact tgcgagcgat ccgatgctac gagaaagcgg ggtttgagag gcaaggtacc 420

gtaaccaccc cagatggtcc agccgtgtac atggttcaaa cacgccaggc attcgagcga 480

acacgcagtg atgcctaa 498

<210> SEQ ID NO 169
<211> LENGTH: 2007
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 169

atgaaaaaga taaaaattgt tccacttatt ttaatagttg tagttgtcgg gtttggtata 60

tatttttatg cttcaaaaga taaagaaatt aataatacta ttgatgcaat tgaagataaa 120

aatttcaaac aagtttataa agatagcagt tatatttcta aaagcgataa tggtgaagta 180

gaaatgactg aacgtccgat aaaaatatat aatagtttag gcgttaaaga tataaacatt 240

caggatcgta aaataaaaaa agtatctaaa aataaaaaac gagtagatgc tcaatataaa 300

attaaaacaa actacggtaa cattgatcgc aacgttcaat ttaattttgt taaagaagat 360

ggtatgtgga agttagattg ggatcatagc gtcattattc caggaatgca gaaagaccaa 420

agcatacata ttgaaaattt aaaatcagaa cgtggtaaaa ttttagaccg aaacaatgtg 480

gaattggcca atacaggaac acatatgaga ttaggcatcg ttccaaagaa tgtatctaaa 540

aaagattata aagcaatcgc taaagaacta agtatttctg aagactatat caacaacaaa 600

tggatcaaaa ttgggtacaa gatgatacct tcgttccact ttaaaaccgt taaaaaaatg 660

gatgaatatt taagtgattt cgcaaaaaaa tttcatctta caactaatga aacagaaagt 720

cgtaactatc ctctagaaaa agcgacttca catctattag gttatgttgg tcccattaac 780

tctgaagaat taaaacaaaa agaatataaa ggctataaag atgatgcagt tattggtaaa 840

aagggactcg aaaaacttta cgataaaaag ctccaacatg aagatggcta tcgtgtcaca 900

atcgttgacg ataatagcaa tacaatcgca catacattaa tagagaaaaa gaaaaaagat 960

ggcaaagata ttcaactaac tattgatgct aaagttcaaa agagtattta taacaacatg 1020

aaaaatgatt atggctcagg tactgctatc caccctcaaa caggtgaatt attagcactt 1080

gtaagcacac cttcatatga cgtctatcca tttatgtatg gcatgagtaa cgaagaatat 1140

aataaattaa ccgaagataa aaaagaacct ctgctcaaca agttccagat tacaacttca 1200

ccaggttcaa ctcaaaaaat attaacagca atgattgggt taaataacaa aacattagac 1260

gataaaacaa gttataaaat cgatggtaaa ggttggcaaa aagataaatc ttggggtggt 1320

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tacaacgtta caagatatga agtggtaaat ggtaatatcg acttaaaaca agcaatagaa   1380
tcatcagata acattttctt tgctagagta gcactcgaat taggcagtaa gaaatttgaa   1440
aaaggcatga aaaaactagg tgttggtgaa gatataccaa gtgattatcc attttataat   1500
gctcaaattt caaacaaaaa tttagataat gaaatattat tagctgattc aggttacgga   1560
caaggtgaaa tactgattaa cccagtacag atcctttcaa tctatagcgc attagaaaat   1620
aatggcaata ttaacgcacc tcacttatta aaagacacga aaaacaaagt ttggaagaaa   1680
aatattattt ccaaagaaaa tatcaatcta ttaaatgatg gtatgcaaca agtcgtaaat   1740
aaaacacata aagaagatat ttatagatct tatgcaaact taattggcaa atccggtact   1800
gcagaactca aaatgaaaca aggagaaagt ggcagacaaa ttgggtggtt tatatcatat   1860
gataaagata atccaaacat gatgatggct attaatgtta aagatgtaca agataaagga   1920
atggctagct acaatgccaa aatctcaggt aaagtgtatg atgagctata tgagaacggt   1980
aataaaaaat acgatataga tgaataa                                       2007
```

<210> SEQ ID NO 170
<211> LENGTH: 2607
<212> TYPE: DNA
<213> ORGANISM: Enterococcus faecium

<400> SEQUENCE: 170

```
atgaataaca tcggcattac tgtttatgga tgtgagcagg atgaggcaga tgcattccat     60
gctctttcgc ctcgctttgg cgttatggca acgataatta acgccaacgt gtcggaatcc    120
aacgccaaat ccgcgccttt caatcaatgt atcagtgtgg gacataaatc agagatttcc    180
gcctctattc ttcttgcgct gaagagagcc ggtgtgaaat atatttctac ccgaagcatc    240
ggctgcaatc atatagatac aactgctgct aagagaatgg gcatcactgt cgacaatgtg    300
gcgtactcgc cggatagcgt tgccgattat actatgatgc taattcttat ggcagtacgc    360
aacgtaaaat cgattgtgcg ctctgtggaa aaacatgatt tcaggttgga cagcgaccgt    420
ggcaaggtac tcagcgacat gacagttggt gtggtgggaa cgggccagat aggcaaagcg    480
gttattgagc ggctgcgagg atttggatgt aaagtgttgg cttatagtcg cagccgaagt    540
atagaggtaa actatgtacc gtttgatgag ttgctgcaaa atagcgatat cgttacgctt    600
catgtgccgc tcaatacgga tacgcactat attatcagcc acgaacaaat acagagaatg    660
aagcaaggag catttcttat caatactggg cgcggtccac ttgtagatac ctatgagttg    720
gttaaagcat tagaaaacgg gaaactgggc ggtgccgcat tggatgtatt ggaaggagag    780
gaagagtttt tctactctga ttgcacccaa aaaccaattg ataatcaatt tttacttaaa    840
cttcaaagaa tgcctaacgt gataatcaca ccgcatacgg cctattatac cgagcaagcg    900
ttgcgtgata ccgttgaaaa aaccattaaa aactgtttgg attttgaaag gagacaggag    960
catgaataga ataaaagttg caatactgtt tggggttgc tcagaggagc atgacgtatc   1020
ggtaaaatct gcaatagaga tagccgctaa cattaataaa gaaaaatacg agccgttata   1080
cattggaatt acgaaatctg gtgtatggaa aatgtgcgaa aaaccttgcg cggaatggga   1140
aaacgacaat tgctattcag ctgtactctc gccggataaa aaaatgcacg gattacttgt   1200
taaaaagaac catgaatatg aaatcaacca tgttgatgta gcattttcag ctttgcatgg   1260
caagtcaggt gaagatggat ccatacaagg tctgtttgaa ttgtccggta tcccttttgt   1320
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aggctgcgat attcaaagct cagcaatttg tatggacaaa tcgttgacat acatcgttgc   1380

gaaaaatgct gggatagcta ctcccgcctt ttgggttatt aataaagatg ataggccggt   1440

ggcagctacg tttacctatc ctgtttttgt taagccggcg cgttcaggct catccttcgg   1500

tgtgaaaaaa gtcaatagcg cggacgaatt ggactacgca attgaatcgg caagacaata   1560

tgacagcaaa atcttaattg agcaggctgt ttcgggctgt gaggtcggtt gtgcggtatt   1620

gggaaacagt gccgcgttag ttgttggcga ggtggaccaa atcaggctgc agtacggaat   1680

ctttcgtatt catcaggaag tcgagccgga aaaaggctct gaaaacgcag ttataaccgt   1740

tcccgcagac ctttcagcag aggagcgagg acggatacag gaaacggcaa aaaaaatata   1800

taaagcgctc ggctgtagag gtctagcccg tgtggatatg tttttacaag ataacggccg   1860

cattgtactg aacgaagtca atactctgcc cggtttcacg tcatacagtc gttatccccg   1920

tatgatggcc gctgcaggta ttgcacttcc cgaactgatt gaccgcttga tcgtattagc   1980

gttaaagggg tgataagcat ggaaatagga tttacttttt tagatgaaat agtacacggt   2040

gttcgttggg acgctaaata tgccacttgg gataatttca ccggaaaacc ggttgacggt   2100

tatgaagtaa atcgcattgt agggacatac gagttggctg aatcgctttt gaaggcaaaa   2160

gaactggctg ctacccaagg gtacggattg cttctatggg acggttaccg tcctaagcgt   2220

gctgtaaact gttttatgca atgggctgca cagccggaaa ataacctgac aaaggaaagt   2280

tattatccca atattgaccg aactgagatg atttcaaaag gatacgtggc ttcaaaatca   2340

agccatagcc gcggcagtgc cattgatctt acgctttatc gattagacac gggtgagctt   2400

gtaccaatgg ggagccgatt tgatttttatg gatgaacgct ctcatcatgc ggcaaatgga   2460

atatcatgca atgaagcgca aaatcgcaga cgtttgcgct ccatcatgga aaacagtggg   2520

tttgaagcat atagcctcga atggtggcac tatgtattaa gagacgaacc ataccccaat   2580

agctattttg atttccccgt taaataa                                       2607
```

<210> SEQ ID NO 171
<211> LENGTH: 1288
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 171

```
ggatccatca ggcaacgacg ggctgctgcc ggccatcagc ggacgcaggg aggactttcc     60

gcaaccggcc gttcgatgcg gcaccgatgg ccttcgcgca ggggtagtga atccgccagg    120

attgacttgc gctgccctac ctctcactag tgaggggcgg cagcgcatca agcggtgagc    180

gcactccggc accgccaact ttcagcacat gcgtgtaaat catcgtcgta gagacgtcgg    240

aatggccgag cagatcctgc acggttcgaa tgtcgtaacc gctgcggagc aaggccgtcg    300

cgaacgagtg gcggagggtg tgcggtgtgg cgggcttcgt gatgcctgct tgttctacgg    360

cacgtttgaa ggcgcgctga aaggtctggt catacatgtg atggcgacgc acgacaccgc    420

tccgtggatc ggtcgaatgc gtgtgctgcg caaaaaccca gaaccacggc caggaatgcc    480

cggcgcgcgg atacttccgc tcaagggcgt cgggaagcgc aacgccgctg cggccctcgg    540

cctggtcctt cagccaccat gcccgtgcac gcgacagctg ctcgcgcagg ctgggtgcca    600

agctctcggg taacatcaag gcccgatcct tggagccctt gccctcccgc acgatgatcg    660

tgccgtgatc gaaatccaga tccttgaccc gcagttgcaa accctcactg atccgcatgc    720
```

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ccgttccata cagaagctgg gcgaacaaac gatgctcgcc ttccagaaaa ccgaggatgc    780

gaaccacttc atccggggtc agcaccaccg gcaagcgccg cgacggccga ggtcttccga    840

tctcctgaag ccagggcaga tccgtgcaca gcaccttgcc gtagaagaac agcaaggccg    900

ccaatgcctg acgatgcgtg gagaccgaaa ccttgcgctc gttcgccagc caggacagaa    960

atgcctcgac ttcgctgctg cccaaggttg ccgggtgacg cacaccgtgg aaacggatga   1020

aggcacgaac ccagtggaca taagcctgtt cggttcgtaa gctgtaatgc aagtagcgta   1080

tgcgctcacg caactggtcc agaaccttga ccgaacgcag cggtggtaac ggcgcagtgg   1140

cggttttcat ggcttgttat gactgttttt ttgtacagtc tatgcctcgg gcatccaagc   1200

agcaagcgcg ttacgccgtg ggtcgatgtt tgatgttatg gagcagcaac gatgttacgc   1260

agcagggcag tcgccctaaa acaaagtt                                      1288
```

```
<210> SEQ ID NO 172
<211> LENGTH: 1650
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 172

gttagatgca ctaagcacat aattgctcac agccaaacta tcaggtcaag tctgctttta     60

ttatttttaa gcgtgcataa taagccctac acaaattggg agatatatca tgaaaggctg    120

gctttttctt gttatcgcaa tagttggcga agtaatcgca acatccgcat taaaatctag    180

cgagggcttt actaagcttg ccccttccgc cgttgtcata atcggttatg gcatcgcatt    240

ttattttctt tctctggttc tgaaatccat ccctgtcggt gttgcttatg cagtctggtc    300

gggactcggc gtcgtcataa ttacagccat tgcctggttg cttcatgggc aaaagcttga    360

tgcgtggggc tttgtaggta tggggctcat aattgctgcc tttttgctcg cccgatcccc    420

atcgtggaag tcgctgcgga ggccgacgcc atggtgacgg tgttcggcat tctgaatctc    480

accgaggact ccttcttcga tgagagccgg cggctagacc ccgccggcgc tgtcaccgcg    540

gcgatcgaaa tgctgcgagt cggatcagac gtcgtggatg tcggaccggc cgccagccat    600

ccggacgcga ggcctgtatc gccggccgat gagatcagac gtattgcgcc gctcttagac    660

gccctgtccg atcagatgca ccgtgtttca atcgacagct tccaaccgga aacccagcgc    720

tatgcgctca agcgcggcgt gggctacctg aacgatatcc aaggatttcc tgaccctgcg    780

ctctatcccg atattgctga ggcggactgc aggctggtgg ttatgcactc agcgcagcgg    840

gatggcatcg ccacccgcac cggtcacctt cgacccgaag acgcgctcga cgagattgtg    900

cggttcttcg aggcgcgggt ttccgccttg cgacggagcg gggtcgctgc cgaccggctc    960

atcctcgatc cggggatggg atttttcttg agccccgcac cggaaacatc gctgcacgtg   1020

ctgtcgaacc ttcaaaagct gaagtcggcg ttggggcttc cgctattggt ctcggtgtcg   1080

cggaaatcct tcttgggcgc caccgttggc cttcctgtaa aggatctggg tccagcgagc   1140

cttgcggcgg aacttcacgc gatcggcaat ggcgctgact acgtccgcac ccacgcgcct   1200

ggagatctgc gaagcgcaat caccttctcg gaaaccctcg cgaaatttcg cagtcgcgac   1260

gccagagacc gagggttaga tcatgcctag cattcacctt ccggccgccc gctagcggac   1320

cctggtcagg ttccgcgaag gtgggcgcag acatgctggg ctcgtcagga tcaaactgca   1380

ctatgaggcg gcggttcata ccgcgccagg ggagcgaatg gacagcgagg agcctccgaa   1440
```

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```
cgttcgggtc gcctgctcgg gtgatatcga cgaggttgtg cggctgatgc acgacgctgc   1500

ggcgtggatg tccgccaagg gaacgcccgc ctgggacgtc gcgcggatcg accggacatt   1560

cgcggagacc ttcgtcctga gatccgagct cctagtcgcg agttgcagcg acggcatcgt   1620

cggctgttgc accttgtcgg ccgaggatcc                                    1650
```

<210> SEQ ID NO 173
<211> LENGTH: 630
<212> TYPE: DNA
<213> ORGANISM: Enterococcus faecium

<400> SEQUENCE: 173

```
atgggtccga atcctatgaa aatgtatcct atagaaggaa acaaatcagt acaatttatc     60

aaacctattt tagaaaaatt agaaaatgtt gaggttggag aatactcata ttatgattct    120

aagaatggag aaacttttga taagcaaatt ttatatcatt atccaatctt aaacgataag    180

ttaaaaatag gtaaattttg ctcaatagga ccaggtgtaa ctattattat gaatggagca    240

aatcatagaa tggatggctc aacatatcca tttaatttat ttggtaatgg atgggagaaa    300

catatgccaa aattagatca actacctatt aaggggggata caataatagg taatgatgta    360

tggataggaa aagatgttgt aattatgcca ggagtaaaaa tcggggatgg tgcaatagta    420

gctgctaatt ctgttgttgt aaaagatata gcgccataca tgttagctgg aggaaatcct    480

gctaacgaaa taaaacaaag atttgatcaa gatacaataa atcagctgct tgatataaaa    540

tggtggaatt ggccaataga cattattaat gagaatatag ataaaattct tgataatagc    600

atcattagag aagtcatatg gaaaaaatga                                     630
```

<210> SEQ ID NO 174
<211> LENGTH: 1440
<212> TYPE: DNA
<213> ORGANISM: Enterococcus faecalis

<400> SEQUENCE: 174

```
atgaatatag ttgaaaatga aatatgtata agaactttaa tagatgatga ttttcctttg     60

atgttaaaat ggttaactga tgaaagagta ttagaatttt atggtggtag agataaaaaa    120

tatacattag aatcattaaa aaaacattat acagagcctt gggaagatga agtttttaga    180

gtaattattg aatataacaa tgttcctatt ggatatggac aaatatataa aatgtatgat    240

gagttatata ctgattatca ttatccaaaa actgatgaga tagtctatgg tatggatcaa    300

tttataggag agccaaatta ttggagtaaa ggaattggta caagatatat taaattgatt    360

tttgaatttt tgaaaaaaga aagaaatgct aatgcagtta ttttagaccc tcataaaaat    420

aatccaagag caataagggc ataccaaaaa tctggtttta gaattattga agatttgcca    480

gaacatgaat tacacgaggg caaaaaagaa gattgttatt taatggaata tagatatgat    540

gataatgcca caaatgttaa ggcaatgaaa tatttaattg agcattactt tgataatttc    600

aaagtagata gtattgaaat aatcggtagt ggttatgata gtgtggcata tttagttaat    660

aatgaataca tttttaaaac aaaatttagt actaataaga aaaaaggtta tgcaaaagaa    720

aaagcaatat ataatttttt aaatacaaat ttagaaacta atgtaaaaat tcctaatatt    780

gaatattcgt atattagtga tgaattatct atactaggtt ataaagaaat taaaggaact    840

tttttaacac cagaaattta ttctactatg tcagaagaag aacaaaattt gttaaaacga    900
```

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gatattgcca gtttttttaag acaaatgcac ggtttagatt atacagatat tagtgaatgt    960
actattgata ataaacaaaa tgtattagaa gagtatatat tgttgcgtga aactatttat   1020
aatgatttaa ctgatataga aaaagattat atagaaagtt ttatggaaag actaaatgca   1080
acaacagttt ttgagggtaa aaagtgttta tgccataatg attttagttg taatcatcta   1140
ttgttagatg gcaataatag attaactgga ataattgatt ttggagattc tggaattata   1200
gatgaatatt gtgattttat atacttactt gaagatagtg aagaagaaat aggaacaaat   1260
tttggagaag atatattaag aatgtatgga aatatagata ttgagaaagc aaaagaatat   1320
caagatatag ttgaagaata ttatcctatt gaaactattg tttatggaat taaaaatatt   1380
aaacaggaat ttatcgaaaa tggtagaaaa gaaatttata aaaggactta taaagattga   1440
```

<210> SEQ ID NO 175
<211> LENGTH: 660
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 175

```
ttgaatttaa acaatgacca tggacctgat cccgaaaata ttttaccgat aaaagggaat     60
cggaatcttc aatttataaa acctactata acgaacgaaa acattttggt gggggaatat    120
tcttattatg atagtaagcg aggagaatcc tttgaagatc aagtcttata tcattatgaa    180
gtgattggag ataagttgat tataggaaga ttttgttcaa ttggtcccgg aacaacattt    240
attatgaatg gtgcaaacca tcggatggat ggatcaacat atccttttca tctattcagg    300
atgggttggg agaagtatat gccttcctta aaagatcttc ccttgaaagg ggacattgaa    360
attggaaatg atgtatggat aggtagagat gtaaccatta tgcctggggt gaaaattggg    420
gacggggcaa tcattgctgc agaagctgtt gtcacaaaga atgttgctcc ctattctatt    480
gtcggtggaa atcccttaaa atttataaga aaaaggtttt ctgatggagt tatcgaagaa    540
tggttagctt tacaatggtg gaatttagat atgaaaatta ttaatgaaaa tcttcccttc    600
ataataaatg gagatatcga aatgctgaag agaaaaagaa aacttctaga tgacacttga    660
```

<210> SEQ ID NO 176
<211> LENGTH: 1569
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 176

```
atgaaaataa tgttagaggg acttaatata aaacattatg ttcaagatcg tttattgttg     60
aacataaatc gcctaaagat ttatcagaat gatcgtattg gtttaattgg taaaaatgga    120
agtggaaaaa caacgttact tcacatatta tataaaaaaa ttgtgcctga agaaggtatt    180
gtaaaacaat tttcacattg tgaacttatt cctcaattga agctcataga atcaactaaa    240
agtggtggtg aagtaacacg aaactatatt cggcaagcgc ttgataaaaa tccagaactg    300
ctattagcag atgaaccaac aactaactta gataataact atatagaaaa attagaacag    360
gatttaaaaa attggcatgg agcatttatt atagtttcac atgatcgcgc tttttttagat    420
aacttgtgta ctactatatg ggaaattgac gagggaagaa taactgaata taaggggaat    480
tatagtaact atgttgaaca aaaagaatta gaaagacatc gagaagaatt agaatatgaa    540
aaatatgaaa aagaaaagaa acgattggaa aaagctataa atataaaaga acagaaagct    600
```

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```
caacgagcaa ctaaaaaacc gaaaaactta agtttatctg aaggcaaaat aaaaggagca    660
aagccatact ttgcaggtaa gcaaaagaag ttacgaaaaa ctgtaaaatc tctagaaacc    720
agactagaaa aacttgaaag cgtcgaaaag agaaacgaac ttcctccact taaaatggat    780
ttagtgaact tagaaagtgt aaaaaataga actataatac gtggtgaaga tgtctcgggt    840
acaattgaag gacgggtatt gtggaaagca aaaagtttta gtattcgcgg aggagacaag    900
atggcaatta tcggatctaa tggtacagga aagacaacgt ttattaaaaa aattgtgcat    960
gggaatcctg gtatttcatt atcgccatct gtcaaaatcg gttattttag ccaaaaaata   1020
gatacattag aattagataa gagcatttta gaaaatgttc aatcttcttc acaacaaaat   1080
gaaactctta ttcgaactat tctagctaga atgcattttt ttagagatga tgtttataaa   1140
ccaataagtg tcttaagtgg tggagagcga gttaaagtag cactaactaa agtattctta   1200
agtgaagtta atacgttggt actagatgaa ccaacaaact ttcttgatat ggaagctata   1260
gaggcgtttg aatctttgtt aaaggaatat aatggcagta taatctttgt atctcacgat   1320
cgtaaattta tcgaaaaagt agccactcga ataatgacaa ttgataataa agaaataaaa   1380
atatttgatg gcacatatga acaatttaaa caagctgaaa agccaacaag gaatattaaa   1440
gaagataaaa aacttttact tgagacaaaa attacagaag tactcagtcg attgagtatt   1500
gaaccttcgg aagaattaga acaagagttt caaaacttaa taaatgaaaa aagaaatttg   1560
gataaataa                                                           1569
```

<210> SEQ ID NO 177
<211> LENGTH: 1467
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus epidermidis

<400> SEQUENCE: 177

```
atggaacaat atacaattaa atttaaccaa atcaatcata aattgacaga tttacgatca     60
cttaacatcg atcatcttta tgcttaccaa tttgaaaaaa tagcacttat tgggggtaat    120
ggtactggta aaaccacatt actaaatatg attgctcaaa aaacaaaacc agaatctgga    180
acagttgaaa cgaatggcga aattcaatat tttgaacagc ttaacatgga tgtggaaaat    240
gattttaaca cgttagacgg tagtttaatg agtgaactcc atatacctat gcatacaacc    300
gacagtatga gtggtggtga aaaagcaaaa tataaattac gtaatgtcat atcaaattat    360
agtccgatat tacttttaga tgaacctaca aatcacttgg ataaaattgg taaagattat    420
ctgaataata ttttaaaata ttactatggt actttaatta tagtaagtca cgatagagca    480
cttatagacc aaattgctga cacaatttgg gatatacaag aagatggcac aataagagtg    540
tttaaaggta attacacaca gtatcaaaat caatatgaac aagaacagtt agaacaacaa    600
cgtaaatatg aacagtatat aagtgaaaaa caaagattgt cccaagccag taaagctaaa    660
cgaaatcaag cgcaacaaat ggcacaagca tcatcaaaac aaaaaaataa aagtatagca    720
ccagatcgtt taagtgcatc aaaagaaaaa ggcacggttg agaaggctgc tcaaaaacaa    780
gctaagcata ttgaaaaaag aatggaacat ttggaagaag ttgaaaaacc acaaagttat    840
catgaattca attttccaca aaataaaatt tatgatatcc ataataatta tccaatcatt    900
gcacaaaatc taacattggt taaaggaagt caaaaactgc taacacaagt acgattccaa    960
ataccatatg gcaaaaatat agcgctcgta ggtgcaaatg gtgtaggtaa gacaacttta   1020
```

-continued

```
cttgaagcta tttaccacca aatagaggga attgattgtt ctcctaaagt gcaaatggca   1080

tactatcgtc aacttgctta tgaagacatg cgtgacgttt cattattgca atatttaatg   1140

gatgaaacgg attcatcaga atcattcagt agagctattt taaataactt gggtttaaat   1200

gaagcacttg agcgttcttg taatgttttg agtggtgggg aaagaacgaa attatcgtta   1260

gcagtattat tttcaacgaa agcgaatatg ttaattttgg atgaaccaac taattttta    1320

gatattaaaa cattagaagc attagaaatg tttatgaata aatatcctgg aatcattttg   1380

tttacatcac atgatacaag gtttgttaaa catgtatcag ataaaaaatg ggaattaaca   1440

ggacaatcta ttcatgatat aacttaa                                       1467
```

What is claimed is

1. A method using probes (fragments and/or oligonucleotides) and/or amplification primers which are specific, ubiquitous and sensitive for determining the presence and/or amount of nucleic acids from bacterial species selected from the group consisting of *Escherichia coli, Klebsiells pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis, Streptococcus pneumoniae, Staphlyococcus aureus, Staphylococcus epidermidis, Enterococcus faecalis, Staphlyococcus saprophyticus, Streptococcus pyogenes, Haemophilus influenzae* and *Moraxells catarrhalis* in a any sample suspected of containing said bacterial nucleic acid, wherein said bacterial nucleic acid or variant or part thereof comprises a selected target region hybridizable with said probes or primers; said method comprising the steps of contacting said sample with said probes or primers and detecting the presence and/or amount of hybridized probes and/or amplified products as an indication of the presence and/or amount of said bacterial species.

2. A method as defined in claim 1 further using probes (fragments and/or oligonucleotides) and/or amplification primers which are universal and sensitive for determining the presence and/or amount of nucleic acids from any bacteria from any sample suspected of containing said bacterial nucleic acid, wherein said bacterial nucleic acid or variant or part thereof comprises a selected target region hybridizable with said probes or primers; said method comprising the steps of contacting said sample with said probes or primers and detecting the presence and/or amount of hybridized probes and/or amplified products as an indication of the presence and/or amount of said any bacteria.

3. A method as defined in claim 1 further using probes (fragments and/or oligonucleotides) and/or amplification primers which are specific, ubiquitous and sensitive for determining the presence and/or amount of nucleic acids from an antibiotic resistance gene selected from the group consisting of bla_{tem}, Bla_{rob}, Bla_{shv}, aadB, aacC1, aacC2, aacC3, aacA4, mecA, vanA, vanH, vanX, satA, aacA-aphD, vat, vga, msrA, sul and int in any sample suspected of containing said bacterial nucleic acid, wherein said bacterial nucleic acid or variant or part thereof comprises a selected target region hybridizable with said probes or primers; said method comprising the steps of contacting said sample with said probes or primers and detecting the presence and/or amount of hybridized probes and/or amplified products as an indication of the presence and/or amount of said antibiotic resistance gene.

4. The method of any one of claims **1**, **2** and **3** which is performed directly on a sample obtained from human patients, animals, environment or food.

5. The method of any one of claims **1**, **2** and **3** which is performed directly on a sample consisting of one or more bacterial colonies.

6. The method of any one of claims 1 to 5, wherein the bacterial nucleic acid is amplified by a method selected from the group consisting of:

a) polymerase chain reaction (PCR),

b) ligase chain reaction,

c) nucleic acid sequence-based amplification,

d) self-sustained sequence replication,

e) strand displacement amplification,

f) branched DNA signal amplification,

g) nested PCR, and

h) multiplex PCR.

7. The method of claim 6 wherein said bacterial nucleic acid is amplified by PCR.

8. The method of claim 7 wherein the PCR protocol is modified to determine within one hour the presence of said bacterial nucleic acids by performing for each amplification cycle an annealing step of only one second at 55° C. and a denaturation step of only one second at 95° C. without any elongation step.

9. A method for the detection, identification and/or quantification of *Escherichia coli* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic

acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO:3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Escherichia coli,* under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Escherichia coli* in said test sample.

10. A method as defined in claim 9, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-227 nucleotides in length which sequence is comprised in SEQ ID NO: 3 or a complementary sequence thereof,

2) an oligonucleotide of 12-278 nucleotides in length which sequence is comprised in SEQ ID NO: 4 or a complementary sequence thereof,

3) an oligonucleotide of 12-1596 nucleotides in length which sequence is comprised in SEQ ID NO: 5 or a complementary sequence thereof,

4) an oligonucleotide of 12-2703 nucleotides in length which sequence is comprised in SEQ ID NO: 6 or a complementary sequence thereof,

5) an oligonucleotide of 12-1391 nucleotides in length which sequence is comprised in SEQ ID NO: 7 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Escherichia coli.*

11. The method of claim 10, wherein the probe for detecting nucleic acid sequences from *Escherichia coli* is selected from the group consisting of SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54 and a sequence complementary thereof.

12. A method for detecting the presence and/or amount of *Escherichia coli* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Escherichia coli* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6 and SEQ ID NO: 7;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Escherichia coli* in said test sample.

13. The method of claim 12, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 42 and SEQ ID NO: 43,

b) SEQ ID NO: 46 and SEQ ID NO: 47,

c) SEQ ID NO: 55 and SEQ ID NO: 56, and

d) SEQ ID NO: 131 and SEQ ID NO: 132.

14. A method for the detection, identification and/or quantification of *Klebsiella pneumoniae* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO:8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Klebsiella pneumoniae,* under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Klebsiella pneumoniae* in said test sample.

15. A method as defined in claim 14, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-238 nucleotides in length which sequence is comprised in SEQ ID NO: 8 or a complementary sequence thereof,

2) an oligonucleotide of 12-385 nucleotides in length which sequence is comprised in SEQ ID NO: 9 or a complementary sequence thereof,

3) an oligonucleotide of 12-462 nucleotides in length which sequence is comprised in SEQ ID NO: 10 or a complementary sequence thereof,

4) an oligonucleotide of 12-730 nucleotides in length which sequence is comprised in SEQ ID NO: 11 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Klebsiella pneumoniae*.

16. The method of claim 15, wherein the probe for detecting nucleic acid sequences from *Klebsiella pneumoniae* is selected from the group consisting of SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 69 and a sequence complementary thereof.

17. A method for detecting the presence and/or amount of *Klebsiella pneumoniae* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Klebsiella pneumoniae* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, and SEQ ID NO: 11;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Klebsiella pneumoniae* in said test sample.

18. The method of claim 17, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 61 and SEQ ID NO: 62,

b) SEQ ID NO: 67 and SEQ ID NO: 68,

c) SEQ ID NO: 135 and SEQ ID NO: 136, and

d) SEQ ID NO: 137 and SEQ ID NO: 138.

19. A method for the detection, identification and/or quantification of *Proteus mirabilis* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Proteus mirabilis,* under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Proteus mirabilis* in said test sample.

20. A method as defined in claim 19, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-225 nucleotides in length which sequence is comprised in SEQ ID NO: 12 or a complementary sequence thereof,

2) an oligonucleotide of 12-402 nucleotides in length which sequence is comprised in SEQ ID NO: 13 or a complementary sequence thereof,

3) an oligonucleotide of 12-157 nucleotides in length which sequence is comprised in SEQ ID NO: 14 or a complementary sequence thereof,

4) an oligonucleotide of 12-1348 nucleotides in length which sequence is comprised in SEQ ID NO: 15 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Proteus mirabilis.*

21. The method of claim 20, wherein the probe for detecting nucleic acid sequences from *Proteus mirabilis* is selected from the group consisting of SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 82 and a sequence complementary thereof.

22. A method for detecting the presence and/or amount of *Proteus mirabilis* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Proteus mirabilis* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, and SEQ ID NO: 15;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Proteus mirabilis* in said test sample.

23. The method of claim 22, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 74 and SEQ ID NO: 75, and

b) SEQ ID NO: 133 and SEQ ID NO: 134.

24. A method for the detection, identification and/or quantification of *Staphylococcus saprophyticus* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Staphylococcus saprophyticus,* under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Staphylococcus saprophyticus* in said test sample.

25. A method as defined in claim 24, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-172 nucleotides in length which sequence is comprised in SEQ ID NO: 21 or a complementary sequence thereof,

2) an oligonucleotide of 12-155 nucleotides in length which sequence is comprised in SEQ ID NO: 22 or a complementary sequence thereof,

3) an oligonucleotide of 12-145 nucleotides in length which sequence is comprised in SEQ ID NO: 23 or a complementary sequence thereof,

4) an oligonucleotide of 12-265 nucleotides in length which sequence is comprised in SEQ ID NO: 24 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Staphylococcus saprophyticus.*

26. The method of claim 25, wherein the probe for detecting nucleic acid sequences from *Staphylococcus saprophyticus* is selected from the group consisting of SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104 and a sequence complementary thereof.

27. A method for detecting the presence and/or amount of *Staphylococcus saprophyticus* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Staphylococcus saprophyticus* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, and SEQ ID NO: 24;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Staphylococcus saprophyticus* in said test sample.

28. The method of claim 27, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 98 and SEQ ID NO: 99, and

b) SEQ ID NO: 139 and SEQ ID NO: 140.

29. A method for the detection, identification and/or quantification of *Moraxella catarrhalis* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 28, SEQ ID NO: 29, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Moraxella catarrhalis,* under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said label-

ling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Moraxella catarrhalis* in said test sample.

30. A method as defined in claim 29, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-526 nucleotides in length which sequence is comprised in SEQ ID NO: 28 or a complementary sequence thereof,

2) an oligonucleotide of 12-466 nucleotides in length which sequence is comprised in SEQ ID NO: 29 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Moraxella catarrhalis.*

31. The method of claim 30, wherein the probe for detecting nucleic acid sequences from *Moraxella catarrhalis* is selected from the group consisting of SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117 and a sequence complementary thereof.

32. A method for detecting the presence and/or amount of *Moraxella catarrhalis* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Moraxella catarrhalis* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 28 and SEQ ID NO: 29;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Moraxella catarrhalis* in said test sample.

33. The method of claim 32, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 112 and SEQ ID NO: 113,

b) SEQ ID NO: 118 and SEQ ID NO: 119, and

c) SEQ ID NO: 160 and SEQ ID NO: 119.

34. A method for the detection, identification and/or quantification of *Pseudomonas aeruginosa* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Pseudomonas aeruginosa,* under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Pseudomonas aeruginosa* in said test sample.

35. A method as defined in claim 34, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-2167 nucleotides in length which sequence is comprised in SEQ ID NO: 16 or a complementary sequence thereof,

2) an oligonucleotide of 12-1872 nucleotides in length which sequence is comprised in SEQ ID NO: 17 or a complementary sequence thereof,

3) an oligonucleotide of 12-3451 nucleotides in length which sequence is comprised in SEQ ID NO: 18 or a complementary sequence thereof,

4) an oligonucleotide of 12-744 nucleotides in length which sequence is comprised in SEQ ID NO: 19 or a complementary sequence thereof,

5) an oligonucleotide of 12-2760 nucleotides in length which sequence is comprised in SEQ ID NO: 20 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Pseudomonas aeruginosa.*

36. The method of claim 35, wherein the probe for detecting nucleic acid sequences from *Pseudomonas aeruginosa* is selected from the group consisting of SEQ ID NO: 87, SEQ ID NO: 88, SEQ ID NO: 89, SEQ ID NO: 90, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95 and a sequence complementary thereof.

37. A method for detecting the presence and/or amount of *Pseudomonas aeruginosa* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers

being capable of hybridizing selectively with one of the two complementary strands of *Pseudomonas aeruginosa* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19 and SEQ ID NO: 20;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Pseudomonas aeruginosa* in said test sample.

38. The method of claim 37, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 83 and SEQ ID NO: 84, and

b) SEQ ID NO: 85 and SEQ ID NO: 86.

39. A method for the detection, identification and/or quantification of *Staphylococcus epidermidis* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 36, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Staphylococcus epidermidis,* under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Staphylococcus epidermidis* in said test sample.

40. A method as defined in claim 39, wherein said probe is selected from the group consisting of an oligonucleotide of 12-705 nucleotides in length which sequence is comprised in SEQ ID NO: 36 and variants thereof which specifically and ubiquitously anneal with strains and representatives of *Staphylococcus epidermidis.*

41. A method for detecting the presence and/or amount of *Staphylococcus epidermidis* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Staphylococcus epidermidis* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the following sequence: SEQ ID NO: 36;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Staphylococcus epidermidis* in said test sample.

42. The method of claim 41, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 145 and SEQ ID NO: 146, and

b) SEQ ID NO: 147 and SEQ ID NO: 148.

43. A method for the detection, identification and/or quantification of *Staphylococcus aureus* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 37, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Staphylococcus aureus*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Staphylococcus aureus* in said test sample.

44. A method as defined in claim 43, wherein said probe is selected from the group consisting of an oligonucleotide of 12-442 nucleotides in length which sequence is comprised in SEQ ID NO: 37 and variants thereof which specifically and ubiquitously anneal with strains and representatives of *Staphylococcus aureus.*

45. A method for detecting the presence and/or amount of *Staphylococcus aureus* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Staphylococcus aureus* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the following sequence: SEQ ID NO: 37;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Staphylococcus aureus* in said test sample.

46. The method of claim 45, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 149 and SEQ ID NO: 150,

b) SEQ ID NO: 149 and SEQ ID NO: 151, and

c) SEQ ID NO: 152 and SEQ ID NO: 153.

47. A method for the detection, identification and/or quantification of *Haemophilus influenzae* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Haemophilus influenzae,* under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Haemophilus influenzae* in said test sample.

48. A method as defined in claim 47, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-845 nucleotides in length which sequence is comprised in SEQ ID NO: 25 or a complementary sequence thereof,

2) an oligonucleotide of 12-1598 nucleotides in length which sequence is comprised in SEQ ID NO: 26 or a complementary sequence thereof,

3) an oligonucleotide of 12-9100 nucleotides in length which sequence is comprised in SEQ ID NO: 27 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Haemophilus influenzae.*

49. The method of claim 48, wherein the probe for detecting nucleic acid sequences from *Haemophilus influenzae* is selected from the group consisting of SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107 and a sequence complementary thereof.

50. A method for detecting the presence and/or amount of *Haemophilus influenzae* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Haemophilus influenzae* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 25, SEQ ID NO: 26 and SEQ ID NO: 27;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Haemophilus influenzae* in said test sample.

51. The method of claim 50, wherein said at least one pair of primers comprises the following pair: SEQ ID NO: 154 and SEQ ID NO: 155.

52. A method for the detection, identification and/or quantification of *Streptococcus pneumoniae* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 34, SEQ ID NO: 35, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Streptococcus pneumoniae,* under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Streptococcus pneumoniae* in said test sample.

53. A method as defined in claim 52, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-631 nucleotides in length which sequence is comprised in SEQ ID NO: 30 or a complementary sequence thereof,

2) an oligonucleotide of 12-3754 nucleotides in length which sequence is comprised in SEQ ID NO: 31 or a complementary sequence thereof,

3) an oligonucleotide of 12-841 nucleotides in length which sequence is comprised in SEQ ID NO: 34 or a complementary sequence thereof,

4) an oligonucleotide of 12-4500 nucleotides in length which sequence is comprised in SEQ ID NO: 35 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Streptococcus pneumoniae.*

54. The method of claim 53, wherein the probe for detecting nucleic acid sequences from *Streptococcus pneumoniae* is selected from the group consisting of SEQ ID NO: 120, SEQ ID NO: 121 and a sequence complementary thereof.

55. A method for detecting the presence and/or amount of *Streptococcus pneumoniae* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Streptococcus pneumoniae* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 34 and SEQ ID NO: 35;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Streptococcus pneumoniae* in said test sample.

56. The method of claim 55, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 78 and SEQ ID NO: 79,

b) SEQ ID NO: 156 and SEQ ID NO: 157, and

c) SEQ ID NO: 158 and SEQ ID NO: 159.

57. A method for the detection, identification and/or quantification of *Streptococcus pyogenes* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 32, SEQ ID NO: 33, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Streptococcus pyogenes,* under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Streptococcus pyogenes* in said test sample.

58. A method as defined in claim 57, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-1337 nucleotides in length which sequence is comprised in SEQ ID NO: 32 or a complementary sequence thereof,

2) an oligonucleotide of 12-1837 nucleotides in length which sequence is comprised in SEQ ID NO: 33 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Streptococcus pyogenes*.

59. A method for detecting the presence and/or amount of *Streptococcus pyogenes* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Streptococcus pyogenes* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 32 and SEQ ID NO: 33;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Streptococcus pyogenes* in said test sample.

60. The method of claim 59, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 141 and SEQ ID NO: 142, and

b) SEQ ID NO: 143 and SEQ ID NO: 144.

61. A method for the detection, identification and/or quantification of *Enterococcus faecalis* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Enterococcus faecalis,* under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Enterococcus faecalis* in said test sample.

62. A method as defined in claim 61, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-1817 nucleotides in length which sequence is comprised in SEQ ID NO: 1 or a complementary sequence thereof,

2) an oligonucleotide of 12-2275 nucleotides in length which sequence is comprised in SEQ ID NO: 2, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Enterococcus faecalis.*

63. A method for detecting the presence and/or amount of *Enterococcus faecalis* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Enterococcus faecalis* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 1 and SEQ ID NO: 2;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Enterococcus faecalis* in said test sample.

64. The method of claim 63, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 38 and SEQ ID NO: 39, and

b) SEQ ID NO: 40 and SEQ ID NO: 41.

65. A method for the detection of the presence and/or amount of any bacterial species directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this

sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a universal probe which sequence is selected from the group consisting of SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130 and a sequence complementary thereof, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of said any bacterial species in said test sample.

66. A method for detecting the presence and/or amount of any bacterial species in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing a pair of universal primers which sequence is defined in SEQ ID NO: 126 and SEQ ID NO: 127, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said any bacterial species DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of said any bacterial species in said test sample.

67. A method for evaluating a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene bla_{tem} (TEM-1) directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 161, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a β-lactamase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene TEM-1.

68. A method as defined in claim 67, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 161.

69. A method for evaluating a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene bla_{tem} (TEM-1) in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for a β-lactamase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 161;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene TEM-1.

70. A method for evaluating a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene bla_{rob} (ROB-1) directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 162, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a β-lactamase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene ROB-1.

71. A method as defined in claim 70, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 162.

72. A method for evaluating a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene bla_{rob} (ROB-1) in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for a β-lactamase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 162;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene ROB-1.

73. A method for evaluating a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene bla_{shv} (SHV-1) directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 163, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a β-lactamase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene SHV-1.

74. A method as defined in claim 73, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 163.

75. A method for evaluating a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene bla_{shv} (SHV-1) in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for a β-lactamase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 163;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene SHV-1.

76. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aadB directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 164, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside adenylyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aadB.

77. A method as defined in claim 76, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 164.

78. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aadB in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside adenylyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 164;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aadB.

79. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacC1 directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 165, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacC1.

80. A method as defined in claim 79, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 165.

81. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aaccl in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 165;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacC1.

82. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacC2 directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 166, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacC2.

83. A method as defined in claim 82, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 166.

84. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacC2 in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 166;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacC2.

85. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacC3 directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 167, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacC3.

86. A method as defined in claim 85, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 167.

87. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacC3 in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 167;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacC3.

88. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial anti-

biotic resistance gene aacA4 directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 168, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacA4.

89. A method as defined in claim 88, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 168.

90. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacA4 in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 168;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacA4.

91. A method for evaluating a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene mecA directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 169, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a penicillin-binding protein, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene mecA.

92. A method as defined in claim 91, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 169.

93. A method for evaluating a bacterial resistance to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene mecA in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for a penicillin-binding protein that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 169;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance

to β-lactam antibiotics mediated by the bacterial antibiotic resistance gene mecA.

94. A method for evaluating a bacterial resistance to vancomycin mediated by the bacterial antibiotic resistance genes vanH, vanA and vanX directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 170, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance genes coding for vancomycin-resistance proteins, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to vancomycin mediated by the bacterial antibiotic resistance genes vanH, vanA and vanX.

95. A method as defined in claim 94, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 170.

96. A method for evaluating a bacterial resistance to vancomycin mediated by the bacterial antibiotic resistance genes vanH, vanA and vanX in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance genes coding for vancomycin-resistance proteins that contain a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 170;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to vancomycin mediated by the bacterial antibiotic resistance genes vanH, vanA and vanX.

97. A method for evaluating a bacterial resistance to streptogramin A mediated by the bacterial antibiotic resistance gene satA directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 173, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a streptogramin A acetyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to streptogramin A mediated by the bacterial antibiotic resistance gene satA.

98. A method as defined in claim 97, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 173.

99. A method for evaluating a bacterial resistance to streptogramin A mediated by the bacterial antibiotic resistance gene satA in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for streptogramin A acetyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 173;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to streptogramin A mediated by the bacterial antibiotic resistance gene satA.

100. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacA-aphD directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 174, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase-phosphotransferase under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacA-aphD.

101. A method as defined in claim 100, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 174.

102. A method for evaluating a bacterial resistance to aminoglycoside; antibiotics mediated by the bacterial antibiotic resistance gene aacA-aphD in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase-phosphotransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 174;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacA-aphD.

103. A method for evaluating a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene vat directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 175, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a virginiamycin acetyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene vat.

104. A method as defined in claim 103, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 175.

105. A method for evaluating a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene vat in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for a virginiamycin acetyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said

at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 175;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene vat.

106. A method for evaluating a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene vga directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 176, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an ATP-binding protein, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene vga.

107. A method as defined in claim 106, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 176.

108. A method for evaluating a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene vga in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an ATP-binding protein that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 176;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene vga.

109. A method for evaluating a bacterial resistance to erythromycin mediated by the bacterial antibiotic resistance gene msrA directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 177, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an erythromycin resistance protein under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to erythromycin mediated by the bacterial antibiotic resistance gene msrA.

110. A method as defined in claim 109, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 177.

111. A method for evaluating a bacterial resistance to erythromycin mediated by the bacterial antibiotic resistance gene msrA in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an erythromycin resistance protein that contains a target sequence, and the other of

said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 177;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to erythromycin mediated by the bacterial antibiotic resistance gene msrA.

112. A method for evaluating potential bacterial resistance to β-lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene int directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 171, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an integrase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of potential bacterial resistance to β-lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene int.

113. A method as defined in claim 112, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 171.

114. A method for evaluating potential bacterial resistance to β-lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene int in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an integrase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 171;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of potential bacterial resistance to β-lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene int.

115. A method for evaluating potential bacterial resistance to β-lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene sul directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 172, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a sulfonamide resistance protein under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of potential bacterial resistance to β-lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene sul.

116. A method as defined in claim 115, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 172.

117. A method for evaluating potential bacterial resistance to β-lactams, aminoglycosides, chloramphenicol and/or tri-

methoprim mediated by the bacterial antibiotic resistance gene sul in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for a sulfonamide resistance protein that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 172;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of potential bacterial resistance to β-lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene sul.

118. A nucleic acid having the nucleotide sequence of any one of SEQ ID NOs: 1 to 37, SEQ ID NOs: 161 to 177, a part thereof and variants thereof which, when in single stranded form, ubiquitously and specifically hybridize with a target bacterial DNA as a probe or as a primer.

119. An oligonucleotide having a nucleotidic sequence of any one of SEQ ID NOs: 38 to 160.

120. A recombinant plasmid comprising a nucleic acid as defined in claim 118.

121. A recombinant host which has been transformed by a recombinant plasmid according to claim 120.

122. A recombinant host according to claim 121 wherein said host is *Escherichia coli.*

123. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial species defined in any one of claims **9, 14, 19, 24, 29, 34, 39, 43, 47, 52, 57** and **61,** comprising any combination of probes defined therein.

124. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial species defined in any one of claims **10, 11, 15, 16, 20, 21, 25, 26, 30, 31, 35, 36, 40, 44, 48, 49, 53, 54, 58, 62** and **65,** comprising any combination of oligonucleotide probes defined therein.

125. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial species defined in any one of claims **12, 13, 17, 18, 22, 23, 27, 28, 32, 33, 37, 38, 41, 42, 45, 46, 50, 51, 55, 56, 59, 60, 63, 64** and **66** comprising any combination of primers defined therein.

126. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial resistance genes defined in any one of claims **67, 70, 73, 76, 79, 82, 85, 88, 91, 94, 97, 100, 103, 106** and **109** comprising any combination of probes defined therein.

127. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial resistance genes defined in any one of claims **68, 71, 74, 77, 80, 83, 86, 89, 92, 95, 98, 101, 104, 107** and **110** comprising any combination of oligonucleotide probes defined therein.

128. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial resistance genes defined in any one of claims **69, 72, 75, 78, 81, 84, 87, 90, 93, 96, 99, 102, 105, 108** and **111** comprising any combination of primers defined therein.

129. A diagnostic kit for the simultaneous detection and quantification of nucleic acids of any combination of the bacterial species defined in claim 123, comprising any combination of the bacterial probes defined therein and any combination of the probes to the antibiotic resistance genes defined in any one of SEQ ID NOs: 161 to 177 in whole or in part.

130. A diagnostic kit for the simultaneous detection and quantification of nucleic acids of any combination of the bacterial species defined in claim 124, comprising any combination of the bacterial oligonucleotide probes defined therein and any combination of oligonucleotide probes that hybridize to the antibiotic resistance genes defined in any one of SEQ ID NOs: 161 to 177.

131. A diagnostic kit for the simultaneous detection and quantification of nucleic acids of any combination of the bacterial species defined in claim 125, comprising any combination of the primers defined therein and any combination of primers that anneal to the antibiotic resistance genes defined in any one of SEQ ID NOs: 161 to 177.

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