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(72) Inventeurs/Inventors:
BERGERON, MICHEL G., CA;
PICARD, FRANCOIS J., CA;
OUELLETTE, MARC, CA;
ROY, PAUL H., CA
(73) Propriétaire/Owner:
GENEOHM SCIENCES CANADA INC., CA
(74) Agent: GOUDREAU GAGE DUBUC

(54) Titre : METHODE DE DETECTION ET D'IDENTIFICATION RAPIDE D'AGENTS PATHOGENES BACTERIENS
COMMUNS ET DE GENES DE RESISTANCE AUX ANTIBIOTIQUES COMMUNS DANS DES SPECIMENS
CLINIQUES

(54) Title: METHOD TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC
RESISTANCE GENES FROM CLINICAL SPECIMENS

(57) **Abrégé/Abstract:**

DNA-based methods employing amplification primers or probes for detecting, identifying, and quantifying in a test sample DNA from (i) any bacterium, (ii) the species *Streptococcus agalactiae*, *Staphylococcus saprophyticus*, *Enterococcus faecium*, *Neisseria meningitidis*, *Listeria monocytogenes* and *Candida albicans*, and (iii) any species of the genera *Streptococcus*, *Staphylococcus*, *Enterococcus*, *Neisseria* and *Candida* are disclosed. DNA-based methods employing amplification primers or probes for detecting, identifying, and quantifying in a test sample antibiotic resistance genes selected from the group consisting of bla_{tem} , bla_{rob} , bla_{shv} , bla_{oxa} , bla_Z , $aadB$, $aacC1$, $aacC2$, $aacC3$, $aacA4$, $aac6'-IIa$, $ermA$, $ermB$, $ermC$, $mecA$, $vanA$, $vanB$, $vanC$, $satA$, $aac(6'-aph(2''))$, $aad(6')$, vat , vga , $msrA$, sul and int are also disclosed. The above microbial species, genera and resistance genes are all clinically relevant and commonly encountered in a variety of clinical specimens. These DNA-based assays are rapid, accurate and can be used in clinical microbiology laboratories for routine diagnosis. These novel diagnostic tools should be useful to improve the speed and accuracy of diagnosis of microbial infections, thereby allowing more effective treatments. Diagnostic kits for (i) the universal detection and quantification of bacteria, and/or (ii) the detection, identification and quantification of the above-mentioned bacterial and fungal species and/or genera, and/or (iii) the detection, identification and quantification of the above-mentioned antibiotic resistance genes are also claimed.



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(21) International Application Number: PCT/CA97/00829 (22) International Filing Date: 4 November 1997 (04.11.97) (30) Priority Data: 08/743,637 4 November 1996 (04.11.96) US (71) Applicant (for all designated States except US): INFECTIO DIAGNOSTIC (I.D.I.) INC. [CA/CA]; 4 ^{ème} étage, 2050, boulevard René Lévesque Ouest, Sainte-Foy, Québec G1V 2K8 (CA). (72) Inventors; and (75) Inventors/Applicants (for US only): BERGERON, Michel, G. [CA/CA]; 2069, rue Brûlard, Sillery, Québec G1T 1G2 (CA). PICARD, François, J. [CA/CA]; 1245, rue de la Sapinière, Cap-Rouge, Québec G1Y 1A1 (CA). OUELLETTE, Marc [CA/CA]; 1035 de Ploermel, Sillery, Québec G1S 3S1 (CA). ROY, Paul, H. [US/US]; 28, rue Charles Garnier, Loretteville, Québec G2A 2X8 (CA). (74) Agents: DUBUC, Jean, H. et al.; Goudreau Gage Dubuc & Martineau Walker, The Stock Exchange Tower, Suite 3400, 800 Place Victoria, P.O. Box 242, Montreal, Québec H4Z 1E9 (CA).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims</i> <i>and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 13 August 1998 (13.08.98)
(54) Title: SPECIES-SPECIFIC, GENUS-SPECIFIC AND UNIVERSAL DNA PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL AND FUNGAL PATHOGENS AND ASSOCIATED AN- TIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS FOR DIAGNOSIS IN MICROBIOLOGY LABORATO- RIES (57) Abstract DNA-based methods employing amplification primers or probes for detecting, identifying, and quantifying in a test sample DNA from (i) any bacterium, (ii) the species <i>Streptococcus agalactiae</i> , <i>Staphylococcus saprophyticus</i> , <i>Enterococcus faecium</i> , <i>Neisseria meningitidis</i> , <i>Listeria monocytogenes</i> and <i>Candida albicans</i> , and (iii) any species of the genera <i>Streptococcus</i> , <i>Staphylococcus</i> , <i>Enterococcus</i> , <i>Neisseria</i> and <i>Candida</i> are disclosed. DNA-based methods employing amplification primers or probes for detecting, identifying, and quantifying in a test sample antibiotic resistance genes selected from the group consisting of <i>bla_{tem}</i> , <i>bla_{rob}</i> , <i>bla_{shv}</i> , <i>bla_{oxa}</i> , <i>bla_Z</i> , <i>aadB</i> , <i>aacC1</i> , <i>aacC2</i> , <i>aacC3</i> , <i>aacA4</i> , <i>aac6'-IIa</i> , <i>ermA</i> , <i>ermB</i> , <i>ermC</i> , <i>mecA</i> , <i>vanA</i> , <i>vanB</i> , <i>vanC</i> , <i>satA</i> , <i>aac(6'-aph(2'))</i> , <i>aad(6')</i> , <i>vat</i> , <i>vga</i> , <i>msrA</i> , <i>sul</i> and <i>int</i> are also disclosed. The above microbial species, genera and resistance genes are all clinically relevant and commonly encountered in a variety of clinical specimens. These DNA-based assays are rapid, accurate and can be used in clinical microbiology laboratories for routine diagnosis. These novel diagnostic tools should be useful to improve the speed and accuracy of diagnosis of microbial infections, thereby allowing more effective treatments. Diagnostic kits for (i) the universal detection and quantification of bacteria, and/or (ii) the detection, identification and quantification of the above-mentioned bacterial and fungal species and/or genera, and/or (iii) the detection, identification and quantification of the above-mentioned antibiotic resistance genes are also claimed.		

TITLE OF THE INVENTION

**METHOD TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL
PATHOGENS AND ANTIBIOTIC RESISTANCE GENES FROM CLINICAL
SPECIMENS**

BACKGROUND OF THE INVENTION**Classical methods for the identification and susceptibility testing of bacteria**

10 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 (bioMérieux). For susceptibility testing, clinical microbiology
laboratories use methods including disk diffusion, agar dilution and broth microdilution.
Although identifications based on biochemical tests and antibacterial susceptibility
15 tests are cost-effective, at least two days are required to obtain preliminary results due
to the necessity of two successive overnight incubations to identify the bacteria from
clinical specimens as well as to determine their susceptibility to antimicrobial agents.
There are some commercially available automated systems (i.e. the MicroScan™ system
from Dade Diagnostics Corp. and the Vitek™ system from bioMérieux) which use
20 sophisticated and expensive apparatus for faster microbial identification and
susceptibility testing (Stager and Davis, 1992, Clin. Microbiol. Rev. 5:302-327). These
systems require shorter incubation periods, thereby allowing most bacterial
identifications and susceptibility testing to be performed in less than 6 hours.
Nevertheless, these faster systems always require the primary isolation of the bacteria
25 as a pure culture, a process which takes at least 18 hours for a pure culture or 2 days
for a mixed culture. The fastest identification system, the autoSCAN-Walk-Away™
system (Dade Diagnostics Corp.) identifies both gram-negative and gram-positive
bacterial species from standardized inoculum in as little as 2 hours and gives
susceptibility patterns to most antibiotics in 5.5 hours. However, this system has a
30 particularly high percentage (i.e. 3.3 to 40.5%) of non-conclusive identifications with
bacterial species other than *Enterobacteriaceae* (Croizé J., 1995, Lett. Infectiol.
10:109-113; York et al., 1992, J. Clin. Microbiol. 30:2903-2910). For
Enterobacteriaceae, the percentage of non-conclusive identifications was 2.7 to 11.4%.

35 A wide variety of bacteria and fungi are routinely isolated and identified from
clinical specimens in microbiology laboratories. Tables 1 and 2 give the incidence for
the most commonly isolated bacterial and fungal pathogens from various types of
clinical specimens. These pathogens are the most frequently associated with
nosocomial and community-acquired human infections and are therefore considered
the most clinically important.

Clinical specimens tested in clinical microbiology laboratories

Most clinical specimens received in clinical microbiology laboratories are urine and blood samples. At the microbiology laboratory of the Centre Hospitalier de l'Université Laval (CHUL), urine and blood account for approximately 55% and 30% of the specimens received, respectively (Table 3). The remaining 15% of clinical specimens comprise various biological fluids including sputum, pus, cerebrospinal fluid, synovial fluid, and others (Table 3). Infections of the urinary tract, the respiratory tract and the bloodstream are usually of bacterial etiology and require antimicrobial therapy. In fact, all clinical samples received in the clinical microbiology laboratory are tested routinely for the identification of bacteria and susceptibility testing.

Conventional pathogen identification from clinical specimens**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. However, the gold standard remains the classical semi-quantitative plate culture method in which 1 µL 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 urinary tract infection (UTI) is normally associated with a bacterial count of 10^7 CFU/L or more 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, approximately 80% of urine specimens tested in clinical microbiology laboratories are considered negative (i.e. bacterial count of less than 10^7 CFU/L; Table 3). 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. The biochemical and susceptibility testing normally require 18-24 hours of incubation.

Accurate and rapid urine screening methods for bacterial pathogens would allow a faster identification of negative specimens and a more efficient treatment and care management of patients. Several rapid identification methods (Uriscreen™, UTIscreen™, Flash Track™ DNA probes and others) have been 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 poor specificities as well as a high number of false negative and false positive results (Koenig *et al.*, 1992, J. Clin. Microbiol. 30:342-345; Pezzlo *et al.*, 1992, J. Clin. Microbiol. 30:640-684).

Blood specimens

The blood specimens received in the microbiology laboratory are always submitted for culture. Blood culture systems may be manual, semi-automated or completely automated. The BACTEC system (from Becton Dickinson) and the

BacTAlert system (from Organon Teknika Corporation) are the two most widely used automated blood culture systems. These systems incubate blood culture bottles under optimal conditions for bacterial growth. Bacterial growth is monitored continuously to detect early positives by using highly sensitive bacterial growth detectors. Once growth is detected, a Gram stain is performed directly from the blood culture and then used to inoculate nutrient agar plates. Subsequently, bacterial identification and susceptibility testing are carried out from isolated bacterial colonies with automated systems as described previously. The bottles are normally reported as negative if no growth is detected after an incubation of 6 to 7 days. Normally, the vast majority of blood cultures are reported negative. For example, the percentage of negative blood cultures at the microbiology laboratory of the CHUL for the period February 1994-January 1995 was 93.1% (Table 3).

Other clinical samples

Upon receipt by the clinical microbiology laboratory, all body fluids other than blood and urine that are from normally sterile sites (i.e. cerebrospinal, synovial, pleural, pericardial and others) are processed for direct microscopic examination and subsequent culture. Again, most clinical samples are negative for culture (Table 3).

Regarding clinical specimens which are not from sterile sites such as sputum or stool specimens, the laboratory diagnosis by culture is more problematic because of the contamination by the normal flora. The bacterial pathogens potentially associated with the infection are purified from the contaminants and then identified as described previously. Of course, the universal detection of bacteria would not be useful for the diagnosis of bacterial infections at these non sterile sites. On the other hand, DNA-based assays for species or genus detection and identification as well as for the detection of antibiotic resistance genes from these specimens would be very useful and would offer several advantages over classical identification and susceptibility testing methods.

DNA-based assays with any clinical specimens

There is an obvious need for rapid and accurate diagnostic tests for bacterial detection and identification directly from clinical specimens. DNA-based technologies are rapid and accurate and offer a great potential to improve the diagnosis of infectious diseases (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). The DNA probes and amplification primers which are objects of the present invention are applicable for bacterial or fungal detection and identification directly from any clinical specimens such as blood cultures, blood, urine, sputum, cerebrospinal fluid, pus and other type of specimens (Table 3). The DNA-based tests proposed in this invention are superior in terms of both rapidity and accuracy to standard biochemical methods currently used for routine diagnosis from any clinical specimens in microbiology laboratories. Since

these tests are performed in around only one hour, they provide the clinicians with new diagnostic tools which should contribute to increase the efficiency of therapies with antimicrobial agents. Clinical specimens from organisms other than humans (e.g. other primates, birds, plants, mammals, farm animals, livestock and others) may also be tested with these assays.

A high percentage of culture negative specimens

Among all the clinical specimens received for routine diagnosis, approximately 80% of urine specimens and even more (around 95%) for other types of clinical specimens are negative for the presence of bacterial pathogens (Table 3). It would also be desirable, in addition to identify bacteria at the species or genus level in a given specimen, to screen out the high proportion of negative clinical specimens with a test detecting the presence of any bacterium (i.e. universal bacterial detection). Such a screening test may be based on the DNA amplification by PCR of a highly conserved genetic target found in all bacteria. Specimens negative for bacteria would not be amplified by this assay. On the other hand, those that are positive for bacteria would give a positive amplification signal with this assay.

Towards the development of rapid DNA-based diagnostic tests

A rapid diagnostic test should have a significant impact on the management of infections. DNA probe and DNA amplification technologies offer several advantages over conventional methods for the identification of pathogens and antibiotic resistance genes from clinical samples (Persing et al., 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.; Ehrlich and Greenberg, 1994, PCR-based Diagnostics in Infectious Disease, Blackwell Scientific Publications, Boston, MA). There is no need for culture of the bacterial pathogens, hence the organisms can be detected directly from clinical samples, thereby reducing the time associated with the isolation and identification of pathogens. Furthermore, DNA-based assays are more accurate for bacterial identification than currently used phenotypic identification systems which are based on biochemical tests. Commercially available DNA-based technologies are currently used in clinical microbiology laboratories, mainly for the detection and identification of fastidious bacterial pathogens such as *Mycobacterium tuberculosis*, *Chlamydia trachomatis*, *Neisseria gonorrhoeae* as well as for the detection of a variety of viruses (Podzorski and Persing, Molecular detection and identification of microorganisms. In : P. Murray et al., 1995, Manual of Clinical Microbiology, ASM press, Washington D.C.). There are also other commercially available DNA-based assays which are used for culture confirmation assays.

Others have developed DNA-based tests for the detection and identification of bacterial pathogens which are objects of the present invention: *Staphylococcus* spp. (US patent No. US 5 437 978), *Neisseria* spp. (US patent No. US 5 162 199 and European patent publication No. EP 0 337 896 131) and *Listeria monocytogenes* (US patents Nos 5 389 513 and 5 089 386). However, the diagnostic tests described in

these patents are based either on rRNA genes or on genetic targets different from those described in the present invention.

Although there are diagnostic kits or methods already used in clinical microbiology laboratories, there is still a need for an advantageous alternative to the conventional culture identification methods in order to improve the accuracy and the speed of the diagnosis of commonly encountered bacterial infections. 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. metabolic level).

Knowledge of the genomic sequences of bacterial and fungal species continuously increases as testified by the number of sequences available from databases. From the sequences readily available from databases, there is no indication therefrom as to their potential for diagnostic purposes. For determining good candidates for diagnostic purposes, one could select sequences for DNA-based assays for (i) the species-specific detection and identification of commonly encountered bacterial or fungal pathogens, (ii) the genus-specific detection and identification of commonly encountered bacterial or fungal pathogens, (iii) the universal detection of bacterial or fungal pathogens and/or (iv) the specific detection and identification of antibiotic resistance genes. All of the above types of DNA-based assays may be performed directly from any type of clinical specimens or from a microbial culture.

In WO 96/08502 patent publication, we described DNA sequences suitable for (i) the species-specific detection and identification of 12 clinically important bacterial pathogens, (ii) the universal detection of bacteria, and (iii) the detection of 17 antibiotic resistance genes. This co-pending application described proprietary DNA sequences and DNA sequences selected from databases (in both cases, fragments of at least 100 base pairs), as well as oligonucleotide probes and amplification primers derived from these sequences. All the nucleic acid sequences described in this patent application enter the composition of diagnostic kits and methods capable of a) detecting the presence of bacteria, b) detecting specifically the presence of 12 bacterial species and 17 antibiotic resistance genes. However, these methods and kits need to be improved, since the ideal kit and method should be capable of diagnosing close to 100% of microbial pathogens and antibiotic resistance genes. For example, infections caused by *Enterococcus faecium* have become a clinical problem because of its resistance to many antibiotics. Both the detection of these bacteria and the evaluation of their resistance profiles are desirable. It is worthwhile noting that the French patent publication FR-A-2,699,539 discloses the sequence of vancomycin B gene, which gene may be derived from *Enterococcus faecium* strains resistant to this antibiotic. Besides that, novel DNA sequences (probes and primers) capable of recognizing the same and other microbial pathogens or the same and additional antibiotic resistance genes are also desirable to aim at detecting more target genes and complement our

earlier patent application.

STATEMENT OF THE INVENTION

5 It is an object of the present invention to provide a specific, ubiquitous and sensitive method using probes and/or amplification primers for determining the presence and/or amount of nucleic acids:

- from specific microbial species or genera selected from the group consisting of *Streptococcus* species, *Streptococcus agalactiae*, *Staphylococcus* species,
10 *Staphylococcus saprophyticus*, *Enterococcus* species, *Enterococcus faecium*, *Neisseria* species, *Neisseria meningitidis*, *Listeria monocytogenes*, *Candida* species and *Candida albicans*

- from an antibiotic resistance gene selected from the group consisting of *bla_{tem}*, *bla_{rob}*, *bla_{SHV}*, *bla_{oxA}*, *bla_Z*, *aadB*, *aacC1*, *aacC2*, *aacC3*, *aacA4*, *aac6'-IIa*, *ermA*, *ermB*,
15 *ermC*, *mecA*, *vanA*, *vanB*, *vanC*, *satA*, *aac(6'')-aph(2'')*, *aad(6')*, *vat*, *vga*, *msrA*, *sul* and *int*, and optionally,

- from any bacterial species

in any sample suspected of containing said nucleic acids,

wherein each of said nucleic acids or a variant or part thereof comprises a
20 selected target region hybridizable with said probe 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 or amplified products as an indication of the presence and/or amount of said any bacterial species, specific microbial species or genus and antibiotic resistance gene.

25 In a specific embodiment, a similar method directed to each specific microbial species or genus detection and identification, antibiotic resistance genes detection, and universal bacterial detection, separately, is provided.

In a more specific embodiment, the method makes use of DNA fragments (proprietary fragments and fragments obtained from databases), selected for their
30 capacity to sensitively, specifically and ubiquitously detect the targeted bacterial or fungal nucleic acids.

In a particularly preferred embodiment, oligonucleotides of at least 12 nucleotides in length have been derived from the longer DNA fragments, and are used in the present method as probes or amplification primers.

35 The proprietary oligonucleotides (probes and primers) are also another object of the invention.

Diagnostic kits comprising probes or amplification primers for the detection of

a microbial species or genus selected from the group consisting of *Streptococcus* species, *Streptococcus agalactiae*, *Staphylococcus* species, *Staphylococcus saprophyticus*, *Enterococcus* species, *Enterococcus faecium*, *Neisseria* species, *Neisseria meningitidis*, *Listeria monocytogenes*, *Candida* species and *Candida albicans* are also objects of the present invention.

Diagnostic kits further comprising probes or amplification primers for the detection of an antibiotic resistance gene selected from the group consisting of *bla_{tem}*, *bla_{rob}*, *bla_{shv}*, *bla_{oxa}*, *bla_Z*, *aadB*, *aacC1*, *aacC2*, *aacC3*, *aacA4*, *aac6'-IIa*, *ermA*, *ermB*, *ermC*, *mecA*, *vanA*, *vanB*, *vanC*, *satA*, *aac(6')-aph(2'')*, *aad(6')*, *vat*, *vga*, *msrA*, *sul* and *int* are also objects of this invention.

Diagnostic kits further comprising probes or amplification primers for the detection of any bacterial or fungal species, comprising or not comprising those for the detection of the specific microbial species or genus listed above, and further comprising or not comprising probes and primers for the antibiotic resistance genes listed above, are also objects of this invention.

In a preferred embodiment, such a kit allows for the separate or the simultaneous detection and identification of the above-listed microbial species or genus, antibiotic resistance genes and for the detection of any bacterium.

In the above methods and kits, amplification reactions may include 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) transcription-mediated amplification, h) cycling probe technology (CPT) i) nested PCR, or j) multiplex PCR.

In a preferred embodiment, a PCR protocol is used as an amplification reaction.

In a particularly preferred embodiment, a PCR protocol is provided, comprising, for each amplification cycle, an annealing step of 30 seconds at 45-55°C and a denaturation step of only one second at 95°C, without any time allowed specifically for the elongation step. This PCR protocol has been standardized to be suitable for PCR reactions with all selected primer pairs, which greatly facilitates the testing because each clinical sample can be tested with universal, species-specific, genus-specific and antibiotic resistance gene PCR primers under uniform cycling conditions. Furthermore, various combinations of primer pairs may be used in multiplex PCR assays.

We aim at developing a rapid test or kit to discard rapidly all the samples which are negative for bacterial cells and to subsequently detect and identify the above bacterial and/or fungal species and genera and to determine rapidly the bacterial resistance to antibiotics. Although the sequences from the selected antibiotic resistance genes are available from databases and have been used to develop DNA-based tests for their detection, our approach is unique because it represents a major improvement over current gold standard diagnostic methods based on bacterial

cultures. Using an amplification method for the simultaneous bacterial detection and identification and antibiotic resistance genes detection, there is no need for culturing the clinical sample prior to testing. Moreover, a modified PCR protocol has been developed to detect all target DNA sequences in approximately one hour under uniform amplification conditions. This procedure will save lives by optimizing treatment, will diminish antibiotic resistance because less antibiotics will be prescribed, will reduce the use of broad spectrum antibiotics which are expensive, decrease overall health care costs by preventing or shortening hospitalizations, and decrease the time and costs associated with clinical laboratory testing.

In the methods and kits described herein below, the oligonucleotide probes and amplification primers have been derived from larger sequences (i.e. DNA fragments of at least 100 base pairs). All DNA fragments have been obtained either from proprietary fragments or from databases. DNA fragments selected from databases are newly used in a method of detection according to the present invention, since they have been selected for their diagnostic potential.

It is clear to the individual skilled in the art that other oligonucleotide sequences appropriate for (i) the universal bacterial detection, (ii) the detection and identification of the above microbial species or genus and (iii) the detection of antibiotic resistance genes other than those listed in Annex VI may also be derived from the proprietary fragments or selected database sequences. For example, the oligonucleotide primers or probes may be shorter or longer than the ones we have chosen; they may also be selected anywhere else in the proprietary DNA fragments or in the sequences selected from databases; they may be also variants of the same oligonucleotide. If the target DNA or a variant thereof hybridizes to a given oligonucleotide, or if the target DNA or a variant thereof can be amplified by a given oligonucleotide PCR primer pair, the converse is also true; a given target DNA may hybridize to a variant oligonucleotide probe or be amplified by a variant oligonucleotide PCR primer. Alternatively, the oligonucleotides may be designed from any DNA fragment sequences for use in amplification methods other than PCR. Consequently, the core of this invention is the identification of universal, species-specific, genus-specific and resistance gene-specific genomic or non-genomic DNA fragments which are used as a source of specific and ubiquitous oligonucleotide probes and/or amplification primers. Although the selection and evaluation of oligonucleotides suitable for diagnostic purposes requires much effort, it is quite possible for the individual skilled in the art to derive, from the selected DNA fragments, oligonucleotides other than the ones listed in Annex VI which are suitable for diagnostic purposes. When a proprietary fragment or a database sequence is selected for its specificity and ubiquity, it increases the probability that subsets thereof will also be specific and ubiquitous.

Since a high percentage of clinical specimens are negative for bacteria (Table

3), DNA fragments having a high potential for the selection of universal oligonucleotide probes or primers were selected from proprietary and database sequences. The amplification primers were selected from a gene highly conserved in bacteria and fungi, and are used to detect the presence of any bacterial pathogen in clinical specimens in order to determine rapidly (approximately one hour) whether it is positive or negative for bacteria. The selected gene, designated *tuf*, encodes a protein (EF-Tu) involved in the translational process during protein synthesis. The *tuf* gene sequence alignments used to derive the universal primers include both proprietary and database sequences (Example 1 and Annex I). This strategy allows the rapid screening of the numerous negative clinical specimens (around 80% of the specimens received, see Table 3) submitted for bacteriological testing. Tables 4, 5 and 6 provide a list of the bacterial or fungal species used to test the specificity of PCR primers and DNA probes. Table 7 gives a brief description of each species-specific, genus-specific and universal amplification assays which are objects of the present invention. Tables 8, 9 and 10 provide some relevant information about the proprietary and database sequences selected for diagnostic puposes.

DETAILED DESCRIPTION OF THE INVENTION

Development of species-specific, genus-specific, universal and antibiotic resistance gene-specific DNA probes and amplification primers for microorganisms

Selection from databases of sequences suitable for diagnostic purposes

In order to select sequences which are suitable for species-specific or genus-specific detection and identification of bacteria or fungi or, alternatively, for the universal detection of bacteria, the database sequences (GenBank, EMBL and Swiss-Prot) were chosen based on their potential for diagnostic purposes according to sequence information and computer analysis performed with these sequences. Initially, all sequence data available for the targeted microbial species or genus were carefully analyzed. The gene sequences which appeared the most promising for diagnostic purposes based on sequence information and on sequence comparisons with the corresponding gene in other microbial species or genera performed with the Genetics Computer Group (GCG, Wisconsin) programs were selected for testing by PCR. Optimal PCR amplification primers were chosen from the selected database sequences with the help of the Oligo™ 4.0 primer analysis software (National Biosciences Inc., Plymouth, Minn.). The chosen primers were tested in PCR assays for their specificity and ubiquity for the target microbial species or genus. In general, the identification of database sequences from which amplification primers suitable for species-specific or genus-specific detection and identification were selected involved the computer analysis and PCR testing of several candidate gene sequences before

obtaining a primer pair which is specific and ubiquitous for the target microbial species or genus. Annex VI provides a list of selected specific and ubiquitous PCR primer pairs. Annexes I to V and Examples 1 to 4 illustrate the strategy used to select genus-specific, species-specific and universal PCR primers from *tuf* sequences or from the *recA* gene.

Oligonucleotide primers and probes design and synthesis

The DNA fragments sequenced by us or selected from databases (GenBank and EMBL) were used as sources of oligonucleotides for diagnostic purposes. 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 databases were tested for their specificity and ubiquity in PCR and hybridization assays as described later. It is important to note that the database sequences were selected based on their potential for being species-specific, genus-specific or universal for the detection of bacteria or fungi according to available sequence information and extensive analysis and that, in general, several candidate database sequences had to be tested in order to obtain the desired specificity, ubiquity and sensitivity.

Oligonucleotide probes and amplification primers derived from species-specific fragments selected from database sequences were synthesized using an automated DNA synthesizer (Perkin-Elmer Corp., Applied Biosystems Division). 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 (i.e. the Genetics Computer Group (GCG) programs and the primer analysis software Oligo™ 4.0). 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 and a high proportion of G or C residues at the 3' end (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.).

The oligonucleotide primers or probes may be derived from either strand of the duplex DNA. The primers or probes may consist of the bases A, G, C, or T or analogs and they may be degenerated at one or more chosen nucleotide position(s). The primers or probes may be of any suitable length and may be selected anywhere within the DNA sequences from proprietary fragments or from selected database sequences which are suitable for (i) the universal detection of bacteria, (ii) the species-specific detection and identification of *Enterococcus faecium*, *Listeria monocytogenes*, *Neisseria meningitidis*, *Staphylococcus saprophyticus*, *Streptococcus agalactiae* and *Candida albicans* (iii) the genus-specific detection of *Streptococcus* species, *Enterococcus* species, *Staphylococcus* species and *Neisseria* species or (iv) the detection of the 26 above-mentioned clinically important antibiotic resistance genes.

5 Variants for a given target bacterial gene are naturally occurring and are attributable to sequence variation within that gene during evolution (Watson *et al.*, 1987, Molecular Biology of the Gene, 4th ed., The Benjamin/Cummings Publishing Company, Menlo Park, CA; Lewin, 1989, Genes IV, John Wiley & Sons, New York, NY). For example, different strains of the same bacterial species may have a single or more nucleotide variation(s) at the oligonucleotide hybridization site. The person skilled in the art is well aware of the existence of variant bacterial or fungal DNA sequences for a specific gene and that the frequency of sequence variations depends on the selective pressure during evolution on a given gene product. The detection of a variant
10 sequence for a region between two PCR primers may be demonstrated by sequencing the amplification product. In order to show the presence of sequence variants at the primer hybridization site, one has to amplify a larger DNA target with PCR primers outside that hybridization site. Sequencing of this larger fragment will allow the detection of sequence variation at this site. A similar strategy may be applied to show
15 variants at the hybridization site of a probe. Insofar as the divergence of the target sequences or a part thereof does not affect the specificity and ubiquity of the amplification primers or probes, variant bacterial DNA is under the scope of this invention. Variants of the selected primers or probes may also be used to amplify or hybridize to a variant DNA.

20 **Sequencing of *tuf* sequences from a variety of bacterial and fungal species**

The nucleotide sequence of a portion of *tuf* genes was determined for a variety of bacterial and fungal species. The amplification primers SEQ ID NOs: 107 and 108, which amplify a *tuf* gene portion of approximately 890 bp, were used for the sequencing of bacterial *tuf* sequences. The amplification primers SEQ ID NOs: 109
25 and 172, which amplify a *tuf* gene portion of approximately 830 bp, were used for the sequencing of fungal *tuf* sequences. Both primer pairs can amplify *tufA* and *tufB* genes. This is not surprising because these two genes are nearly identical. For example, the entire *tufA* and *tufB* genes from *E. coli* differ at only 13 nucleotide positions (Neidhardt *et al.*, 1996, *Escherichia coli* and *Salmonella*: Cellular and
30 Molecular Biology, 2nd ed., American Society for Microbiology Press, Washington, D.C.). These amplification primers are degenerated at several nucleotide positions and contain inosines in order to allow the amplification of a wide range of *tuf* sequences. The strategy used to select these amplification primers is similar to that illustrated in Annex I for the selection of universal primers. The amplification primers SEQ ID NOs:
35 107 and 108 could be used to amplify the *tuf* genes from any bacterial species. The amplification primers SEQ ID NOs: 109 and 172 could be used to amplify the *tuf* genes from any fungal species.

The *tuf* genes were amplified directly from bacterial or yeast cultures using the following amplification protocol: One μ L of cell suspension was transferred directly to

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19 μ L of a PCR reaction mixture containing 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% TritonTMX-100, 2.5 mM MgCl₂, 1 μ M of each of the 2 primers, 200 μ M of each of the four dNTPs, 0.5 unit of *Taq* DNA polymerase (Promega Corp., Madison, WI). PCR reactions were subjected to cycling using a MJ Research PTC-200 thermal cycler (MJ Research Inc., Watertown, Mass.) as follows: 3 min at 96°C followed by 30-35 cycles of 1 min at 95°C for the denaturation step, 1 min at 30-50°C for the annealing step and 1 min at 72°C for the extension step. Subsequently, twenty microliters of the PCR-amplified mixture were resolved by electrophoresis in a 1.5% agarose gel. The gel was then visualized by staining with methylene blue (Flores *et al.*, 1992, Biotechniques, 13:203-205). The size of the amplification products was estimated by comparison with a 100-bp molecular weight ladder. The band corresponding to the specific amplification product (i.e. approximately 890 or 830 bp for bacterial or fungal *tuf* sequences, respectively) was excised from the agarose gel and purified using the QIAquickTM gel extraction kit (QIAGEN Inc., Chatsworth, CA). The gel-purified DNA fragment was then used directly in the sequencing protocol. Both strands of the *tuf* genes amplification product were sequenced by the dideoxynucleotide chain termination sequencing method by using an Applied Biosystems automated DNA sequencer (model 373A) with their PRISMTM Sequenase[®] Terminator Double-stranded DNA Sequencing Kit (Perkin-Elmer Corp., Applied Biosystems Division, Foster City, CA). The sequencing reactions were all performed by using the amplification primers (SEQ ID NOs: 107 to 109 and 172) and 100 ng per reaction of the gel-purified amplicon. In order to ensure that the determined sequence did not contain errors attributable to the sequencing of PCR artefacts, we have sequenced two preparations of the gel-purified *tuf* amplification product originating from two independent PCR amplifications. For all target microbial species, the sequences determined for both amplicon preparations were identical. Furthermore, the sequences of both strands were 100% complementary thereby confirming the high accuracy of the determined sequence. The *tuf* sequences determined using the above strategy are all in the Sequence Listing (i.e. SEQ ID NOs:118 to 146). Table 13 gives the originating microbial species and the source for each *tuf* sequence in the Sequence Listing.

The alignment of the *tuf* sequences determined by us or selected from databases reveals clearly that the length of the sequenced portion of the *tuf* genes is variable. There may be insertions or deletions of several amino acids. This explains why the size of the sequenced *tuf* amplification product was variable for both bacterial and fungal species. Among the *tuf* sequences determined by our group, we found insertions and deletions adding up to 5 amino acids or 15 nucleotides. Consequently, the nucleotide positions indicated on top of each of Annexes I to V do not correspond for *tuf* sequences having insertions or deletions.

It should also be noted that the various *tuf* sequences determined by us

occasionally contain degenerescences. These degenerated nucleotides correspond to sequence variations between *tufA* and *tufB* genes because the amplification primers amplify both *tuf* genes. These nucleotide variations were not attributable to nucleotide misincorporations by the *tag* DNA polymerase because the sequence of both strands were identical and also because the sequences determined with both preparations of the gel-purified *tuf* amplicons were identical.

The selection of amplification primers from *tuf* sequences

The *tuf* sequences determined by us or selected from databases were used to select PCR primers for (i) the universal detection of bacteria, (ii) the genus-specific detection and identification of *Enterococcus* spp. and *Staphylococcus* spp. and (iii) the species-specific detection and identification of *Candida albicans*. The strategy used to select these PCR primers was based on the analysis of multiple sequence alignments of various *tuf* sequences. For more details about the selection of PCR primers from *tuf* sequences, please refer to Examples 1 to 3 and Annexes I to IV.

The selection of amplification primers from *recA*

The comparison of the nucleotide sequence for the *recA* gene from various bacterial species including 5 species of streptococci allowed the selection of *Streptococcus*-specific PCR primers. For more details about the selection of PCR primers from *recA*, please refer to Example 4 and Annex V.

DNA fragment isolation from *Staphylococcus saprophyticus* by arbitrarily primed PCR

DNA sequences of unknown coding potential for the species-specific detection and identification of *Staphylococcus saprophyticus* were obtained by the method of arbitrarily primed PCR (AP-PCR).

AP-PCR is a method which can be used to generate specific DNA probes for microorganisms (Fani *et al.*, 1993, Mol. Ecol. 2:243-250). A description of the AP-PCR protocol used to isolate a species-specific genomic DNA fragment from *Staphylococcus saprophyticus* follows. Twenty different oligonucleotide primers of 10 nucleotides in length (all included in the AP-PCR kit OPAD (Operon Technologies, Inc., Alameda, CA)) were tested systematically with DNAs from 3 bacterial strains of *Staphylococcus saprophyticus* (all obtained from the American Type Culture Collection (ATCC): numbers 15305, 35552 and 43867) as well as with DNA from four other staphylococcal species (*Staphylococcus aureus* ATCC 25923, *Staphylococcus epidermidis* ATCC 14990, *Staphylococcus haemolyticus* ATCC 29970 and *Staphylococcus hominis* ATCC 35982). For all bacterial species, amplification was performed from a bacterial suspension adjusted to a standard 0.5 McFarland which corresponds to approximately 1.5×10^8 bacteria/mL. One μ L of the standardized bacterial suspension was transferred directly to 19 μ L of a PCR reaction mixture containing 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM $MgCl_2$,

1.2 μ M of only one of the 20 different AP-PCR primers OPAD, 200 μ M of each of the four dNTPs and 0.5 unit of *Taq* DNA polymerase (Promega Corp., Madison, WI). PCR reactions were subjected to cycling using a MJ Research PTC-200 thermal cycler (MJ Research Inc.) as follows: 3 min at 96°C followed by 35 cycles of 1 min at 95°C for the denaturation step, 1 min at 32°C for the annealing step and 1 min at 72°C for the extension step. A final extension step of 7 min at 72°C was made after the 35 cycles to ensure complete extension of PCR products. Subsequently, twenty microliters of the PCR amplified mixture were resolved by electrophoresis in a 2% agarose gel containing 0.25 μ g/mL of ethidium bromide. The size of the amplification products was estimated by comparison with a 50-bp molecular weight ladder.

Amplification patterns specific for *Staphylococcus saprophyticus* were observed with the AP-PCR primer OPAD-9 (SEQ ID NO: 25). Amplification with this primer consistently showed a band corresponding to a DNA fragment of approximately 450 bp for all *Staphylococcus saprophyticus* strains tested but not for any of the four other staphylococcal species tested. This species-specific pattern was confirmed by testing 10 more clinical isolates of *S. saprophyticus* selected from the culture collection of the microbiology laboratory of the CHUL as well as strains selected from the gram-positive bacterial species listed in Table 5.

The band corresponding to the approximately 450 bp amplicon which was specific and ubiquitous for *S. saprophyticus* based on AP-PCR was excised from the agarose gel and purified using the QIAquick™ gel extraction kit (QIAGEN Inc.). The gel-purified DNA fragment was cloned into the T/A cloning site of the pCR 2.1™ plasmid vector (Invitrogen Inc.) using T4 DNA ligase (New England BioLabs). Recombinant plasmids were transformed into *E. coli* DH5α competent cells using standard procedures. Plasmid DNA isolation was done by the method of Birnboim and Doly (Nucleic Acids Res. 7:1513-1523) for small-scale preparations. All plasmid DNA preparations were digested with the *Eco*RI restriction endonuclease to ensure the presence of the approximately 450 bp AP-PCR insert into the recombinant plasmids. Subsequently, a large-scale and highly purified plasmid DNA preparation was performed from two selected clones shown to carry the AP-PCR insert by using the QIAGEN plasmid purification kit. These plasmid preparations were used for automated DNA sequencing.

Both strands of the AP-PCR insert from the two selected clones were sequenced by the dideoxynucleotide chain termination sequencing method with SP6 and T7 sequencing primers, by using an Applied Biosystems automated DNA sequencer as described previously. The analysis of the obtained sequences revealed that the DNA sequences for both strands from each clone were 100% complementary. Furthermore, it showed that the entire sequence determined for each clone were both identical. These sequencing data confirm the 100% accuracy for the determined 438

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bp sequence (SEQ ID NO: 29). Optimal amplification primers have been selected from the sequenced AP-PCR *Staphylococcus saprophyticus* DNA fragment with the help of the primer analysis software Oligo™ 4.0. The selected primer sequences have been tested in PCR assays to verify their specificity and ubiquity (Table 7). These PCR primers were specific since there was no amplification with DNA from bacterial species other than *S. saprophyticus* selected from Tables 4 and 5. Furthermore, this assay was ubiquitous since 245 of 260 strains of *S. saprophyticus* were efficiently amplified with this PCR assay. When used in combination with another *S. saprophyticus*-specific PCR assay, which is an object of our U.S. Patent No. 6,001,564 and PCT WO 96/08582 patent application, the ubiquity reaches 100% for these 260 strains.

DNA amplification

For DNA amplification by the widely used PCR (polymerase chain reaction) method, primer pairs were derived from proprietary DNA fragments or from database sequences. Prior to synthesis, the potential primer pairs were analyzed by using the Oligo™ 4.0 software to verify that they are good candidates for PCR amplification.

During DNA amplification by PCR, two oligonucleotide primers binding respectively to each strand of the heat-denatured 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 follow: Treated clinical specimens or standardized bacterial or fungal suspensions (see below) were amplified in a 20 µL PCR reaction mixture containing 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 2.5 mM MgCl₂, 0.4 µM of each primer, 200 µM of each of the four dNTPs and 0.5 unit of *Taq* DNA polymerase (Promega) combined with the TaqStart™ antibody (Clontech Laboratories Inc., Palo Alto, CA). The TaqStart™ antibody, which is a neutralizing monoclonal antibody to *Taq* DNA polymerase, was added to all PCR reactions to enhance the specificity and the sensitivity of the amplifications (Kellogg *et al.*, 1994, Biotechniques 16:1134-1137). The treatment of the clinical specimens varies with the type of specimen tested, since the composition and the sensitivity level required are different for each specimen type. It consists in a rapid protocol to lyse the bacterial cells and eliminate the PCR inhibitory effects (see example 11 for urine specimen preparation). For amplification from bacterial or fungal cultures, the samples were added directly to the PCR amplification mixture without any pre-treatment step (see example 10). Primer sequences derived from highly conserved regions of the bacterial 16S ribosomal RNA gene were used to provide an internal control for all PCR reactions. Alternatively, the

internal control was derived from sequences not found in microorganisms or in the human genome. The internal control was integrated into all amplification reactions to verify the efficiency of the PCR assays and to ensure that significant PCR inhibition was absent. The internal control derived from rRNA was also useful to monitor the efficiency of bacterial lysis protocols.

PCR reactions were then subjected to thermal cycling (3 min at 95°C followed by 30 cycles of 1 second at 95°C for the denaturation step and 30 second at 55°C for the annealing-extension step) using a PTC-200 thermal cycler (MJ Research Inc.) and subsequently analyzed by standard ethidium bromide-stained agarose gel electrophoresis. The number of cycles performed for the PCR assays varies according to the sensitivity level required. For example, the sensitivity level required for microbial detection directly from clinical specimens is higher for blood specimens than for urine specimens because the concentration of microorganisms associated with a septicemia can be much lower than that associated with a urinary tract infection. Consequently, more sensitive PCR assays having more thermal cycles are required for direct detection from blood specimens. Similarly, PCR assays performed directly from bacterial or fungal cultures may be less sensitive than PCR assays performed directly from clinical specimens because the number of target organisms is normally much lower in clinical specimens than in microbial cultures.

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). Methods based on the detection of fluorescence are particularly promising for utilization in routine diagnosis as they are very rapid, quantitative and can be automated (Example 14).

Microbial pathogens detection and identification may also be performed by solid support or liquid hybridization using species-specific internal DNA probes hybridizing to an amplification product. Such probes may be generated from any species-specific or genus-specific DNA amplification products which are objects of the present invention. Alternatively, the internal probes for species or genus detection and identification may be derived from the amplicons produced by the universal amplification assay. The oligonucleotide probes may be labeled with biotin or with digoxigenin or with any other reporter molecules.

To assure PCR efficiency, glycerol, 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 a target DNA having a high GC content or forming strong secondary structures (Dieffenbach and Dveksler, 1995, PCR Primer : A Laboratory Manual, Cold Spring Harbor Laboratory Press, Plainview, New York). The

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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 MgCl_2 are 0.1-1.5 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 9 to 14.

The person skilled in the art of DNA amplification knows the existence of other rapid amplification procedures such as ligase chain reaction (LCR), transcription-mediated amplification (TMA), self-sustained sequence replication (3SR), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA), branched DNA (bDNA) and cycling probe technology (CPT) (Lee *et al.*, 1997, Nucleic Acid Amplification Technologies: Application to Disease Diagnosis, Eaton Publishing, Boston, MA ; 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 method or any other procedure which may be used to increase rapidity and sensitivity of the tests. Any oligonucleotide suitable for the amplification of nucleic acids by approaches other than PCR and derived from the species-specific, genus-specific and universal DNA fragments as well as from selected antibiotic resistance gene sequences included in this document are also under the scope of this invention.

Hybridization assays with oligonucleotide probes

In hybridization experiments, single-stranded oligonucleotides (size less than 100 nucleotides) have some advantages over DNA fragment probes for the detection of bacteria, such as ease of synthesis 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 $\gamma\text{-}^{32}\text{P}(\text{dATP})$ using T4 polynucleotide kinase (Pharmacia) (Sambrook *et al.*, 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY). The unincorporated radionucleotide was removed by passing the labeled oligonucleotide through a SephadexTMG-50 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.

Each oligonucleotide probe was then tested for its specificity by hybridization to DNAs from a variety of bacterial and fungal species selected from Tables 4, 5 and 6. All of the bacterial or fungal species tested were likely to be pathogens associated

with common infections or potential contaminants which can be isolated from clinical specimens. Each target DNA was released from bacterial cells using standard chemical treatments to lyse the cells (Sambrook *et al.*, 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY). Subsequently, the DNA was 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 oligonucleotide probe cells (Sambrook *et al.*, 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY). Pre-hybridization conditions were in 1 M NaCl + 10% dextran sulfate + 1% SDS + 100 μ g/mL salmon sperm DNA at 65°C for 15 min. Hybridization was performed in fresh pre-hybridization solution containing the labeled probe at 65°C overnight. Post-hybridization washing conditions were as follows: twice in 3X SSC containing 1% SDS, twice in 2X SSC containing 1% SDS and twice in 1X SSC containing 1% SDS (all of these washes were at 65°C for 15 min), and a final wash in 0.1X SSC containing 1% SDS at 25°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 because of the high stringency of the washes.

An oligonucleotide probe was considered specific only when it hybridized solely to DNA from the species or genus from which it was isolated. Oligonucleotide probes found to be specific were subsequently tested for their ubiquity (i.e. ubiquitous probes recognized most or all isolates of the target species or genus) by hybridization to microbial DNAs from clinical isolates of the species or genus of interest including ATCC strains. The DNAs from strains of the target species or genus were denatured, fixed onto nylon membranes and hybridized as described above. Probes were considered ubiquitous when they hybridized specifically with the DNA from at least 80% of the isolates of the target species or genus.

Specificity and ubiquity tests for oligonucleotide primers and probes

The specificity of oligonucleotide primers and probes, derived either from the DNA fragments sequenced by us or selected from databases, was tested by amplification of DNA or by hybridization with bacterial or fungal species selected from those listed in Tables 4, 5 and 6, as described in the two previous sections. Oligonucleotides found to be specific were subsequently tested for their ubiquity by amplification (for primers) or by hybridization (for probes) with bacterial DNAs from isolates of the target species or genus. Results for specificity and ubiquity tests with the oligonucleotide primers are summarized in Table 7. The specificity and ubiquity of the PCR assays using the selected amplification primer pairs were tested directly from cultures (see Examples 9 and 10) of bacterial or fungal species.

The various species-specific and genus-specific PCR assays which are objects of the present invention are all specific. For the PCR assays specific to bacterial species or genus, this means that DNA isolated from a wide variety of bacterial species, other than that from the target species or genus and selected from Tables 4 and 5, could not be amplified. For the PCR assay specific to *Candida albicans*, it means there was no amplification with genomic DNA from the fungal species listed in Table 6 as well as with a variety of bacterial species selected from Tables 4 and 5.

The various species-specific and genus-specific PCR assays which are objects of the present invention are also all ubiquitous (Table 7). (i) The species-specific PCR assays for *E. faecium*, *L. monocytogenes*, *S. saprophyticus*, *S. agalactiae* and *C. albicans* amplified genomic DNA from all or most strains of the target species tested, which were obtained from various sources and which are representative of the diversity within each target species (Table 7). The species identification of all of these strains was based on classical biochemical methods which are routinely used in clinical microbiology laboratories. (ii) The genus-specific PCR assays specific for *Enterococcus* spp., *Staphylococcus* spp., *Streptococcus* spp. and *Neisseria* spp. amplified genomic DNA from all or most strains of the target genus tested, which represent all clinically important bacterial species for each target genus. These strains were obtained from various sources and are representative of the diversity within each target genus. Again, the species identification of all of these strains was based on classical biochemical methods which are routinely used in clinical microbiology laboratories. More specifically, the four genus-specific PCR assays amplified the following species: (1) The *Enterococcus*-specific assay amplified efficiently DNA from all of the 11 enterococcal species tested including *E. avium*, *E. casseliflavus*, *E. dispar*, *E. durans*, *E. faecalis*, *E. faecium*, *E. flavescens*, *E. gallinarum*, *E. hirae*, *E. mundtii* and *E. raffinosus*. (2) The *Neisseria*-specific assay amplified efficiently DNA from all of the 12 neisserial species tested including *N. canis*, *N. cinerea*, *N. elongata*, *N. flavescens*, *N. gonorrhoeae*, *N. lactamica*, *N. meningitidis*, *N. mucosa*, *N. polysaccharea*, *N. sicca*, *N. subflava* and *N. weaveri*. (3) The *Staphylococcus*-specific assay amplified efficiently DNA from 13 of the 14 staphylococcal species tested including *S. aureus*, *S. auricularis*, *S. capitis*, *S. cohnii*, *S. epidermidis*, *S. haemolyticus*, *S. hominis*, *S. lugdunensis*, *S. saprophyticus*, *S. schleiferi*, *S. simulans*, *S. warneri* and *S. xylosus*. The staphylococcal species which could not be amplified is *S. sciuri*. (4) Finally, the *Streptococcus*-specific assay amplified efficiently DNA from all of the 22 streptococcal species tested including *S. agalactiae*, *S. anginosus*, *S. bovis*, *S. constellatus*, *S. crista*, *S. dysgalactiae*, *S. equi*, *S. gordonii*, *S. intermedius*, *S. mitis*, *S. mutans*, *S. oralis*, *S. parasanguis*, *S. pneumoniae*, *S. pyogenes*, *S. salivarius*, *S. sanguis*, *S. sabrinus*, *S. suis*, *S. uberis*, *S. vestibularis* and *S. viridans*. On the other hand, the *Streptococcus*-specific assay did not amplify 3 out of 9 strains

of *S. mutans* and 1 out of 23 strains of *S. salivarius*, thereby showing a slight lack of ubiquity for these two streptococcal species.

All specific and ubiquitous amplification primers for each target microbial species or genus or antibiotic resistance gene investigated are listed in Annex VI.

5 Divergence in the sequenced DNA fragments can occur, 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.

The PCR amplification primers listed in Annex VI were all tested for their specificity and ubiquity using reference strains as well as clinical isolates from various

10 geographical locations. The 351 reference strains used to test the amplification and hybridization assays (Tables 4, 5 and 6) were obtained from (i) the American Type Culture Collection (ATCC): 85%, (ii) the Laboratoire de santé publique du Québec (LSPQ): 10%, (iii) the Centers for Disease Control and Prevention (CDC): 3% , (iv) the National Culture Type Collection (NCTC): 1% and (v) several other reference

15 laboratories throughout the world: 1%. These reference strains are representative of (i) 90 gram-negative bacterial species (169 strains; Table 4), (ii) 97 gram-positive bacterial species (154 strains; Table 5) and (iii) 12 fungal species (28 strains; Table 6).

Antibiotic resistance genes

Antimicrobial resistance complicates treatment and often leads to therapeutic

20 failures. Furthermore, overuse of antibiotics inevitably leads to the emergence of bacterial resistance. Our goal is to provide clinicians, in approximately 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

25 species- and/or genus-specific DNA-based tests, 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 clinically important antibiotic resistance genes (i.e. DNA-based tests for the detection

30 of antibiotic resistance genes). Since the sequence from the most important and common bacterial antibiotic resistance genes are available from databases, our strategy was to use the sequence from a portion or from the entire resistance gene to design specific oligonucleotide primers or probes which will be used as a basis for the development of rapid DNA-based tests. The sequence from each of the bacterial

35 antibiotic resistance genes selected on the basis of their clinical relevance (i.e. high incidence and importance) is given in the Sequence Listing. Tables 9 and 10 summarize some characteristics of the selected antibiotic resistance genes. Our approach is unique because the antibiotic resistance genes detection and the bacterial detection and identification are performed simultaneously in multiplex assays under

uniform PCR amplification conditions (Example 13).

Annex VI provides a list of all amplification primers selected from 26 clinically important antibiotic resistance genes which were tested in PCR assays. The various PCR assays for antibiotic resistance genes detection and identification were validated by testing several resistant bacterial isolates known to carry the targeted gene and obtained from various countries. The testing of a large number of strains which do not carry the targeted resistance gene was also performed to ensure that all assays were specific. So far, all PCR assays for antibiotic resistance genes are highly specific and have detected all control resistant bacterial strains known to carry the targeted gene. The results of some clinical studies to validate the array of PCR assays for the detection and identification of antibiotic resistance genes and correlate these DNA-based assays with standard antimicrobials susceptibility testing methods are presented in Tables 11 and 12.

Universal bacterial detection

In the routine microbiology laboratory, a high percentage of clinical specimens sent for bacterial identification are negative by culture (Table 4). Testing clinical samples with universal amplification primers or universal probes 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 amplification primers and probes were therefore synthesized from highly conserved portions of bacterial sequences from the *tuf* genes (Table 8). The universal primer selection was based on a multiple sequence alignment constructed with sequences determined by us or selected from available database sequences as described in Example 1 and Annex I.

For the identification of database sequences suitable for the universal detection of bacteria, we took advantage of the fact that the complete genome sequences for two distant microorganisms (i.e. *Mycoplasma genitalium* and *Haemophilus influenzae*) are available. A comparison of the amino acid sequence for all proteins encoded by the genome of these two distant microorganisms led to the identification of highly homologous proteins. An analysis of these homologous proteins allowed to select some promising candidates for the development of universal DNA-based assays for the detection of bacteria. Since the complete nucleotide sequence of several other microbial genomes are presently available in databases, a person skilled in the art could arrive to the same conclusions by comparing genomes sequences other than those of *Mycoplasma genitalium* and *Haemophilus influenzae*. The selected *tuf* gene encodes a protein (EF-Tu) involved in the translation process during protein synthesis. Subsequently, an extensive nucleotide sequence analysis was performed with the *tuf* gene sequences available in databases as well as with novel *tuf* sequences which we have determined as described previously. All computer analysis of amino acid and

nucleotide sequences were performed by using the GCG programs. Subsequently, optimal PCR primers for the universal amplification of bacteria were selected with the help of the Oligo™ program. The selected primers are degenerated at several nucleotide positions and contain several inosines in order to allow the amplification of all clinically relevant bacterial species (Annex I). Inosine is a nucleotide analog able to specifically bind to any of the four nucleotides A, C, G or T. Degenerated oligonucleotides consist of an oligonucleotide mix having two or more of the four nucleotides A, C, G or T at the site of mismatches. The inclusion of inosine and/or of degenerescences in the amplification primers allow mismatch tolerance thereby permitting the amplification of a wider array of target nucleotide sequences (Dieffenbach and Dveksler, 1995 PCR Primer: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Plainview, NY).

The amplification conditions with the universal primers were identical to those used for the species- and genus-specific amplification assays except that the annealing temperature was 50°C instead of 55°C. This universal PCR assay was specific and nearly ubiquitous for the detection of bacteria. The specificity for bacteria was verified by amplifying genomic DNA isolated from the 12 fungal species listed in Table 6 as well as genomic DNA from *Leishmania donovani*, *Saccharomyces cerevisiae* and human lymphocytes. None of the above eukaryotic DNA preparations could be amplified by the universal assay, thereby suggesting that this test is specific for bacteria. The ubiquity of the universal assay was verified by amplifying genomic DNAs from 116 reference strains which represent 95 of the most clinically relevant bacterial species. These species have been selected from the bacterial species listed in Tables 4 and 5. We found that 104 of these 116 strains could be amplified. The bacterial species which could not be amplified belong to the following genera: *Corynebacterium* (11 species) and *Stenotrophomonas* (1 species). Sequencing of the *tuf* genes from these bacterial species has been recently performed. This sequencing data has been used to select new universal primers which may be more ubiquitous. These primers are in the process of being tested. We also observed that for several species the annealing temperature had to be reduced to 45°C in order to get an efficient amplification. These bacterial species include *Gemella morbilbrum*, *Listeria* spp. (3 species) and *Gardnerella vaginalis*. It is important to note that the 95 bacterial species selected from Tables 4 and 5 to test the ubiquity of the universal assay include all of the most clinically relevant bacterial species associated with a variety of human infections acquired in the community or in hospitals (nosocomial infections). The most clinically important bacterial and fungal pathogens are listed in Tables 1 and 2.

EXAMPLES AND ANNEXES

The following examples and annexes are intended to be illustrative of the various methods and compounds of the invention, rather than limiting the scope thereof.

5 The various annexes show the strategies used for the selection of amplification primers from *tuf* sequences or from the *recA* gene: (i) Annex I illustrates the strategy used for the selection of the universal amplification primers from *tuf* sequences. (ii) Annex II shows the strategy used for the selection of the amplification primers specific for the genus *Enterococcus* from *tuf* sequences. (iii) Annex III illustrates the strategy
10 used for the selection of the amplification primers specific for the genus *Staphylococcus* from *tuf* sequences. (iv) Annex IV shows the strategy used for the selection of the amplification primers specific for the species *Candida albicans* from *tuf* sequences. (v) Annex V illustrates the strategy used for the selection of the amplification primers specific for the genus *Streptococcus* from *recA* sequences. (vi)
15 Annex VI gives a list of all selected primer pairs. As shown in these annexes, the selected amplification primers may contain inosines and/or degenerescences. Inosine is a nucleotide analog able to specifically bind to any of the four nucleotides A, C, G or T. Alternatively, degenerated oligonucleotides which consist of an oligonucleotide mix having two or more of the four nucleotides A, C, G or T at the site of mismatches
20 were used. The inclusion of inosine and/or of degenerescences in the amplification primers allow mismatch tolerance thereby permitting the amplification of a wider array of target nucleotide sequences (Dieffenbach and Dveksler, 1995 PCR Primer: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Plainview, New York).

EXAMPLES**25 EXAMPLE 1 :**

Selection of universal PCR primers from *tuf* sequences. As shown in Annex I, the comparison of *tuf* sequences from a variety of bacterial and eukaryotic species allowed the selection of PCR primers which are universal for the detection of bacteria. The strategy used to design the PCR primers was based on the analysis of a multiple
30 sequence alignment of various *tuf* sequences. This multiple sequence alignment includes *tuf* sequences from 38 bacterial species and 3 eukaryotic species either determined by us or selected from databases (Table 13). A careful analysis of this multiple sequence alignment allowed the selection of primer sequences which are conserved within eubacteria but which discriminate sequences from eukaryotes,
35 thereby permitting the universal detection of bacteria. As shown in Annex I, the selected primers contain several inosines and degenerescences. This was necessary because there is a relatively high polymorphism among bacterial *tuf* sequences despite the fact that this gene is highly conserved. In fact, among the *tuf* sequences that we determined, we found many nucleotide variations as well as some deletions and/or

insertions of amino acids. The selected universal primers were specific and ubiquitous for bacteria (Table 7). Of the 95 most clinically important bacterial species tested, 12 were not amplified. These species belong to the genera *Corynebacterium* (11 species) and *Stenotrophomonas* (1 species). The universal primers did not amplify DNA of non-bacterial origin, including human and other types of eukaryotic DNA.

EXAMPLE 2 :

Selection of genus-specific PCR primers from *tuf* sequences. As shown in Annexes 2 and 3, the comparison of *tuf* sequences from a variety of bacterial species allowed the selection of PCR primers specific for *Enterococcus* spp. or for *Staphylococcus* spp. The strategy used to design the PCR primers was based on the analysis of a multiple sequence alignment of various *tuf* sequences. These multiple sequence alignments include the *tuf* sequences of four representative bacterial species selected from each target genus as well as *tuf* sequences from species of other closely related bacterial genera. A careful analysis of those alignments allowed the selection of oligonucleotide sequences which are conserved within the target genus but which discriminate sequences from other closely related genera, thereby permitting the genus-specific and ubiquitous detection and identification of the target bacterial genus.

For the selection of primers specific for *Enterococcus* spp. (Annex II), we have sequenced a portion of approximately 890 bp of the *tuf* genes for *Enterococcus avium*, *E. faecalis*, *E. faecium* and *E. gallinarum*. All other *tuf* sequences used in the alignment were either sequenced by us or selected from databases. The analysis of this sequence alignment led to the selection of a primer pair specific and ubiquitous for *Enterococcus* spp. (Table 7). All of the 11 enterococcal species tested were efficiently amplified and there was no amplification with genomic DNA from bacterial species of other genera.

For the selection of primers specific for *Staphylococcus* spp. (Annex III), we have also sequenced a portion of approximately 890 bp of the *tuf* genes for *Staphylococcus aureus*, *S. epidermidis*, *S. saprophyticus* and *S. simulans*. All other *tuf* sequences used in the alignment were either sequenced by us or selected from databases. The analysis of this sequence alignment led to the selection of two primer pairs specific and ubiquitous for *Staphylococcus* spp. (Table 7). Annex III shows the strategy used to select one of these two PCR primer pairs. The same strategy was used to select the other primer pair. Of the 14 staphylococcal species tested, one (*S. sciuri*) could not be amplified by the *Staphylococcus*-specific PCR assays using either one of these two primer pairs. For PCR assays using either one of these two primer pairs, there was no amplification with DNA from species of other bacterial genera.

EXAMPLE 3 :

Selection from *tuf* sequences of PCR primers specific for *Candida albicans*. As shown in Annex IV, the comparison of *tuf* sequences from a variety of bacterial and eukaryotic species allowed the selection of PCR primers specific for *Candida albicans*.

5 The strategy used to design the PCR primers was based on the analysis of a multiple sequence alignment of various *tuf* sequences. This multiple sequence alignment includes *tuf* sequences of five representative fungal species selected from the genus *Candida* which were determined by our group (i.e. *C. albicans*, *C. glabrata*, *C. krusei*, *C. parapsilosis* and *C. tropicalis*) as well as *tuf* sequences from other closely related

10 fungal species. *tuf* sequences from various bacterial species were also included. A careful analysis of this sequence alignment allowed the selection of primers from the *C. albicans* *tuf* sequence; these primers discriminate sequences from other closely related *Candida* species and other fungal species, thereby permitting the species-specific and ubiquitous detection and identification of *C. albicans* (Table 7). All of 88

15 *Candida albicans* strains tested were efficiently amplified and there was no amplification with genomic DNA from other fungal or bacterial species.

EXAMPLE 4:

Selection of PCR primers specific for *Streptococcus* from *recA*. As shown in Annex V, the comparison of the various bacterial *recA* gene sequences available from

20 databases (GenBank and EMBL) was used as a basis for the selection of PCR primers which are specific and ubiquitous for the bacterial genus *Streptococcus*. Since sequences of the *recA* gene are available for many bacterial species including five species of streptococci, it was possible to choose sequences well conserved within the genus *Streptococcus* but distinct from the *recA* sequences for other bacterial genera.

25 When there were mismatches between the *recA* gene sequences from the five *Streptococcus* species, an inosine residue was incorporated into the primer (Annex V). The selected primers, each containing one inosine and no degenerescence, were specific and ubiquitous for *Streptococcus* species (Table 7). This PCR assay amplified all of the 22 streptococcal species tested. However, the *Streptococcus*-specific assay

30 did not amplify DNA from 3 out of 9 strains of *S. mutans* and 1 out of 3 strains of *S. salivarius*. There was no amplification with genomic DNA from other bacterial genera (Table 7).

EXAMPLE 5:

Nucleotide sequencing of DNA fragments. The nucleotide sequence of a portion

35 of the *tuf* genes from a variety of bacterial or fungal species was determined by using the dideoxynucleotide chain termination sequencing method (Sanger *et al.*, 1977, Proc. Natl. Acad. Sci. USA. 74:5463-5467). The sequencing was performed by using an Applied Biosystems automated DNA sequencer (model 373A) with their PRISM™ Sequenase® Terminator Double-stranded DNA Sequencing Kit (Perkin-Elmer Corp.,

Applied Biosystems Division, Foster City, CA). The sequencing strategy does not discriminate *tufA* and *tufB* genes because the sequencing primers hybridize efficiently to both bacterial *tuf* genes. These DNA sequences are shown in the sequence listing (SEQ ID Nos: 118 to 146). The presence of several degenerated nucleotides in the various *tuf* sequences determined by our group (Table 13) corresponds to sequence variations between *tufA* and *tufB*.

Oligonucleotide primers and probes selection. Oligonucleotide probes and amplification primers were selected from the given proprietary DNA fragments or database sequences using the Oligo™ program and were synthesized with an automated ABI DNA synthesizer (Model 391, Perkin-Elmer Corp., Applied Biosystems Division) using phosphoramidite chemistry.

EXAMPLE 6 :

Labeling of oligonucleotides for hybridization assays. Each oligonucleotide was 5' end-labeled with γ -³²P (dATP) by the T4 polynucleotide kinase (Pharmacia) as described earlier. The label could also be non-radioactive.

Specificity test for oligonucleotide probes. All labeled oligonucleotide probes were tested for their specificity by hybridization to DNAs from a variety of bacterial and fungal species selected from Tables 4, 5 and 6 as described earlier. Species-specific or genus-specific probes were those hybridizing only to DNA from the microbial species or genus from which it was isolated. Oligonucleotide probes found to be specific were submitted to ubiquity tests as follows.

Ubiquity test for oligonucleotide probes. Specific oligonucleotide probes were then used in ubiquity tests with strains of the target species or genus including reference strains and other strains obtained from various countries and which are representative of the diversity within each target species or genus. Chromosomal DNAs from the isolates were transferred onto nylon membranes and hybridized with labeled oligonucleotide probes as described for specificity tests. The batteries of isolates constructed for each target species or genus 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 or genus.

EXAMPLE 7:

Same as example 6 except that a pool of specific oligonucleotide probes is used for microbial identification (i) to increase sensitivity and assure 100% ubiquity or (ii) to identify simultaneously more than one microbial species and/or genus. Microbial identification could be performed from microbial cultures or directly from any clinical specimen.

EXAMPLE 8:

Same as example 6 except that bacteria or fungi were detected directly from clinical samples. Any biological sample was loaded directly onto a dot blot apparatus and cells were lysed *in situ* for bacterial or fungal detection and identification. Blood samples should be heparinized in order to avoid coagulation interfering with their convenient loading on a dot blot apparatus.

EXAMPLE 9:

PCR amplification. The technique of PCR was used to increase the sensitivity and the rapidity of the assays. The sets of primers were tested in PCR assays performed directly from bacterial colonies or from a standardized bacterial suspension (see Example 10) to determine their specificity and ubiquity (Table 7). Examples of specific and ubiquitous PCR primer pairs are listed in Annex VI.

Specificity and ubiquity tests for amplification primers. The specificity of all selected PCR primer pairs was tested against DNAs from a variety of bacterial and fungal species selected from Tables 4, 5 and 6 as described earlier. Primer pairs found specific for each species or genus were then tested for their ubiquity to ensure that each set of primers could amplify at least 90% of DNAs from a battery of isolates of the target species or genus. The batteries of isolates constructed for each species contain reference ATCC strains and various clinical isolates from around the world which are representative of the diversity within each species or genus.

Standard precautions to avoid false positive PCR results should be taken (Kwok and Higuchi, 1989, Nature, 239:237-238). Methods to inactivate PCR amplification products such as the inactivation by uracil-N-glycosylase may be used to control PCR carryover.

EXAMPLE 10:

Amplification directly from bacterial or yeast cultures. 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 approximately 1.5×10^8 bacteria/mL). In the case of direct amplification from a colony, a portion of a colony was transferred using a plastic rod directly into a 20 μ L PCR reaction mixture containing 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM $MgCl_2$, 0.4 μ M of each primer, 200 μ M of each of the four dNTPs and 0.5 unit of Taq DNA polymerase (Promega) combined with the TaqStart™ antibody (Clontech Laboratories Inc.). For the bacterial suspension, 1 μ L of the cell suspension was added to 19 μ L of the same PCR reaction mixture. For the identification from yeast cultures, 1 μ L of a standard McFarland 1.0 (corresponds to approximately 3.0×10^8 bacteria/mL) concentrated 100 times by centrifugation was added directly to the PCR reaction. This concentration step for yeast cells was performed because a McFarland 0.5 for yeast cells has approximately 200 times fewer cells than a McFarland 0.5 for bacterial cells.

PCR reactions were then subjected to thermal cycling (3 min at 95°C followed by 30 cycles of 1 second at 95°C for the denaturation step and 30 seconds at 55°C for the annealing-extension step) using a PTC-200 thermal cycler. PCR amplification products were then analyzed by standard agarose gel (2%) electrophoresis. Amplification products were visualized in agarose gels containing 0.25 µg/mL of ethidium bromide under UV at 254 nm. The entire PCR assay can be completed in approximately one hour.

Primer sequences derived from highly conserved regions of the bacterial 16S ribosomal RNA gene were used to provide an internal control for all PCR reactions. Alternatively, the internal control was derived from sequences not found in microorganisms or in the human genome. The internal control was integrated into all amplification reactions to verify the efficiency of the PCR assays and to ensure that significant PCR inhibition was absent. The internal control derived from rRNA was also useful to monitor the efficiency of the bacterial lysis protocols. The internal control and the species-specific or genus-specific amplifications were performed simultaneously in multiplex PCR assays.

EXAMPLE 11:

Amplification directly from urine specimens. For PCR amplification performed directly from urine specimens, 1 µL of urine was mixed with 4 µL of a lysis solution containing 500 mM KCl, 100 mM tris-HCl (pH 9.0), 1% triton X-100. After incubation for at least 15 minutes at room temperature, 1 µL of the treated urine specimen was added directly to 19 µL of the PCR reaction mixture. The final concentration of the PCR reagents was 50 mM KCl, 10 mM Tris (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl₂, 0.4 µM of each primer, 200 µM of each of the four dNTPs. In addition, each 20 µL reaction contained 0.5 unit of *Taq* DNA polymerase (Promega) combined with the TaqStart™ antibody (Clontech Laboratories Inc.).

Strategies for the internal control, PCR amplification and agarose gel detection of the amplicons are as previously described in example 10.

EXAMPLE 12:

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 previously. Specific oligonucleotides used as a basis for the DNA-based tests are selected from the antibiotic resistance gene sequences. These tests, which allow the rapid evaluation of bacterial resistance to antimicrobial agents, can be performed either directly from clinical specimens, from a standardized bacterial suspension or from a bacterial colony and should complement diagnostic tests for the universal detection of bacteria as well as for the species-specific and genus-specific microbial detection and identification.

EXAMPLE 13:

Same as examples 10 and 11 except that assays were performed by multiplex PCR (i.e. using several pairs of primers in a single PCR reaction) to reach an ubiquity of 100% for the specific targeted pathogen(s). For more heterogeneous microbial species or genus, a combination of PCR primer pairs may be required to detect and identify all representatives of the target species or genus.

Multiplex PCR assays could also be used to (i) detect simultaneously several microbial species and/or genera or, alternatively, (ii) to simultaneously detect and identify bacterial and/or fungal pathogens and detect specific antibiotic resistance genes either directly from a clinical specimen or from bacterial cultures.

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 fluorescent dyes emitting at different wavelengths. The fluorescent dyes can be each coupled with a specific oligonucleotide linked to a fluorescence quencher which is degraded during amplification to release the fluorescent dyes (e.g. TaqMan™, Perkin Elmer).

EXAMPLE 14:

Detection of amplification products. The person skilled in the art will appreciate that alternatives other than standard agarose gel electrophoresis (Example 10) may be used for the revelation of amplification products. Such methods may be based on fluorescence polarization or on the detection of fluorescence after amplification (e.g. Amplisensor™, Biotronics; TaqMan™, Perkin-Elmer Corp.) or other labels such as biotin (SHARP Signal™ system, Digene Diagnostics). These methods are quantitative and may be automated. One of the amplification primers or an internal oligonucleotide probe specific to the amplicon(s) derived from the species-specific, genus-specific or universal DNA fragments is coupled with the fluorescent dyes 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 fluorescent dyes emitting at different wavelengths are available.

EXAMPLE 15:

Species-specific, genus-specific, universal and antibiotic resistance gene amplification primers can be used in other rapid amplification procedures such as the ligase chain reaction (LCR), transcription-mediated amplification (TMA), self-sustained sequence replication (3SR), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA), cycling probe technology (CPT) and branched DNA (bDNA) or any other methods to increase the sensitivity of the test. Amplifications can be performed from isolated bacterial cultures or directly from any clinical specimen. The scope of this invention is therefore not limited to the use of the

DNA sequences from the enclosed Sequence Listing for PCR only but rather includes the use of any procedures to specifically detect bacterial DNA and which may be used to increase rapidity and sensitivity of the tests.

EXAMPLE 16:

5 A test kit would contain sets of probes specific for each microbial species or genus 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 species- or genus-specific probes for the detection of each pathogen of interest in specific types of clinical samples. The kit will also include test
10 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.

15 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:

- A kit for the universal detection of bacterial or fungal pathogens from all clinical
20 specimens which contains sets of probes specific for highly conserved regions of the microbial genomes.

- A kit for the detection of microbial pathogens retrieved from urine samples, which contains 5 specific test components (sets of probes for the detection of *Enterococcus faecium*, *Enterococcus* species, *Staphylococcus saprophyticus*,
25 *Staphylococcus* species and *Candida albicans*).

- A kit for the detection of respiratory pathogens which contains 3 specific test components (sets of probes for the detection of *Staphylococcus* species, *Enterococcus* species and *Candida albicans*).

- A kit for the detection of pathogens retrieved from blood samples, which
30 contains 10 specific test components (sets of probes for the detection of *Streptococcus* species, *Streptococcus agalactiae*, *Staphylococcus* species, *Staphylococcus saprophyticus*, *Enterococcus* species, *Enterococcus faecium*, *Neisseria* species, *Neisseria meningitidis*, *Listeria monocytogenes* and *Candida albicans*). This kit can also be applied for direct detection and identification from blood
35 cultures.

- A kit for the detection of pathogens causing meningitis, which contains 5 specific test components (sets of probes for the detection of *Streptococcus* species, *Listeria monocytogenes*, *Neisseria meningitidis*, *Neisseria* species and *Staphylococcus* species).

- 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 26 following genes associated with antibiotic resistance: *bla_{tem}*, *bla_{rob}*, *bla_{shv}*, *bla_{oxa}*, *bla_Z*, *aadB*, *aacC1*, *aacC2*, *aacC3*, *aacA4*, *aac6'-IIa*, *ermA*, *ermB*, *ermC*, *mecA*, *vanA*, *vanB*, *vanC*,
5 *satA*, *aac(6')-aph(2'')*, *aad(6')*, *vat*, *vga*, *msrA*, *sul* and *int*.

- Other kits adapted for the detection of pathogens from skin, abdominal wound or any other clinically relevant infections may also be developed.

EXAMPLE 17:

Same as example 16 except that the test kits contain all reagents and controls
10 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 microbial cultures. Components required for (i) universal bacterial detection, (ii) species-specific and genus-specific bacterial and/or fungal detection and identification and (iii) detection of antibiotic resistance genes will be included.

15 Amplification assays could be performed either in tubes or in microtitration plates having multiple wells. For assays in plates, the wells will contain 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
20 required for species-specific and genus-specific bacterial and/or fungal detection and identification as well as for the simultaneous antibiotic resistance genes detection will be included in kits for testing directly from bacterial or fungal cultures as well as in kits for testing directly from any type of clinical specimen.

The kits will be adapted for use with each type of specimen as described in
25 example 16 for hybridization-based diagnostic kits.

EXAMPLE 18:

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

This invention has been described herein above, and it is readily apparent that modifications can be made thereto without departing from the spirit of this invention. These modifications are under the scope of this invention, as defined in the appended claims.

Table 1. Distribution (%) of nosocomial pathogens for various human infections in USA (1990-1992)¹.

	Pathogen	UTI ²	SSI ³	BSI ⁴	Pneumonia	CSF ⁵
5	<i>Escherichia coli</i>	27	9	5	4	2
	<i>Staphylococcus aureus</i>	2	21	17	21	2
	<i>Staphylococcus epidermidis</i>	2	6	20	0	1
	<i>Enterococcus faecalis</i>	16	12	9	2	0
	<i>Enterococcus faecium</i>	1	1	0	0	0
10	<i>Pseudomonas aeruginosa</i>	12	9	3	18	0
	<i>Klebsiella pneumoniae</i>	7	3	4	9	0
	<i>Proteus mirabilis</i>	5	3	1	2	0
	<i>Streptococcus pneumoniae</i>	0	0	3	1	18
	Group B <i>Streptococci</i>	1	1	2	1	6
15	Other <i>Streptococci</i>	3	5	2	1	3
	<i>Haemophilus influenzae</i>	0	0	0	6	45
	<i>Neisseria meningitidis</i>	0	0	0	0	14
	<i>Listeria monocytogenes</i>	0	0	0	0	3
	Other <i>Enterococci</i>	1	1	0	0	0
20	Other <i>Staphylococci</i>	2		8	13	20
	<i>Candida albicans</i>	9	3	5	5	0
	Other <i>Candida</i>	2		1	3	10
	<i>Enterobacter</i> spp.	5	7	4	12	2
	<i>Acinetobacter</i> spp.	1	1	2	4	2
25	<i>Citrobacter</i> spp.	2	1	1	1	0
	<i>Serratia marcescens</i>	1	1	1	3	1
	Other <i>Klebsiella</i>	1	1	1	2	1
	Others	0	6	4	5	0

30 ¹ Data recorded by the National Nosocomial Infections Surveillance (NNIS) from 80 hospitals (Emori and Gaynes, 1993, Clin. Microbiol. Rev., 6:428-442).

² Urinary tract infection.

³ Surgical site infection.

⁴ Bloodstream infection.

35 ⁵ Cerebrospinal fluid.

Table 2. Distribution (%) of bloodstream infection pathogens in Quebec (1995), Canada (1992), UK (1969-1988) and USA (1990-1992).

5	Organism	Quebec ¹	Canada ²	UK ³		USA ⁴
				Community-acquired	Hospital-acquired	Hospital-acquired
	<i>E. coli</i>	15.6	53.8	24.8	20.3	5.0
	<i>S. epidermidis</i> and other CoNS ⁵	25.8	NI ⁶	0.5	7.2	31.0
10	<i>S. aureus</i>	9.6	NI	9.7	19.4	16.0
	<i>S. pneumoniae</i>	6.3	NI	22.5	2.2	NR ⁷
	<i>E. faecalis</i>	3.0	NI	1.0	4.2	NR
	<i>E. faecium</i>	2.6	NI	0.2	0.5	NR
	<i>Enterococcus</i> spp.	NR	NI	NR	NR	9.0
15	<i>H. influenzae</i>	1.5	NR	3.4	0.4	NR
	<i>P. aeruginosa</i>	1.5	8.2	1.0	8.2	3.0
	<i>K. pneumoniae</i>	3.0	11.2	3.0	9.2	4.0
	<i>P. mirabilis</i>	NR	3.9	2.8	5.3	1.0
20	<i>S. pyogenes</i>	NR	NI	1.9	0.9	NR
	<i>Enterobacter</i> spp.	4.1	5.5	0.5	2.3	4.0
	<i>Candida</i> spp.	8.5	NI	NR	1.0	8.0
	Others	18.5	17.4 ⁸	28.7	18.9	19.0

25 ¹ Data obtained for 270 isolates collected at the Centre Hospitalier de l'Université Laval (CHUL) during a 5 month period (May to October 1995).

² Data from 10 hospitals throughout Canada representing 941 gram-negative bacterial isolates. (Chamberland *et al.*, 1992, Clin. Infect. Dis., 15:615-628).

30 ³ Data from a 20-year study (1969-1988) for nearly 4000 isolates (Eykyn *et al.*, 1990, J. Antimicrob. Chemother., Suppl. C, 25:41-58).

⁴ Data recorded by the National Nosocomial Infections Surveillance (NNIS) from 80 hospitals (Emori and Gaynes, 1993, Clin. Microbiol. Rev., 6:428-442).

⁵ Coagulase-negative staphylococci.

⁶ NI, not included. This survey included only gram-negative species.

35 ⁷ NR, incidence not reported for these species or genera.

⁸ In this case, 17.4 stands for other gram-negative bacterial species.

Table 3. Distribution of positive and negative clinical specimens tested at the microbiology laboratory of the CHUL (February 1994 – January 1995).

	Clinical specimens and/or sites	No. of samples tested (%)	% of positive specimens	% of negative specimens
5	Urine	17,981 (54.5)	19.4	80.6
	Blood culture/marrow	10,010 (30.4)	6.9	93.1
	Sputum	1,266 (3.8)	68.4	31.6
	Superficial pus	1,136 (3.5)	72.3	27.7
10	Cerebrospinal fluid	553 (1.7)	1.0	99.0
	Synovial fluid	523 (1.6)	2.7	97.3
	Respiratory tract	502 (1.5)	56.6	43.4
	Deep pus	473 (1.4)	56.8	43.2
	Ears	289 (0.9)	47.1	52.9
15	Pleural and pericardial fluid	132 (0.4)	1.0	99.0
	Peritoneal fluid	101(0.3)	28.6	71.4
	Total:	32,966 (100.0)	20.0	80.0

Table 4. Gram-negative bacterial species (90) used to test the specificity of PCR primers and DNA probes (continues on next page).

	Bacterial species	Number of reference strains tested ^a	Bacterial species	Number of reference strains tested ^a
5	<i>Acinetobacter baumannii</i>	1	<i>Moraxella phenylpyruvica</i>	1
	<i>Acinetobacter lwoffii</i>	3	<i>Morganella morganii</i>	1
	<i>Actinobacillus lignieresii</i>	1	<i>Neisseria animalis</i>	1
	<i>Alcaligenes faecalis</i>	1	<i>Neisseria canis</i>	1
	<i>Alcaligenes odorans</i>	1	<i>Neisseria caviae</i>	1
10	<i>Alcaligenes xylosoxydans</i>		<i>Neisseria cinerea</i>	1
	subsp. <i>denitrificans</i>	1	<i>Neisseria cuniculi</i>	1
	<i>Bacteroides distasonis</i>	1	<i>Neisseria elongata</i>	1
			subsp. <i>elongata</i>	
	<i>Bacteroides fragilis</i>	1	<i>Neisseria elongata</i>	1
15			subsp. <i>glycoytica</i>	
	<i>Bacteroides ovatus</i>	1	<i>Neisseria flavescens</i>	1
	<i>Bacteroides</i>	1	<i>Neisseria flavescens</i>	1
	<i>thetaiotaomicron</i>		<i>Branham</i>	
	<i>Bacteroides vulgatus</i>	1	<i>Neisseria gonorrhoeae</i>	18
20	<i>Bordetella bronchiseptica</i>	1	<i>Neisseria lactamica</i>	1
	<i>Bordetella parapertussis</i>	1	<i>Neisseria meningitidis</i>	4
	<i>Bordetella pertussis</i>	2	<i>Neisseria mucosa</i>	2
	<i>Burkholderia cepacia</i>	1	<i>Neisseria polysaccharea</i>	1
	<i>Citrobacter amalonaticus</i>	1	<i>Neisseria sicca</i>	3
25	<i>Citrobacter diversus</i>	2	<i>Neisseria subflava</i>	3
	subsp. <i>koseri</i>			
	<i>Citrobacter freundii</i>	1	<i>Neisseria weaveri</i>	1
	<i>Comamonas acidovorans</i>	1	<i>Ochrobactrum antropi</i>	1
	<i>Enterobacter aerogenes</i>	1	<i>Pasteurella aerogenes</i>	1
30	<i>Enterobacter</i>	1	<i>Pasteurella multocida</i>	1
	<i>agglomerans</i>			
	<i>Enterobacter cloacae</i>	1	<i>Prevotella melaninogenica</i>	1
	<i>Escherichia coli</i>	9	<i>Proteus mirabilis</i>	3
	<i>Escherichia fergusonii</i>	1	<i>Proteus vulgaris</i>	1

	Bacterial species	Number of reference strains tested ^a	Bacterial species	Number of reference strains tested ^a
	<i>Escherichia hermannii</i>	1	<i>Providencia alcalifaciens</i>	1
	<i>Escherichia vulneris</i>	1	<i>Providencia rettgeri</i>	1
	<i>Flavobacterium meningosepticum</i>	1	<i>Providencia rustigianii</i>	1
5	<i>Flavobacterium indologenes</i>	1	<i>Providencia stuartii</i>	1
	<i>Flavobacterium odoratum</i>	1	<i>Pseudomonas aeruginosa</i>	14
	<i>Fusobacterium necrophorum</i>	2	<i>Pseudomonas fluorescens</i>	2
10	<i>Gardnerella vaginalis</i>	1	<i>Pseudomonas stutzeri</i>	1
	<i>Haemophilus haemolyticus</i>	1	<i>Salmonella arizonae</i>	1
	<i>Haemophilus influenzae</i>	12	<i>Salmonella choleraesuis</i>	1
	<i>Haemophilus parahaemolyticus</i>	1	<i>Salmonella gallinarum</i>	1
15	<i>Haemophilus parainfluenzae</i>	2	<i>Salmonella typhimurium</i>	3
	<i>Hafnia alvei</i>	1	<i>Serratia liquefaciens</i>	1
	<i>Kingella indologenes</i>	1	<i>Serratia marcescens</i>	1
20	subsp. <i>suttonella</i>			
	<i>Kingella kingae</i>	1	<i>Shewanella putida</i>	1
	<i>Klebsiella ornithinolytica</i>	1	<i>Shigella boydii</i>	1
	<i>Klebsiella oxytoca</i>	1	<i>Shigella dysenteriae</i>	1
	<i>Klebsiella pneumoniae</i>	8	<i>Shigella flexneri</i>	1
25	<i>Moraxella atlantae</i>	1	<i>Shigella sonnei</i>	1
	<i>Moraxella catarrhalis</i>	5	<i>Stenotrophomonas maltophilia</i>	1
	<i>Moraxella lacunata</i>	1	<i>Yersinia enterocolitica</i>	1
	<i>Moraxella osloensis</i>	1		

- 30 ^a Most reference strains were obtained from the American Type Culture Collection (ATCC). The other reference strains were obtained from (i) the Laboratoire de Santé Publique du Québec (LSPQ), (ii) the Center for Disease Control and Prevention (CDC) and (iii) the National Culture Type Collection (NCTC).

Table 5. Gram-positive bacterial species (97) used to test the specificity of PCR primers and DNA probes (continues on next page).

	Bacterial species	Number of reference strains tested ^a	Bacterial species	Number of reference strains tested ^a
5	<i>Abiotrophia adiacens</i>	1	<i>Micrococcus kristinae</i>	1
	<i>Abiotrophia defectiva</i>	1	<i>Micrococcus luteus</i>	1
	<i>Actinomyces israelii</i>	1	<i>Micrococcus lylae</i>	1
	<i>Clostridium perfringens</i>	1	<i>Micrococcus roseus</i>	1
	<i>Corynebacterium accolens</i>	1	<i>Micrococcus varians</i>	1
10	<i>Corynebacterium aquaticum</i>	1	<i>Peptococcus niger</i>	1
	<i>Corynebacterium bovis</i>	1	<i>Peptostreptococcus anaerobius</i>	1
	<i>Corynebacterium cervicis</i>	1	<i>Peptostreptococcus asaccharolyticus</i>	1
15	<i>Corynebacterium diphtheriae</i>	6	<i>Staphylococcus aureus</i>	10
	<i>Corynebacterium flavescens</i>	1	<i>Staphylococcus auricularis</i>	1
	<i>Corynebacterium genitalium</i>	6	<i>Staphylococcus capitis</i> subsp. <i>urealyticus</i>	1
20	<i>Corynebacterium jeikeium</i>	1	<i>Staphylococcus cohnii</i>	1
	<i>Corynebacterium kutcheri</i>	1	<i>Staphylococcus epidermidis</i>	2
	<i>Corynebacterium matruchotii</i>	1	<i>Staphylococcus haemolyticus</i>	2
	<i>Corynebacterium minutissimum</i>	1	<i>Staphylococcus hominis</i>	2
25	<i>Corynebacterium mycetoides</i>	1	<i>Staphylococcus lugdunensis</i>	1
	<i>Corynebacterium pseudodiphtheriticum</i>	1	<i>Staphylococcus saprophyticus</i>	3
	<i>Corynebacterium pseudogenitalium</i>	6	<i>Staphylococcus schleiferi</i>	1
30	<i>Corynebacterium renale</i>	1	<i>Staphylococcus sciuri</i>	1
	<i>Corynebacterium striatum</i>	1	<i>Staphylococcus simulans</i>	1
	<i>Corynebacterium ulcerans</i>	1	<i>Staphylococcus warneri</i>	1

	Bacterial species	Number of reference strains tested ^a	Bacterial species	Number of reference strains tested ^a
	<i>Corynebacterium urealyticum</i>	1	<i>Staphylococcus xylosus</i>	1
	<i>Corynebacterium xerosis</i>	1	<i>Streptococcus agalactiae</i>	6
	<i>Enterococcus avium</i>	1	<i>Streptococcus anginosus</i>	2
5	<i>Enterococcus casseliflavus</i>	1	<i>Streptococcus bovis</i>	2
	<i>Enterococcus cecorum</i>	1	<i>Streptococcus constellatus</i>	1
	<i>Enterococcus dispar</i>	1	<i>Streptococcus crista</i>	1
	<i>Enterococcus durans</i>	1	<i>Streptococcus dysgalactiae</i>	1
10	<i>Enterococcus faecalis</i>	6	<i>Streptococcus equi</i>	1
	<i>Enterococcus faecium</i>	3	<i>Streptococcus gordonii</i>	1
	<i>Enterococcus flavescens</i>	1	Group C <i>Streptococci</i>	1
	<i>Enterococcus gallinarum</i>	3	Group D <i>Streptococci</i>	1
	<i>Enterococcus hirae</i>	1	Group E <i>Streptococci</i>	1
15	<i>Enterococcus mundtii</i>	1	Group F <i>Streptococci</i>	1
	<i>Enterococcus pseudoavium</i>	1	Group G <i>Streptococci</i>	1
	<i>Enterococcus raffinosus</i>	1	<i>Streptococcus intermedius</i>	1
	<i>Enterococcus saccharolyticus</i>	1	<i>Streptococcus mitis</i>	2
20	<i>Enterococcus solitarius</i>	1	<i>Streptococcus mutans</i>	1
	<i>Eubacterium lentum</i>	1	<i>Streptococcus oralis</i>	1
	<i>Gemella haemolysans</i>	1	<i>Streptococcus parasanguis</i>	1
	<i>Gemella morbillorum</i>	1	<i>Streptococcus pneumoniae</i>	6
25	<i>Lactobacillus acidophilus</i>	1	<i>Streptococcus pyogenes</i>	3
	<i>Listeria innocua</i>	1	<i>Streptococcus salivarius</i>	2
	<i>Listeria ivanovii</i>	1	<i>Streptococcus sanguis</i>	2
	<i>Listeria grayi</i>	1	<i>Streptococcus sobrinus</i>	1
	<i>Listeria monocytogenes</i>	3	<i>Streptococcus suis</i>	1
30	<i>Listeria murrayi</i>	1	<i>Streptococcus uberis</i>	1
	<i>Listeria seeligeri</i>	1	<i>Streptococcus vestibularis</i>	1
	<i>Listeria welshimeri</i>	1		

^a Most reference strains were obtained from the American Type Culture Collection (ATCC). The other reference strains were obtained from (i) the Laboratoire de Santé Publique du Québec (LSPQ), (ii) the Center for Disease Control and Prevention (CDC) and (iii) the National Culture Type Collection (NCTC).

Table 6. Fungal species (12) used to test the specificity of PCR primers and DNA probes.

	Fungal species	Number of reference strains tested ^a
5	<i>Candida albicans</i>	12
	<i>Candida glabrata</i>	1
	<i>Candida guilliermondii</i>	1
	<i>Candida kefyr</i>	3
10	<i>Candida krusei</i>	2
	<i>Candida lusitaniae</i>	1
	<i>Candida parapsilosis</i>	2
	<i>Candida tropicalis</i>	3
	<i>Rhodotorula glutinis</i>	1
15	<i>Rhodotorula minuta</i>	1
	<i>Rhodotorula rubra</i>	1
	<i>Saccharomyces cerevisiae</i>	1

^a Most reference strains were obtained from (i) the American Type Culture Collection (ATCC) and (ii) the Laboratoire de Santé Publique du Québec (LSPQ).

Table 7. PCR assays developed for several clinically important bacterial and fungal pathogens (continues on next page).

	Organism	Primer Pair ^a SEQ ID NO	Amplicon size (bp)	Ubiquity ^b	DNA amplification from	
					culture ^c	specimens ^d
5	<i>Enterococcus faecium</i>	1-2	216	79/80	+	+
	<i>Listeria monocytogenes</i>	3-4	130	164/168 ^e	+	+
	<i>Neisseria meningitidis</i>	5-6	177	258/258	+	+
	<i>Staphylococcus saprophyticus</i>	7-8	149	245/260	+	NT
	<i>Streptococcus agalactiae</i>	9-10	154	29/29	+	+
10	<i>Candida albicans</i>	11-12	149	88/88	+	NT
	<i>Enterococcus</i> spp. (11 species) ^f	13-14	112	87/87	+	NT
	<i>Neisseria</i> spp. (12 species) ^f	15-16	103	321/321	+	+
	<i>Staphylococcus</i> spp. (14 species)	17-18	192	13/14	+	NT
	<i>Streptococcus</i> spp. (22 species) ^f	19-20	221	13/14	+	NT
20	<i>Streptococcus</i> spp. (22 species) ^f	21-22	153	210/214 ^g	+	+
	Universal detection ^h (95 species) ⁱ	23-24	309	104/ 116 ⁱ	+	+

^a All primer pairs are specific in PCR assays since no amplification was observed with DNA from the bacterial and fungal species other than the species of interest listed in Tables 4, 5 and 6.

^b Ubiquity was tested by using reference strains as well as strains from throughout the world, which are representative of the diversity within each target species or genus.

^c For all primer pairs, PCR amplifications performed directly from a standardized microbial suspension (MacFarland) or from a colony were all specific and ubiquitous.

^d PCR assays performed directly from blood cultures, urine specimens or

cerebrospinal fluid. NT, not tested.

- ° The four *L. monocytogenes* strains undetected are not clinical isolates. These strains were isolated from food and are not associated with a human infection.
- f The bacterial species tested include all those clinically relevant for each genus (Tables 4 and 5). All of these species were efficiently amplified by their respective genus-specific PCR assay, except for the *Staphylococcus*-specific assay, which does not amplify *S. sciuri*.
- g The *Streptococcus*-specific PCR assay did not amplify 3 out of 9 strains of *S. mutans* and 1 out of 3 strains of *S. salivarius*.
- h The primers selected for universal bacterial detection do not amplify DNA of non-bacterial origin, including human and other types of eukaryotic genomic DNA.
- i For the universal amplification, the 95 bacterial species tested represent the most clinically important bacterial species listed in Tables 4 and 5. The 12 strains not amplified are representatives of genera *Corynebacterium* (11 species) and *Stenotrophomonas* (1 species).

Table 8. Target genes for the various genus-specific, species-specific and universal amplification assays.

20	Microorganisms	Gene	Protein encoded
	<i>Candida albicans</i>	<i>tuf</i>	translation elongation factor EF-Tu
	<i>Enterococcus faecium</i>	<i>ddl</i>	D-alanine:D-alanine ligase
	<i>Listeria monocytogenes</i>	<i>actA</i>	actin-assembly inducing protein
	<i>Neisseria meningitidis</i>	<i>omp</i>	outer membrane protein
25	<i>Streptococcus agalactiae</i>	<i>cAMP</i>	cAMP factor
	<i>Staphylococcus saprophyticus</i>	unknown	unknown
	<i>Enterococcus</i> spp.	<i>tuf</i>	translation elongation factor EF-Tu
	<i>Neisseria</i> spp.	<i>asd</i>	ASA-dehydrogenase
30	<i>Staphylococcus</i> spp.	<i>tuf</i>	translation elongation factor EF-Tu
	<i>Streptococcus</i> spp.	<i>recA</i>	RecA protein
	Universal detection	<i>tuf</i>	translation elongation factor EF-Tu

Table 9. Antibiotic resistance genes selected for diagnostic purposes.

	Genes	SEQ ID NOs		Antibiotics	Bacteria ^a
		selected primers	originating fragment		
5	<i>bla_{oxa}</i>	49-50	110	β-lactams	<i>Enterobacteriaceae</i> , <i>Pseudomonadaceae</i>
	<i>blaZ</i>	51-52	111	β-lactams	<i>Enterococcus</i> spp.
	<i>aac6'-IIa</i>	61-64	112	Aminoglycosides	<i>Pseudomonadaceae</i>
	<i>ermA</i>	91-92	113	Macrolides	<i>Staphylococcus</i> spp.
10	<i>ermB</i>	93-94	114	Macrolides	<i>Staphylococcus</i> spp.
	<i>ermC</i>	95-96	115	Macrolides	<i>Staphylococcus</i> spp.
	<i>vanB</i>	71-74	116	Vancomycin	<i>Enterococcus</i> spp.
	<i>vanC</i>	75-76	117	Vancomycin	<i>Enterococcus</i> spp.
15	<i>aad(6')</i>	173-174	-	Streptomycin	<i>Enterococcus</i> spp.

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

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Table 10. Antibiotic resistance genes from our US Patent No. 6,001,564 and PCT WO 96/08582 patent application for which we have selected PCR primers pairs.

5	Genes	SEQ ID NOs	Antibiotics	Bacteria ^a
	of selected primers			
	<i>bla_{tem}</i>	37-40	β-lactams	<i>Enterobacteriaceae</i> , <i>Pseudomonadaceae</i> , <i>Haemophilus</i> spp., <i>Neisseria</i> spp.
	<i>bla_{rob}</i>	45-48	β-lactams	<i>Haemophilus</i> spp., <i>Pasteurella</i> spp.
10	<i>bla_{shv}</i>	41-44	β-lactams	<i>Klebsiella</i> spp. and other <i>Enterobacteriaceae</i>
	<i>aadB</i>	53-54	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonadaceae</i>
	<i>aacC1</i>	55-56		
	<i>aacC2</i>	57-58		
15	<i>aacC3</i>	59-60		
	<i>aacA4</i>	65-66		
	<i>mecA</i>	97-98	β-lactams	<i>Staphylococcus</i> spp.
	<i>vanA</i>	67-70	Vancomycin	<i>Enterococcus</i> spp.
	<i>satA</i>	81-82	Macrolides	<i>Enterococcus</i> spp.
20	<i>aac(6')-aph(2'')</i>	83-86	Aminoglycosides	<i>Enterococcus</i> spp., <i>Staphylococcus</i> spp.
	<i>vat</i>	87-88	Macrolides	<i>Staphylococcus</i> spp.
	<i>vga</i>	89-90	Macrolides	<i>Staphylococcus</i> spp.
	<i>msrA</i>	77-80	Erythromycin	<i>Staphylococcus</i> spp.
25	<i>int</i>	99-102	β-lactams, trimethoprim,	<i>Enterobacteriaceae</i> ,
	<i>sul</i>	103-106	aminoglycosides, antiseptic, chloramphenicol	<i>Pseudomonadaceae</i>

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

Table 11. Correlation between disk diffusion and PCR amplification of antibiotic resistance genes in *Staphylococcus* species^a.

				Disk diffusion (Kirby-Bauer) ^b		
5	Antibiotic	Phenotype	PCR	Resistant	Intermediate	Sensitive
	Penicillin	<i>blaZ</i>	+	165	0	0
			-	0	0	31
	Oxacillin	<i>mecA</i>	+	51	11	4
			-	2	0	128
10	Gentamycin	<i>aac(6')aph(2'')</i>	+	24	18	6
			-	0	0	148
	Erythromycin	<i>ermA</i>	+	15	0	0
		<i>ermB</i>	+	0	0	0
		<i>ermC</i>	+	43	0	0
		15	<i>msrA</i>	+	4	0
	-		0	1	136	

^a The *Staphylococcus* strains studied include *S. aureus* (82 strains), *S. epidermidis* (83 strains), *S. hominis* (2 strains), *S. capitis* (3 strains), *S. haemolyticus* (9 strains), *S. simulans* (12 strains) and *S. warneri* (5 strains), for a total of 196 strains.

^b Susceptibility testing was performed by the method of Kirby-Bauer according to the protocol recommended by the National Committee of Clinical Laboratory Standards (NCCLS).

Table 12. Correlation between disk diffusion profiles and PCR amplification of antibiotic resistance genes in *Enterococcus* species^a.

	Antibiotic	Phenotype	PCR	Disk diffusion (Kirby-Bauer) ^b	
				Resistant	Sensitive
5	Ampicillin	<i>blaZ</i>	+	0	2
			-	1	30
	Gentamycin	<i>aac(6')aph(2'')</i>	+	51	1
			-	3	38
10	Streptomycin	<i>aad(6')</i>	+	26	15
			-	6	27
	Vancomycin	<i>vanA</i>	+	36	0
		<i>vanB</i>	+	26	0
15			-	0	40

^a The *Enterococcus* strains studied include *E. faecalis* (33 strains) and *E. faecium* (69 strains), for a total of 102 strains.

^b Susceptibility testing was performed by the method of Kirby-Bauer according to the protocol recommended by the National Committee of Clinical Laboratory Standards (NCCLS).

Table 13. Origin of *tuf* sequences in the Sequence Listing (continues on next page).

	SEQ ID NO	Bacterial or fungal species	Source
5	118	<i>Abiotrophia adiacens</i>	This patent
	119	<i>Abiotrophia defectiva</i>	This patent
	120	<i>Candida albicans</i>	This patent
	121	<i>Candida glabrata</i>	This patent
	122	<i>Candida krusei</i>	This patent
10	123	<i>Candida parapsilosis</i>	This patent
	124	<i>Candida tropicalis</i>	This patent
	125	<i>Corynebacterium accolens</i>	This patent
	126	<i>Corynebacterium diphtheriae</i>	This patent
	127	<i>Corynebacterium genitalium</i>	This patent
15	128	<i>Corynebacterium jeikeium</i>	This patent
	129	<i>Corynebacterium pseudotuberculosis</i>	This patent
	130	<i>Corynebacterium striatum</i>	This patent
	131	<i>Enterococcus avium</i>	This patent
	132	<i>Enterococcus faecalis</i>	This patent
20	133	<i>Enterococcus faecium</i>	This patent
	134	<i>Enterococcus gallinarum</i>	This patent
	135	<i>Gardnerella vaginalis</i>	This patent
	136	<i>Listeria innocua</i>	This patent
	137	<i>Listeria ivanovii</i>	This patent
25	138	<i>Listeria monocytogenes</i>	This patent
	139	<i>Listeria seeligeri</i>	This patent
	140	<i>Staphylococcus aureus</i>	This patent
	141	<i>Staphylococcus epidermidis</i>	This patent
	142	<i>Staphylococcus saprophyticus</i>	This patent
30	143	<i>Staphylococcus simulans</i>	This patent
	144	<i>Streptococcus agalactiae</i>	This patent
	145	<i>Streptococcus pneumoniae</i>	This patent

	SEQ ID NO	Bacterial or fungal species	Source
	146	<i>Streptococcus salivarius</i>	This patent
	147	<i>Agrobacterium tumefaciens</i>	Database
	148	<i>Bacillus subtilis</i>	Database
	149	<i>Bacteroides fragilis</i>	Database
5	150	<i>Borrelia burgdorferi</i>	Database
	151	<i>Brevibacterium linens</i>	Database
	152	<i>Burkholderia cepacia</i>	Database
	153	<i>Chlamydia trachomatis</i>	Database
	154	<i>Escherichia coli</i>	Database
10	155	<i>Fibrobacter succinogenes</i>	Database
	156	<i>Flavobacterium ferrugineum</i>	Database
	157	<i>Haemophilus influenzae</i>	Database
	158	<i>Helicobacter pylori</i>	Database
	159	<i>Micrococcus luteus</i>	Database
15	160	<i>Mycobacterium tuberculosis</i>	Database
	161	<i>Mycoplasma genitalium</i>	Database
	162	<i>Neisseria gonorrhoeae</i>	Database
	163	<i>Rickettsia prowazekii</i>	Database
	164	<i>Salmonella typhimurium</i>	Database
20	165	<i>Shewanella putida</i>	Database
	166	<i>Stigmatella aurantiaca</i>	Database
	167	<i>Streptococcus pyogenes</i>	Database
	168	<i>Thiobacillus cuprinus</i>	Database
	169	<i>Treponema pallidum</i>	Database
25	170	<i>Ureaplasma urealyticum</i>	Database
	171	<i>Wolinella succinogenes</i>	Database

Annex I: Strategy for the selection from *tuf* sequences of the universal amplification primers (continues on pages 49 to 51).

		SEQ ID
	491	NO
	517...776	118
5	<i>Abiotrophia</i> <i>adiacens</i>	802
	<i>Abiotrophia</i> <i>defectiva</i>	119
	<i>Agrobacterium</i> <i>tumefaciens</i>	147
10	<i>Bacillus</i> <i>subtilis</i>	148
	<i>Bacteroides</i> <i>fragilis</i>	149
15	<i>Borrelia</i> <i>burgdorferi</i>	150
	<i>Brevibacterium</i> <i>linens</i>	151
	<i>Burkholderia</i> <i>cepacia</i>	152
20	<i>Chlamydia</i> <i>trachomatis</i>	153
	<i>Corynebacterium</i> <i>diphtheriae</i>	126

5	Corynebacterium genitalium	CCACCGTTAC CTCATCGAG ATGTTCA...AGATGGT TATGCCGGGC GACAACGTTG	127
	Corynebacterium jeikeium	CCACCGTTAC CTCATCGAG ATGTTCA...AGATGGT TATGCCGGGC GACAACGTTG	128
	Enterococcus faecalis	CAACYGTTAC AGGTGTTGAA ATGTTCC...AAATGGT AATGCCCTGGT GATAACGTTG	132
	Enterococcus faecium	CAACAGTTAC TGGTGTGAA ATGTTCC...AAATGGT CATGCCCGGT GACAACGT..	133
	Escherichia coli	CTACCTGTAC TGGCGTTGAA ATGTTCC...AGATGGT AATGCCGGGC GACAACATCA	154
10	Fibrobacter succinogenes	ACGTCAATCAC CGGTGTTGAA ATGTTCC...AAATGGT TACTCCGGGT GACACGGTCA	155
	Flavobacterium ferrugineum	CTACCGTTAC AGGTGTTGAG ATGTTCC...AAATGGT TATGCCCTGGT GATAACACCA	156
	Gardnerella vaginalis	CCACCGTCAC CTCTATCGAG ACCTTCC...AAATGGT TCAGCCAGGC GATCAGGCAA	135
	Haemophilus influenzae	CTACTGTAAC GGGTGTGAA ATGTTCC...AAATGGT AATGCCAGGC GATAACATCA	157
	Helicobacter pylori	CRACTGTAAC CGGTGTAGAA ATGTTTA...AAATGGT TATGCCCTGGC GATAATGTGA	158
20	Listeria monocytogenes	TAGTAGTAAC TGGAGTAGAA ATGTTCC...AAATGGT AAYGCCCTGGT GATAACATTG	138
	Micrococcus luteus	CCACTGTAC CGGCATCGAG ATGTTCC...AGATGGT CATGCCCGGC GACAACACCG	159
	Mycobacterium tuberculosis	CCACCGTCAC CGGTGTGGAG ATGTTCC...AGATGGT GATGCCCGGT GACAACACCA	160

5	<i>Mycoplasma genitalium</i>	<u>CAGTGTGTTAC</u> <u>TGGAATTGAA</u> <u>ATGTTCA</u> ... <u>AAATGGT</u> <u>TCTACCTGGT</u> <u>GATAATGCTT</u>	161
	<i>Neisseria gonorrhoeae</i>	<u>CCACCTGTAC</u> <u>CGGCGTTGAA</u> <u>ATGTTCC</u> ... <u>AAATGGT</u> <u>AATGCCGGGT</u> <u>GAGAACGTAA</u>	162
	<i>Rickettsia prowazekii</i>	<u>CGACTTGTAC</u> <u>AGGTGTAGAA</u> <u>ATGTTCA</u> ... <u>AGATGGT</u> <u>TATGCCCTGGA</u> <u>GATAATGCTA</u>	163
	<i>Salmonella typhimurium</i>	<u>CTACCTGTAC</u> <u>TGGCGTTGAA</u> <u>ATGTTCC</u> ... <u>AGATGGT</u> <u>AATGCCGGGC</u> <u>GACAACATCA</u>	164
	<i>Shewanella putida</i>	<u>CAACGTGTAC</u> <u>TGGTGTAGAA</u> <u>ATGTTCC</u> ... <u>AGATGGT</u> <u>AATGCCAGGC</u> <u>GATAACATCA</u>	165
10	<i>Stigmatella aurantiaca</i>	<u>CGGTCAATCAC</u> <u>GGGGTGGAG</u> <u>ATGTTCC</u> ... <u>AGATGGT</u> <u>GATGCCGGGA</u> <u>GACAACATCG</u>	166
	<i>Staphylococcus aureus</i>	<u>CAACTGTTAC</u> <u>AGGTGTTGAA</u> <u>ATGTTCC</u> ... <u>AAATGGT</u> <u>AATGCCCTGGT</u> <u>GATAACGTTG</u>	140
15	<i>Staphylococcus epidermidis</i>	<u>CAACTGTTAC</u> <u>TGGTGTAGAA</u> <u>ATGTTCC</u> ... <u>AAATGGT</u> <u>TATGCCCTGGC</u> <u>GACAACGTTG</u>	141
	<i>Streptococcus agalactiae</i>	<u>CAGTGTGTTAC</u> <u>TGGTGTGTTGAA</u> <u>ATGTTCC</u> ... <u>AAATGGT</u> <u>TATGCCCTGGT</u> <u>GATAACGTTA</u>	144
20	<i>Streptococcus pneumoniae</i>	<u>CAGTGTGTTAC</u> <u>TGGTGTGTTGAA</u> <u>ATGTTCC</u> ... <u>AAATGGT</u> <u>AATGCCCTGGT</u> <u>GATAACGTGA</u>	145
	<i>Streptococcus pyogenes</i>	<u>CTGTTGTTAC</u> <u>TGGTGTGTTGAA</u> <u>ATGTTCC</u> ... <u>AAATGGT</u> <u>TATGCCCTGGT</u> <u>GATAACGTGA</u>	167
	<i>Thiobacillus cuprinus</i>	<u>CCACCTGCAC</u> <u>CGGCGTGGAA</u> <u>ATGTTCA</u> ... <u>AAATGGT</u> <u>CATGCCCGGC</u> <u>GATAATGTGA</u>	168
25	<i>Treponema pallidum</i>	<u>CAGTGGTTAC</u> <u>TGGCATTGAG</u> <u>ATGTTTA</u> ... <u>ACATGGT</u> <u>GAAGCCGGGG</u> <u>GATAACACCA</u>	169

Ureaplasma	CTGTTGTTAC AGGAATTGAA ATGTTTA...ATTGGT TAIGCCAGGT GATGACGTTG	170
urealyticum		
Wolinella	CAACCCTAAC TGGCGTTGAG ATGTTCC...AGATGGT TAIGCCTGGT GACAACGTTA	171
succinogenes		
Candida	GTGTTACCAC TGAAGTCAAR TCCGTTG...AGRAATT GGAAGAAAAT CCAAAATTCG	120
albicans		
Schizo-	GTGTCACTAC CGAAGTCAAG TCTGTTG...AGAAGAT TGAGGAGTCC CCTAAGTTTG	
saccharomyces pombe		
Human	TGACAGGCAT TGAGATGTTT CACAAGA...AGAAGGAGCTTGCCATG CCCGGGGAGG	
Selected ^a	ACIKKIAC IGGIGTIGAR ATGTT ATGGT IATGCCIGGI GAIAAYRT	
equences ^a		
Selected	SEQ ID NO:23	SEQ ID NO: 24 ^b
universal		
15 primer	ACIKKIAC IGGIGTIGAR ATGTT	AYRTT ITCICCIGGC ATIACCAT
sequences ^a :		

The sequence numbering refers to the E. coli tuf gene fragment. Underlined nucleotides are identical to the selected sequence or match that sequence.

20 ^a "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T. "K", "R" and "Y" designate nucleotide positions which are degenerated. "K" stands for T or G; "R" stands for A or G; "Y" stands for C or T.

^b This sequence is the reverse complement of the above tuf sequence.

Annex II: Strategy for the selection from tuf sequences of the amplification primers specific for the genus Enterococcus (continues on pages 53 and 54).

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314	348	401	435	SEQ
5	Bacillus subtilis	CGCGACACTG <u>AAAAACCAT</u> <u>CATGATGCCA</u> GTTGA...CGCGG <u>ACAAGTTAAA</u> <u>GTCGGTGACG</u> <u>AAGTTGAAAT</u>	148	ID NO
	Bacteroides fragilis	CGCGAIGTTG <u>ATAAACCTTT</u> <u>CTTGAIGCCG</u> GTAGA...ACTGG <u>TGTTATCCAT</u> <u>GTAGGTGATG</u> <u>AAATCGAAAT</u>	149	
10	Burkholderia cepacia	CGTGCAGTTG <u>ACGGCGCGTT</u> <u>CCTGAIGCCG</u> GTGGA...CGCGG <u>CATCGTGAAG</u> <u>GTCGGCGAAG</u> <u>AAATCGAAAT</u>	152	
	Chlamydia trachomatis	AGAGAAATIG <u>ACAAGCCTTT</u> <u>CTTAAATGCCCT</u> ATTGA...CGTGG <u>AATTGTTAAA</u> <u>GTTCCTCGATA</u> <u>AAGTTCAGTT</u>	153	
	Corynebacterium diphtheriae	CGTGAGACCG <u>ACAAGCCATT</u> <u>CCTCAIGCCT</u> ATCGA...CGTGG <u>CTCCCTGAAG</u> <u>GTC AACCGAGG</u> <u>ACGTCGAGAT</u>	126	
15	Enterococcus avium	CGTGATACTG <u>ACA AACCAT</u> <u>CATGATGCCA</u> GTCGA...CGTGG <u>ACAAGTTCGC</u> <u>GTTGGTGACG</u> <u>AAGTTGAAAT</u>	131	
	Enterococcus faecalis	CGTGATACTG <u>ACA AACCAT</u> <u>CATGATGCCA</u> GTCGA...CGTGG <u>TGAAGTTCGC</u> <u>GTTGGTGACG</u> <u>AAGTTGAAAT</u>	132	
	Enterococcus faecium	CGTGACAACG <u>ACA AACCAT</u> <u>CATGATGCCA</u> GTTGA...CGTGG <u>ACAAGTTCGC</u> <u>GTTGGTGACG</u> <u>AAGTTGAAAT</u>	133	
20	Enterococcus gallinarum	CGTGATACTG <u>ACA AACCAT</u> <u>CATGATGCCA</u> GTCGA...CGTGG <u>ACAAGTTCGC</u> <u>GTTGGTGATG</u> <u>AAGTAGAAAT</u>	134	
	Escherichia coli	CGTGCGATTG <u>ACAAGCCGTT</u> <u>CCTGCTGCCG</u> ATCGA...CGCGG <u>TATCATCAAA</u> <u>GTTGGTGAAG</u> <u>AAGTTGAAAT</u>	154	

Gardnerella vaginalis	CACGATCTTG <u>ACAAGCCATT</u> CTTGATGCCA ATCGA...CGTGG TAAGCTCCCA ATCAACACCC CAGTTGAGAT	135
Haemophilus influenzae	CGTGCGATTG <u>ACCAACCGTT</u> CCTTCTTCCA ATCGA...CGAGG TATTATCCGT ACAGGTGATG <u>AAGTAGAAAT</u>	157
5 Helicobacter pylori	AGAGACACTG <u>AAAAA</u> CTTT CTTGATGCCG GTTGA...AGAGG CGTGGTGAAA <u>GTAGCGGATG</u> <u>AAGTGGAAAT</u>	158
Listeria monocytogenes	CGTGATACTG <u>ACAAACCAT</u> T CATGATGCCA GTTGA...CGTGG ACAAGTTAAA <u>GTTGGTGACG</u> <u>AAGTAGAAGT</u>	138
Micrococcus luteus	CGCGACAAGG <u>ACAAGCCGTT</u> CCTGATGCCG ATCGA...CGCGG CACCCCTGAAG ATCAACTCCG <u>AGTCGAGAT</u>	159
Mycobacterium tuberculosis	CGCGAGACCG <u>ACAAGCCGTT</u> CCTGATGCCG GTCGA...CGCGG CGTGATCAAC <u>GTTAACGAGG</u> <u>AAGTTGAGAT</u>	160
Mycoplasma genitalium	CGTGAAGTAG <u>ATAAACCTTT</u> CTTATTAGCA ATTGA...AGAGG TGAACCTCAA <u>GTAGTCAAG</u> <u>AAGTTGAAAT</u>	161
15 Neisseria gonorrhoeae	CGTGCCGTGG <u>ACAAACCAT</u> T CCTGCTGCCT ATCGA...CGAGG TATCATCCAC <u>GTTGGTGACG</u> <u>AGATTGAAAT</u>	162
Salmonella typhimurium	CGTGCGATTG <u>ACAAGCCGTT</u> CCTGCTGCCG ATCGA...CGCGG TATCATCAAA <u>GTTGGCGAAG</u> <u>AAGTTGAAAT</u>	164
Shewanella putida	CGTGACATCG <u>ATAAGCCGTT</u> CCTACTGCCA ATCGA...CGTGG TATTGTACGC <u>GTAGGCGACG</u> <u>AAGTTGAAAT</u>	165
20 Staphylococcus aureus	CGTGATTCTG <u>ACAAACCAT</u> T CATGATGCCA GTTGA...CGTGG TCAAAATCAA <u>GTTGGTGAAG</u> <u>AAGTTGAAAT</u>	140
Staphylococcus epidermidis	CGTGATTCTG <u>ACAAACCAT</u> T CATGATGCCA GTTGA...CGTGG TCAAAATCAA <u>GTTGGTGAAG</u> <u>AAGTTGAAAT</u>	141
25 Staphylococcus saprophyticus	CGTGATTCTG <u>ACAAACCAT</u> T CATGATGCCA GTTGA...CGTGG TCAAAATCAA <u>GTCGGTGAAG</u> <u>AAATCGARAT</u>	142

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PCT/CA97/00829 -

Streptococcus CGTGATCTG ACAAACCTTT ACTTCTTCCA GTTGA...CGTGG TACTGTTCTG GTCAACGACG AAGTTGAAAT 144
agactiae
Streptococcus CGTGACACTG ACAAACCAT GCTTCTTCCA GTCGA...CGTGG TATCGTTAAA GTCAACGACG AAATCGAAAT 145
pneumoniae
5 Streptococcus CGCGACACTG ACAAACCAT GCTTCTTCCA GTCGA...CGTGG TACTGTTCTG GTCAACGACG AAATCGAAAT 167
pyogenes
Ureaplasma CGTAGTACTG ACAAACCAT CTATATAGCA ATTGA...CGTGG TGTATTAAAA GTTAATGATG AGTTTGAAAT 170
urealyticum
Selected TACTG ACAAACCAT CATGATG GTTCGC GTTGGTGACG AAGTT

10 sequences

Selected SEQ ID NO: 13 SEQ ID NO: 14^a

genus-specific

primer TACTG ACAAACCAT CATGATG AACTTC GTCAACCAACG CGAAC

15 sequences:

The sequence numbering refers to the *E. faecalis* *tuf* gene fragment. Underlined nucleotides are identical to the selected sequence or match that sequence.

20 ^a This sequence is the reverse complement of the above *tuf* sequence.

NOTE: The above primers also amplify *tuf* sequences from *Abiotrophia* species; this genus has recently been related to the *Enterococcus* genus by 16S rRNA analysis.

Annex III: Strategy for the selection from tuf sequences of the amplification primers specific for the genus Staphylococcus (continues on pages 56 and 57).

385	420.....579	611 SEQ ID
5	<i>Bacillus subtilis</i>	NO
	TGGCCGTTGTA GAACGCGGAC AAGTTAAAGT CGG.....TTG CTAAACCAGG TACAATCACT CCACACAGCA	148
	<i>Bacteroides fragilis</i>	
	AGGTCGTATC GAAACTGGTG TTATCCATGT AGG.....TTT GTAAACCGGG TCAGATTAA CCTCACTCTA	149
	<i>Burkholderia cepacia</i>	
	GGGTCGTGTC GAGCGCGGCA TCGTGAAGGT CGG.....TGG CGAAGCCGGG TTCGATCAG CCGCACACGC	152
	<i>Chlamydia trachomatis</i>	
	TGGACGTATT GAGCGTGGAA TTGTAAAGT TTC.....TTT GCTTGCCAAA CAGTGTTAA CCTCATACAC	153
	<i>Corynebacterium diptheriae</i>	
	CGGCCGTGTT GAGCGTGGCT CCCTGAAGGT CAA.....TTG TTAAGCCAGG CGCTTACAC CCTCACACCG	126
15	<i>Enterococcus faecalis</i>	
	AGGACGTGTT GAACGTGGTG AAGTTCGCGT TGG.....TAG CTAAACCAGC TACAATCACT CCACACACAA	132
	<i>Enterococcus faecium</i>	
	AGGTCGTGTT GAACGTGGAC AAGTTCGCGT TGG.....TAG CTAAACCAGG TACAATCACA CCTCCTACAA	133
	<i>Escherichia coli</i>	
	CGGTCGTGTA GAACGCGGTA TCATCAAAAGT TGG.....TGG CTAAGCCGGG CACCATCAAG CCGCACACCA	154
20	<i>Gardnerella vaginalis</i>	
	CGGTCGTGTT GAGCGTGGTA AGCTCCCAAT CAA.....TGG CTGCTCCAGG TTCGTGACT CCACACACCA	135

Haemophilus influenzae	AGGTCG TGTA <u>GAACGAGGTA</u> <u>TTATCCGTAC</u> AGG.....TAG CGAAACCAGG <u>TTCAATCACA</u> <u>CCACACACTG</u> 157
Helicobacter pylori	AGGTAGGATT <u>GAAAGAGGCG</u> TGGTGA AAGT AGG.....TAT GCAAACCAGG <u>TTCTATCACT</u> <u>CCGCACAAGA</u> 158
5 Listeria monocytogenes	TGGACG TGTT <u>GAACGTGGAC</u> <u>AAGTTAAAGT</u> TGG.....TAG CTAAACCAGG <u>TTCGATTACT</u> <u>CCACACACTA</u> 138
Micrococcus luteus	CGGTCGCGCC <u>GAGCGCGGCA</u> CCTG GAAGAT CAA.....TGG TGGAGCGGGG <u>CTCCATCAC</u> <u>CCGCACACCA</u> 159
Mycobacterium tuberculosis	CGGACG TGTG <u>GAGCGCGGCG</u> TGATCA ACGT GAA.....TCA CCAAGCCCGG <u>CACCACCAG</u> <u>CCGCACACCG</u> 160
Mycoplasma genitalium	AGGAAGAGTT <u>GAAAGAGGTG</u> <u>AACTCAAAGT</u> AGG.....TAG CAAAACCAGG <u>CTCTATTAA</u> <u>CCGCACAAGA</u> 161
Neisseria gonorrhoeae	CGGCCG TGTA <u>GAGCGAGGTA</u> TCATCC ACGT TGG.....TGG CCAAACGGGG <u>TACTATCACT</u> <u>CCTCACACCA</u> 162
15 Salmonella typhimurium	CGGTCG TGTA <u>GAGCGCGGTA</u> TCATCA AAAGT GGG.....TGG CTAAGCCGGG <u>CACCATCAAG</u> <u>CCGCACACCA</u> 164
Shewanella putida	AGGTCG TGTT <u>GAGCGTGTA</u> TTGTACGCGT AGG.....TAG CGAAGCCAGG <u>TTCAATCAAC</u> <u>CCACACACTA</u> 165
Staphylococcus aureus	AGGCCG TGTT <u>GAACGTGGTC</u> <u>AAATCAAAGT</u> TGG.....TAG CTGCTCCTGG <u>TTCAATTACA</u> <u>CCACATACTG</u> 140
20 Staphylococcus epidermidis	AGGCCG TGTT <u>GAACGTGGTC</u> <u>AAATCAAAGT</u> WGG.....TAG CTGCTCCTGG <u>TTCTATTACA</u> <u>CCACACACAA</u> 141
Staphylococcus saprophyticus	AGGCCG TGTT <u>GAACGTGGTC</u> <u>AAATCAAAGT</u> CGG.....TAG CTGCTCCTGG <u>TACTATCACA</u> <u>CCACATACAA</u> 142
25 Staphylococcus simulans	AGGCCG TGTT <u>GAACGTGGTC</u> <u>AAATCAAAGT</u> CGG.....TAG CAGCTCCTGG <u>CTCTATTACT</u> <u>CCACACACAA</u> 143

Streptococcus AGGACGTATC GACCGTGGTA CTGTTCTGT CAA.....TTG CTAAACCAGG TTCAATCAAC CCACACACTA 144
agalactiae
Streptococcus AGGACGTATC GACCGTGGTA TCGTTAAAGT CAA.....TCG CTAAACCAGG TTCAATCAAC CCACACACTA 145
pneumoniae
5 Ureaplasma TGGACGTGTT GAACGTGGTG TATTAAAGT TAA.....TTG TAAACCAGG ATCAATTAA CCTCACCGTA 170
urealyticum
Selected CCGTGTT GAACGTGGTC AAATCAAA GCTCCTGG YNCWATYACA CCACAYA
sequences^a

10 Selected SEQ ID NO: 17 SEQ ID NO: 18^b

genus-specific
primer CCGTGTT GAACGTGGTC AAATCAAA TRTGTGGT GTRATGWRC CAGGAGC
sequences^a:

15 The sequence numbering refers to the *S.aureus* *tuf* gene fragment. Underlined nucleotides are identical to the selected sequence or match that sequence.

^a "R", "W" and "Y" designate nucleotide positions which are degenerated. "R" stands for A or G; "W", for A or T; "Y", for C or T.

20 ^b This sequence is the reverse complement of the above *tuf* sequence.

Annex IV: Strategy for the selection from tuf sequences of the amplification primers specific for the species Candida albicans (continues on pages 59 and 60).

	58	90	181	213 SEQ ID NO	
<u>Candida albicans</u>	CGTCAAGAAG GTTGGTTACA ACCCAAGAC TGT...CAA ATCCGGTAAA GTTACTGGTA AGACCTTGTT				120
<u>Candida glabrata</u>	CATCAAGAAG GTCGGTTACA ACCCAAGAC TGT...CAA GGCTGGTGTC GTCAAGGGTA AGAYCTTGTT				121
<u>Candida krusei</u>	CATCAAGAAG GTTGGTTACA ACCCAAGAC TGT...CAA GGCAAGTGTT GTTAAGGGTA AGACCTTATT				122
<u>Candida parapsilosis</u>	CGTCAAGAAG GTTGGTTACA ACCCTAAAGC TGT...TAA AGCTGGTAAG GTTACCGGTA AGACCTTGTT				123
<u>Candida tropicalis</u>	CGTCAAGAAG GTTGGTTACA ACCCTAAGGC TGT...CAA GGCTGGTAAG GTTACCGGTA AGACTTTGTT				124
<u>Schizo-saccharomyces pombe</u>	CATCAAGAAG GTCGGTTTCA ACCCAAGAC CGT...CAA GGCTGGTGTC GTCAAGGGTA AGACTCTTTT				
<u>Human</u>	GGAGATCCGG GAGCTGCTCA CCGAGTTTGG CTA...GTT AGGCCTGAAG TCTGTGCAGA AGCTACTGGA				
<u>15 Chlamydia trachomatis</u>	GGAGCTCCGC GAGCTGCTCA GCAAGTACGG CTT...CAA ATG..... TATTCTGG AGCTGATGAA				153
<u>Corynebacterium diptheriae</u>	GGAGATCCRT GAGCTGCTCG CTGAGCAGGA TTA...GAA GTGGACCCAG TCCATCATCG ACCTCATGCA				126
<u>Enterococcus faecalis</u>	GGAAGTTCGT GACTTATTAT CAGAAATACGA TTT..... TGAAGAA AAAATCTTAG AATTAATGGC				132
<u>Escherichia coli</u>	GGAAGTTCGT GAACTTCTGT CTCAGTACGA CTT..... GGGAGCG AAAATCCTGG AACTGGCTGG				154

Flavobacterium ferrugineum	CGAGGTTCCG <u>G</u> AAGAACTGA <u>C</u> TAAACGCGG TTT..... ..GG <u>CTTAAA</u> <u>G</u> AAATGAAA <u>A</u> CCTGATGGA	156
Gardnerella vaginalis	AGAGGTCCGT <u>G</u> ACCTCCTCG <u>A</u> AGAAAACGG CTT...CAA <u>G</u> TGGGTAGAG ACCGTCAAGG <u>A</u> ACTCATGAA	135
5 Haemophilus influenzae	GGAAGTTCGT <u>G</u> AACTTCTAT <u>C</u> TCAATATGA CTT..... ..GGGAAGAA <u>A</u> AAATCCTTG <u>A</u> GTTAGCAAA	157
Listeria monocytogenes	GGAAATTCGT <u>G</u> ATCTATTAA <u>C</u> TGAATATGA ATT..... ..GGGAAGCT <u>A</u> AAATGACG <u>A</u> GTTAATGGA	138
Micrococcus 10 luteus	GGAAGTCCGT <u>G</u> AGTTGCTGG <u>C</u> TGCCCAGGA ATT...CAA <u>G</u> TGGGTCGAG <u>T</u> CTGTACAC <u>A</u> GTTGATGGA	159
Neisseria gonorrhoeae	GGAAATCCGC <u>G</u> ACCTGCTGT <u>C</u> CAGCTACGA CTT..... ..ACGAAGAA <u>A</u> AAATCTTCG <u>A</u> ACTGGCTAC	162
Salmonella typhimurium	GGAAGTTCGC <u>G</u> AACTGCTGT <u>C</u> TCAGTACGA CTT..... ..GGGAAGCG <u>A</u> AAATCATCG <u>A</u> ACTGGCTGG	164
15 Staphylococcus aureus	GGAAGTTCGT <u>G</u> ACTTATTAA <u>G</u> CGAATATGA CTT..... ..CGAAGAA <u>A</u> AAATCTTAG <u>A</u> ATTAATGGA	140
Streptococcus pneumoniae	GGAAATCCGT <u>G</u> ACCTATTGT <u>C</u> AGAATACGA CTT..... ..CGAAGAC <u>A</u> TCGTTATGG <u>A</u> ATTGATGAA	145
Treponema 20 pallidum	AGAGGTGCGT <u>G</u> ATGCGCTTG <u>C</u> TGGATATGG GTT...GGA <u>G</u> GATGCAGCT <u>T</u> GTATTGAGG <u>A</u> ACTGCTTGC	169

Selected sequences	CAAGAAG GTTGGTTACA ACCCAAAGA	ATCCGGTAAA GTTACTGGTA AGACCT
Selected	SEQ ID NO: 11	SEQ ID NO: 12 ^a
5 species-specific primer sequences:	CAAGAAG GTTGGTTACA ACCCAAAGA	AGGTCTTACC AGTAACTTTAC CGGAT

10 The sequence numbering refers to the *Candida albicans* tuf gene fragment. Underlined nucleotides are identical to the selected sequence or match that sequence.

^a This sequence is the reverse-complement of the above tuf sequence.

Annex V: Strategy for the selection from the *recA* gene of the amplification primers specific for the genus *Streptococcus* (continues on pages 62 and 63).

	415	449...540	574 SEQ	
				ID NO
5 Bordetella pertussis	CTCGAGATCA	CCGACGGGCT GGTGGCTCG GGCTC...GGCC GCTGATGAG	CCAGGCGCTG	CGCAAGCTGA
Burkholderia cepacia	CTCGAAATCA	CCGATGGGCT GGTGGCTCG GGCTC...GGCC GCTGATGTC	GCAGGCGCTG	CGCAAGCTGA
Campylobacter jejuni	TTAGAAATTG	TAGAACTAT AGCAAGAAGT GGCGC...AGCA GACTTATGTC	TCAAGCTCTA	AGAAACTTA
Chlamydia trachomatis	TTGAGTATTG	CAGAGCTCTT AGCGGTTCT GGAGC...AGCT GCATGATGTC	GCAGGCTCTA	CGCAAATTAA
Clostridium perfringens	TTAGAAATAA	CAGAAGCTTT AGTTAGATCA GGAGC...AGCTA GATTAATGTC	ACAAGCCTTA	AGAAAGTTAA
15 Corynebacterium pseudotuberculosis	CTGGAGATTG	CAGATATGCT TGTTCGCTCT GGAGC...AGCG GTTGTGATGAG	TCAGGCGCTG	CGTAAGATGA
Enterobacter agglomerans	CTGGAAATCT	GTGATGGGCT GACCCGTTCA GGCGC...AGCTC GTATGATGAG	CCAGGCGATG	CGTAAGCTTG
Enterococcus faecium	TTAGAGATTG	CCGATGCCTT AGTTTCAAGT GGTGC...AGCTC GACTAATGTC	TCAAGCACTA	CGTAAATTAT
20 Escherichia coli	CTGGAAATCT	GTGACGCCCT GGCGGTTCT GGCGC...GGCAC GTATGATGAG	CCAGGCGATG	CGTAAGCTGG

Haemophilus influenzae	GCGAAACAGAA GAATAGAATT TTAATGCATT ACCGC...GACCT GTGAGTTTAC GCAAAGCTTG AGACATTAA
Helicobacter pylori	TTAGAAATTT TAGAAACGAT CACCAGAAGC GGAGG...AGCAA GGCTTATGAG CCATGCGTTA AGAAAAATCA
5 Lactococcus lactis	CTTCAAAATG CTGAAAATT GATTACTTCT GGAGC...AGCAC GTATGATGTC ACAAGCCATG CGTAAACTTG
Legionella pneumophila	CTGGAAATTA CTGATATGCT GGTGCGTTCT GCAGC...GGCAA GATTGATGTC GCAAGCCCTG CGTAAATTGA
Mycoplasma genitalium	TTTGCTCTTA TCGAATCATT AATTAAACA AACAA...TGCAA GAATGATGTC AAAAGGTTTG CGAAGAATAC
Neisseria gonorrhoeae	TTGGAAATCT GCGACACGCT CGTCCGTTCT GGCGG...GGCGC GCCTGATGAG TCAGGCTTG CGCAAACTGA
Proteus mirabilis	CTGGAAATTT GTGATGCATT ATCTCGCTCT GTTGC...CGCAC GTATGATGAG CCAAGCTATG CGTAAACTAG
15 Pseudomonas aeruginosa	CTGGAAATCA CCGACATGCT GGTGCGCTCC AACGC...GGCAC GCCTGATGTC CCAGGCGCTG CGCAAGATCA
Serratia marcescens	CTGGAAATCT GTGATGCGCT GACCCGCTCC GGCGC...GGCGC GCATGATGAG CCAGGCGATG CGTAAAGCTGG
Shigella flexneri	CTGGAAATCT GTGACGCCCT GGCGCGTTCT GGCGC...GGCAC GTATGATGAG CCAGGCGATG CGTAAAGCTGG
20 Staphylococcus aureus	CTTGAAATCG CCGAAGCATT TGTTAGAAGT GTTGC...AGCTC GTTAAATGTC ACAAGCGTTA CGTAAACTTT
Streptococcus gordonii	TTAGAAATG CAGGAAAATT GATTGACTCT GGGGC..... 32
25 Streptococcus mutans	CTTGAAATG CAGGGAATT GATTGATTCT GGCGC...AGCAC GCATGATGAG TCAAGCGATG CGTAAATTAT 33

Streptococcus CTTGAGATTG CCGGAAATT GATTGACTCA GGTGC...GGCTC GTATGATGAG CCAGGCCCATG CGTAAACTTG 34
pneumoniae
Streptococcus CTTGAAATTG CAGGTAAATT GATTGATTCT GGTGC...AGCAC GTATGATGAG TCAGGCCCATG CGTAAATTAT 35
pyogenes
5 Streptococcus CTCGAAATTG CAGGTAAGCT GATTGACTCT GGTGC...AGCGC GTATGATGAG TCAAGCCCATG CGTAAACTTT 36
salivarius
Vibrio CTGGAAATT GTGATGCACT GGCTCGCTCT GGTGC...AGCGC GTATGTTGTC GCAAGCAATG CGTAAACTGA
cholerae
Yersinia CTGGAAATT GTGATGCGCT GACTCGCTCT GGTGC...CGCGC GTATGATGAG CCAGGCTATG CGTAAAGCTGG
10 pestis
Selected GAAATTG CAGGIAAATT GATTGA ATGATGAG TCAIGCCCATG CGTAA
sequences^a

SEQ ID NO: 22^b

SEQ ID NO: 21

15 genus-specific primer GAAATTG CAGGIAAATT GATTGA TTACGCAT GGCITGACTC ATCAT
sequences^a:

The sequence numbering refers to the *S.pneumoniae* *recA* sequence. Underlined nucleotides are identical
20 to the selected sequence or match that sequence.

^a "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides
A, C, G or T.
^b This sequence is the reverse complement of the above *recA* sequence.

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Annex VI: Specific and ubiquitous primers for DNA amplification

	SEQ ID NO	Nucleotide sequence	Originating DNA fragment		
			SEQ ID NO	Nucleotide position	
5	<u>Bacterial species:</u> <i>Enterococcus faecium</i>				
	1	5'-TGC TTT AGC AAC AGC CTA TCA G	26 ^a	273-294	
	2 ^b	5'-TAA ACT TCT TCC GGC ACT TCG	26 ^a	468-488	
10	<u>Bacterial species:</u> <i>Listeria monocytogenes</i>				
	3	5'-TGC GGC TAT AAA TGA AGA GGC	27 ^a	339-359	
	4 ^b	5'-ATC CGA TGA TGC TAT GGC TTT	27 ^a	448-468	
15	<u>Bacterial species:</u> <i>Neisseria meningitidis</i>				
	5	5'-CCA GCG GTA TTG TTT GGT GGT	28 ^a	56-76	
	6 ^b	5'-CAG GCG GCC TTT AAT AAT TTC	28 ^a	212-232	
20	<u>Bacterial species:</u> <i>Staphylococcus saprophyticus</i>				
	7	5'- AGA TCG AAT TCC ACA TGA AGG TTA TTA TGA	29 ^c	290-319	
	8 ^b	5'- TCG CTT CTC CCT CAA CAA TCA AAC TAT CCT	29 ^c	409-438	
25	<u>Bacterial species:</u> <i>Streptococcus agalactiae</i>				
	9	5'-TTT CAC CAG CTG TAT TAG AAG TA	30 ^a	59-81	
	10 ^b	5'-GTT CCC TGA ACA TTA TCT TTG AT	30 ^a	190-212	
30	<u>Fungal species:</u> <i>Candida albicans</i>				
	11	5'-CAA GAA GGT TGG TTA CAA CCC AAA GA	120 ^c	61-86	
	12 ^b	5'-AGG TCT TAC CAG TAA CTT TAC CGG AT	120 ^c	184-209	

^a Sequences from databases.

35 ^b These sequences are from the opposite DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^c Sequences determined by our group.

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Annex VI: Specific and ubiquitous primers for DNA amplification
(continues on next page)

	SEQ ID NO	Nucleotide sequence	Originating DNA fragment		
			SEQ ID NO	Nucleotide position	
5	<u>Bacterial genus: Enterococcus</u>				
	13	5'-TAC TGA CAA ACC ATT CAT GAT G	131-134 ^{a,b}	319-340 ^c	
	14 ^d	5'-AAC TTC GTC ACC AAC GCG AAC	131-134 ^{a,b}	410-430 ^c	
10	<u>Bacterial genus: Neisseria</u>				
	15	5'-CTG GCG CGG TAT GGT CGG TT	31 ^e	21-40 ^f	
	16 ^d	5'-GCC GAC GTT GGA AGT GGT AAA G	31 ^e	102-123 ^f	
	<u>Bacterial genus: Staphylococcus</u>				
15	17	5'-CCG TGT TGA ACG TGG TCA AAT CAA A	140-143 ^{a,b}	391-415 ^g	
	18 ^d	5'-TRT GTG GTG TRA TWG WRC CAG GAG C	140-143 ^{a,b}	584-608 ^g	
	19	5'-ACA ACG TGG WCA AGT WTT AGC WGC T	140-143 ^{a,b}	562-583 ^g	
	20 ^d	5'-ACC ATT TCW GTA CCT TCT GGT AAG T	140-143 ^{a,b}	729-753 ^g	
20	<u>Bacterial genus: Streptococcus</u>				
	21	5'-GAA ATT GCA GGI AAA TTG ATT GA	32-36 ^e	418-440 ^h	
	22 ^d	5'-TTA CGC ATG GCI TGA CTC ATC AT	32-36 ^e	547-569 ^h	
25	Universal primers				
	23	5'-ACI KKI ACI GGI GTI GAR ARG TT	118-146 ^{a,b} 147-171 ^{a,e}	493-515 ⁱ	
	24 ^d	5'-AYR TTI TCI CCI GGC ATI ACC AT	118-146 ^{a,b} 147-171 ^{a,e}	778-800 ⁱ	

- 30 ^a These sequences were aligned to derive the corresponding primer.
- ^b tuf sequences determined by our group.
- ^c The nucleotide positions refer to the *E. faecalis* tuf gene fragment (SEQ ID NO: 132).
- 35 ^d These sequences are from the opposite DNA strand of the sequence of the originating fragment given in the Sequence Listing.
- ^e Sequences from databases.
- ^f The nucleotide positions refer to the *N. meningitidis* asd gene fragment (SEQ ID NO: 31).

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- ^g The nucleotide positions refer to the *S. aureus tuf* gene fragment (SEQ ID NO: 140).
- ^h The nucleotide positions refer to the *S. pneumoniae recA* gene (SEQ ID NO: 34).
- 5 ⁱ The nucleotide positions refer to the *E. coli tuf* gene fragment (SEQ ID NO: 154).

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Annex VI: Specific and ubiquitous primers for DNA amplification

SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO	Nucleotide position
<u>Antibiotic resistance gene: bla_{tem}</u>			
5	37 5'-CTA TGT GGC GCG GTA TTA TC	-	-
	38 5'-CGC AGT GTT ATC ACT CAT GG	-	-
	39 5'-CTG AAT GAA GCC ATA CCA AA	-	-
	40 5'-ATC AGC AAT AAA CCA GCC AG	-	-
<u>Antibiotic resistance gene: bla_{shv}</u>			
15	41 5'-TTA CCA TGA GCG ATA ACA GC	-	-
	42 5'-CTC ATT CAG TTC CGT TTC CC	-	-
	43 5'-CAG CTG CTG CAG TGG ATG GT	-	-
	44 5'-CGC TCT GCT TTG TTA TTC GG	-	-
<u>Antibiotic resistance gene: bla_{rob}</u>			
20	45 5'-TAC GCC AAC ATC GTG GAA AG	-	-
	46 5'-TTG AAT TTG GCT TCT TCG GT	-	-
	47 5'-GGG ATA CAG AAA CGG GAC AT	-	-
	48 5'-TAA ATC TTT TTC AGG CAG CG	-	-
<u>Antibiotic resistance gene: bla_{oxa}</u>			
30	49 5'-GAT GGT TTG AAG GGT TTA TTA TAA G	110 ^a	686-710
	50 ^b 5'-AAT TTA GTG TGT TTA GAA TGG TGA T	110 ^a	802-826
<u>Antibiotic resistance gene: bla_Z</u>			
35	51 5'-ACT TCA ACA CCT GCT GCT TTC	111 ^a	511-531
	52 ^b 5'-TGA CCA CTT TTA TCA GCA ACC	111 ^a	663-683
<u>Antibiotic resistance gene: aadB</u>			
40	53 5'-GGC AAT AGT TGA AAT GCT CG	-	-
	54 5'-CAG CTG TTA CAA CGG ACT GG	-	-
<u>Antibiotic resistance gene: aacC1</u>			
45	55 5'-TCT ATG ATC TCG CAG TCT CC	-	-
	56 5'-ATC GTC ACC GTA ATC TGC TT	-	-

^a Sequences from databases.^b These sequences are from the opposite DNA strand of the sequence of the originating fragment given in the Sequence Listing.

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Annex VI: Specific and ubiquitous primers for DNA amplification

	SEQ ID NO	Nucleotide sequence	Originating DNA fragment		
			SEQ ID NO	Nucleotide position	
5	<u>Antibiotic resistance gene: aacC2</u>				
	57	5'-CAT TCT CGA TTG CTT TGC TA	-	-	
	58	5'-CCG AAA TGC TTC TCA AGA TA	-	-	
10	<u>Antibiotic resistance gene: aacC3</u>				
	59	5'-CTG GAT TAT GGC TAC GGA GT	-	-	
	60	5'-AGC AGT GTG ATG GTA TCC AG	-	-	
15	<u>Antibiotic resistance gene: aac6'-IIa</u>				
	61	5'-GAC TCT TGA TGA AGT GCT GG	112 ^a	123-142	
	62 ^b	5'-CTG GTC TAT TCC TCG CAC TC	112 ^a	284-303	
20	63	5'-TAT GAG AAG GCA GGA TTC GT	112 ^a	445-464	
	64 ^b	5'-GCT TTC TCT CGA AGG CTT GT	112 ^a	522-541	
25	<u>Antibiotic resistance gene: aacA4</u>				
	65	5'-GAG TTG CTG TTC AAT GAT CC	-	-	
	66	5'-GTG TTT GAA CCA TGT ACA CG	-	-	
30	<u>Antibiotic resistance gene: aad(6')</u>				
	173	5'-TCT TTA GCA GAA CAG GAT GAA	-	-	
	174	5'-GAA TAA TTC ATA TCC TCC G	-	-	
35	<u>Antibiotic resistance gene: vanA</u>				
	67	5'-TGT AGA GGT CTA GCC CGT GT	-	-	
	68	5'-ACG GGG ATA ACG ACT GTA TG	-	-	
	69	5'-ATA AAG ATG ATA GGC CGG TG	-	-	
	70	5'-TGC TGT CAT ATT GTC TTG CC	-	-	
40	<u>Antibiotic resistance gene: vanB</u>				
	71	5'-ATT ATC TTC GGC GGT TGC TC	116 ^a	22-41	
	72 ^b	5'-GAC TAT CGG CTT CCC ATT CC	116 ^a	171-190	
45	73	5'-CGA TAG AAG CAG CAG GAC AA	116 ^a	575-594	
	74 ^b	5'-CTG ATG GAT GCG GAA GAT AC	116 ^a	713-732	

^a Sequences from databases.^b These sequences are from the opposite DNA strand of the sequence of the originating fragment given in the Sequence Listing.**SUBSTITUTE SHEET (RULE 26)**

Annex VI: Specific and ubiquitous primers for DNA amplification

	SEQ ID NO	Nucleotide sequence	Originating DNA fragment		
			SEQ ID NO	Nucleotide position	
5	<u>Antibiotic resistance gene: <i>vanC</i></u>				
	75	5'-GCC TTA TGT ATG AAC AAA TGG	117 ^a	373-393	
	76 ^b	5'-GTG ACT TTW GTG ATC CCT TTT GA	117 ^a	541-563	
10	<u>Antibiotic resistance gene: <i>msrA</i></u>				
	77	5'-TCC AAT CAT TGC ACA AAA TC	-	-	
	78	5'-AAT TCC CTC TAT TTG GTG GT	-	-	
	79	5'-TCC CAA GCC AGT AAA GCT AA	-	-	
15	80	5'-TGG TTT TTC AAC TTC TTC CA	-	-	
	<u>Antibiotic resistance gene: <i>sata</i></u>				
	81	5'-TCA TAG AAT GGA TGG CTC AA	-	-	
20	82	5'-AGC TAC TAT TGC ACC ATC CC	-	-	
	<u>Antibiotic resistance gene: <i>aac(6')-aph(2'')</i></u>				
	83	5'-CAA TAA GGG CAT ACC AAA AAT C	-	-	
25	84	5'-CCT TAA CAT TTG TGG CAT TAT C	-	-	
	85	5'-TTG GGA AGA TGA AGT TTT TAG A	-	-	
	86	5'-CCT TTA CTC CAA TAA TTT GGC T	-	-	
30	<u>Antibiotic resistance gene: <i>vat</i></u>				
	87	5'-TTT CAT CTA TTC AGG ATG GG	-	-	
	88	5'-GGA GCA ACA TTC TTT GTG AC	-	-	
35	<u>Antibiotic resistance gene: <i>vga</i></u>				
	89	5'-TGT GCC TGA AGA AGG TAT TG	-	-	
	90	5'-CGT GTT ACT TCA CCA CCA CT	-	-	
40	<u>Antibiotic resistance gene: <i>ermA</i></u>				
	91	5'-TAT CTT ATC GTT GAG AAG GGA TT	113 ^a	370-392	
	92 ^b	5'-CTA CAC TTG GCT TAG GAT GAA A	113 ^a	487-508	

45 ^a Sequences from databases.

^b These sequences are from the opposite DNA strand of the sequence of the originating fragment given in the Sequence Listing.

Annex VI: Specific and ubiquitous primers for DNA amplification

SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
		SEQ ID NO	Nucleotide position
<u>Antibiotic resistance gene: <i>ermB</i></u>			
5	93 5'-CTA TCT GAT TGT TGA AGA AGG ATT	114 ^a	366-389
	94 ^b 5'-GTT TAC TCT TGG TTT AGG ATG AAA	114 ^a	484-507
<u>Antibiotic resistance gene: <i>ermC</i></u>			
10	95 5'-CTT GTT GAT CAC GAT AAT TTC C	115 ^a	214-235
	96 ^b 5'-ATC TTT TAG CAA ACC CGT ATT C	115 ^a	382-403
<u>Antibiotic resistance gene: <i>mecA</i></u>			
15	97 5'-AAC AGG TGA ATT ATT AGC ACT TGT AAG	-	-
	98 5'-ATT GCT GTT AAT ATT TTT TGA GTT GAA	-	-
<u>Antibiotic resistance gene: <i>int</i></u>			
20	99 5'-GTG ATC GAA ATC CAG ATC C	-	-
	100 5'-ATC CTC GGT TTT CTG GAA G	-	-
25	101 5'-CTG GTC ATA CAT GTG ATG G	-	-
	102 5'-GAT GTT ACC CGA GAG CTT G	-	-
<u>Antibiotic resistance gene: <i>sul</i></u>			
30	103 5'-TTA AGC GTG CAT AAT AAG CC	-	-
	104 5'-TTG CGA TTA CTT CGC CAA CT	-	-
	105 5'-TTT ACT AAG CTT GCC CCT TC	-	-
	106 5'-AAA AGG CAG CAA TTA TGA GC	-	-

35 ^a Sequences from databases.

^b These sequences are from the opposite DNA strand of the sequence of the originating fragment given in the Sequence Listing.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: BERGERON, Michel G.
PICARD, Francois J.
OUELLETTE, Marc
ROY, Paul H.
- (ii) TITLE OF INVENTION: SPECIES-SPECIFIC, GENUS-SPECIFIC AND
UNIVERSAL DNA PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY
DETECT AND IDENTIFY COMMON BACTERIAL AND FUNGAL PATHOGENS
AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES ...
- (iii) NUMBER OF SEQUENCES: 174
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: GOUDREAU GAGE DUBUC & MARTINEAU WALKER
 - (B) STREET: 3400-800 Place-Victoria, P.O. Box 242
 - (C) CITY: Montreal
 - (D) STATE: Quebec
 - (E) COUNTRY: CANADA
 - (F) ZIP: H4Z 1E9
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: CA 2,270,281
 - (B) FILING DATE: 04-NOV-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/743,637
 - (B) FILING DATE: 04-NOV-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: LECLERC, Alain M.
 - (B) REGISTRATION NUMBER: 37036
 - (C) REFERENCE/DOCKET NUMBER: DH/12287.21
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (514) 397-4335
 - (B) TELEFAX: (514) 397-4382

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Enterococcus faecium
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGCTTTAGCA ACAGCCTATC AG

22

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Enterococcus faecium
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TAAACTTCTT CCGGCACTTC G

21

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Listeria monocytogenes
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGCGGCTATA AATGAAGAGG C

21

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Listeria monocytogenes

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATCCGATGAT GCTATGGCTT T

21

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCAGCGGTAT TGTTTGGTGG T

21

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAGGCGGCCT TTAATAATTT C

21

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGATCGAATT CCACATGAAG GTTATTATGA

30

(2) INFORMATION FOR SEQ ID NO:8:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TCGCTTCTCC CTCAACAATC AAATATCCT

30

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTTCACCAGC TGTATTAGAA GTA

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTTCCCTGAA CATTATCTTT GAT

23

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Candida albicans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CAAGAAGGTT GGTACAACC CAAAGA

26

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Candida albicans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGGTCTTACC AGTAACTTTA CCGGAT

26

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TACTGACAAA CCATTCATGA TG

22

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AACTTCGTCA CCAACGCGAA C

21

(2) INFORMATION FOR SEQ ID NO:15:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTGGCGCGGT ATGGTCGGTT

20

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCGACGTTG GAAGTGGTAA AG

22

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCGTGTTGAA CGTGGTCAAA TCAA

25

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TRTGTGGTGT RATWGWCCA GGAGC

25

(2) INFORMATION FOR SEQ ID NO:19:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACAACGTGGW CAAGTWTAG CWGCT

25

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ACCATTTCWG TACCTTCTGG TAAGT

25

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAAATTGCAG GNAAATTGAT TGA

23

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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- (B) LOCATION: 12
- (D) OTHER INFORMATION: /note= "n = inosine"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTACGCATGG CNTGACTCAT CAT

23

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 3
 - (D) OTHER INFORMATION: /note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 6
 - (D) OTHER INFORMATION: /note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 9
 - (D) OTHER INFORMATION: /note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 12
 - (D) OTHER INFORMATION: /note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 15
 - (D) OTHER INFORMATION: /note= "n = inosine"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ACNKKNACNG GNGTNGARAT GTT

23

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

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- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "n = inosine"

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 9
 - (D) OTHER INFORMATION: /note= "n = inosine"

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 12
 - (D) OTHER INFORMATION: /note= "n = inosine"

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 18
 - (D) OTHER INFORMATION: /note= "n = inosine"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AYRTTNTCNC CNGGCATNAC CAT

23

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCGCTTCTCC

10

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 600 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Enterococcus faecium
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTCTTAGAGA CATTGAATAT GCCTTATGTC GCGCAGGCG TATTGACCAG TGCATGTGCC	60
ATGGATAAAA TCATGACCAA GTATATTTTA CAAGCTGCTG GTGTGCCGCA AGTTCCTTAT	120
GTACCAGTAC TTAAGAATCA ATGGAAAGAA AATCCTAAAA AAGTATTTGA TCAATGTGAA	180

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GGTTCTTTGC TTTATCCGAT GTTTGTCAAA CCTGCGAATA TGGGTTCTAG TGTCGGCATT	240
ACAAAGGCAG AAAACCGAGA AGAGCTGCAA AATGCTTTAG CAACAGCCTA TCAGTATGAT	300
TCTCGAGCAA TCGTTGAACA AGGAATTGAA GCGCGCGAAA TCGAAGTTGC TGTATTAGGA	360
AATGAAGATG TTCGGACGAC TTTGCCTGGC GAAGTCGTAA AAGACGTAGC ATTCTATGAT	420
TATGAAGCCA AATATATCAA TAATAAAATC GAAATGCAGA TTCCAGCCGA AGTGCCGGAA	480
GAAGTTTATC AAAAAGCGCA AGAGTACGCG AAGTTAGCTT ACACGATGTT AGGTGGAAGC	540
GGATTGAGCC GGTGCGATTT CTTTTTGACA AATAAAAATG AATTATTCCT GAATGAATTA	600

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1920 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTGGGATTAA ACAGATTTAT GCGTGCGATG ATGGTGGTTT TCATTACTGC CAATTGCATT	60
ACGATTAACC CCGACATAAT ATTTGCAGCG ACAGATAGCG AAGATTCTAG TCTAAACACA	120
GATGAATGGG AAGAAGAAAA AACAGAAGAG CAACCAAGCG AGGTAAATAC GGGACCAAGA	180
TACGAAACTG CACGTGAAGT AAGTTCACGT GATATTAAAG AACTAGAAAA ATCGAATAAA	240
GTGAGAAATA CGAACAAAGC AGACCTAATA GCAATGTTGA AAGAAAAAGC AGAAAAAGGT	300
CCAAATATCA ATAATAACAA CAGTGAACAA ACTGAGAATG CGGCTATAAA TGAAGAGGCT	360
TCAGGAGCCG ACCGACCAGC TATACAAGTG GAGCGTCGTC ATCCAGGATT GCCATCGGAT	420
AGCGCAGCGG AAATTAAAAA AAGAAGGAAA GCCATAGCAT CATCGGATAG TGAGCTTGAA	480
AGCCTTACTT ATCCGGATAA ACCAACAAAA GTAAATAAGA AAAAAGTGGC GAAAGAGTCA	540
GTTGCGGATG CTTCTGAAAG TGACTTAGAT TCTAGCATGC AGTCAGCAGA TGAGTCTTCA	600
CCACAACCTT TAAAAGCAAA CCAACAACCA TTTTCCCTA AAGTATTTAA AAAAATAAAA	660
GATGCGGGGA AATGGGTACG TGATAAAATC GACGAAAATC CTGAAGTAAA GAAAGCGATT	720
GTTGATAAAA GTGCAGGGTT AATTGACCAA TTATTAACCA AAAAGAAAAG TGAAGAGGTA	780
AATGCTTCGG ACTTCCCGCC ACCACCTACG GATGAAGAGT TAAGACTTGC TTTGCCAGAG	840

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ACACCAATGC TTCTTGGTTT TAATGCTCCT GCTACATCAG AACCGAGCTC ATTCGAATTT	900
CCACCACCAC CTACGGATGA AGAGTTAAGA CTTGCTTTGC CAGAGACGCC AATGCTTCTT	960
GGTTTTAATG CTCCTGCTAC ATCGGAACCG AGCTCGTTTCG AATTTCCACC GCCTCCAACA	1020
GAAGATGAAC TAGAAATCAT CCGGGAAACA GCATCCTCGC TAGATTCTAG TTTTACAAGA	1080
GGGGATTTAG CTAGTTTGAG AAATGCTATT AATCGCCATA GTCAAAATTT CTCTGATTTC	1140
CCACCAATCC CAACAGAAGA AGAGTTGAAC GGGAGAGGCG GTAGACCAAC ATCTGAAGAA	1200
TTTAGTTCGC TGAATAGTGG TGATTTTACA GATGACGAAA ACAGCGAGAC AACAGAAGAA	1260
GAAATTGATC GCCTAGCTGA TTTAAGAGAT AGAGGAACAG GAAAACACTC AAGAAATGCG	1320
GGTTTTTTTAC CATTAAATCC GTTTGCTAGC AGCCCGGTTT CTTCGTTAAG TCCAAAGGTA	1380
TCGAAAATAA GCGACCGGGC TCTGATAAGT GACATAACTA AAAAAACGCC ATTTAAGAAT	1440
CCATCACAGC CATTAAATGT GTTTAATAAA AAAACTACAA CGAAAACAGT GACTAAAAAA	1500
CCAACCCCTG TAAAGACCGC ACCAAAGCTA GCAGAACTTC CTGCCACAAA ACCACAAGAA	1560
ACCGTACTTA GGGAAAATAA AACACCCTTT ATAGAAAAAC AAGCAGAAAC AAACAAGCAG	1620
TCAATTAATA TGCCGAGCCT ACCAGTAATC CAAAAAGAAG CTACAGAGAG CGATAAAGAG	1680
GAAATGAAAC CACAAACCGA GGAAAAAATG GTAGAGGAAA GCGAATCAGC TAATAACGCA	1740
AACGGAAAAA ATCGTTCTGC TGGCATTGAA GAAGGAAAAC TAATTGCTAA AAGTGCAGAA	1800
GACGAAAAAG CGAAGGAAGA ACCAGGGAAC CATACGACGT TAATTCTTGC AATGTTAGCT	1860
ATTGGCGTGT TCTCTTTAGG GGC GTTTATC AAAATTATTC AATTAAGAAA AAATAATTAA	1920

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TACCGGTACG CTAAATATTG GTGATGTATT GGATATTATG ATTTGGGAAG CGCCGCCAGC	60
GGTATTGTTT GGTGGTGGCC TTTCTTCGAT GGGCTCGGGT AGTGCGCAAC AAACCAAGTT	120
GCCGGAGCAA CTGGTGACGG CACGTGGTAC GGTTTCTGTG CCGTTTGTTG GCGATATTTC	180

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GGTGGTCGGT AAAACGCCTG GTCAGGTTCA GGAAATTATT AAAGGCCGCC TGAAAAAAT 240
 GGCCAATCAG CCGCAAGTGA TGGTGCCTT GGTGCAGAAT AATGCGGCAA ATGTATCGGT 300
 GATTCGCGCA GGCAATAGTG TCGTATGCC GTTGACGGCA GCCGGTGAGC GTGTGTTGGA 360
 TGCGGTGGCT GCGGTAGGTG GTTCAACGGC AAATGTGCAG GATACGAATG TGCAG 415

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TCGCTTCTCC AGAAGAAATT TTAGAAACAT ATCTAGAAAA TCCCAAATTA GATAAACCGT 60
 TTATATTATG TGAATACGCA CATGCAATGG GAAATTCACC AGGAGATCTT AATGCATATC 120
 AAACATTAAT TGAAAAATAT GATAGTTTTA TTGGCGGTTT TGTTTGGGAA TGGTGTGATC 180
 ATAGCATTCA GGTGTTGGATA AAGGAAGGTA AACCAATTTT TAGATATGGT GGAGATTTTG 240
 GTGAGGCCTT ACATGACGGT AATTTTTGTG TTGATGGTAT TGTTTCGCCA GATCGAATTC 300
 CACATGAAGG TTATTATGAG TTAAACATG AACATAGACC TTTGAGATTG GTTAACGAAG 360
 AGGATTATCG GTTTACATTG AAGAATCAAT TTGATTTTAC AAATGCGGAG GATAGTTTGA 420
 TTGTTGAGGG AGAAGCGA 438

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATGAACGTTA CACATATGAT GTATCTATCT GGAACCTAG TGGCTGGTGC ATTGTTATTT 60

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TCACCAGCTG TATTAGAAGT ACATGCTGAT CAAGTGACAA CTCCACAAGT GGTAATCAT	120
GTAAATAGTA ATAATCAAGC CCAGCAAATG GCTCAAAAGC TTGATCAAGA TAGCATTCAG	180
TTGAGAAATA TCAAAGATAA TGTTCAAGGA ACAGATTATG AAAAACCGGT TAATGAGGCT	240
ATTACTAGCG TGGAAAAATT AAAGACTTCA TTGCGTGCCA ACCCTGAGAC AGTTTATGAT	300
TTGAATTCTA TTGGTAGTCG TGTAGAAGCC TTAACAGATG TGATTGAAGC AATCACTTTT	360
TCAACTCAAC ATTTAACAAA TAAGGTTAGT CAAGCAAATA TTGATATGGG ATTTGGGATA	420
ACTAAGCTAG TTATTCGCAT TTTAGATCCA TTTGCTTCAG TTGATTCAAT TAAAGCTCAA	480
GTTAACGATG TAAAGGCATT AGAACAAAAA GTTTTAACTT ATCCTGATTT AAAACCAACT	540
GATAGAGCTA CCATCTATAC AAAATCAAAA CTTGATAAGG AAATCTGGAA TACACGCTTT	600
ACTAGAGATA AAAAAGTACT TAACGTCAAA GAATTTAAAG TTTACAATAC TTAAATAAAA	660
GCAATCACAC ATGCTGTTGG AGTTCAGTTG AATCCAAATG TTACGGTACA ACAAGTTGAT	720
CAAGAGATTG TAACATTACA AGCAGCACTT CAAACAGCAT TAAATAA	768

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGAAAGTAG GTTTCGTCGG CTGGCGCGGT ATGGTCGGTT CGGTTTTGAT GCAGCGTATG	60
AAAGAAGAAA ACGACTTCGC CCACATTCCC GAAGCGTTTT TCTTTACCAC TTCCAACGTC	120
GGCGGCGCAC GCCCTGATTT CGGTCAGGCG GCTAAAACAT TATTGGACGC GAACAACGTT	180
GCCGAGCTGG CAAAATGGA CATCATCGTT ACCTGCCAAG GCGGCGACTA CACCAAATCC	240
GTCTTCCAAG CCCTGCGCGA CAGCGGCTGG AACGGCTACT GGATTGACGC GGCATCCTCG	300
CTGCGTATGA AAGACGACGC GATTATCGTC CTCGACCCCG TCAACCGCAA CGTCATCGAC	360
AACGGCCTCA AAAACGGCGT GAAAACTAC ATCGGCGGCA ACTGTACCGT TTCCCTGATG	420
C	421

(2) INFORMATION FOR SEQ ID NO:32:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus gordonii*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

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TTCATAGACG CTGAGCACGC TTTGGATCCA TCTTACGCGG CTGCTCTAGG TGTAATATT      60
GATGAGCTGT TGCTATCTCA ACCAGATTCT GGTGAGCAAG GTTTAGAAAT TGCAGGAAAA      120
TTGATTGACT CTGGGGCAGT TGATTTAGTT GTCATCGACT CTGTTGCAGC TCTTGTACCA      180
CGTGCGGAAA TCGATGGAGA TATCGGTGAT AGC                                213

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(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mutans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```

GGGCCGGAAT CTTCTGGTAA GACAACTGTC GCTCTTCATG CTGCTGCTCA GGCGCAAAAA      60
GATGGCGGTA TTGCCGCTTT CATTGATGCA GAACATGCCC TTGATCCAGC CTATGCTGCT      120
GCTCTTGGCG TTAATATTGA TGAGCTTTTG CTTTCACAAC CAGATTCAGG AGAACAGGGT      180
CTTGAAATTG CAGGGAAATT GATTGATTCT GGCGCTGTTG ATTTAGTTGT TGTGACTCA      240
GTGGCAGCTT TAGTACCACG TCGCGAGATT GACGGAGATA TTGGTAATAG TCATGTTGGC      300
TTACAAGCAC GCATGATGAG TCAAGCGATG CGTAAATTAT CAGCTTCAAT CAATAAAACA      360
AAAACCATTG CTATTTTTTAT TAATCAATTG CGGGAAAAAG TTGGTATTAT GTTTGGTAAT      420
CCAGAAACAA CCCCTGGCGG GCGTGCCTTG AAGTTTTATT CTTCTGTGCG TCTTGATGTC      480
CGCGGCAATA CTCAAATTAA AGGAACCGGG GAACAAAAAG ACAGCAATAT TGGTAAAGAG      540
ACCAAAATTA AAGTTGTTAA AAATAAAGTT GCTCCACCAT TTAAGGAAGC TTTTGTAGAA      600

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ATTATATATG GTGAAGGCAT TTCTCGTACA GGTGAATTAG TTAAGATTGC CAGTGATTTG 660
 GGAATTATCC AAAAAGCTGG AGCTTGGTAC TC 692

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ATGGCGAAAA AACCAAAAAA ATTAGAAGAA ATTTCAAAAA AATTTGGGGC AGAACGTGAA 60
 AAGGCCTTGA ATGACGCTCT TAAATTGATT GAGAAAGACT TTGGTAAAGG ATCAATCATG 120
 CGTTTGGGTG AACGTGCGGA GCAAAGGTG CAAGTGATGA GCTCAGGTTC TTTAGCTCTT 180
 GACATTGCCC TTGGCTCAGG TGGTTATCCT AAGGGACGTA TCATCGAAAT CTATGGCCCA 240
 GAGTCATCTG GTAAGACAAC GGTTGCCCTT CATGCAGTTG CACAAGCGCA AAAAGAAGGT 300
 GGGATTGCTG CCTTTATCGA TGCGGAACAT GCCCTTGATC CAGCTTATGC TGCGGCCCTT 360
 GGTGTCAATA TTGACGAATT GCTCTTGTCT CAACCAGACT CAGGAGAGCA AGGTCTTGAG 420
 ATTGCGGGAA AATTGATTGA CTCAGGTGCA GTTGATCTTG TCGTAGTCGA CTCAGTTGCT 480
 GCCCTTGTTT CTCGTGCGGA AATTGATGGA GATATCGGAG ATAGCCATGT TGGTTTGCAG 540
 GCTCGTATGA TGAGCCAGGC CATGCGTAAA CTTGGCGCCT CTATCAATAA AACCAAAACA 600
 ATTGCCATTT TTATCAACCA ATTGCGTGAA AAAGTTGGAG TGATGTTTGG AAATCCAGAA 660
 ACAACACCGG GCGGACGTGC TTTGAAATTC TATGCTTCAG TCCGCTTGGA TGTTCGTGGT 720
 AATACACAAA TTAAGGGAAC TGGTGATCAA AAAGAAACCA ATGTCGGTAA AGAAACTAAG 780
 ATTAAGGTTG TAAAAAATAA GGTAGCTCCA CCGTTTAAGG AAGCCGTAGT TGAAATTATG 840
 TACGGAGAAG GAATTTCTAA GACTGGTGAG CTTTGAAGA TTGCAAGCGA TTTGGATATT 900
 ATCAAAAAAG CAGGGGCTTG GTATTCTTAC AAAGATGAAA AAATTGGGCA AGGTTCTGAG 960
 AATGCTAAGA AATACTTGGC AGAGCACCCA GAAATCTTTG ATGAAATTGA TAAGCAAGTC 1020
 CGTTCTAAAT TTGGCTTGAT TGATGGAGAA GAAGTTTCAG AACAAGATAC TGAAAACAAA 1080
 AAAGATGAGC CAAAGAAAGA AGAAGCAGTG AATGAAGAAG TTCCGCTTGA CTTAGGCGAT 1140

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GAACCTTGAAA TCGAAATTGA AGAATAAGCT GTTAAAGCAG TGGAGAAATC CGCTACTTTT 1200
TCGA 1204

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pyogenes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATGCGTTCAG GAAGTCTAGC TCTTGATATT GCTTGGATAG CTGGTGGTTA TCCTAAAGGA 60
CGTATCATCG AAATCTATGG TCCAGAGTCT TCCGGTAAAA CGACTGTGGC TTTACATGCT 120
GTAGCACAAG CTCAAAAAGA AGGTGGAATC GCAGCCTTTA TCGATGCCGA GCATGCGCTT 180
GATCCAGCTT ATGCTGCTGC GCTTGGGGTT AATATTGATG AACTTCTCTT GTCTCAACCA 240
GATTCTGGAG AACAAGGACT TGAAATTGCA GGTAATTGA TTGATTCTGG TCGGGTTGAC 300
CTGGTTGTTG TCGATTCAGT AGCAGCTTTA GTGCCACGTG CTGAAATTGA TGGTGATATT 360
GGCGATAGCC ATGTCGGATT GCAAGCACGT ATGATGAGTC AGGCCATGCG TAAATTATCA 420
GCTTCTATTA ATAAAACAAA AACTATCGCA ATCTTTATCA ACCAATTGCG TGAAAAAGTT 480
GGTGTGATGT TTGGAAATCC TGAAACAACA CCAGGTGGTC GAGCTTTGAA ATTCTATGCT 540
TCTGTTCGGC TGGATGTGCG TGGAAACAAC CAAATTAAAG GAACTGGTGA CCAAAGATA 600
GCCAGCATTG GTAAGGAGAC CAAAATCAAG GTTGTAAAA ACAAGGTCGC TCCGCCATTT 660
AAGGTAGCAG AAGTTGAAAT CATGTATGGG GAAGGTATTT CTCGTACAGG GGAGCTTGTG 720
AAAATTGCTT CTGATTTGGA CATTATCCAA AAAGCAGGTG CTTGGTTCTC TTATAATGGT 780
GAGAAGATTG GCCAAGGTTC TGAAAATGCT AAGCGTTATT TGGCCGATCA TCCACAATTG 840
TTTGATGAAA TCGACCGTAA AGTACGTGTT AAATTTGGTT TGCTTGAAGA AAGCGAAGAA 900
GAATCTGCTA TGGCAGTAGC ATCAGAAGAA ACCGATGATC TTGCTTTAGA TTTAGATAAT 960
GGTATTGAAA TTGAAGATTA A 981

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus salivarius

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCGTATGCAC GAGCTCTAGG TGTTAATATC GATGAGCTTC TTTTGTGCGA GCCTGATTCT	60
GGTGAGCAAG GTCTCGAAAT TGCAGGTAAG CTGATTGACT CTGGTGCAGT GGATTTAGTT	120
GTTGTTGACT CAGTTGCGGC CTTCGTACCA CGTGCAGAAA TTGATGGAGA TAGTGGTGAC	180
AGTCATGTAG GACTTCAAGC GCGTATGATG AGTCAAGCCA TGCGTAAACT TTCTGCATCT	240
ATTAATAAAA CAAAACGAT TGCTATCTTT ATTAACCAGT TCGTGAAAA AGTTGGTATC	300
ATGTTTGGTA AC	312

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CTATGTGGCG CGGTATTATC	20
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(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGCAGTGTTA TCACTCATGG	20
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(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTGAATGAAG CCATACCAAA

20

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATCAGCAATA AACCAGCCAG

20

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TTACCATGAG CGATAACAGC

20

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTCATTCAGT TCCGTTTCCC

20

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CAGCTGCTGC AGTGGATGGT

20

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CGCTCTGCTT TGTATTCGG

20

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TACGCCAACA TCGTGGAAG

20

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TTGAATTTGG CTTCTTCGGT

20

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

- 90 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGGATACAGA AACGGGACAT

20

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TAAATCTTTT TCAGGCAGCG

20

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GATGGTTTGA AGGGTTTATT ATAAG

25

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AATTTAGTGT GTTTAGAATG GTGAT

25

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs

- 91 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

ACTTCAACAC CTGCTGCTTT C

21

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGACCACTTT TATCAGCAAC C

21

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGCAATAGTT GAAATGCTCG

20

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CAGCTGTTAC AACGGACTGG

20

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

- 92 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TCTATGATCT CGCAGTCTCC

20

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

ATCGTCACCG TAATCTGCTT

20

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CATTCTCGAT TGCTTTGCTA

20

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CCGAAATGCT TCTCAAGATA

20

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

- 93 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CTGGATTATG GCTACGGAGT

20

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

AGCAGTGTGA TGGTATCCAG

20

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GACTCTTGAT GAAGTGCTGG

20

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTGGTCTATT CCTCGCACTC

20

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

- 94 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TATGAGAAGG CAGGATTCGT

20

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCTTTCTCTC GAAGGCTTGT

20

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GAGTTGCTGT TCAATGATCC

20

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GTGTTTGAAC CATGTACACG

20

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

- 95 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TGTAGAGGTC TAGCCCGTGT

20

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ACGGGGATAA CGACTGTATG

20

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ATAAAGATGA TAGGCCGGTG

20

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TGCTGTCATA TTGTCTTGCC

20

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

- 96 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ATTATCTTCG GCGGTTGCTC

20

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GACTATCGGC TTCCCATTC

20

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CGATAGAAGC AGCAGGACAA

20

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CTGATGGATG CGGAAGATAC

20

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs

- 97 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GCCTTATGTA TGAACAAATG G

21

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GTGACTTTWG TGATCCCTTT TGA

23

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TCCAATCATT GCACAAAATC

20

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

AATTCCTCT ATTTGGTGGT

20

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

- 98 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCCCAAGCCA GTAAAGCTAA

20

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TGGTTTTTCA ACTTCTTCCA

20

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TCATAGAATG GATGGCTCAA

20

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGCTACTATT GCACCATCCC

20

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs

- 99 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CAATAAGGGC ATACCAAAAA TC

22

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CCTTAACATT TGTGGCATT TC

22

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTGGGAAGAT GAAGTTTTTA GA

22

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CCTTTACTCC AATAATTGG CT

22

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

- 100 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TTTCATCTAT TCAGGATGGG

20

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GGAGCAACAT TCTTTGTGAC

20

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TGTGCCTGAA GAAGGTATTG

20

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CGTGTTACTT CACCACCACT

20

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs

- 101 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TATCTTATCG TTGAGAAGGG ATT

23

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTACACTTGG CTTAGGATGA AA

22

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CTATCTGATT GTTGAAGAAG GATT

24

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GTTTACTCTT GGTTTAGGAT GAAA

24

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs

- 102 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

CTTGTTGATC ACGATAATTT CC

22

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ATCTTTTAGC AAACCCGTAT TC

22

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

AACAGGTGAA TTATTAGCAC TTGTAAG

27

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATTGCTGTTA ATATTTTTTG AGTTGAA

27

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs

- 103 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTGATCGAAA TCCAGATCC

19

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ATCCTCGGTT TTCTGGAAG

19

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CTGGTCATAC ATGTGATGG

19

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GATGTTACCC GAGAGCTTG

19

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

- 104 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TTAAGCGTGC ATAATAAGCC

20

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTGCGATTAC TTCGCCAACT

20

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TTTACTAAGC TTGCCCCTTC

20

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

AAAAGGCAGC AATTATGAGC

20

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs

- 105 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

AAYATGATNA CNGGNGCNGC NCARATGGA

29

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "n = inosine"

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 12
 - (D) OTHER INFORMATION: /note= "n = inosine"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CCNACNGTNC KNCCRCCYTC RCG

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(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 6
 - (D) OTHER INFORMATION: /note= "n = inosine"

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 12
 - (D) OTHER INFORMATION: /note= "n = inosine"

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 15
 - (D) OTHER INFORMATION: /note= "n = inosine"

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 18
 - (D) OTHER INFORMATION: /note= "n = inosine"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CARYTNATHG TNGCNGTNAA YAARATGGA

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(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 831 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

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ATGAAAAACA CAATACATAT CAACTTCGCT ATTTTTTTTAA TAATTGCAAA TATTATCTAC	60
AGCAGCGCCA GTGCATCAAC AGATATCTCT ACTGTTGCAT CTCCATTATT TGAAGGAACT	120
GAAGGTTGTT TTTTACTTTA CGATGCATCC ACAAACGCTG AAATTGCTCA ATTCAATAAA	180
GCAAAGTGTG CAACGCAAAT GGCACCAGAT TCAACTTTCA AGATCGCATT ATCACTTATG	240
GCATTTGATG CGGAAATAAT AGATCAGAAA ACCATATTCA AATGGGATAA AACCCCCAAA	300
GGAATGGAGA TCTGGAACAG CAATCATACA CCAAAGACGT GGATGCAATT TTCTGTTGTT	360
TGGGTTTCGC AAGAAATAAC CCAAAAAATT AGATTAAATA AAATCAAGAA TTATCTCAAA	420
GATTTTGATT ATGGAAATCA AGACTTCTCT GGAGATAAAG AAAGAAACAA CGGATTAACA	480
GAAGCATGGC TCGAAAGTAG CTTAAAAATT TCACCAGAAG AACAAATTCA ATTCCTGCGT	540
AAAATTATTA ATCACAATCT CCCAGTTAAA AACTCAGCCA TAGAAAACAC CATAGAGAAC	600
ATGTATCTAC AAGATCTGGA TAATAGTACA AAAGTGTATG GGAAAACTGG TGCAGGATTC	660
ACAGCAAATA GAACCTTACA AAACGGATGG TTTGAAGGGT TTATTATAAG CAAATCAGGA	720
CATAAATATG TTTTGTGTC CGCACTTACA GGAAACTTGG GGTCGAATTT AACATCAAGC	780
ATAAAAGCCA AGAAAAATGC GATCACCATT CTAAACACAC TAAATTTATA A	831

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TTGAAAAAGT TAATATTTTT AATTGTAATT GCTTTAGTTT TAAGTGCATG TAATTCAAAC	60
AGTTCACATG CCAAAGAGTT AAATGATTTA GAAAAAAAT ATAATGCTCA TATTGGTGTG	120
TATGCTTTAG ATACTAAAAG TGGTAAGGAA GTAAAATTTA ATTCAGATAA GAGATTTGCC	180
TATGCTTCAA CTTCAAAGC GATAAATAGT GCTATTTTGT TAGAACAAGT ACCTTATAAT	240
AAGTTAAATA AAAAAGTACA TATTAACAAA GATGATATAG TTGCTTATTC TCCTATTTTA	300
GAAAAATATG TAGGAAAAGA TATCACTTTA AAAGCACTTA TTGAGGCTTC AATGACATAT	360
AGTGATAATA CAGCAAACAA TAAATTTATA AAAGAAATCG GTGGAATCAA AAAAGTTAAA	420
CAACGTCTAA AAGAACTAGG AGATAAAGTA ACAAATCCAG TTAGATATGA GATAGAATTA	480

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AATTACTATT CACCAAAGAG CAAAAAAGAT ACTTCAACAC CTGCTGCTTT CGGTAAGACT	540
TTAAATAAAC TTATCGCAAA TGGAAAATTA AGCAAAGAAA ACAAAAAATT CTTACTTGAT	600
TTAATGTTAA ATAATAAAAG CGGAGATACT TTAATTAAAG ACGGTGTTCC AAAAGACTAT	660
AAGGTTGCTG ATAAAAGTGG TCAAGCAATA ACATATGCTT CTAGAAATGA TGTTGCTTTT	720
GTTTATCCTA AGGGCCAATC TGAACCTATT GTTTTAGTCA TTTTACGAA TAAAGACAAT	780
AAAAGTGATA AGCCAAATGA TAAGTTGATA AGTGAAACCG CCAAGAGTGT AATGAAGGAA	840
TTTTAA	846

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

ATGTCCGCGA GCACCCCCC CATAACTCTT CGCCTCATGA CCGAGCGCGA CCTGCCGATG	60
CTCCATGACT GGCTCAACCG GCCGCACATC GTTGAGTGGT GGGGTGGCGA CGAAGAGCGA	120
CCGACTCTTG ATGAAGTGCT GGAACACTAC CTGCCAGAG CGATGGCGGA AGAGTCCGTA	180
ACACCGTACA TCGCAATGCT GGGCGAGGAA CCGATCGGCT ATGCTCAGTC GTACGTCGCG	240
CTCGGAAGCG GTGATGGCTG GTGGGAAGAT GAAACTGATC CAGGAGTGCG AGGAATAGAC	300
CAGTCTCTGG CTGACCCGAC ACAGTTGAAC AAAGGCCTAG GAACAAGGCT TGTCCGCGCT	360
CTCGTTGAAC TACTGTTCTC GGACCCACC GTGACGAAGA TTCAGACCGA CCCGACTCCG	420
AACAACCATC GAGCCATACG CTGCTATGAG AAGGCAGGAT TCGTGCGGGA GAAGATCATC	480
ACCACGCCTG ACGGGCCGGC GGTTTACATG GTTCAAACAC GACAAGCCTT CGAGAGAAAG	540
CGCGGTGTTG CCTAA	555

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

ATGAACCAGA AAAACCCTAA AGACACGCAA AATTTTATTA CTTCTAAAAA GCATGTAAAA	60
GAAATATTGA ATCACACGAA TATCAGTAAA CAAGACAACG TAATAGAAAT CGGATCAGGA	120
AAAGGACATT TTACCAAAGA GCTAGTCAAA ATGAGTCGAT CAGTTACTGC TATAGAAATT	180
GATGGAGGCT TATGTCAAGT GACTAAAGAA GCGGTAAACC CCTCTGAGAA TATAAAAGTG	240
ATTCAAACGG ATATTCTAAA ATTTTCCTTC CCAAACATA TAAACTATAA GATATATGGT	300
AATATTCCTT ATAACATCAG TACGGATATT GTCAAAAGAA TTACCTTTGA AAGTCAGGCT	360
AAATATAGCT ATCTTATCGT TGAGAAGGGA TTTGCGAAAA GATTGCAAAA TCTGCAACGA	420
GCTTTGGGTT TACTATTAAT GGTGGAGATG GATATAAAAA TGCTCAAAAA AGTACCACCA	480
CTATATTTTC ATCCTAAGCC AAGTGTAGAC TCTGTATTGA TTGTTCTTGA ACGACATCAA	540
CCATTGATTT CAAAGAAGGA CTACAAAAAG TATCGATCTT TTGTTTATAA GTGGGTAAAC	600
CGTGAATATC GTGTTCTTTT CACTAAAAAC CAATTCCGAC AGGCTTTGAA GCATGCAAAT	660
GTCACATAA TTAATAAACT ATCGAAGGAA CAATTTCTTT CTATTTTCAA TAGTTACAAA	720
TTGTTTCACT AA	732

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 738 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

ATGAACAAAA ATATAAAATA TTCTCAAAAC TTTTAAACGA GTGAAAAAGT ACTCAACCAA	60
ATAATAAAAC AATTGAATTT AAAAGAAACC GATACCGTTT ACGAAATTGG AACAGGTAAA	120
GGGCATTTAA CGACGAAACT GGCTAAAATA AGTAAACAGG TAACGTCTAT TGAATTAGAC	180
AGTCATCTAT TCAACTTATC GTCAGAAAAA TTAAAATCGA ATACTCGTGT CACTTTAATT	240
CACCAAGATA TTCTACAGTT TCAATTCCTT AACAAACAGA GGTATAAAAT TGTTGGGAAT	300
ATTCCTTACC ATTTAAGCAC ACAAATTATT AAAAAAGTGG TTTTGGAAAG CCATGCGTCT	360
GACATCTATC TGATTGTTGA AGAAGGATTC TACAAGCGTA CCTTGGATAT TCACCGAACA	420
CTAGGGTTGC TCTTGACAC TCAAGTCTCG ATTCAGCAAT TGCTTAAGCT GCCAGCGGAA	480

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TGCTTTCATC CTAAACCAAG AGTAAACAGT GTCTTAATAA AACTTACCCG CCATACCACA	540
GATGTTCCAG ATAAATATTG GAAGCTATAT ACGTACTTTG TTTCAAAATG GGTCAATCGA	600
GAATATCGTC AACTGTTTAC TAAAAATCAG TTTCATCAAG CAATGAAACA CGCCAAAGTA	660
AACAATTTAA GTACCGTTAC TTATGAGCAA GTATTGTCTA TTTTTAATAG TTATCTATTA	720
TTTAACGGGA GGAAATAA	738

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

ATGAACGAGA AAAATATAAA ACACAGTCAA AACTTTATTA CTTCAAAACA TAATATAGAT	60
AAAATAATGA CAAATATAAG ATTAAATGAA CATGATAATA TCTTTGAAAT CGGCTCAGGA	120
AAAGGGCATT TTACCCTTGA ATTAGTACAG AGGTGTAATT TCGTAACTGC CATTGAAATA	180
GACCATAAAT TATGCAAAAC TACAGAAAAT AAAGTTGTTG ATCACGATAA TTTCCAAGTT	240
TTAAACAAGG ATATATTGCA GTTTAAATTT CCTAAAAACC AATCCTATAA AATATTTGGT	300
AATATACCTT ATAACATAAG TACGGATATA ATACGCAAAA TTGTTTTTTGA TAGTATAGCT	360
GATGAGATTT ATTTAATCGT GGAATACGGG TTTGCTAAAA GATTATTAAA TACAAAACGC	420
TCATTGGCAT TATTTTTAAT GGCAGAAGTT GATATTTCTA TATTAAGTAT GGTTCGAAGA	480
GAATATTTTC ATCCTAAACC TAGAGTGAAT AGCTCACTTA TCAGATTAAA TAGAAAAAAA	540
TCAAGAATAT CACACAAAGA TAAACAGAAG TATAATTATT TCGTTATGAA ATGGGTTAAC	600
AAAGAATACA AGAAAATATT TACAAAAAAT CAATTTAACA ATTCCTTAAA ACATGCAGGA	660
ATTGACGATT TAAACAATAT TAGCTTTGAA CAATTCTTAT CTCTTTTCAA TAGCTATAAA	720
TTATTTAATA AGTAA	735

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ATGAATAAAA TAAAAGTCGC AATTATCTTC GGCGGTTGCT CGGAGGAACA TGATGTGTCG	60
GTAAAATCCG CAATAGAAAT TGCTGCGAAC ATTAATACTG AAAAATTCGA TCCGCACTAC	120
ATCGGAATTA CAAAAACGG CGTATGGAAG CTATGCAAGA AGCCATGTAC GGAATGGGAA	180
GCCGATAGTC TCCCCGCCAT ATTCTCCCCG GATAGGAAAA CGCATGGTCT GCTTGTCATG	240
AAAGAAAGAG AATACGAAAC TCGGCGTATT GACGTGGCTT TCCCGGTTTT GCATGGCAAA	300
TGCGGGGAGG ATGGTGCGAT ACAGGGTCTG TTTGAATTGT CTGGTATCCC CTATGTAGGC	360
TGCGATATTC AAAGCTCCGC AGCTTGCATG GACAAATCAC TGGCCTACAT TCTTACAAAA	420
AATGCGGGCA TCGCCGTCCC CGAATTTCAA ATGATTGAAA AAGGTGACAA ACCGGAGGCG	480
AGGACGCTTA CCTACCCTGT CTTTGTGAAG CCGGCACGGT CAGGTTTCGTC CTTTGGCGTA	540
ACCAAAGTAA ACAGTACGGA AGAACTAAAC GCTGCGATAG AAGCAGCAGG ACAATATGAT	600
GGAAAAATCT TAATTGAGCA AGCGATTTCG GGCTGTGAGG TCGGCTGCGC GGTCATGGGA	660
AACGAGGATG ATTTGATTGT CGGCGAAGTG GATCAAATCC GGTGAGCCA CGGTATCTTC	720
CGCATCCATC AGGAAAACGA GCCGGAAAAA GGCTCAGAGA ATGCGATGAT TATCGTTCCA	780
GCAGACATTC CGGTCGAGGA ACGAAATCGG GTGCAAGAAA CGGCAAAGAA AGTATATCGG	840
GTGCTTGGAT GCAGAGGGCT TGCTCGTGTT GATCTTTTTT TGCAGGAGGA TGGCGGCATC	900
GTTCTAAACG AGGTCAATAC CCTGCCCCGGT TTTACATCGT ACAGCCGCTA TCCACGCATG	960
GCGGCTGCCG CAGGAATCAC GCTTCCCGCA CTAATTGACA GCCTGATTAC ATTGGCGATA	1020
GAGAGGTGA	1029

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ATGAAAAAAA TTGCCGTTTT ATTTGGAGGG AATTCTCCAG AATACTCAGT GTCACTAACC	60
TCAGCAGCAA GTGTGATCCA AGCTATTGAC CCGCTGAAAT ATGAAGTAAT GACCATTGGC	120

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ATCGCACCAA CAATGGATTG GTATTGGTAT CAAGGAAACC TCGCGAATGT TCGCAATGAT	180
ACTTGGCTAG AAGATCACAA AAAGTGTAC CAGCTGACTT TTTCTAGCCA AGGATTTATA	240
TTAGGAGAAA AACGAATCGT CCCTGATGTC CTCTTTCCAG TCTTGCATGG GAAGTATGGC	300
GAGGATGGCT GTATCCAAGG ACTGCTTGAA CTAATGAACC TGCCTTATGT TGGTTGCCAT	360
GTCGCTGCCT CCGCATTATG TATGAACAAA TGGCTCTTGC ATCAACTTGC TGATACCATG	420
GGAATCGCTA GTGCTCCAC TTTGCTTTTA TCCCGCTATG AAAACGATCC TGCCACAATC	480
GATCGTTTTA TTCAAGACCA TGGATTCCCG ATCTTTATCA AGCCGAATGA AGCCGGTTCT	540
TCAAAGGGA TCACAAAAGT AACTGACAAA ACAGCGCTCC AATCTGCATT AACGACTGCT	600
TTTGCTTACG GTTCTACTGT GTTGATCCAA AAGGCGATAG CGGGTATTGA AATTGGCTGC	660
GGCATCTTAG GAAATGAGCA ATTGACGATT GGTGCTTGTG ATGCGATTTC TCTTGTCGAC	720
GGTTTTTTTG ATTTTGAAGA GAAATACCAA TTAATCAGCG CCACGATCAC TGTCCCAGCA	780
CCATTGCCTC TCGCGCTTGA ATCACAGATC AAGGAGCAGG CACAGCTGCT TTATCGAAAC	840
TTGGGATTGA CGGGTCTGGC TCGAATCGAT TTTTTCGTCA CCAATCAAGG AGCGATTTAT	900
TTAAACGAAA TCAACACCAT GCCGGGATTT ACTGGGCACT CCCGCTACCC AGCTATGATG	960
GCGGAAGTCG GGTATCCTA CGAAATATTA GTAGAGCAAT TGATTGCACT GGCAGAGGAG	1020
GACAAACGAT G	1031

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TGGTGCTATC TTAGTAGTAT CTGCAGCTGA TGGTCCAATG CCTCAAACAC GTGAACACAT	60
CTTATTATCA CGTCAAGTAG GTGTTCTTA CATCGTTGTA TTCTTAAACA AAGTTGACAT	120
GGTTGACGAT GAAGAATTAT TAGAATTAGT AGAAATGGAA GTTCGTGACT TATTATCAGA	180
ATACGATTTC CCAGGCGATG ACACTCCAGT TGTTGCAGGT TCTGCTTTAC GCGCTTTAGA	240
AGGCGACGCT TCATACRAAG AAAAAATCTT AGAATTAATG GCTGCTGTTG ACGAATACAT	300

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TCCA	ACTCCA	GAACGYGACG	TTGACAAACC	ATTCATGATG	CCAGTTGAAG	ACGTGTTCTC	360
AATC	CACAGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	CGTGGACAAG	TTCGTGTTGG	420
TGAC	GAAAGTT	GAAATCGTTG	GTATTTTCTA	AGAAACTTCA	AAAACAACTG	TAACTGGTGT	480
TGAA	ATGTTT	CGTAAATTGT	TAGACTACGC	TGAAGCAGGG	GATAACATTG	GTACATTATT	540
ACGT	GGTGT	ACACGTGACA	ACATCGAACG	TGGACAAGTT	CTTGCTAAAC	CAGGAACAAT	600
CACT	CCACAT	ACTAAATTCA	AAGCTGAAGT	TTACGTATTA	ACTAAAGAAG	AAGGTGGACG	660
TCAT	ACTCCA	TTCTTCTCTA	ACTACCGTCC	TCAATTCTAC	TTCCGTACAA	CAGACATCAC	720
TGGT	GTTTGT	GTGTTACCAG	AAGGCGTTGA	AATGGTAATG	CCTGGTGATA	ACGTAACAT	780
GGA	AGTTGAA	TTAATTCACC	CAGTAGCGA				809

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Abiotrophia defectiva

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CGGCGCGATC	CTCGTTGTAT	CTGCTGCTGA	CGGCCCAATG	CCACAAACTC	GTGAACACAT	60
CCTCTTGTCT	CGTCAAGTTG	GTGTTCTTA	CATCGTAGTA	TTCTTGAACA	AAGTTGACAT	120
GGTTGACGAC	GAAGAATTGC	TCGAATTAGT	TGAAATGGAA	GTTTCGTGACC	TCTTGTCTGA	180
ATACGACTTC	CCAGGCGACG	ACACTCCAGT	TATCGCTGGT	TCAGCTTTGA	AAGCTTTAGA	240
AGGCGACGCT	AACTACGAAG	CTAAAGTTTT	AGAATTGATG	GAACAAGTTG	ATGCTTACAT	300
TCCAGAACCA	GAACGTGACA	CTGACAAGCC	ATTCATGATG	CCAGTCGAAG	ACGTATTCTC	360
TATCACTGGT	CGTGGTACTG	TTGCAACTGG	TCGTGTTGAA	CGTGGTCAAG	TTCGCGTTGG	420
TGACGAAGTT	GAAATCGTTG	GTATCGAAGA	AGAAACTTCT	AAGACTACCG	TTACCGGTGT	480
TGAAATGTTT	CGTAAGTTAT	TGGATTACGC	TGAAGCTGGG	GACAACGTTG	GTACCTTGTT	540
ACGTGGTGTA	ACTCGTGACC	AAATCCAACG	TGGTCAAGTA	TTATCTAAAC	CAGGTTCAAT	600
CACTCCGYAC	ACTAAGTTCG	AAGCTGAAGT	GTACGTATTG	TCTAAAGAAG	AAGGTGGTCG	660
TCACACTCCA	TTCTTCTCTA	ACTACCGTCC	ACAATTCTAC	TTCCGTACAA	CTGACGTAAC	720

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TGGTGTGTT ACTTTACCAG AAGGTACTGA AATGGTTATG CCAGGCGACA ACGTACAAAT 780
GGTTGTTGAA TTGATCCACC CAATCGCGAT CGAAGAA 817

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Candida albicans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

CTCTGTCAAA TGGGACAAAA ACAGATTGTA AGAAATCATC AAGGAAACCT CCAACTTCGT 60
CAAGAAGGTT GGTTACAACC CAAAGACTGT TCCATTCGTT CCAATCTCTG GTTGAATGG 120
TGACAACWTG ATTGAASCAT CCACCAACTG TCCATGGTAC AAGGGTTGGG AAAAGGAAAC 180
CAAATCCGGT AAAGTTACTG GTAAGACCTT GTTAGAAGCT ATTGACGCTA TTGAACCACC 240
AACCAGACCA ACCGACAAAC CATTGAGATT GCCATTRCAA GATGTTTACA AGATCGGTGG 300
TATTGGTACT GTGCCAGTCG GTAGAGTTGA AACTGGTATC ATCAAAGCCG GTATGGTWGT 360
TACTTTCGCC CCAGCTGGTG TTACCACTGA AGTCAARTCC GTTGAAATGC ATCACGAACA 420
ATTGGCTGAA GGTGTTCCAG GTGACAATGT TRGTTTCAAC GTTAAGAACR TTTCCGTAA 480
AGAAATTAGA AGAGGTAACG TTTGTGGTGA CTCCAAGAAC GATCCACCAA AGGGTTGTGA 540
CTCTTTCAAT GCCCAAGTCA TTGTTTTGAA CCATCCAGGT CAAATCTCTG CTGGTTACTC 600
TCCAGTCTTG GATTGTCACR CTGCCCACAT TGCTTGTAAG TCGACRCTT TGGTTGAAAA 660
GATTGACAGA AGAACTGGTA AGRAATTGGA AGAAAATCCA AAATTCGTCA AATCCGGTGA 720
TGCTGCTATC GTCAAGATGG TCCCAACCAA ACCA 754

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Candida glabrata*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TCTGTCAAGT GGGATGAATC CAGATTCGCT GAAATCGTTA AGGAAACCTC CAACTTCATC	60
AAGAAGGTCG GTTACAACCC AAAGACTGTT CCATTCGTCC CAATCTCTGG TTGGAACGGT	120
GACAACATGA TTGAAGCCAC CACCAACGCT TCCTGGTACA AGGGTTGGGA AAAGGAAACC	180
AAGGCTGGTG TCGTCAAGGG TAAGACCTTG TTGGAAGCCA TTGACGCTAT CGAACCACCA	240
ACCAGACCAA CTGACAAGCC ATTGAGATTG CCATTGCAAG ATGTCTACAA GATCGGTGGT	300
ATCGGTACGG TGCCAGTCGG TAGAGTCGAA ACCGGTGTCA TCAAGCCAGG TATGGTTGTT	360
ACCTTCGCCC CAGCTGGTGT TACCACTGAA GTCAAGTCCG TTGAAATGCA CCACGAACAA	420
TTGACTGAAG GTTTGCCAGG TGACAACGTT GGTTTCAACG TTAAGAACGT TTCCGTTAAG	480
GAAATCAGAA GAGGTAATGT CTGTGGTGAC TCCAAGAACG ACCCACCAA GGCTGCTGCT	540
TCTTTCAACG CTACCGTCAT TGTCTTGAAC CACCCAGGTC AAATCTCTGC TGGTTACTCT	600
CCAGTTTTGG ACTGTCACAC CGCCACATT GCTTGTAAGT TCGAAGAATT GTTGGAAAAG	660
AACGACAGAA GATCCGGTAA GAAGTTGGAA GACTCTCCAA AGTTCTTGAA GTCCGGTGAC	720
GCTGCTTTGG TTAAGTTCGT TCCATCCAAG CCA	753

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida krusei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CCGTTAAGTG GGATGAAAAC AGATTTGAAG AAATTGTCAA GGAAACCCAA AACTTCATCA	60
AGAAGGTTGG TTACAACCCA AAGACTGTTC CATTCGTTCC AATCTCTGGT TGGAATGGTG	120
ACAACATGAT TGAAGCATCC ACCAACTGTC CATGGTACAA GGGTTGGACT AAGGAAACCA	180
AGGCAGGTGT TGTTAAGGGT AAGACCTTAT TAGAAGCAAT CGATGCTATT GAACCACCTG	240
TCAGACCAAC CGAAAAGCCA TTAAGATTAC CATTACAAGA TGTTTACAAG ATTGGTGGTA	300
TTGGTACTGT GCCAGTCGGT AGAGTCGAAA CCGGTGTCAT TAAGCCAGGT ATGGTTGTCA	360

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CTTTTGCTCC AGCAGGTGTC ACCACCGAAG TCAAATCCGT TGAAATGCAC CATGAACAAT	420
TAGAACAAGG TGTTCCAGGT GATAACGTTG GTTTCAACGT TAAGAACGTY TCTGTCAAGG	480
ATATCAAGAG AGGTAACGTT TGTGGTGACT CCAAGAACGA CCCACCAATG GGTGCAGCTT	540
CTTTCAATGC TCAAGTCATT GTCTTGAACC ACCCTGGTCA AATTTCCGCT GGTTACTCTC	600
CAGTCTTGGA TTGTCACACT GCCCACATTG CATGTAAGTT CGACGAATTA ATCGAAAAGA	660
TTGACAGAAG AACTGGTAAG TCTGTTGAAG ACCATCCAAA GTCYGTCAAG TCTGGTGATG	720
CAGCTATCGT CAAGATGGTC CCAACCAAGC CA	752

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Candida parapsilosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CTCAGTCAAA TGGGACAAGA RCAGATACGA AGAAATTGTC AAGGAAACTT CCAACTTCGT	60
CAAGAAGGTT GGTTACAACC CTAAAGCTGT CCCATTCGTC CCAATCTCTG GTTGGAACGG	120
TGACAATATG ATTGAACCAT CAACCAACTG TCCATGGTAC AAGGGTTGGG AAAAGGAAAC	180
TAAAGCTGGT AAGGTTACCG GTAAGACCTT GTTGGAAGCT ATCGATGCTA TCGARCCACC	240
AACCAGACCA ACTGACAAGC CATTGAGATT GCCATTGCAA GATGTCTACA AGATTGGTGG	300
TATTGGAAC TGTGCCAGTTG GTAGAGTTGA AACCGGTATC ATCAAGGCTG GTATGGTTGT	360
TACTTTTGCC CCAGCTGGTG TTACCACTGA AGTCAAGTCC GTTGAAATGC ACCACGAACA	420
ATTGACTGAA GGTGTCCCAG GTGACAATGT TGGTTTCAAC GTCAAGAACG TTTCAGTTAA	480
GGAAATCAGA AGAGGTAACG TYTGTGGTGA CTCCAAGAAC GATCCACCAA AGGGATGTGA	540
YTCCTTCAAT GCTCAAGTTA TTGTCTTGAA CCACCCAGGT CAAATCTCTG CTGGTTACTC	600
ACCAGTCTTG GATTGTCACA CTGCCACAT TGCTTGTAAT TTCGACACTT TGATTGAAAA	660
GATTGACAGA AGAACCGGTA AGAAATTGGA AGWTGAACCA AAATTCATCA AGTCCGGTGA	720
TGCTGCTATC GTCAAGATGG TCCCAACCAA GCCA	754

(2) INFORMATION FOR SEQ ID NO:124:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

TCTGTTAAAT GGGACAARAA CAGATTTGAA GAAATTATCA AGGAAACYTC TAACTTCGTC	60
AAGAAGGTTG GTTACAACCC TAAGGCTGTT CCATTCGTTC CAATCTCWGG TTGGAATGGT	120
GACAACATGA TTGAAGCTTC TACCAACTGT CCATGGTACA AGGGTTGGGA AAAAGAAACC	180
AAGGCTGGTA AGGTTACCGG TAAGACTTTG TTGGAAGCCA TTGATGCTAT TGAACCACCT	240
TCAAGACCAA CTGACAAGCC ATTGAGATTG CCATTGCAAG ATGTTTACAA GATTGGTGGT	300
ATTGGTACTG TGCCAGTCGG TAGAGTTGAA ACTGGTGTCA TCAAAGCCGG TATGGTTGTT	360
ACTTTYGCCC CAGCTGGTGT TACCACTGAA GTCAAATCCG TYGAAATGCA CCACGAACAA	420
TTGGCTGAAG GTGTCCCAGG TGACAATGTT GGTTTCAACG TTAAGAACGT TTCTGTTAAA	480
GAAATTAGAA GAGGTAACGT TTGTGGTGAC TCCAAGAACG ATCCACCAAA GGGTTGTGAC	540
TCTTTCAACG CTCAAGTTAT TGTCTTGAAC CACCCAGGTC AAATYTCTGC TGGTTACTCT	600
CCAGTCTTGG ATTGTCACAC TGCTCATATT GCTTGTAAT TCGACACCTT GGTTGAAAAG	660
ATTGACAGAA GAACTGGTAA GAAATTGGAA GAAAATCCAA AATTCGTCAA ATCCGGTGAT	720
GCTGCTATTG TCAAGATGGT TCCAACCAAA CCA	753

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium accolens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CGGCGCTATC CTGGTTGTTG CTGCAACCGA TGGCCCGATG CCGCAGACCC GCGAGCACGT	60
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TCTGCTTGCT CGCCAGGTTG GCGTTCCTTA CATCCTCGTT GCACTGAACA AGTGCGACAT	120
GGTTGATGAT GAGGAAATCA TCGAGCTCGT GGAGATGGAG ATCTCCGAGC TGCTCGCAGA	180
GCAGGACTAC GATGAGGAAG CTCCTATCGT TCACATCTCC GCTCTGAAGG CACTCGAGGG	240
TGACGAGAAG TGGGTACAGT CCATCGTTGA CCTGATGGAT GCCTGCGACA ACTCCATCCC	300
TGATCCGGAG CGCGCTACCG ATCAGCCGTT CTTGATGCCT ATCGAGGACA TCTTCACCAT	360
TACCGGCCGC GGTACCGTTG TTACCGGCCG TGTTGAGCGT GGTCGTCTGA ACGTCAACGA	420
GGACGTTGAG ATCATCGGTA TCCAGGAGAA GTCCCAGAAC ACCACCGTTA CCGGTATCGA	480
GATGTTCCGC AAGATGATGG ACTACACCGA GGCTGGCGAC AACTGTGGTC TGCTTCTGCG	540
TGGTACCAAG CGTGAGGACG TTGAGCGTGG CCAGGTTGTT ATCAAGCCGG GCGCTTACAC	600
CCCTCACACC AAGTTCGAGG GTTCCGTCTA CGTCCTGAAG AAGGAAGAGG GCGGCCGCCA	660
CACCCGYTC ATGAACAACT ACCGTCCTCA GTTCTACTTC CGCACCACCG ACGTTACCGG	720
TGTTGTGAAC CTGCCTGAGG GCACCGAGAT GGTATGCCT GCGACAACG TTGAGATGTC	780
TGTTGAGCTC ATCCAGCCTG TTGCTATGGA CGAG	814

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CGGCGCAATC CTCGTTGTTG CTGCCACCGA CGGCCCAATG CCTCAGACCC GTGAGCACGT	60
TCTGCTCGCT CGCCAGGTCG GCGTTCCTTA CATCCTCGTT GCTCTGAACA AGTGCGACAT	120
GGTTGATGAT GAGGAAATCA TCGAGCTCGT CGAGATGGAG ATCCRTGAGC TGCTCGCTGA	180
GCAGGATTAC GACGAAGAGG CTCCAATCAT CCACATCTCC GCACTGAAGG CTCTTGAGGG	240
CGACGAGAAG TGGACCCAGT CCATCATCGA CCTCATGCAG GCTTGCKATG ATTCCATCCC	300
AGACCCAGAG CGTGAGACCG ACAAGCCATT CCTCATGCCT ATCGAGGACA TCTTCACCAT	360
CACCGGCCGC GGTACCGTTG TTACCGGCCG TGTTGAGCGT GGCTCCCTGA AGGTCAACGA	420
GGACGTCGAG ATCATCGGTA TCCGCGAGAA KGCTACCACC ACCACCGTTA CCGGTATCGA	480

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GATGTTCCGT AAGCTTCTCG ACTACACCGA GGCTGGCGAC AACTGTGGTC TGCTTCTCCG 540
 TGGCGTTAAG CGCGAAGACG TTGAGCGTGG CCAGGTTGTT GTTAAGCCAG GCGCTTACAC 600
 CCCTCACACC GAGTTCGAGG GCTCTGTCTA CGTTCTGTCC AAGGACGAGG GTGGCCGCCA 660
 CACCCCATTC TTCGACAACT ACCGCCACA GTTCTACTTC CGCACCACCG ACGTTACCGG 720
 TGTGTGAAG CTTCTGAGG GCACCGAGAT GGTCATGCCT GGCGACAACG TCGACATGTC 780
 CGTCACCCTG ATCCAGCCTG TCGCTATGGA TGAG 814

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium genitalium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

CGGCGCCATC CTGGTTGTTG CTGCAACCGA TGGCCCGATG CCGCAGACCC GTGAGCACGT 60
 TCTGCTGGCT CGCCAGGTTG GCGTTCCGTA CATCCTAGTT GCACTGAACA AGTGCGACAT 120
 GGTGATGAT GAGGAGCTGC TGGAGCTCGT CGAGATGGAG GTCCGCGAGC TGCTGGCTGA 180
 GCAGGACTTC GACGAGGAAG CACCTGTTGT TCACATCTCC GCACTGAAGG CCCTGGAGGG 240
 CGACGAGAAG TGGGCTAAGC AGATCCTGGA GCTCATGGAG GCTTGCGACA ACTCCATCCC 300
 GGATCCGGAG CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGRGGACA TCTTCACCAT 360
 TACCGGCCGC GGTACCGTTG TTACCGGCCG TGTTGAGCGT GGCGTCCTGA ACCTGAACGA 420
 CGAGGTCGAG ATCCTGGGCA TCCGCGAGAA GTCCACCAAG ACCACCGTTA CCTCCATCGA 480
 GATGTTCAAC AAGCTGCTGG ACACCGCAGA GGCTGGCGAC AACGCCGCAC TGCTGCTGCG 540
 TGGCCTGAAG CGCGAAGATG TTGAGCGTGG TCAGATCGTT GCTAAGCCGG GCGAGTACAC 600
 CCCGCACACC GAGTTCGAGG GCTCCGTCTA CGTTCTGTCC AAGGACGAGG GTGGCCGCCA 660
 CACCCCGTTC TTCGACAACT ACCGTCCGCA GTTCTATTTC CGCACCACCG ACGTTACCGG 720
 TGTGTGAAG CTGCCGGAGG GCACCGAGAT GGTTATGCCG GGCGACAACG TTGACATGTC 780
 CGTCACCCTG ATCCAGCCGG TTGCTATGGA CGAG 814

(2) INFORMATION FOR SEQ ID NO:128:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium jeikeium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CGGCGCCATC CTGGTTGTTG CCGCAACCGA TGGCCCGATG CCGCAGACCC GCGAGCACGT	60
TCTGCTGGCY CGCCAGGTTG GCGTTCCGTA CATCCTGGTT GCACTGAACA AGTGTGACAT	120
GGTTGACGAT GAGGAGCTGC TGGAGCTCGT CGAGATGGAG GTCCGCGAGC TGCTGGCTGA	180
GCAGGACTTC GACGAGGAAG CTCCGGTTGT TCACATCTCC GCACTGAAGG CCCTGGAGGG	240
CGACGAGAAG TGGGCTAACC AGATTCTCGA GCTGATGCAG GCTTGCGACG AGTCTATCCC	300
GGATCCGGAG CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGWGGACA TCTTCACCAT	360
TACCGGTCGC GGTACCGTTG TTACCGGCCG TGTTGAGCGT GGCATCCTGA ACCTGAACGA	420
CGAGGTTGAG ATCCTGGGTA TCCGCGAGAA GTCCCAGAAG ACCACCGTTA CCTCCATCGA	480
GATGTTCAAC AAGCTGCTGG ACACCGCAGA GGCTGGCRAC AACGCTGCAC TGCTGCTGCG	540
TGGTCTGAAG CGCGAGGACG TTGAGCGTGG CCAGATCATC GCTAAGCCGG GCGAGTACAC	600
CCCGCACACC GAGTTCGAGG GCTCCGTCTA CGTTCTGTCC AAGGACGAGG GCGGCCGCCA	660
CACCCCGTTC TTCGACAACT ACCGTCCGCA GTTCTACTTC CGCACCACCG ACGTTACCGG	720
TGTTGTGAAG CTGCCTGAGG GCACCGAGAT GGTTATGCCG GCGACAACG TYGACATGTC	780
CGTCACCCTG ATCCAGCCGG TTGCTATGGA CGAG	814

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudodiphtheriticum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

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CGGCGCTATC TTGGTTGTTG CAGCTACCGA CGGCCCAATG CCACAGACTC GCGAGCACGT	60
TCTGCTGGCT CGCCAGGTTG GCGTTCCTTA CATCCTGGTT GCACTAAACA AGTGCGACAT	120
GGTTGACGAC GAGGAAATCC TCGAGCTCGT CGAGATGGAG ATCCGCGAAT TGCTGGCTGA	180
CCAGGAATTC GACGAAGAAG CTCCAATCGT TCACATCTCC GCAGTCGGCG CCTTGGAAGG	240
CGAAGAGAGG TGGGTTAACG CCATCGTTGA ACTGATGGAT GCTTGTGACG AGTCGATCCC	300
TGATCCAGAC CGTGCTACCG ACAAGCCATT CCTGATGCCT ATCGAGGACA TCTTCACCAT	360
TACCGGTCGT GGCACCGTTG TTACGGGTCG TGTTGAGCGT GGTTCCCTGA AGGTCAACGA	420
AGAAGTCGAG ATCATCGGCA TCAAGGAAAA GTCCCAGAAG ACCACCATCA CCGGTATCGA	480
AATGTTCCGC AAGATGCTGG ACTACACCGA GGCCGGCGAC AACGCTGGTC TGCTGCTTCG	540
CGGTACCAAG CGTGAAGACG TTGAGCGTGG ACAGGTTATC GTTGCTCCAG GTGCTTACAG	600
CACCCACAAG AAGTTCGAAG GTTCCGTCTA CGTTCTTTCC AAGGACGAGG GCGGCCGCCA	660
CACCCCGTTC TTCGACAACT ACCGTCCTCA GTTCTACTTC CGCACCACCG ACGTTACCGG	720
TGTTGTTACC CTGCCTGAGG GCACCGAG	748

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium striatum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GGCGCTATCT TGGTTGTTGC TGCAACCGAT GGCCCGRTGC CGCAGACCCG CGAGCACGTT	60
CTTCTGGCTC GCCAGGTTGG CGTTCCTTAC ATCCTCGTTG CACTGAACAA GTGCGACATG	120
GTTGACGACG AGGAAATTAT CGAGCTCGTC GAGATGGAGA TCCGCGAACT GCTCGCAGAG	180
CAGGACTACG ATGAGGAAGC TCCGATCGTT CACATCTCTG CTCTGAAGGC TCTTGAGGGC	240
GRCGAGAAGT GGGTACAGGC TATCGTTGAC CTGATGCAGG CTTGCGATGA CTCCATCCCG	300
GATCCGGAGC GCGAGCTGGA CAAGCCGTTC CTGATGCCAA TCGAGGACAT CTTCAACCATC	360
ACCGGCCGCG GTACCGTTGT TACTGGCCGT GTTGAGCGTG GCTCCCTGAA CGTCAACGAG	420
GACGTTGAGA TCATCGGTAT CCAGGACARG TCCATCTCCA CCACCGTTAC CCGTATCGAG	480

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ATGYTCCGCA AGATGATGGA CTACACCGAG GCTGGCGACA ACTGTGGTCT GCTTCTGCGT 540
 GGTACCAAGC GTGAAGAGGT TGAGCGCGGC CAGGTTGTTA TTAAGCCGGG CGCTTACACC 600
 CCTCACACCC AGTTCGAGGG TTCCGTCTAC GTCCTGAAGA AGGAAGAGGG CGGCCGCCAC 660
 ACCCCGTTCA TGGACAATA CCGTCCGCAG TTCTACTTCC GCACCACCGA CGTTACCGGC 720
 GTCATCAAGC TGCCTGAGGG CACCGAGATG GTTATGCCTG GCGACAACGT CGAGATGTCY 780
 GTCGAGCTGA TCCAGCCGGT CGCTATGGAC GAG 813

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCTATG CCTCAAACCTC GTGAACACAT 60
 CTTGTTATCT CGTAACGTTG GTGTTCTTA CATCGTTGTA TTCTTAAACA AAATGGATAT 120
 GGTGACGAT GAAGAATTAC TTGAATTAGT TGAAATGGAA GTTCGTGACT TATTAACCTGA 180
 ATACGACTTC CCAGGCGACG ACACTCCAGT TATCGCAGGT TCAGCGTTGA AAGCTTTAGA 240
 AGGCGACGCT TCATACGAAG AAAAAATCTT AGAATTAATG GCTGCTGTTG ACGAATATAT 300
 CCCAACACCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG ACGTATTCTC 360
 AATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTTGAA CGTGGACAAG TTCGCGTTGG 420
 TGACGAAGTT GAAATCGTAG GTATCGCTGA CGAAACTGCT AAAACAACCTG TTACAGGTGT 480
 TGAAATGTTC CGTAAATTGT TAGACTACGC TGAAGCAGGT GACAACATCG GTGCTTTGTT 540
 ACGTGGTGTT GCACGTGAAG ATATCCAACG TGGACAAGTA TTGGCTAAAC CAGCTTCAAT 600
 CACTCCACAT ACAAATTCT CTGCAGAAGT TTATGTTCTA ACTAAAGAAG AAGGTGGACG 660
 TCATACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC TTCCGTACAA CTGACGTAAC 720
 TGGTGTAGTT GATCTACCAG AAGGTACTGA AATGGTWATG CCTGGGGATA ACGTAACTAT 780
 GGAAGTTGAA TTGATYCACC CAATYCGGT AGAAGAC 817

(2) INFORMATION FOR SEQ ID NO:132:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGTCCTATG CCTCAAACAC GTGAACATAT	60
CTTATTATCA CGTAACGTTG GTGTACCATA CATCGTTGTA TTCTTAAACA AAATGGATAT	120
GGTTGATGAC GAAGAATTAT TAGAATTAGT AGAAATGGAA GTTCGTGACT TATTATCAGA	180
ATACGATTTT CCAGGCGATG ATGTTCCAGT TATCGCAGGT TCTGCTTTGA AAGCTTTAGA	240
AGGCGACGAG TCTTATGAAG AAAAAATCTT AGAATTAATG GCTGCAGTTG ACGAATATAT	300
CCCAACTCCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG ACGTATTCTC	360
AATCACTGGA CGTGGTACTG TTGCTACAGG ACGTGTTGAA CGTGGTGAAG TTCGCGTTGG	420
TGACGAAGTT GAAATCGTTG GTATTAAAGA CGAAACATCT AAAACAACYG TTACAGGTGT	480
TGAAATGTTC CGTAAATTAT TAGACTACGC TGAAGCAGGC GACAACMTCG GTGCTTTATT	540
ACGTGGTGTA GCACGTGAAG ATATCGAACG TGGACAAGTA TTAGCTAAAC CAGCTACAAT	600
CACTCCACAC ACAAATTCA AAGCTGAAGT ATACGTATTA TCAAAGAAG AAGGCGGACG	660
TCACACTCCA TTCTTCACTA ACTACCGTCC TCAATTCTAC TTCCGTACAA CAGACGTTAC	720
TGGTGTTGTA GAATTGCCAG AAGGTACTGA AATGGTAATG CCTGGTGATA ACGTTGCTAT	780
GGACGTTGAA TTAATTCACC CAATCGCTAT CGAAGAC	817

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

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CGGAGCTATC TTGGTAGTTT CTGCTGCTGA CGGCCCAATG CCTCAAACCTC GTGAACACAT	60
CCTATTGTCT CGTCAAGTTG GTGTTCTTA CATCGTTGTA TTCTTGAACA AAGTAGACAT	120
GGTTGATGAC GAAGAATTAC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTAACAGA	180
ATACRAATTC CCTGGTGRCG ATGTTCTGT AGTTGCTGGA TCAGCTTTGA AAGCTCTAGA	240
AGGCGACGCT TCATACGAAG AAAAAATTCT TGAATTAATG GCTGCAGTTG ACGAATACAT	300
CCCAACTCCA GAACGTGACA ACGACAAACC ATTCATGATG CCAGTTGAAG ACGTGTTCTC	360
AATTACTGGA CGTGGTACTG TTGCTACAGG TCGTGTTGAA CGTGGACAAG TTCGCGTTGG	420
TGACGAAGTT GAAGTTGTTG GTATTGCTGA AGAACTTCA AAAACAACAG TTAGTGGTGT	480
TGAAATGTTT CGTAAATTGT TAGACYACGC TGAAGCTGGA GACRACATTG GTGCTTTACT	540
ACGTGGTGTG GCACGTGAAG ACATCCAACG TGGACAAGTT TTAGCTAAAC CAGGTACAAT	600
CACACCTCRT ACAAATTCT CTGCAGAAGT ATACGTGTTG ACAAAGAAG AAGGTGGACG	660
TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC TTCCGTACAA CTGACGTAAC	720
AGGTGTTGTT GAATTACCAG AAGGAACTGA AATGGTCATG CCCGGTGACA ACGT	774

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

CGGTGCGATC TTAGTAGTAT CTGCTGCTGA CGGTCCTATG CCTCAAACCTC GTGAACACAT	60
CTTGTTATCA CGTAACGTTG GCGTACCATA CATCGTTGTT TTCTTGAACA AAATGGATAT	120
GGTTGAYGAC GAAGAATTGC TAGAATTAGT TGAAATGGAA GTTCGTGACC TATTGTCTGA	180
ATATGACTTC CCAGGCGACG ATGTTCTGT AATCGCCGGT TCTGCTTTGA AAGCTCTTGA	240
AGGAGATCCT TCATACGAAG AAAAAATCAT GGAATTGATG GCTGCAGTTG ACGAATACGT	300
TCCAACCTCCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG ACGTATTCTC	360
AATCACTGGA CGTGGTACTG TTGCTACAGG CCGTGTTGAA CGTGGACAAG TTCGCGTTGG	420
TGATGAAGTA GAAATCGTTG GTATTGCTGA CGAACTGCT AAAACAACCTG TAACAGGTGT	480

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TGAAATGTTT	CGTAAATTGT	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	540
ACGTGGGGTT	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAG	CTGGTACAAT	600
CACACCTCAT	ACAAAATTCA	AAGCTGAAGT	TTATGTTTTG	ACAAAAGAAG	AAGGTGGACG	660
TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	TTCCGTACAA	CTGACGTAAC	720
TGGTGTGTGT	GAATTACCAG	AAGGAACTGA	AATGGTGATG	CCTGGCGACA	ACGTGACCAT	780
CGACGTTGAA	TTGATRCACC	CAATCGCTC				809

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gardnerella vaginalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

TGGCGCAATC	CTCGTGGTTG	CTGCTACCGA	CGGTCCAATG	GCTCAGACCC	GTGAACACGT	60
CTTGCTTGCT	AAGCAGGTCG	GCGTTCCAAA	AATTCTTGTT	GCTTTGAACA	AGTGCGATAT	120
GGTTGACGAC	GAAGAGCTTA	TCGATCTCGT	TGAAGAAGAG	GTCCGTGACC	TCCTCGAAGA	180
AAACGGCTTC	GATCGCGATT	GCCCAGTCYT	CCGTACTTCC	GCTTACGGCG	CTTTGCATGA	240
TGACGCTCCA	GACCACGACA	AGTGGGTAGA	GACCGTCAAG	GAATCATGA	AGGCTGTTGA	300
CGAGTACATC	CCAACCCCAA	CTCACGATCT	TGACAAGCCA	TTCTTGATGC	CAATCGAAGA	360
TGTGTTCAAC	ATCTCCGGTC	GTGGTYCCGT	TGTCACCGGT	CGTGTTGAGC	GTGGTAAGCT	420
CCCAATCAAC	ACCCAGTTG	AGATCGTTGG	TTTGCGCGAT	ACCCAGACCA	CCACCGTCAC	480
CTCTATCGAG	ACCTTCCACA	AGCAGATGGA	TGAGGCAGAG	GCTGGCGATA	AACTGGTCT	540
TCTTCTCCGC	GGTATCAACC	GTACCGACGT	TGAGCGTGGT	CAGGTGTGG	CTGCTCCAGG	600
TTCTGTGACT	CCACACACCA	AGTTCGAAGG	CGAAGTTTAC	GTCTTGACCA	AGGACGAAGG	660
TGGCCGTCAC	TCGCCATTCT	TCTCCAACTA	CCGTCCACAG	TTCTACTTCC	GTACCACCGA	720
TGTTACTGGC	GTTATCACCT	TGCCAGACGG	CATCGAAATG	GTTGAGCCAG	GCGATCACGC	780
AACCTTCACT	GTTGAGTTGA	TCCAGGCTAT	CGCAATGGAA	GAG		823

(2) INFORMATION FOR SEQ ID NO:136:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria innocua*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC GTGAACATAT	60
CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA TTCATGAACA AATGTGACAT	120
GGTTGACGAT GAAGAATTAC TAGAATTAGT TGAAATGGAA ATTCGTGATC TATTAAGTGA	180
ATATGAATTC CCTGGCGATG ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA	240
AGGTGAAGCT GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT	300
TCCAACCTCCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG ATGTATTCTC	360
AATCACTGGT CGTGGAACAG TTGCAACTGG ACGTGTTGAA CGTGGACAAG TTAAAGTTGG	420
TGACGAAGTA GAAGTTATCG GTATTGAAGA AGAAAGCAAA AAAGTAGTAG TAACTGGAGT	480
AGAAATGTTC CGTAAATTAC TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT	540
ACGTGGTGTT GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTAGCTAAAC CAGGTTCGAT	600
TACTCCACAC ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG AAGGTGGACG	660
TCACACTCCA TTCTTCAACA ACTACCGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC	720
TGGTATTGTT ACACTTCCAG AAGGTACTGA AATGGTAATG CCTGGTGATA ACATTGAGCT	780
TGCAGTTGAA CTAATTGCAC CAATCGCTAT CGAAGAC	817

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria ivanovii*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

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CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAAACTC GTGAACATAT	60
TCTTACTTTC ACGTCAAGTT GGTGTTCCAT ACATCGTTGT ATTCATGAAC AAATGTGACA	120
TGGTTGACGA TGAAGAATTA CTTGAATTAG TTGAAATGGA AATTCGTGAT CTATTAAGTG	180
AATATGAATT CCCTGGCGAC GACATTCCTG TAATCAAAGG TTCAGCTCTT AAAGCACTTC	240
AAGGTGAAGC TGATTGGGAA GCTAAAATTG ACGAGTTAAT GGAAGCTGTA GATTCTTACA	300
TTCCAAGTCC AGAACGTGAT ACTGACAAAC CATTGATGAT GCCAGTTGAG GATGTATTCT	360
CAATCACTGG TCGTGGAACA GTTGCAACTG GACGTGTTGA ACGTGGACAA GTTAAAGTTG	420
GTGACGAAGT AGAAGTTATC GGTATTGAAG AAGAAAGCAA AAAAGTAGTA GTAAGTGGAG	480
TAGAAATGTT CCGTAAATTA CTAGACTACG CTGAAGCTGG CGACAACATT GGCGCACTTC	540
TACGTGGTGT TGCTCGTGAA GATATCCAAC GTGGTCAAGT ATTAGCTAAA CCAGGTTCGA	600
TTACTCCACA TACTAACTTC AAAGCTGAAA CTTATGTTTT AACTAAAGAA GAAGGTGGAC	660
GTCATACTCC ATTCTTCAAC AACTACCGCC CACAATTCTA TTTCCGTACT ACTGACGTAA	720
CTGGTATTGT TACACTTCCA GAAGGTACTG AAATGGTAAT GCCTGGTGAT AACATTGAGC	780
TTGCAGTTGA ACTAATTGCA CCAATCGCTA TCGAAGAC	818

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC GTGAACATAT	60
CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA TTCATGAACA AATGTGACAT	120
GGTTGACGAT GAAGAATTAC TAGAATTAGT TGAAATGGAA ATTCGTGATC TATTAAGTGA	180
ATATGAATTC CCTGGCGATG ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA	240
AGGTGAAGCT GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT	300
TCCAAGTCCW GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG ATGTATTCTC	360
AATCACTGGT CGTGGAACAG TTGCAACTGG ACGTGTTGAA CGTGGACAAG TTAAAGTTGG	420

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TGACGAAGTA GAAGTTATCG GTATCGAAGA AGAAAGCAAA AAAGTAGTAG TAACTGGAGT	480
AGAAATGTTC CGTAAATTAC TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT	540
ACGTGGTGTT GCTCGTGAAG ATATCCAACR TGGTCAAGTA TTAGCTAAAC CAGGTTCGAT	600
TACTCCACAC ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG AAGGTGGACG	660
TCACACTCCA TTCTTCAACA ACTACCGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC	720
TGGTATTGTT ACACTTCCAG AAGGTACTGA AATGGTAAYG CCTGGTGATA ACATTGAGCT	780
TGCAGTTGAA CTAATTGCAC CAATCGCTAT CGAAGAC	817

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria seeligeri*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC GTGAACATAT	60
CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA TTCATGAACA AATGTGACAT	120
GGTTGACGAT GAAGAATTAC TTGAATTAGT TGAAATGGAA ATTCGTGATC TATTAAGTGA	180
ATATGAATTC CCTGGTGATG ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA	240
AGGTGAAGCT GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT	300
TCCAACCTCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG ATGTATTCTC	360
AATCACTGGT CGTGGAAGT TTGCAACTGG ACGTGTTGAA CGTGGACAAG TTAAAGTTGG	420
TGACGAAGTA GAAGTTATCG GTATTGAAGA AGAAAGCAAA AAAGTAATAG TAACTGGAGT	480
AGAAATGTTC CGTAAATTAC TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT	540
ACGTGGTGTT GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTAGCTAAAC CAGGTTCGAT	600
TACTCCACAT ACTAACTTCA AAGCTGAAAC TTATGTTTTA ACTAAAGAAG AAGGTGGACG	660
TCACACTCCA TTCTTCAACA ACTACCGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC	720
TGGTATTGTT ACACTTCCAG AAGGTACTGA AATGGTAATG CCTGGTGATA ACATTGAGCT	780
TGCAGTTGAA CTAATTGCAC CAATCGCTAT CGAAGAC	817

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(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

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CGGTGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCACAAACTC GTGAACACAT      60
TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA TTCTTAAACA AAGTTGACAT      120
GGTTGACGAT GAAGAATTAT TAGAATTAGT AGAAATGGAA GTTCGTGACT TATTAAGCGA      180
ATATGACTTC CCAGGTGACG ATGTACCTGT AATCGCTGGT TCAGCATTAR AAGCTTTAGA      240
AGGCGATGCT CAATACGAAG AAAAAATCTT AGAATTARTG GAAGCTGTAG ATACTTACAT      300
TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG ACGTATTCTC      360
AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA CGTGGTCAAA TCAAAGTTGG      420
TGAAGAAGTT GAAATCATCG GTTTACATGA CACATCTAAA ACAACTGTTA CAGGTGTTGA      480
AATGTTCCGT AAATTATTAG ACTACGCTGA AGCTGGTGAC AACATTGGTG CATTATTACG      540
TGGTGTTGCT CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC      600
ACCACATACT GAATTCAAAG CAGAAGTATA CGTATTATCA AAAGACGAAG GTGGACGTCA      660
CACTCCATTC TTCTCAAAC ATCGTCCACA ATTCTATTTC CGTACTACTG ACGTAACTGG      720
TGTTGTTTAC TTACCAGAAG GTACTGAAAT GGTAATGCCT GGTGATAACG TTGAAATGAC      780
AGTAGAATTA ATCGCTCCAA TCGCGATTGA AGAC                                814

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(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

CGGCGGTATC TTAGTTGTAT CTGCTGCTGA CGGTCCAATG CCACAACTC GTGAACACAT	60
CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA TTCTTAAACA AAGTTGACAT	120
GGTAGACGAC GAAGAATTAT TAGAATTAGT TGAAATGGAA GTTCGTGACT TATTAAGCGA	180
ATATGACTTC CCAGGTGACG ATGTACCTGT AATCGCTGGT TCTGCATTAA AAGCATTAGA	240
AGGCGATGCT GAATACGAAC AAAAAATCTT AGACTTAATG CAAGCAGTTG ATGATTACAT	300
TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG ACGTATTCTC	360
AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA CGTGGTCAAA TCAAAGTWGG	420
TGAAGAAGTT GAAATCATCG GTATGCACGA AACTTCTAAA ACAACTGTTA CTGGTGTAGA	480
AATGTTCCGT AAATTATTAG ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG	540
TGGTGTTGCA CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCTATTAC	600
ACCACACACA AAATTCAAAG CTGAAGTATA CGTATTATCT AAAGATGAAG GTGGACGTCA	660
CACTCCATTC TTCACTAACT ATCGCCACA ATTCTATTTC CRTACTACTG ACGTAACTGG	720
TGTTGTAAAC TTACCAGAAG GTACAGAAAT GGTTATGCCT GGCGACAACG TTGAAATGAC	780
AGTTGAATTA ATCGCTCCAA TCGCTATCGA AGAC	814

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAACTC GTGAACACAT	60
TCTTTTATCA CGTRACGTTG GTGYTCCAGC ATTAGTTGTA TTCTTAAACA AAGTTGACAT	120
GGTTGACGAY GAAGAATTAT TAGAATTRGT AGAAATGGAA GTTCGTGRCT TATTAAGCGA	180
ATATGACTTC CCAGGTGACG ATGTACCTGT AATCTCTGGT TCTGCATTAA AAGCTTTAGA	240
AGGCGACGCT GACTATGAGC AAAAAATCTT AGACTTAATG CAAGCTGTTG ATGACTYCAT	300
TCCAACACCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG ACGTATTCTC	360

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AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA CGTGGTCAAA TCAAAGTCGG	420
TGAAGAAATC GARATCATCG GTATGCAAGA AGAATCAAGC AAAACAACCTG TTACTGGTGT	480
AGAAATGTTC CGTAAATTAT TAGACTACGC TGAAGCTGGT GACAACATTG GTGCATTATT	540
ACGTGGTGTT TCACGTGATG ATGTACAACG TGGTCAAGTT TTAGCTGCTC CTGGTACTAT	600
CACACCACAT ACAAATTTCA AAGCGGATGT TTACGTTTTA TCTAAAGATG AAGGTGGTCG	660
TCATACGCCA TTCTTCACTA ACTACCGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC	720
TGGTGTTGTT AACTTACCAG AAGGTACTGA AATGGTTATG CCTGGCGATA ACGTTGAAAT	780
GGATGTTGAA TTAATTTCTC CAATCGCTAT TGAAGAC	817

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus simulans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

CGGCGGTATC TTAGTAGTAT CTGCTGCAGA TGGTCCAATG CCACAAACTC GTGAACACAT	60
CTTATTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA TTCTTAAACA AAGCTGACAT	120
GTTTGACGAC GAAGAATTAT TAGAATTAGT TGAAATGGAA GTTCGTGACT TATTATCTGA	180
ATACGACTTC CCTGGTGACG ATGTACCAGT TATCGTTGGT TCTGCATTAA AAGCTTTAGA	240
AGGCGACCCA GAATACGAAC AAAAAATCTT AGACTTAATG CAAGCTGTAG ATGACTACAT	300
CCCAACTCCA GAACGTGACT CTGATAAACC ATTCATGATG CCAGTTGAGG ACGTATTCTC	360
AATCACTGGT CGTGGTACTG TAGCAACAGG CCGTGTTGAA CGTGGTCAAA TCAAAGTCGG	420
TGAAGAAGTT GAAATCATCG GTATCACTGA AGAAAGCAAG AAAACAACAG TTACAGGTGT	480
AGAAATGTTC CGTAAATTAT TAGACTACGC TGAAGCTGGT GACAACATCG GTGCTTTATT	540
ACGTGGTGTT GCACGTGAAG ACGTACAACG TGGACAAGTA TTAGCAGCTC CTGGCTCTAT	600
TACTCCACAC ACAAATTTCA AAGCTGATGT TTACGTTTTA TCTAAAGAAG AAGGTGGACG	660
TCATACTCCA TTCTTCACTA ACTACCGCCC ACAATTCTAC TTCCGTACTA CTGACGTAAC	720
TGGCGTTGTT CACTTACCAG AAGGTACTGA AATGGTTATG CCTGGCGATA ACGTAGAAAT	780

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GACTGTTGAA TTGATCGCTC CAATCGCGAT TGAAGAC

817

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

CGGAGCTATC CTTGTAGTTG CTTCAACTGA TGGACCAATG CCACAAACTC GTGAGCACAT	60
CCTTCTTTCA CGTCAAGTTG GTGTTAAACA CCTTATCGTA TTCATGAACA AAGTTGACCT	120
TGTTGATGAT GAAGAATTGC TTGAATTGGT TGAAATGGAA ATTCGTGACC TTCTTTCAGA	180
ATACGACTTC CCAGGTGATG ACCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCACTTGA	240
AGGCGACGAA AAATACGAAG ACATCATCAT GGAATTGATG AGCACTGTTG ATGAGTACAT	300
TCCAGAACCA GAACGTGATA CTGACAAACC TTTACTTCTT CCAGTTGAAG ATGTATTCTC	360
AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC CGTGGTACTG TTCGTGTCAA	420
CGACGAAGTT GAAATCGTTG GTATTAAAGA AGATATCCAA AAAGCAGTTG TTA CTGGTGT	480
TGAAATGTTC CGTAAACAAC TTGACGAAGG TCTTGCAGGG GACAACGTTG GTGTTCTTCT	540
TCGTGGTGTT CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT	600
CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT TCTAAAGAAG AAGGTGGACG	660
TCATACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC TTCCGTACAA CTGACGTAAC	720
AGGTTCAATC GAACTTCCAG CAGGAACAGA AATGGTTATG CCTGGTGATA ACGTTACTAT	780
CGAAGTTGAA TTGATTCACC CAATCGCCGT AGAACAA	817

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

CGGAGCTATC CTTGTAGTAG CTTCAACTGA CGGACCAATG CCACAAACTC GTGAGCACAT	60
CCTTCTTTCA CGTCAGGTTG GTGTTAAACA CCTTATCGTC TTCATGAACA AAGTTGACTT	120
GGTTGACGAC GAAGAATTGC TTGAATTGGT TGAAATGGAA ATCCGTGACC TATTGTCAGA	180
ATACGACTTC CCAGGTGACG ATCTTCCAGT TATCCAAGGT TCAGCACTTA AAGCTCTTGA	240
AGGTGACTCT AAATACGAAG ACATCGTTAT GGAATTGATG AACACAGTTG ATGAGTATAT	300
CCCAGAACCA GAACGTGACA CTGACAAACC ATTGCTTCTT CCAGTCGAGG ACGTATTCTC	360
AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC CGTGGTATCG TTAAAGTCAA	420
CGACGAAATC GAAATCGTTG GSTATCAAAGA AGAACTCRA AAAGCAGTTG TTAAGTGGTGT	480
TGAAATGTTC CGTAAACAAC TTGACGAAGG TCTTGCTGGA GATAACGTAG GTGTCCTTCT	540
TCGTGGTGTT CAACGTGATG AAATCGAACG TGGACAAGTT ATCGCTAAAC CAGGTTCAAT	600
CAACCCACAC ACTAAATTCA AAGGTGAAGT CTACATCCTT ACTAAAGAAG AAGGTGGACG	660
TCACACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC TTCCGTACTA CTGACGTTAC	720
AGGTTCAATC GAACTTCCAG CAGGTACTGA AATGGTAATG CCTGGTGATA ACGTGACAAT	780
CGACGTTGAG TTGATTCACC CAATCGCCGT AGAACAA	817

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus salivarius*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

CGGTGCGATC CTTGTAGTAG CATCTACTGA CGGACCAATG CCACAAACTC GTGAGCACAT	60
CCTTCTTTCA CGTCAGGTTG GTGTTAAACA CCTTATCGTC TTCATGAACA AAGTTGACTT	120
GGTTGACGAT GAAGAATTGC TTGAATTGGT TGAAATGGAA ATCCGTGACC TTCTTTCAGA	180
ATACGATTTT CCAGGTGATG ACATTCCAGT TATCCAAGGT TCAGCTCTTA AAGCTCTTGA	240
AGGTGATTCT AAATACGAAG ACATCATCAT GGAATTGATG AACACTGTTG ACGAATACAT	300

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CCCAGAACCA GAACGTGACA CTGACAAACC ATTGTTGCTT CCAGTCGAAG ACGTATTCTC	360
AATCACTGGT CGTGGTACTG TTGCTTCAGG ACGTATCGAC CGTGGTGTTG TTCGTGTCAA	420
TGACGAAGTT GAAATCGTTG GTCTTAAAGA AGACATCCAA AAAGCAGTTG TTA CTGGTGT	480
TGAAATGTTC CGTAAACAAC TTGACGRAGG TATTGCCGGA GATAACGTCG GTGTTCTTCT	540
TCGTGGTATC CAACGTGATG AAATCGAACG TGGTCAAGTA TTGGCTGCAC CTGGTTCAAT	600
CAACCCACAC ACTAAATTCA AAGGTGAAGT TTACATCCTT TCTAAAGAAG AAGGTGGACG	660
TCACACTCCA TTCTTCAACA ACTACCGTCC ACAGTTCTAC TTCCGTACAA CTGACGTAAC	720
AGGTTCAATC GAACTTCCTG CAGGTACTGA AATGGTTATG CCTGGTGATA ACGTGACTAT	780
CGACGTTGAG TTGATCCACC CAATCGCCGT TGAACAA	817

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Agrobacterium tumefaciens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

AACATGATCA CCGGTGCTGC CGAGATGGAC GGC GCGATCC TGGTTTGCTC GGCTGCCGAC	60
GGCCCGATGC CACAGACCCG CGAGCACATC CTGCTTGCCC GTCAGGTGGG CGTTCCGGCC	120
ATCGTCGTGT TCCTCAACAA GGTCGACCAG GTTGACGACG CCGAGCTTCT CGAGCTCGTC	180
GAGCTTGAAG TTCGCGAACT TCTGTCGTCC TACGACTTCC CGGGCGACGA TATCCCGATC	240
ATCAAGGGTT CGGCACTTGC TGCTCTTGAA GATTCTGACA AGAAGATCGG TGAAGACGCG	300
ATCCGCGAGC TGATGGCTGC TGTCGACGCC TACATCCCGA CGCCTGAGCG TCCGATCGAC	360
CAGCCGTTCC TGATGCCGAT CGAAGACGTG TTCTCGATCT CGGGTCGTGG TACGGTTGTG	420
ACGGGTCGCG TTGAGCGCGG TATCGTCAAG GTTGGTGAAG AAGTCGAAAT CGTCGGCATC	480
CGTCCGACCT CGAAGACGAC TGTTACCGGC GTTGAAATGT TCCGCAAGCT GCTCGACCAG	540
GGCCAGGCCG GCGACAACAT CGGTGCACTC GTTCGCGGCG TTACCCGTGA CGGCGTCGAG	600
CGTGGTCAGA TCCTGTGCAA GCCGGGTTTCG GTCAAGCCGC ACAAGAAGTT CATGGCAGAA	660
GCCTACATCC TGACGAAGGA AGAAGGCGGC CGTCATACGC CGTTCTTCAC GAACTACCGT	720

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CCGCAGTTCT ACTTCCGTAC GACTGACGTT ACCGGTATCG TTTCGCTTCC TGAAGGCACG 780
 GAAATGGTTA TGCCTGGCGA CAACGTCACT GTTGAAGTCG AGCTGATCGT TCCGATCGCG 840
 ATGGAAGAAA AGCTGCGCTT CGCTATCCGC GAAGGCGGCC GTACCGTCGG CGCCGGC 897

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus subtilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ATGATCACTG GTGCTGCGCA AATGGACGGA GCTATCCTTG TAGTATCTGC TGCTGATGGC 60
 CCAATGCCAC AAACCTCGTA GCACATCCTT CTTTCTAAAA ACGTTGGTGT ACCATACATC 120
 GTTGTATTCT TAAACAAATG CGACATGGTA GACGACGAAG AGCTTCTTGA ACTAGTTGAA 180
 ATGGAAGTTC GCGATCTTCT TAGCGAATAC GACTTCCCTG GTGATGATGT ACCAGTTGTT 240
 AAAGGTTCTG CTCTTAAAGC TCTTGAAGGA GACGCTGAGT GGAAGCTAA AATCTTCGAA 300
 CTTATGGATG CGGTTGATGA GTACATCCCA ACTCCAGAAC GCGACACTGA AAAACCATTC 360
 ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACAGTTGC TACTGGCCGT 420
 GTAGAACGCG GACAAGTTAA AGTCGGTGAC GAAGTTGAAA TCATCGGTCT TCAAGAAGAG 480
 AACAAGAAAA CAACTGTTAC AGGTGTTGAA ATGTTCCGTA AGCTTCTTGA TTACGCTGAA 540
 GCTGGTGACA ACATTGGTGC CCTTCTTCGC GGTGTATCTC GTGAAGAAAT CCAACGTGGT 600
 CAAGTACTTG CTAAACCAGG TACAATCACT CCACACAGCA AATTCAAAGC TGAAGTTTAC 660
 GTTCTTTCTA AAGAAGAGGG TGGACGTCAT ACTCCATTCT TCTCTAACTA CCGTCCTCAG 720
 TTCTACTTCC GTACAACTGA CGTAACTGGT ATCATCCATC TTCCAGAAGG CGTAGAAATG 780
 GTTATGCCTG GAGATAACAC TGAAATGAAC GTTGAACCTA TTTCTACAAT CGCTATCGAA 840
 GAAGGAACTC GTTTCTCTAT TCGTGAAGGC GGACGTACTG TTGGT 885

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacteroides fragilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ATGGTTACTG GTGCTGCTCA GATGGACGGT GCTATCATTG TAGTTGCTGC TACTGATGGT	60
CCGATGCCTC AGACTCGTGA GCACATCCTT TTGGCTCGTC AGGTAAACGT TCCGAAGCTG	120
GTTGTATTCA TGAACAAGTG CGATATGGTT GAAGATGCTG AGATGTTGGA ACTTGTTGAA	180
ATGGAAATGA GAGAATTGCT TTCATTCTAT GATTTCGACG GTGACAATAC TCCGATCATT	240
CAGGGTTCTG CTCTTGGTGC ATTGAACGGC GTAGAAAAAT GGGAAGACAA AGTAATGGAA	300
CTGATGGAAG CTGTTGATAC TTGGATTCCA CTGCCTCCGC GCGATGTTGA TAAACCTTTC	360
TTGATGCCGG TAGAAGACGT GTTCTCTATC ACAGGTCGTG GTACTGTAGC TACAGGTCGT	420
ATCGAAACTG GTGTTATCCA TGTAGGTGAT GAAATCGAAA TCCTCGGTTT GGGTGAAGAT	480
AAGAAATCAG TTGTAAACAGG TGTTGAAATG TTCCGCAAAC TTCTGGATCA GGGTGAAGCT	540
GGTGACAACG TAGGTCTGTT GCTTCGTGGT GTTGACAAGA ACGAAATCAA ACGTGGTATG	600
GTTCTTTGTA AACCGGGTCA GATTAAACCT CACTCTAAAT TCAAAGCAGA GGTTTATATC	660
CTGAAGAAAG AAGAAGGTGG TCGTCACACT CCATTCCATA ACAAATATCG TCCTCAGTTC	720
TACCTGCGTA CTATGGACTG TACAGGTGAA ATCACTCTTC CGGAAGGAAC TGAAATGGTA	780
ATGCCGGGTG ATAACGTAAC TATCACTGTA GAGTTGATCT ATCCGGTTGC ACTGAACATC	840
GGTCTTCGTT TCGCTATCCG CGAAGGTGGA CGTACAGTAG GT	882

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Borrelia burgdorferi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

AATATGATTA CAGGAGCAGC TCAAATGGAT GCAGCGATAC TTTTAGTTGC TGCTGATAGT	60
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GGTGCTGAGC CTCAAACAAA AGAGCATTTG CTTCTTGCTC AAAGAATGGG AATAAAGAAA	120
ATAATAGTTT TTTTAAATAA ATTGGACTTA GCAGATCCTG AACTTGTTGA GCTTGTTGAA	180
GTTGAAGTTT TAGAACTTGT TGAAAAATAT GGCTTTTCAG CTGATACTCC AATAATCAAA	240
GGTTCAGCTT TTGGGGCTAT GTCAAATCCA GAAGATCCTG AATCTACAAA ATGCGTTAAA	300
GAAGTTCTTG AATCTATGGA TAATTATTTT GATCTTCCAG AAAGAGATAT TGACAAGCCA	360
TTTTTGCTTG CTGTTGAAGA TGTATTTTCT ATTTTCAGGAA GAGGCACTGT TGCTACTGGG	420
CGTATTGAAA GAGGTATTAT TAAAGTTGGT CAAGAAGTTG AAATAGTTGG AATTAAAGAA	480
ACCAGAAAAA CTACTGTTAC TGGTGTTGAA ATGTTCCAGA AAATTCTTGA GCAAGGTCAA	540
GCAGGGGATA ATGTTGGTCT TCTTTTGAGA GCGTTGATA AAAAAGACAT TGAGAGGGGG	600
CAAGTTTTGT CAGCTCCAGG TACAATTACT CCACACAAGA AATTTAAAGC TTCAATTTAT	660
TGTTTGACTA AAGAAGAAGG CGGTAGGCAC AAGCCATTTT TCCCAGGGTA TAGACCACAG	720
TTCTTTTTTA GAACAACCGA TGTTACTGGA GTTGTTGCTT TAGAGGGCAA AGAAATGGTT	780
ATGCCTGGTG ATAATGTTGA TATTATTGTT GAGCTGATCT CTTCAATAGC TATGGATAAG	840
AATGTAGAAT TTGCTGTTCG AGAAGGTGGA AGAACCGTTG CTTCAGGA	888

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Brevibacterium linens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AACATGATCA CCGGTGCCGC TCAGATGGAC GGTGCGATCC TCGTCGTCGC CGCTACCGAC	60
GGACCGATGC CCCAGACCCG TGAGCACGTG CTGCTCGCGC GTCAGGTCGG CGTTCCCTAC	120
ATCGTCGTGG CTCTGAACAA GTCCGACATG GTCGATGACG AGGAGCTCCT CGAGCTCGTC	180
GAATTCGAGG TCCGCGACCT GCTCTCGAGC CAGGACTTCG ACGGAGACAA CGCTCCGGTC	240
ATTCCGGTGT CCGCTCTCAA GGCGCTGGAA GGCGACGAGA AGTGGGTCAA GAGCGTTCAG	300
GATCTCATGG CTGCCGTCGA TGACAACGTT CCGGAGCCGG AGCGCGATGT CGACAAGCCG	360
TTCCTCATGC CCGTCGAGGA CGTCTTCACG ATCACCGGTC GTGGAACCGT CGTCACCGGT	420

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CGTGTCGAGC GCGGCGTGCT CCTGCCTAAC GACGAAATCG AAATCGTCGG CATCAAGGAG	480
AAGTCGTCCA AGACGACTGT CACCGCTATC GAGATGTTCC GCAAGACCCT GCCGGATGCC	540
CGTGCAGGTG AGAACGTCGG TCTGCTCCTC CGCGGCACCA AGCGCGAGGA TGTTGAGCGC	600
GGTCAGGTCA TCGTGAAGCC GGGTTCGATC ACCCCGCACA CCAAGTTCGA GGCTCAGGTC	660
TACATCCTGA GCAAGGACGA GGGCGGACGT CACAACCCGT TCTACTCGAA CTACCGTCCG	720
CAGTTCTACT TCCGGACCAC GGACGTCACC GGTGTCATCA CGCTGCCCCA GGGCACCGAG	780
ATGGTCATGC CCGGCGACAA CACCGATATG TCGGTCGAGC TCATCCAGCC GATCGCTATG	840
GAGGACCGCC TCCGCTTCGC AATCCGCGAA GGTGGCCGCA CCGTCGGCGC CGGT	894

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Burkholderia cepacia

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ATGATCACGG GCGCAGCGCA GATGGACGGC GCGATCCTGG TTTGCTCGGC AGCAGACGGC	60
CCGATGCCGC AAACGCGTGA GCACATCCTG CTGGCGCGTC AGGTTGGTGT TCCGTACATC	120
ATCGTGTTCC TGAACAAGTG CGACAGTGTG GACGACGCTG AACTGCTCGA GCTGGTCGAG	180
ATGGAAGTTC GCGAACTCCT GTCGAAGTAC GACTTCCCGG GCGACGACAC GCCGATCGTG	240
AAGGGTTCGG CCAAGCTGGC GCTGGAAGGC GACACGGGCG AGCTGGGCGA AGTGGCGATC	300
ATGAGCCTGG CAGACGCGCT GGACACGTAC ATCCCGACGC CGGAGCGTGC AGTTGACGGC	360
GCGTTCCTGA TGCCGGTGGA AGACGTGTTC TCGATCTCGG GCCGTGGTAC GGTGGTGACG	420
GGTCGTGTCTG AGCGCGGCAT CGTGAAGGTC GGCGAAGAAA TCGAAATCGT CCGTATCAAG	480
CCGACGGTGA AGACGACCTG CACGGGCGTT GAAATGTTCC GCAAGCTGCT GGACCAAGGT	540
CAGGCAGGCG ACAACGTCGG TATCCTGCTG CGCGGCACGA AGCGTGAAGA CGTGGAGCGT	600
GGCCAGGTTC TGGCGAAGCC GGGTTCGATC ACGCCGCACA CGCACTTCAC GGCTGAAGTG	660
TACGTGCTGA GCAAGGACGA AGGCGGCCGT CACACGCCGT TCTTCAACAA CTACCGTCCG	720
CAGTTCTACT TCCGTACGAC GGACGTGACG GGCTCGATCG AGCTGCCGAA GGACAAGGAA	780

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ATGGTGATGC CGGGCGACAA CGTGTCGATC ACGGTGAAGC TGATTGCTCC GATCGCGATG 840
 GAAGAAGGTC TCGCTTCGC AATCCGTGAA GGCGGCCGTA CGGTCGGC 888

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Chlamydia trachomatis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

AACATGATCA CCGGTGCGGC TCAAATGGAC GGGGCTATTC TAGTAGTTTC TGCAACAGAC 60
 GGAGCTATGC CTCAAATAA AGAGCATATT CTTTGGCAA GACAAGTTGG GGTTCCTTAC 120
 ATCGTTGTTT TTCTCAATAA AATTGACATG ATTTCCGAAG AAGACGCTGA ATTGGTCGAC 180
 TTGGTTGAGA TGGAGTTGGC TGAGCTTCTT GAAGAGAAAG GATACAAAGG GTGTCCAATC 240
 ATCAGAGGTT CTGCTCTGAA AGCTTTGGAA GGAGATGCTG CACATAGTA GAAAGTTCTG 300
 GAGCTAATGC AAGCCGTCGA TGATAATATC CCTACTCCAG AAAGAGAAAT TGACAAGCCT 360
 TTCTTAATGC CTATTGAGGA CGTGTTCTCT ATCTCCGGAC GAGGAACTGT AGTAACTGGA 420
 CGTATTGAGC GTGGAATTGT TAAAGTTTCC GATAAAGTTC AGTTGGTCGG TCTTAGAGAT 480
 ACTAAAGAAA CGATTGTTAC TGGGGTTGAA ATGTTTCAGAA AAGAACTCCC AGAAGGTCGT 540
 GCAGGAGAGA ACGTTGGATT GCTCCTCAGA GGTATTGGTA AGAACGATGT GGAAAGAGGA 600
 ATGGTTGTTT GCTTGCCAAA CAGTGTTAAA CCTCATAAC AGTTTAAGTG TGCTGTTTAC 660
 GTTCTGCAAA AAGAAGAAGG TGGACGACAT AAGCCTTTCT TCACAGGATA TAGACCTCAA 720
 TTCTTCTTCC GTACAACAGA CGTTACAGGT GTGGTAACTC TGCCTGAGGG AGTTGAGATG 780
 GTCATGCCTG GGGATAACGT TGAGTTTGAA GTGCAATTGA TTAGCCCTGT GGCTTTAGAA 840
 GAAGGTATGA GATTGCGAT TCGTGAAGGT GGTCGTACAA TCGGTGCTGG A 891

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

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AACATGATCA CCGGTGCTGC GCAGATGGAC GGCGCGATCC TGGTAGTTGC TGCGACTGAC      60
GGCCCGATGC CGCAGACTCG TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC      120
ATCATCGTGT TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT      180
GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGGCGACGA CACTCCGATC      240
GTTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGGAAGC GAAAATCCTG      300
GAACTGGCTG GCTTCCTGGA TTCTTACATT CCGGAACCAG AGCGTGCGAT TGACAAGCCG      360
TTCCTGCTGC CGATCGAAGA CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT      420
CGTGTAGAAC GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG      480
ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT      540
GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT CGAACGTGGT      600
CAGGTACTGG CTAAGCCGGG CACCATCAAG CCGCACACCA AGTTCGAATC TGAAGTGTAC      660
ATTCTGTCCA AAGATGAAGG CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG      720
TTCTACTTCC GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG      780
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCGATGGAC      840
GACGGTCTGC GTTTCGCAAT CCGTGAAGGC GGCCGTACCG TTGGCGCGGG C              891

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(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fibrobacter succinogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

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AACATGGTGA CTGGTGCTGC TCAGATGGAC GGCGCTATCC TCGTTGTTGC CGCTACTGAC      60
GGTCCGATGC CGCAGACTCG CGAACACATC CTTCTCGCTC ACCAGGTTGG CGTGCCGAAG      120

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ATCGTCGTGT TCATGAACAA GTGCGACATG GTTGACGATG CTGAAATTCT CGACCTCGTC	180
GAAATGGAAG TTCGCGAACT CCTCTCCAAG TATGACTTCG ACGGTGACAA CACCCCGATC	240
ATCCGTGGTT CCGCTCTCAA GGCCCTCGAA GCGGATCCGG AATACCAGGA CAAGGTCATG	300
GAACTCATGA ACGCTTGCGA CGAATACATC CCGCTCCCGC AGCGCGATAC CGACAAGCCG	360
TTCCTCATGC CGATCGAAGA CGTGTTACAG ATTACTGGCC GCGGCACTGT CGCTACTGGC	420
CGTATCGAAC GCGGTGTCGT TCGCTTGAAC GACAAGGTTG AACGTATCGG TCTCGGTGAA	480
ACCACCGAAT ACGTCATCAC CGGTGTTGAA ATGTTCCGTA AGCTCCTCGA CGACGCTCAG	540
GCAGGTGACA ACGTTGGTCT CTCCTCCGT GGTGCTGAAA AGAAGGACAT CGTCCGTGGC	600
ATGGTTCTCG CAGCTCCGAA GTCTGTCACT CCGCACACCG AATTTAAGGC TGAAATCTAC	660
GTTCTCACGA AGGACGAAGG TGGCCGTCAC ACGCCGTTCA TGAATGGCTA CCGTCCGCAG	720
TTCTACTTCC GCACCACCGA CGTTACTGGT ACGATCCAGC TCCCGGAAGG TGTCGAAATG	780
GTTACTCCGG GTGACACGGT CACGATCCAC GTGAACCTCA TCGCTCCGAT CGCTATGGAA	840
AAGCAGCTCC GCTTCGCTAT CCGTGAAGGT GGACGTACTG TTGGTGCTGG C	891

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Flavobacterium ferrugineum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

AACATGATCA CCGGTGCTGC CCAGATGGAC GGTGCTATCT TAGTTGTGGC TGCATCAGAC	60
GGTCCTATGC CTCAAACAAA AGAACACATC CTGCTTGCTG CCCAGGTAGG TGTACCTAAA	120
ATGGTTGTGT TTCTGAATAA AGTTGACCTC GTTGACGACG AAGAGCTCCT GGAGCTGGTT	180
GAGATCGAGG TTCGCGAAGA ACTGACTAAA CGCGGTTTCG ACGGCGACAA CACTCCAATC	240
ATCAAAGGTT CCGCTACAGG CGCCCTCGCT GGTGAAGAAA AGTGGGTAA AGAAATTGAA	300
AACCTGATGG ACGCTGTTGA CAGCTACATC CCACTGCCTC CTCGTCCGGT TGATCTGCCG	360
TTCCTGATGA GCGTAGAGGA CGTATTCTCT ATCACTGGTC GTGGTACTGT TGCTACCGGT	420
CGTATCGAGC GTGGCCGTAT CAAAGTTGGT GAGCCTGTTG AGATCGTAGG TCTGCAGGAG	480

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TCTCCCCTGA ACTCTACCGT TACAGGTGTT GAGATGTTCC GCAAACCTCCT CGACGAAGGT	540
GAAGCTGGTG ATAACGCCGG TCTCCTCCTC CGTGGTGTTG AAAAAACACA GATCCGTCGC	600
GGTATGGTAA TCGTTAAACC CGGTTCCATC ACTCCGCACA CGGACTTCAA AGGCGAAGTT	660
TACGTACTGA GCAAAGACGA AGGTGGCCGT CACACTCCAT TCTTCAACAA ATACCGTCCT	720
CAATTCTACT TCCGTACAAC TGACGTTACA GGTGAAGTAG AACTGAACGC AGGAACAGAA	780
ATGGTTATGC CTGGTGATAA CACCAACCTG ACCGTTAAAC TGATCCAACC GATCGCTATG	840
GAAAAGGTC TGAAATTCGC GATCCGCGAA GGTGGCCGTA CCGTAGGTGC AGGA	894

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

AATATGATTA CTGGTGCGGC ACAAATGGAT GGTGCTATTT TAGTAGTAGC AGCAACAGAT	60
GGTCCTATGC CACAACTCG TGAACACATC TTATTAGGTC GCCAAGTAGG TGTTCATAC	120
ATCATCGTAT TCTTAAACAA ATGCGACATG GTAGATGACG AAGAGTTATT AGAATTAGTC	180
GAAATGGAAG TTCGTGAACT TCTATCTCAA TATGACTTCC CAGGTGACGA TACACCAATC	240
GTACGTGGTT CAGCATTACA AGCGTTAAAC GGC GTAGCAG AATGGGAAGA AAAAATCCTT	300
GAGTTAGCAA ACCACTTAGA TACTTACATC CCAGAACCAG AACGTGCGAT TGACCAACCG	360
TTCTTTCTTC CAATCGAAGA TGTGTTCTCA ATCTCAGGTC GTGGTACTGT AGTAACAGGT	420
CGTGTTAGAAC GAGGTATTAT CCGTACAGGT GATGAAGTAG AAATCGTCGG TATCAAAGAT	480
ACAGCGAAAA CTACTGTAAC GGGTGTTGAA ATGTTCCGTA AATTACTTGA CGAAGGTCGT	540
GCAGGTGAAA ACATCGGTGC ATTATTACGT GGTACCAAAC GTGAAGAAAT CGAACGTGGT	600
CAAGTATTAG CGAAACCAGG TTCAATCACA CCACACACTG ACTTCGAATC AGAAGTGTAC	660
GTATTATCAA AAGATGAAGG TGGTCGTCAT ACTCCATTCT TCAAAGGTTA CCGTCCACAA	720
TTCTATTTCC GTACAACAGA CGTGACTGGT ACAATCGAAT TACCAGAAGG CGTGGAATG	780
GTAATGCCAG GCGATAACAT CAAGATGACA GTAAGCTTAA TCCACCCAAT TGCGATGGAT	840

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CAAGGTTTAC GTTTCGCAAT CCGTGAAGGT GGCCGTACAG TAGGTGCAGG C

891

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

AACATGATCA CCGGTGCGGC GCAAATGGAC GGAGCGATTT TGGTTGTTTC TGCAGCTGAT	60
GGCCCTATGC CTCAAAC TAG GGAGCATATC TTATTGTCTC GTCAAGTAGG CGTGCCTCAC	120
ATCGTTGTTT TCTTAAACAA ACAAGACATG GTAGATGACC AAGAATTGTT AGAACTTGTA	180
GAAATGGAAG TGC GCGAATT GTTGAGCGCG TATGAATTTC CTGGCGATGA CACTCCTATC	240
GTAGCGGGTT CAGCTTTAAG AGCTTTAGAA GAAGCAAAGG CTGGTAATGT GGGTGAATGG	300
GGTGAAAAAG TGCTTAAACT TATGGCTGAA GTGGATGCCT ATATCCCTAC TCCAGAAAGA	360
GAACTGAAA AAAC TTTCTT GATGCCGGTT GAAGATGTGT TCTCTATTGC GGGTAGAGGG	420
ACTGTGGTTA CAGGTAGGAT TGAAAGAGGC GTGGTGAAAG TAGGCGATGA AGTGGAATC	480
GTTGGTATCA GACCTACACA AAAAACGACT GTAACCGGTG TAGAAATGTT TAGGAAAGAG	540
TTGGAAAAAG GTGAAGCCGG CGATAATGTG GGCGTGCTTT TGAGAGGAAC TAAAAAGAA	600
GAAGTGGAAC GCGGTATGGT TCTATGCAA CCAGGTTCTA TCACTCCGCA CAAGAAATTT	660
GAGGGAGAAA TTTATGTCCT TTCTAAAGAA GAAGGCGGGA GACACACTCC ATTCTTCACC	720
AATTACCGCC CGCAATTCTA TGTGCGCACA ACTGATGTGA CTGGCTCTAT CACCCTTCCT	780
GAAGGCGTAG AAATGGTTAT GCCTGGCGAT AATGTGAAAA TCACTGTAGA GTTGATTAGC	840
CCTGTTGCGT TAGAGTTGGG AACTAAATTT GCGATTCGTG AAGGCGGTAG GACCGTTGGT	900
GCTGGT	906

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Micrococcus luteus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

AACATGATCA CCGGCGCCGC TCAGATGGAC GGCGCGATCC TCGTGGTCGC CGCTACCGAC	60
GGCCCGATGG CCCAGACCCG TGAGCACGTG CTCCTGGCCC GCCAGGTCGG CGTGCCGGCC	120
CTGCTCGTGG CCCTGAACAA GTCGGACATG GTGGAGGACG AGGAGCTCCT CGAGCGTGTC	180
GAGATGGAGG TCCGGCAGCT GCTGTCCTCC AGGAGCTTCG ACGTCGACGA GGCCCCGGTC	240
ATCCGCACCT CCGCTCTGAA GGCCCTCGAG GGCGACCCCC AGTGGGTCAA GTCCGTCGAG	300
GACCTCATGG ATGCCGTGGA CGAGTACATC CCGGACCCGG TGC GCGACAA GGACAAGCCG	360
TTCCTGATGC CGATCGAGGA CGTCTTCACG ATCACCGGCC GTGGCACCGT GGTGACCGGT	420
CGCGCCGAGC GCGGCACCCT GAAGATCAAC TCCGAGGTCG AGATCGTCGG CATCCGCGAC	480
GTGCAGAAGA CCACTGTCAC CGGCATCGAG ATGTTCCACA AGCAGCTCGA CGAGGCCTGG	540
GCCGGCGAGA ACTGCGGTCT GCTCGTGCGC GGTCTGAAGC GCGACGACGT CGAGCGCGGC	600
CAGGTGCTGG TGGAGCCGGG CTCCATCACC CCGCACACCA ACTTCGAGGC GAACGTCTAC	660
ATCCTGTCCA AGGACGAGGG TGGGCGTCAC ACCCCGTTCT ACTCGAACTA CCGCGCGCAG	720
TTCTACTTCC GCACCACCGA CGTCACCGGC GTCATCACGC TGCCCGAGGG CACCGAGATG	780
GTCATGCCCC GCGACACCAC CGAGATGTCG GTCGAGCTCA TCCAGCCGAT CGCCATGGAG	840
GAGGGCCTCG GCTTCGCCAT CCGCGAGGGT GGCCGCACCG TGGGCTCCGG C	891

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 891 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

AACATGATCA CCGGCGCCGC GCAGATGGAC GGTGCGATCC TGGTGGTCGC CGCCACCGAC	60
GGCCCGATGC CCCAGACCCG CGAGCACGTT CTGCTGGCGC GTCAAGTGGG TGTGCCCTAC	120

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ATCCTGGTAG CGCTGAACAA GGCCGACGCA GTGGACGACG AGGAGCTGCT CGAACTCGTC	180
GAGATGGAGG TCCGCGAGCT GCTGGCTGCC CAGGAATTCG ACGAGGACGC CCCGGTTGTG	240
CGGGTCTCGG CGCTCAAGGC GCTCGAGGGT GACGCGAAGT GGGTTGCCTC TGTCGAGGAA	300
CTGATGAACG CGGTCGACGA GTCGATTCCG GACCCGGTCC GCGAGACCGA CAAGCCGTTC	360
CTGATGCCGG TCGAGGACGT CTTCAACATT ACCGGCCGCG GAACCGTGGT CACCGGACGT	420
GTGGAGCGCG GCGTGATCAA CGTGAACGAG GAAGTTGAGA TCGTCGGCAT TCGCCCATCG	480
ACCACCAAGA CCACCGTCAC CGGTGTGGAG ATGTTCCGCA AGCTGCTCGA CCAGGGCCAG	540
GCGGGCGACA ACGTTGGTTT GCTGCTGCGG GGCGTCAAGC GCGAGGACGT CGAGCGTGGC	600
CAGGTTGTCA CCAAGCCCGG CACCACCACG CCGCACACCG AGTTCGAAGG CCAGGTCTAC	660
ATCCTGTCCA AGGACGAGGG CGGCCGGCAC ACGCCGTTCT TCAACAATA CCGTCCGCAG	720
TTCTACTTCC GCACCACCGA CGTGACCGGT GTGGTGACAC TGCCGGAGGG CACCGAGATG	780
GTGATGCCCC GTGACAACAC CAACATCTCG GTGAAGTTGA TCCAGCCCGT CGCCATGGAC	840
GAAGGTCTGC GTTTCGCGAT CCGCGAGGGT GGCCGCACCG TGGGCGCCGG C	891

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycoplasma genitalium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

AATATGATCA CAGGTGCTGC ACAAATGGAT GGAGCTATTC TAGTTGTTTC AGCAACTGAT	60
AGTGTGATGC CCCAAACCCG CGAGCACATC TTAATTGCCC GCCAAGTAGG GGTTCCTAAA	120
ATGGTAGTTT TTCTAAACAA GTGTGATATT GCTAGTGATG AAGAGGTACA AGAACTTGTT	180
GCTGAAGAAG TACGTGATCT GTTAACTTCC TATGGTTTTG ATGGTAAGAA CACTCCTATT	240
ATTTATGGCT CAGCTTTAAA AGCATTGGAA GGTGATCCAA AGTGGGAGGC TAAGATCCAT	300
GATTTGATTA AAGCAGTTGA TGAATGGATT CCAACTCCTA CACGTGAAGT AGATAAACCT	360
TTCTTATTAG CAATTGAAGA TACGATGACC ATTACTGGTA GAGGTACAGT TGTTACAGGA	420
AGAGTTGAAA GAGGTGAACT CAAAGTAGGT CAAGAAGTTG AAATTGTTGG TTAAAAACCA	480

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ATTAGAAAAG CAGTTGTTAC TGGAATTGAA ATGTTCAAAA AGGAACTTGA TTCAGCAATG 540
 GCTGGTGACA ATGCTGGGGT ATTATTACGT GGTGTTGAAC GTAAAGAAGT TGAAAGAGGT 600
 CAAGTTTTAG CAAAACCAGG CTCTATTAAA CCGCACAAGA AATTTAAAGC TGAGATCTAT 660
 GCTTTAAAGA AAGAAGAAGG TGGTAGACAC ACTGGTTTTT TAAACGGTTA CCGTCCTCAA 720
 TTCTATTTCC GTACCACTGA TGTAAGTGGT TCTATTGCTT TAGCTGAAAA TACTGAAATG 780
 GTTCTACCTG GTGATAATGC TTCTATTACT GTTGAGTTAA TTGCTCCTAT CGCTTGTGAA 840
 AAAGGTAGTA AGTTCTCAAT TCGTGAAGGT GGTAAGACTG TAGGGGCAGG C 891

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria gonorrhoeae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

AACATGATTA CCGGCGCCGC ACAAATGGAC GGTGCAATCC TGGTATGTTT TGCTGCCGAC 60
 GGCCCTATGC CGCAAACCCG CGAACACATC CTGCTGGCCC GTCAAGTAGG CGTACCTTAC 120
 ATCATCGTGT TCATGAACAA ATGCGACATG GTCGACGATG CCGAGCTGTT CCAACTGGTT 180
 GAAATGGAAA TCCGCGACCT GCTGTCCAGC TACGACTTCC CCGGCGACGA CTGCCCAGATC 240
 GTACAAGGTT CCGCACTGAA AGCCTTGGAA GGCGATGCCG CTTACGAAGA AAAAATCTTC 300
 GAACTGGCTA CCGCATTGGA CAGATACATC CCGACTCCCG AGCGTGCCGT GGACAAACCA 360
 TTCCTGCTGC CTATCGAAGA CGTGTTCTCC ATTTCCGGCC GCGGTACCGT AGTCACCGGC 420
 CGTGTAAGAGC GAGGTATCAT CCACGTTGGT GACGAGATTG AAATCGTCGG TCTGAAAGAA 480
 ACCCAAAAAA CCACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGTCAG 540
 GCGGGCGACA ACGTAGGCGT ATTGCTGCGC GGTACCAAAC GTGAAGACGT AGAACGCGGT 600
 CAGGTATTGG CCAAACGGGG TACTATCACT CCTCACACCA AGTTCAAAGC AGAAGTGTAC 660
 GTATTGAGCA AAGAAGAGGG CGGCCCCCAT ACCCGTTTTT TCGCCAATA CCGTCCCCAA 720
 TTCTACTTCC GTACCACTGA CGTAACCGGC ACGATTACTT TGGAAAAAGG TGTGGAATG 780
 GTAATGCCGG GTGAGAACGT AACCATTACT GTAGAAGTGA TTGCGCCTAT CGCTATGGAA 840

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GAAGGTCTGC GCTTTGCGAT TCGCGAAGGC GGCCGTACCG TGGGTGCCGG C

891

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rickettsia prowazekii*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

AATATGATAA CTGGTGCCGC TCAGATGGAT GGTGCTATAT TAGTAGTTTC TGCTGCTGAT	60
GGTCCTATGC CTCAAACTAG AGAACATATA TTA CTGGCAA AACAGGTAGG TGTACCTGCT	120
ATGGTAGTAT TTTTGAATAA AGTAGATATG GTAGATGATC CTGACCTATT AGAATTAGTT	180
GAGATGGAAG TAAGAGAATT ATTATCAAAA TATGGTTTCC CTGGTAATGA AATACCTATT	240
ATTAAAGGTT CTGCACTTCA AGCTTTAGAA GGAAAACCTG AAGGTGAAAA AGCTATTAAT	300
GAGTTAATGA ATGCAGTAGA TACGTATATA CCTCAGCCTA TAGAGCTACA AGATAAACCT	360
TTTTTAATGC CAATAGAGGA TGTATTTTCT ATTT CAGGCA GAGGTACCGT TGTA ACTGGT	420
AGAGTGGAGT CAGGCATAAT TAAGGTGGGT GAAGAAATTG AAATAGTAGG TCTAAAAAAT	480
ACGCAAAAAA CGACTTGTAC AGGTGTAGAA ATGTT CAGAA AATTACTTGA TGAAGGACAA	540
TCTGGAGATA ATGTCGGTAT ATTACTACGT GGTACAAAAA GAGAAGAAGT AGAAAGAGGA	600
CAAGTACTTG CAAAACCTGG GAGCATAAAA CCGCATGATA AATTTGAAGC TGAAGTGTAT	660
GTGCTTAGTA AAGAGGAAGG TGGACGTCAT ACCCCATTTA CTAATGATTA TCGCCCACAG	720
TTCTATTTTA GAACAACAGA TGTTACCGGC ACAATAAAAT TGCCTTCTGA TAAGCAGATG	780
GTTATGCCTG GAGATAATGC TACTTTTTCA GTAGAATTAA TTAAGCCGAT TGCTATGCAA	840
GAAGGGTTAA AATTCTCTAT ACGTGAAGGT GG TAGAACAG TAGGAGCCGG T	891

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella typhimurium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

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AACATGATCA CCGGTGCTGC TCAGATGGAC GGCGCGATCC TGGTTGTTGC TGCGACTGAC      60
GGCCCGATGC CGCAGACCCG TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC      120
ATCATCGTGT TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT      180
GAGATGGAAG TTCGCGAACT GCTGTCTCAG TACGACTTCC CGGGCGACGA CACTCCGATC      240
GTTCTGTGGT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGGAAGC GAAAATCATC      300
GAACTGGCTG GCTTCCTGGA TTCTTATATT CCGGAACCAG AGCGTGCGAT TGACAAGCCG      360
TTCCTGCTGC CGATCGAAGA CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT      420
CGTGTAAGAG GCGGTATCAT CAAAGTGGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAG      480
ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT      540
GCCGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT CGAACGTGGT      600
CAGGTACTGG CTAAGCCGGG CACCATCAAG CCGCACACCA AGTTCGAATC TGAAGTGTAC      660
ATTCTGTCCA AAGATGAAGG CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG      720
TTCTACTTCC GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG      780
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCGATGGAC      840
GACGGTCTGC GTTTCGCAAT CCGTGAAGGC GGCCGTACCG TTGGCGCGGG C              891

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(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 881 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Shewanella putida*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

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ATGATCACTG GTGCTGCACA GATGGACGGC GCGATTCTGG TAGTCGCTTC AACAGACGGT      60
CCAATGCCAC AGACTCGTGA GCACATCCTG CTTTCTCGTC AGGTTGGCGT ACCATTCATC      120
ATCGTATTCA TGAACAAATG TGACATGGTA GATGACGAAG AGCTGTTAGA GCTAGTTGAG      180

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ATGGAAGTGC GTGAACTGTT ATCAGAATAC GATTTCCCAG GTGATGACTT ACCGGTAATC	240
CAAGGTTTCAG CTCTGAAAGC GCTAGAAGGC GAGCCAGAGT GGGAAGCAAA AATCCTTGAA	300
TTAGCAGCGG CGCTGGATTC TTACATTCCA GAACCACAAC GTGACATCGA TAAGCCGTTC	360
CTACTGCCAA TCGAAGACGT ATTCTCAATT TCAGGCCGTG GTACAGTAGT AACAGGTCGT	420
GTTGAGCGTG GTATTGTACG CGTAGGCGAC GAAGTTGAAA TCGTTGGTGT ACGTGCGACA	480
ACTAAGACAA CGTGTACTGG TGTAGAAATG TTCCGTAAAC TGCTTGACGA AGGTCGTGCA	540
GGTGAGAACT GTGGTATTTT GTTACGTGGT ACTAAGCGTG ATGACGTAGA ACGTGGTCAA	600
GTATTAGCGA AGCCAGGTTT AATCAACCCA CACACTACTT TTGAATCAGA AGTTTACGTA	660
CTGTCAAAAG AAGAAGGTGG TCGTCACACG CCATTCTTCA AAGGCTACCG TCCACAGTTC	720
TACTTCCGTA CAACTGACGT AACCGGTACT ATCGAACTGC CAGAAGGCGT AGAGATGGTA	780
ATGCCAGGCG ATAACATCAA GATGGTAGTG AACTGATTT GCCCAATCGC GATGGACGAA	840
GGTTTACGCT TCGCAATCCG TGAAGGCGGT CGTACAGTGG T	881

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stigmatella aurantiaca*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

AACATGATCA CGGGCGCGGC GCAGATGGAC GGAGCGATTC TGGTGGTGTC CGCGGCCGAC	60
GGCCCGATGC CCCAGACGCG TGAGCACATC CTGCTGGCCA GGCAGGTGGG CGTGCCCTAC	120
ATCGTCGTCT TCCTGAACAA GGTGGACATG CTGGACGATC CGGAGCTGCG CGAGCTGGTG	180
GAGATGGAGG TGCGCGACCT GCTCAAGAAG TACGAGTTCC CGGGCGACAG CATCCCCATC	240
ATCCCTGGCA GCGCGCTCAA GGCGCTGGAG GGAGACACCA GCGACATCGG CGAGGGAGCG	300
ATCCTGAAGC TGATGGCGGC GGTGGACGAG TACATCCCGA CGCCGCAGCG TGCGACGGAC	360
AAGCCGTTCC TGATGCCGGT GGAAGACGTG TTCTCCATCG CAGGCCGAGG AACGGTGGCG	420
ACGGGCCGAG TGGAGCGCGG CAAGATCAAG GTGGGCGAGG AAGTGGAGAT CGTGGGGATC	480
CGTCCGACGC AGAAGACGGT CATCACGGGG GTGGAGATGT TCCGCAAGCT GCTGGACGAG	540

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GGCATGGCGG GAGACAACAT CGGAGCGCTG CTGCGAGGCC TGAAGCGCGA GGACCTGGAG	600
CGTGGGCAGG TGCTGGCGAA CTGGGGGAGC ATCAACCCGC ACACGAAGTT CAAGGCGCAG	660
GTGTACGTGC TGTCGAAGGA AGAGGGAGGG CGGCACACGC CGTTCTTCAA GGGATACCGG	720
CCGCAGTTCT ACTTCCGGAC GACGGACGTG ACCGGAACGG TGAAGCTGCC GGACAACGTG	780
GAGATGGTGA TGCCGGGAGA CAACATCGCC ATCGAGGTGG AGCTCATTAC TCCGGTCGCC	840
ATGGAGAAGG AGCTGCCGTT CGCCATCCGT GAGGGTGGCC GCACGGTGGG CGCCGGC	897

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

AACATGATCA CTGGTGCCGC TCAAATGGAC GGAGCTATCC TTGTAGTTGC TTCAACTGAT	60
GGACCAATGC CACAACTCG TGAGCACATC CTTCTTTCAC GTCAGGTTGG TGTAAACAC	120
CTTATCGTGT TCATGAACAA AGTTGACCTT GTTGATGACG AAGAGTTGCT TGAATTAGTT	180
GAGATGGAAA TTCGTGACCT TCTTTCAGAA TACGATTTCC CAGGTGATGA CCTTCCAGTT	240
ATCCAAGGTT CAGCTCTTAA AGCTCTTGAA GGCACACTA AATTTGAAGA CATCATCATG	300
GAATTGATGG ATACTGTTGA TTCATACATT CCAGAACCAG AACGCGACAC TGACAAACCA	360
TTGCTTCTTC CAGTCGAAGA CGTATTCTCA ATTACAGGTC GTGGTACAGT TGCTTCAGGA	420
CGTATCGACC GTGGTACTGT TCGTGTCAAC GACGAAATCG AAATCGTTGG TATCAAAGAA	480
GAAACTAAAA AAGCTGTTGT TACTGGTGTT GAAATGTTCC GTAAACAACT TGACGAAGGT	540
CTTGCAGGAG ACAACGTAGG TATCCTTCTT CGTGGTGTTT AACGTGACGA AATCGAACGT	600
GGTCAAGTTA TTGCTAAACC AAGTTCAATC AACCCACACA CTAAATTCAA AGGTGAAGTA	660
TATATCCTTT CTAAAGACGA AGGTGGACGT CACACTCCAT TCTTCAACAA CTACCGTCCA	720
CAATTCTACT TCCGTACAAC TGACGTAACA GGTTCATCG AACTTCCAGC AGGTACAGAA	780
ATGGTTATGC CTGGTGATAA CGTGACAATC AACGTTGAGT TGATCCACCC AATCGCCGTA	840
GAACAAGGTA CTACTTTCTC AATCCGTGAA GGTGGACGTA CTGTTGGTTC AGGT	894

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(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Thiobacillus cuprinus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

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AACATGATCA CCGGTGCGGC CCAGATGGAC GCGCCATCC TGGTCGTGTC CGCCGCCGAC      60
GGCCCCATGC CCCAAACCCG CGAGCACATC CTGCTGGCGC GTCAGGTGGG CGTGCCCTAC      120
ATCATCGTGT TCCTCAACAA GTGCGACATG GTCGACGACG CCGAGCTGCT CGAACTCGTC      180
GAGATGGAAG TGC GCGAGCT GCTGTCCAAG TACGACTTCC CCGGTGACGA CACCCCCATC      240
ATCAAGGGCT CGGCCAAGCT GGCCCTCGAA GGCGACAAGG GCGAACTGGG CGAAGGCGCC      300
ATTCTCAAGC TGGCCGAGGC CCTGGACACC TACATCCCCA CGCCCGAGCG GGCCGTCGAC      360
GGCGCGTTCC TCATGCCCGT GGAAGACGTG TTCTCCATCT CCGGGCGCGG CACGGTGGTC      420
ACCGGGCGTG TGGAGCGCGG CATCATCAAG GTCGGCGAGG AAATCGAGAT TGTCGGCCTC      480
AAGCCCACCC TCAAGACCAC CTGCACCGGC GTGGAAATGT TCAGGAAGCT GCTCGACCAG      540
GGCCAGGCCG GCGACAACGT CGGCATCTTG CTGCGCGGCA CCAAGCGCGA GGAAGTCGAG      600
CGCGGCCAGG TGCTGTGCAA ACCCGGCTCG ATCAAGCCCC ACACCCACTT CACCGCCGAG      660
GTGTACGTGC TGAGCAAGGA CGAGGGCGGC CGCCACACCC CCTTCTTCAA CAACTACCGC      720
CCGCAGTTCT ACTTCCGCAC CACCGACGTC ACCGGCGCCA TCGAACTGCC CAAGGACAAG      780
GAAATGGTCA TGCCCGGCGA TAATGTGAGC ATCACCGTCA AGCTCATCGC CCCCATCGCC      840
ATGGAAGAAG GCCTGCGCTT CGCCATCCGC GAAGGCGGCC GCACCGTCGG CGCCGGC      897

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(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Treponema pallidum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

AATATGATCA CGGGTGCTGC GCAGATGGAC GGTGGTATTC TCGTCGTGTC TGCGCCTGAC	60
GGCGTTATGC CACAGACGAA GGAGCATCTT CTGCTCGCCC GTCAGGTTGG TGTTCCCTCC	120
ATCATTGTTT TTTTGAACAA GGTTGATTTG GTTGATGATC CTGAGTTGCT AGAGCTGGTG	180
GAAGAAGAGG TCGTGATGC GCTTGCTGGA TATGGGTTTT CGCGTGAGAC GCCTATCGTC	240
AAGGGGTCTG CGTTTAAAGC TCTGCAGGAT GGCGCTTCCC CGGAGGATGC AGCTTGATT	300
GAGGAACTGC TTGCGGCCAT GGATTCCTAC TTTGAAGACC CAGTGCGTGA CGACGCAAGA	360
CCTTTCTTGC TCTCTATCGA GGATGTGTAC ACTATTTCTG GGCGTGGTAC CGTTGTCACG	420
GGGCGCATCG AATGTGGGGT AATTAGTCTG AATGAAGAGG TCGAGATCGT CGGGATTAAG	480
CCCACTAAGA AAACAGTGGT TACTGGCATT GAGATGTTTA ATAAGTTGCT TGATCAGGGA	540
ATTGCAGGTG ATAACGTGGG GCTGCTTTTG CGCGGGGTGG ATAAAAAGA GGTGAGCGC	600
GGTCAGGTGC TTTCTAAGCC CGGTTCTATT AAGCCACACA CCAAGTTTGA GGCGCAGATC	660
TACGTGCTCT CTAAGGAAGA GGGTGGCCGT CACAGTCCTT TTTTCAAGG TTATCGTCCG	720
CAGTTTTATT TTAGAACTAC TGACATTACC GGTACGATTT CTCTTCCTGA AGGGGTAGAC	780
ATGGTGAAGC CGGGGGATAA CACCAAGATT ATAGGTGAGC TCATCCACCC GATAGCTATG	840
GACAAGGGTC TGAAGCTTGC GATTCGTGAA GGGGGGCGCA CTATTGCTTC TGGT	894

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Ureaplasma urealyticum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

AATATGATTA CAGGGGCAGC ACAAATGGAT GGAGCAATTT TAGTTATTGC TGCATCTGAT	60
GGGGTTATGG CTCAAATAA AGAACATATT TTATTAGCAC GTCAAGTTGG TGTTCCAAAA	120
ATCGTTGTTT TCTTAAACAA ATGTGATTTT ATGACAGATC CAGATATGCA AGATCTTGTT	180
GAAATGGAAG TTCGTGAATT ATTATCTAAA TATGGATTTG ATGGCGATAA CACACCAGTT	240

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ATTCGTGGTT CAGGTCTTAA GGCTTTAGAA GGAGATCCAG TTTGAGAAGC AAAAATTGAT	300
GAATTAATGG ACGCAGTTGA TTCATGAATT CCATTACCAG AACGTAGTAC TGACAAACCA	360
TTCTTATTAG CAATTGAAGA TGTATTCACA ATTTCAGGAC GTGGTACAGT AGTAACTGGA	420
CGTGTTGAAC GTGGTGTATT AAAAGTTAAT GATGAGGTTG AAATTGTTGG TCTAAAAGAC	480
ACTCAAAAAA CTGTTGTTAC AGGAATTGAA ATGTTTAGAA AATCATTAGA TCAAGCTGAA	540
GCTGGTGATA ATGCTGGTAT TTTATTACGT GGTATTAAAA AAGAAGATGT TGAACGTGGT	600
CAAGTACTTG TAAAACCAGG ATCAATTAAA CCTCACCGTA CTTTTACTGC TAAAGTTTAT	660
ATTCTTAAAA AAGAAGAAGG TGGACGTCAT ACACCTATTG TTTCAGGATA CCGTCCACAA	720
TTCTATTTTA GAACAACAGA TGTAACAGGT GCTATTTTCAT TACCTGCTGG TGTTGATTTG	780
GTTATGCCAG GTGATGACGT TGAAATGACT GTAGAATTAA TTGCTCCAGT TGC GATTGAA	840
GATGGATCTA AATTCTCAAT CCGTGAAGGT GGTAAACTG TAGGTCATGG T	891

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 909 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Wolinella succinogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

AACATGATTA CAGGTGCTGC TCAAATGGAT GGCGCGATTC TTGTTGTTTC TCGGCGGAT	60
GGCCCCATGC CCCAACTAG GGAGCACATT CTTCTTTCTC GACAAGTAGG CGTTCCTTAC	120
ATCGTGGTTT TCTTGAACAA AGAAGATATG GTTGATGACG CTGAGCTTCT TGAGCTTGTT	180
GAAATGGAAG TTAGAGAACT TCTTAGCAAC TACGACTTCC CTGGAGATGA CACTCCTATC	240
GTTGCAGGTT CCGCTCTTAA AGCTCTTGAA GAGGCTAACG ACCAGGAAAA TGTTGGCGAG	300
TGGGGCGAGA AAGTATTGAA GCTTATGGCT GAGGTTGACC GATATATTCC TACGCCTGAG	360
CGAGATGTGG ATAAGCCTTT CCTTATGCCT GTTGAAGACG TATTCTCCAT CGCGGGTCGT	420
GGAACCGTTG TGACAGGAAG AATTGAAAGA GCGTGTTA AAGTCGGTGA CGAAGTAGAA	480
ATCGTTGGTA TCCGAAACAC ACAAAAAACA ACCGTAAGT GCGTTGAGAT GTTCCGAAAA	540
GAGCTCGACA AGGGTGAGGC GGGTGACAAC GTTGGTGTTT TTTTGAGAGG CACCAAGAAA	600

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GAAGATGTTG AGAGAGGTAT GGTTCTTTGT AAAATAGGTT CTATCACTCC TCACACTAAC 660
 TTTGAAGGTG AAGTTTACGT TCTTTCCAAA GAGGAAGGCG GACGACACAC TCCATTCTTC 720
 AATGGATACC GACCTCAGTT CTATGTTAGA ACTACAGACG TTACCGGTTC TATCTCTCTT 780
 CCTGAGGGCG TAGAGATGGT TATGCCTGGT GACAACGTTA AGATCAATGT TGAGCTTATC 840
 GCTCCTGTAG CCCTCGAAGA GGGAACACGA TTCGCGATCC GTGAAGGTGG TCGAACCGTT 900
 GGTGCGGGT 909

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

TARTCNGTRA ANGCTCNAC RCACAT 26

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

TCTTTAGCAG AACAGGATGA A 21

(2) INFORMATION FOR SEQ ID NO:174:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GAATAATTCC ATATCCTCCG

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WHAT IS CLAIMED IS:

1. A method using one or more oligonucleotides for determining or detecting the presence, amount or both of one or more bacterial and fungal nucleic acids in a sample, wherein said one or more nucleic acids or parts thereof comprise a selected target region hybridizable with said one or more oligonucleotides, said method comprising:

a) contacting said sample with said one or more oligonucleotides that anneal in an annealing step of an amplification reaction under conditions comprising 50 mM KCl, 10 mM Tris-HCl (pH 9.0) and 2.5 mM MgCl₂ at 45°C to:

i) at least 12 nucleotides of each of the bacterial nucleotide sequences defined in the group consisting of SEQ ID NOs: 118, 119 and 125-171, or complementary sequences thereof; or

ii) at least 12 nucleotides of each of the fungal nucleotide sequences defined in the group consisting of SEQ ID NOs: 120-124, or complementary sequences thereof;

so as to perform an amplification reaction or a hybridization assay; and

b) detecting the presence, amount or both of hybridized oligonucleotides or amplified products in a) as an indication of the presence, amount or both of said one or more nucleic acids.

2. The method of claim 1, wherein said one or more oligonucleotides comprise nucleotide sequence SEQ ID NOs: 23, 24, 107, 108, 109 or 172.

3. The method of claim 1 or 2, further comprising using one or more oligonucleotides for determining the presence, amount or both of one or more nucleic acids from a bacterial and/or fungal species and/or genus of: *Enterococcus faecium*, *Listeria monocytogenes*, *Neisseria meningitidis*, *Staphylococcus saprophyticus*, *Streptococcus agalactiae*, *Candida albicans*, *Enterococcus* genus, *Neisseria* genus, *Staphylococcus* genus, *Streptococcus* genus or *Candida* genus,

a) wherein said one or more oligonucleotides for determining the presence, amount or both of one or more nucleic acids from a bacterial and/or fungal species anneal in an annealing step of an amplification reaction under conditions

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comprising 50 mM KCl, 10 mM Tris-HCl (pH 9.0) and 2.5 mM MgCl₂ at 45°C to at least 12 nucleotides of one and only one of nucleotide sequences:

SEQ ID NO: 26 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Enterococcus faecium*;

SEQ ID NO: 27 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Listeria monocytogenes*;

SEQ ID NO: 28 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Neisseria meningitidis*;

SEQ ID NO: 29 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Staphylococcus saprophyticus*;

SEQ ID NO: 30 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Streptococcus agalactiae*;
or

SEQ ID NO: 120 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Candida albicans*; or

b) wherein said one or more oligonucleotides for determining the presence and/or amount of one or more nucleic acids from a bacterial and/or fungal genus anneal in an annealing step of an amplification reaction under conditions comprising 50 mM KCl, 10 mM Tris-HCl (pH 9.0) and 2.5 mM MgCl₂ at 45°C to at least 12 nucleotides of one and only one of genus-specific nucleotide sequences:

SEQ ID NOs: 131 to 134 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Enterococcus* genus;

SEQ ID NO: 31 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Neisseria* genus;

SEQ ID NOs: 140 to 143 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Staphylococcus* genus;

SEQ ID NOs: 32 to 36 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Streptococcus* genus; or

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SEQ ID NOs: 120 to 124 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Candida* genus.

4. The method of claim 3, wherein the presence, amount or both of said one or more nucleic acids from a bacterial and/or fungal species and/or genus is determined using one or more oligonucleotides which anneal in an annealing step of an amplification reaction under conditions comprising 50 mM KCl, 10 mM Tris-HCl (pH 9.0) and 2.5 mM MgCl₂ at 45°C to a nucleotide sequence which is:

SEQ ID NOs: 1 and 2, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Enterococcus faecium*;

SEQ ID NOs: 3 and 4, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Listeria monocytogenes*;

SEQ ID NOs: 5 and 6, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Neisseria meningitidis*;

SEQ ID NOs: 7 and 8, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Staphylococcus saprophyticus*;

SEQ ID NOs: 9 and 10, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Streptococcus agalactiae*;

SEQ ID NOs: 11 and 12, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Candida albicans*;

SEQ ID NOs: 13 and 14, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from one or more members of the *Enterococcus* genus;

SEQ ID NOs: 15 and 16, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof, for determining the presence or

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amount of one or more nucleic acids from one or more members of the *Neisseria* genus;

SEQ ID NOs: 17 to 20, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from one or more members of the *Staphylococcus* genus; or

SEQ ID NO. 21 and 22, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from one or more members of the *Streptococcus* genus.

5. The method of any one of claims 1-4, further comprising using one or more oligonucleotides for determining the presence of a nucleic acid from one or more bacterial antibiotic resistance genes which is: *bla_{oxa}*, *blaZ*, *aac6'-IIa*, *vanB*, *vanC*, *ermA*, *ermB* or *ermC*, wherein said one or more oligonucleotides for determining the presence of a nucleic acid from one or more bacterial antibiotic resistance genes consist of at least 12 nucleotides in length and anneal in an annealing step of an amplification reaction under conditions comprising 50 mM KCl, 10 mM Tris-HCl (pH 9.0) and 2.5 mM MgCl₂ at 45°C to one or more of nucleotide sequences:

SEQ ID NO: 110 or a complementary sequence thereof for the detection of *bla_{oxa}*;

SEQ ID NO: 111 or a complementary sequence thereof for the detection of *blaZ*;

SEQ ID NO: 112 or a complementary sequence thereof for the detection of *aac6'-IIa*;

SEQ ID NO: 113 or a complementary sequence thereof for the detection of *ermA*;

SEQ ID NO: 114 or a complementary sequence thereof for the detection of *ermB*;

SEQ ID NO: 115 or a complementary sequence thereof for the detection of *ermC*;

SEQ ID NO: 116 or a complementary sequence thereof for the detection of *vanB*; or

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SEQ ID NO: 117 or a complementary sequence thereof for the detection of *vanC*.

6. The method of any one of claims 1-4, further comprising using one or more oligonucleotides for determining the presence of a nucleic acid from one or more bacterial antibiotic resistance genes which is: *bla_{tem}*, *bla_{shv}*, *bla_{rob}*, *bla_{oxa}*, *bla_Z*, *aadB*, *aacC1*, *aacC2*, *aacC3*, *aac6'-IIa*, *aacA4*, *aad(6')*, *vanA*, *vanB*, *vanC*, *msrA*, *satA*, *aac(6')-aph(2'')*, *vat*, *vga*, *ermA*, *ermB*, *ermC*, *mecA*, *int* or *sul*;

a) wherein said one or more oligonucleotides comprise a sequence which is:

SEQ ID NO: 37-40, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *bla_{tem}*;

SEQ ID NO: 41-44, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *bla_{shv}*;

SEQ ID NO: 45-48, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *bla_{rob}*;

SEQ ID NO: 49-50, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *bla_{oxa}*;

SEQ ID NO: 51-52, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *bla_Z*;

SEQ ID NO: 53-54, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *aadB*;

SEQ ID NO: 55-56, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *aacC1*;

SEQ ID NO: 57-58, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *aacC2*;

SEQ ID NO: 59-60, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *aacC3*;

SEQ ID NO: 61-64, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *aac6'-IIa*;

SEQ ID NO: 65-66, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *aacC4*;

SEQ ID NO: 67-70, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *vanA*;

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SEQ ID NO: 71-74, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *vanB*;

SEQ ID NO: 75-76, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *vanC*;

SEQ ID NO: 77-80, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *msrA*;

SEQ ID NO: 81-82, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *satA*;

SEQ ID NO: 83-86, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *aac(6')-aph(2'')*;

SEQ ID NO: 87-88, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *vat*;

SEQ ID NO: 89-90, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *vga*;

SEQ ID NO: 91-92, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *ermA*;

SEQ ID NO: 93-94, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *ermB*;

SEQ ID NO: 95-96, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *ermC*;

SEQ ID NO: 97-98, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *mecA*;

SEQ ID NO: 99-102, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *int*; or

SEQ ID NO: 103-106, parts thereof having at least 12 nucleotides in length or a complementary sequence thereof for the detection of *sul*; and

b) wherein said one or more oligonucleotides anneal in an annealing step of an amplification reaction to their target antibiotic resistance gene nucleic acid under conditions comprising 50 mM KCl, 10 mM Tris-HCl (pH 9.0) and 2.5 mM MgCl₂ at 45°C.

7. A method according to any one of claims 1-6, wherein the presence of bacterial and fungal nucleic acids is determined or detected simultaneously.

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8. The method according to any one of claims 1-7, which is performed directly from a test sample.

9. The method according to any one of claims 1-7, which is performed directly from a test sample consisting of:

- a) a bacterial culture or suspension;
- b) a fungal culture or suspension, or
- c) both a) and b).

10. The method according to any one of claims 1-9, wherein said nucleic acids are amplified by a method which is:

- a) polymerase chain reaction (PCR),
- b) ligase chain reaction (LCR),
- c) nucleic acid sequence-based amplification (NASBA),
- d) self-sustained sequence replication (3SR),
- e) strand displacement amplification (SDA),
- f) branched DNA signal amplification (bDNA),
- g) transcription-mediated amplification (TMA),
- h) cycling probe technology (CPT),
- i) nested PCR, or
- j) multiplex PCR.

11. The method of claim 10, wherein said nucleic acids are amplified by PCR.

12. The method of claim 11, wherein said PCR comprises an annealing step and a denaturing step but no time specifically allowed for an elongation step.

13. The method of any one of claims 1 to 7, comprising:

- a) i) depositing and fixing on an inert support or leaving in solution the bacterial or fungal DNA of the sample or of a substantially homogeneous population of bacteria or fungi isolated from this sample; or
- ii) inoculating said sample or said substantially homogeneous population of bacteria or fungi isolated from this sample on an inert support;

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b) lysing *in situ* said inoculated sample or isolated bacteria or fungi to release the bacterial or fungal DNA, said bacterial or fungal DNA being made in a substantially single-stranded form;

c) contacting said single-stranded DNA with a probe having at least 12 nucleotides in length and hybridizing under conditions comprising 1M NaCl, 10% dextran sulfate, 1% SDS and 100 µg/ml salmon sperm DNA at 65°C to:

i) each of the bacterial nucleotide sequences defined in the group consisting of SEQ ID NOs: 118, 119 and 125-171, or complementary sequences thereof; or

ii) each of the fungal nucleotide sequences defined in the group consisting of SEQ ID NOs: 120-124, or complementary sequences thereof;

so as to form a hybridization complex; and

d) detecting the presence of said hybridization complex on said inert support or in said solution as an indication of the presence, amount or both of bacterial or fungal nucleic acids in said sample.

14. The method of any of claims 1 to 7, comprising:

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 annealing in an annealing step of an amplification reaction under conditions comprising 50 mM KCl, 10 mM Tris-HCl (pH 9.0) and 2.5 mM MgCl₂ at 45°C with one of the two complementary strands of said microorganism DNA that contains a target sequence, and the other of said primers being capable of annealing 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 annealing under said conditions to:

i) each of the bacterial nucleotide sequences defined in the group consisting of SEQ ID NOs: 118, 119 and 125-171, or complementary sequences thereof; or

ii) each of the fungal nucleotide sequences defined in the group consisting of SEQ ID NOs: 120-124, or complementary sequences thereof; and

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

c) detecting the presence, amount or both of said amplified target sequence as an indication of the presence, amount or both of bacterium or fungus in said test sample.

15. The method of claim 14, wherein said pair of primers comprises a pair of nucleotide sequences which is SEQ ID NOs: 23 and 24; 107 and 108; or 109 and 172.

16. An oligonucleotide primer or probe consisting of 12 to 100 nucleotides in length and having the nucleotide sequence of any one of SEQ ID NOs: 23, 24, 107, 108, 109 or 172, part thereof having at least 12 nucleotides or a sequence complementary thereof, which anneals in an annealing step of an amplification reaction under conditions comprising 50 mM KCl, 10 mM Tris-HCl (pH 9.0) and 2.5 mM MgCl₂ at 45°C to:

a) each of the bacterial nucleotide sequences defined in the group consisting of SEQ ID NOs: 118, 119 and 125-171, or complementary sequences thereof; or

b) each of the fungal nucleotide sequences defined in the group consisting of SEQ ID NOs: 120-124, or complementary sequences thereof;

wherein said oligonucleotide primer or probe having the nucleotide sequence of any one of SEQ ID NOs: 23, 24, 107 and 108, part thereof having at least 12 nucleotides or a sequence complementary thereof, anneals to bacterial nucleotide sequences defined in a) and wherein said oligonucleotide primer or probe having the nucleotide sequence of any one of SEQ ID NOs: 109 and 172, part thereof having at least 12 nucleotides or a sequence complementary thereof anneals to fungal nucleotide sequences defined in b).

17. A recombinant plasmid comprising an oligonucleotide primer or probe as defined in claim 16.

18. A recombinant host cell which has been transformed by a recombinant plasmid according to claim 17.

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19. A recombinant host cell according to claim 18, wherein said host is *Escherichia coli*.

20. A diagnostic kit for the universal detection, quantification or both of nucleic acids of a bacterium, fungus or both, comprising any suitable combination of probes and/or primers consisting of 12 to 100 nucleotides in length and comprising a nucleotide sequence which is SEQ ID NOs: 23, 24, 107, 108, 109 or 172, part thereof having at least 12 nucleotides in length, or sequences complementary thereof, which anneals in an annealing step of an amplification reaction under conditions comprising 50 mM KCl, 10 mM Tris-HCl (pH 9.0) and 2.5 mM MgCl₂ at 45°C to:

a) each of the bacterial nucleotide sequences defined in the group consisting of SEQ ID NOs: 118, 119 and 125-171, or complementary sequences thereof for the detection, quantification or both of nucleic acids from bacteria; or

b) each of the fungal nucleotide sequences defined in the group consisting of SEQ ID NOs: 120-124, or complementary sequences thereof for the detection, quantification or both of nucleic acids from fungus;

wherein said oligonucleotide primers and/or probes comprising the nucleotide sequence which is SEQ ID NOs: 23, 24, 107 or 108, part thereof having at least 12 nucleotides, or a sequence complementary thereof, anneal to bacterial nucleotide sequences defined in a) and wherein said oligonucleotide primers and/or probes comprising the nucleotide sequence which is SEQ ID NOs: 109 or 172, part thereof having at least 12 nucleotides, or a sequence complementary thereof, anneal to fungal nucleotide sequences defined in b).

21. The diagnostic kit of claim 20, further comprising any suitable combination of probes and/or primers for the detection and/or quantification of the nucleic acids of any combination of bacterial resistance genes *bla_{oxa}*, *blaZ*, *aac6'-IIa*, *ermA*, *ermB*, *ermC*, or *vanC*, wherein said primers and/or probes are at least 12 nucleotides in length and anneal in an annealing step of an amplification reaction under conditions comprising 50 mM KCl, 10 mM Tris-HCl (pH 9.0) and 2.5 mM MgCl₂ at 45°C to one or more of nucleotide sequences:

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SEQ ID NO: 110 or a complementary sequence thereof for the detection of *bla_{oxa}*;

SEQ ID NO: 111 or a complementary sequence thereof for the detection of *bla_Z*;

SEQ ID NO: 112 or a complementary sequence thereof for the detection of *aac6'-IIa*;

SEQ ID NO: 113 or a complementary sequence thereof for the detection of *ermA*;

SEQ ID NO: 114 or a complementary sequence thereof for the detection of *ermB*;

SEQ ID NO: 115 or a complementary sequence thereof for the detection of *ermC*;

SEQ ID NO: 116 or a complementary sequence thereof for the detection of *vanB*; or

SEQ ID NO: 117 or a complementary sequence thereof for the detection of *vanC*.

22. The diagnostic kit of claim 20 or 21, further comprising any suitable combination of primers comprising a nucleotide sequence of any one of SEQ ID NOs: 1 to 22, parts thereof having at least 12 nucleotides in length, or sequences complementary thereof, for the detection and/or quantification of nucleic acids of bacterial and fungal species and/or genus of: *Enterococcus faecium*, *Listeria monocytogenes*, *Neisseria meningitidis*, *Staphylococcus saprophyticus*, *Streptococcus agalactiae*, *Candida albicans*, *Enterococcus* genus, *Neisseria* genus, *Staphylococcus* genus or *Streptococcus* genus.

23. The diagnostic kit of claim 20 or 21, further comprising any suitable combination of probes and/or primers consisting of 12 to 100 nucleotides in length for determining the presence, amount or both of one or more nucleic acids from a bacterial and/or fungal species and/or genus of: *Enterococcus faecium*, *Listeria monocytogenes*, *Neisseria meningitidis*, *Staphylococcus saprophyticus*, *Streptococcus agalactiae*, *Candida albicans*, *Enterococcus* genus, *Neisseria* genus, *Staphylococcus* genus, *Streptococcus* genus or *Candida* genus,

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a) wherein probes and/or primers for determining the presence, amount or both of one or more nucleic acids from a bacterial and/or fungal species anneal in an annealing step of an amplification reaction under conditions comprising 50 mM KCl, 10 mM Tris-HCl (pH 9.0) and 2.5 mM MgCl₂ at 45°C to at least 12 nucleotides of one and only one of nucleotide sequences:

SEQ ID NO: 26 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Enterococcus faecium*;

SEQ ID NO: 27 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Listeria monocytogenes*;

SEQ ID NO: 28 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Neisseria meningitidis*;

SEQ ID NO: 29 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Staphylococcus saprophyticus*;

SEQ ID NO: 30 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Streptococcus agalactiae*;
or

SEQ ID NO: 120 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Candida albicans*; or

b) wherein said probes and/or primers for determining the presence and/or amount of one or more nucleic acids from a bacterial and/or fungal genus anneal in an annealing step of an amplification reaction under conditions comprising 50 mM KCl, 10 mM Tris-HCl (pH 9.0) and 2.5 mM MgCl₂ at 45°C to at least 12 nucleotides of one and only one of genus-specific nucleotide sequences:

SEQ ID NOs: 131 to 134 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Enterococcus* genus;

SEQ ID NO: 31 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Neisseria* genus;

SEQ ID NOs: 140 to 143 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Staphylococcus* genus;

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SEQ ID NOs: 32 to 36 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Streptococcus* genus; or

SEQ ID NOs: 120 to 124 or a complementary sequence thereof, for determining the presence or amount of one or more nucleic acids from *Candida* genus.

24. The diagnostic kit of claim 22, further comprising any suitable combination of primers comprising a nucleotide sequence of SEQ ID NOs: 37 to 106, 173 or 174, parts thereof having at least 12 nucleotides in length, or sequences complementary thereof, for the simultaneous detection, quantification or both of nucleic acids of one or more bacterial antibiotic resistance genes which is: of *bla_{tem}*, *bla_{rob}*, *bla_{shv}*, *bla_{oxa}*, *bla_Z*, *aadB*, *aacC1*, *aacC2*, *aacC3*, *aacA4*, *aac6'-IIa*, *aad(6')*, *ermA*, *ermB*, *ermC*, *mecA*, *vanA*, *vanB*, *vanC*, *satA*, *aac(6')-aph(2'')*, *vat*, *vga*, *msrA*, *sul* or *int*.

25. The oligonucleotide of claim 16, wherein said oligonucleotide consists of 12 to 30 nucleotides in length.

26. The diagnostic kit of any one of claims 20 to 24, wherein said probes and/or primers are from 12 to 30 nucleotides in length.

27. The oligonucleotide of claim 16, wherein said oligonucleotide consists of 19 to 30 nucleotides in length.

28. The diagnostic kit of any one of claims 20 to 24, wherein said probes and/or primers are from 19 to 30 nucleotides in length.

29. The method of any one of claims 1 to 12, 14 and 15 comprising in step a) contacting said sample with at least one primer pair which is:

- a) SEQ ID NOs: 23 and 24;
- b) SEQ ID NOs: 107 and 108; or
- c) SEQ ID NOs: 109 and 172.

30. The diagnostic kit of any one of claims 20 to 24, comprising at least one primer pair which is:

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- a) SEQ ID NOs: 23 and 24;
- b) SEQ ID NOs: 107 and 108; or
- c) SEQ ID NOs: 109 and 172.

31. The method of any one of claims 1-12, 14 and 29, wherein multiplex amplification is used.