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(54) Titre : GENES FORTEMENT CONSERVES ET UTILISATION DE CES GENES POUR PRODUIRE DES SONDAS D'ACIDE NUCLEIQUE SPECIFIQUES A L'ESPECE, SPECIFIQUES AU GENRE, SPECIFIQUES A LA FAMILLE, SPECIFIQUES AU GROUPE ET UNIVERSELLES ET AMORCES D'AMPLIFICATION PERMETTANT DE DETECTER ET D'IDENTIFIER RAPIDEMENT LES PATHOGENES BACTERIENS, FONGIQUES ET PARASITIQUES D'APRES DES SPECIMENS

(54) Title: HIGHLY CONSERVED GENES AND THEIR USE TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC, FAMILY-SPECIFIC, GROUP-SPECIFIC AND UNIVERSAL NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY BACTERIAL, FUNGAL AND PARASITIC PATHOGENS FROM CLINICAL SPECIMENS FOR DIAGNOSIS



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TITLE OF THE INVENTION

**HIGHLY CONSERVED GENES AN THEIR USE TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC, FAMILY-SPECIFIC, GROUP-SPECIFIC AND
5 UNIVERSAL NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO
RAPIDLY DETECT AND IDENTIFY BACTERIAL, FUNGAL AND PARASITICAL
PATHOGENS FROM CLINICAL SPECIMENS FOR DIAGNOSIS**

BACKGROUND OF THE INVENTION

Classical methods for the identification of bacteria, fungi, and parasites

15 Bacteria and fungi 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
20 antibacterial susceptibility 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
25 the Vitek™ system from bioMérieux) which use 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
30 require the primary isolation of the bacteria or fungi as a pure culture, a process which takes at least 18 hours for a pure culture or 2 days for a mixed culture. So, the shortest time from sample reception to identification of the pathogen is around 24 hours. Moreover, fungi other than yeasts are often difficult or very slow to cultivate from clinical specimens. Identification must rely on labor-intensive techniques such
35 as direct microscopic examination of the specimens and by direct and/or indirect immunological assays. Cultivation of most parasites is impractical in the clinical laboratory. Hence, microscopic examination of the specimen, a few immunological tests and clinical symptoms are often the only methods used for an identification that frequently remains presumptive.

40 The fastest bacterial 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 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%.

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 main organisms associated with nosocomial and community-acquired human infections and are therefore considered the most clinically important.

15 *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

30 *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). In these normally sterile sites, a test for the universal detection of bacteria, fungi and

parasites would be very useful.

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 or fungal pathogens potentially associated with the infection are grown and separated from the colonizing microbes using selective methods 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 or family or group 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 specimen

There is an obvious need for rapid and accurate diagnostic tests for the detection and identification of bacteria, fungi and parasites 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.; Bergeron and Ouellette, 1995, Infection **23**:69-72; Bergeron and Ouellette, 1998, J Clin Microbiol. **36**:2169-72). The DNA probes and amplification primers which are objects of the present invention are applicable for the detection and identification of bacteria, fungi, and parasites directly from any clinical specimen such as blood cultures, blood, urine, sputum, cerebrospinal fluid, pus, genital and gastro-intestinal tracts, skin or any 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 can be performed in one hour or less, they provide the clinician with new diagnostic tools which should contribute to a better management of patients with infectious diseases. Specimens from sources other than humans (e.g. other primates, birds, plants, mammals, farm animals, livestock, food products, environment such as water or soil, 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 normally sterile 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 or family or group 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 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 any bacterium would give a positive amplification signal with this assay. Similarly, highly conserved genes of fungi and parasites could serve not only to identify particular species or genus or family or group but also to detect the presence of any fungi or parasite in the specimen.

10 ***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 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 microbial identification than currently used phenotypic identification systems which are based on biochemical tests and/or microscopic examination. 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 for example: *Staphylococcus* sp. (US patent serial no. 5,437,978), *Neisseria* sp. (US patent serial no. 5,162,199 and European patent serial no. 0,337,896,131) and *Listeria monocytogenes* (US patent serial 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. To our knowledge there are only three patents published by others mentioning the use of any of the three targets described in the present invention for diagnostic purposes (PCT

international publication number WO92/03455, European patent publication number 0 133 671 B1, and European patent publication number 0 133 288 A2). WO92/03455 is focused on the inhibition of *Candida* species for therapeutic purposes. It describes antisense oligonucleotide probes hybridizing to *Candida* messenger RNA. Two of the numerous mRNA proposed as target are coding for translation elongation factor 1 (tef1) and the beta subunit of ATPase. DNA amplification or hybridization are not under the scope of their invention and although diagnostic use is briefly mentioned in the body of the application, no specific claim is made regarding diagnostics. In the main body of the text, EP 0 133 671 B1 describes the use of bacterial *tuf* sequence for diagnostics based on hybridization with bacterial RNA. To hybridize RNA, an oligonucleotide probe must be antisense. DNA amplification techniques require the use of both sense and antisense primers. Hence, claim number one from EP 0 133 671 B1 precludes PCR or other DNA-based amplification techniques. Furthermore, EP 0 133 671 B1 makes no specific claim on the use of *tuf* sequences for diagnostics; only ribosomal RNA sequences are claimed. Patent EP 0 133 288 A2 describes and claims the use of bacterial *tuf* sequence for diagnostics based on hybridization of a *tuf* probe with bacterial DNA. DNA amplification is not in the scope of EP 0 133 288 A2. Nowhere it is mentioned that multiple *tuf* probes could be used simultaneously. The sensitivity of the *tuf* hybridizations reported are, at 1×10^6 bacteria or 1-100 ng of DNA, much lower than those achievable by nucleic acid amplification technologies.

Although there are phenotypic identification methods which have been used for more than 125 years in clinical microbiology laboratories, these methods do not provide information fast enough to be useful in the initial management of patients. There is a need to increase the speed of the diagnosis of commonly encountered bacterial, fungal and parasitical infections. Besides being much faster, DNA-based diagnostic tests are more accurate than standard biochemical tests presently used for diagnosis because the microbial genotype (e.g. DNA level) is more stable than the phenotype (e.g. physiologic level).

Knowledge of the genomic sequences of bacterial, fungal and parasitical species continuously increases as testified by the number of sequences available from public databases such as GenBank. From the sequences readily available from those public 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, fungal and parasitical pathogens, (ii) the genus-specific detection and identification of commonly encountered bacterial, fungal or parasitical pathogens, (iii) the family-specific detection and identification of commonly encountered bacterial, fungal or parasitical pathogens, (iv) the group-specific detection and identification of commonly encountered bacterial, fungal or parasitical pathogens, (v) the universal detection of bacterial,

fungal or parasitical pathogens, and/or (vi) the specific detection and identification of antibiotic resistance genes, and/or (vii) the specific detection and identification of bacterial toxin 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.

5 In our co-pending U.S. patent 6,001,564 and WO98/20157 patent application, we described DNA sequences suitable for (i) the species-specific detection and identification of clinically important bacterial pathogens, (ii) the universal detection of bacteria, and (iii) the detection of antibiotic resistance genes.

10 The latter co-pending application described proprietary *tuf* DNA sequences as well as *tuf* sequences selected from public 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 that patent application can enter in the composition of diagnostic kits or product and methods capable of a) detecting the presence of bacteria, fungi and parasites b) detecting
15 specifically at the species, genus, family or group levels, the presence of bacteria, fungi and parasites and antibiotic resistance genes associated with these pathogens. 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 associated antibiotic resistance genes and toxins genes. For example, infections caused by
20 *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. 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
25 target genes and complement our earlier patent applications.

The present invention improves the co-pending application by disclosing new proprietary *tuf* sequences as well as describing new ways to obtain *tuf* sequences. In addition we disclose new proprietary *atpD* and *recA* sequences. In addition, new uses of *tuf*, *atpD* and *recA* DNA sequences selected from public databases (Table 11) are
30 disclosed.

Highly conserved genes for identification and diagnostics

Highly conserved genes are useful for identification of microorganisms. For
35 bacteria, the most studied genes for identification of microorganisms are the universally conserved ribosomal RNA genes (rRNA). Among those, the principal targets used for identification purposes are the small subunit (SSU) ribosomal 16S rRNA genes (in prokaryotes) and 18S rRNA genes (in eukaryotes) (Relman and Persing, Genotyping Methods for Microbial Identification, *In*: D.H. Persing, 1996, PCR Protocols for Emerging Infectious Diseases, ASM Press, Washington D.C.). The
40 rRNA genes are also the most commonly used targets for universal identification of bacteria (Chen *et al.*, 1988, FEMS Microbiol. Lett. **57**:19-24; McCabe *et al.*, 1999, Mol. Genet. Metabol. **66**:205-211) and fungi (Van Burik *et al.*, 1998, J. Clin. Microbiol. **36**:1169-1175).

However, it may be difficult to discriminate between closely related species when using primers derived from the 16S rRNA. In some instances, 16S rRNA sequence identity may not be sufficient to guarantee species identity (Fox *et al.*, 1992, Int. J. Syst. Bacteriol. **42**:166-170) and it has been shown that inter-operon sequence variation as well as strain to strain variation could undermine the application of 16S rRNA for identification purposes (Clayton *et al.*, 1995, Int. J. Syst. Bacteriol. **45**:595-599).

STATEMENT OF THE INVENTION

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 any bacterial, fungal or parasitical species in any sample suspected of containing said nucleic acids, and optionally,
- from specific microbial species or genera selected from the group consisting of the species or genera listed in Table 4
- from an antibiotic resistance gene selected from the group consisting of the genes listed in Table 5, and optionally,
- from a toxin gene selected from the group consisting of the genes listed in Table 6,

wherein each of said nucleic acids or a variant or part thereof comprises a 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 microbial species, specific microbial species or genus or family or group and antibiotic resistance gene and/or toxin gene.

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

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

In another particularly preferred embodiment, oligonucleotides primers and probes of at least 12 nucleotides in length are designed for their specificity and ubiquity based upon analysis of our databases of *tuf*, *atpD* and *recA* sequences. These databases are generated using both proprietary and public sequence information. Altogether, these databases form a sequence repertory useful for the design of primers and probes for the detection and identification of bacterial, fungal and parasitical microorganisms. The repertory can also be subdivided into subrepertories for analysis leading to the design of primers and probes.

The *tuf*, *atpD* and *recA* sequences databases as a product to assist the design of oligonucleotides primers and probes for the detection and identification of bacterial, fungal and parasitical microorganisms are also an object of this invention.

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 or family or group selected from the following list consisting of *Bordetella* sp., *Candida albicans*, *Candida dubliniensis*, *Candida* sp., *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium* sp., *Corynebacterium* sp., *Cryptosporidium parvum*, *Entamoeba* sp., *Enterobacteriaceae* group, *Enterococcus casseliflavus-flavescens-gallinarum* group, *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus gallinarum*, *Enterococcus* sp., *Escherichia coli*, *Giardia* sp., *Haemophilus influenzae*, *Trypanosomatidae* family, *Leishmania* sp., *Mycobacteriaceae* family, *Neisseria gonorrhoeae*, platelets contaminants group (see Table 14), *Pseudomonads* group, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus saprophyticus*, *Staphylococcus* sp., *Streptococcus agalactiae*, *Streptococcus* sp., *Trypanosoma brucei*, *Trypanosoma cruzi*, *Trypanosoma* sp., 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 listed in Table 5 are also objects of this invention.

Diagnostic kits further comprising probes or amplification primers for the detection of a toxin gene selected from the group listed in Table 6 are also objects of this invention.

Diagnostic kits further comprising probes or amplification primers for the detection of any bacterial, fungal or parasitical species, comprising or not comprising those for the detection of the specific microbial species or genus or family or group listed above, and further comprising or not comprising probes and primers for the antibiotic resistance genes listed above, and further comprising or not comprising

probes and primers for the toxin 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 or family or group, antibiotic resistance genes, toxin genes and for the
5 detection of any microorganism (bacteria, fungi or parasite).

In the above methods and kits, amplification reactions may include but are not restricted to: 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
10 signal amplification (bDNA), g) transcription-mediated amplification (TMA), h) cycling probe technology (CPT), i) nested PCR, j) multiplex PCR, k) solid phase amplification (SPA), l) nuclease dependent signal amplification (NDSA), m) rolling circle amplification technology (RCAT).

In the above methods and kits, detection of the nucleic acids of target genes
15 may include real-time or post-amplification technologies. These detection technologies can include, but are not limited to, fluorescence resonance energy transfer (FRET)-based methods such as adjacent hybridization to FRET probes (including probe-probe and probe-primer methods), Taqman, molecular beacons and Scorpions. Other detection methods include target genes nucleic acids detection via
20 immunological methods, solid phase hybridization methods on filters, chips or any other solid support, whether the hybridization is monitored by fluorescence, chemiluminescence, potentiometry, mass spectrometry, plasmon resonance, polarimetry, or colorimetry. Sequencing, including sequencing by dideoxy termination or sequencing by hybridization, is another possible method to detect and
25 identify the nucleic acids of target genes.

In a preferred embodiment, a PCR protocol is used for nucleic acid amplification.

In a particularly preferred embodiment, a PCR protocol is provided, comprising, an initial denaturation step of 1-3 minutes at 95 °C, followed by an
30 amplification cycle including a denaturation step of one second at 95 °C and an annealing step of 30 seconds at 45-65 °C, without any time allowed specifically for the elongation step. This PCR protocol has been standardized to be suitable for PCR reactions with most selected primer pairs, which greatly facilitates the testing because each clinical sample can be tested with universal, species-specific, genus-specific,
35 antibiotic resistance gene and toxin gene PCR primers under uniform cycling conditions. Furthermore, various combinations of primer pairs may be used in multiplex PCR assays.

It is also an object of the present invention that *tuf* sequences, *atpD* sequences and *recA* sequences could serve as drug targets and these sequences and means to
40 obtain them revealed in the present invention can assist the screening, design and modeling of these drugs.

It is also an object of the present invention that *tuf* sequences, *atpD* sequences and *recA* sequences could serve for vaccine purposes and these sequences and means to obtain them revealed in the present invention can assist the screening, design and modeling of these vaccines.

5

We aim at developing a rapid test or kit (universal) to discard rapidly all the samples which are negative for bacterial, fungal or parasitical cells. This test could be used alone or combined with more specific identification to detect and identify the above bacterial and/or fungal and/or parasitical species and genera and to determine rapidly the bacterial resistance to antibiotics and/or presence of bacterial toxins. Although the sequences from the selected antibiotic resistance genes are available from public 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 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.

The diagnostic kits, primers and probes mentioned above can be used to identify bacteria, fungi, parasites, antibiotic resistance genes and toxin genes on any type of sample, whether said diagnostic kits, primers and probes are used for *in vitro* or *in situ* applications. The said samples may include but are not limited to: any clinical sample, any environment sample, any microbial culture, any microbial colony, any tissue, and any cell line.

It is also an object of the present invention that said diagnostic kits, primers and probes can be used alone or in conjunction with any other assay suitable to identify microorganisms, including but not limited to: any immunoassay, any enzymatic assay, any biochemical assay, any lysotypic assay, any serological assay, any differential culture medium, any enrichment culture medium, any selective culture medium, any specific assay medium, any identification culture medium, any enumeration culture medium, any cellular stain, any culture on specific cell lines, and any infectivity assay on animals.

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 public databases. DNA fragments selected from public databases are newly used in a method of detection according to the present invention, since they have been selected for their diagnostic potential.

In another embodiment, the amino acid sequences translated from the repertory of *tuf*, *atpD* and *recA* sequences are also an object of the present invention.

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 or family or group, and (iii) the detection of antibiotic resistance genes, and (iv) the detection of toxin genes other than those listed in Annexes I to III and XXI may also be derived from the proprietary fragments or selected public databases 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 public 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, resistance gene-specific, toxin 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 Annexes I to III and XXI which are suitable for diagnostic purposes. When a proprietary fragment or a public databases 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 public databases sequences. The amplification primers were selected from genes highly conserved in bacteria, fungi and parasites, and are used to detect the presence of any bacterial or fungal or parasitical pathogen in clinical specimens in order to determine rapidly (less than one hour) whether it is positive or negative for bacteria, fungi or parasites. The selected genes, designated *tuf*, *atpD* and *recA*, encode respectively 2 proteins (elongation factors Tu and G) involved in the translational process during protein synthesis, a protein (beta subunit) responsible for the catalytic activity of

proton pump ATPase and a protein responsible for the homologous recombination of genetic material. The alignments of *tuf*, *atpD* and *recA* sequences used to derive the universal primers include both proprietary and public databases sequences. The universal primer strategy allows the rapid screening of the numerous negative clinical specimens (around 80% of the specimens received, see Table 3) submitted for bacteriological testing.

Table 4 provides a list of the bacterial, fungal and parasitical species for which *tuf* and/or *atpD* and/or *recA* sequences are revealed in the present invention. Tables 5 and 6 provide a list of antibiotics resistance genes and toxin genes selected for diagnostic purposes. Table 7 provides the origin of *tuf*, *atpD* and *recA* sequences listed in the sequence listing. Tables 8-10 provide lists of species used to test specificity and ubiquity of some assays described in examples.

DETAILED DESCRIPTION OF THE INVENTION

HIGHLY CONSERVED GENES AND THEIR USE TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC, FAMILY-SPECIFIC, GROUP-SPECIFIC AND UNIVERSAL NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY BACTERIAL, FUNGAL AND PARASITICAL PATHOGENS FROM CLINICAL SPECIMENS FOR DIAGNOSIS

10 The present inventors compared the published *Haemophilus influenzae* and *Mycoplasma genitalium* genomes and searched for the most conserved genes, which would then serve, as paradigm to develop primers and probes. This sequence comparison is highly informative as these two bacteria are distantly related and most genes present in the minimal genome of *M. genitalium* are likely to be present in every bacterium. Therefore genes conserved between these two bacteria are likely to be conserved in all other bacteria.

15 Following the genomic comparison, it was found that several protein-coding genes were conserved in evolution. Highly conserved proteins included the translation elongation factor Tu (EF-Tu) and the β subunit of F₀F₁ type ATP-synthase, and to a lesser extent, the RecA recombinase.

20 Translation elongation factor Tu is a member of a family of GTP-binding proteins which intervene in the interactions of tRNA molecules with the ribosome machinery during essential steps of protein synthesis. The role of elongation factor Tu is to facilitate the binding of aminoacylated tRNA molecules to the A site of the ribosome. The eukaryotic and archaeobacterial homolog of EF-Tu is called elongation factor 1 alpha (EF-1 α). All protein synthesis factors originated from a common ancestor via gene duplications and fusions (Cousineau *et al.*, 1997, J. Mol. Evol. **45**:661-670). In particular, elongation factor G (EF-G), although having a functional role in promoting the translocation of aminoacyl-tRNA molecules from the A site to the P site of the ribosome, shares sequence homologies with EF-Tu and is thought to have arisen from the duplication and fusion of an ancestor of the EF-Tu gene.

30 In addition, EF-Tu is known to be the target for antibiotics belonging to the elfamycin's group as well as to other structural classes (Anborgh and Parmeggiani, 1991, EMBO J. **10**:779-784; Luiten *et al.*, 1992, European patent application serial No. EP 0 466 251 A1). EF-G for its part, is the target of the antibiotic fusidic acid. In addition to its crucial activities in translation, EF-Tu has chaperone-like functions in protein folding, protection against heat denaturation of proteins and interactions with unfolded proteins (Caldas *et al.*, 1998, J. Biol. Chem. **273**:11478-11482). Interestingly, a form of the EF-Tu protein has been identified as a dominant component of the periplasm of *Neisseria gonorrhoeae* (Porcella *et al.*, 1996, Microbiology **142**:2481-2489), hence suggesting that at least in some bacterial species, EF-Tu might be an antigen with vaccine potential.

40 F₀F₁ type ATP-synthase belongs to a superfamily of proton-translocating ATPases divided in three major families: P, V and F (Nelson and Taiz,

1989, TIBS **14**:113-116). P-ATPases (or E₁-E₂ type) operate via a phosphorylated intermediate and are not evolutionarily related to the other two families. V-ATPases (or V₀V₁ type) are present on the vacuolar and other endomembranes of eukaryotes, on the plasma membrane of archaeobacteria and also on the plasma membrane of some eubacteria especially species belonging to the order *Spirochaetales* as well as to the *Chlamydiaceae* and *Deinococcaceae* families. F-ATPases (or F₀F₁ type) are found on the plasma membrane of most eubacteria, on the inner membrane of mitochondria and on the thylakoid membrane of chloroplasts. They function mainly in ATP synthesis. They are large multimeric enzymes sharing numerous structural and functional features with the V-ATPases. F and V-type ATPases have diverged from a common ancestor in an event preceding the appearance of eukaryotes. The β subunit of the F-ATPases is the catalytic subunit and it possesses low but significant sequence homologies with the catalytic A subunit of V-ATPases.

The translation elongation factors EF-Tu, EF-G and EF-1 α , and the catalytic subunit of F or V-types ATP-synthase, are highly conserved proteins sometimes used for phylogenetic analysis and their genes are also known to be highly conserved (Iwabe *et al.*, 1989, Proc. Natl. Acad. Sci. USA **86**:9355-9359, Gogarten *et al.*, 1989, Proc. Natl. Acad. Sci. USA **86**:6661-6665, Ludwig *et al.*, 1993, Antonie van Leeuwenhoek **64**:285-305). A recent BLAST (Altschul *et al.*, 1997, J. Mol. Biol. **215**:403-410) search performed by the present inventors on the GenBank, EMBL, DDBJ and specific genome project databases indicated that throughout bacteria, the EF-Tu and the β subunit of F₀F₁ type ATP-synthase genes may be more conserved than other genes that are well conserved between *H. influenzae* and *M. genitalium*.

The RecA recombinase is a multifunctional protein encoded by the *recA* gene. It plays a central role in homologous recombination, it is critical for the repair of DNA damage and it is involved in the regulation of the SOS system by promoting the proteolytic digestion the LexA repressor. It is highly conserved in bacteria and could serve as a useful genetic marker to reconstruct bacterial phylogeny (Miller and Kokjohn, 1990, Annu. Rev. Microbiol. **44**:365-394). Although *recA* possesses some highly conserved sequence segments that we used to design universal primers aimed at sequencing the *recA* fragments, it is clearly not as well conserved as *tuf* and *atpD*. Hence, *recA* may not be optimal for universal detection of bacteria with high sensitivity but it was chosen because preliminary data indicated that *tuf* and *atpD* may sometimes be too closely related to find specific primer pairs that could discriminate between certain very closely related species and genera. While RecA, like *tuf* and *atpD*, possesses highly conserved regions suitable for the design of universal sequencing primers, the less conserved region between primers should be divergent enough to allow species-specific and genus-specific primers in those cases.

Thus, as targets to design primers and probes for the genetic detection of microorganisms, the present inventors have focused on the genes encoding these three proteins: *tuf*, the gene for elongation factor Tu; *atpD*, the gene for β subunit of F₀F₁ type ATP-synthase; and *recA*, the gene encoding the RecA recombinase. In several bacterial genomes *tuf* is often found in two highly similar duplicated copies named *tufA* and *tufB* (Filer and Furano, 1981, J. Bacteriol. **148**:1006-1011, Sela *et al.*,

1989, J. Bacteriol. **171**:581-584). In some particular cases, more divergent copies of the *tuf* genes can exist in some bacterial species such as some Actinomycetes (Luiten *et al.* European patent application publication No. EP 0 446 251 A1; Vijgenboom *et al.*, 1994, Microbiology **140**:983-998) and, as revealed as part of this invention, in several enterococcal species. In several bacterial species, *tuf* is organized in an operon with its homolog gene for the elongation factor G (EF-G) encoded by the *fusA* gene. This operon is often named the *str* operon. The *tuf*, *atpD* and *recA* genes were chosen as they are well conserved in evolution and have highly conserved stretches as well as more variable segments. Moreover, these three genes have eukaryotic orthologs which are described in the present invention as targets to identify fungi and parasites. The eukaryotic homolog of elongation factor Tu is called elongation factor 1-alpha (EF-1 α) (gene name: *tef*, *tef1*, *ef1*, *ef-1* or *EF-1*). In fungi, the gene for EF-1 α occurs sometimes in two or more highly similar duplicated copies (often named *tef1*, *tef2*, *tef3*...). In addition, eukaryotes have a copy of elongation factor Tu which is originating from their organelle genome ancestry (gene name: *tuf1*, *tufM* or *tufA*). For the purpose of the current invention, the genes for these four functionally and evolutionarily linked elongation factors (bacterial EF-Tu and EF-G, eukaryotic EF-1 α , and organellar EF-Tu) will hereafter be designated as «*tuf* sequences». The eukaryotic (mitochondrial) F₀F₁ type ATP-synthase beta subunit gene is named *atp2* in yeast. For the purpose of the current invention, the genes of catalytic subunit of either F or V-type ATP-synthase will hereafter be designated as «*atpD* sequences». The eukaryotic homologs of RecA are distributed in two families, typified by the Rad51 and Dmc1 proteins. For the purpose of the current invention, the genes corresponding to the latter proteins will hereafter be designated as «*recA* sequences».

Analysis of multiple sequence alignments of *tuf* and *atpD* sequences permitted the design of oligonucleotide primers (and probes) capable of amplifying (or hybridizing to) segments of *tuf* and *atpD* genes from a wide variety of bacterial species (see Examples 1 to 4 and Table 7). Sequencing primer pairs for *tuf* sequences are listed in Annex I and hybridization probes are listed in Annex III. Sequencing primer pairs for *atpD* sequences are listed in Annex II. Analysis of the main subdivisions of *tuf* and *atpD* sequences (see Figures 1 and 2) permitted to design sequencing primers amplifying specifically each of these subdivisions. It should be noted that these sequencing primers could also be used as universal primers. However, since some of these sequencing primers include several variable sequence (degenerated) positions, their sensitivity could be lower than that of universal primers developed for diagnostic purposes. Further subdivisions could be done on the basis of the various phyla where these genes are encountered.

Similarly, analysis of multiple sequence alignments of *recA* sequences present in the public databases permitted the design of oligonucleotide primers capable of amplifying segments of *recA* genes from a wide variety of bacterial species. Sequencing primer pairs for *recA* sequences are listed in Annex XXI. The main subdivisions of *recA* sequences comprise *recA*, *rad51* and *dmc1*. Further subdivisions could be done on the basis of the various phyla where these genes are encountered.

The present inventor's strategy is to get as much sequence data information from the three conserved genes (*tuf*, *atpD* and *recA*). This ensemble of sequence data forming a repertory (with subrepertories corresponding to each target gene and their main sequence subdivisions) and then using the sequence information of the sequence repertory (or subrepertories) to design primer pairs that could permit either universal detection of bacteria or fungi or parasites, detection of a family or group of microorganism (e.g. *Enterobacteriaceae*), detection of a genus (e.g. *Streptococcus*) or finally a specific species (e.g. *Staphylococcus aureus*). It should be noted that for the purpose of the present invention a group of microorganisms is defined depending on the needs of the particular diagnostic test. It does not need to respect a particular taxonomical grouping or phylum. See example 12 where primers were designed to amplify a group a bacteria consisting of the 17 major bacterial species encountered as contaminants of platelet concentrates. Also remark that in that example, the primers' specificity is not perfect since the objective of that particular test is to be able to sensitively and rapidly detect at least the 17 important bacterial species, but the primers could also detect other species as well, as shown in Table 14. In these circumstances the primers shown in example 12 are considered universal for platelet-contaminating bacteria. To develop an assay specific for the latter, one or more primers or probes specific to each species could be designed. Another example of primers and/or probes for group detection is given by the Pseudomonad group primers. These primers were designed based upon alignment of *tuf* sequences from real *Pseudomonas* species as well as from former *Pseudomonas* species such as *Stenotrophomonas maltophilia*. The resulting primers are able to amplify all *Pseudomonas* species tested as well as several species belonging to different genera, hence as being specific for a group including *Pseudomonas* and other species, we defined that group as Pseudomonads as several members were former *Pseudomonas*.

For certain applications, it may be possible to develop a universal, group, family or genus-specific reaction and to proceed to species identification using sequence information within the amplicon to design species-specific internal probes or primers, or alternatively, to proceed directly by sequencing the amplicon. The various strategies will be discussed further below.

The ensembles formed by public and proprietary *tuf*, *atpD* and *recA* sequences are used in a novel fashion so they constitute three databases containing useful information for the identification of microorganisms.

Oligonucleotide primers and probes design and synthesis

The *tuf*, *atpD* and *recA* DNA fragments sequenced by us or selected from public databases (GenBank and EMBL) were used to design oligonucleotides primers and probes for diagnostic purposes. We also relied on the corresponding peptide sequence of *tuf*, *atpD* and *recA* sequences to facilitate the identification of regions suitable for primers and probes design. As part of the design rules, 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™ 5.0). The potential suitability of the PCR primer pairs was also evaluated prior to the synthesis by
 5 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.). Oligonucleotide probes and amplification primers were synthesized using an automated DNA synthesizer (Perkin-Elmer Corp.,
 10 Applied Biosystems Division).

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
 15 the DNA sequences from proprietary fragments or from selected database sequences which are suitable for (i) the universal detection of bacteria or fungi or parasites, (ii) the species-specific detection and identification of any microorganism, including but not limited to: *Candida albicans*, *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Cryptosporidium parvum*, *Enterococcus faecalis*,
 20 *Enterococcus faecium*, *Enterococcus gallinarum*, *Escherichia coli*, *Haemophilus influenzae*, *Neisseria gonorrhoeae*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus saprophyticus*, *Streptococcus agalactiae*, *Trypanosoma brucei*, *Trypanosoma cruzi*,
 25 (iii) the genus-specific detection of *Bordetella* species, *Candida* species, *Clostridium* species, *Corynebacterium* species, *Entamoeba* species, *Enterococcus* species, *Giardia* species, *Leishmania* species, *Staphylococcus* species, *Streptococcus* species, *Trypanosoma* species, (iv) the family-specific detection of *Enterobacteriaceae* family members, *Mycobacteriaceae* family members, (v) the detection of *Enterococcus casseliflavus-flavescens-gallinarum* group, *Trypanosomatidae* family, Pseudomonads
 30 extended group, Platelet-contaminating bacteria group, or (vi) the detection of clinically important antibiotic resistance genes listed in Table 5, or (vii) the detection of clinically important toxin genes listed in Table 6.

Variants for a given target bacterial gene are naturally occurring and are attributable to sequence variation within that gene during evolution (Watson *et al.*,
 35 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
 40 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 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
 5 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 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
 10 invention. Variants of the selected primers or probes may also be used to amplify or hybridize to a variant DNA.

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

15 The nucleotide sequence of a portion of *tuf* sequences was determined for a variety of bacterial, fungal and parasitical species. The amplification primers (SEQ ID NOs. 107 and 108 in previous patent application WO98/20157), which amplify a *tuf* gene portion of approximately 890 bp, were used along with newly designed
 20 sequencing primer pairs (See Annex I for the sequencing primers for *tuf* sequences). Most primer pairs can amplify different copies of *tuf* genes (*tufA* and *tufB*). This is not surprising since it is known that for several bacterial species 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*:
 25 Cellular and Molecular Biology, 2nd ed., American Society for Microbiology Press, Washington, D.C.). Similarly, some fungi are known to have two nearly identical copies of *tuf* sequences (EF-1 α). 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
 30 primers is similar to that illustrated in Annex I for the selection of universal primers. The *tuf* sequencing primers even sometimes amplified highly divergent copies of *tuf* genes (*tufC*) as illustrated in the case of some enterococcal species (SEQ ID NOs.: 73, 75, 76, 614 to 618, 621 and 987 to 989). To prove this we first had to clone PCR products before being able to sequence them. Using the cloned sequence data we
 35 designed a new pair of sequencing primers specific to the divergent (*tufC*) copy of enterococci (SEQ ID NOs.: 658-659 and 661) and then sequenced directly the *tufC* amplicons. The amplification primers (SEQ ID NOs.: 543, 556, 557, 660, 664, 694, 696 and 697) could be used to amplify the *tuf* sequences from any bacterial species. The amplification primers (SEQ ID NOs.: 558, 559, 560, 653, 654, 655, 813 and 815)
 40 could be used to amplify the *tuf* (EF-1 α) genes from any fungal and parasitical

species. The amplification primers SEQ ID NOs. 1221-1228 could be used to amplify bacterial *tuf* sequences of the EF-G subdivision (*fusA*) (Figure 3). The amplification primer SEQ ID NOs 1224, and 1227-1229 could be used to amplify bacterial *tuf* sequences comprising the end of EF-G (*fusA*) and the beginning of EF-Tu (*tuf*), as shown in Figure 3.

The *tuf* fragments to be sequenced were amplified using the following amplification protocol: One μ l of cell suspension (or of purified genomic DNA 0.1-0.5 ng/ μ l) was transferred directly to 19 μ l of a PCR reaction mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-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 PTC-200 thermal cycler (MJ Research Inc., Watertown, Mass.) as follows: 3 min at 96 °C followed by 30-45 cycles of 1 min at 95 °C for the denaturation step, 1 min at 50-55 °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 amplicon 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 was excised from the agarose gel and purified using the QIAquick™ 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 377) with their Big Dye™ Terminator Cycle Sequencing Ready Reaction Kit (Perkin-Elmer Corp., Applied Biosystems Division, Foster City, CA). The sequencing reactions were performed by using the same amplification primers and 10 ng/100 bp of the gel-purified amplicon per reaction. For the sequencing of long amplicons such as those of eukaryotic *tuf* (EF-1 α) sequences, we designed internal sequencing primers (SEQ ID NOs.: 654, 655 and 813) to be able to obtain sequence data on both strands for most of the fragment length. 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 most target microbial species, the sequences determined for both amplicon preparations were identical. In case of discrepancies, a third independent PCR amplification was sequenced. 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 described in the Sequence Listing. Table 7 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. In addition, in
 5 several fungi introns were observed. Intron sequences are part of *tuf* sequences and could be useful in the design of species-specific primers and probes. This explains why the size of the sequenced *tuf* amplification products was variable from one species to another. Consequently, the nucleotide positions indicated on top of each of Annexes IV to XXI, XXIII to XXXI, XXXVIII and XLII do not correspond for
 10 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 (or copies of the EF-G subdivision of *tuf* sequences, or copies of EF-1 α subdivision of *tuf* sequences for fungi and
 15 parasites) because the amplification primers amplify both *tuf* genes. These nucleotide variations were not attributable to nucleotide misincorporations by the *Taq* DNA polymerase because the sequence of both strands was 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 public databases were used to select PCR primers for (i) the universal detection of bacteria, (ii) the genus-specific
 25 detection and identification of *Enterococcus* sp. and *Staphylococcus* sp. 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 and Annexes.

Sequencing of *atpD* and *recA* sequences from a variety of bacterial, fungal and parasitical species

The method use to obtain *atpD* and *recA* sequences is similar to that described
 35 above for *tuf* sequences.

The selection of amplification primers from *atpD* or *recA*

The comparison of the nucleotide sequence for the *atpD* or *recA* genes from

various bacterial fungal and parasitical species allowed the selection of PCR primers (refer to Examples 1, 2 and 6 and Annexes IV, V, X, XX, XXI).

DNA amplification

5

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™ 5.0 software to verify that they were good candidates for PCR amplification.

10 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
15 Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.).

Briefly, the PCR protocols were as follows: Treated clinical specimens or standardized bacterial or fungal or parasitical suspensions (see below) or purified genomic DNA from bacteria, fungi or parasites were amplified in a 20 µl PCR
20 reaction mixture. Each PCR reaction contained 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
25 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. For amplification
30 from bacterial or fungal cultures or from purified genomic DNA, the samples were added directly to the PCR amplification mixture without any pre-treatment step. An internal control was derived from sequences not found in the target 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
35 PCR inhibition was absent. Alternatively, an internal control derived from rRNA was also useful to monitor the efficiency of microbial 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 seconds at 50-65 °C for the annealing-extension step) using a PTC-200 thermal cycler (MJ Research
40 Inc.). 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.

5 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 or parasitical 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.

10 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), cycling probe technology (CPT), solid
15 phase amplification (SPA), rolling circle amplification technology (RCAT), and nuclease dependent signal amplification (NDSA) (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
20 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 nucleic acid-based tests. The scope of the present invention also covers the use of any nucleic acids amplification and detection technology including real-time or post-amplification detection
25 technologies, any amplification technology combined with detection, any hybridization nucleic acid chips or arrays technologies, any amplification chips or combination of amplification and hybridization chips technologies. Detection and identification by any sequencing method is also under the scope of the present invention.

30 Any oligonucleotide suitable for the amplification of nucleic acids by approaches other than PCR or for DNA hybridization and derived from the species-specific, genus-specific and universal DNA fragments as well as from selected antibiotic resistance or toxin gene sequences included in this document are also under the scope of this invention.

35

Detection of amplification products

Classically, detection of amplification is performed by standard ethidium bromide-stained agarose gel electrophoresis. It is clear that other methods for the
40 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 or during amplification. One simple method for monitoring

amplified DNA is to measure its rate of formation by measuring the increase in fluorescence of intercalating agents such as ethidium bromide or SYBR[®] Green I. If more specific detection is required, fluorescence-based technologies can monitor the appearance of a specific product during the reaction. The use of dual-labeled fluorogenic probes such as in the TaqMan[™] system which utilizes the 5'-3' exonuclease activity of the *Taq* polymerase is a good example (Livak K.J. *et al.* 1995, PCR Methods Appl. 4:357-362). TaqMan[™] can be performed during amplification and this "real-time" detection can be done in a single closed tube hence eliminating post-PCR sample handling and consequently preventing the risk of amplicon carryover (TaqMan[™] system from Perkin Elmer or Amplisensor[™] from Biotronics). Several other fluorescence-based detection methods can be performed in real-time. Fluorescence resonance energy transfer (FRET) is the principle behind the use of adjacent hybridization probes and molecular beacons. Adjacent hybridization probes are designed to be internal to the amplification primers. The 3' end of one probe is labelled with a donor fluorophore while the 5' end of an adjacent probe is labelled with an acceptor fluorophore. When the two probes are specifically hybridized in closed proximity (spaced by 1 to 5 nucleotides) the donor fluorophore which has been excited by an external light source emits light that is absorbed by a second acceptor that emit more fluorescence and yields a FRET signal. Molecular beacons possess a stem-and-loop structure where the loop is the probe and at the bottom of the stem a fluorescent moiety is at one end while a quenching moiety is at the other end. The beacons undergo a fluorogenic conformational change when they hybridize to their targets hence separating the fluorochrome from its quencher. The FRET principle is also used in an air thermal cycler with a built-in fluorometer (Wittwer, C.T. *et al.* 1997. BioTechniques 22:130-138). The amplification and detection are extremely rapid as reactions are performed in capillaries : it takes 18 min to complete 45 cycles. Those techniques are suitable especially in the case where few pathogens are searched for. Boehringer-Roche Inc. sells the LightCycler[™], an apparatus capable of rapid cycle PCR combined with fluorescent SYBR[®] Green I or FRET detection. We recently demonstrated in our laboratory, real-time detection of 10 CFU in less than 40 minutes using adjacent hybridization probes on the LightCycler[™]. 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.

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 sequences from our repertory and designed to specifically hybridize to DNA amplification products which are objects of the present invention. Alternatively, the internal probes for species or genus or family or group detection and identification may be derived from the amplicons produced by a universal, family, group or genus

amplification assay. The oligonucleotide probes may be labeled with biotin or with digoxigenin or with any other reporter molecule (for more details see below the section on hybrid capture). Hybridization on a solid support is amenable to miniaturization.

5 At present the oligonucleotide nucleic acid microarray technology is appealing. Currently, available low to medium density arrays (Heller *et al.*, An integrated microelectronics hybridization system for genomic research and diagnostic applications. *In*: Harrison, D.J., and van den Berg, A., 1998, Micro total analysis systems '98, Kluwer Academic Publisher, Dordrecht.) could specifically capture
10 fluorescent-labelled amplicons. Detection methods for hybridization are not limited to fluorescence; potentiometry, colorimetry and plasmon resonance are some examples of alternative detection methods. In addition to detection by hybridization, nucleic acid microarrays could be used to perform rapid sequencing by hybridization. Mass spectrometry could also be applicable for rapid identification of the amplicon or
15 even for sequencing of the amplification products (Chiu and Cantor, 1999, Clinical Chemistry **45**:1578; Berkenkamp *et al.*, 1998, Science **281**:260).

We also keep in mind the major challenge of molecular diagnostics tools, *i.e.* : integration of the major steps including sample preparation, genetic amplification, detection, data analysis and presentation (Anderson *et al.*, Advances in integrated
20 genetic analysis. *In*: Harrison, D.J., and van den Berg, A., 1998, Micro total analysis systems '98, Kluwer Academic Publisher, Dordrecht.).

To ensure 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
25 forming strong secondary structures (Dieffenbach and Dveksler, 1995, PCR Primer: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Plainview, New York). The concentration ranges for glycerol and DMSO are 5-15% (v/v) and 3-10% (v/v), respectively. For the PCR reaction mixture, the concentration ranges for the amplification primers and $MgCl_2$ are 0.1-1.5 μM and 1.0-10.0 mM, respectively.
30 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.

35

Hybrid capture and chemiluminescence detection of amplification products

Hybridization and detection of amplicons by chemiluminescence were adapted from Nikiforov *et al.* (1994, PCR Methods and Applications **3**:285-291 and 1995, Anal. Biochem. **227**:201-209) and from the DIGTM system protocol of Boehringer
40 Mannheim. Briefly, 50 μl of a 25 picomoles solution of capture probe diluted in EDC {1-ethyl-3-(3-dimethylaminopropyl) carbodiimide hydrochloride} are immobilized in

each well of 96-wells plates (Microlite™ 2, Dynex) by incubation overnight at room temperature. The next day, the plates are incubated with a solution of 1% BSA diluted into TNTw (10 mM Tris-HCl, pH 7.5; 150 mM NaCl; 0.05% Tween™ 20) for 1 hour at 37 °C. The plates are then washed on a Wellwash Ascent™
 5 (Labystems) with TNTw followed by Washing Buffer (100 mM maleic acid pH7.5; 150 mM NaCl; 0.3% Tween™ 20).

The amplicons were labelled with DIG-11-dUTP during PCR using the PCR DIG Labelling Mix from Boehringer Mannheim according to the manufacturer's instructions. Hybridization of the amplicons to the capture probes is performed in
 10 triplicate at stringent temperature (generally, probes are designed to allow hybridization at 55 °C, the stringent temperature) for 30 minutes in 1.5 M NaCl; 10 mM EDTA. It is followed by two washes in 2 X SSC; 0.1% SDS, then by four washes in 0.1X SSC; 0.1% SDS at the stringent temperature (55 °C). Detection with 1,2 dioxetane chemiluminescent alkaline phosphatase substrates like CSPD® (Tropix inc.) is
 15 performed according to the manufacturer's instructions but with shorter incubations times and a different antibody concentration. The plates are agitated at each step, the blocking incubation is performed for only 5 minutes, the anti-DIG-AP1 is used at a 1:1000 dilution, the incubation with antibody lasts 15 minutes, the plates are washed twice for only 5 minutes. Finally, after a 2 minutes incubation into the detection
 20 buffer, the plates are incubated 5 minutes with CSPD® at room temperature followed by a 10 minutes incubation at 37 °C without agitation. Luminous signal detection is performed on a Dynex Microtiter Plate Luminometer using RLU (Relative Light Units).

25 ***Specificity and ubiquity tests for oligonucleotide primers and probes***

The specificity of oligonucleotide primers and probes was tested by amplification of DNA or by hybridization with bacterial or fungal or parasitical species selected from a panel comprising closely related species and species sharing
 30 the same anatomo-pathological site (see Annexes and Examples). All of the bacterial, fungal and parasitical species tested were likely to be pathogens associated with infections or potential contaminants which can be isolated from clinical specimens. Each target DNA could be released from bacterial cells using standard chemical and/or physical treatments to lyse the cells (Sambrook *et al.*, 1989, Molecular
 35 Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY) or alternatively, genomic DNA purified with the GNOME™ DNA kit (Bio101, Vista, CA) was used. Subsequently, the DNA was subjected to amplification with the primer pairs.

Oligonucleotides primers found to amplify specifically the target species, genus,
 40 family or group were subsequently tested for their ubiquity by amplification (i.e.

ubiquitous primers amplified most or all isolates of the target species or genus or family or group). The specificity and ubiquity of the PCR assays using the selected amplification primer pairs were tested either directly from cultures of microbial species or from purified microbial genomic DNA.

5 Probes were tested in hybrid capture assays as described above. An oligonucleotide probe was considered specific only when it hybridized solely to DNA from the species or genus or family or group from which it was selected. 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
10 genus or family or group) by hybridization to microbial DNAs from different clinical isolates of the species or genus or family or group of interest including ATCC reference strains. Similarly, oligonucleotide primers and probes could be derived from antibiotic resistance or toxin genes which are objects of the present invention.

15 ***Reference strains***

The reference strains used to built proprietary *tuf*, *atpD* and *recA* sequence data subrepertories, as well as to test the amplification and hybridization assays were obtained from (i) the American Type Culture Collection (ATCC), (ii) the Laboratoire
20 de santé publique du Québec (LSPQ), (iii) the Centers for Disease Control and Prevention (CDC), (iv) the National Culture Type Collection (NCTC) and (v) several other reference laboratories throughout the world. The identity of our reference strains was confirmed by phenotypic testing and reconfirmed by analysis of *tuf*, *atpD* and *recA* sequences (see example 13).

25 ***Antibiotic resistance genes***

Antimicrobial resistance complicates treatment and often leads to therapeutic failures. Furthermore, overuse of antibiotics inevitably leads to the emergence of
30 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 species- and/or genus- and/or family- and/or group-specific DNA-based tests,
35 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 of antibiotic resistance genes). Since the sequence from
40 the most important and common bacterial antibiotic resistance genes are available

from public databases, our strategy is 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 list of each of the bacterial antibiotic resistance genes selected on the basis of their clinical
 5 relevance (i.e. high incidence and importance) is given in Table 5. Our approach is unique because the antibiotic resistance genes detection and the bacterial detection and identification can be performed simultaneously in multiplex assays under uniform PCR amplification conditions. These amplifications can also be done separately.

10 *Toxin genes*

Toxin identification is often very important to prescribe optimal treatments. Besides the rapid identification of negative clinical specimens with DNA-based tests
 15 for universal bacterial detection and the identification of the presence of a specific pathogen in the positive specimens with species- and/or genus- and/or family- and/or group-specific DNA-based tests, clinicians sometimes need timely information about the ability of certain bacterial pathogens to produce toxins. Since the sequence from the most important and common bacterial toxin genes are available from public
 20 databases, our strategy is to use the sequence from a portion or from the entire toxin gene to design specific oligonucleotide primers or probes which will be used as a basis for the development of rapid DNA-based tests. The list of each of the bacterial toxin genes selected on the basis of their clinical relevance (i.e. high incidence and importance) is given in Table 6. Our approach is unique because the toxin genes
 25 detection and the bacterial detection and identification can be performed simultaneously in multiplex assays under uniform PCR amplification conditions.

Universal bacterial detection

30 In the routine microbiology laboratory, a high percentage of clinical specimens sent for bacterial identification are negative by culture. Testing clinical samples with universal amplification primers or universal probes to detect the presence of bacteria prior to specific identification and screening out the numerous negative specimens is thus useful as it reduces costs and may rapidly orient the clinical management of the
 35 patients. Several amplification primers and probes were therefore synthesized from highly conserved portions of bacterial sequences from the *tuf* and *atpD* sequences. The universal primers selection was based on a multiple sequence alignment constructed with sequences from our repertoire.

All computer analysis of amino acid and nucleotide sequences were performed
 40 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 are very similar to those used for the species- and genus-specific amplification assays except that the annealing temperature is slightly lower. The original universal PCR assay described in our co-pending WO98/20157 (SEQ ID NOs. 23-24 of the latter application) 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 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 Table 4. We found that at least 104 of these species could be amplified. However, the assay could be improved since bacterial species which could not be amplified with the original *tuf* sequences-based assay included species belonging to the following genera: *Corynebacterium* (11 species) and *Stenotrophomonas* (1 species). Sequencing of the *tuf* genes from these bacterial species and others has been performed in the scope of the present invention in order to improve the universal assay. This sequencing data has been used to select new universal primers which may be more ubiquitous. Also, we improved our primer and probes design strategy by taking into consideration the phylogeny observed in analysing our repertoire of *tuf*, *atpD* and *recA* sequences. Data from each of the 3 main subrepertoires (*tuf*, *atpD* and *recA*) was subjected to a basic phylogenetic analysis using the Pileup command from version 10 of the GCG package (Genetics Computer Group, inc.). This analysis indicated the main branches or phyla reflecting the relationships between sequences. Instead of trying to design primers or probes able to hybridize to all phyla, we designed primers or probes able to hybridize to the main phyla while trying to use the largest phylum possible. This strategy should allow less degenerated primers hence improving sensitivity and by combining primers in a multiplex assay, improve ubiquity. Universal primers SEQ ID NOs. 643-645 based on *tuf* sequences have been designed

to amplify most pathogenic bacteria except *Actinomycetaceae*, *Clostridiaceae* and the *Cytophaga*, *Flexibacter* and *Bacteroides* phylum (pathogenic bacteria of this phylum include mostly *Bacteroides*, *Porphyromonas* and *Prevotella* species). Primers to fill these gaps have been designed for *Actinomycetaceae* (SEQ ID NOs. 646-648),
 5 *Clostridiaceae* (SEQ ID NOs. 796-797, 808-811), and the *Cytophaga*, *Flexibacter* and *Bacteroides* phylum (SEQ ID NOs. 649-651). These primers sets could be used alone or in conjunction to render the universal assay more ubiquitous. These primers are in the process of being tested.

Universal primers derived from *atpD* sequences include SEQ ID NOs. 562-565.
 10 Combination of these primers does not amplify human DNA but should amplify almost all pathogenic bacterial species except proteobacteria belonging to the epsilon subdivision (*Campylobacter* and *Helicobacter*), the bacteria from the *Cytophaga*, *Flexibacter* and *Bacteroides* group and some actinomycetes and corynebacteria. By analysing *atpD* sequences from the latter species, primers and probes to specifically
 15 fill these gaps could be designed and used in conjunction with primers SEQ ID NOs. 562-565. These primers are in the process of being tested.

In addition, universality of the assay could be expanded by mixing *atpD* sequences-derived primers with *tuf* sequences-derived primers. Ultimately, even *recA* sequences-derived primers could be added to fill some gaps in the universal assay.

20 It is important to note that the 95 bacterial species selected 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.

25

Amino acid sequences derived from *tuf*, *atpD* and *recA* sequences

The amino acid sequences translated from the repertory of *atpD*, *tuf* and *recA* sequences are also an object of the present invention. The amino acid sequence data
 30 will be particularly useful for homology modeling of three-dimensional (3D) structure of the elongation factor Tu, elongation factor G, elongation factor 1 α , ATPase subunit beta and RecA recombinase. For all these proteins, at least one structure model has been published using X-ray diffraction data from crystals. Based on those structural informations it is possible to use computer software to build 3D
 35 model structures for any other protein having peptide sequence homologies with the known structure (Greer, 1991, Methods in Enzymology, **202**:239-252, Taylor, 1994, Sali, 1995, Curr. Opin. Biotechnol. **6**:437-451, Sanchez and Sali, 1997, Curr. Opin. Struct. Biol. **7**:206-214, Fischer and Eisenberg, 1999, Curr. Opin. Struct. Biol. **9**:208-211, Guex *et al.*, 1999, Trends Biochem. Sci. **24**: 364-367). Model structures of target
 40 proteins are used for the design or to predict the behavior of ligands and inhibitors

such as antibiotics. Since EF-Tu and EF-G are already known as antibiotic targets (see above) and since the beta subunit of ATPase and RecA recombinase are essential to the survival of the microbial cells in natural conditions of infection, all four proteins could be considered antibiotic targets. Sequence data, especially the new
5 data generated by us could be very useful to assist the creation of new antibiotic molecules with desired spectrum of activity. In addition, model structures could be used to improve protein function for commercial purposes such as improving antibiotic production by microbial strains or increasing biomass.

BRIEF SUMMARY OF THE INVENTION

Three highly conserved genes, encoding translation elongation factor Tu, the catalytic subunit of proton-translocating ATPase and the RecA recombinase, are used to generate species-specific, genus-specific, group-specific and universal nucleic acid probes and amplification primers to rapidly detect and identify bacterial, fungal and parasitical pathogens from clinical specimens for diagnosis. The concomittant detection of associated antibiotic resistance and toxin genes are also under the scope of the present invention.

DESCRIPTION OF THE DRAWINGS

Figures 1 and 2 illustrate the principal subdivisions of the *tuf* and *atpD* sequences repertories, respectively. For the design of primers and probes, depending on the needs, one may want to use the complete data set illustrated on the top of the pyramid or use only a subset illustrated by the different branching points. Smaller subdivisions, representing groups, families, genus and species, could even be made to extend to the bottom of the pyramid. Because the *tuf* and *atpD* sequences are highly conserved and evolved with each species, the design of primers and probes does not need to include all the sequences within the database or its subdivisions. As illustrated, in Annexes IV to XX, depending on the use, sequences from a limited number of species can be carefully selected to represent: i) only the main phylogenetic branches from which the intended probes and primers need to be differentiating, and ii) only the species for which they need to be matching. However, for ubiquity purposes, and especially for primers and probes identifying large groups of species (genus, family, group or universal, or sequencing primers), the more data is included into the sequence analysis, the better the probes and primers will be suitable for each particular intended use. Similarly, for specificity purposes, a larger data set (or repertory) ensures optimal primers and probes design by reducing the chance of employing nonspecific oligonucleotides.

Figure 3 illustrates the approach used to design specific amplification primers from *fusA* as well as from the region between the end of *fusA* and the beginning of *tuf* in the streptomycin (*str*) operon.

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.

The various annexes show the strategies used for the selection of DNA amplification primers, nucleic acid hybridization probes or molecular beacon internal probes from *tuf*, *atpD*, *recA*, *speA*, *stx*, *van*, *pbp*, *mecA*, *hexA*, *pcp*, *ddl*, *mtl* or unknown gene sequences:

- (i) Annex I shows the amplification primers used for *tuf* sequences.
- (ii) Annex II shows the amplification primers used for *atpD* sequences.
- (iii) Annex III shows the internal probes for nucleic acid hybridization and specific detection of *tuf* sequences.
- 10 (iv) Annex IV illustrates the strategy used for the selection of the amplification primers specific for *atpD* sequences of the F-type.
- (v) Annex V illustrates the strategy used for the selection of the amplification primers specific for *atpD* sequences of the V-type.
- 15 (vi) Annex VI illustrates the strategy used for the selection of the amplification primers specific for the *tuf* sequences of organelle lineage (M, the letter M is used to indicate that in most cases, the organelle is the mitochondria).
- (vii) Annex VII illustrates the strategy used for the selection of the amplification primers specific for the *tuf* sequences of eukaryotes (EF-1).
- (viii) Annex VIII illustrates the strategy for the selection of *Streptococcus agalactiae*-specific amplification primers from *tuf* sequences.
- 20 (ix) Annex IX illustrates the strategy for the selection of *Streptococcus agalactiae*-specific hybridization probes from *tuf* sequences.
- (x) Annex X illustrates the strategy for the selection of *Streptococcus agalactiae*-specific amplification primers from *atpD* sequences.
- 25 (xi) Annex XI illustrates the strategy for the selection from *tuf* sequences of *Candida albicans/dubliniensis*-specific amplification primers, *Candida albicans*-specific hybridization probe and *Candida dubliniensis*-specific hybridization probe.
- (xii) Annex XII illustrates the strategy for the selection of *Staphylococcus*-specific amplification primers from *tuf* sequences.
- 30 (xiii) Annex XIII illustrates the strategy for the selection of the *Staphylococcus* genus-specific hybridization probe from *tuf* sequences.
- (xiv) Annex XIV illustrates the strategy for the selection of *Staphylococcus saprophyticus*-specific and *Staphylococcus haemolyticus*-specific hybridization probes from *tuf* sequences.
- 35 (xv) Annex XV illustrates the strategy for the selection of *Staphylococcus aureus*-specific and *Staphylococcus epidermidis*-specific hybridization probes from *tuf* sequences.
- 40 (xvi) Annex XVI illustrates the strategy for the selection of the *Staphylococcus hominis*-specific hybridization probe from *tuf* sequences.

- (xvii) Annex XVII illustrates the strategy for the selection of the *Enterococcus* genus-specific amplification primers from *tuf* sequences.
- (xviii) Annex XVIII illustrates the strategy for the selection of the *Enterococcus faecalis*-specific hybridization probe, of the *Enterococcus faecium*-specific hybridization probe and of the *Enterococcus casseliflavus-flavescens-gallinarum* group-specific hybridization probe from *tuf* sequences.
- (xix) Annex XIX illustrates the strategy for the selection of primers from *tuf* sequences for the identification of platelets contaminants.
- (xx) Annex XX illustrates the strategy for the selection of the universal amplification primers from *atpD* sequences.
- (xxi) Annex XXI illustrates the amplification primers used for nucleic acid amplification from *recA* sequences.
- (xxii) Annex XXII shows the specific and ubiquitous primers for nucleic acid amplification from *speA* sequences.
- (xxiii) Annex XXIII illustrates the first strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *speA* sequences.
- (xxiv) Annex XXIV illustrates the second strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *speA* sequences.
- (xxv) Annex XXV illustrates the strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *tuf* sequences.
- (xxvi) Annex XXVI illustrates the strategy for the selection of Shiga toxin-producing, *Escherichia coli*-specific amplification primers and hybridization probe from *stx₁* sequences.
- (xxvii) Annex XXVII illustrates the strategy for the selection of Shiga toxin-producing, *Escherichia coli*-specific amplification primers and hybridization probe from *stx₂* sequences.
- (xxviii) Annex XXVIII illustrates the strategy for the selection of *vanA*-specific amplification primers from *van* sequences.
- (xxix) Annex XXIX illustrates the strategy for the selection of *vanB*-specific amplification primers from *van* sequences.
- (xxx) Annex XXX illustrates the strategy for the selection of *vanC*-specific amplification primers from *vanC* sequences.
- (xxxi) Annex XXXI illustrates the strategy for the selection of *Streptococcus pneumoniae*-specific amplification primers and hybridization probes from *pbp1a* sequences.
- (xxxii) Annex XXXII shows the specific and ubiquitous primers for nucleic acid amplification from *stx* sequences.
- (xxxiii) Annex XXXIII shows the molecular beacon internal probes for hybridization and specific detection of toxin sequences.
- (xxxiv) Annex XXXIV shows the specific and ubiquitous primers for nucleic acid

amplification from *van* sequences.

- (xxxv) Annex XXXV shows the internal probes for nucleic acid hybridization and specific detection of *van* sequences.
- (xxxvi) Annex XXXVI shows the specific and ubiquitous primers for nucleic acid amplification from *pbp* sequences.
- (xxxvii) Annex XXXVII shows the internal probes for nucleic acid hybridization and specific detection of *pbp* sequences.
- (xxxviii) Annex XXXVIII illustrates the strategy for the selection of *vanAB*-specific amplification primers and specific hybridization probes *vanA* and *vanB* from *van* sequences.
- (xxxix) Annex XXXIX shows the internal probe for nucleic acid hybridization and specific detection of *mecA*.
- (xl) Annex XL shows the specific and ubiquitous primers for nucleic acid amplification from *hexA* sequences.
- (xli) Annex XLI shows the internal probe for nucleic acid hybridization and specific detection of *hexA*.
- (xlii) Annex XLII illustrates the strategy for the selection of *Streptococcus pneumoniae* species-specific amplification primers and hybridization probe from *hexA* sequences.
- (xlili) Annex XLIII shows the specific and ubiquitous primers for nucleic acid amplification from *pcp* sequences.
- (xliv) Annex XLIV shows the specific and ubiquitous primers for nucleic acid amplification from unknown *S. saprophyticus* gene sequences.
- (xlv) Annex XLV shows the molecular beacon internal probes for hybridization and specific detection of antibiotic resistance gene sequences.
- (xlvi) Annex XLVI shows the molecular beacon internal probe for hybridization and specific detection of an unknown *S. aureus* gene sequence.
- (xlvii) Annex XLVII shows the molecular beacon internal probe for hybridization and specific detection of *tuf* sequences.
- (xlviii) Annex XLVIII shows the molecular beacon internal probes for hybridization and specific detection of *ddl* and *mtl* gene sequences.
- (xlix) Annex XLIX shows the internal probe for nucleic acid hybridization and specific detection of the unknown *S. aureus* gene.

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 were used. The inclusion of inosine and/or of degenerescences in the amplification primers allows 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

EXAMPLE 1:

Sequencing of bacterial *atpD* (F-type and V-type) gene fragments. As shown in Annex IV, the comparison of publicly available *atpD* (F-type) sequences from a variety of bacterial species revealed conserved regions allowing the design of PCR primers able to amplify *atpD* sequences (F-type) from a wide range of bacterial species. Using primers pairs SEQ ID NOs. 566 and 567, 566 and 814, 568 and 567, 570 and 567, 572 and 567, 569 and 567, 571 and 567, and 700 and 567, it was possible to amplify and sequence *atpD* sequences SEQ ID NOs. 242-270, 272-398, 673-674, 737-767, 866-867 and 942-955.

Similarly, Annex V shows how were designed the PCR primers able to amplify *atpD* sequences of the V-type from a wide range of bacterial species. Using primers SEQ ID NOs. 681-683, it was possible to amplify and sequence *atpD* sequences SEQ ID Nos. 827-832, 929-931, 958 and 966. As the gene was difficult to amplify for several species, additional amplification primers were designed inside the original amplicon (SEQ ID NOs.1203-1207).

EXAMPLE 2:

Sequencing of eukaryotic *atpD* (F-type and V-type) gene fragments. The comparison of publicly available *atpD* (F-type) sequences from a variety of fungal and parasitical species revealed conserved regions allowing the design of PCR primers able to amplify *atpD* sequences from a wide range of fungal and parasitical species. Using primers pairs SEQ ID NOs. 568 and 573, 574 and 573, 574 and 708, and 566 and 567, it was possible to amplify and sequence *atpD* sequences SEQ ID NOs. 458-497, 530-538, 663, 667, 676, 678-680, 768-778, 856-862, 889-896 and 941.

In the same manner, the primers described in Annex V (SEQ ID NOs. 681-683) could amplify the *atpD* (V-type) gene from fungal and parasitical species. We were thus able to sequence SEQ ID Nos. 834-839, 956-957, and 959-965.

EXAMPLE 3:

Sequencing of eukaryotic *tuf* (EF-1) gene fragments. As shown in Annex VII, the comparison of publicly available *tuf* (EF-1) sequences from a variety of fungal and

parasitical species revealed conserved regions allowing the design of PCR primers able to amplify *tuf* sequences from a wide range of fungal and parasitical species. Using primers pairs SEQ ID NOs. 558 and 559, 813 and 559, 558 and 815, 560 and 559, 653 and 559, 558 and 655, and 654 and 559, it was possible to amplify and
 5 sequence *tuf* sequences SEQ ID NOs. 399-457, 509-529, 622-624, 677, 779-790, 840-842, 865, and 897-903.

EXAMPLE 4:

10 Sequencing of eukaryotic *tuf* (organelle origin, M) gene fragments. As shown in Annex VI, the comparison of publicly available *tuf* (organelle origin, M) sequences from a variety of fungal and parasitical organelles revealed conserved regions allowing the design of PCR primers able to amplify *tuf* sequences of several
 15 organelles belonging to a wide range fungal and parasitical species. Using primers pairs SEQ ID NOs. 664 and 652, 664 and 561, 911 and 914, 912 and 914, 913 and 915, 916 and 561, and 664 and 917, it was possible to amplify and sequence *tuf* sequences SEQ ID NOs. 498-508, 791-792, 843-855, and 904-910.

EXAMPLE 5:

20 Specific identification of *Streptococcus agalactiae* using *tuf* sequences. As shown in Annex VIII, the comparison of *tuf* sequences from a variety of bacterial species allowed the selection of PCR primers specific for *S. agalactiae*. The strategy used to design the PCR primers was based on the analysis of a multiple sequence alignment
 25 of various *tuf* sequences. The multiple sequence alignment includes the *tuf* sequences of four bacterial strains from the target species as well as *tuf* sequences from other species and bacterial genera, especially representatives of closely related species. A careful analysis of this alignment allowed the selection of oligonucleotide sequences which are conserved within the target species but which discriminate sequences from
 30 other species and genera, especially from the closely related species, thereby permitting the species-specific and ubiquitous detection and identification of the target bacterial species.

The chosen primer pair, oligos SEQ ID NO. 549 and SEQ ID NO. 550, gives an
 35 amplification product of 252 bp. Standard PCR was carried out using 0.4 μ M of each primer, 2.5 mM $MgCl_2$, BSA 0.05 mM, 1X Taq Buffer (Promega), dNTP 0.2 mM (Pharmacia), 1 μ l Taq DNA polymerase (Promega) 0.025 U/ μ l combined with TaqStart 5 ng/ μ l (Clontech Laboratories Inc., Palo Alto), 1 μ l of genomic DNA sample in a final volume of 20 μ l using a PTC-200 thermocycler (MJ Research Inc.).
 40 The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 62 °C, followed by terminal extension at 72 °C for

2 minutes. Amplification was monitored on agarose gel electrophoresis by staining the DNA with ethidium bromide.

Specificity of the assay was tested by adding into the PCR reactions, 0.1 ng of genomic DNA from each of the bacterial species listed in Table 8. Strong amplification was observed only for the 5 *S. agalactiae* strains listed. Of the other bacterial species, including 32 species representative of the vaginal flora and 27 other streptococcal species, only *S. acidominimus* yielded amplification. The signal for 0.1 ng of *S. acidominimus* genomic DNA was weak and the detection limit for this species was 10 pg (corresponding to more than 4000 genome copies) while the detection limit for *S. agalactiae* was 2.5 fg (corresponding to one genome copy) of genomic DNA.

To increase the specificity of the assay, internal probes were designed for FRET (Fluorescence Resonance Energy Transfer) detection using the LightCycler (Idaho Technology). As illustrated in Annex IX, a multiple sequence alignment of streptococcal *tuf* sequence fragments corresponding to the 252 bp region amplified by primers SEQ ID NO. 549 and SEQ ID NO. 550, was used for the design of internal probes TSagHF436 (SEQ ID NO. 582) and TSagHF465 (SEQ ID NO. 583). The region of the amplicon selected for internal probes contained sequences unique and specific to *S. agalactiae*. SEQ ID NO. 583, the more specific probe, is labelled with fluorescein in 3', while SEQ ID NO. 582, the less discriminant probe, is labelled with CY5 in 5' and blocked in 3' with a phosphate group. However, since the FRET signal is only emitted if both probes are adjacently hybridized on the same target amplicon, detection is highly specific.

Real-time detection of PCR products using the LightCycler™ was carried out using 0.4 μ M of each primer (SEQ ID NO. 549-550), 0.2 μ M of each probe (SEQ ID NO. 582-583), 2.5 mM MgCl₂, BSA 450 μ g/ml, 1X PC2 Buffer (AB Peptides, St-Louis, MO), dNTP 0.2 mM (Pharmacia), KlenTaq1™ DNA polymerase 0.5 U (AB Peptides) 0.025 U/ μ l combined with TaqStart (Clontech Laboratories Inc., Palo Alto), 0.7 μ l of genomic DNA sample in a final volume of 7 μ l using a LightCycler thermocycler (Idaho Technology). The optimal cycling conditions for maximum sensitivity and specificity were 3 minutes at 94 °C for initial denaturation, then forty cycles of three steps consisting of 0 second (this setting meaning the LightCycler will reach the target temperature and stay at it for its minimal amount of time) at 94 °C, 10 seconds at 64 °C, 20 seconds at 72 °C. Amplification was monitored during each annealing steps using the fluorescence ratio. The streptococcal species having close sequence homologies with the *tuf* sequence of *S. agalactiae* (*S. acidominimus*, *S. anginosus*, *S. bovis*, *S. dysgalactiae*, *S. equi*, *S. ferus*, *S. gordonii*, *S. intermedius*, *S.*

parasanguis, *S. parauberis*, *S. salivarius*, *S. sanguis*, *S. suis*, and of course *S. agalactiae*) were tested in the LightCycler with 0.07 ng of genomic DNA per reaction. This time, only *S. agalactiae* yielded an amplification signal, hence demonstrating that the assay is species-specific. With the LightCycler assay using the internal FRET probes, the detection limit for *S. agalactiae* was 12.5 fg (corresponding to five genome copies) of genomic DNA.

EXAMPLE 6:

10 Specific identification of *Streptococcus agalactiae* using *atpD* sequences. As shown in Annex XIV, the comparison of *atpD* sequences from a variety of bacterial species allowed the selection of PCR primers specific for *S. agalactiae*. The primer design strategy is similar to the strategy described in the preceding example except that *atpD* sequences were used in the alignment (see Annex X).

15 Four primers were selected, ASag42 (SEQ ID NO. 627), ASag52 (SEQ ID NO. 628), ASag206 (SEQ ID NO. 625) and ASag371 (SEQ ID NO. 626). The following combinations of these four primers give four amplicons; SEQ ID NO. 627 + SEQ ID NO. 625 = 190 bp, SEQ ID NO. 628 + SEQ ID NO. 625 = 180 bp, SEQ ID NO. 627 + SEQ ID NO. 626 = 355 bp, and SEQ ID NO. 628 + SEQ ID NO. 626 = 345 bp.

25 Standard PCR was carried out on PTC-200 thermocyclers (MJ Research Inc) using 0.4 μ M of each primers pair, 2.5 mM $MgCl_2$, BSA 0.05 mM, 1X *taq* Buffer (Promega), dNTP 0.2 mM (Pharmacia), 1 μ l *taq* DNA polymerase (Promega) 0.025 U/ μ l combined with TaqStart 5 ng/ μ l (Clontech Laboratories Inc., Palo Alto), 1 μ l of genomic DNA sample in a final volume of 20 μ l using a PTC-200 thermocycler (MJ Research Inc.). The optimal cycling conditions for maximum sensitivity and specificity were adjusted for each primer pair. Three minutes at 95 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at the optimal temperature specified below were followed by terminal extension at 72 °C for 2 minutes. Amplification was monitored on agarose gel electrophoresis by staining the DNA with ethidium bromide. Since *atpD* sequences are relatively more specific than *tuf* sequences, only the more closely related species namely, the streptococcal species listed in table 9, were tested.

35 All four primer pairs only amplified the six *S. agalactiae* strains. With an annealing temperature of 63 °C, the primer pair SEQ ID NO. 627 + SEQ ID NO. 625 had a sensitivity of 1-5 fg (equivalent to 1-2 genome copies). At 55 °C, the primer pair SEQ ID NO. 628 + SEQ ID NO. 625 had a sensitivity of 2.5 fg (equivalent to 1 genome copy). At 60 °C, the primer pair SEQ ID NO. 627 + SEQ ID NO. 626 had a

sensitivity of 10 fg (equivalent to 4 genome copies). At 58 °C, the primer pair SEQ ID NO. 628 + SEQ ID NO. 626 had a sensitivity of 2.5-5 fg (equivalent to 1-2 genome copies). This proves that all four primer pairs can detect *S. agalactiae* with high specificity and sensitivity. Together with example 5, this example demonstrates that both *tuf* and *atpD* sequences are suitable targets for the identification of microorganisms at the species level.

EXAMPLE 7:

10 Development of a PCR assay for detection and identification of staphylococci at genus and species levels.

Materials and Methods

15 **Bacterial strains.** The specificity of the PCR assay was verified by using a panel of ATCC (America Type Culture Collection) and DSMZ (Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH ; German Collection of Microorganisms and Cell Cultures) reference strains consisting of 33 gram-negative and 47 gram-positive bacterial species (Table 12). In addition, 295 clinical isolates representing 11 different species of staphylococci from the microbiology laboratory of the Centre Hospitalier Universitaire de Québec, Pavillon Centre Hospitalier de l'Université Laval (CHUL) (Ste-Foy, Québec, Canada) were also tested to further validate the *Staphylococcus*-specific PCR assay. These strains were all identified by using (i) conventional methods or (ii) the automated MicroScan Autoscan-4 system equipped with the Positive BP Combo Panel Type 6 (Dade Diagnostics, Mississauga, Ontario, Canada). Bacterial strains from frozen stocks kept at -80 °C in brain heart infusion (BHI) broth containing 10% glycerol were cultured on sheep blood agar or in BHI broth (Quelab Laboratories Inc, Montréal, Québec, Canada).

30 **PCR primers and internal probes.** Based on multiple sequence alignments, regions of the *tuf* gene unique to staphylococci were identified. *Staphylococcus* genus-specific PCR primers TStaG422 (SEQ ID NO. 553) and TStaG765 (SEQ ID NO. 575) were derived from these regions (Annex XII). These PCR primers are displaced by two nucleotide positions compared to original *Staphylococcus* genus-specific PCR primers described in previous patent application WO98/20157 (SEQ ID NOs. 17 and 20 in the said patent application). These modifications were done to ensure specificity and ubiquity of the primer pair, in the light of new *tuf* sequence data revealed in the present patent application for several additional streptococcal species and strains.

40 Similarly, sequence alignments analysis were performed to design genus and species-

specific internal probes (see Annexes XIII to XVI). Two internal probes for *Staphylococcus*-genus (SEQ ID NOs. 605-606), five for *S. aureus* (SEQ ID NOs. 584-588), five for *S. epidermidis* (SEQ ID NO. 589-593), two for *S. haemolyticus* (SEQ ID NOs. 594-595), three for *S. hominis* (SEQ ID NOs. 596-598), four for *S. saprophyticus* (SEQ ID NOs. 599-601 and 695), and two for coagulase-negative *Staphylococcus* species *S. epidermidis*, *S. hominis*, *S. saprophyticus*, *S. auricularis*, *S. capitis*, *S. haemolyticus*, *S. lugdunensis*, *S. simulans*, *S. cohnii* and *S. warneri* (SEQ ID NOs. 1175-1176) were designed. The range of mismatches between the *Staphylococcus*-specific 371-bp amplicon and each of the 20-mer species-specific internal probes was from 1 to 5, in the middle of the probe when possible. No mismatches were present in the two *Staphylococcus*-genus probes for the 11 species analyzed: *S. aureus*, *S. auricularis*, *S. capitis*, *S. cohnii*, *S. epidermidis*, *S. haemolyticus*, *S. hominis*, *S. lugdunensis*, *S. saprophyticus*, *S. simulans* and *S. warneri*. In order to verify the intra-specific sequence conservation of the nucleotide sequence, sequences were obtained for the 371-bp amplicon from five unrelated ATCC and clinical strains for each of the species *S. aureus*, *S. epidermidis*, *S. haemolyticus*, *S. hominis* and *S. saprophyticus*. The Oligo™ (version 5.0) primer analysis software (National Biosciences, Plymouth, Minn.) was used to confirm the absence of self-complementary regions within and between the primers or probes. When required, the primers contained inosines or degenerated nucleotides at one or more variable positions. Oligonucleotide primers and probes were synthesized on a model 394 DNA synthesizer (Perkin-Elmer Corp., Applied Biosystems Division, Mississauga, Ontario, Canada). Detection of the hybridization was performed with the DIG-labeled dUTP incorporated during the amplification with the *Staphylococcus*-specific PCR assay, and the hybridization signal was detected with a luminometer (Dynex Technologies) as described above in the section on luminescent detection of amplification products. Annexes XIII to XVI illustrate the strategy for the selection of several internal probes.

PCR amplification. For all bacterial species, amplification was performed from purified genomic DNA or from a bacterial suspension whose turbidity was adjusted to that of a 0.5 McFarland standard, which corresponds to approximately 1.5×10^8 bacteria per ml. One nanogram of genomic DNA or 1 µl of the standardized bacterial suspension was transferred directly to a 19 µl PCR mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl₂, 0.2 µM (each) of the two *Staphylococcus* genus-specific primers (SEQ ID NOs. 553 and 575), 200 µM (each) of the four deoxynucleoside triphosphates (Pharmacia Biotech), 3.3 µg/µl bovine serum albumin (BSA) (Sigma-Aldrich Canada Ltd, Oakville, Ontario, Canada), and 0.5 U *Taq* polymerase (Promega) coupled with *TaqStart*™ Antibody (Clontech). The PCR amplification was performed as follows : 3 min. at 94

°C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 55 °C, plus a terminal extension at 72 °C for 2 minutes. Amplification was monitored on agarose gel electrophoresis by staining the amplified DNA with ethidium bromide.

5

For determination of the sensitivities of the PCR assays, two-fold dilutions of purified genomic DNA were used to determine the minimal number of genome copies which can be detected.

10

Results

Amplifications with the *Staphylococcus* genus-specific PCR assay. The specificity of the assay was assessed by performing 30-cycle and 40-cycle PCR amplifications with the panel of gram-positive (47 species from 8 genera) and gram-negative (33 species from 22 genera) bacterial species listed in Table 12. The PCR assay was able to detect 27 of 27 staphylococcal species tested in both 30-cycle and 40-cycle regimens. For 30-cycle PCR, all bacterial species tested other than staphylococci were negative. For 40-cycle PCR, *Enterococcus faecalis*, *Lactobacillus acidophilus*, *Lactococcus lactis*, *Macrococcus caseolyticus*, *Streptococcus agalactiae* and *S. mutans* were slightly positive for the *Staphylococcus*-specific PCR assay. The other species tested remained negative. Ubiquity tests performed on a collection of 295 clinical isolates provided by the microbiology laboratory of the Centre Hospitalier Universitaire de Québec, Pavillon Centre Hospitalier de l'Université Laval (CHUL), including *Staphylococcus aureus* (n=34), *S. auricularis* (n=2), *S. capitis* (n=19), *S. cohnii* (n=5), *S. epidermidis* (n=18), *S. haemolyticus* (n=21), *S. hominis* (n=73), *S. lugdunensis* (n=17), *S. saprophyticus* (n=6), *S. simulans* (n=3), *S. warneri* (n=32) and *Staphylococcus* sp. (n=65), showed a uniform amplification signal with the 30-cycle PCR assays and a perfect relation between the genotype and classical identification schemes.

The sensitivity of the *Staphylococcus*-specific assay with 30-cycle and 40-cycle PCR protocols was determined by using purified genomic DNA from the 11 staphylococcal species previously mentioned. For PCR with 30 cycles, a detection limit of 50 copies of genomic DNA was consistently obtained. In order to enhance the sensitivity of the assay, the number of cycles was increased. For 40-cycle PCR assays, the detection limit was lowered to a range of 5-10 genome copies, depending on the staphylococcal species tested.

Hybridization between the *Staphylococcus*-specific 371-bp amplicon and species-specific or genus-specific internal probes. Inter-species polymorphism was sufficient to generate species-specific internal probes for each of the principal

species involved in human diseases (*S. aureus*, *S. epidermidis*, *S. haemolyticus*, *S. hominis* and *S. saprophyticus*). In order to verify the intra-species sequence conservation of the nucleotide sequence, sequences comparisons were performed on the 371-bp amplicon from five unrelated ATCC and clinical strains for each of 5 staphylococcal species: *S. aureus*, *S. epidermidis*, *S. haemolyticus*, *S. hominis* and *S. saprophyticus*. Results showed a high level of conservation of nucleotide sequence between different unrelated strains from the same species. This sequence information allowed the development of staphylococcal species identification assays using species-specific internal probes hybridizing to the 371-bp amplicon. These assays are specific and ubiquitous for those five staphylococcal species. In addition to the species-specific internal probes, the genus-specific internal probes were able to recognize most *Staphylococcus* species.

15 **EXAMPLE 8:**

Differentiating between the two closely related yeast species *Candida albicans* and *Candida dubliniensis*. It is often useful for the clinician to be able to differentiate between two very closely related species of microorganisms. *Candida albicans* is the most important cause of invasive human mycose. In the recent years, a very closely related species, *Candida dubliniensis*, was isolated in immunosuppressed patients. These two species are difficult to distinguish by classic biochemical methods. This example demonstrates the use of *tuf* sequences to differentiate *Candida albicans* and *Candida dubliniensis*. PCR primers TCal528 and TCal676 were selected for their ability to specifically amplify a *tuf* (elongation factor 1 alpha type) fragment from both species (see Annex XI for primer positions and previous patent application WO98/20157 for SEQ ID NOs. 11-12). Within this *tuf* fragment, a region differentiating *C. albicans* and *C. dubliniensis* by two nucleotides was selected and used to design two internal probes (see Annex XI for probe design, SEQ ID NOs. 577 and 578) specific for each species. Amplification of genomic DNA from *C. albicans* and *C. dubliniensis* was carried out using DIG-11-dUTP as described above in the section on chemiluminescent detection of amplification products. Internal probes SEQ ID NOs. 577 and 578 were immobilized on the bottom of individual microtiter plates and hybridization was carried out as described above in the above section on luminescent detection of amplification products. Luminometer data showed that the amplicon from *C. albicans* hybridized only to probe SEQ ID NO. 577 while the amplicon from *C. dubliniensis* hybridized only to probe SEQ ID NO. 578, thereby demonstrating that each probe was species-specific.

40 **EXAMPLE 9:**

Specific identification of *Entamoeba histolytica*. Upon analysis of *tuf* (elongation factor 1 alpha) sequence data, it was possible to find four regions where *Entamoeba histolytica* sequences remained conserved while other parasitical and eukaryotic species have diverged. Primers TEntG38 (SEQ ID NO. 703), TEntG442 (SEQ ID NO. 704), TEntG534 (SEQ ID NO. 705), and TEntG768 (SEQ ID NO. 706) were designed so that SEQ ID NO. 703 could be paired with the three other primers. On PTC-200 thermocyclers (MJ Research), the cycling conditions for initial sensitivity and specificity testing were 3 min. at 94 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 55 °C, followed by terminal extension at 72 °C for 2 minutes. Amplification was monitored on agarose gel electrophoresis by staining the amplified DNA with ethidium bromide. The three primer pairs could detect the equivalent of less than 200 *E. histolytica* genome copies. Specificity was tested using 0.5 ng of purified genomic DNA from a panel of microorganisms including *Babesia bovis*, *Babesia microtti*, *Candida albicans*, *Crithidia fasciculata*, *Leishmania major*, *Leishmania hertigi* and *Neospora caninum*. Only *E. histolytica* DNA could be amplified, thereby suggesting that the assay was species-specific.

20 **EXAMPLE 10:**

Sensitive identification of *Chlamydia trachomatis*. Upon analysis of *tuf* sequence data, it was possible to find two regions where *Chlamydia trachomatis* sequences remained conserved while other species have diverged. Primers Ctr82 (SEQ ID NO. 554) and Ctr249 (SEQ ID NO. 555) were designed. With the PTC-200 thermocyclers (MJ Research), the optimal cycling conditions for maximum sensitivity and specificity were determined to be 3 min. at 94 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 60 °C, followed by terminal extension at 72 °C for 2 minutes. Amplification was monitored on agarose gel electrophoresis by staining the amplified DNA with ethidium bromide. The assay could detect the equivalent of 8 *C. trachomatis* genome copies. Specificity was tested on 0.1 ng of purified genomic DNA from a panel of microorganisms including 22 species commonly encountered in the vaginal flora (*Bacillus subtilis*, *Bacteroides fragilis*, *Candida albicans*, *Clostridium difficile*, *Corynebacterium cervicis*, *Corynebacterium urealyticum*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Fusobacterium nucleatum*, *Gardnerella vaginalis*, *Haemophilus influenzae*, *Klebsiella oxytoca*, *Lactobacillus acidophilus*, *Peptococcus niger*, *Peptostreptococcus prevotii*, *Porphyromonas asaccharolytica*, *Prevotella melaninogenica*, *Propionibacterium acnes*, *Staphylococcus aureus*, *Streptococcus acidominimus*, and *Streptococcus agalactiae*). Only *C. trachomatis* DNA could be

amplified, thereby suggesting that the assay was species-specific.

EXAMPLE 11:

5 Genus-specific identification of enterococci. Upon analysis of *tuf* sequence data and comparison with the repertory of *tuf* sequences, it was possible to find two regions where *Enterococcus* sequences remained conserved while other genera have diverged (Annex XVII). Primer pair Encg313dF and Encg599c (SEQ ID NOs. 1137 and 1136) was tested for its specificity by using purified genomic DNA from a panel of bacteria
10 listed in Table 10. Using the PTC-200 thermocycler (MJ Research), the optimal cycling conditions for maximum sensitivity and specificity were determined to be 3 min. at 94 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 55 °C, followed by terminal extension at 72 °C for 2 minutes. Amplification was monitored on agarose gel electrophoresis by staining
15 the amplified DNA with ethidium bromide. The 18 enterococcal species listed in Table 10 were all amplified efficiently. The only other species amplified were *Abiotrophia adiacens*, *Gemella haemolysans* and *Gemella morbillorum*, three gram-positive species. Sensitivity tested with several strains of *E. casseliflavus*, *E. faecium*, *E. faecalis*, *E. flavescens* and *E. gallinarum* and with one strain of each other
20 *Enterococcus* species listed in Table 10 ranged from 1 to 10 genome copies. The sequence variation within the 308-bp amplicon was sufficient so that nested PCR or internal probes could be used to speciate the amplicon and differentiate enterococci from *Abiotrophia adiacens*, *Gemella haemolysans* and *Gemella morbillorum*, thereby allowing to achieve excellent specificity. Species-specific internal probes were
25 generated for each of the clinically important species, *E. faecalis* (SEQ ID NO. 1174), *E. faecium* (SEQ ID NO. 602), and the *E. casseliflavus*, *E. flavescens*, *E. gallinarum* group (SEQ ID NO. 1122) (Annex XVIII). The species-specific internal probes were able to differentiate their respective *Enterococcus* species from all other *Enterococcus* species. These assays are sensitive, specific and ubiquitous for those
30 five *Enterococcus* species.

EXAMPLE 12:

35 Identification of the major bacterial platelets contaminants using *tuf* sequences in a multiplex test. Blood platelets preparations need to be monitored for bacterial contaminations. The *tuf* sequences of 17 important bacterial contaminants of platelets were aligned. As shown in Annex XIX, analysis of these sequences allowed the design PCR primers. Since in the case of contamination of platelet concentrates, detecting all species (not just the more frequently encountered ones) is desirable,
40 perfect specificity of primers was not an issue in the design. However, sensitivity is

important. That is why, to avoid having to put too much degeneracy, only the most frequent contaminants were included in primer design, knowing that the selected primers would anyway be able to amplify more species than the 17 used in the design. Oligonucleotide sequences which are conserved in these 17 major bacterial contaminants of platelet concentrates were chosen (oligos Tplaq 769 and Tplaq 991, respectively SEQ ID NOs. 636 and 637) thereby permitting the detection of these bacterial species. However, sensitivity was slightly deficient with staphylococci. To ensure maximal sensitivity in the detection of all the more frequent bacterial contaminants, a multiplex assay also including oligonucleotide primers targetting the *Staphylococcus* genera (oligos Stag 422, SEQ ID NO. 553; and Stag 765, SEQ ID NO. 575) was developed. The bacterial species detected with the assay are listed in Table 14.

The primer pairs, oligos SEQ ID NO. 636 and SEQ ID NO. 637 that give an amplification product of 245 pb, and oligos SEQ ID NO. 553 and SEQ ID NO. 575 that give an amplification product of 368 pb, were used simultaneously in the multiplex PCR assay. Real-time detection of these PCR products was made on the LightCycler thermocycler (Idaho Technology) using SYBR[®] Green I (Molecular Probe Inc.). SYBR[®] Green I is a fluorescent dye that binds specifically to double-stranded DNA. It thus binds to DNA products as they are synthesized. The measure of SYBR[®] Green I fluorescence at the end of each elongation cycle indicates the amount of DNA duplex generated by specific DNA fragment amplification and primer-dimer formation.

Fluorogenic detection of PCR products with the LightCycler was carried out using 1.0 mM of both Tplaq primers (SEQ ID NOs. 636-637) and 0.4 mM of both TStaG primers (SEQ ID NOs. 553 and 575), 2.5 mM MgCl₂, BSA 500 mg/ml, dNTP 0.2 mM (Pharmacia), 10X PCR reaction buffer (Boehringer Mannheim) and *taq* DNA polymerase (Boehringer Mannheim) 0.025 U/ml combined with TaqStart 5 ng/ml (Clontech), and 0.7 ml of genomic DNA sample in a final volume of 7 ml. The optimal cycling conditions for maximum sensitivity were 1 minute at 94 °C for initial denaturation, then forty-five cycles of three steps consisting of 0 second at 95 °C, 5 seconds at 60 °C and 9 seconds at 72 °C. Amplification was monitored during each elongation cycle by measuring the level of SYBR[®] Green I. However, real analysis takes place after PCR. Melting curves are done for each sample and transformation of the melting peak allows determination of T_m. Thus primer-dimer and specific PCR product are discriminated. With this assay, all prominent bacterial contaminants of platelet concentrates listed in Annex XIX and Table 14 were detected. Sensitivity tests were performed on the 9 most frequent bacterial contaminants of platelets. The detection limit was less than 20 genome copies for *E. cloacae*, *B. cereus*, *S.*

choleraesuis and *S. marcescens*; less than 15 genome copies for *P. aeruginosa*; and 2 to 3 copies were detected for *S. aureus*, *S. epidermidis*, *E. coli* and *K. pneumoniae*. Further refinements of assay conditions should increase sensitivity levels.

5 **EXAMPLE 13:**

The resolving power of the *tuf* and *atpD* sequences databases is comparable to the biochemical methods for bacterial identification. The present gold standard for bacterial identification is mainly based on key morphological traits and batteries of biochemical tests. Here we demonstrate that the use of *tuf* and *atpD* sequences combined with simple phylogenetic analysis of databases formed by these sequences is comparable to the gold standard. In the process of acquiring data for the *tuf* sequences, we sequenced the *tuf* gene of a strain that was given to us labelled as *Staphylococcus hominis* ATCC 35982. That *tuf* sequence (SEQ ID NO. 192) was incorporated into the *tuf* sequences database and subjected to a basic phylogenetic analysis using the Pileup command from version 10 of the GCG package (Genetics Computer Group, inc.). This analysis indicated that SEQ ID NO. 192 is not associated with other *S. hominis* strains but rather with the *S. warneri* strains. The ATCC 35982 strain was sent to the reference laboratory of the Laboratoire de Santé publique du Québec (LSPQ). They used the classic identification scheme for staphylococci (Kloos and Schleifer, 1975., J. Clin. Microbiol. 1:82-88). Their results shown that although the colonial morphology could correspond to *S. hominis*, the more precise biochemical assays did not. These assays included discriminant mannitol, mannose and ribose acidification tests as well as rapid and dense growth in deep thioglycolate agar. The LSPQ report identified strain ATCC 35982 as *S. warneri* which confirms our database analysis. The same thing happened for *S. warneri* (SEQ ID NO. 187) which had initially been identified as *S. haemolyticus* by a routine clinical laboratory using a low resolving power automated system (MicroScan, AutoScan-4™). Again, the *tuf* and LSPQ analysis agreed on its identification as *S. warneri*. In numerous other instances, in the course of acquiring *tuf* and *atpD* sequence data from various species and genera, analysis of our *tuf* and/or *atpD* sequence databases permitted the exact identification of mislabelled or erroneously identified strains. These results clearly demonstrate the usefulness and the high resolving power of our sequence-based identification assays using the *tuf* and *atpD* sequences databases.

EXAMPLE 14:

Detection of group B streptococci in clinical specimens.

Introduction

Streptococcus agalactiae, the group B streptococcus (GBS), is responsible for a severe illness affecting neonate infants. The bacterium is passed from the healthy carrier mother to the baby during delivery. To prevent this infection, it is recommended to treat expectant mothers susceptible of carrying GBS in their anovaginal flora. Carrier status is often a transient condition and rigorous monitoring requires cultures and classic bacterial identification weeks before delivery. To improve the diagnostic and identification of GBS we developed a rapid, specific and sensitive PCR test fast enough to be performed right at delivery.

Materials and Methods

GBS Clinical Specimens. A total of 66 duplicate anovaginal swabs were collected from 41 consenting pregnant women admitted for delivery at the Centre Hospitalier Universitaire de Québec, Pavillon Saint-François d'Assise following the CDC recommendations. The samples were obtained either before or after rupture of membranes. The swab samples were tested at the Centre de Recherche en Infectiologie de l'Université Laval within 24 hours of collection. Upon receipt, one swab was cut and then the tip of the swab was added to GNS selective broth for identification of group B streptococci (GBS) by the standard culture methods recommended by the Center for Diseases Control. The other swab was processed following the instruction of the IDI DNA extraction kit (Infectio Diagnostics (IDI) Inc.) prior to PCR amplification.

Oligonucleotides. PCR primers, Tsag340 (SEQ ID NO. 549) and Tsag552 (SEQ ID NO. 550) complementary to the regions of the *tuf* gene unique for GBS were designed based upon a multiple sequence alignment using our repertory of *tuf* sequences. Oligo primer analysis software (version 5.0) (National Biosciences) was used to analyse primers annealing temperature, secondary structure potential as well as mispriming and dimerization potential. The primers were synthesized using a model 391 DNA synthesizer (Perkin-Elmer).

A pair of fluorescently labeled adjacent hybridization probes Sag465-F (SEQ ID NO. 583) and Sag436-C (SEQ ID NO. 582) were synthesized and purified by Operon Technologies. They were designed to meet the recommendations of the manufacturer (Idaho Technology) and based upon multiple sequence alignment analysis using our repertory of *tuf* sequences to be specific and ubiquitous for GBS. These adjacent probes, which are separated by one nucleotide, allow fluorescence resonance energy transfer (FRET), generating an increased fluorescence signal when both hybridized simultaneously to their target sequences. The probe SEQ ID NO. 583 was labeled with FITC in 3 prime while SEQ ID NO. 582 was labeled with Cy5 in 5 prime. The

Cy5-labeled probes contained a 3'-blocking phosphate group to prevent extension of the probes during the PCR reactions.

PCR Amplification. Conventional amplifications were performed either from 2 μ l of a purified genomic DNA preparation or cell lysates of anovaginal specimens. The 20 μ l PCR mixture contained 0.4 μ M of each GBS-specific primer (SEQ ID NOs. 549-550), 200 μ M of each deoxyribonucleotide (Pharmacia Biotech), 10 mM Tris-HCl (pH 9.0), 50 mM KCl, 0.1% Triton X-100, 2.5 mM MgCl₂, 3.3 mg/ml bovine serum albumin (BSA) (Sigma), and 0.5 U of *Taq* polymerase (Promega) combined with the TaqStart antibody (Clontech). The TaqStart antibody, which is a neutralizing monoclonal antibody of *Taq* DNA polymerase, was added to all PCR reactions to enhance the efficiency of the amplification. The PCR mixtures were subjected to thermal cycling (3 min at 95 °C and then 40 cycles of 1 s at 95 °C, and 30 s at 62 °C with a 2-min final extension at 72 °C) with a PTC-200 DNA Engine thermocycler (MJ research). The PCR-amplified reaction mixture was resolved by agarose gel electrophoresis.

The LightCyclerTM PCR amplifications were performed with 1 μ l of the same preparation as described above. The 10 μ l amplification mixture consisted of 0.4 μ M each GBS-specific primer (SEQ ID NOs. 549-550), 200 μ M each dNTP, 0.2 μ M each fluorescently labeled probe (SEQ ID NOs. 582-583), 300 μ g/ml BSA (Sigma), and 1 μ l of 10x PC2 buffer (containing 50 mM Tris-HCl (pH 9.1), 16 mM ammonium sulfate, 3.5 mM Mg²⁺, and 150 μ g/ml BSA) and 0.5 U KlenTaq1TM (AB Peptides) coupled with TaqStartTM antibody (Clontech). KlenTaq1TM is a highly active and more heat-stable DNA polymerase without 5'-exonuclease activity. This prevents hydrolysis of hybridized probes by the 5' to 3' exonuclease activity. A volume of 7 μ l of the PCR mixture was transferred into a composite capillary tube (Idaho Technology). The tubes were then centrifuged to move the reaction mixture to the tips of the capillaries and then cleaned with optical-grade methanol. Subsequently the capillaries were loaded into the carousel of a LC32 LightCyclerTM (Idaho Technology), an instrument that combines rapid-cycle PCR with fluorescence analysis for continuous monitoring during amplification. The PCR reaction mixtures were subjected to a denaturation step at 94 °C for 3 min followed by 45 cycles of 0 s at 94 °C, 20 s at 64 °C and 10 s at 72 °C with a temperature transition rate of 20 °C/s. Fluorescence signals were obtained at each cycle by sequentially positioning each capillary on the carousel at the focus of optical elements affiliated to the built-in fluorimeter for 100 milliseconds. Complete amplification and analysis required about 35 min.

Specificity And Sensitivity Tests. The specificity of the conventional and LightCyclerTM PCR assays was verified by using purified genomic DNA (0.1 ng/reaction) from a battery of ATCC reference strains representing 35 clinically relevant gram-positive species (*Abiotrophia defectiva* ATCC 49176, *Bifidobacterium*

breve ATCC 15700, *Clostridium difficile* ATCC 9689, *Corynebacterium urealyticum* ATCC 43042, *Enterococcus casseliflavus* ATCC 25788, *Enterococcus durans* ATCC 19432, *Enterococcus faecalis* ATCC 29212, *Enterococcus faecium* ATCC 19434, *Enterococcus gallinarum* ATCC 49573, *Enterococcus raffinosus* ATCC 49427, *Lactobacillus reuteri* ATCC 23273, *Lactococcus lactis* ATCC 19435, *Listeria monocytogenes* ATCC 15313, *Peptococcus niger* ATCC 27731, *Peptostreptococcus anaerobius* ATCC 27337, *Peptostreptococcus prevotii* ATCC 9321, *Staphylococcus aureus* ATCC 25923, *Staphylococcus epidermidis* ATCC 14990, *Staphylococcus haemolyticus* ATCC 29970, *Staphylococcus saprophyticus* ATCC 15305, *Streptococcus agalactiae* ATCC 27591, *Streptococcus anginosus* ATCC 33397, *Streptococcus bovis* ATCC 33317, *Streptococcus constellatus* ATCC 27823, *Streptococcus dysgalactiae* ATCC 43078, *Streptococcus gordonii* ATCC 10558, *Streptococcus mitis* ATCC 33399, *Streptococcus mutans* ATCC 25175, *Streptococcus oralis* ATCC 35037, *Streptococcus parauberis* ATCC 6631, *Streptococcus pneumoniae* ATCC 6303, *Streptococcus pyogenes* ATCC 19615, *Streptococcus salivarius* ATCC 7073, *Streptococcus sanguinis* ATCC 10556, *Streptococcus uberis* ATCC 19436). These microbial species included 15 species of streptococci and many members of the normal vaginal and anal floras. In addition, 40 GBS isolates of human origin, whose identification was confirmed by the Latex agglutination test (Streptex, Murex), were also used to evaluate the ubiquity of the assay.

For determination of the sensitivities (i.e., the minimal number of genome copies that could be detected) for conventional and LightCycler™ PCR assays, serial 10-fold or 2-fold dilutions of purified genomic DNA from 5 GBS ATCC strains were used.

Results

Evaluation of the GBS-specific conventional and LightCycler™ PCR assay.

The specificity of the two assays demonstrated that only DNAs from GBS strains could be amplified. Both PCR assays did not amplify DNAs from any other bacterial species tested including 14 streptococcal species other than GBS as well as phylogenetically related species belonging to the genera *Enterococcus*, *Peptostreptococcus* and *Lactococcus*. Important members of the vaginal or anal flora, including coagulase-negative staphylococci, *Lactobacillus* sp., and *Bacteriodes* sp. were also negative with the GBS-specific PCR assay. The LightCycler™ PCR assays detected only GBS DNA by producing an increased fluorescence signal which was interpreted as a positive PCR result. Both PCR methods were able to amplify all of 40 GBS clinical isolates, showing a perfect correlation with the phenotypic identification methods.

The sensitivity of the assay was determined by using purified genomic DNA

from the 5 ATCC strains of GBS. The detection limit for all of these 5 strains was one genome copy of GBS. The detection limit of the assay with the LightCycler™ was 3.5 fg of genomic DNA (corresponding to 1-2 genome copies of GBS). These results confirmed the high sensitivity of our GBS-specific PCR assay.

5 **Direct Detection of GBS from anovaginal specimens.** Among 66 anovaginal specimens tested, 12 were positive for GBS by culture. 11 of them were also identified by both PCR assays. The sensitivity of both PCR methods with vaginal/anal specimens for identifying colonization status in pregnant women at delivery was 91.7% when compared to culture results. The specificity and positive
10 predictive values were both 100% and the negative predictive value was 97.8%. The time for obtaining results was approximately 45 min for LightCycler™ PCR, approximately 100 min for conventional PCR and 48 hours for culture.

Conclusion

15 We have developed for the detection of GBS two PCR assays (conventional and LightCycler™) which are specific (i.e., no amplification of DNA from a variety of bacterial species other than GBS) and sensitive (i.e., able to detect around 1 genome copy for several reference ATCC strains of GBS). Both PCR assays are able to detect
20 GBS directly from anovaginal specimens in a very short turnaround time. Using the real-time PCR assay on LightCycler™, we can detect GBS carriage in pregnant women at delivery within 45 minutes.

EXAMPLE 15:

25 Simultaneous identification of *Streptococcus pyogenes* and its pyrogenic exotoxin A.
The rapid detection of *Streptococcus pyogenes* and of its pyrogenic exotoxin A is of clinical importance. We developed a multiplex assay which permits the detection of strains of *S. pyogenes* carrying the pyrogenic toxin A gene, which is associated with
30 scarlet fever and other pathologies. In order to specifically detect *S. pyogenes*, nucleotide sequences of the pyrrolidone carboxyl peptidase gene (*pcp*) were aligned to design PCR primers Spy291 (SEQ ID NO. 1211) and Spy473 (SEQ ID NO. 1210). Next, we designed primers for the specific detection of the pyrogenic exotoxin A. Nucleotide sequences of the *speA* gene, carried on the bacteriophage T12, were
35 aligned as shown in Annex XXIII to design PCR primers Spytx814 (SEQ ID NO. 994) and Spytx 927 (SEQ ID NO. 995).

The primer pairs : oligos SEQ ID NOs. 1210-1211, yielding an amplification product of 207 bp, and oligos SEQ ID NOs. 994-995, yielding an amplification product of
40 135 bp, were used in the PCR assay.

PCR amplification was carried out using 0.4 μ M of both pairs of primers, 2.5 mM MgCl_2 , BSA 0.05 μ M, dNTP 0.2 μ M (Pharmacia), 10X PCR reaction buffer (Promega), 0.025 U/ml *Taq* DNA polymerase (Promega) combined with TaqStart (Clontech Laboratories Inc.), and 1 μ l of genomic DNA sample in a final volume of 20 μ l. PCR amplification was performed using a PTC-200 thermal cycler (MJ Research). The optimal cycling conditions for maximum sensitivity were 3 minutes at 94 °C for initial denaturation, then forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 63 °C, followed by a final step of 2 minutes at 72 °C. Detection of the PCR products was made by agarose gel (2%) electrophoresis containing 0.25 μ g/ml of ethidium bromide. Visualization of the PCR products was made under UV at 254 nm.

The detection limit was less than 5 genome copies for both *S. pyogenes* and its pyrogenic exotoxin A. The assay was specific for pyrogenic exotoxin A-producing *S. pyogenes*: strains of the 27 other species of *Streptococcus* tested were all negative, as well as 20 strains of various gram-positive and gram-negative bacterial species.

A similar approach was used to design an alternative set of *speA*-specific primers (SEQ ID NOs. 996 to 998, see Annex XXIV). In addition, another set of primers based on the *tuf* gene (SEQ ID NOs. 999 to 1001, see Annex XXV) could be used to specifically detect *Streptococcus pyogenes*.

EXAMPLE 16 :

Real-time identification of Shiga toxin-producing bacteria. Shiga toxin-producing *Escherichia coli* and *Shigella dysenteriae* cause bloody diarrhea. Currently, identification relies mainly on the phenotypic identification of *S. dysenteriae* and *E. coli* serotype O157:H7. However, other serotypes of *E. coli* are increasingly found to be producers of type 1 and/or type 2 Shiga toxins. Two pairs of PCR primers targeting highly conserved regions present in each of the Shiga toxin genes *stx*₁ and *stx*₂ were designed to amplify all variants of those genes (see Annexes XXVI and XXVII). The first primer pair, oligonucleotides 1SLT224 (SEQ ID NO. 1081) and 1SLT385 (SEQ ID NO. 1080), yields an amplification product of 186 bp from the *stx*₁ gene. For this amplicon, the 1SLTB1-Fam (SEQ ID NO. 1084) molecular beacon was designed for the specific detection of *stx*₁ using the fluorescent label 6-carboxy-fluorescein. A second pair of PCR primers, oligonucleotides 2SLT537 (SEQ ID NO. 1078) and 2SLT678b (SEQ ID NO. 1079), yields an amplification product of 160 bp from the *stx*₂ gene. Molecular beacon 2SLTB1-Tet (SEQ ID NO. 1085) was designed for the specific detection of *stx*₂ using the fluorescent label 5-tetrachloro-fluorescein.

Both primer pairs were combined in a multiplex PCR assay.

PCR amplification was carried out using 0.8 μ M of primers pair SEQ ID NOs. 1080-1081, 0.5 μ M of primer pair SEQ ID NOs. 1078-1079, 0.3 μ M of each molecular beacon, 8 mM MgCl₂, 12.25 μ g BSA, 0.2 mM dNTPs (Pharmacia), 50 mM Tris-HCl, 16 mM NH₄SO₄, 1X TaqMaster (Eppendorf), 2.5 U KlenTaq1 DNA polymerase (AB Peptides) combined with TaqStart (Clontech Laboratories Inc.), and 1 μ l of genomic DNA sample in a final volume of 25 μ l. PCR amplification was performed using a SmartCycler thermal cycler (Cepheid). The optimal cycling conditions for maximum sensitivity were 60 seconds at 95 °C for initial denaturation, then 45 cycles of three steps consisting of 10 seconds at 95 °C, 15 seconds at 56 °C and 5 seconds at 72 °C. Detection of the PCR products was made in real-time by measuring the fluorescent signal emitted by the molecular beacon when it hybridizes to its target at the end of the annealing step at 56 °C.

The detection limit was the equivalent of less than 5 genome copies. The assay was specific for the detection of both toxins, as demonstrated by the perfect correlation between PCR results and the phenotypic characterization performed using antibodies specific for each Shiga toxin type. The assay was successfully performed on several Shiga toxin-producing strains isolated from various geographic areas of the world, including 10 O157:H7 *E. coli*, 5 non-O157:H7 *E. coli* and 4 *S. dysenteriae*.

EXAMPLE 17:

Development of a PCR assay for the detection and identification of staphylococci at genus and species levels and its associated *mecA* gene. The *Staphylococcus* genus-specific PCR primers described in Example 7 (SEQ ID NOs. 553 and 575) were used in multiplex with the *mecA*-specific PCR primers described in previous US patent serial no. 5,994,066 (SEQ ID NOs. 261 and 262 in the said patent) as well as with the *S. aureus*-specific PCR primers SEQ ID NOs. 152 and 153 described in the said patent. Sequence alignment analysis of 10 publicly available *mecA* gene sequences were performed to design an internal probe for *mecA* (SEQ ID NO. 1177). An internal probe was also designed for the *S. aureus*-specific amplicon (SEQ ID NO 1234). PCR amplification and agarose gel analysis of the amplified products were performed as described in Example 7, with the exception that 0.4 μ M (each) of the two *Staphylococcus* genus-specific primers (SEQ ID NOs. 553 and 575) and 0.4 μ M (each) of the *mecA* gene primers and 0.4 μ M (each) of the *S. aureus*-specific primers were used in the PCR mixture. The specificity of the multiplex assay with 40-cycle PCR protocols was verified by using purified genomic DNA from five methicillin-resistant and fifteen methicillin-sensitive staphylococcal strains. The sensitivity of the

5 multiplex assay with 40-cycle PCR protocols was determined by using purified genomic DNA from five methicillin-resistant and seven methicillin-sensitive staphylococcal strains. A detection limit of 3-5 genome copies was obtained, depending on the staphylococcal species tested. Furthermore, the *mecA*-specific internal probe and the *S. aureus*-specific internal probe combined with (i) the species-specific internal probes, (ii) the genus-specific internal probes and (iii) the coagulase-negative staphylococci specific internal probes (described in Example 7) were able to recognize three methicillin-resistant staphylococcal strains with high sensitivity and specificity.

10 The format of the assay is not limited to the one described above. A person skilled in the art could adapt the assay for different formats such as PCR with real-time detection using molecular beacon probes. Molecular beacon probes designed to be used in this assay include, but are not limited to, SEQ ID NO. 1232 for detection of the *S. aureus*-specific amplicon, SEQ ID NO. 1233 for detection of coagulase-negative staphylococci and SEQ ID NO. 1231 for detection of *mecA*.

EXAMPLE 18:

20 Sequencing of *pbp1a*, *pbp2b* and *pbp2x* genes of *Streptococcus pneumoniae*. The comparison of publicly available *pbp1a*, *pbp2b* and *pbp2x* sequences from a variety of *S. pneumoniae* strains revealed conserved regions allowing the design of PCR primers able to amplify *pbp1a*, *pbp2b*, and *pbp2x* sequences of several strains of *S. pneumoniae* having various levels of resistance to penicillin and third-generation cephalosporins. Using primer pairs Spnpbp1a876 and Spnpbp1a2163 (SEQ ID NOs. 1125 and 1126), Spnpbp2b580 and Spnpbp2b2045 (SEQ ID NOs. 1142 and 1143), and Spnpbp2x469 and Spnpbp2x2212 (SEQ ID NOs. 1146 and 1147), it was possible to amplify and sequence *pbp1a* sequences SEQ ID NOs. 1004-1018, *pbp2b* sequences SEQ ID NOs. 1019-1033, and *pbp2x* sequences SEQ ID NOs. 1034-1048. Six other PCR primers (SEQ ID NOs. 1127-1128, 1144-1145, 1148-1149) were also designed and used to complete the sequencing of *pbp1a*, *pbp2b* and *pbp2x* amplification products.

EXAMPLE 19:

35 Sequencing of *hexA* genes of *Streptococcus* species. The *hexA* sequence of *S. pneumoniae* described in previous US patent serial no. 5,994,066 (SEQ ID NO. 31 in the said patent, SEQ ID NO. 1183 in the present application) allowed the design of a PCR primer (SEQ ID NO. 1182) which was used with primer Spn1401 described in previous US patent serial no. 5,994,066 (SEQ ID NO. 156 in the said patent, SEQ ID

NO. 1179 in the present application) to amplify the *hexA* gene of one strain of *S. oralis*, three strains of *S. mitis* and four strains of *S. pneumoniae* (Annex XLII). Using primers SEQ ID NO. 1179 and SEQ ID NO. 1182, it was possible to amplify and sequence *S. pneumoniae hexA* (SEQ ID NOs. 1184-1187), *S. mitis hexA* (SEQ ID
 5 NOs. 1189-1191) and *S. oralis hexA* (SEQ ID NO. 1188).

EXAMPLE 20:

10 Development of a multiplex PCR assay for the detection of *Streptococcus pneumoniae* and its penicillin resistance genes.

Material and Methods

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Bacterial strains. The specificity of the multiplex PCR assay was verified by using a panel of ATCC (American Type Culture Collection) reference strains consisting of 33 gram-negative and 67 gram-positive bacterial species (Table 13). In addition, 55 clinical isolates of *Streptococcus pneumoniae* and 16 strains of *S. mitis*
 20 and 3 strains of *S. oralis* from the microbiology laboratory of the Centre Hospitalier Universitaire de Québec, Pavillon Centre Hospitalier de l'Université Laval (CHUL) (Ste-Foy, Québec, Canada) and from the Laboratoire de santé publique du Québec (LSPQ) (Sainte-Anne de Bellevue, Québec, Canada) were also tested to further validate the *Streptococcus pneumoniae*-specific PCR assay. The penicillin MICs
 25 (minimal inhibitory concentration) of 55 isolates were measured by the broth dilution method according to the recommended protocol of NCCLS.

PCR primers and internal probes. The comparison of *hexA* sequences from a variety of streptococcal species described in Example 19 (SEQ ID NOs. 1184-1191)
 30 allowed the selection of a PCR primer specific for *S. pneumoniae*, Spnhexa1613 (SEQ ID NO. 1181). This primer was used with the *S. pneumoniae* species-specific primer SEQ ID NO. 1179 to generate an amplification product of 213 bp (Annex XLII). The PCR primer SEQ ID NO. 1181 is located 87 nucleotides downstream on the *hexA* sequence compared to the original *S. pneumoniae* species-specific PCR
 35 primer Spn1515 described in previous US patent serial no. 5,994,066 (SEQ ID NO. 157 in the said patent). These modifications were done to ensure the design of the *S. pneumoniae* species-specific internal probe according to the new *hexA* sequences of several close streptococcal species (SEQ ID NOs. 1184-1191). The comparison of *pbp1a* sequences from *S. pneumoniae* strains with various levels of penicillin
 40 resistance allowed the identification of amino acid substitutions Ile-459 to Met and

Ser-462 to Ala that occur in isolates with high-level penicillin resistance (MICs $\geq 1\mu\text{g/ml}$), and amino acid substitutions Ser-575 to Thr, Gln-576 to Gly and Phe-577 to Tyr that are common to all penicillin-resistant isolates with MICs $\geq 0.25\mu\text{g/ml}$. As shown in annex XXXI, PCR primer pair Spnpbp1a1365 and Spnpbp1a1747 (SEQ ID NOs. 1130 and 1131) were designed to detect high-level penicillin resistance (MICs $\geq 1\mu\text{g/ml}$), whereas PCR primer pair Spnpbp1a1591 (SEQ ID NO. 1129) and SEQ ID NO. 1131 were designed to detect intermediate-level penicillin resistance ($0.25 \leq \text{MICs} \leq 0.5\mu\text{g/ml}$).

The comparison of *hexA* sequences allowed the design of an internal probe specific for *S. pneumoniae* (SEQ ID NO. 1180) (Annex XLII). The range of mismatches between the *S. pneumoniae*-specific 213-bp amplicon was from 2 to 5, in the middle of the 19-bp probe. Five internal probes containing all possible mutations were designed to detect the high-level penicillin resistance 383-bp amplicon (SEQ ID NOs. 1197, 1217-1220) and five internal probes containing all possible mutations were designed to detect the 156-bp amplicon which includes both high-level and intermediate penicillin resistance (SEQ ID NOs. 1094, 1192, 1193, 1214 and 1216). Design and synthesis of primers and probes, and detection of the hybridization were performed as described in Example 7. Annex XXXI illustrates one of the internal probes for detection of the high-level penicillin resistance 383-bp amplicon (SEQ ID NO. 1197) and one of the internal probes for detection of the intermediate level penicillin resistance 156-bp amplicon (SEQ ID NO. 1193).

PCR amplification. For all bacterial species, amplification was performed from purified genomic DNA. One μl of 0.1 nanogram of genomic DNA was transferred directly to a 19 μl PCR mixture. Each PCR reaction contained 50 mM KCl; 10 mM Tris-HCl (pH 9.0); 0.1% Triton X-100; 2.5 mM MgCl_2 ; 0.1 μM (each) of the *S. pneumoniae* species-specific primers SEQ ID NO. 1179 and SEQ ID NO. 1181, 0.1 μM of the penicillin resistance primer SEQ ID NO. 1129, 0.7 μM of the other penicillin resistance primer SEQ ID NO. 1130, and 0.6 μM of the high-level penicillin resistance primer SEQ ID NO. 1131; 200 μM (each) of the four deoxynucleoside triphosphates; 3.3 $\mu\text{g}/\mu\text{l}$ bovine serum albumin (BSA); and 0.5 U *Taq* polymerase coupled with *TaqStart*TM Antibody.

For determination of the sensitivities of the PCR assays, two-fold dilutions of purified genomic DNA were used to determine the minimal number of genome copies which can be detected.

Results

Amplifications with the multiplex PCR assay. The specificity of the assay was

assessed by performing 40-cycle PCR amplifications with the panel of gram-positive (67 species from 12 genera) and gram-negative (33 species from 17 genera) bacterial species listed in Table 13. All bacterial species tested other than *S. pneumoniae* were negative except *S. mitis* and *S. oralis*. Ubiquity tests were performed using a collection of 55 clinical *S. pneumoniae* isolates provided by the microbiology laboratory of the CHUL and the LSPQ, including high-level penicillin resistance (n=37), intermediate resistance (n=11) and sensitive (n=7) strains. There was a perfect correlation between PCR and standard susceptibility testing for 37 isolates with high-level penicillin resistance and 7 penicillin-sensitive isolates. Among 11 isolates with intermediate penicillin resistance, 9 had intermediate resistance based on PCR but two isolates with MIC of 0.5 µg/ml showed a high-level penicillin resistance based on genotyping. This demonstrated that MIC of 0.5 µg/ml may represent intermediate or high-level penicillin resistance. In general, there was a good correlation between the genotype and classical identification schemes.

The sensitivity of the *S. pneumoniae*-specific assay with 40-cycle PCR protocols was determined by using purified genomic DNA from 9 isolates of *S. pneumoniae*. The detection limit was 2-10 genome copies, depending on the *pbp* amplification pattern.

Hybridization between multiplex PCR amplicons and internal probes. The *S. pneumoniae*-specific internal probe did not hybridize to the *S. mitis* and *S. oralis* non-specific PCR amplification products generated from the *S. pneumoniae*-specific PCR primers. More precisely, this specificity was tested by using genomic DNA purified from 16 strains of *S. mitis* and from 3 strains of *S. oralis*. The ubiquity of the assay was tested by using genomic DNA from 15 strains of *S. pneumoniae*. In summary, the combination of the PCR and hybridization assays results in a highly specific test for the detection of penicillin-resistant *Streptococcus pneumoniae*.

EXAMPLE 21:

Sequencing of the vancomycin resistance *vanA*, *vanC1*, *vanC2* and *vanC3* genes. The publicly available sequences of the *vanH-vanA-vanX-vanY* locus of transposon Tn1546 from *E. faecalis*, *vanC1* sequence from one strain of *E. gallinarum*, *vanC2* and *vanC3* sequences from a variety of *E. casseliflavus* and *Enterococcus flavescens* strains, respectively, allowed the design of PCR primers able to amplify the *vanA*, *vanC1*, *vanC2* and *vanC3* sequences of several *Enterococcus* species. Using primer pairs van6877 and van9106 (SEQ ID NOs. 1150 and 1155), vanC1-122 and vanC1-1315 (SEQ ID NOs. 1110 and 1109), and vanC2C3-1 and vanC2C3-1064 (SEQ ID NOs. 1108 and 1107), it was possible to amplify and sequence *vanA* sequences

SEQ ID NOs. 1049-1057, *vanC1* sequences SEQ ID NOs. 1058-1059, *vanC2* sequences SEQ ID NOs. 1060-1063 and *vanC3* sequences SEQ ID NOs. 1064-1066, respectively. Three other PCR primers (SEQ ID NOs. 1151-1154) were also designed and used to complete the sequencing of *vanA* amplification products.

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EXAMPLE 22:

Development of a PCR assay for the detection and identification of enterococci at genus and species levels and its associated resistance genes *vanA* and *vanB*. The comparison of *vanA* and *vanB* sequences revealed conserved regions allowing the design of PCR primers specific for both *vanA* and *vanB* sequences (Annex XXXVIII). The PCR primer pair vanAB459 and vanAB830R (SEQ ID NOs. 1112 and 1111) was used in multiplex with the *Enterococcus* genus-specific primers Encg313dF and Encg599c (SEQ ID NOs. 1137 and 1136) described in Example 11. Sequence alignment analysis of *vanA* and *vanB* sequences revealed regions suitable for the design of internal probes specific for *vanA* (SEQ ID NO. 1170) and *vanB* genes (SEQ ID NO. 1171). PCR amplification and agarose gel analysis of the amplified products were performed as described in Example 11. The specificity of the multiplex assay with 40-cycle PCR was verified by using 0.1 nanogram of purified genomic DNA from a panel of bacteria listed in Table 10. The sensitivity of the multiplex assay with 40-cycle PCR was verified with three strains of *E. casseliflavus*, eight strains of *E. gallinarum*, two strains of *E. flavescens*, two vancomycin-resistant strains of *E. faecalis* and one vancomycin-sensitive strain of *E. faecalis*, three vancomycin-resistant strains of *E. faecium* and one vancomycin-sensitive strain of *E. faecium*, and one strain of each of the other enterococcal species listed in Table 10. A detection limit of 1-10 genome copies was obtained, depending on the enterococcal species tested. In addition to the species-specific internal probes described in Example 11, the *vanA*- and *vanB*-specific internal probes were able to recognize vancomycin-resistant enterococcal species with high sensitivity, specificity and ubiquity and with a perfect correlation between the genotypic and phenotypic analysis.

The format of the assay is not limited to the one described above. A person skilled in the art could adapt the assay for different formats such as PCR with real-time detection using molecular beacon probes. Molecular beacon probes designed to be used in this assay include, but are not limited to, SEQ ID NO. 1236 for the detection of *E. faecalis*, SEQ ID NO. 1235 for the detection of *E. faecium*, SEQ ID NO. 1240 for the detection of *vanA*, and SEQ ID NO. 1241 for the detection of *vanB*.

EXAMPLE 23:

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Development of a multiplex PCR assay for detection and identification of vancomycin-resistant *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus gallinarum*, *Enterococcus casseliflavus*, and *Enterococcus flavescens*. The comparison of *vanA* and *vanB* sequences revealed conserved regions allowing design of a PCR primer pair (SEQ ID NOs. 1089 and 1090) specific for *vanA* sequences (Annex XXVIII) and a PCR primer pair (SEQ ID NOs. 1095 and 1096) specific for *vanB* sequences (Annex XXIX). The *vanA*-specific PCR primer pair (SEQ ID NOs. 1089 and 1090) was used in multiplex with the *vanB*-specific PCR primer pair (SEQ ID NOs. 1095 and 1096). The comparison of *vanC1*, *vanC2* and *vanC3* sequences revealed conserved regions allowing design of PCR primers (SEQ ID NOs. 1101 and 1102) able to generate a 158-bp amplicon specific for *E. gallinarum*, *E. casseliflavus* and *E. flavescens* (Annex XXX). The *vanC*-specific PCR primer pair (SEQ ID NOs. 1101 and 1102) was used in multiplex with the *E. faecalis* species-specific PCR primer pair described in previous US patent serial no. 5,994,066 (SEQ ID NOs. 40 and 41 in the said patent) and with the *E. faecium* species-specific PCR primer pair described in previous patent application WO98/20157 (SEQ ID NOs. 1 and 2 in the said application). For both multiplexes, the optimal cycling conditions for maximum sensitivity and specificity were found to be 3 min. at 94 °C, followed by forty cycles of two steps consisting of 1 second at 95 °C and 30 seconds at 58 °C, plus a terminal extension at 72 °C for 2 minutes. Amplification was monitored on agarose gel electrophoresis by staining the amplified DNA with ethidium bromide. The *vanA*-specific PCR primer pair (SEQ ID NOs. 1089 and 1090), the *vanB*-specific primers pair (SEQ ID NOs. 1095 and 1096) and the *vanC*-specific primer pair (SEQ ID NOs. 1101 and 1102) were tested for their specificity by using 0.1 nanogram of purified genomic DNA from a panel of 5 vancomycin-sensitive *Enterococcus* species, 3 vancomycin-resistant *Enterococcus* species, 13 other gram-positive bacteria and one gram-negative bacterium. Specificity tests using the *E. faecium* species-specific PCR primer pair described in previous patent application WO98/20157 (SEQ ID NOs. 1 and 2 in the said application) and the *E. faecalis* species-specific PCR primer pair described in previous US patent serial no. 5,994,066 (SEQ ID NOs. 40 and 41 in the said patent) were performed on a panel of 37 gram-positive bacterial species. All *Enterococcus* strains were amplified with high specificity and there was a perfect correlation between the genotypic and phenotypic analysis. Finally, the sensitivity of the assays was determined for several strains of *E. gallinarum*, *E. casseliflavus*, *E. flavescens* and vancomycin-resistant *E. faecalis* and *E. faecium*. Using each of the *E. faecalis* and *E. faecium* species-specific PCR primer pairs as well as *vanA*, *vanB* and *vanC*-specific PCR primers used alone or in multiplex as described above, the sensitivity ranged from 1 to 10 genome copies.

The format of the assay is not limited to the one described above. A person skilled in the art could adapt the assay for different formats such as PCR with real-time

detection using molecular beacon probes. Molecular beacon probes designed to be used in this assay include, but are not limited to, SEQ ID NO. 1238 for the detection of *E. faecalis*, SEQ ID NO. 1237 for the detection of *E. faecium*, SEQ ID NO. 1239 for the detection of *vanA*, and SEQ ID NO. 1241 for the detection of *vanB*.

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EXAMPLE 24:

Universal amplification involving the EF-G (*fusA*) subdivision of *tuf* sequences. As shown in Figure 3, primers SEQ ID NOs. 1228 and 1229 were designed to amplify the region between the end of *fusA* and the beginning of *tuf* genes in the *str* operon. Genomic DNAs from a panel of 35 strains were tested for PCR amplification with those primers. The following strains showed a positive result: *Abiotrophia adiacens* ATCC 49175, *Abiotrophia defectiva* ATCC 49176, *Bacillus subtilis* ATCC 27370, *Clostridium difficile* ATCC 9689, *Enterococcus avium* ATCC 14025, *Enterococcus casseliflavus* ATCC 25788, *Enterococcus cecorum* ATCC 43198, *Enterococcus faecalis* ATCC 29212, *Enterococcus faecium* ATCC 19434, *Enterococcus flavescens* ATCC 49996, *Enterococcus gallinarum* ATCC 49573, *Enterococcus solitarius* ATCC 49428, *Escherchia coli* ATCC 11775, *Haemophilus influenzae* ATCC 9006, *Lactobacillus acidophilus* ATCC 4356, *Peptococcus niger* ATCC 27731, *Proteus mirabilis* ATCC 25933, *Staphylococcus aureus* ATCC 43300, *Staphylococcus auricularis* ATCC 33753, *Staphylococcus capitis* ATCC 27840, *Staphylococcus epidemidis* ATCC 14990, *Staphylococcus haemolyticus* ATCC 29970, *Staphylococcus hominis* ATCC 27844, *Staphylococcus lugdunensis* ATCC 43809, *Staphylococcus saprophyticus* ATCC 15305, *Staphylococcus simulans* ATCC 27848, and *Staphylococcus warneri* ATCC 27836. This primer pair could amplify additional bacterial species; however, there was no amplification for some species, suggesting that the PCR cycling conditions could be optimized or the primers modified. For example, SEQ ID NO. 1227 was designed to amplify a broader range of species. In addition to other possible primer combinations to amplify the region covering *fusA* and *tuf*, Figure 3 illustrates the positions of amplification primers SEQ ID NOs. 1221-1227 which could be used for universal amplification of *fusA* segments. All of the above mentioned primers (SEQ ID NOs. 1221-1229) could be useful for the universal and/or the specific detection of bacteria.

EXAMPLE 25:

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, Molecular Ecology 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 5 bacterial strains of *Staphylococcus saprophyticus* as well as with bacterial strains of 27 other staphylococcal (non-*S. saprophyticus*) species. For all bacterial species, amplification was performed directly from one μL (0.1 ng/ μL) of purified genomic DNA. The 25 μL PCR reaction mixture contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl_2 , 1.2 μM of only one of the 20 different AP-PCR primers OPAD, 200 μM of each of the four dNTPs, 0.5 U of *Taq* DNA polymerase (Promega Corp., Madison, Wis.) combined with TaqStartTM antibody (Clontech Laboratories Inc., Palo Alto, CA). PCR reactions were subjected to cycling using a MJ Research PTC-200 thermal cycler as follows: 3 min at 96 °C followed by 42 cycles of 1 min at 94 °C for the denaturation step, 1 min at 31 °C for the annealing step and 2 min at 72 °C for the extension step. A final extension step of 7 min at 72 °C followed the 42 cycles to ensure complete extension of PCR products. Subsequently, twenty microliters of the PCR-amplified mixture were resolved by electrophoresis on a 1.5 % agarose gel containing 0.5 $\mu\text{g/mL}$ 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-16 (sequence: 5'-AACGGGCGTC-3'). Amplification with this primer consistently showed a band corresponding to a DNA fragment of approximately 380 bp for all *Staphylococcus saprophyticus* strains tested but not for any of the other staphylococcal species tested.

The band corresponding to the 380 bp amplicon, specific and ubiquitous for *S. saprophyticus* based on AP-PCR, was excised from the agarose gel and purified using the QIAquickTM gel extraction kit (QIAGEN Inc.). The gel-purified DNA fragment was cloned into the T/A cloning site of the pCR 2.1TM plasmid vector (Invitrogen Inc.) using T4 DNA ligase (New England BioLabs). Recombinant plasmids were transformed into *E. coli* DH5 α competent cells using standard procedures. All reactions were performed according to the manufacturer's instructions. Plasmid DNA isolation was done by the method of Birnboim and Doly (Nucleic Acid Res., 1979, 7:1513-1523) for small-scale preparations. All plasmid DNA preparations were digested with the EcoRI restriction endonuclease to ensure the presence of the approximately 380 bp AP-PCR insert into the plasmid. 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 (midi format). These large-scale plasmid preparations were used for automated DNA sequencing.

The 380 bp nucleotide sequence was determined for three strains of *S. saprophyticus* (SEQ ID NOs. 74, 1093, and 1198). 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 the Applied Biosystems automated DNA sequencer (model 373A) with their PRISMTM Sequenase^{RTM} Terminator Double-stranded DNA Sequencing Kit (Perkin-Elmer Corp., Applied Biosystems Division, Foster City, CA).

Optimal species-specific amplification primers (SEQ ID NOs. 1208 and 1209) have been selected from the sequenced AP-PCR *Staphylococcus saprophyticus* DNA fragments with the help of the primer analysis software Oligo™ 4.0 (National BioSciences Inc.). The selected primers were tested in PCR assays to verify their
5 specificity and ubiquity. Data obtained with DNA preparations from reference ATCC strains of 49 gram-positive and 31 gram-negative bacterial species, including 28 different staphylococcal species, indicate that the selected primer pairs are specific for *Staphylococcus saprophyticus* since no amplification signal has been observed with DNAs from the other staphylococcal or bacterial species tested.

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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
15 claims.

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

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Pathogen	UTI ²	SSI ³	BSI ⁴	Pneumonia	CSF 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
<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
Other streptococci	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 enterococci	1	1	0	0	0
Other staphylococci	2	8	13	2	0
<i>Candida albicans</i>	9	3	5	5	0
Other <i>Candida</i>	2	1	3	1	0
<i>Enterobacter</i> sp.	5	7	4	12	2
<i>Acinetobacter</i> sp.	1	1	2	4	2
<i>Citrobacter</i> sp.	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

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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.

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	
	<i>E. coli</i>	15.6	53.8	24.8	20.3	5.0
10	<i>S. epidermidis</i> and other CoNS ⁵	25.8	-	0.5	7.2	31.0
	<i>S. aureus</i>	9.6	-	9.7	19.4	16.0
	<i>S. pneumoniae</i>	6.3	-	22.5	2.2	-
	<i>E. faecalis</i>	3.0	-	1.0	4.2	-
15	<i>E. faecium</i>	2.6	-	0.2	0.5	-
	<i>Enterococcus</i> sp.	-	-	-	-	9.0
	<i>H. influenzae</i>	1.5	-	3.4	0.4	-
	<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
20	<i>P. mirabilis</i>	-	3.9	2.8	5.3	1.0
	<i>S. pyogenes</i>	-	-	1.9	0.9	-
	<i>Enterobacter</i> sp.	4.1	5.5	0.5	2.3	4.0
	<i>Candida</i> sp.	8.5	-	-	1.0	8.0
	Others	18.5	17.4	28.7	18.9	19.0

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- 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 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.

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

5	Clinical specimens and/or sites	No. of samples tested (%)	% of positive specimens	% of negative specimens
10	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
	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
	Pleural and pericardial fluid	132 (0.4)	1.0	99.0
15	Peritoneal fluid	101(0.3)	28.6	71.4
	Total:	32,966 (100.0)	20.0	80.0

Table 4. Non-limiting example of microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are used in the present invention.

Bacterial species	
5	<i>Achromobacter xylosoxidans</i> subsp. <i>denitrificans</i>
	<i>Acetobacterium woodi</i>
	<i>Acetobacter aceti</i>
	<i>Acetobacter altoacetigenes</i>
10	<i>Acetobacter polyoxogenes</i>
	<i>Acholeplasma laidlawii</i>
	<i>Acidiphilum facilis</i>
	<i>Acinetobacter baumannii</i>
	<i>Acinetobacter calcoaceticus</i>
15	<i>Acinetobacter lwoffii</i>
	<i>Actinomyces meyeri</i>
	<i>Aerococcus viridans</i>
	<i>Aeromonas salmonicida</i>
	<i>Agrobacterium tumefaciens</i>
20	<i>Alcaligenes faecalis</i>
	<i>Allochromatium vinosum</i>
	<i>Anabaena variabilis</i>
	<i>Anacystis nidulans</i>
	<i>Anaerorhabdus furcosus</i>
25	<i>Aquifex aeolicus</i>
	<i>Aquifex pyrophilus</i>
	<i>Azotobacter vinelandii</i>
	<i>Bacillus anthracis</i>
	<i>Bacillus cereus</i>
30	<i>Bacillus firmus</i>
	<i>Bacillus halodurans</i>
	<i>Bacillus megaterium</i>
	<i>Bacillus stearothermophilus</i>
	<i>Bacillus subtilis</i>
35	<i>Bacteroides distasonis</i>
	<i>Bacteroides fragilis</i>
	<i>Bacteroides ovatus</i>
	<i>Bacteroides vulgatus</i>
	<i>Bartonella henselae</i>
40	<i>Bifidobacterium adolescentis</i>
	<i>Bifidobacterium breve</i>
	<i>Bifidobacterium dentium</i>
	<i>Bifidobacterium longum</i>
	<i>Blastochloris viridis</i>
45	<i>Borrelia burgdorferi</i>
	<i>Bordetella pertussis</i>
	<i>Bordetella bronchiseptica</i>
	<i>Branhamella catarrhalis</i>
	<i>Brucella abortus</i>
50	<i>Brevibacterium linens</i>
	<i>Brevibacterium flavum</i>
	<i>Buchnera aphidicola</i>
	<i>Burkholderia cepacia</i>
	<i>Burkholderia mallei</i>
55	<i>Burkholderia pseudomallei</i>
	<i>Campylobacter jejuni</i>
	<i>Cedecea davisae</i>
	<i>Cedecea lapagei</i>
	<i>Cedecea neteri</i>
60	<i>Chlamydia pneumoniae</i>
	<i>Chlamydia psittaci</i>
	<i>Chlamydia trachomatis</i>
	<i>Chlorobium vibrioforme</i>
	<i>Chloroflexus aurantiacus</i>
65	<i>Chryseobacterium meningosepticum</i>
	<i>Citrobacter amalonaticus</i>
	<i>Citrobacter braakii</i>
	<i>Citrobacter farmeri</i>
	<i>Citrobacter freundii</i>
70	<i>Citrobacter koseri</i>
	<i>Citrobacter sedlakii</i>
	<i>Citrobacter werkmanii</i>
	<i>Citrobacter youngae</i>
	<i>Clostridium acetobutylicum</i>
75	<i>Clostridium beijerinckii</i>
	<i>Clostridium bifermentans</i>
	<i>Clostridium botulinum</i>
	<i>Clostridium difficile</i>
	<i>Clostridium innocuum</i>
80	<i>Clostridium histolyticum</i>
	<i>Clostridium novyi</i>
	<i>Clostridium septicum</i>
	<i>Clostridium perfringens</i>
	<i>Clostridium ramosum</i>
85	<i>Clostridium sordellii</i>
	<i>Clostridium tertium</i>
	<i>Clostridium tetani</i>
	<i>Comamonas acidovorans</i>
	<i>Corynebacterium bovis</i>
90	<i>Corynebacterium cervicis</i>
	<i>Corynebacterium diphtheriae</i>
	<i>Corynebacterium flavescens</i>
	<i>Corynebacterium glutamicum</i>
	<i>Corynebacterium kutscheri</i>
95	<i>Corynebacterium minutissimum</i>
	<i>Corynebacterium mycetoides</i>
	<i>Corynebacterium pseudodiphtheriticum</i>
	<i>Corynebacterium pseudogenitalium</i>
	<i>Corynebacterium pseudotuberculosis</i>
100	<i>Corynebacterium renale</i>
	<i>Corynebacterium ulcerans</i>
	<i>Corynebacterium urealyticum</i>
	<i>Corynebacterium xerosis</i>
	<i>Coxiella burnetii</i>
105	<i>Cytophaga lytica</i>
	<i>Deinococcus radiodurans</i>
	<i>Deinonema</i> sp.
	<i>Edwardsiella hoshinae</i>
	<i>Edwardsiella tarda</i>
110	<i>Ehrlichia canis</i>
	<i>Ehrlichia risticii</i>
	<i>Eikenella corrodens</i>
	<i>Enterobacter aerogenes</i>
	<i>Enterobacter agglomerans</i>
115	<i>Enterobacter amnigenus</i>
	<i>Enterobacter asburiae</i>
	<i>Enterobacter cancerogenus</i>

Table 4. Non-limiting example of microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are used in the present invention (continued).

Bacterial species (continued)

5	<i>Enterobacter cloacae</i>		<i>Helicobacter pylori</i>
	<i>Enterobacter gergoviae</i>	65	<i>Herpetosiphon aurantiacus</i>
	<i>Enterobacter hormaechei</i>		<i>Kingella kingae</i>
	<i>Enterobacter sakazakii</i>		<i>Klebsiella ornithinolytica</i>
10	<i>Enterococcus avium</i>		<i>Klebsiella oxytoca</i>
	<i>Enterococcus casseliflavus</i>		<i>Klebsiella planticola</i>
	<i>Enterococcus cecorum</i>	70	<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>
	<i>Enterococcus columbae</i>		<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>
	<i>Enterococcus dispar</i>		<i>Klebsiella pneumoniae</i> subsp.
15	<i>Enterococcus durans</i>		<i>rhinoscleromatis</i>
	<i>Enterococcus faecalis</i>		<i>Kluyvera ascorbata</i>
	<i>Enterococcus faecium</i>	75	<i>Kluyvera cryocrescens</i>
	<i>Enterococcus flavescens</i>		<i>Kluyvera georgiana</i>
	<i>Enterococcus gallinarum</i>		<i>Lactobacillus acidophilus</i>
20	<i>Enterococcus hirae</i>		<i>Lactobacillus garvieae</i>
	<i>Enterococcus malodoratus</i>		<i>Lactobacillus paracasei</i>
	<i>Enterococcus mundtii</i>	80	<i>Lactobacillus casei</i> subsp. <i>casei</i>
	<i>Enterococcus pseudoavium</i>		<i>Lactococcus lactis</i> subsp. <i>lactis</i>
	<i>Enterococcus raffinosus</i>		<i>Leclercia adecarboxylata</i>
25	<i>Enterococcus saccharolyticus</i>		<i>Legionella micdadei</i>
	<i>Enterococcus solitarius</i>		<i>Legionella pneumophila</i> subsp. <i>pneumophila</i>
	<i>Enterococcus sulfureus</i>	85	<i>Leminorella grimontii</i>
	<i>Erwinia carotovora</i>		<i>Leminorella richardii</i>
	<i>Escherichia coli</i>		<i>Leptospira biflexa</i>
30	<i>Escherichia fergusonii</i>		<i>Leptospira interrogans</i>
	<i>Escherichia hermannii</i>		<i>Listeria monocytogenes</i>
	<i>Escherichia vulneris</i>	90	<i>Macrococcus caseolyticus</i>
	<i>Eubacterium lentum</i>		<i>Magnetospirillum magnetotacticum</i>
	<i>Eubacterium nodatum</i>		<i>Megamonas hypermegale</i>
35	<i>Ewingella americana</i>		<i>Methanobacterium thermoautotrophicum</i>
	<i>Francisella tularensis</i>		<i>Methanococcus jannaschii</i>
	<i>Frankia alni</i>	95	<i>Methanococcus vanniellii</i>
	<i>Fervidobacterium islandicum</i>		<i>Methanosarcina barkeri</i>
	<i>Fibrobacter succinogenes</i>		<i>Methanosarcina jannaschii</i>
40	<i>Flavobacterium ferrigeneum</i>		<i>Methylobacillus flagellatum</i>
	<i>Flexistipes sinusarabici</i>		<i>Methylomonas clara</i>
	<i>Fusobacterium gonidiaformans</i>	100	<i>Micrococcus luteus</i>
	<i>Fusobacterium necrophorum</i> subsp. <i>necrophorum</i>		<i>Micrococcus lylae</i>
	<i>Fusobacterium nucleatum</i> subsp. <i>polymorphum</i>		<i>Mitsuokella multacida</i>
45	<i>Gardnerella vaginalis</i>		<i>Mobiluncus curtisii</i> subsp. <i>holmesii</i>
	<i>Gemella haemolysans</i>		<i>Moellerella thermoacetica</i>
	<i>Gemella morbillorum</i>	105	<i>Moellerella wisconsensis</i>
	<i>Gloeobacter violaceus</i>		<i>Moraxella osloensis</i>
	<i>Gloeotheca</i> sp.		<i>Morganella morganii</i> subsp. <i>morganii</i>
50	<i>Gluconobacter oxydans</i>		<i>Mycobacterium avium</i>
	<i>Haemophilus actinomycetemcomitans</i>		<i>Mycobacterium bovis</i>
	<i>Haemophilus aphrophilus</i>	110	<i>Mycobacterium gordonae</i>
	<i>Haemophilus ducreyi</i>		<i>Mycobacterium leprae</i>
	<i>Haemophilus haemolyticus</i>		<i>Mycobacterium tuberculosis</i>
55	<i>Haemophilus influenzae</i>		<i>Mycoplasma capricolum</i>
	<i>Haemophilus parahaemolyticus</i>		<i>Mycoplasma gallisepticum</i>
	<i>Haemophilus parainfluenzae</i>	115	<i>Mycoplasma genitalium</i>
	<i>Haemophilus paraphrophilus</i>		<i>Mycoplasma hominis</i>
	<i>Haemophilus segnis</i>		<i>Mycoplasma pirum</i>
60	<i>Hafnia alvei</i>		<i>Mycoplasma mycetoides</i>
	<i>Haloarcula marismortui</i>		<i>Mycoplasma pneumoniae</i>
	<i>Halobacterium salinarum</i>	120	<i>Mycoplasma pulmonis</i>
	<i>Haloferax volcanii</i>		

Table 4. Non-limiting example of microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are used in the present invention (continued).

Bacterial species (continued)

5	<i>Mycoplasma salivarium</i>		<i>Rhodospirillum rubrum</i>
	<i>Myxococcus xanthus</i>	65	<i>Ruminococcus albus</i>
	<i>Neisseria animalis</i>		<i>Salmonella bongori</i>
	<i>Neisseria canis</i>		<i>Salmonella choleraesuis</i> subsp. <i>arizonae</i>
10	<i>Neisseria cinerea</i>		<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>
	<i>Neisseria cuniculi</i>		<i>Salmonella choleraesuis</i> subsp. <i>diarizonae</i>
	<i>Neisseria elongata</i> subsp. <i>elongata</i>	70	<i>Salmonella choleraesuis</i> subsp. <i>houtenae</i>
	<i>Neisseria elongata</i> subsp. <i>intermedia</i>		<i>Salmonella choleraesuis</i> subsp. <i>indica</i>
	<i>Neisseria flava</i>		<i>Salmonella choleraesuis</i> subsp. <i>salamae</i>
15	<i>Neisseria flavescens</i>		<i>Serpulina hyodysenteriae</i>
	<i>Neisseria gonorrhoeae</i>		<i>Serratia ficaria</i>
	<i>Neisseria lactamica</i>	75	<i>Serratia fonticola</i>
	<i>Neisseria meningitidis</i>		<i>Serratia grimesii</i>
	<i>Neisseria mucosa</i>		<i>Serratia liquefaciens</i>
20	<i>Neisseria perflava</i>		<i>Serratia marcescens</i>
	<i>Neisseria pharyngis</i>		<i>Serratia odorifera</i>
	<i>Neisseria polysaccharea</i>	80	<i>Serratia plymuthica</i>
	<i>Neisseria sicca</i>		<i>Serratia rubidaea</i>
	<i>Neisseria subflava</i>		<i>Shewanella putida</i>
25	<i>Neisseria weaveri</i>		<i>Shewanella putrefaciens</i>
	<i>Ochrobactrum anthropi</i>		<i>Shigella boydii</i>
	<i>Pantoea agglomerans</i>	85	<i>Shigella dysenteriae</i>
	<i>Pantoea dispersa</i>		<i>Shigella flexneri</i>
	<i>Paracoccus denitrificans</i>		<i>Shigella sonnei</i>
30	<i>Pasteurella multocida</i>		<i>Spirochaeta aurantia</i>
	<i>Pectinatus frisingensis</i>		<i>Staphylococcus aureus</i>
	<i>Peptococcus niger</i>	90	<i>Staphylococcus aureus</i> subsp. <i>aureus</i>
	<i>Peptostreptococcus anaerobius</i>		<i>Staphylococcus auricularis</i>
	<i>Peptostreptococcus asaccharolyticus</i>		<i>Staphylococcus capitis</i> subsp. <i>capitis</i>
35	<i>Peptostreptococcus prevotii</i>		<i>Staphylococcus cohnii</i>
	<i>Phormidium ectocarpi</i>		<i>Staphylococcus epidermidis</i>
	<i>Pirellula marina</i>	95	<i>Staphylococcus haemolyticus</i>
	<i>Planobispora rosea</i>		<i>Staphylococcus hominis</i>
	<i>Plectonema boryanum</i>		<i>Staphylococcus lugdunensis</i>
40	<i>Porphyromonas asaccharolytica</i>		<i>Staphylococcus saprophyticus</i>
	<i>Porphyromonas gingivalis</i>		<i>Staphylococcus sciuri</i> subsp. <i>sciuri</i>
	<i>Pragia fontium</i>	100	<i>Staphylococcus simulans</i>
	<i>Prevotella melaninogenica</i>		<i>Staphylococcus warneri</i>
	<i>Prevotella oralis</i>		<i>Stigmatella aurantiaca</i>
45	<i>Prevotella ruminicola</i>		<i>Stenotrophomonas maltophilia</i>
	<i>Prochlorothrix hollandica</i>		<i>Streptococcus acidominimus</i>
	<i>Propionibacterium acnes</i>	105	<i>Streptococcus agalactiae</i>
	<i>Propionigenium modestum</i>		<i>Streptococcus anginosus</i>
	<i>Proteus mirabilis</i>		<i>Streptococcus bovis</i>
50	<i>Proteus penneri</i>		<i>Streptococcus cricetus</i>
	<i>Proteus vulgaris</i>		<i>Streptococcus cristatus</i>
	<i>Providencia alcalifaciens</i>	110	<i>Streptococcus downei</i>
	<i>Providencia rettgeri</i>		<i>Streptococcus dysgalactiae</i>
	<i>Providencia rustigianii</i>		<i>Streptococcus equi</i> subsp. <i>equi</i>
55	<i>Providencia stuartii</i>		<i>Streptococcus ferus</i>
	<i>Pseudomonas aeruginosa</i>		<i>Streptococcus gordonii</i>
	<i>Pseudomonas fluorescens</i>	115	<i>Streptococcus macacae</i>
	<i>Pseudomonas stutzeri</i>		<i>Streptococcus mitis</i>
	<i>Psychrobacter phenylpyruvicus</i>		<i>Streptococcus mutans</i>
60	<i>Rahnella aquatilis</i>		<i>Streptococcus oralis</i>
	<i>Rickettsia prowazekii</i>		<i>Streptococcus parasanguinis</i>
	<i>Rhodobacter capsulatus</i>	120	
	<i>Rhodobacter sphaerolides</i>		

Table 4. Non-limiting example of microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are used in the present invention (continued).

Bacterial species (continued)

	<i>Streptococcus pneumoniae</i>		<i>Aspergillus oryzae</i>
	<i>Streptococcus pyogenes</i>		<i>Aspergillus flavus</i>
	<i>Streptococcus ratti</i>	65	<i>Aspergillus fumigatus</i>
	<i>Streptococcus salivarius</i>		<i>Aspergillus niger</i>
10	<i>Streptococcus salivarius</i> subsp. <i>thermophilus</i>		<i>Aureobasidium pullulans</i>
	<i>Streptococcus sanguinis</i>		<i>Bipolaris hawaiiensis</i>
	<i>Streptococcus sobrinus</i>	70	<i>Blastoschizomyces capitatus</i>
	<i>Streptococcus suis</i>		<i>Candida albicans</i>
	<i>Streptococcus uberis</i>		<i>Candida catenulata</i>
15	<i>Streptococcus vestibularis</i>		<i>Candida dubliniensis</i>
	<i>Streptomyces anbofaciens</i>		<i>Candida famata</i>
	<i>Streptomyces aureofaciens</i>	75	<i>Candida glabrata</i>
	<i>Streptomyces cinnamomeus</i>		<i>Candida guilliermondii</i>
	<i>Streptomyces coelicolor</i>		<i>Candida haemulonii</i>
20	<i>Streptomyces collinus</i>		<i>Candida inconspicua</i>
	<i>Streptomyces lividans</i>		<i>Candida kefyr</i>
	<i>Streptomyces ramocissimus</i>	80	<i>Candida krusei</i>
	<i>Streptomyces rimosus</i>		<i>Candida lambica</i>
	<i>Streptomyces venezuelae</i>		<i>Candida lusitanae</i>
25	<i>Synechococcus</i> sp.		<i>Candida norvegensis</i>
	<i>Synechocystis</i> sp.		<i>Candida parapsilosis</i>
	<i>Tatumella ptyseos</i>		<i>Candida rugosa</i>
	<i>Taxeobacter ocealus</i>	85	<i>Candida sphaerica</i>
	<i>Thermoplasma acidophilum</i>		<i>Candida tropicalis</i>
30	<i>Thermotoga maritima</i>		<i>Candida utilis</i>
	<i>Thermus aquaticus</i>		<i>Candida viswanathii</i>
	<i>Thermus thermophilus</i>		<i>Candida zeylanoides</i>
	<i>Thiobacillus ferrooxydans</i>	90	<i>Cladophialophora carrionii</i>
	<i>Thiomonas cuprina</i>		<i>Coccidioides immitis</i>
35	<i>Trabulsirella guamensis</i>		<i>Coprinus cinereus</i>
	<i>Treponema pallidum</i>		<i>Cryptococcus albidus</i>
	<i>Ureaplasma urealyticum</i>		<i>Cryptococcus humicola</i>
	<i>Veillonella parvula</i>	95	<i>Cryptococcus neoformans</i>
	<i>Vibrio alginolyticus</i>		<i>Cunninghamella bertholletiae</i>
40	<i>Vibrio anguillarum</i>		<i>Curvularia lunata</i>
	<i>Vibrio cholerae</i>		<i>Emericella nidulans</i>
	<i>Wolinella succinogenes</i>		<i>Exophiala jeanselmei</i>
	<i>Xanthomonas citri</i>	100	<i>Eremothecium gossypii</i>
	<i>Xanthomonas oryzae</i>		<i>Fonsecaea pedrosoi</i>
45	<i>Xenorhabdus bovienii</i>		<i>Fusarium oxysporum</i>
	<i>Xenorhabdus nematophilus</i>		<i>Geotrichum</i> sp.
	<i>Yersinia bercovieri</i>		<i>Histoplasma capsulatum</i>
	<i>Yersinia enterocolitica</i>	105	<i>Issatchenkia orientalis</i>
	<i>Yersinia frederiksenii</i>		<i>Kluyveromyces lactis</i>
50	<i>Yersinia intermedia</i>		<i>Malassezia furfur</i>
	<i>Yersinia pestis</i>		<i>Malassezia pachydermatidis</i>
	<i>Yersinia pseudotuberculosis</i>		<i>Malbranchea filamentosa</i>
	<i>Yersinia rohdei</i>	110	<i>Metschnikowia pulcherrima</i>
	<i>Yokenella regensburgi</i>		<i>Microsporium audouinii</i>
55	<i>Zoogloea ramigera</i>		<i>Mucor circinelloides</i>
			<i>Neurospora crassa</i>
	Fungal species		<i>Paeciliomyces lilacinus</i>
	<i>Absidia corymbifera</i>	115	<i>Paracoccidioides brasiliensis</i>
60	<i>Absidia glauca</i>		<i>Penicillium marneffeii</i>
	<i>Alternaria alternata</i>		<i>Phialaphora verrucosa</i>
	<i>Arxula adenivorans</i>		<i>Pichia anomala</i>

Table 4. Non-limiting example of microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are used in the present invention (continued).

Fungal species (continued)

5	<i>Piedraia hortai</i>	<i>Trypanosoma brucei</i> subsp. <i>brucei</i>
	<i>Podospora anserina</i>	<i>Trypanosoma congolense</i>
	<i>Puccinia graminis</i>	65 <i>Trypanosoma cruzi</i>
	<i>Pseudallescheria boydii</i>	
10	<i>Rhizomucor racemosus</i>	
	<i>Rhizopus oryzae</i>	
	<i>Rhodotorula minuta</i>	
	<i>Rhodotorula mucilaginosa</i>	
	<i>Saccharomyces cerevisiae</i>	
15	<i>Saksenaea vasiformis</i>	
	<i>Schizosaccharomyces pombe</i>	
	<i>Scopulariopsis koningii</i>	
	<i>Sporobolomyces salmonicolor</i>	
	<i>Sporothrix schenckii</i>	
20	<i>Stephanoascus ciferrii</i>	
	<i>Syncephalastrum racemosum</i>	
	<i>Trichoderma reesei</i>	
	<i>Trichophyton mentagrophytes</i>	
	<i>Trichophyton tonsurans</i>	
25	<i>Trichosporon cutaneum</i>	
	<i>Ustilago maydis</i>	
	<i>Wangiella dermatitidis</i>	
	<i>Yarrowia lipolytica</i>	

30 **Parasitical species**

	<i>Babesia bigemina</i>
	<i>Babesia bovis</i>
	<i>Babesia microti</i>
35	<i>Blastocystis hominis</i>
	<i>Crithidia fasciculata</i>
	<i>Cryptosporidium parvum</i>
	<i>Entamoeba histolytica</i>
	<i>Giardia lamblia</i>
40	<i>Kentrophoros</i> sp.
	<i>Leishmania aethiopica</i>
	<i>Leishmania amazonensis</i>
	<i>Leishmania braziliensis</i>
	<i>Leishmania donovani</i>
45	<i>Leishmania infantum</i>
	<i>Leishmania enriettii</i>
	<i>Leishmania gerbilli</i>
	<i>Leishmania guyanensis</i>
	<i>Leishmania hertigi</i>
50	<i>Leishmania major</i>
	<i>Leishmania mexicana</i>
	<i>Leishmania tarentolae</i>
	<i>Leishmania tropica</i>
	<i>Neospora caninum</i>
55	<i>Onchocerca volvulus</i>
	<i>Plasmodium berghei</i>
	<i>Plasmodium falciparum</i>
	<i>Plasmodium knowlesi</i>
	<i>Porphyra purpurea</i>
60	<i>Toxoplasma gondii</i>
	<i>Treponema pallidum</i>
	<i>Trichomonas vaginalis</i>

Table 5. Antibiotic resistance genes selected for diagnostic purposes.

	Genes	Antibiotics	Bacteria ¹	ACCESSION NO.	SEQ ID NO. (genes)
5	<i>aac(3)-Ib</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> <i>Pseudomonads</i>	L06157	
	<i>aac(3)-IIb</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	M97172	
10	<i>aac(3)-IVa</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i>	X01385	
	<i>aac(3)-VIa</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	M88012	
	<i>aac(2')-1a</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	X04555	
15	<i>aac(6')-aph(2'')</i> ²	Aminoglycosides	<i>Enterococcus</i> sp., <i>Staphylococcus</i> sp.		83-86 ³
	<i>aac(6')-Ia</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	M18967	
20	<i>aac(6')-Ic</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	M94066	
	<i>aac(6')-IIa</i> ²	Aminoglycosides	<i>Pseudomonads</i>		112 ⁴
	<i>aadB</i> [<i>ant(2'')-Ia</i> ²]	Aminoglycosides	<i>Enterobacteriaceae</i>		53-54 ³
	<i>aacC1</i> [<i>aac(3)-Ia</i> ²]	Aminoglycosides	<i>Pseudomonads</i>		55-56 ³
	<i>aacC2</i> [<i>aac(3)-IIa</i> ²]	Aminoglycosides	<i>Pseudomonads</i>		57-58 ³
25	<i>aacC3</i> [<i>aac(3)-III</i> ²]	Aminoglycosides	<i>Pseudomonads</i>		59-60 ³
	<i>aacA4</i> [<i>aac(6')-Ib</i> ²]	Aminoglycosides	<i>Pseudomonads</i>		65-66 ³
	<i>ant(3'')-Ia</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Enterococcus</i> sp., <i>Staphylococcus</i> sp.	X02340 M10241	
30	<i>ant(4')-Ia</i> ²	Aminoglycosides	<i>Staphylococcus</i> sp.	V01282	
	<i>aph(3')-Ia</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	J01839	
	<i>aph(3')-IIa</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	V00618	
35	<i>aph(3')-IIIa</i> ²	Aminoglycosides	<i>Enterococcus</i> sp., <i>Staphylococcus</i> sp.	V01547	
	<i>aph(3')-VIa</i> ²	Aminoglycosides	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>	X07753	
40	<i>rrs</i> ²	Streptomycin	<i>M. tuberculosis</i>	L15307 S62531	
	<i>rpsL</i> ²	Streptomycin	<i>M. tuberculosis</i> , <i>M. avium</i> complex	X80120 U14749 X70995 L08011	
45	<i>blaOXA</i> ^{5,6}	β -lactams	<i>Enterobacteriaceae</i> , <i>Pseudomonads</i>		110 ⁴
	<i>blaROB</i> ⁵	β -lactams	<i>Haemophilus</i> sp. <i>Pasteurella</i> sp.		45-48 ³
50	<i>blaSHV</i> ^{5,6}	β -lactams	<i>Enterobacteriaceae</i> , <i>Pseudomonas aeruginosa</i>		41-44 ³
	<i>blaTEM</i> ^{5,6}	β -lactams	<i>Enterobacteriaceae</i> , <i>Neisseria</i> sp., <i>Haemophilus</i> sp.		37-40 ³
55	<i>blaCARB</i> ⁵	β -lactams	<i>Pseudomonas</i> sp., <i>Enterobacteriaceae</i>	J05162 S46063 M69058	

Table 5. Antibiotic resistance genes selected for diagnostic purposes (continued).

	Genes	Antibiotics	Bacteria ¹	ACCESSION NO.	SEQ ID NO. (genes)
5	<i>bla</i> _{CTX-M-1} ⁵	β-lactams	<i>Enterobacteriaceae</i>	X92506	
	<i>bla</i> _{CTX-M-2} ⁵	β-lactams	<i>Enterobacteriaceae</i>	X92507	
	<i>bla</i> _{CMY-2} ⁷	β-lactams	<i>Enterobacteriaceae</i>	X91840	
	<i>bla</i> _{PER-1} ⁵	β-lactams	<i>Enterobacteriaceae</i> , <i>Pseudomonas aeruginosa</i>	Z21957	
10	<i>bla</i> _{PER-2} ⁷	β-lactams	<i>Enterobacteriaceae</i>	X93314	
	<i>bla</i> _{IMP} ⁵	β-lactams	<i>Enterobacteriaceae</i> , <i>Pseudomonas aeruginosa</i>	AJ223604	
	<i>bla</i> _Z ¹²	β-lactams	<i>Enterococcus</i> sp., <i>Staphylococcus</i> sp.		111 ⁴
15	<i>mecA</i> ¹²	β-lactams	<i>Staphylococcus</i> sp.		97-98 ³
	<i>penA</i> ¹³	β-lactams	<i>Neisseria gonorrhoeae</i>	X54021	
	<i>pbp1a</i> ¹³	β-lactams	<i>Streptococcus pneumoniae</i>		SEE TABLE 7
20				M90527 X67872 AB006868 AB006874 X67873 AB006878 AB006875 AB006877 AB006879 AF046237 AF046235 AF026431 AF046232 AF046233 AF046236 X67871 Z49095 AF046234 AB006873 X67866 X67868 AB006870 AB006869 AB006872 X67870 AB006871 X67867 X67869 AB006876 AF046230 AF046238 Z49094	
25					
30					
35					
40					
45					
50	<i>pbp2b</i> ¹³	β-lactams	<i>Streptococcus pneumoniae</i>	X16022 M25516 M25518 M25515 U20071 U20084 U20082 U20067 U20079 Z22185 U20072	SEE TABLE 7
55					
60					

Table 5. Antibiotic resistance genes selected for diagnostic purposes (continued).

	Genes	Antibiotics	Bacteria ¹	ACCESSION NO.	SEQ ID NO. (genes)
5	<i>pbp2b</i> ¹³	β -lactams	<i>Streptococcus pneumoniae</i>	U20083	
				U20081	
				M25522	
				U20075	
10				U20070	
				U20077	
				U20068	
				Z22184	
				U20069	
15				U20078	
				M25521	
				M25525	
				M25519	
				Z21981	
20				M25523	
				M25526	
				M25524	
				Z22230	
25	<i>pbp2x</i> ¹³	β -lactams	<i>Streptococcus pneumoniae</i>	U20073	SEE TABLE 7
				U20080	
				U20074	
				U20076	
				M25520	
				M25517	
30				X16367	
				X65135	
				AB011204	
				AB011209	
35				AB011199	
				AB011200	
				AB011201	
				AB011202	
				AB011198	
40				AB011208	
				AB011205	
				AB015852	
				AB011210	
				AB015849	
45				AB015850	
				AB015851	
				AB015847	
				AB015846	
				AB011207	
50				AB015848	
				Z49096	
	<i>int</i>	β -lactams, trimethoprim	<i>Enterobacteriaceae</i> ,		99-102 ³
	<i>sul</i>	aminoglycosides, antiseptic, chloramphenicol	<i>Pseudomonads</i>		103-106 ³
55	<i>ermA</i> ¹⁴	Macrolides, lincosamides, streptogramin B	<i>Staphylococcus</i> sp.		113 ⁴
60	<i>ermB</i> ¹⁴	Macrolides, lincosamides, streptogramin B	<i>Enterobacteriaceae</i> , <i>Staphylococcus</i> sp. <i>Enterococcus</i> sp. <i>Streptococcus</i> sp.		114 ⁴
65					

Table 5. Antibiotic resistance genes selected for diagnostic purposes (continued).

	Genes	Antibiotics	Bacteria ¹	ACCESSION NO.	SEQ ID NO. (genes)
5	<i>ermC</i> ¹⁴	Macrolides, lincosamides, streptogramin B	<i>Enterobacteriaceae</i> , <i>Staphylococcus</i> sp.		115 ⁴
10	<i>ereA</i> ¹²	Macrolides	<i>Enterobacteriaceae</i> , <i>Staphylococcus</i> sp.	M11277	
	<i>ereB</i> ¹²	Macrolides	<i>Enterobacteriaceae</i> <i>Staphylococcus</i> sp.	A15097	
	<i>msrA</i> ¹²	Macrolides	<i>Staphylococcus</i> sp.		77-80 ³
15	<i>mtr</i> ⁸	Macrolides	<i>Neisseria gonorrhoeae</i>	S42418 S40252 S42417 S40251 Z25796 U14993 Q51007 Q51006 Q51073 AF037040 AF037041	
20					
25	<i>mefA, mefE</i> ⁸	Macrolides	<i>Streptococcus</i> sp.	U70055 U83667	
	<i>mphA</i> ⁸	Macrolides	<i>Enterobacteriaceae</i> , <i>Staphylococcus</i> sp.	D16251	
30	<i>linA/linA'</i> ⁹	Lincosamides	<i>Staphylococcus</i> sp.	J03947 M14039	
	<i>linB</i> ¹⁰	Lincosamides	<i>Enterococcus faecium</i>	AF110130	
	<i>rrna</i> ¹¹	Macrolides	<i>Mycobacterium</i> <i>avium</i> complex	U74494	
35	<i>vga</i> ¹⁵	Streptogramin	<i>Staphylococcus</i> sp.		89-90 ³
	<i>vgb</i> ¹⁵	Streptogramin	<i>Staphylococcus</i> sp.	M36022	
	<i>vat</i> ¹⁵	Streptogramin	<i>Staphylococcus</i> sp.		87-88 ³
	<i>vatB</i> ¹⁵	Streptogramin	<i>Staphylococcus</i> sp.	U19456 L38809	
40	<i>satA</i> ¹⁵	Streptogramin	<i>Enterococcus faecium</i>		81-82 ³
	<i>ileS</i> ¹²	Mupirocin	<i>Staphylococcus aureus</i>	X74219	
	<i>mupA</i> ¹²	Mupirocin	<i>Staphylococcus aureus</i>	X75439	
45	<i>gyrA</i> ¹⁶	Quinolones	Gram-positive and gram-negative bacteria	X95718 X06744 X57174 X16817 X71437 AF065152 AF060881 D32252	
50	<i>parC/grlA</i> ¹⁶	Quinolones	Gram-positive and gram-negative bacteria	AB005036 AF056287 X95717 AF129764 AB017811 AF065152	
55					
60					

Table 5. Antibiotic resistance genes selected for diagnostic purposes (continued).

	Genes	Antibiotics	Bacteria ¹	ACCESSION NO.	SEQ ID NO. (genes)
5	<i>parE/grlB</i> ¹⁶	Quinolones	Gram-positive bacteria	X95717 AF065153 AF058920	
10	<i>norA</i> ¹⁶	Quinolones	<i>Staphylococcus</i> sp.	D90119 M80252 M97169	
	<i>mexR (nalB)</i> ¹⁶	Quinolones	<i>Pseudomonas aeruginosa</i>	U23763	
	<i>nfxB</i> ¹⁶	Quinolones	<i>Pseudomonas aeruginosa</i>	X65646	
15	<i>cat</i> ¹²	Chloramphenicol	Gram-positive and gram-negative bacteria	M55620 X15100 A24651 M28717 A00568 A00569 X74948 Y00723 A24362 A00569 M93113 M62822 M58516	
20					
25					
30	<i>rpoB</i> ¹⁷	Rifampin	<i>Mycobacterium tuberculosis</i>	AF055891 AF055892 S71246 L27989 AF055893	
	<i>inhA</i> ¹⁷	Isoniazid	<i>Mycobacterium tuberculosis</i>	AF106077 U02492	
35	<i>katG</i> ¹⁷	Isoniazid	<i>Mycobacterium tuberculosis</i>	U40593 U06259 U06260 U06261 U06262 U40594 U40595	
40					
	<i>ahpC</i> ¹⁷	Isoniazid	<i>Mycobacterium tuberculosis</i>	U43812 U57761 U24085 U16243 U58030 U18264	
45					
	<i>embB</i> ¹⁷	Ethambutol	<i>Mycobacterium tuberculosis</i>	U68480	
	<i>pncA</i> ¹⁷	Pyrazinamide	<i>Mycobacterium tuberculosis</i>	U59967	
50	<i>vanA</i> ¹²	Vancomycin	<i>Enterococcus</i> sp.		67-70 ³ SEE TABLE 7
	<i>vanB</i> ¹²	Vancomycin	<i>Enterococcus</i> sp.		116 ⁴
	<i>vanC1</i> ¹²	Vancomycin	<i>Enterococcus gallinarum</i>		117 ⁴ SEE TABLE 7
55	<i>vanC2</i> ¹²	Vancomycin	<i>Enterococcus casseliflavus</i>		SEE TABLE 7
60				U94521 U94522 U94523 U94524 U94525 L29638	

Table 5. Antibiotic resistance genes selected for diagnostic purposes (continued).

	Genes	Antibiotics	Bacteria ¹	ACCESSION NO.	SEQ ID NO. (genes)
5	<i>vanC3</i> ¹²	Vancomycin	<i>Enterococcus flavescens</i>	L29639 U72706 L29640	SEE TABLE 7
10	<i>vanD</i> ¹⁸	Vancomycin	<i>Enterococcus faecium</i>	AF130997	
	<i>tetB</i> ¹⁹	Tetracycline	Gram-negative bacteria	J01830	
	<i>tetM</i> ¹⁹	Tetracycline	Gram-negative and Gram-positive bacteria	X52632	
15	<i>sulII</i> ²⁰	Sulfonamides	Gram-negative bacteria	D37827 M36657 AF017389 AF017391	
	<i>dhfrIa</i> ²⁰	Trimethoprim	Gram-negative bacteria	AJ238350 X17477	
20	<i>dhfrIb</i> ²⁰	Trimethoprim	Gram-negative bacteria	Z50805 Z50804	
	<i>dhfrV</i> ²⁰	Trimethoprim	Gram-negative bacteria	X12868	
	<i>dhfrVII</i> ²⁰	Trimethoprim	Gram-negative bacteria	U31119	
	<i>dhfrVIII</i> ²⁰	Trimethoprim	Gram-negative bacteria	U10186	
25	<i>dhfrIX</i> ²⁰	Trimethoprim	Gram-negative bacteria	X57730	
	<i>dhfrXII</i> ²⁰	Trimethoprim	Gram-negative bacteria	Z21672	
	<i>dfrA</i> ²⁰	Trimethoprim	<i>Staphylococcus</i> sp.	AF045472 U40259 AF051916	
30	¹ Bacteria having high incidence for the specified antibiotic resistance gene. The presence of the antibiotic resistance genes in other bacteria is not excluded. ² Shaw, K. J., P. N. Rather, R. S. Hare, and G. H. Miller. 1993. Molecular genetics of aminoglycoside resistance genes and familial relationships of the aminoglycoside-modifying enzymes. <i>Microbiol. Rev.</i> 57:138-163. ³ Antibiotic resistance genes from our co-pending US patent no. 6,001,564 for which we have selected PCR primer pairs. ⁴ These SEQ ID NOs. refer to a previous patent (application WO98/20157). ⁵ Bush, K., G.A. Jacoby and A. Medeiros. 1995. A functional classification scheme for β-lactamase and its correlation with molecular structure. <i>Antimicrob. Agents. Chemother.</i> 39:1211-1233. ⁶ Nucleotide mutations in <i>bla_{SHV}</i>, <i>bla_{TEM}</i>, and <i>bla_{OXA}</i>, are associated with extended-spectrum β-lactamase or inhibitor-resistant β-lactamase. ⁷ Bauerfeind, A., Y. Chong, and K. Lee. 1998. Plasmid-encoded AmpC beta-lactamases: how far have we gone 10 ears after discovery? <i>Yonsei Med. J.</i> 39:520-525. ⁸ Sutcliffe, J., T. Grebe, A. Tait-Kamradt, and L. Wondrack. 1996. Detection of erythromycin-resistant determinants by PCR. <i>Antimicrob. Agent Chemother.</i> 40:2562-2566. ⁹ Leclerc, R., A., Brisson-Noël, J. Duval, and P. Courvalin. 1991. Phenotypic expression and genetic heterogeneity of lincosamide inactivation in <i>Staphylococcus</i> sp. <i>Antimicrob. Agents. Chemother.</i> 31:1887-1891. ¹⁰ Bozdogan, B., L. Berrezouga, M.-S. Kuo, D. A. Yurek, K. A. Farley, B. J. Stockman, and R. Leclercq. 1999. A new gene, <i>linB</i>, conferring resistance to lincosamides by nucleotidylation in <i>Enterococcus faecium</i> HM1025. <i>Antimicrob. Agents. Chemother.</i> 43:925-929. ¹¹ Cockerill III, F.R. 1999. Genetic methods for assessing antimicrobial resistance. <i>Antimicrob. Agents. Chemother.</i> 43:199-212. ¹² Tenover, F. C., T. Popovic, and O. Olsvik. 1996. Genetic methods for detecting antibacterial resistance genes. pp. 1368-1378. In Murray, P. R., E. J. Baron, M. A. Pfaller, F. C. Tenover, R. H. Tenover (eds). <i>Manual of clinical microbiology</i>. 6th ed., ASM Press, Washington, D.C. USA ¹³ Dowson, C. G., T. J. Tracey, and B. G. Spratt. 1994. Origin and molecular epidemiology of penicillin-				

- binding-protein-mediated resistance to β -lactam antibiotics. Trends Molec. Microbiol. **2**: 361-366.
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Table 6. List of bacterial toxins selected for diagnostic purposes.

	Organism	Toxin	Accession number
5	<i>Actinobacillus actinomycetemcomitans</i>	Cytolethal distending toxin (<i>cdtA</i> , <i>cdtB</i> , <i>cdtC</i>) Leukotoxin (<i>ltxA</i>)	AF006830 M27399
	<i>Actinomyces pyogenes</i>	Hemolysin (pyolysin)	U84782
	<i>Aeromonas hydrophila</i>	Aerolysin (<i>aerA</i>) Haemolysin (<i>hlyA</i>) Cytotoxic enterotoxin (<i>alt</i>)	M16495 U81555 L77573
10	<i>Bacillus anthracis</i>	Anthrax toxin (<i>cya</i>)	M23179
	<i>Bacillus cereus</i>	Enterotoxin (<i>bceT</i>)	D17312 AF192766, AF192767 AJ237785 Y19005
15	<i>Bacillus mycoides</i>	Enterotoxic hemolysin BL Non-haemolytic enterotoxins A,B and C (<i>nhe</i>)	AJ243150 to AJ243153
	<i>Bacillus pseudomycoides</i>	Hemolytic enterotoxin HBL	AJ243154 to AJ243156
	<i>Bacteroides fragilis</i>	Enterotoxin (<i>bftP</i>) Matrix metalloprotease/enterotoxin (fragilysin) Metalloprotease toxin-2	U67735 S75941, AF038459 U90931 AF081785 AF056297
20		Metalloprotease toxin-3	Z37112, U22953 U59687 AB020025
	<i>Bordetella bronchiseptica</i>	Adenylate cyclase hemolysin (<i>cyaA</i>) Dermonecrotic toxin (<i>dnt</i>)	
25	<i>Bordetella pertussis</i>	Pertussis toxin (S1 subunit, <i>tox</i>)	AJ006151 AJ006153 AJ006155 AJ006157 AJ006159 AJ007363 M14378, M16494 AJ007364 M13223 X16347 18323 U10527
30		<u>Patents:</u> EP0322533-A 2 05jul89 EP0322115-A 5 28jun89 EP0396964-A 1 14nov90 JP1987228286-A 1 7oct87	
35	<i>Campylobacter jejuni</i>	Adenyl cyclase (<i>cya</i>) Dermonecrotic toxin (<i>dnt</i>)	U51121
	<i>Citrobacter freundii</i>	Cytolethal distending toxin (<i>cdtA</i> , <i>cdtB</i> , <i>cdtC</i>) Shiga-like toxin (<i>slt-IIcA</i>)	X67514, S53206
40	<i>Clostridium botulinum</i>	Botulism toxin (BoNT)	X52066, X52088 X73423 M30196 X70814 X70819 X71343 Z11934 X70817 M81186 X70818 X70815 X62089 X62683 S76749 X81714 X70816 X70820 X70281 L35496 M92906
45		The A,B,E and F serotypes are neurotoxic for humans	
		The other serotypes have not been considered	
50		Partial sequences (<200 bp) have not been considered	
55			
60	<i>Clostridium difficile</i>	A toxin (enterotoxin) (<i>tcdA</i>)	AB012304 AF053400 Y12616 X51797 X17194 M30307
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Table 6. List of bacterial toxins selected for diagnostic purposes (continued).

	Organism	Toxin	Accession number
5	<i>Clostridium difficile</i>	B toxin (cytotoxin) (<i>toxB</i>)	Z23277 X53138
10	<i>Clostridium perfringens</i>	Alpha (phospholipase C) (<i>cpa</i>)	L43545 L43546 L43547 L43548 X13608 X17300 D10248
15		Beta (dermonecrotic protein) (<i>cpb</i>)	L13198 X83275 L77965
20		Enterotoxin (<i>cpe</i>)	AJ000766 M98037 X81849 X71844 Y16009
25		Enterotoxin pseudogene (not expressed)	AF037328 AF037329 AF037330
		Epsilon toxin (<i>etxD</i>)	M80837 M95206 X60694
		Iota (Ia and Ib)	X73562
		Lambda (metalloprotease)	D45904
		Theta (perfringolysin O)	M36704
30	<i>Clostridium sordellii</i>	Cytotoxin L	X82638
	<i>Clostridium tetani</i>	Tetanos toxin	X06214 X04436
35	<i>Corynebacterium diphtheriae</i>	Diphtheriae toxin <u>Patent:</u> JP 1985227681-A/1	X00703
	<i>Corynebacterium pseudotuberculosis</i>	Phospholipase C <u>Patent:</u> WO 9011351-A 2	A21336
	<i>Eikenella corrodens</i>	lysine decarboxylase (<i>cadA</i>)	U89166
40	<i>Enterobacter cloacae</i>	Shiga-like toxin II	Z50754, U33502
	<i>Enterococcus faecalis</i>	Cytolysin B (<i>cytB</i>)	M38052
	<i>Escherichia coli</i> (EHEC)	Hemolysin toxin (<i>hlyA</i> and <i>ehxA</i>)	AF043471 X94129 X79839 X86087 AB011549 AF074613
45		Shiga-like (Vero cytotoxin) (<i>stx</i>)	X81418 M14107 M10133 M12863
50		Contains the sequences for both the A and B subunits <u>Patent:</u> JP 1995008280-A/1	X81417 X81416 X81415 Z36900 L11078 L04539 L11079 X65949 M21534 M29153 Z37725 Z36901 X61283 AB017524 U72191
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Table 6. List of bacterial toxins selected for diagnostic purposes (continued).

	Organism	Toxin	Accession number
5	<i>Escherichia coli</i> (ETEC)	Enterotoxin (heat-labile) (<i>eltB</i>) Patents: EP 0145486-A 5 WO 9313202-A 42 JP 1986005097-A JP 1992320675-A	M17874 M17873 J01605 AB011677
10		Enterotoxin (heat-stable) (<i>astA</i>) (<i>estA1</i>)	L11241 M58746 M29255 V00612 J01831
15	<i>Escherichia coli</i> (other)	Cytolethal-distending toxin (<i>cdt</i>) (3 genes)	U03293 U04208 U89305
		Cytotoxic necrotizing factor 1 (<i>cnf1</i>) Microcin 24 (<i>mtfS</i>)	U42629 U47048
20	<i>Haemophilus ducreyi</i>	Autotransporter enterotoxin (<i>Pet</i>) (cytotoxin)	AF056581
	<i>Helicobacter pylori</i>	Cytolethal distending toxin (<i>cdtA</i> , <i>cdtB</i> , <i>cdtC</i>) Vacuolating toxin (<i>vacA</i>)	U53215 U07145 U80067 U80068 AF077938 AF077939 AF077940 AF077941
25			
	<i>Legionella pneumophila</i>	Structural toxin protein (<i>rtxA</i>)	AF057703
30	<i>Listeria monocytogenes</i>	Listeriolysin O (<i>lisA</i> , <i>hlyA</i>)	X15127 M24199 X60035 U25452 U25443 U25446 U25449
35			
	<i>Pasteurella multocida</i>	Mitogenic toxin (dermonecrotic toxin)	X57775, Z28388 X51512 X52478
	<i>Proteus mirabilis</i>	Hemolysin (<i>hpmA</i>)	M30186
40	<i>Pseudomonas aeruginosa</i>	Cytotoxin (Enterotoxin A)	X14956
	<i>Salmonella typhimurium</i>	Calmodulin-sensitive adenylate cyclase toxin (<i>cya</i>) Cytolysin (salmolysin) (<i>slyA</i>) Enterotoxin (<i>stn</i>)	AF060869 U03842 L16014
	<i>Serratia marcescens</i>	Hemolysin (<i>shlA</i>)	M22618
45	<i>Shigella dysenteriae</i> type 1	Shiga toxin (2 subunits) (<i>stxA</i> and <i>stxB</i>)	X07903, M32511 M19437 M24352, M21947
	<i>Shigella flexneri</i>	ShET2 enterotoxin (<i>senA</i>)	Z54211 Z47381
50		Enterotoxin 1 (<i>set1A</i> and <i>set1B</i>) Hemolysin E (<i>hlyE</i> , <i>clyA</i> , <i>sheA</i>)	U35656 AF200955
	<i>Shigella sonnei</i>	Shiga toxin (2 subunits) (<i>stxA</i> and <i>stxB</i>)	AJ132761
	<i>Sphingomonas paucimobilis</i>	Beta-hemolysin (<i>hlyA</i>)	L01270
55	<i>Staphylococcus aureus</i>	Gamma-hemolysin (<i>hlg2</i>)	D42143 L01055 U93688 L22565, L22566 M18970 M11118
		Enterotoxin Enterotoxin A (<i>sea</i>)	
60		Enterotoxin B Enterotoxin C1 (<i>entC1</i>) Enterotoxin C2 (<i>entC2</i>) Enterotoxin C3 (<i>entC3</i>) Enterotoxin D (<i>sed</i>) Enterotoxin E	X05815 P34071 X51661 M94872 M21319
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Table 6. List of bacterial toxins selected for diagnostic purposes (continued).

	Organism	Toxin	Accession number
5	<i>Staphylococcus aureus</i>	Enterotoxin G (<i>seg</i>) Enterotoxin H (<i>seh</i>) Enterotoxin I (<i>sei</i>) Enterotoxin J Exfoliative toxin A (ETA) (Epidermolytic toxin A)	AF064773 U11702 AF064774 AF053140 M17347 M17357 L25372, M20371
10		Exfoliative toxin B (ETB) Leukocidin R (F and S component, <i>lukF</i> and <i>lukS</i>) (Hemolysin B and C)	M17348, M13775 X64389, S53213 X72700 L01055
15		Toxic shock syndrome toxin 1 (TSST-1) (alpha toxin) (alpha hemolysin)	X01645 M90536 J02615 U93688
20	<i>Staphylococcus epidermidis</i> <i>Staphylococcus intermedius</i>	Delta toxin (<i>hld</i>) Enterotoxin 1 Leukocidin R (F and S component, <i>lukF</i> and <i>lukS</i>) (synergohymenotropic toxin)	AF068634 U91526 X79188
25	<i>Streptococcus pneumoniae</i> <i>Streptococcus pyogenes</i>	Pneumolysin <i>Streptococcus pyrogenic</i> exotoxin A (<i>speA</i>)	X52474 X61560 (and 19 others) X03929 U40453, M19350 U63134 M86905, M35110
30		Pyrogenic exotoxin B (<i>speB</i>)	
35	<i>Vibrio cholerae</i>	Cholerae toxin (<i>ctxA</i> and <i>ctxB</i> subunits) <u>Patents:</u> JP 1995008279-A 1 EP 0368819-A 12 (<i>ctxB</i>) WO 9313202-A 45 (<i>ctxA</i>)	X00171 X76390 X58786 X58785, S55782 D30052 D30053 K02679 AF175708 Z22569, AF175708 X74108, M85198 M97591, L03220 M83563, AF175708
40		Accessory cholera enterotoxin (<i>ace</i>) Heat-stable enterotoxin (<i>stx</i>) <i>Zonula occludens</i> toxin (<i>zot</i>)	
	<i>Vibrio parahaemolyticus</i>	Thermostable direct hemolysin (<i>tdh</i>)	S67841
	<i>Vibrio vulnificus</i>	Cytolysin (<i>vvhA</i>)	M34670
45	<i>Yersinia enterocolitica</i>	Heat-stable enterotoxin (<i>ystI</i>) Heat-stable enterotoxin type B (<i>ystB</i>) Heat-stable enterotoxin type C (<i>ystC</i>)	U09235, X65999 D88145 D63578
	<i>Yersinia kristensenii</i>	Enterotoxin	X69218
50	<i>Yersinia pestis</i>	Toxin	X92727

Table 7. Origin of the sequences in the sequence listing.

SEQ ID NO.		Bacterial,fungal or parasitical species	Source	Comments*
5	1	<i>Acinetobacter baumannii</i>	This patent	tuf
	2	<i>Actinomyces meyeri</i>	This patent	tuf
	3	<i>Aerococcus viridans</i>	This patent	tuf
	4	<i>Achromobacter xylosoxidans</i> subsp. <i>denitrificans</i>	This patent	tuf
	5	<i>Anaerorhabdus furcosus</i>	This patent	tuf
10	6	<i>Bacillus anthracis</i>	This patent	tuf
	7	<i>Bacillus cereus</i>	This patent	tuf
	8	<i>Bacteroides distasonis</i>	This patent	tuf
	9	<i>Enterococcus casseliflavus</i>	This patent	tuf
15	10	<i>Staphylococcus saprophyticus</i>	This patent	tuf
	11	<i>Bacteroides ovatus</i>	This patent	tuf
	12	<i>Bartonella henselae</i>	This patent	tuf
	13	<i>Bifidobacterium adolescentis</i>	This patent	tuf
	14	<i>Bifidobacterium dentium</i>	This patent	tuf
20	15	<i>Brucella abortus</i>	This patent	tuf
	16	<i>Burkholderia cepacia</i>	This patent	tuf
	17	<i>Cedecea davisae</i>	This patent	tuf
	18	<i>Cedecea neteri</i>	This patent	tuf
	19	<i>Cedecea lapagei</i>	This patent	tuf
25	20	<i>Chlamydia pneumoniae</i>	This patent	tuf
	21	<i>Chlamydia psittaci</i>	This patent	tuf
	22	<i>Chlamydia trachomatis</i>	This patent	tuf
	23	<i>Chryseobacterium meningosepticum</i>	This patent	tuf
	24	<i>Citrobacter amalonaticus</i>	This patent	tuf
30	25	<i>Citrobacter braakii</i>	This patent	tuf
	26	<i>Citrobacter koseri</i>	This patent	tuf
	27	<i>Citrobacter farmeri</i>	This patent	tuf
	28	<i>Citrobacter freundii</i>	This patent	tuf
	29	<i>Citrobacter sedlakii</i>	This patent	tuf
35	30	<i>Citrobacter werkmanii</i>	This patent	tuf
	31	<i>Citrobacter youngae</i>	This patent	tuf
	32	<i>Clostridium perfringens</i>	This patent	tuf
	33	<i>Comamonas acidovorans</i>	This patent	tuf
	34	<i>Corynebacterium bovis</i>	This patent	tuf
40	35	<i>Corynebacterium cervicis</i>	This patent	tuf
	36	<i>Corynebacterium flavescens</i>	This patent	tuf
	37	<i>Corynebacterium kutscheri</i>	This patent	tuf
	38	<i>Corynebacterium minutissimum</i>	This patent	tuf
	39	<i>Corynebacterium mycetoides</i>	This patent	tuf
45	40	<i>Corynebacterium pseudogenitalium</i>	This patent	tuf
	41	<i>Corynebacterium renale</i>	This patent	tuf
	42	<i>Corynebacterium ulcerans</i>	This patent	tuf
	43	<i>Corynebacterium urealyticum</i>	This patent	tuf
	44	<i>Corynebacterium xerosis</i>	This patent	tuf
50	45	<i>Coxiella burnetii</i>	This patent	tuf
	46	<i>Edwardsiella hoshinae</i>	This patent	tuf
	47	<i>Edwardsiella tarda</i>	This patent	tuf
	48	<i>Eikenella corrodens</i>	This patent	tuf
	49	<i>Enterobacter aerogenes</i>	This patent	tuf
55	50	<i>Enterobacter agglomerans</i>	This patent	tuf
	51	<i>Enterobacter amnigenus</i>	This patent	tuf
	52	<i>Enterobacter asburiae</i>	This patent	tuf
	53	<i>Enterobacter cancerogenus</i>	This patent	tuf
	54	<i>Enterobacter cloacae</i>	This patent	tuf
60	55	<i>Enterobacter gergoviae</i>	This patent	tuf
	56	<i>Enterobacter hormaechei</i>	This patent	tuf
	57	<i>Enterobacter sakazakii</i>	This patent	tuf
	58	<i>Enterococcus casseliflavus</i>	This patent	tuf
	59	<i>Enterococcus cecorum</i>	This patent	tuf
65	60	<i>Enterococcus dispar</i>	This patent	tuf
	61	<i>Enterococcus durans</i>	This patent	tuf

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial,fungal or parasitcal species	Source	Comments*
5	62 <i>Enterococcus faecalis</i>	This patent	tuf
	63 <i>Enterococcus faecalis</i>	This patent	tuf
	64 <i>Enterococcus faecium</i>	This patent	tuf
	65 <i>Enterococcus flavescens</i>	This patent	tuf
	66 <i>Enterococcus gallinarum</i>	This patent	tuf
10	67 <i>Enterococcus hirae</i>	This patent	tuf
	68 <i>Enterococcus mundtii</i>	This patent	tuf
	69 <i>Enterococcus pseudoavium</i>	This patent	tuf
	70 <i>Enterococcus raffinosus</i>	This patent	tuf
	71 <i>Enterococcus saccharolyticus</i>	This patent	tuf
15	72 <i>Enterococcus solitarius</i>	This patent	tuf (C)
	73 <i>Enterococcus casseliflavus</i>	This patent	unknown
	74 <i>Staphylococcus saprophyticus</i>	This patent	tuf (C)
	75 <i>Enterococcus flavescens</i>	This patent	tuf (C)
	76 <i>Enterococcus gallinarum</i>	This patent	tuf
20	77 <i>Ehrlichia canis</i>	This patent	tuf
	78 <i>Escherichia coli</i>	This patent	tuf
	79 <i>Escherichia fergusonii</i>	This patent	tuf
	80 <i>Escherichia hermannii</i>	This patent	tuf
	81 <i>Escherichia vulneris</i>	This patent	tuf
25	82 <i>Eubacterium lentum</i>	This patent	tuf
	83 <i>Eubacterium nodatum</i>	This patent	tuf
	84 <i>Ewingella americana</i>	This patent	tuf
	85 <i>Francisella tularensis</i>	This patent	tuf
	86 <i>Fusobacterium nucleatum</i> subsp. <i>polymorphum</i>	This patent	tuf
30	87 <i>Gemella haemolysans</i>	This patent	tuf
	88 <i>Gemella morbillorum</i>	This patent	tuf
	89 <i>Haemophilus actinomycetemcomitans</i>	This patent	tuf
	90 <i>Haemophilus aphrophilus</i>	This patent	tuf
	91 <i>Haemophilus ducreyi</i>	This patent	tuf
35	92 <i>Haemophilus haemolyticus</i>	This patent	tuf
	93 <i>Haemophilus parahaemolyticus</i>	This patent	tuf
	94 <i>Haemophilus parainfluenzae</i>	This patent	tuf
	95 <i>Haemophilus paraphrophilus</i>	This patent	tuf
	96 <i>Haemophilus segnis</i>	This patent	tuf
40	97 <i>Hafnia alvei</i>	This patent	tuf
	98 <i>Kingella kingae</i>	This patent	tuf
	99 <i>Klebsiella ornithinolytica</i>	This patent	tuf
	100 <i>Klebsiella oxytoca</i>	This patent	tuf
	101 <i>Klebsiella planticola</i>	This patent	tuf
45	102 <i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	This patent	tuf
	103 <i>Klebsiella pneumoniae pneumoniae</i>	This patent	tuf
	104 <i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	This patent	tuf
	105 <i>Kluyvera ascorbata</i>	This patent	tuf
	106 <i>Kluyvera cryocrescens</i>	This patent	tuf
50	107 <i>Kluyvera georgiana</i>	This patent	tuf
	108 <i>Lactobacillus casei</i> subsp. <i>casei</i>	This patent	tuf
	109 <i>Lactococcus lactis</i> subsp. <i>lactis</i>	This patent	tuf
	110 <i>Leclercia adecarboxylata</i>	This patent	tuf
	111 <i>Legionella micdadei</i>	This patent	tuf
55	112 <i>Legionella pneumophila</i> subsp. <i>pneumophila</i>	This patent	tuf
	113 <i>Leminorella grimontii</i>	This patent	tuf
	114 <i>Leminorella richardii</i>	This patent	tuf
	115 <i>Leptospira interrogans</i>	This patent	tuf
	116 <i>Megamonas hypermegale</i>	This patent	tuf
60	117 <i>Mitsuokella multacidus</i>	This patent	tuf
	118 <i>Mobiluncus curtisii</i> subsp. <i>holmesii</i>	This patent	tuf
	119 <i>Moellerella wisconsensis</i>	This patent	tuf
	120 <i>Moraxella catarrhalis</i>	This patent	tuf
	121 <i>Morganella morganii</i> subsp. <i>morganii</i>	This patent	tuf
65	122 <i>Mycobacterium tuberculosis</i>	This patent	tuf

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial,fungal or parasitical species	Source	Comments*
5	123 <i>Neisseria cinerea</i>	This patent	tuf
	124 <i>Neisseria elongata</i> subsp. <i>elongata</i>	This patent	tuf
	125 <i>Neisseria flavescens</i>	This patent	tuf
	126 <i>Neisseria gonorrhoeae</i>	This patent	tuf
	127 <i>Neisseria lactamica</i>	This patent	tuf
10	128 <i>Neisseria meningitidis</i>	This patent	tuf
	129 <i>Neisseria mucosa</i>	This patent	tuf
	130 <i>Neisseria sicca</i>	This patent	tuf
	131 <i>Neisseria subflava</i>	This patent	tuf
	132 <i>Neisseria weaveri</i>	This patent	tuf
15	133 <i>Ochrobactrum anthropi</i>	This patent	tuf
	134 <i>Pantoea agglomerans</i>	This patent	tuf
	135 <i>Pantoea dispersa</i>	This patent	tuf
	136 <i>Pasteurella multocida</i>	This patent	tuf
	137 <i>Peptostreptococcus anaerobius</i>	This patent	tuf
20	138 <i>Peptostreptococcus asaccharolyticus</i>	This patent	tuf
	139 <i>Peptostreptococcus prevotii</i>	This patent	tuf
	140 <i>Porphyromonas asaccharolytica</i>	This patent	tuf
	141 <i>Porphyromonas gingivalis</i>	This patent	tuf
	142 <i>Pragia fontium</i>	This patent	tuf
25	143 <i>Prevotella melaninogenica</i>	This patent	tuf
	144 <i>Prevotella oralis</i>	This patent	tuf
	145 <i>Propionibacterium acnes</i>	This patent	tuf
	146 <i>Proteus mirabilis</i>	This patent	tuf
	147 <i>Proteus penneri</i>	This patent	tuf
30	148 <i>Proteus vulgaris</i>	This patent	tuf
	149 <i>Providencia alcalifaciens</i>	This patent	tuf
	150 <i>Providencia rettgeri</i>	This patent	tuf
	151 <i>Providencia rustigianii</i>	This patent	tuf
	152 <i>Providencia stuartii</i>	This patent	tuf
35	153 <i>Pseudomonas aeruginosa</i>	This patent	tuf
	154 <i>Pseudomonas fluorescens</i>	This patent	tuf
	155 <i>Pseudomonas stutzeri</i>	This patent	tuf
	156 <i>Psychrobacter phenylpyruvicum</i>	This patent	tuf
	157 <i>Rahnella aquatilis</i>	This patent	tuf
40	158 <i>Salmonella choleraesuis</i> subsp. <i>arizonae</i>	This patent	tuf
	159 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Choleraesuis	This patent	tuf
	160 <i>Salmonella choleraesuis</i> subsp. <i>diarizonae</i>	This patent	tuf
	161 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Heidelberg	This patent	tuf
	162 <i>Salmonella choleraesuis</i> subsp. <i>houtenae</i>	This patent	tuf
45	163 <i>Salmonella choleraesuis</i> subsp. <i>indica</i>	This patent	tuf
	164 <i>Salmonella choleraesuis</i> subsp. <i>salamae</i>	This patent	tuf
	165 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Typhi	This patent	tuf
	166 <i>Serratia fonticola</i>	This patent	tuf
	167 <i>Serratia liquefaciens</i>	This patent	tuf
50	168 <i>Serratia marcescens</i>	This patent	tuf
	169 <i>Serratia odorifera</i>	This patent	tuf
	170 <i>Serratia plymuthica</i>	This patent	tuf
	171 <i>Serratia rubidaea</i>	This patent	tuf
	172 <i>Shigella boydii</i>	This patent	tuf
55	173 <i>Shigella dysenteriae</i>	This patent	tuf
	174 <i>Shigella flexneri</i>	This patent	tuf
	175 <i>Shigella sonnei</i>	This patent	tuf
	176 <i>Staphylococcus aureus</i>	This patent	tuf
	177 <i>Staphylococcus aureus</i>	This patent	tuf
60	178 <i>Staphylococcus aureus</i>	This patent	tuf
	179 <i>Staphylococcus aureus</i>	This patent	tuf
	180 <i>Staphylococcus aureus</i> subsp. <i>aureus</i>	This patent	tuf
	181 <i>Staphylococcus auricularis</i>	This patent	tuf
	182 <i>Staphylococcus capitis</i> subsp. <i>capitis</i>	This patent	tuf

Table 7. Origin of the sequences in the sequence listing (continued).

	SEQ ID NO.	Bacterial,fungal or parasitical species	Source	Comments*
5	183	<i>Macrococcus caseolyticus</i>	This patent	tuf
	184	<i>Staphylococcus cohnii</i>	This patent	tuf
	185	<i>Staphylococcus epidermidis</i>	This patent	tuf
	186	<i>Staphylococcus haemolyticus</i>	This patent	tuf
	187	<i>Staphylococcus warneri</i>	This patent	tuf
10	188	<i>Staphylococcus haemolyticus</i>	This patent	tuf
	189	<i>Staphylococcus haemolyticus</i>	This patent	tuf
	190	<i>Staphylococcus haemolyticus</i>	This patent	tuf
	191	<i>Staphylococcus hominis</i> subsp. <i>hominis</i>	This patent	tuf
	192	<i>Staphylococcus warneri</i>	This patent	tuf
15	193	<i>Staphylococcus hominis</i>	This patent	tuf
	194	<i>Staphylococcus hominis</i>	This patent	tuf
	195	<i>Staphylococcus hominis</i>	This patent	tuf
	196	<i>Staphylococcus hominis</i>	This patent	tuf
	197	<i>Staphylococcus lugdunensis</i>	This patent	tuf
20	198	<i>Staphylococcus saprophyticus</i>	This patent	tuf
	199	<i>Staphylococcus saprophyticus</i>	This patent	tuf
	200	<i>Staphylococcus saprophyticus</i>	This patent	tuf
	201	<i>Staphylococcus sciuri</i> subsp. <i>sciuri</i>	This patent	tuf
	202	<i>Staphylococcus warneri</i>	This patent	tuf
25	203	<i>Staphylococcus warneri</i>	This patent	tuf
	204	<i>Bifidobacterium longum</i>	This patent	tuf
	205	<i>Stenotrophomonas maltophilia</i>	This patent	tuf
	206	<i>Streptococcus acidominimus</i>	This patent	tuf
	207	<i>Streptococcus agalactiae</i>	This patent	tuf
30	208	<i>Streptococcus agalactiae</i>	This patent	tuf
	209	<i>Streptococcus agalactiae</i>	This patent	tuf
	210	<i>Streptococcus agalactiae</i>	This patent	tuf
	211	<i>Streptococcus anginosus</i>	This patent	tuf
	212	<i>Streptococcus bovis</i>	This patent	tuf
35	213	<i>Streptococcus anginosus</i>	This patent	tuf
	214	<i>Streptococcus cricetus</i>	This patent	tuf
	215	<i>Streptococcus cristatus</i>	This patent	tuf
	216	<i>Streptococcus downei</i>	This patent	tuf
	217	<i>Streptococcus dysgalactiae</i>	This patent	tuf
40	218	<i>Streptococcus equi</i> subsp. <i>equi</i>	This patent	tuf
	219	<i>Streptococcus ferus</i>	This patent	tuf
	220	<i>Streptococcus gordonii</i>	This patent	tuf
	221	<i>Streptococcus anginosus</i>	This patent	tuf
	222	<i>Streptococcus macacae</i>	This patent	tuf
45	223	<i>Streptococcus gordonii</i>	This patent	tuf
	224	<i>Streptococcus mutans</i>	This patent	tuf
	225	<i>Streptococcus parasanguinis</i>	This patent	tuf
	226	<i>Streptococcus ratti</i>	This patent	tuf
	227	<i>Streptococcus sanguinis</i>	This patent	tuf
50	228	<i>Streptococcus sobrinus</i>	This patent	tuf
	229	<i>Streptococcus suis</i>	This patent	tuf
	230	<i>Streptococcus uberis</i>	This patent	tuf
	231	<i>Streptococcus vestibularis</i>	This patent	tuf
	232	<i>Tatumella ptyseos</i>	This patent	tuf
55	233	<i>Trabulsiella guamensis</i>	This patent	tuf
	234	<i>Veillonella parvula</i>	This patent	tuf
	235	<i>Yersinia enterocolitica</i>	This patent	tuf
	236	<i>Yersinia frederiksenii</i>	This patent	tuf
	237	<i>Yersinia intermedia</i>	This patent	tuf
60	238	<i>Yersinia pestis</i>	This patent	tuf
	239	<i>Yersinia pseudotuberculosis</i>	This patent	tuf
	240	<i>Yersinia rohdei</i>	This patent	tuf
	241	<i>Yokenella regensburgei</i>	This patent	tuf
	242	<i>Achromobacter xylosoxidans</i> subsp. <i>denitrificans</i>	This patent	atpD
65	243	<i>Acinetobacter baumannii</i>	This patent	atpD
	244	<i>Acinetobacter lwoffii</i>	This patent	atpD

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial,fungal or parasitical species	Source	Comments*
5	245 <i>Staphylococcus saprophyticus</i>	This patent	<i>atpD</i>
	246 <i>Alcaligenes faecalis</i>	This patent	<i>atpD</i>
	247 <i>Bacillus anthracis</i>	This patent	<i>atpD</i>
	248 <i>Bacillus cereus</i>	This patent	<i>atpD</i>
	249 <i>Bacteroides distasonis</i>	This patent	<i>atpD</i>
10	250 <i>Bacteroides ovatus</i>	This patent	<i>atpD</i>
	251 <i>Leclercia adecarboxylata</i>	This patent	<i>atpD</i>
	252 <i>Stenotrophomonas maltophilia</i>	This patent	<i>atpD</i>
	253 <i>Bartonella henselae</i>	This patent	<i>atpD</i>
	254 <i>Bifidobacterium adolescentis</i>	This patent	<i>atpD</i>
15	255 <i>Brucella abortus</i>	This patent	<i>atpD</i>
	256 <i>Cedecea davisae</i>	This patent	<i>atpD</i>
	257 <i>Cedecea lapagei</i>	This patent	<i>atpD</i>
	258 <i>Cedecea neteri</i>	This patent	<i>atpD</i>
	259 <i>Chryseobacterium meningosepticum</i>	This patent	<i>atpD</i>
20	260 <i>Citrobacter amalonaticus</i>	This patent	<i>atpD</i>
	261 <i>Citrobacter braakii</i>	This patent	<i>atpD</i>
	262 <i>Citrobacter koseri</i>	This patent	<i>atpD</i>
	263 <i>Citrobacter farmeri</i>	This patent	<i>atpD</i>
	264 <i>Citrobacter freundii</i>	This patent	<i>atpD</i>
25	265 <i>Citrobacter koseri</i>	This patent	<i>atpD</i>
	266 <i>Citrobacter sedlakii</i>	This patent	<i>atpD</i>
	267 <i>Citrobacter werkmanii</i>	This patent	<i>atpD</i>
	268 <i>Citrobacter youngae</i>	This patent	<i>atpD</i>
	269 <i>Clostridium innocuum</i>	This patent	<i>atpD</i>
30	270 <i>Clostridium perfringens</i>	This patent	<i>atpD</i>
	272 <i>Corynebacterium diphtheriae</i>	This patent	<i>atpD</i>
	273 <i>Corynebacterium pseudodiphtheriticum</i>	This patent	<i>atpD</i>
	274 <i>Corynebacterium ulcerans</i>	This patent	<i>atpD</i>
	275 <i>Corynebacterium urealyticum</i>	This patent	<i>atpD</i>
35	276 <i>Coxiella burnetii</i>	This patent	<i>atpD</i>
	277 <i>Edwardsiella hoshinae</i>	This patent	<i>atpD</i>
	278 <i>Edwardsiella tarda</i>	This patent	<i>atpD</i>
	279 <i>Eikenella corrodens</i>	This patent	<i>atpD</i>
	280 <i>Enterobacter agglomerans</i>	This patent	<i>atpD</i>
40	281 <i>Enterobacter amnigenus</i>	This patent	<i>atpD</i>
	282 <i>Enterobacter asburiae</i>	This patent	<i>atpD</i>
	283 <i>Enterobacter cancerogenus</i>	This patent	<i>atpD</i>
	284 <i>Enterobacter cloacae</i>	This patent	<i>atpD</i>
	285 <i>Enterobacter gergoviae</i>	This patent	<i>atpD</i>
45	286 <i>Enterobacter hormaechei</i>	This patent	<i>atpD</i>
	287 <i>Enterobacter sakazakii</i>	This patent	<i>atpD</i>
	288 <i>Enterococcus avium</i>	This patent	<i>atpD</i>
	289 <i>Enterococcus casseliflavus</i>	This patent	<i>atpD</i>
	290 <i>Enterococcus durans</i>	This patent	<i>atpD</i>
50	291 <i>Enterococcus faecalis</i>	This patent	<i>atpD</i>
	292 <i>Enterococcus faecium</i>	This patent	<i>atpD</i>
	293 <i>Enterococcus gallinarum</i>	This patent	<i>atpD</i>
	294 <i>Enterococcus saccharolyticus</i>	This patent	<i>atpD</i>
	295 <i>Escherichia fergusonii</i>	This patent	<i>atpD</i>
55	296 <i>Escherichia hermannii</i>	This patent	<i>atpD</i>
	297 <i>Escherichia vulneris</i>	This patent	<i>atpD</i>
	298 <i>Eubacterium lentum</i>	This patent	<i>atpD</i>
	299 <i>Ewingella americana</i>	This patent	<i>atpD</i>
	300 <i>Francisella tularensis</i>	This patent	<i>atpD</i>
60	301 <i>Fusobacterium gonidiaformans</i>	This patent	<i>atpD</i>
	302 <i>Fusobacterium necrophorum</i> subsp. <i>necrophorum</i>	This patent	<i>atpD</i>
	303 <i>Fusobacterium nucleatum</i> subsp. <i>polymorphum</i>	This patent	<i>atpD</i>
	304 <i>Gardnerella vaginalis</i>	This patent	<i>atpD</i>
65	305 <i>Gemella haemolysans</i>	This patent	<i>atpD</i>
	306 <i>Gemella morbillorum</i>	This patent	<i>atpD</i>

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial, fungal or parasitical species	Source	Comments*
5	307 <i>Haemophilus ducreyi</i>	This patent	<i>atpD</i>
	308 <i>Haemophilus haemolyticus</i>	This patent	<i>atpD</i>
	309 <i>Haemophilus parahaemolyticus</i>	This patent	<i>atpD</i>
	310 <i>Haemophilus parainfluenzae</i>	This patent	<i>atpD</i>
	311 <i>Hafnia alvei</i>	This patent	<i>atpD</i>
10	312 <i>Kingella kingae</i>	This patent	<i>atpD</i>
	313 <i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	This patent	<i>atpD</i>
	314 <i>Klebsiella ornithinolytica</i>	This patent	<i>atpD</i>
	315 <i>Klebsiella oxytoca</i>	This patent	<i>atpD</i>
	316 <i>Klebsiella planticola</i>	This patent	<i>atpD</i>
15	317 <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	This patent	<i>atpD</i>
	318 <i>Kluyvera ascorbata</i>	This patent	<i>atpD</i>
	319 <i>Kluyvera cryocrescens</i>	This patent	<i>atpD</i>
	320 <i>Kluyvera georgiana</i>	This patent	<i>atpD</i>
	321 <i>Lactobacillus acidophilus</i>	This patent	<i>atpD</i>
20	322 <i>Legionella pneumophila</i> subsp. <i>pneumophila</i>	This patent	<i>atpD</i>
	323 <i>Leminorella grimontii</i>	This patent	<i>atpD</i>
	324 <i>Listeria monocytogenes</i>	This patent	<i>atpD</i>
	325 <i>Micrococcus lylae</i>	This patent	<i>atpD</i>
	326 <i>Moellerella wisconsensis</i>	This patent	<i>atpD</i>
25	327 <i>Moraxella catarrhalis</i>	This patent	<i>atpD</i>
	328 <i>Moraxella osloensis</i>	This patent	<i>atpD</i>
	329 <i>Morganella morganii</i> subsp. <i>morganii</i>	This patent	<i>atpD</i>
	330 <i>Pantoea agglomerans</i>	This patent	<i>atpD</i>
	331 <i>Pantoea dispersa</i>	This patent	<i>atpD</i>
30	332 <i>Pasteurella multocida</i>	This patent	<i>atpD</i>
	333 <i>Pragia fontium</i>	This patent	<i>atpD</i>
	334 <i>Proteus mirabilis</i>	This patent	<i>atpD</i>
	335 <i>Proteus vulgaris</i>	This patent	<i>atpD</i>
	336 <i>Providencia alcalifaciens</i>	This patent	<i>atpD</i>
35	337 <i>Providencia rettgeri</i>	This patent	<i>atpD</i>
	338 <i>Providencia rustigianii</i>	This patent	<i>atpD</i>
	339 <i>Providencia stuartii</i>	This patent	<i>atpD</i>
	340 <i>Psychrobacter phenylpyruvicus</i>	This patent	<i>atpD</i>
	341 <i>Rahnella aquatilis</i>	This patent	<i>atpD</i>
40	342 <i>Salmonella choleraesuis</i> subsp. <i>arizonae</i>	This patent	<i>atpD</i>
	343 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Choleraesuis	This patent	<i>atpD</i>
	344 <i>Salmonella choleraesuis</i> subsp. <i>diarizonae</i>	This patent	<i>atpD</i>
	345 <i>Salmonella choleraesuis</i> subsp. <i>houtenae</i>	This patent	<i>atpD</i>
	346 <i>Salmonella choleraesuis</i> subsp. <i>indica</i>	This patent	<i>atpD</i>
45	347 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Paratyphi A	This patent	<i>atpD</i>
	348 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Paratyphi B	This patent	<i>atpD</i>
	349 <i>Salmonella choleraesuis</i> subsp. <i>salamae</i>	This patent	<i>atpD</i>
	350 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Typhi	This patent	<i>atpD</i>
	351 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Typhimurium	This patent	<i>atpD</i>
50	352 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Virchow	This patent	<i>atpD</i>
	353 <i>Serratia ficaria</i>	This patent	<i>atpD</i>
	354 <i>Serratia fonticola</i>	This patent	<i>atpD</i>
	355 <i>Serratia grimesii</i>	This patent	<i>atpD</i>
	356 <i>Serratia liquefaciens</i>	This patent	<i>atpD</i>
55	357 <i>Serratia marcescens</i>	This patent	<i>atpD</i>
	358 <i>Serratia odorifera</i>	This patent	<i>atpD</i>
	359 <i>Serratia plymuthica</i>	This patent	<i>atpD</i>
	360 <i>Serratia rubidaea</i>	This patent	<i>atpD</i>
	361 <i>Pseudomonas putida</i>	This patent	<i>atpD</i>
60	362 <i>Shigella boydii</i>	This patent	<i>atpD</i>
	363 <i>Shigella dysenteriae</i>	This patent	<i>atpD</i>

Table 7. Origin of the sequences in the sequence listing (continued).

	SEQ ID NO.	Bacterial,fungal or parasitical species	Source	Comments*
5	364	<i>Shigella flexneri</i>	This patent	<i>atpD</i>
	365	<i>Shigella sonnei</i>	This patent	<i>atpD</i>
	366	<i>Staphylococcus aureus</i>	This patent	<i>atpD</i>
	367	<i>Staphylococcus auricularis</i>	This patent	<i>atpD</i>
	368	<i>Staphylococcus capitis</i> subsp. <i>capitis</i>	This patent	<i>atpD</i>
10	369	<i>Staphylococcus cohnii</i>	This patent	<i>atpD</i>
	370	<i>Staphylococcus epidermidis</i>	This patent	<i>atpD</i>
	371	<i>Staphylococcus haemolyticus</i>	This patent	<i>atpD</i>
	372	<i>Staphylococcus hominis</i> subsp. <i>hominis</i>	This patent	<i>atpD</i>
	373	<i>Staphylococcus hominis</i>	This patent	<i>atpD</i>
15	374	<i>Staphylococcus lugdunensis</i>	This patent	<i>atpD</i>
	375	<i>Staphylococcus saprophyticus</i>	This patent	<i>atpD</i>
	376	<i>Staphylococcus simulans</i>	This patent	<i>atpD</i>
	377	<i>Staphylococcus warneri</i>	This patent	<i>atpD</i>
	378	<i>Streptococcus acidominimus</i>	This patent	<i>atpD</i>
20	379	<i>Streptococcus agalactiae</i>	This patent	<i>atpD</i>
	380	<i>Streptococcus agalactiae</i>	This patent	<i>atpD</i>
	381	<i>Streptococcus agalactiae</i>	This patent	<i>atpD</i>
	382	<i>Streptococcus agalactiae</i>	This patent	<i>atpD</i>
	383	<i>Streptococcus agalactiae</i>	This patent	<i>atpD</i>
25	384	<i>Streptococcus dysgalactiae</i>	This patent	<i>atpD</i>
	385	<i>Streptococcus equi</i> subsp. <i>equi</i>	This patent	<i>atpD</i>
	386	<i>Streptococcus anginosus</i>	This patent	<i>atpD</i>
	387	<i>Streptococcus salivarius</i>	This patent	<i>atpD</i>
	388	<i>Streptococcus suis</i>	This patent	<i>atpD</i>
30	389	<i>Streptococcus uberis</i>	This patent	<i>atpD</i>
	390	<i>Tatumella ptyseos</i>	This patent	<i>atpD</i>
	391	<i>Trabulsiella guamensis</i>	This patent	<i>atpD</i>
	392	<i>Yersinia bercovieri</i>	This patent	<i>atpD</i>
	393	<i>Yersinia enterocolitica</i>	This patent	<i>atpD</i>
35	394	<i>Yersinia frederiksenii</i>	This patent	<i>atpD</i>
	395	<i>Yersinia intermedia</i>	This patent	<i>atpD</i>
	396	<i>Yersinia pseudotuberculosis</i>	This patent	<i>atpD</i>
	397	<i>Yersinia rohdei</i>	This patent	<i>atpD</i>
	398	<i>Yokenella regensburgei</i>	This patent	<i>atpD</i>
40	399	<i>Yarrowia lipolytica</i>	This patent	<i>tuf</i> (EF-1)
	400	<i>Absidia corymbifera</i>	This patent	<i>tuf</i> (EF-1)
	401	<i>Alternaria alternata</i>	This patent	<i>tuf</i> (EF-1)
	402	<i>Aspergillus flavus</i>	This patent	<i>tuf</i> (EF-1)
	403	<i>Aspergillus fumigatus</i>	This patent	<i>tuf</i> (EF-1)
45	404	<i>Aspergillus fumigatus</i>	This patent	<i>tuf</i> (EF-1)
	405	<i>Aspergillus niger</i>	This patent	<i>tuf</i> (EF-1)
	406	<i>Blastoschizomyces capitatus</i>	This patent	<i>tuf</i> (EF-1)
	407	<i>Candida albicans</i>	This patent	<i>tuf</i> (EF-1)
	408	<i>Candida albicans</i>	This patent	<i>tuf</i> (EF-1)
50	409	<i>Candida albicans</i>	This patent	<i>tuf</i> (EF-1)
	410	<i>Candida albicans</i>	This patent	<i>tuf</i> (EF-1)
	411	<i>Candida albicans</i>	This patent	<i>tuf</i> (EF-1)
	412	<i>Candida dubliniensis</i>	This patent	<i>tuf</i> (EF-1)
	413	<i>Candida catenulata</i>	This patent	<i>tuf</i> (EF-1)
55	414	<i>Candida dubliniensis</i>	This patent	<i>tuf</i> (EF-1)
	415	<i>Candida dubliniensis</i>	This patent	<i>tuf</i> (EF-1)
	416	<i>Candida famata</i>	This patent	<i>tuf</i> (EF-1)
	417	<i>Candida glabrata</i>	This patent	<i>tuf</i> (EF-1)
	418	<i>Candida guilliermondii</i>	This patent	<i>tuf</i> (EF-1)
60	419	<i>Candida haemulonii</i>	This patent	<i>tuf</i> (EF-1)
	420	<i>Candida inconspicua</i>	This patent	<i>tuf</i> (EF-1)
	421	<i>Candida kefyr</i>	This patent	<i>tuf</i> (EF-1)
	422	<i>Candida krusei</i>	This patent	<i>tuf</i> (EF-1)
	423	<i>Candida lambica</i>	This patent	<i>tuf</i> (EF-1)
65	424	<i>Candida lusitaniae</i>	This patent	<i>tuf</i> (EF-1)
	425	<i>Candida norvegensis</i>	This patent	<i>tuf</i> (EF-1)

Table 7. Origin of the sequences in the sequence listing (continued).

	SEQ ID NO.	Bacterial,fungal or parasitical species	Source	Comments*
5	426	<i>Candida parapsilosis</i>	This patent	tuf (EF-1)
	427	<i>Candida rugosa</i>	This patent	tuf (EF-1)
	428	<i>Candida sphaerica</i>	This patent	tuf (EF-1)
	429	<i>Candida tropicalis</i>	This patent	tuf (EF-1)
	430	<i>Candida utilis</i>	This patent	tuf (EF-1)
10	431	<i>Candida viswanathii</i>	This patent	tuf (EF-1)
	432	<i>Candida zeylanoides</i>	This patent	tuf (EF-1)
	433	<i>Coccidioides immitis</i>	This patent	tuf (EF-1)
	434	<i>Cryptococcus albidus</i>	This patent	tuf (EF-1)
	435	<i>Exophiala jeanselmei</i>	This patent	tuf (EF-1)
15	436	<i>Fusarium oxysporum</i>	This patent	tuf (EF-1)
	437	<i>Geotrichum</i> sp.	This patent	tuf (EF-1)
	438	<i>Histoplasma capsulatum</i>	This patent	tuf (EF-1)
	439	<i>Issatchenkia orientalis kudrjanzev</i>	This patent	tuf (EF-1)
	440	<i>Malassezia furfur</i>	This patent	tuf (EF-1)
20	441	<i>Malassezia pachydermatis</i>	This patent	tuf (EF-1)
	442	<i>Malbranchea filamentosa</i>	This patent	tuf (EF-1)
	443	<i>Metschnikowia pulcherrima</i>	This patent	tuf (EF-1)
	444	<i>Paecilomyces lilacinus</i>	This patent	tuf (EF-1)
	445	<i>Paracoccidioides brasiliensis</i>	This patent	tuf (EF-1)
25	446	<i>Penicillium marneffeii</i>	This patent	tuf (EF-1)
	447	<i>Pichia anomala</i>	This patent	tuf (EF-1)
	448	<i>Pichia anomala</i>	This patent	tuf (EF-1)
	449	<i>Pseudallescheria boydii</i>	This patent	tuf (EF-1)
	450	<i>Rhizopus oryzae</i>	This patent	tuf (EF-1)
30	451	<i>Rhodotorula minuta</i>	This patent	tuf (EF-1)
	452	<i>Sporobolomyces salmonicolor</i>	This patent	tuf (EF-1)
	453	<i>Sporothrix schenckii</i>	This patent	tuf (EF-1)
	454	<i>Stephanoascus ciferrii</i>	This patent	tuf (EF-1)
	455	<i>Trichophyton mentagrophytes</i>	This patent	tuf (EF-1)
35	456	<i>Trichosporon cutaneum</i>	This patent	tuf (EF-1)
	457	<i>Wangiella dermatitidis</i>	This patent	tuf (EF-1)
	458	<i>Aspergillus fumigatus</i>	This patent	atpD
	459	<i>Blastoschizomyces capitatus</i>	This patent	atpD
	460	<i>Candida albicans</i>	This patent	atpD
40	461	<i>Candida dubliniensis</i>	This patent	atpD
	462	<i>Candida famata</i>	This patent	atpD
	463	<i>Candida glabrata</i>	This patent	atpD
	464	<i>Candida guilliermondii</i>	This patent	atpD
	465	<i>Candida haemulonii</i>	This patent	atpD
45	466	<i>Candida inconspicua</i>	This patent	atpD
	467	<i>Candida kefyr</i>	This patent	atpD
	468	<i>Candida krusei</i>	This patent	atpD
	469	<i>Candida lambica</i>	This patent	atpD
	470	<i>Candida lusitanae</i>	This patent	atpD
50	471	<i>Candida norvegensis</i>	This patent	atpD
	472	<i>Candida parapsilosis</i>	This patent	atpD
	473	<i>Candida rugosa</i>	This patent	atpD
	474	<i>Candida sphaerica</i>	This patent	atpD
	475	<i>Candida tropicalis</i>	This patent	atpD
55	476	<i>Candida utilis</i>	This patent	atpD
	477	<i>Candida viswanathii</i>	This patent	atpD
	478	<i>Candida zeylanoides</i>	This patent	atpD
	479	<i>Coccidioides immitis</i>	This patent	atpD
	480	<i>Cryptococcus albidus</i>	This patent	atpD
60	481	<i>Fusarium oxysporum</i>	This patent	atpD
	482	<i>Geotrichum</i> sp.	This patent	atpD
	483	<i>Histoplasma capsulatum</i>	This patent	atpD
	484	<i>Malassezia furfur</i>	This patent	atpD
	485	<i>Malassezia pachydermatis</i>	This patent	atpD
65	486	<i>Metschnikowia pulcherrima</i>	This patent	atpD
	487	<i>Penicillium marneffeii</i>	This patent	atpD

Table 7. Origin of the sequences in the sequence listing (continued).

	SEQ ID NO.	Bacterial,fungal or parasitical species	Source	Comments*
5	488	<i>Pichia anomala</i>	This patent	<i>atpD</i>
	489	<i>Pichia anomala</i>	This patent	<i>atpD</i>
	490	<i>Rhodotorula minuta</i>	This patent	<i>atpD</i>
	491	<i>Rhodotorula mucilaginosa</i>	This patent	<i>atpD</i>
	492	<i>Sporobolomyces salmonicolor</i>	This patent	<i>atpD</i>
10	493	<i>Sporothrix schenckii</i>	This patent	<i>atpD</i>
	494	<i>Stephanoascus ciferrii</i>	This patent	<i>atpD</i>
	495	<i>Trichophyton mentagrophytes</i>	This patent	<i>atpD</i>
	496	<i>Wangiella dermatitidis</i>	This patent	<i>atpD</i>
	497	<i>Yarrowia lipolytica</i>	This patent	<i>atpD</i>
15	498	<i>Aspergillus fumigatus</i>	This patent	<i>tuf (M)</i>
	499	<i>Blastoschizomyces capitatus</i>	This patent	<i>tuf (M)</i>
	500	<i>Candida rugosa</i>	This patent	<i>tuf (M)</i>
	501	<i>Coccidioides immitis</i>	This patent	<i>tuf (M)</i>
	502	<i>Fusarium oxysporum</i>	This patent	<i>tuf (M)</i>
20	503	<i>Histoplasma capsulatum</i>	This patent	<i>tuf (M)</i>
	504	<i>Paracoccidioides brasiliensis</i>	This patent	<i>tuf (M)</i>
	505	<i>Penicillium marneffeii</i>	This patent	<i>tuf (M)</i>
	506	<i>Pichia anomala</i>	This patent	<i>tuf (M)</i>
	507	<i>Trichophyton mentagrophytes</i>	This patent	<i>tuf (M)</i>
25	508	<i>Yarrowia lipolytica</i>	This patent	<i>tuf (M)</i>
	509	<i>Babesia bigemina</i>	This patent	<i>tuf (EF-1)</i>
	510	<i>Babesia bovis</i>	This patent	<i>tuf (EF-1)</i>
	511	<i>Crithidia fasciculata</i>	This patent	<i>tuf (EF-1)</i>
	512	<i>Entamoeba histolytica</i>	This patent	<i>tuf (EF-1)</i>
30	513	<i>Giardia lamblia</i>	This patent	<i>tuf (EF-1)</i>
	514	<i>Leishmania tropica</i>	This patent	<i>tuf (EF-1)</i>
	515	<i>Leishmania aethiopica</i>	This patent	<i>tuf (EF-1)</i>
	516	<i>Leishmania tropica</i>	This patent	<i>tuf (EF-1)</i>
	517	<i>Leishmania donovani</i>	This patent	<i>tuf (EF-1)</i>
35	518	<i>Leishmania infantum</i>	This patent	<i>tuf (EF-1)</i>
	519	<i>Leishmania enriettii</i>	This patent	<i>tuf (EF-1)</i>
	520	<i>Leishmania gerbilli</i>	This patent	<i>tuf (EF-1)</i>
	521	<i>Leishmania hertigi</i>	This patent	<i>tuf (EF-1)</i>
	522	<i>Leishmania major</i>	This patent	<i>tuf (EF-1)</i>
40	523	<i>Leishmania amazonensis</i>	This patent	<i>tuf (EF-1)</i>
	524	<i>Leishmania mexicana</i>	This patent	<i>tuf (EF-1)</i>
	525	<i>Leishmania tarentolae</i>	This patent	<i>tuf (EF-1)</i>
	526	<i>Leishmania tropica</i>	This patent	<i>tuf (EF-1)</i>
	527	<i>Neospora caninum</i>	This patent	<i>tuf (EF-1)</i>
45	528	<i>Trichomonas vaginalis</i>	This patent	<i>tuf (EF-1)</i>
	529	<i>Trypanosoma brucei</i> subsp. <i>brucei</i>	This patent	<i>tuf (EF-1)</i>
	530	<i>Crithidia fasciculata</i>	This patent	<i>atpD</i>
	531	<i>Leishmania tropica</i>	This patent	<i>atpD</i>
	532	<i>Leishmania aethiopica</i>	This patent	<i>atpD</i>
50	533	<i>Leishmania donovani</i>	This patent	<i>atpD</i>
	534	<i>Leishmania infantum</i>	This patent	<i>atpD</i>
	535	<i>Leishmania gerbilli</i>	This patent	<i>atpD</i>
	536	<i>Leishmania hertigi</i>	This patent	<i>atpD</i>
	537	<i>Leishmania major</i>	This patent	<i>atpD</i>
55	538	<i>Leishmania amazonensis</i>	This patent	<i>atpD</i>
	607	<i>Enterococcus faecalis</i>	WO98/20157	<i>tuf</i>
	608	<i>Enterococcus faecium</i>	WO98/20157	<i>tuf</i>
	609	<i>Enterococcus gallinarum</i>	WO98/20157	<i>tuf</i>
	610	<i>Haemophilus influenzae</i>	Database	<i>tuf</i>
60	611	<i>Staphylococcus epidermidis</i>	WO98/20157	<i>tuf</i>
	612	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i>	This patent	<i>tuf</i>
		serotype Paratyphi A		
	613	<i>Serratia ficaria</i>	This patent	<i>tuf</i>
	614	<i>Enterococcus malodoratus</i>	This patent	<i>tuf (C)</i>
65	615	<i>Enterococcus durans</i>	This patent	<i>tuf (C)</i>
	616	<i>Enterococcus pseudoavium</i>	This patent	<i>tuf (C)</i>

Table 7. Origin of the sequences in the sequence listing (continued).

	SEQ ID NO.	Bacterial,fungal or parasitical species	Source	Comments*
5	617	<i>Enterococcus dispar</i>	This patent	tuf (C)
	618	<i>Enterococcus avium</i>	This patent	tuf (C)
	619	<i>Saccharomyces cerevisiae</i>	Database	tuf (M)
	621	<i>Enterococcus faecium</i>	This patent	tuf (C)
	622	<i>Saccharomyces cerevisiae</i>	This patent	tuf (EF-1)
10	623	<i>Cryptococcus neoformans</i>	This patent	tuf (EF-1)
	624	<i>Candida albicans</i>	This patent	tuf (EF-1)
	662	<i>Corynebacterium diphtheriae</i>	WO98/20157	tuf
	663	<i>Candida catenulata</i>	This patent	atpD
	665	<i>Saccharomyces cerevisiae</i>	Database	tuf (EF-1)
15	666	<i>Saccharomyces cerevisiae</i>	Database	atpD
	667	<i>Trypanosoma cruzi</i>	This patent	atpD
	668	<i>Corynebacterium glutamicum</i>	Database	tuf
	669	<i>Escherichia coli</i>	Database	atpD
	670	<i>Helicobacter pylori</i>	Database	atpD
20	671	<i>Clostridium acetobutylicum</i>	Database	atpD
	672	<i>Cytophaga lytica</i>	Database	atpD
	673	<i>Ehrlichia risticii</i>	This patent	atpD
	674	<i>Vibrio cholerae</i>	This patent	atpD
	675	<i>Vibrio cholerae</i>	This patent	tuf
25	676	<i>Leishmania enriettii</i>	This patent	atpD
	677	<i>Babesia microti</i>	This patent	tuf (EF-1)
	678	<i>Cryptococcus neoformans</i>	This patent	atpD
	679	<i>Cryptococcus neoformans</i>	This patent	atpD
	680	<i>Cunninghamella bertholletiae</i>	This patent	atpD
30	684	<i>Candida tropicalis</i>	Database	atpD (V)
	685	<i>Enterococcus hirae</i>	Database	atpD (V)
	686	<i>Chlamydia pneumoniae</i>	Database	atpD (V)
	687	<i>Halobacterium salinarum</i>	Database	atpD (V)
	688	Human	Database	atpD (V)
35	689	<i>Plasmodium falciparum</i>	Database	atpD (V)
	690	<i>Saccharomyces cerevisiae</i>	Database	atpD (V)
	691	<i>Schizosaccharomyces pombe</i>	Database	atpD (V)
	692	<i>Trypanosoma congolense</i>	Database	atpD (V)
	693	<i>Thermus thermophilus</i>	Database	atpD (V)
40	698	<i>Escherichia coli</i>	Database	tuf
	709	<i>Borrelia burgdorferi</i>	genome project	atpD (V)
	710	<i>Treponema pallidum</i>	genome project	atpD (V)
	711	<i>Chlamydia trachomatis</i>	genome project	atpD (V)
	712	<i>Enterococcus faecalis</i>	genome project	atpD (V)
45	713	<i>Methanosarcina barkeri</i>	Database	atpD (V)
	714	<i>Methanococcus jannaschii</i>	Database	atpD (V)
	715	<i>Porphyromonas gingivalis</i>	genome project	atpD (V)
	716	<i>Streptococcus pneumoniae</i>	genome project	atpD (V)
	717	<i>Burkholderia mallei</i>	This patent	tuf
50	718	<i>Burkholderia pseudomallei</i>	This patent	tuf
	719	<i>Clostridium beijerinckii</i>	This patent	tuf
	720	<i>Clostridium innocuum</i>	This patent	tuf
	721	<i>Clostridium novyi</i>	This patent	tuf
	722	<i>Clostridium septicum</i>	This patent	tuf
55	723	<i>Clostridium tertium</i>	This patent	tuf
	724	<i>Clostridium tetani</i>	This patent	tuf
	725	<i>Enterococcus malodoratus</i>	This patent	tuf
	726	<i>Enterococcus sulfureus</i>	This patent	tuf
	727	<i>Lactococcus garvieae</i>	This patent	tuf
60	728	<i>Mycoplasma pirum</i>	This patent	tuf
	729	<i>Mycoplasma salivarium</i>	This patent	tuf
	730	<i>Neisseria polysaccharea</i>	This patent	tuf
	731	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Enteritidis	This patent	tuf

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial,fungal or parasitical species	Source	Comments*
5	732 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Gallinarum	This patent	tuf
	733 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Paratyphi B	This patent	tuf
	734 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Virchow	This patent	tuf
10	735 <i>Serratia grimesii</i>	This patent	tuf
	736 <i>Clostridium difficile</i>	This patent	tuf
	737 <i>Burkholderia pseudomallei</i>	This patent	atpD
15	738 <i>Clostridium bifermentans</i>	This patent	atpD
	739 <i>Clostridium beijerinckii</i>	This patent	atpD
	740 <i>Clostridium difficile</i>	This patent	atpD
20	741 <i>Clostridium ramosum</i>	This patent	atpD
	742 <i>Clostridium septicum</i>	This patent	atpD
	743 <i>Clostridium tertium</i>	This patent	atpD
25	744 <i>Comamonas acidovorans</i>	This patent	atpD
	745 <i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	This patent	atpD
	746 <i>Neisseria canis</i>	This patent	atpD
30	747 <i>Neisseria cinerea</i>	This patent	atpD
	748 <i>Neisseria cuniculi</i>	This patent	atpD
	749 <i>Neisseria elongata</i> subsp. <i>elongata</i>	This patent	atpD
35	750 <i>Neisseria flavescens</i>	This patent	atpD
	751 <i>Neisseria gonorrhoeae</i>	This patent	atpD
	752 <i>Neisseria gonorrhoeae</i>	This patent	atpD
40	753 <i>Neisseria lactamica</i>	This patent	atpD
	754 <i>Neisseria meningitidis</i>	This patent	atpD
	755 <i>Neisseria mucosa</i>	This patent	atpD
45	756 <i>Neisseria subflava</i>	This patent	atpD
	757 <i>Neisseria weaveri</i>	This patent	atpD
	758 <i>Neisseria animalis</i>	This patent	atpD
50	759 <i>Proteus penneri</i>	This patent	atpD
	760 <i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Enteritidis	This patent	atpD
	761 <i>Yersinia pestis</i>	This patent	atpD
55	762 <i>Burkholderia mallei</i>	This patent	atpD
	763 <i>Clostridium sordellii</i>	This patent	atpD
	764 <i>Clostridium novyi</i>	This patent	atpD
60	765 <i>Clostridium botulinum</i>	This patent	atpD
	766 <i>Clostridium histolyticum</i>	This patent	atpD
	767 <i>Peptostreptococcus prevotii</i>	This patent	atpD
65	768 <i>Absidia corymbifera</i>	This patent	atpD
	769 <i>Alternaria alternata</i>	This patent	atpD
	770 <i>Aspergillus flavus</i>	This patent	atpD
70	771 <i>Mucor circinelloides</i>	This patent	atpD
	772 <i>Piedraia hortai</i>	This patent	atpD
	773 <i>Pseudallescheria boydii</i>	This patent	atpD
75	774 <i>Rhizopus oryzae</i>	This patent	atpD
	775 <i>Scopulariopsis koningii</i>	This patent	atpD
	776 <i>Trichophyton mentagrophytes</i>	This patent	atpD
80	777 <i>Trichophyton tonsurans</i>	This patent	atpD
	778 <i>Trichosporon cutaneum</i>	This patent	tuf (EF-1)
	779 <i>Cladophialophora carrionii</i>	This patent	tuf (EF-1)
85	780 <i>Cunninghamella bertholletiae</i>	This patent	tuf (EF-1)
	781 <i>Curvularia lunata</i>	This patent	tuf (EF-1)
	782 <i>Fonsecaea pedrosoi</i>	This patent	tuf (EF-1)
90	783 <i>Microsporum audouinii</i>	This patent	tuf (EF-1)
	784 <i>Mucor circinelloides</i>	This patent	tuf (EF-1)
	785 <i>Phialophora verrucosa</i>	This patent	tuf (EF-1)
95	786 <i>Saksenaea vasiformis</i>	This patent	tuf (EF-1)
	787 <i>Syncephalastrum racemosum</i>	This patent	tuf (EF-1)
	788 <i>Trichophyton tonsurans</i>	This patent	tuf (EF-1)
100	789 <i>Trichophyton mentagrophytes</i>	This patent	tuf (EF-1)

Table 7. Origin of the sequences in the sequence listing (continued).

	SEQ ID NO.	Bacterial,fungal or parasitical species	Source	Comments*
5	790	<i>Bipolaris hawaiiensis</i>	This patent	<i>tuf</i> (EF-1)
	791	<i>Aspergillus fumigatus</i>	This patent	<i>tuf</i> (M)
	792	<i>Trichophyton mentagrophytes</i>	This patent	<i>tuf</i> (M)
	827	<i>Clostridium novyi</i>	This patent	<i>atpD</i> (V)
	828	<i>Clostridium difficile</i>	This patent	<i>atpD</i> (V)
10	829	<i>Clostridium septicum</i>	This patent	<i>atpD</i> (V)
	830	<i>Clostridium botulinum</i>	This patent	<i>atpD</i> (V)
	831	<i>Clostridium perfringens</i>	This patent	<i>atpD</i> (V)
	832	<i>Clostridium tetani</i>	This patent	<i>atpD</i> (V)
	833	<i>Streptococcus pyogenes</i>	Database	<i>atpD</i> (V)
15	834	<i>Babesia bovis</i>	This patent	<i>atpD</i> (V)
	835	<i>Cryptosporidium parvum</i>	This patent	<i>atpD</i> (V)
	836	<i>Leishmania infantum</i>	This patent	<i>atpD</i> (V)
	837	<i>Leishmania major</i>	This patent	<i>atpD</i> (V)
	838	<i>Leishmania tarentolae</i>	This patent	<i>atpD</i> (V)
20	839	<i>Trypanosoma brucei</i>	This patent	<i>atpD</i> (V)
	840	<i>Trypanosoma cruzi</i>	This patent	<i>tuf</i> (EF-1)
	841	<i>Trypanosoma cruzi</i>	This patent	<i>tuf</i> (EF-1)
	842	<i>Trypanosoma cruzi</i>	This patent	<i>tuf</i> (EF-1)
	843	<i>Babesia bovis</i>	This patent	<i>tuf</i> (M)
25	844	<i>Leishmania aethiopica</i>	This patent	<i>tuf</i> (M)
	845	<i>Leishmania amazonensis</i>	This patent	<i>tuf</i> (M)
	846	<i>Leishmania donovani</i>	This patent	<i>tuf</i> (M)
	847	<i>Leishmania infantum</i>	This patent	<i>tuf</i> (M)
	848	<i>Leishmania enriettii</i>	This patent	<i>tuf</i> (M)
30	849	<i>Leishmania gerbilli</i>	This patent	<i>tuf</i> (M)
	850	<i>Leishmania major</i>	This patent	<i>tuf</i> (M)
	851	<i>Leishmania mexicana</i>	This patent	<i>tuf</i> (M)
	852	<i>Leishmania tarentolae</i>	This patent	<i>tuf</i> (M)
	853	<i>Trypanosoma cruzi</i>	This patent	<i>tuf</i> (M)
35	854	<i>Trypanosoma cruzi</i>	This patent	<i>tuf</i> (M)
	855	<i>Trypanosoma cruzi</i>	This patent	<i>tuf</i> (M)
	856	<i>Babesia bigemina</i>	This patent	<i>atpD</i>
	857	<i>Babesia bovis</i>	This patent	<i>atpD</i>
	858	<i>Babesia microti</i>	This patent	<i>atpD</i>
40	859	<i>Leishmania guyanensis</i>	This patent	<i>atpD</i>
	860	<i>Leishmania mexicana</i>	This patent	<i>atpD</i>
	861	<i>Leishmania tropica</i>	This patent	<i>atpD</i>
	862	<i>Leishmania tropica</i>	This patent	<i>atpD</i>
	863	<i>Bordetella pertussis</i>	Database	<i>tuf</i>
45	864	<i>Trypanosoma brucei</i>	Database	<i>tuf</i> (EF-1)
	865	<i>Cryptosporidium parvum</i>	This patent	<i>tuf</i> (EF-1)
	866	<i>Staphylococcus saprophyticus</i>	This patent	<i>atpD</i>
	867	<i>Zoogloea ramigera</i>	This patent	<i>atpD</i>
	868	<i>Staphylococcus saprophyticus</i>	This patent	<i>tuf</i>
50	869	<i>Enterococcus casseliflavus</i>	This patent	<i>tuf</i>
	870	<i>Enterococcus casseliflavus</i>	This patent	<i>tuf</i>
	871	<i>Enterococcus flavescens</i>	This patent	<i>tuf</i>
	872	<i>Enterococcus gallinarum</i>	This patent	<i>tuf</i>
	873	<i>Enterococcus gallinarum</i>	This patent	<i>tuf</i>
55	874	<i>Staphylococcus haemolyticus</i>	This patent	<i>tuf</i>
	875	<i>Staphylococcus epidermidis</i>	This patent	<i>tuf</i>
	876	<i>Staphylococcus epidermidis</i>	This patent	<i>tuf</i>
	877	<i>Staphylococcus epidermidis</i>	This patent	<i>tuf</i>
	878	<i>Staphylococcus epidermidis</i>	This patent	<i>tuf</i>
60	879	<i>Enterococcus gallinarum</i>	This patent	<i>tuf</i>
	880	<i>Pseudomonas aeruginosa</i>	This patent	<i>tuf</i>
	881	<i>Enterococcus casseliflavus</i>	This patent	<i>tuf</i>
	882	<i>Enterococcus casseliflavus</i>	This patent	<i>tuf</i>
	883	<i>Enterococcus faecalis</i>	This patent	<i>tuf</i>
65	884	<i>Enterococcus faecalis</i>	This patent	<i>tuf</i>
	885	<i>Enterococcus faecium</i>	This patent	<i>tuf</i>

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial, fungal or parasitical species	Source	Comments*
5	886 <i>Enterococcus faecium</i>	This patent	tuf
	887 <i>Zoogloea ramigera</i>	This patent	tuf
	888 <i>Enterococcus faecalis</i>	This patent	tuf
	889 <i>Aspergillus fumigatus</i>	This patent	atpD
	890 <i>Penicillium marneffe</i>	This patent	atpD
10	891 <i>Paecilomyces lilacinus</i>	This patent	atpD
	892 <i>Penicillium marneffe</i>	This patent	atpD
	893 <i>Sporothrix schenckii</i>	This patent	atpD
	894 <i>Malbranchea filamentosa</i>	This patent	atpD
	895 <i>Paecilomyces lilacinus</i>	This patent	atpD
15	896 <i>Aspergillus niger</i>	This patent	atpD
	897 <i>Aspergillus fumigatus</i>	This patent	tuf (EF-1)
	898 <i>Penicillium marneffe</i>	This patent	tuf (EF-1)
	899 <i>Piedraia hortai</i>	This patent	tuf (EF-1)
	900 <i>Paecilomyces lilacinus</i>	This patent	tuf (EF-1)
20	901 <i>Paracoccidioides brasiliensis</i>	This patent	tuf (EF-1)
	902 <i>Sporothrix schenckii</i>	This patent	tuf (EF-1)
	903 <i>Penicillium marneffe</i>	This patent	tuf (EF-1)
	904 <i>Curvularia lunata</i>	This patent	tuf (M)
	905 <i>Aspergillus niger</i>	This patent	tuf (M)
25	906 <i>Bipolaris hawaiiensis</i>	This patent	tuf (M)
	907 <i>Aspergillus flavus</i>	This patent	tuf (M)
	908 <i>Alternaria alternata</i>	This patent	tuf (M)
	909 <i>Penicillium marneffe</i>	This patent	tuf (M)
	910 <i>Penicillium marneffe</i>	This patent	tuf (M)
30	918 <i>Escherichia coli</i>	Database	recA
	929 <i>Bacteroides fragilis</i>	This patent	atpD (V)
	930 <i>Bacteroides distasonis</i>	This patent	atpD (V)
	931 <i>Porphyromonas asaccharolytica</i>	This patent	atpD (V)
	932 <i>Listeria monocytogenes</i>	This patent	tuf
35	939 <i>Saccharomyces cerevisiae</i>	Database	recA (Rad51)
	940 <i>Saccharomyces cerevisiae</i>	Database	recA (Dmc1)
	941 <i>Cryptococcus humicolus</i>	This patent	atpD
	942 <i>Escherichia coli</i>	This patent	atpD
	943 <i>Escherichia coli</i>	This patent	atpD
40	944 <i>Escherichia coli</i>	This patent	atpD
	945 <i>Escherichia coli</i>	This patent	atpD
	946 <i>Neisseria polysaccharea</i>	This patent	atpD
	947 <i>Neisseria sicca</i>	This patent	atpD
	948 <i>Streptococcus mitis</i>	This patent	atpD
45	949 <i>Streptococcus mitis</i>	This patent	atpD
	950 <i>Streptococcus mitis</i>	This patent	atpD
	951 <i>Streptococcus oralis</i>	This patent	atpD
	952 <i>Streptococcus pneumoniae</i>	This patent	atpD
	953 <i>Streptococcus pneumoniae</i>	This patent	atpD
50	954 <i>Streptococcus pneumoniae</i>	This patent	atpD
	955 <i>Streptococcus pneumoniae</i>	This patent	atpD
	956 <i>Babesia microti</i>	This patent	atpD (V)
	957 <i>Entamoeba histolytica</i>	This patent	atpD (V)
	958 <i>Fusobacterium nucleatum</i> subsp. <i>polymorphum</i>	This patent	atpD (V)
55	959 <i>Leishmania aethiopica</i>	This patent	atpD (V)
	960 <i>Leishmania tropica</i>	This patent	atpD (V)
	961 <i>Leishmania guyanensis</i>	This patent	atpD (V)
	962 <i>Leishmania donovani</i>	This patent	atpD (V)
	963 <i>Leishmania hertigi</i>	This patent	atpD (V)
60	964 <i>Leishmania mexicana</i>	This patent	atpD (V)
	965 <i>Leishmania tropica</i>	This patent	atpD (V)
	966 <i>Peptostreptococcus anaerobius</i>	This patent	atpD (V)
	967 <i>Bordetella pertussis</i>	This patent	tuf
	968 <i>Bordetella pertussis</i>	This patent	tuf
65	969 <i>Enterococcus columbae</i>	This patent	tuf

Table 7. Origin of the sequences in the sequence listing (continued).

	SEQ ID NO.	Bacterial,fungal or parasitical species	Source	Comments*
5	970	<i>Enterococcus flavescens</i>	This patent	<i>tuf</i>
	971	<i>Streptococcus pneumoniae</i>	This patent	<i>tuf</i>
	972	<i>Escherichia coli</i>	This patent	<i>tuf</i>
	973	<i>Escherichia coli</i>	This patent	<i>tuf</i>
	974	<i>Escherichia coli</i>	This patent	<i>tuf</i>
10	975	<i>Escherichia coli</i>	This patent	<i>tuf</i>
	976	<i>Mycobacterium avium</i>	This patent	<i>tuf</i>
	977	<i>Streptococcus pneumoniae</i>	This patent	<i>tuf</i>
	978	<i>Mycobacterium gordonae</i>	This patent	<i>tuf</i>
	979	<i>Streptococcus pneumoniae</i>	This patent	<i>tuf</i>
15	980	<i>Mycobacterium tuberculosis</i>	This patent	<i>tuf</i>
	981	<i>Staphylococcus warneri</i>	This patent	<i>tuf</i>
	982	<i>Streptococcus mitis</i>	This patent	<i>tuf</i>
	983	<i>Streptococcus mitis</i>	This patent	<i>tuf</i>
	984	<i>Streptococcus mitis</i>	This patent	<i>tuf</i>
20	985	<i>Streptococcus oralis</i>	This patent	<i>tuf</i>
	986	<i>Streptococcus pneumoniae</i>	This patent	<i>tuf</i>
	987	<i>Enterococcus hirae</i>	This patent	<i>tuf</i> (C)
	988	<i>Enterococcus mundtii</i>	This patent	<i>tuf</i> (C)
	989	<i>Enterococcus raffinosus</i>	This patent	<i>tuf</i> (C)
25	990	<i>Bacillus anthracis</i>	This patent	<i>recA</i>
	991	<i>Prevotella melaninogenica</i>	This patent	<i>recA</i>
	992	<i>Enterococcus casseliflavus</i>	This patent	<i>tuf</i>
	993	<i>Streptococcus pyogenes</i>	Database	<i>speA</i>
	1002	<i>Streptococcus pyogenes</i>	genome project	<i>tuf</i>
30	1003	<i>Bacillus cereus</i>	This patent	<i>recA</i>
	1004	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1005	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1006	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1007	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
35	1008	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1009	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1010	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1011	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1012	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
40	1013	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1014	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1015	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1016	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1017	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
45	1018	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp1a</i>
	1019	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1020	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1021	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1022	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
50	1023	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1024	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1025	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1026	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1027	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
55	1028	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1029	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1030	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1031	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1032	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
60	1033	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2b</i>
	1034	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1035	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1036	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1037	<i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial,fungal or parasitcal species	Source	Comments*
5	1038 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1039 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1040 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1041 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1042 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
10	1043 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1044 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1045 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1046 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1047 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
15	1048 <i>Streptococcus pneumoniae</i>	This patent	<i>pbp2x</i>
	1049 <i>Enterococcus faecium</i>	This patent	<i>vanA</i>
	1050 <i>Enterococcus gallinarum</i>	This patent	<i>vanA</i>
	1051 <i>Enterococcus faecium</i>	This patent	<i>vanA</i>
	1052 <i>Enterococcus faecium</i>	This patent	<i>vanA</i>
20	1053 <i>Enterococcus faecium</i>	This patent	<i>vanA</i>
	1054 <i>Enterococcus faecalis</i>	This patent	<i>vanA</i>
	1055 <i>Enterococcus gallinarum</i>	This patent	<i>vanA</i>
	1056 <i>Enterococcus faecium</i>	This patent	<i>vanA</i>
	1057 <i>Enterococcus flavescens</i>	This patent	<i>vanA</i>
25	1058 <i>Enterococcus gallinarum</i>	This patent	<i>vanC1</i>
	1059 <i>Enterococcus gallinarum</i>	This patent	<i>vanC1</i>
	1060 <i>Enterococcus casseliflavus</i>	This patent	<i>vanC2</i>
	1061 <i>Enterococcus casseliflavus</i>	This patent	<i>vanC2</i>
	1062 <i>Enterococcus casseliflavus</i>	This patent	<i>vanC2</i>
30	1063 <i>Enterococcus casseliflavus</i>	This patent	<i>vanC2</i>
	1064 <i>Enterococcus flavescens</i>	This patent	<i>vanC3</i>
	1065 <i>Enterococcus flavescens</i>	This patent	<i>vanC3</i>
	1066 <i>Enterococcus flavescens</i>	This patent	<i>vanC3</i>
	1067 <i>Enterococcus faecium</i>	This patent	<i>vanXY</i>
35	1068 <i>Enterococcus faecium</i>	This patent	<i>vanXY</i>
	1069 <i>Enterococcus faecium</i>	This patent	<i>vanXY</i>
	1070 <i>Enterococcus faecalis</i>	This patent	<i>vanXY</i>
	1071 <i>Enterococcus gallinarum</i>	This patent	<i>vanXY</i>
	1072 <i>Enterococcus faecium</i>	This patent	<i>vanXY</i>
40	1073 <i>Enterococcus flavescens</i>	This patent	<i>vanXY</i>
	1074 <i>Enterococcus faecium</i>	This patent	<i>vanXY</i>
	1075 <i>Enterococcus gallinarum</i>	This patent	<i>vanXY</i>
	1076 <i>Escherichia coli</i>	Database	<i>stx₁</i>
	1077 <i>Escherichia coli</i>	Database	<i>stx₂</i>
45	1093 <i>Staphylococcus saprophyticus</i>	This patent	unknown
	1117 <i>Enterococcus faecium</i>	Database	<i>vanB</i>
	1138 <i>Enterococcus gallinarum</i>	Database	<i>vanC1</i>
	1139 <i>Enterococcus faecium</i>	Database	<i>vanA</i>
	1140 <i>Enterococcus casseliflavus</i>	Database	<i>vanC2</i>
50	1141 <i>Enterococcus faecium</i>	Database	<i>vanHAXY</i>
	1169 <i>Streptococcus pneumoniae</i>	Database	<i>pbp1a</i>
	1172 <i>Streptococcus pneumoniae</i>	Database	<i>pbp2b</i>
	1173 <i>Streptococcus pneumoniae</i>	Database	<i>pbp2x</i>
	1178 <i>Staphylococcus aureus</i>	Database	<i>mecA</i>
55	1183 <i>Streptococcus pneumoniae</i>	Database	<i>hexA</i>
	1184 <i>Streptococcus pneumoniae</i>	This patent	<i>hexA</i>
	1185 <i>Streptococcus pneumoniae</i>	This patent	<i>hexA</i>
	1186 <i>Streptococcus pneumoniae</i>	This patent	<i>hexA</i>
	1187 <i>Streptococcus pneumoniae</i>	This patent	<i>hexA</i>
60			

Table 7. Origin of the sequences in the sequence listing (continued).

SEQ ID NO.	Bacterial, fungal or parasitical species	Source	Comments*
5	1188 <i>Streptococcus oralis</i>	This patent	<i>hexA</i>
	1189 <i>Streptococcus mitis</i>	This patent	<i>hexA</i>
	1190 <i>Streptococcus mitis</i>	This patent	<i>hexA</i>
	1191 <i>Streptococcus mitis</i>	This patent	<i>hexA</i>
	1198 <i>Staphylococcus saprophyticus</i>	This patent	unknown
10	1215 <i>Streptococcus pyogenes</i>	Database	<i>PCP</i>
	1230 <i>Escherichia coli</i>	Database	<i>tuf</i> (EF-G)
	1242 <i>Enterococcus faecium</i>	Database	<i>ddl</i>
	1243 <i>Enterococcus faecalis</i>	Database	<i>mtlF</i> , <i>mtlD</i>
15	1244 <i>Staphylococcus aureus</i> subsp. <i>aureus</i>	This patent	unknown

* *tuf* indicates *tuf* sequences, *tuf* (C) indicates *tuf* sequences divergent from main (usually A and B) copies of the elongation factor-Tu, *tuf* (EF-1) indicates *tuf* sequences of the eukaryotic type (elongation factor 1 α), *tuf* (M) indicates *tuf* sequences from organellar (mostly mitochondrial) origin.

20 *atpD* indicates *atpD* sequences of the F-type, *atpD* (V) indicates *atpD* sequences of the V-type.

recA indicates *recA* sequences, *recA*(Rad51) indicates *rad51* sequences or homologs and *recA*(Dmc1) indicates *dmc1* sequences or homologs.

speA indicates *speA* sequences.

25 *hexA* indicates *hexA* sequences.

mecA indicates *mecA* sequences.

vanA indicates *vanA* sequences, *vanB* indicates *vanB* sequences, *vanC1* indicates *vanC1* sequences, *vanC2* indicates *vanC2* sequences, *vanC3* indicates *vanC3* sequences, *vanXY* indicates *vanXY* sequences, *vanHAXY* indicates *vanHAXY* sequences.

pbp1a indicates *pbp1a* sequences, *pbp2b* indicates *pbp2b* sequences, *pbp2x* indicates *pbp2x* sequences.

pcp indicates *pcp* sequences.

30 *stx₁* indicates *stx₁* sequences, *stx₂* indicates *stx₂* sequences.

unknown indicates an unknown gene.

Table 8. Bacterial species used to test the specificity of the *Streptococcus agalactiae*-specific amplification primers derived from *tuf* sequences.

5	Strain	Reference number	Strain	Reference number
	<i>Streptococcus acidominimus</i>	ATCC 51726	<i>Bacteroides caccae</i>	ATCC 43185
	<i>Streptococcus agalactiae</i>	ATCC 12403	<i>Bacteroides vulgatus</i>	ATCC 8482
	<i>Streptococcus agalactiae</i>	ATCC 12973	<i>Bacteroides fragilis</i>	ATCC 25285
10	<i>Streptococcus agalactiae</i>	ATCC 13813	<i>Candida albicans</i>	ATCC 11006
	<i>Streptococcus agalactiae</i>	ATCC 27591	<i>Clostridium innoculum</i>	ATCC 14501
	<i>Streptococcus agalactiae</i>	CDCs 1073	<i>Clostridium ramosum</i>	ATCC 25582
	<i>Streptococcus anginosus</i>	ATCC 27335	<i>Lactobacillus casei</i> subsp. <i>casei</i>	ATCC 393
	<i>Streptococcus anginosus</i>	ATCC 33397	<i>Clostridium septicum</i>	ATCC 12464
15	<i>Streptococcus bovis</i>	ATCC 33317	<i>Corynebacterium cervicis</i>	NCTC 10604
	<i>Streptococcus anginosus</i>	ATCC 27823	<i>Corynebacterium genitalium</i>	ATCC 33031
	<i>Streptococcus cricetus</i>	ATCC 19642	<i>Corynebacterium urealyticum</i>	ATCC 43042
	<i>Streptococcus cristatus</i>	ATCC 51100	<i>Enterococcus faecalis</i>	ATCC 29212
	<i>Streptococcus downei</i>	ATCC 33748	<i>Enterococcus faecium</i>	ATCC 19434
20	<i>Streptococcus dysgalactiae</i>	ATCC 43078	<i>Eubacterium lentum</i>	ATCC 43055
	<i>Streptococcus equi</i> subsp. <i>equi</i>	ATCC 9528	<i>Eubacterium nodutum</i>	ATCC 33099
	<i>Streptococcus ferus</i>	ATCC 33477	<i>Gardnerella vaginalis</i>	ATCC 14018
	<i>Streptococcus gordonii</i>	ATCC 10558	<i>Lactobacillus acidophilus</i>	ATCC 4356
	<i>Streptococcus macacae</i>	ATCC 35911	<i>Lactobacillus crispatus</i>	ATCC 33820
25	<i>Streptococcus mitis</i>	ATCC 49456	<i>Lactobacillus gasseri</i>	ATCC 33323
	<i>Streptococcus mutans</i>	ATCC 25175	<i>Lactobacillus johnsonii</i>	ATCC 33200
	<i>Streptococcus oralis</i>	ATCC 35037	<i>Lactococcus lactis</i> subsp. <i>lactis</i>	ATCC 19435
	<i>Streptococcus parasanguinis</i>	ATCC 15912	<i>Lactococcus lactis</i> subsp. <i>lactis</i>	ATCC 11454
	<i>Streptococcus parauberis</i>	DSM 6631	<i>Listeria innocua</i>	ATCC 33090
30	<i>Streptococcus pneumoniae</i>	ATCC 27336	<i>Micrococcus luteus</i>	ATCC 9341
	<i>Streptococcus pyogenes</i>	ATCC 19615	<i>Escherichia coli</i>	ATCC 25922
	<i>Streptococcus rattii</i>	ATCC 19645	<i>Micrococcus lylae</i>	ATCC 27566
	<i>Streptococcus salivarius</i>	ATCC 7073	<i>Porphyromonas asaccharolytica</i>	ATCC 25260
	<i>Streptococcus sanguinis</i>	ATCC 10556	<i>Prevotella corporis</i>	ATCC 33547
35	<i>Streptococcus sobrinus</i>	ATCC 27352	<i>Prevotella melanogenica</i>	ATCC 25845
	<i>Streptococcus suis</i>	ATCC 43765	<i>Staphylococcus aureus</i>	ATCC 13301
	<i>Streptococcus uberis</i>	ATCC 19436	<i>Staphylococcus epidermidis</i>	ATCC 14990
	<i>Streptococcus vestibularis</i>	ATCC 49124	<i>Staphylococcus saprophyticus</i>	ATCC 15305

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Table 9. Bacterial species used to test the specificity of the *Streptococcus agalactiae*-specific amplification primers derived from *atpD* sequences.

	Strain	Reference number	Strain	Reference number
5	<i>Streptococcus acidominimus</i>	ATCC 51726	<i>Streptococcus gordonii</i>	ATCC 10558
	<i>Streptococcus agalactiae</i>	ATCC 12400	<i>Streptococcus macacae</i>	ATCC 35911
	<i>Streptococcus agalactiae</i>	ATCC 12403	<i>Streptococcus mitis</i>	ATCC 49456
10	<i>Streptococcus agalactiae</i>	ATCC 12973	<i>Streptococcus mutans</i>	ATCC 25175
	<i>Streptococcus agalactiae</i>	ATCC 13813	<i>Streptococcus oralis</i>	ATCC 35037
	<i>Streptococcus agalactiae</i>	ATCC 27591	<i>Streptococcus parasanguinis</i>	ATCC 15912
	<i>Streptococcus agalactiae</i>	CDCs-1073	<i>Streptococcus parauberis</i>	DSM 6631
	<i>Streptococcus anginosus</i>	ATCC 27335	<i>Streptococcus pneumoniae</i>	ATCC 27336
15	<i>Streptococcus anginosus</i>	ATCC 27823	<i>Streptococcus pyogenes</i>	ATCC 19615
	<i>Streptococcus bovis</i>	ATCC 33317	<i>Streptococcus rattii</i>	ATCC 19645
	<i>Streptococcus cricetus</i>	ATCC 19642	<i>Streptococcus salivarius</i>	ATCC 7073
	<i>Streptococcus cristatus</i>	ATCC 51100	<i>Streptococcus sanguinis</i>	ATCC 10556
	<i>Streptococcus downei</i>	ATCC 33748	<i>Streptococcus sobrinus</i>	ATCC 27352
20	<i>Streptococcus dysgalactiae</i>	ATCC 43078	<i>Streptococcus suis</i>	ATCC 43765
	<i>Streptococcus equi</i> subsp. <i>equi</i>	ATCC 9528	<i>Streptococcus uberis</i>	ATCC 19436
	<i>Streptococcus ferus</i>	ATCC 33477	<i>Streptococcus vestibularis</i>	ATCC 49124

Table 10. Bacterial species used to test the specificity of the *Enterococcus*-specific amplification primers derived from *tuf* sequences.

	Strain	Reference number	Strain	Reference number
5	Gram-positive species (n=74)			
	<i>Abiotrophia adiacens</i>	ATCC 49176	<i>Listeria innocua</i>	ATCC 33090
	<i>Abiotrophia defectiva</i>	ATCC 49175	<i>Listeria ivanovii</i>	ATCC 19119
	<i>Bacillus cereus</i>	ATCC 14579	<i>Listeria monocytogenes</i>	ATCC 15313
	<i>Bacillus subtilis</i>	ATCC 27370	<i>Listeria seeligeri</i>	ATCC 35967
10	<i>Bifidobacterium adolescentis</i>	ATCC 27534	<i>Micrococcus luteus</i>	ATCC 9341
	<i>Bifidobacterium breve</i>	ATCC 15700	<i>Pediococcus acidilacti</i>	ATCC 33314
	<i>Bifidobacterium dentium</i>	ATCC 27534	<i>Pediococcus pentosaceus</i>	ATCC 33316
	<i>Bifidobacterium longum</i>	ATCC 15707	<i>Peptococcus niger</i>	ATCC 27731
	<i>Clostridium perfringens</i>	ATCC 3124	<i>Peptostreptococcus anaerobius</i>	ATCC 27337
15	<i>Clostridium septicum</i>	ATCC 12464	<i>Peptostreptococcus indolicus</i>	ATCC 29247
	<i>Corynebacterium aquaticus</i>	ATCC 14665	<i>Peptostreptococcus micros</i>	ATCC 33270
	<i>Corynebacterium pseudodiphtheriticum</i>	ATCC 10700	<i>Propionibacterium acnes</i>	ATCC 6919
	<i>Enterococcus avium</i>	ATCC 14025	<i>Staphylococcus aureus</i>	ATCC 43300
20	<i>Enterococcus casseliflavus</i>	ATCC 25788	<i>Staphylococcus capitis</i>	ATCC 27840
	<i>Enterococcus cecorum</i>	ATCC 43199	<i>Staphylococcus epidermidis</i>	ATCC 14990
	<i>Enterococcus columbae</i>	ATCC 51263	<i>Staphylococcus haemolyticus</i>	ATCC 29970
	<i>Enterococcus dispar</i>	ATCC 51266	<i>Staphylococcus hominis</i>	ATCC 27844
	<i>Enterococcus durans</i>	ATCC 19432	<i>Staphylococcus lugdunensis</i>	ATCC 43809
25	<i>Enterococcus faecalis</i>	ATCC 29212	<i>Staphylococcus saprophyticus</i>	ATCC 15305
	<i>Enterococcus faecium</i>	ATCC 19434	<i>Staphylococcus simulans</i>	ATCC 27848
	<i>Enterococcus flavescens</i>	ATCC 49996	<i>Staphylococcus warneri</i>	ATCC 27836
	<i>Enterococcus gallinarum</i>	ATCC 49573	<i>Streptococcus agalactiae</i>	ATCC 13813
	<i>Enterococcus hirae</i>	ATCC 8044	<i>Streptococcus anginosus</i>	ATCC 33397
30	<i>Enterococcus malodoratus</i>	ATCC 43197	<i>Streptococcus bovis</i>	ATCC 33317
	<i>Enterococcus mundtii</i>	ATCC 43186	<i>Streptococcus constellatus</i>	ATCC 27823
	<i>Enterococcus pseudoavium</i>	ATCC 49372	<i>Streptococcus cristatus</i>	ATCC 51100
	<i>Enterococcus raffinosus</i>	ATCC 49427	<i>Streptococcus intermedius</i>	ATCC 27335
	<i>Enterococcus saccharolyticus</i>	ATCC 43076	<i>Streptococcus mitis</i>	ATCC 49456
35	<i>Enterococcus solitarius</i>	ATCC 49428	<i>Streptococcus mitis</i>	ATCC 3639
	<i>Enterococcus sulfureus</i>	ATCC 49903	<i>Streptococcus mutans</i>	ATCC 27175
	<i>Eubacterium lentum</i>	ATCC 49903	<i>Streptococcus parasanguinis</i>	ATCC 15912
	<i>Gemella haemolysans</i>	ATCC 10379	<i>Streptococcus pneumoniae</i>	ATCC 27736
	<i>Gemella morbillorum</i>	ATCC 27842	<i>Streptococcus pneumoniae</i>	ATCC 6303
40	<i>Lactobacillus acidophilus</i>	ATCC 4356	<i>Streptococcus pyogenes</i>	ATCC 19615
	<i>Leuconostoc mesenteroides</i>	ATCC 19225	<i>Streptococcus salivarius</i>	ATCC 7073
	<i>Listeria grayi</i>	ATCC 19120	<i>Streptococcus sanguinis</i>	ATCC 10556
	<i>Listeria grayi</i>	ATCC 19123	<i>Streptococcus suis</i>	ATCC 43765
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Table 10. Bacterial species used to test the specificity of the *Enterococcus* genus-specific amplification primers derived from *tuf* sequences (continued).

	Strain	Reference number	Strain	Reference number
5	Gram-negative species (n=39)			
	<i>Acidominococcus fermentans</i>	ATCC 2508	<i>Hafnia alvei</i>	ATCC 13337
	<i>Acinetobacter baumannii</i>	ATCC 19606	<i>Klebsiella oxytoca</i>	ATCC 13182
	<i>Alcaligenes faecalis</i>	ATCC 8750	<i>Meganomonas hypermegas</i>	ATCC 25560
	<i>Anaerobiospirillum</i>	ATCC 29305	<i>Mitsukoella multiacidus</i>	ATCC 27723
10	<i>succiniproducens</i>		<i>Moraxella catarrhalis</i>	ATCC 43628
	<i>Anaerorhabdus furcosus</i>	ATCC 25662	<i>Morganella morganii</i>	ATCC 25830
	<i>Bacteroides distasonis</i>	ATCC 8503	<i>Neisseria meningitidis</i>	ATCC 13077
	<i>Bacteroides thetaiotaomicron</i>	ATCC 29741	<i>Pasteurella aerogenes</i>	ATCC 27883
	<i>Bacteroides vulgatus</i>	ATCC 8482	<i>Proteus vulgaris</i>	ATCC 13315
15	<i>Bordetella pertussis</i>	LSPQ 3702	<i>Providencia alcalifaciens</i>	ATCC 9886
	<i>Bulkholderia cepacia</i>	LSPQ 2217	<i>Providencia rettgeri</i>	ATCC 9250
	<i>Butyrvibrio fibrinosolvens</i>	ATCC 19171	<i>Pseudomonas aeruginosa</i>	ATCC 27853
	<i>Cardiobacterium hominis</i>	ATCC 15826	<i>Salmonella typhimurium</i>	ATCC 14028
	<i>Citrobacter freundii</i>	ATCC 8090	<i>Serratia marcescens</i>	ATCC 13880
20	<i>Desulfovibrio vulgaris</i>	ATCC 29579	<i>Shigella flexneri</i>	ATCC 12022
	<i>Edwardsiellae tarda</i>	ATCC 15947	<i>Shigella sonnei</i>	ATCC 29930
	<i>Enterobacter cloacae</i>	ATCC 13047	<i>Succinivibrio dextrinosolvens</i>	ATCC 19716
	<i>Escherichia coli</i>	ATCC 25922	<i>Tissierella praeacuta</i>	ATCC 25539
	<i>Fusobacterium russii</i>	ATCC 25533	<i>Veillonella parvula</i>	ATCC 10790
25	<i>Haemophilus influenzae</i>	ATCC 9007	<i>Yersinia enterocolitica</i>	ATCC 9610

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases.

	Species	Strain	Accession number	Coding gene*
Bacteria				
	<i>Agrobacterium tumefaciens</i>		X99673	<i>tuf</i>
	<i>Agrobacterium tumefaciens</i>		X99673	<i>tuf</i> (EF-G)
5	<i>Agrobacterium tumefaciens</i>		X99674	<i>tuf</i>
	<i>Anacystis nidulans</i>	PCC 6301	X17442	<i>tuf</i>
	<i>Aquifex aeolicus</i>	VF5	AE000669	<i>tuf</i>
	<i>Aquifex aeolicus</i>	VF5	AE000669	<i>tuf</i> (EF-G)
	<i>Aquifex pyrophilus</i>		Genome project ²	<i>tuf</i> (EF-G)
10	<i>Aquifex pyrophilus</i>		Y15787	<i>tuf</i>
	<i>Archaeoglobus fulgidus</i>		Genome project ²	<i>tuf</i> (EF-G)
	<i>Bacillus halodurans</i>	C-125	AB017508	<i>tuf</i>
	<i>Bacillus halodurans</i>	C-125	AB017508	<i>tuf</i> (EF-G)
	<i>Bacillus stearothermophilus</i>	CCM 2184	AJ000260	<i>tuf</i>
15	<i>Bacillus subtilis</i>	168	D64127	<i>tuf</i>
	<i>Bacillus subtilis</i>	168	D64127	<i>tuf</i> (EF-G)
	<i>Bacillus subtilis</i>	DSM 10	Z99104	<i>tuf</i>
	<i>Bacteroides forsythus</i>	ATCC 43037	AB035466	<i>tuf</i>
	<i>Bacteroides fragilis</i>	DSM 1151	- ¹	<i>tuf</i>
20	<i>Bordetella bronchiseptica</i>	RB50	Genome project ²	<i>tuf</i>
	<i>Bordetella pertussis</i>	Tohama 1	Genome project ²	<i>tuf</i>
	<i>Borrelia burgdorferi</i>	B31	U78193	<i>tuf</i>
	<i>Borrelia burgdorferi</i>		AE001155	<i>tuf</i> (EF-G)
	<i>Brevibacterium linens</i>	DSM 20425	X76863	<i>tuf</i>
25	<i>Buchnera aphidicola</i>	Ap	Y12307	<i>tuf</i>
	<i>Campylobacter jejuni</i>	NCTC 11168	Y17167	<i>tuf</i>
	<i>Chlamydia pneumoniae</i>	CWL029	AE001592	<i>tuf</i>
	<i>Chlamydia pneumoniae</i>	CWL029	AE001639	<i>tuf</i> (EF-G)
	<i>Chlamydia trachomatis</i>		M74221	<i>tuf</i>
30	<i>Chlamydia trachomatis</i>	D/UW-3/CX	AE001317	<i>tuf</i> (EF-G)
	<i>Chlamydia trachomatis</i>	D/UW-3/CX	AE001305	<i>tuf</i>
	<i>Chlamydia trachomatis</i>	F/IC-Cal-13	L22216	<i>tuf</i>
	<i>Chlorobium vibrioforme</i>	DSM 263	X77033	<i>tuf</i>
	<i>Chloroflexus aurantiacus</i>	DSM 636	X76865	<i>tuf</i>
35	<i>Clostridium acetobutylicum</i>	ATCC 824	Genome project ²	<i>tuf</i>
	<i>Clostridium difficile</i>	630	Genome project ²	<i>tuf</i>
	<i>Corynebacterium glutamicum</i>	ASO 19	X77034	<i>tuf</i>
	<i>Corynebacterium glutamicum</i>	MJ-233	E09634	<i>tuf</i>
	<i>Coxiella burnetii</i>	Nine Mile phase I	AF136604	<i>tuf</i>
40	<i>Cytophaga lytica</i>	DSM 2039	X77035	<i>tuf</i>
	<i>Deinococcus radiodurans</i>	R1	AE001891	<i>tuf</i> (EF-G)
	<i>Deinococcus radiodurans</i>	R1	Genome project ²	<i>tuf</i>
	<i>Deinonema</i> sp.		- ¹	<i>tuf</i>
	<i>Eikenella corrodens</i>	ATCC 23834	Z12610	<i>tuf</i>
45	<i>Eikenella corrodens</i>	ATCC 23834	Z12610	<i>tuf</i> (EF-G)
	<i>Enterococcus faecalis</i>		Genome project ²	<i>tuf</i> (EF-G)
	<i>Escherichia coli</i>		J01690	<i>tuf</i>
	<i>Escherichia coli</i>		J01717	<i>tuf</i>
	<i>Escherichia coli</i>		X00415	<i>tuf</i> (EF-G)
50	<i>Escherichia coli</i>		X57091	<i>tuf</i>
	<i>Escherichia coli</i>	K-12 MG1655	U00006	<i>tuf</i>
	<i>Escherichia coli</i>	K-12 MG1655	U00096	<i>tuf</i>
	<i>Fervidobacterium islandicum</i>	DSM 5733	Y15788	<i>tuf</i>
	<i>Fibrobacter succinogenes</i>	S85	X76866	<i>tuf</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Flavobacterium ferrigeneum</i>	DSM 13524	X76867	<i>tuf</i>
	<i>Flexistipes sinusarabici</i>		X59461	<i>tuf</i>
	<i>Gloeobacter violaceus</i>	PCC 7421	U09433	<i>tuf</i>
	<i>Gloeotheca</i> sp.	PCC 6501	U09434	<i>tuf</i>
5	<i>Haemophilus actinomycetemcomitans</i>	HK1651	Genome project ²	<i>tuf</i>
	<i>Haemophilus ducreyi</i>	35000	AF087414	<i>tuf</i> (EF-G)
	<i>Haemophilus influenzae</i>	Rd	U32739	<i>tuf</i>
	<i>Haemophilus influenzae</i>	Rd	U32739	<i>tuf</i> (EF-G)
	<i>Halobacterium marismortui</i>		X16677	<i>tuf</i>
10	<i>Helicobacter pylori</i>	26695	AE000511	<i>tuf</i>
	<i>Helicobacter pylori</i>	J99	AE001539	<i>tuf</i> (EF-G)
	<i>Helicobacter pylori</i>	J99	AE001541	<i>tuf</i>
	<i>Herpetosiphon aurantiacus</i>	Hpga1	X76868	<i>tuf</i>
	<i>Lactobacillus paracasei</i>		E13922	<i>tuf</i>
15	<i>Leptospira interrogans</i>		AF115283	<i>tuf</i>
	<i>Methanobacterium thermoautrophicum</i>	delta H	AE000877	<i>tuf</i>
	<i>Methanococcus jannaschii</i>	ATCC 43067	U67486	<i>tuf</i>
	<i>Methanococcus jannaschii</i>	DSM 2661	Genome project ²	<i>tuf</i> (EF-G)
	<i>Methanococcus vanniellii</i>		X05698	<i>tuf</i>
20	<i>Micrococcus luteus</i>	IFO 3333	M17788	<i>tuf</i> (EF-G)
	<i>Micrococcus luteus</i>	IFO 3333	M17788	<i>tuf</i>
	<i>Moraxella</i> sp.	TAC II 25	AJ249258	<i>tuf</i>
	<i>Mycobacterium avium</i>	104	Genome project ²	<i>tuf</i>
	<i>Mycobacterium bovis</i>	AF2122/97	Genome project ²	<i>tuf</i>
25	<i>Mycobacterium leprae</i>		L13276	<i>tuf</i>
	<i>Mycobacterium leprae</i>		Z14314	<i>tuf</i>
	<i>Mycobacterium leprae</i>		Z14314	<i>tuf</i> (EF-G)
	<i>Mycobacterium leprae</i>	Thai 53	D13869	<i>tuf</i>
	<i>Mycobacterium tuberculosis</i>	Erdmann	S40925	<i>tuf</i>
30	<i>Mycobacterium tuberculosis</i>	H37Rv	AL021943	<i>tuf</i> (EF-G)
	<i>Mycobacterium tuberculosis</i>	H37Rv	Z84395	<i>tuf</i>
	<i>Mycobacterium tuberculosis</i>	y42	AD000005	<i>tuf</i>
	<i>Mycoplasma capricolum</i>	PG-31	X16462	<i>tuf</i>
	<i>Mycoplasma genitalium</i>	G37	U39732	<i>tuf</i>
35	<i>Mycoplasma genitalium</i>	G37	Genome project ²	<i>tuf</i> (EF-G)
	<i>Mycoplasma hominis</i>		X57136	<i>tuf</i>
	<i>Mycoplasma hominis</i>	PG21	M57675	<i>tuf</i>
	<i>Mycoplasma pneumoniae</i>	M129	AE000019	<i>tuf</i>
	<i>Mycoplasma pneumoniae</i>	M129	AE000058	<i>tuf</i> (EF-G)
40	<i>Neisseria gonorrhoeae</i>	MS11	L36380	<i>tuf</i>
	<i>Neisseria gonorrhoeae</i>	MS11	L36380	<i>tuf</i> (EF-G)
	<i>Neisseria meningitidis</i>		Genome project ²	<i>tuf</i> (EF-G)
	<i>Neisseria meningitidis</i>	Z2491	Genome project ²	<i>tuf</i>
	<i>Peptococcus niger</i>	DSM 20745	X76869	<i>tuf</i>
45	<i>Porphyromonas gingivalis</i>	W83	Genome project ²	<i>tuf</i>
	<i>Phormidium ectocarp</i>	PCC 7375	U09443	<i>tuf</i>
	<i>Planobispora rosea</i>	ATCC 53773	U67308	<i>tuf</i>
	<i>Plectonema boryanum</i>	PCC 73110	U09444	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	W83	Genome project ²	<i>tuf</i>
50	<i>Porphyromonas gingivalis</i>	FDC 381	AB035461	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	W83	AB035462	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	SUNY 1021	AB035463	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	A7A1-28	AB035464	<i>tuf</i>
	<i>Porphyromonas gingivalis</i>	ATCC 33277	AB035465	<i>tuf</i>
55	<i>Porphyromonas gingivalis</i>	ATCC 33277	AB035471	<i>tuf</i> (EF-G)

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Prochlorothrix hollandica</i>		U09445	<i>tuf</i>
	<i>Pseudomonas aeruginosa</i>	PAO-1	Genome project ²	<i>tuf</i>
	<i>Pyrococcus abyssi</i>	Orsay	AJ248285	<i>tuf</i>
	<i>Rickettsia prowazekii</i>	Madrid E	AJ235272	<i>tuf</i>
5	<i>Rickettsia prowazekii</i>	Madrid E	Z54171	<i>tuf</i> (EF-G)
	<i>Salmonella typhimurium</i>		X64591	<i>tuf</i> (EF-G)
	<i>Salmonella typhimurium</i>	LT2 trpE91	X55116	<i>tuf</i>
	<i>Salmonella typhimurium</i>	LT2 trpE91	X55117	<i>tuf</i>
	<i>Serpulina hyodysenteriae</i>	B204	U51635	<i>tuf</i>
10	<i>Serratia marcescens</i>		AF058451	<i>tuf</i>
	<i>Shewanella putida</i>		Genome project ²	<i>tuf</i>
	<i>Shewanella putrefaciens</i>	DSM 50426	- ¹	<i>tuf</i>
	<i>Shewanella putrefaciens</i>	MR-1	Genome project ²	<i>tuf</i>
	<i>Spirochaeta aurantia</i>	DSM 1902	X76874	<i>tuf</i>
15	<i>Staphylococcus aureus</i>		AJ237696	<i>tuf</i> (EF-G)
	<i>Stigmatella aurantiaca</i>	DW4	X82820	<i>tuf</i>
	<i>Stigmatella aurantiaca</i>	Sg a1	X76870	<i>tuf</i>
	<i>Streptococcus mutans</i>	GS-5 Kuramitsu	U75481	<i>tuf</i>
	<i>Streptococcus mutans</i>	UAB159	Genome project ²	<i>tuf</i>
20	<i>Streptococcus oralis</i>	NTCC 11427	P331701	<i>tuf</i>
	<i>Streptococcus pyogenes</i>		Genome project ²	<i>tuf</i> (EF-G)
	<i>Streptococcus pyogenes</i>	M1-GAS	Genome project ²	<i>tuf</i>
	<i>Streptomyces aureofaciens</i>	ATCC 10762	AF007125	<i>tuf</i>
	<i>Streptomyces cinnamomeus</i>	Tue89	X98831	<i>tuf</i>
25	<i>Streptomyces coelicolor</i>	A3(2)	AL031013	<i>tuf</i> (EF-G)
	<i>Streptomyces coelicolor</i>	M145	X77039	<i>tuf</i>
	<i>Streptomyces collinus</i>	BSM 40733	S79408	<i>tuf</i>
	<i>Streptomyces netropsis</i>	Tu1063	AF153618	<i>tuf</i>
	<i>Streptomyces ramocissimus</i>		X67057	<i>tuf</i>
30	<i>Streptomyces ramocissimus</i>		X67057	<i>tuf</i> (EF-G)
	<i>Synechococcus</i> sp.		X17442	<i>tuf</i> (EF-G)
	<i>Synechocystis</i> sp.		X65159	<i>tuf</i> (EF-G)
	<i>Synechocystis</i> sp.	PCC 6803	D90913	<i>tuf</i>
	<i>Taxeobacter ocealus</i>	Myx 2105	X77036	<i>tuf</i>
35	<i>Thermoplasma acidophilum</i>	DSM 1728	X53866	<i>tuf</i>
	<i>Thermotoga maritima</i>		Genome project ²	<i>tuf</i> (EF-G)
	<i>Thermotoga maritima</i>		M27479	<i>tuf</i>
	<i>Thermus aquaticus</i>	EP 00276	X66322	<i>tuf</i>
	<i>Thermus thermophilus</i>	HB8	X16278	<i>tuf</i> (EF-G)
40	<i>Thermus thermophilus</i>	HB8	X05977	<i>tuf</i>
	<i>Thermus thermophilus</i>	HB8	X06657	<i>tuf</i>
	<i>Thiomonas cuprina</i>	DSM 5495	U78300	<i>tuf</i>
	<i>Thiomonas cuprina</i>	DSM 5495	U78300	<i>tuf</i> (EF-G)
	<i>Thiomonas cuprina</i>	Hoe5	X76871	<i>tuf</i>
45	<i>Treponema pallidum</i>		AE001202	<i>tuf</i>
	<i>Treponema pallidum</i>		AE001248	<i>tuf</i> (EF-G)
	<i>Streptomyces ramocissimus</i>		X67058	<i>tuf</i>
	<i>Ureaplasma urealyticum</i>	ATCC 33697	Z34275	<i>tuf</i>
	<i>Vibrio cholerae</i>	N16961	TIGR2	<i>tuf</i>
50	<i>Wolinella succinogenes</i>	DSM 1740	X76872	<i>tuf</i>
	<i>Yersinia pestis</i>	CO-92	Genome project ²	<i>tuf</i>
Fungi				
55	<i>Absidia glauca</i>	CBS 101.48	X54730	<i>tuf</i> (EF-1)

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Arxula adeninivorans</i>	Ls3	Z47379	<i>tuf</i> (EF-1)
	<i>Aspergillus oryzae</i>	KBN616	AB007770	<i>tuf</i> (EF-1)
	<i>Aureobasidium pullulans</i>	R106	U19723	<i>tuf</i> (EF-1)
	<i>Candida albicans</i>	SC5314	M29934	<i>tuf</i> (EF-1)
5	<i>Candida albicans</i>	SC5314	M29935	<i>tuf</i> (EF-1)
	<i>Cryptococcus neoformans</i>	B3501	U81803	<i>tuf</i> (EF-1)
	<i>Cryptococcus neoformans</i>	M1-106	U81804	<i>tuf</i> (EF-1)
	<i>Eremothecium gossypii</i>	ATCC 10895	X73978	<i>tuf</i> (EF-1)
	<i>Fusarium oxysporum</i>	NRRL 26037	AF008498	<i>tuf</i> (EF-1)
10	<i>Histoplasma capsulatum</i>	186AS	U14100	<i>tuf</i> (EF-1)
	<i>Podospora anserina</i>		X74799	<i>tuf</i> (EF-1)
	<i>Puccinia graminis</i>	race 32	X73529	<i>tuf</i> (EF-1)
	<i>Rhizomucor racemosus</i>	ATCC 1216B	X17475	<i>tuf</i> (EF-1)
	<i>Rhizomucor racemosus</i>	ATCC 1216B	J02605	<i>tuf</i> (EF-1)
15	<i>Rhizomucor racemosus</i>	ATCC 1216B	X17476	<i>tuf</i> (EF-1)
	<i>Rhodotorula mucilaginosa</i>		AF016239	<i>tuf</i> (EF-1)
	<i>Saccharomyces cerevisiae</i>		K00428	<i>tuf</i> (M)
	<i>Saccharomyces cerevisiae</i>		M59369	<i>tuf</i> (EF-G)
	<i>Saccharomyces cerevisiae</i>		X00779	<i>tuf</i> (EF-1)
20	<i>Saccharomyces cerevisiae</i>		X01638	<i>tuf</i> (EF-1)
	<i>Schizosaccharomyces pombe</i>		U42189	<i>tuf</i> (EF-1)
	<i>Trichoderma reesei</i>	QM9414	Z23012	<i>tuf</i> (EF-1)
	<i>Yarrowia lipolytica</i>		AF054510	<i>tuf</i> (EF-1)
25	Parasites			
	<i>Blastocystis hominis</i>	HE87-1	D64080	<i>tuf</i> (EF-1)
	<i>Eimeria tenella</i>	LS18	A1755521	<i>tuf</i> (EF-1)
	<i>Giardia lamblia</i>		D14342	<i>tuf</i> (EF-1)
30	<i>Kentrophoros</i> sp.		AF056101	<i>tuf</i> (EF-1)
	<i>Leishmania amazonensis</i>	IFLA/BR/67/PH8	M92653	<i>tuf</i> (EF-1)
	<i>Leishmania braziliensis</i>		U72244	<i>tuf</i> (EF-1)
	<i>Onchocerca volvulus</i>		M64333	<i>tuf</i> (EF-1)
	<i>Porphyra purpurea</i>	Avonport	U08844	<i>tuf</i> (EF-1)
35	<i>Plasmodium berghei</i>	ANKA	AJ224150	<i>tuf</i> (EF-1)
	<i>Plasmodium falciparum</i>	K1	X60488	<i>tuf</i> (EF-1)
	<i>Plasmodium knowlesi</i>	line H	AJ224153	<i>tuf</i> (EF-1)
	<i>Toxoplasma gondii</i>	RH	Y11431	<i>tuf</i> (EF-1)
	<i>Trypanosoma cruzi</i>	Y	L76077	<i>tuf</i> (EF-1)
40	<i>Trypanosoma brucei</i>	LVH/75/ USAMRU-K/18	U10562	<i>tuf</i> (EF-1)
	Human and plants			
	<i>Arabidopsis thaliana</i>	Columbia	X89227	<i>tuf</i> (EF-1)
45	<i>Glycine max</i>	Ceresia	X89058	<i>tuf</i> (EF-1)
	<i>Glycine max</i>	Ceresia	Y15107	<i>tuf</i> (EF-1)
	<i>Glycine max</i>	Ceresia	Y15108	<i>tuf</i> (EF-1)
	<i>Glycine max</i>	Maple Arrow	X66062	<i>tuf</i> (EF-1)
	<i>Homo sapiens</i>		X03558	<i>tuf</i> (EF-1)
50	<i>Pyramimonas disomata</i>		AB008010	<i>tuf</i>
	Bacteria			
	<i>Acetobacterium woodi</i>	DSM 1030	U10505	<i>atpD</i>
55	<i>Bacillus firmus</i>	OF4	M60117	<i>atpD</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Bacillus megaterium</i>	QM B1551	M20255	<i>atpD</i>
	<i>Bacillus stearothermophilus</i>		D38058	<i>atpD</i>
	<i>Bacillus stearothermophilus</i>	IFO1035	D38060	<i>atpD</i>
	<i>Bacillus subtilis</i>	168	Z28592	<i>atpD</i>
5	<i>Bacteroides fragilis</i>	DSM 2151	M22247	<i>atpD</i>
	<i>Bordetella bronchiseptica</i>	RB50	Genome project ²	<i>atpD</i>
	<i>Bordetella pertussis</i>	Tohama 1	Genome project ²	<i>atpD</i>
	<i>Borrelia burgdorferi</i>	B31	AE001122	<i>atpD</i> (V)
	<i>Burkholderia cepacia</i>	DSM50181	X76877	<i>atpD</i>
10	<i>Campylobacter jejuni</i>	NCTC 11168	Genome project ²	<i>atpD</i>
	<i>Chlamydia pneumoniae</i>		Genome project ²	<i>atpD</i> (V)
	<i>Chlamydia trachomatis</i>	MoPn	Genome project ²	<i>atpD</i> (V)
	<i>Chlorobium vibrioforme</i>	DSM 263	X76873	<i>atpD</i>
	<i>Citrobacter freundii</i>	JEO503	AF037156	<i>atpD</i>
15	<i>Clostridium acetobutylicum</i>	ATCC 824	Genome project ²	<i>atpD</i>
	<i>Clostridium acetobutylicum</i>	DSM 792	AF101055	<i>atpD</i>
	<i>Clostridium difficile</i>	630	Genome project ²	<i>atpD</i>
	<i>Corynebacterium glutamicum</i>	ASO 19	X76875	<i>atpD</i>
	<i>Corynebacterium glutamicum</i>	MJ-233	E09634	<i>atpD</i>
20	<i>Cytophaga lytica</i>	DSM 2039	M22535	<i>atpD</i>
	<i>Enterobacter aerogenes</i>	DSM 30053	_3	<i>atpD</i>
	<i>Enterococcus faecalis</i>		M90060	<i>atpD</i>
	<i>Enterococcus faecalis</i>	V583	Genome project ²	<i>atpD</i> (V)
	<i>Enterococcus hirae</i>	ATCC 9790	D17462	<i>atpD</i> (V)
25	<i>Escherichia coli</i>		J01594	<i>atpD</i>
	<i>Escherichia coli</i>		M25464	<i>atpD</i>
	<i>Escherichia coli</i>		V00267	<i>atpD</i>
	<i>Escherichia coli</i>		V00311	<i>atpD</i>
	<i>Escherichia coli</i>	K12 MG1655	L10328	<i>atpD</i>
30	<i>Flavobacterium ferrugineum</i>	DSM 13524	_3	<i>atpD</i>
	<i>Haemophilus actinomycetemcomitans</i>		Genome project ²	<i>atpD</i>
	<i>Haemophilus influenzae</i>	Rd	U32730	<i>atpD</i>
	<i>Halobacterium salinarum</i>		S56356	<i>atpD</i> (V)
	<i>Haloferax volcanii</i>	WR 340	X79516	<i>atpD</i>
35	<i>Helicobacter pylori</i>	NCTC 11638	AF004014	<i>atpD</i>
	<i>Helicobacter pylori</i>	26695	Genome project ²	<i>atpD</i>
	<i>Helicobacter pylori</i>	J99	Genome project ²	<i>atpD</i>
	<i>Lactobacillus casei</i>	DSM 20021	X64542	<i>atpD</i>
	<i>Methanococcus jannaschii</i>	DSM 2661	U67477	<i>atpD</i> (V)
40	<i>Methanosarcina barkeri</i>	DSM 800	J04836	<i>atpD</i> (V)
	<i>Moorella thermoacetica</i>	ATCC 39073	U64318	<i>atpD</i>
	<i>Mycobacterium avium</i>	104	Genome project ²	<i>atpD</i>
	<i>Mycobacterium bovis</i>	AF2122/97	Genome project ²	<i>atpD</i>
	<i>Mycobacterium leprae</i>		U15186	<i>atpD</i>
45	<i>Mycobacterium tuberculosis</i>	H37Rv	Z73419	<i>atpD</i>
	<i>Mycoplasma gallisepticum</i>		X64256	<i>atpD</i>
	<i>Mycoplasma genitalium</i>	G37	U39725	<i>atpD</i>
	<i>Mycoplasma pneumoniae</i>	M129	U43738	<i>atpD</i>
	<i>Neisseria gonorrhoeae</i>	FA 1090	Genome project ²	<i>atpD</i>
50	<i>Neisseria meningitidis</i>	Z2491	Genome project ²	<i>atpD</i>
	<i>Pectinatus frisingensis</i>	DSM 20465	X64543	<i>atpD</i>
	<i>Peptococcus niger</i>	DSM 20475	X76878	<i>atpD</i>
	<i>Pirellula marina</i>	IFAM 1313	X57204	<i>atpD</i>
	<i>Porphyromonas gingivalis</i>	W83	Genome project ²	<i>atpD</i> (V)
55	<i>Propionigenium modestum</i>	DSM 2376	X58461	<i>atpD</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Pseudomonas aeruginosa</i>	PAO1	Genome project ²	<i>atpD</i>
	<i>Pseudomonas putida</i>		Genome project ²	<i>atpD</i>
	<i>Rhodobacter capsulatus</i>	B100	X99599	<i>atpD</i>
	<i>Rhodospirillum rubrum</i>		X02499	<i>atpD</i>
5	<i>Rickettsia prowazekii</i>	F-12	AF036246	<i>atpD</i>
	<i>Rickettsia prowazekii</i>	Madrid	Genome project ²	<i>atpD</i>
	<i>Ruminococcus albus</i>	7ATCC	AB006151	<i>atpD</i>
	<i>Salmonella choleraesuis</i>	S83769	AF037146	<i>atpD</i>
	subsp. <i>arizonae</i>			
10	<i>Salmonella choleraesuis</i>	u24	AF037147	<i>atpD</i>
	subsp. <i>arizonae</i>			
	<i>Salmonella bongori</i>	JEO4162	AF037155	<i>atpD</i>
	<i>Salmonella bongori</i>	BR1859	AF037154	<i>atpD</i>
	<i>Salmonella choleraesuis</i>	DS210/89	AF037149	<i>atpD</i>
15	subsp. <i>diarizonae</i>			
	<i>Salmonella choleraesuis</i>	JEO307	AF037148	<i>atpD</i>
	subsp. <i>diarizonae</i>			
	<i>Salmonella choleraesuis</i>	S109671	AF037150	<i>atpD</i>
	subsp. <i>diarizonae</i>			
20	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Dublin	K228	AF037140	<i>atpD</i>
	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Dublin	K771	AF037139	<i>atpD</i>
	<i>Salmonella choleraesuis</i>	S84366	AF037151	<i>atpD</i>
25	subsp. <i>houtenae</i>			
	<i>Salmonella choleraesuis</i>	S84098	AF037152	<i>atpD</i>
	subsp. <i>houtenae</i>			
	<i>Salmonella choleraesuis</i>	BR2047	AF037153	<i>atpD</i>
	subsp. <i>indica</i>			
30	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Infantis	Div36-86	AF037142	<i>atpD</i>
	<i>Salmonella choleraesuis</i>	NSC72	AF037144	<i>atpD</i>
	subsp. <i>salamae</i>			
	<i>Salmonella choleraesuis</i>	S114655	AF037145	<i>atpD</i>
35	subsp. <i>salamae</i>			
	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Tennessee	Div95-86	AF037143	<i>atpD</i>
	<i>Salmonella choleraesuis</i> subsp. <i>choleraesuis</i> serotype Typhimurium	LT2	AF037141	<i>atpD</i>
40	<i>Shewanella putida</i>		Genome project ²	<i>atpD</i>
	<i>Shewanella putrefaciens</i>	MR-1	Genome project ²	<i>atpD</i>
	<i>Stigmatella aurantiaca</i>	Sga1	X76879	<i>atpD</i>
	<i>Streptococcus bovis</i>	JB-1	AB009314	<i>atpD</i>
	<i>Streptococcus mutans</i>	GS-5	U31170	<i>atpD</i>
45	<i>Streptococcus mutans</i>	UAB159	Genome project ²	<i>atpD</i>
	<i>Streptococcus pneumoniae</i>	Type 4	Genome project ²	<i>atpD</i> (V)
	<i>Streptococcus pneumoniae</i>	Type 4	Genome project ²	<i>atpD</i>
	<i>Streptococcus pyogenes</i>		Genome project ²	<i>atpD</i> (V)
	<i>Streptococcus pyogenes</i>	M1-GAS	Genome project ²	<i>atpD</i>
50	<i>Streptococcus sanguinis</i>	10904	AF001955	<i>atpD</i>
	<i>Streptomyces lividans</i>	1326	Z22606	<i>atpD</i>
	<i>Thermus thermophilus</i>	HB8	D63799	<i>atpD</i> (V)
	<i>Thiobacillus ferrooxidans</i>	ATCC 33020	M81087	<i>atpD</i>
	<i>Treponema pallidum</i>	Nichols	AE001228	<i>atpD</i> (V)
55	<i>Vibrio alginolyticus</i>		X16050	<i>atpD</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Vibrio cholerae</i>	N16961	Genome project ²	<i>atpD</i>
	<i>Wolinella succinogenes</i>	DSM 1470	X76880	<i>atpD</i>
	<i>Yersinia enterocolitica</i>	NCTC 10460	AF037157	<i>atpD</i>
5	<i>Yersinia pestis</i>	CO-92	Genome project ²	<i>atpD</i>
	Fungi			
	<i>Candida tropicalis</i>		M64984	<i>atpD</i> (V)
	<i>Kluyveromyces lactis</i>	2359/152	U37764	<i>atpD</i>
10	<i>Neurospora crassa</i>		X53720	<i>atpD</i>
	<i>Saccharomyces cerevisiae</i>		M12082	<i>atpD</i>
	<i>Saccharomyces cerevisiae</i>	X2180-1A	J05409	<i>atpD</i> (V)
	<i>Schizosaccharomyces pombe</i>	972 h-	S47814	<i>atpD</i> (V)
15	<i>Schizosaccharomyces pombe</i>	972 h-	M57956	<i>atpD</i>
	Parasites			
	<i>Giardia lamblia</i>	WB	U18938	<i>atpD</i>
	<i>Plasmodium falciparum</i>	3D7	L08200	<i>atpD</i> (V)
20	<i>Trypanosoma congolense</i>	IL3000	Z25814	<i>atpD</i> (V)
	Human and plants			
	<i>Homo sapiens</i>		L09234	<i>atpD</i> (V)
25	<i>Homo sapiens</i>		M27132	<i>atpD</i>
	Bacteria			
	<i>Acetobacter aceti</i>	no. 1023	S60630	<i>recA</i>
30	<i>Acetobacter altoacetigenes</i>	MH-24	E05290	<i>recA</i>
	<i>Acetobacter polyoxogenes</i>	NBI 1028	D13183	<i>recA</i>
	<i>Acholeplasma laidlawii</i>	8195	M81465	<i>recA</i>
	<i>Acidiphilium facilis</i>	ATCC 35904	D16538	<i>recA</i>
	<i>Acidothermus cellulolyticus</i>	ATCC 43068	AJ006705	<i>recA</i>
35	<i>Acinetobacter calcoaceticus</i>	BD413/ADP1	L26100	<i>recA</i>
	<i>Aeromonas salmonicida</i>	A449	U83688	<i>recA</i>
	<i>Agrobacterium tumefaciens</i>	C58	L07902	<i>recA</i>
	<i>Allochromatium vinosum</i>		AJ000677	<i>recA</i>
	<i>Aquifex aeolicus</i>	VF5	AE000775	<i>recA</i>
40	<i>Aquifex pyrophilus</i>	Kol5a	L23135	<i>recA</i>
	<i>Azotobacter vinelandii</i>		S96898	<i>recA</i>
	<i>Bacillus stearothermophilus</i>	10	Genome project ²	<i>recA</i>
	<i>Bacillus subtilis</i>	PB1831	U87792	<i>recA</i>
	<i>Bacillus subtilis</i>	168	Z99112	<i>recA</i>
45	<i>Bacteroides fragilis</i>		M63029	<i>recA</i>
	<i>Bifidobacterium breve</i>	NCFB 2258	AF094756	<i>recA</i>
	<i>Blastochloris viridis</i>	DSM 133	AF022175	<i>recA</i>
	<i>Bordetella pertussis</i>	165	X53457	<i>recA</i>
	<i>Borrelia burgdorferi</i>	Sh-2-82	U23457	<i>recA</i>
50	<i>Borrelia burgdorferi</i>	B31	AE001124	<i>recA</i>
	<i>Brevibacterium flavum</i>	MJ-233	E10390	<i>recA</i>
	<i>Brucella abortus</i>	2308	L00679	<i>recA</i>
	<i>Burkholderia cepacia</i>	ATCC 17616	U70431	<i>recA</i>
	<i>Campylobacter jejuni</i>	81-176	U03121	<i>recA</i>
55	<i>Chlamydia trachomatis</i>	L2	U16739	<i>recA</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Chloroflexus aurantiacus</i>	J-10-fl	AF037259	<i>recA</i>
	<i>Clostridium acetobutylicum</i>		M94057	<i>recA</i>
	<i>Clostridium perfringens</i>	13	U61497	<i>recA</i>
	<i>Corynebacterium glutamicum</i>	AS019	U14965	<i>recA</i>
5	<i>Corynebacterium pseudotuberculosis</i>	C231	U30387	<i>recA</i>
	<i>Deinococcus radiodurans</i>	KD8301	AB005471	<i>recA</i>
	<i>Deinococcus radiodurans</i>	R1	U01876	<i>recA</i>
	<i>Enterobacter agglomerans</i>	339	L03291	<i>recA</i>
	<i>Enterococcus faecalis</i>	OGIX	M81466	<i>recA</i>
10	<i>Erwinia carotovora</i>		X55554	<i>recA</i>
	<i>Escherichia coli</i>		J01672	<i>recA</i>
	<i>Escherichia coli</i>		X55552	<i>recA</i>
	<i>Escherichia coli</i>	K-12	AE000354	<i>recA</i>
	<i>Frankia alni</i>	Arl3	AJ006707	<i>recA</i>
15	<i>Gluconobacter oxydans</i>		U21001	<i>recA</i>
	<i>Haemophilus influenzae</i>	Rd	U32687	<i>recA</i>
	<i>Haemophilus influenzae</i>	Rd	U32741	<i>recA</i>
	<i>Haemophilus influenzae</i>	Rd	L07529	<i>recA</i>
	<i>Helicobacter pylori</i>	69A	Z35478	<i>recA</i>
20	<i>Helicobacter pylori</i>	26695	AE000536	<i>recA</i>
	<i>Helicobacter pylori</i>	J99	AE001453	<i>recA</i>
	<i>Lactococcus lactis</i>	ML3	M88106	<i>recA</i>
	<i>Legionella pneumophila</i>		X55453	<i>recA</i>
	<i>Leptospira biflexa</i>	serovar patoc	U32625	<i>recA</i>
25	<i>Leptospira interrogans</i>	serovar pomona	U29169	<i>recA</i>
	<i>Magnetospirillum magnetotacticum</i>	MS-1	X17371	<i>recA</i>
	<i>Methylobacillus flagellatus</i>	MFK1	M35325	<i>recA</i>
	<i>Methylomonas clara</i>	ATCC 31226	X59514	<i>recA</i>
	<i>Mycobacterium leprae</i>		X73822	<i>recA</i>
30	<i>Mycobacterium tuberculosis</i>	H37Rv	X58485	<i>recA</i>
	<i>Mycoplasma genitalium</i>	G37	U39717	<i>recA</i>
	<i>Mycoplasma mycoides</i>	GM9	L22073	<i>recA</i>
	<i>Mycoplasma pneumoniae</i>	ATCC 29342	MPAE000033	<i>recA</i>
	<i>Mycoplasma pulmonis</i>	KD735	L22074	<i>recA</i>
35	<i>Myxococcus xanthus</i>		L40368	<i>recA</i>
	<i>Neisseria animalis</i>	NCTC 10212	U57910	<i>recA</i>
	<i>Neisseria cinerea</i>	LCDC 81-176	AJ223869	<i>recA</i>
	<i>Neisseria cinerea</i>	LNP 1646	U57906	<i>recA</i>
	<i>Neisseria cinerea</i>	NCTC 10294	AJ223871	<i>recA</i>
40	<i>Neisseria cinerea</i>	Vedros M601	AJ223870	<i>recA</i>
	<i>Neisseria elongata</i>	CCUG 2131	AJ223882	<i>recA</i>
	<i>Neisseria elongata</i>	CCUG 4165A	AJ223880	<i>recA</i>
	<i>Neisseria elongata</i>	CCUG 4557	AJ223879	<i>recA</i>
	subsp. <i>intermedia</i>			
45	<i>Neisseria elongata</i>	NCTC 10660	AJ223881	<i>recA</i>
	<i>Neisseria elongata</i>	NCTC 11050	AJ223878	<i>recA</i>
	<i>Neisseria elongata</i>	NHITCC 2376	AJ223877	<i>recA</i>
	<i>Neisseria flava</i>	Bangor 9	AJ223873	<i>recA</i>
	<i>Neisseria flavescens</i>	LNP 444	U57907	<i>recA</i>
50	<i>Neisseria gonorrhoeae</i>	CH95	U57902	<i>recA</i>
	<i>Neisseria gonorrhoeae</i>	FA19	X64842	<i>recA</i>
	<i>Neisseria gonorrhoeae</i>	MS11	X17374	<i>recA</i>
	<i>Neisseria lactamica</i>	CCUG 7757	AJ223866	<i>recA</i>
	<i>Neisseria lactamica</i>	CCUG 7852	Y11819	<i>recA</i>
55	<i>Neisseria lactamica</i>	LCDC 77-143	Y11818	<i>recA</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Neisseria lactamica</i>	LCDC 80-111	AJ223864	<i>recA</i>
	<i>Neisseria lactamica</i>	LCDC 845	AJ223865	<i>recA</i>
	<i>Neisseria lactamica</i>	NCTC 10617	U57905	<i>recA</i>
	<i>Neisseria lactamica</i>	NCTC 10618	AJ223863	<i>recA</i>
5	<i>Neisseria meningitidis</i>	44/46	X64849	<i>recA</i>
	<i>Neisseria meningitidis</i>	Bangor 13	AJ223868	<i>recA</i>
	<i>Neisseria meningitidis</i>	HF116	X64848	<i>recA</i>
	<i>Neisseria meningitidis</i>	HF130	X64844	<i>recA</i>
	<i>Neisseria meningitidis</i>	HF46	X64847	<i>recA</i>
10	<i>Neisseria meningitidis</i>	M470	X64850	<i>recA</i>
	<i>Neisseria meningitidis</i>	N94II	X64846	<i>recA</i>
	<i>Neisseria meningitidis</i>	NCTC 8249	AJ223867	<i>recA</i>
	<i>Neisseria meningitidis</i>	P63	X64845	<i>recA</i>
	<i>Neisseria meningitidis</i>	S3446	U57903	<i>recA</i>
15	<i>Neisseria mucosa</i>	LNP 405	U57908	<i>recA</i>
	<i>Neisseria mucosa</i>	Vedros M1801	AJ223875	<i>recA</i>
	<i>Neisseria perflava</i>	CCUG 17915	AJ223876	<i>recA</i>
	<i>Neisseria perflava</i>	LCDC 85402	AJ223862	<i>recA</i>
	<i>Neisseria pharyngis</i> var. <i>flava</i>	NCTC 4590	U57909	<i>recA</i>
20	<i>Neisseria polysaccharea</i>	CCUG 18031	Y11815	<i>recA</i>
	<i>Neisseria polysaccharea</i>	CCUG 24845	Y11816	<i>recA</i>
	<i>Neisseria polysaccharea</i>	CCUG 24846	Y11814	<i>recA</i>
	<i>Neisseria polysaccharea</i>	INS MA 3008	Y11817	<i>recA</i>
	<i>Neisseria polysaccharea</i>	NCTC 11858	U57904	<i>recA</i>
25	<i>Neisseria sicca</i>	NRL 30016	AJ223872	<i>recA</i>
	<i>Neisseria subflava</i>	NRL 30017	AJ223874	<i>recA</i>
	<i>Paracoccus denitrificans</i>	DSM 413	U59631	<i>recA</i>
	<i>Pasteurella multocida</i>		X99324	<i>recA</i>
	<i>Porphyromonas gingivalis</i>	W83	U70054	<i>recA</i>
30	<i>Prevotella ruminicola</i>	JCM 8958	U61227	<i>recA</i>
	<i>Proteus mirabilis</i>	pG1300	X14870	<i>recA</i>
	<i>Proteus vulgaris</i>		X55555	<i>recA</i>
	<i>Pseudomonas aeruginosa</i>		X05691	<i>recA</i>
	<i>Pseudomonas aeruginosa</i>	PAM 7	X52261	<i>recA</i>
35	<i>Pseudomonas aeruginosa</i>	PAO12	D13090	<i>recA</i>
	<i>Pseudomonas cepacia</i>		D90120	<i>recA</i>
	<i>Pseudomonas fluorescens</i>	OE 28.3	M96558	<i>recA</i>
	<i>Pseudomonas putida</i>		L12684	<i>recA</i>
	<i>Pseudomonas putida</i>	PpS145	U70864	<i>recA</i>
40	<i>Rhizobium leguminosarum</i>	VF39	X59956	<i>recA</i>
	biovar <i>viciae</i>			
	<i>Rhizobium phaseoli</i>	CNPAF512	X62479	<i>recA</i>
	<i>Rhodobacter capsulatus</i>	J50	X82183	<i>recA</i>
	<i>Rhodobacter sphaeroides</i>	2.4.1	X72705	<i>recA</i>
45	<i>Rhodopseudomonas palustris</i>	N 7	D84467	<i>recA</i>
	<i>Rickettsia prowazekii</i>	Madrid E	AJ235273	<i>recA</i>
	<i>Rickettsia prowazekii</i>	Madrid E	U01959	<i>recA</i>
	<i>Serratia marcescens</i>		M22935	<i>recA</i>
	<i>Shigella flexneri</i>		X55553	<i>recA</i>
50	<i>Shigella sonnei</i>	KNIH104S	AF101227	<i>recA</i>
	<i>Sinorhizobium meliloti</i>	2011	X59957	<i>recA</i>
	<i>Staphylococcus aureus</i>		L25893	<i>recA</i>
	<i>Streptococcus gordonii</i>	Challis V288	L20574	<i>recA</i>
	<i>Streptococcus mutans</i>	UA96	M81468	<i>recA</i>
55	<i>Streptococcus pneumoniae</i>		Z17307	<i>recA</i>

Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

	Species	Strain	Accession number	Coding gene*
	<i>Streptococcus pneumoniae</i>	R800	Z34303	<i>recA</i>
	<i>Streptococcus pyogenes</i>	NZ131	U21934	<i>recA</i>
	<i>Streptococcus salivarius</i>		M94062	<i>recA</i>
	subsp. <i>thermophilus</i>			
5	<i>Streptomyces ambofaciens</i>	DSM 40697	Z30324	<i>recA</i>
	<i>Streptomyces coelicolor</i>	A3(2)	AL020958	<i>recA</i>
	<i>Streptomyces lividans</i>	TK24	X76076	<i>recA</i>
	<i>Streptomyces rimosus</i>	R6	X94233	<i>recA</i>
	<i>Streptomyces venezuelae</i>	ATCC10712	U04837	<i>recA</i>
10	<i>Synechococcus</i> sp.	PR6	M29495	<i>recA</i>
	<i>Thermotoga maritima</i>		L23425	<i>recA</i>
	<i>Thermus aquaticus</i>		L20095	<i>recA</i>
	<i>Thermus thermophilus</i>	HB8	D17392	<i>recA</i>
	<i>Thiobacillus ferrooxidans</i>		M26933	<i>recA</i>
15	<i>Treponema pallidum</i>	Nichols	AE001243	<i>recA</i>
	<i>Vibrio anguillarum</i>		M80525	<i>recA</i>
	<i>Vibrio cholerae</i>	017	X71969	<i>recA</i>
	<i>Vibrio cholerae</i>	2740-80	U10162	<i>recA</i>
	<i>Vibrio cholerae</i>	569B	L42384	<i>recA</i>
20	<i>Vibrio cholerae</i>	M549	AF117881	<i>recA</i>
	<i>Vibrio cholerae</i>	M553	AF117882	<i>recA</i>
	<i>Vibrio cholerae</i>	M645	AF117883	<i>recA</i>
	<i>Vibrio cholerae</i>	M793	AF117878	<i>recA</i>
	<i>Vibrio cholerae</i>	M794	AF117880	<i>recA</i>
25	<i>Vibrio cholerae</i>	M967	AF117879	<i>recA</i>
	<i>Xanthomonas citri</i>	XW47	AF006590	<i>recA</i>
	<i>Xanthomonas oryzae</i>		AF013600	<i>recA</i>
	<i>Xenorhabdus bovienii</i>	T228/1	U87924	<i>recA</i>
	<i>Xenorhabdus nematophilus</i>	AN6	AF127333	<i>recA</i>
30	<i>Yersinia pestis</i>	231	X75336	<i>recA</i>
Fungi, parasites, human and plants				
	<i>Anabaena variabilis</i>	ATCC 29413	M29680	<i>recA</i>
35	<i>Arabidopsis thaliana</i>		U43652	<i>recA</i> (Rad51)
	<i>Candida albicans</i>		U39808	<i>recA</i> (Dmc1)
	<i>Coprinus cinereus</i>	Okayama-7	U21905	<i>recA</i> (Rad51)
	<i>Emericella nidulans</i>		Z80341	<i>recA</i> (Rad51)
	<i>Gallus gallus</i>		L09655	<i>recA</i> (Rad51)
40	<i>Homo sapiens</i>		D13804	<i>recA</i> (Rad51)
	<i>Homo sapiens</i>		D63882	<i>recA</i> (Dmc1)
	<i>Leishmania major</i>	Friedlin	AF062379	<i>recA</i> (Rad51)
	<i>Leishmania major</i>	Friedlin	AF062380	<i>recA</i> (Dmc1)
	<i>Mus musculus</i>		D58419	<i>recA</i> (Dmc1)
45	<i>Neurospora crassa</i>	74-OR23-1A	D29638	<i>recA</i> (Rad51)
	<i>Saccharomyces cerevisiae</i>		D10023	<i>recA</i> (Rad51)
	<i>Schizosaccharomyces pombe</i>		Z22691	<i>recA</i> (Rad51)
	<i>Schizosaccharomyces pombe</i>	972h-	AL021817	<i>recA</i> (Dmc1)
	<i>Tetrahymena thermophila</i>	PB9R	AF064516	<i>recA</i> (Rad51)
50	<i>Trypanosoma brucei</i>	stock 427	Y13144	<i>recA</i> (Rad51)
	<i>Ustilago maydis</i>		U62484	<i>recA</i> (Rad51)
	<i>Xenopus laevis</i>		D38488	<i>recA</i> (Rad51)
	<i>Xenopus laevis</i>		D38489	<i>recA</i> (Rad51)

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Table 11. Microbial species for which *tuf* and/or *atpD* and/or *recA* sequences are available in public databases (continued).

Species	Strain	Accession number	Coding gene*
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* *tuf* indicates *tuf* sequences

tuf (C) indicates *tuf* sequences divergent from main (usually A and B) copies of the elongation factor-Tu

tuf (EF-1) indicates *tuf* sequences of the eukaryotic type (elongation factor 1 α)

tuf (M) indicates *tuf* sequences from organellar (mostly mitochondrial) origin

5 *atpD* indicates *atpD* sequences of the F-type

atpD (V) indicates *atpD* sequences of the V-Type

recA indicates *recA* sequences

recA (Rad51) indicates *rad51* sequences or homologs

recA (Dmc1) indicates *dmc1* sequences or homologs

10 ¹ Nucleotides sequences published in Arch. Microbiol. 1990 **153**:241-247

² These sequences are from the TIGR database (<http://www.tigr.org/tdb/tdb.html>)

³ Nucleotides sequences published in FEMS Microbiology Letters 1988 **50**:101-106

Table 12. Bacterial species used to test the specificity of the *Staphylococcus* genus-specific amplification primers derived from *tuf* sequences.

	Strain	Reference number	Strain	Reference number
5	Staphylococci species (n=27)		Other Gram-positive bacteria (n=20)	
	<i>Staphylococcus arlettae</i>	ATCC 43957	<i>Bacillus subtilis</i>	ATCC 27370
	<i>Staphylococcus aureus</i>	ATCC 35844	<i>Enterococcus avium</i>	ATCC 14025
	subsp. <i>anaerobius</i>			
10	<i>Staphylococcus aureus</i>	ATCC 43300	<i>Enterococcus durans</i>	ATCC 19432
	subsp. <i>aureus</i>			
	<i>Staphylococcus auricularis</i>	ATCC 33753	<i>Enterococcus faecalis</i>	ATCC 19433
	<i>Staphylococcus capitis</i>	ATCC 27840	<i>Enterococcus faecium</i>	ATCC 19434
	subsp. <i>capitis</i>			
15	<i>Staphylococcus caprae</i>	ATCC 35538	<i>Enterococcus flavescens</i>	ATCC 49996
	<i>Staphylococcus carnosus</i>	ATCC 51365	<i>Enterococcus gallinarum</i>	ATCC 49573
	<i>Staphylococcus chromogenes</i>	ATCC 43764	<i>Lactobacillus acidophilus</i>	ATCC 4356
	<i>Staphylococcus cohnii</i>	DSM 20260	<i>Lactococcus lactis</i>	ATCC 11454
	subsp. <i>urealyticum</i>			
20	<i>Staphylococcus delphini</i>	ATCC 49171	<i>Listeria innocua</i>	ATCC 33090
	<i>Staphylococcus epidermidis</i>	ATCC 14990	<i>Listeria ivanovii</i>	ATCC 19119
	<i>Staphylococcus equorum</i>	ATCC 43958	<i>Listeria monocytogenes</i>	ATCC 15313
	<i>Staphylococcus felis</i>	ATCC 49168	<i>Macrococcus caseolyticus</i>	ATCC 13548
	<i>Staphylococcus gallinarum</i>	ATCC 35539	<i>Streptococcus agalactiae</i>	ATCC 13813
25	<i>Staphylococcus haemolyticus</i>	ATCC 29970	<i>Streptococcus anginosus</i>	ATCC 33397
	<i>Staphylococcus hominis</i>	ATCC 27844	<i>Streptococcus bovis</i>	ATCC 33317
	<i>Staphylococcus hyicus</i>	ATCC 11249	<i>Streptococcus mutans</i>	ATCC 25175
	<i>Staphylococcus intermedius</i>	ATCC 29663	<i>Streptococcus pneumoniae</i>	ATCC 6303
	<i>Staphylococcus kloosis</i>	ATCC 43959	<i>Streptococcus pyogenes</i>	ATCC 19615
30	<i>Staphylococcus lentus</i>	ATCC 29070	<i>Streptococcus salivarius</i>	ATCC 7073
	<i>Staphylococcus lugdunensis</i>	ATCC 43809		
	<i>Staphylococcus saprophyticus</i>	ATCC 15305		
	<i>Staphylococcus schleiferi</i>	ATCC 49545		
	subsp. <i>coagulans</i>			
35	<i>Staphylococcus sciuri</i>	ATCC 29060		
	subsp. <i>sciuri</i>			
	<i>Staphylococcus simulans</i>	ATCC 27848		
	<i>Staphylococcus warneri</i>	ATCC 27836		
	<i>Staphylococcus xylosus</i>	ATCC 29971		
40	Gram-negative bacteria (n=33)			
	<i>Acinetobacter baumannii</i>	ATCC 19606	<i>Morganella morganii</i>	ATCC 25830
	<i>Bacteroides distasonis</i>	ATCC 8503	<i>Neisseria gonorrhoeae</i>	ATCC 35201
	<i>Bacteroides fragilis</i>	ATCC 25285	<i>Neisseria meningitidis</i>	ATCC 13077
	<i>Bulkholderia cepacia</i>	ATCC 25416	<i>Proteus mirabilis</i>	ATCC 25933
45	<i>Bordetella pertussis</i>	ATCC 9797	<i>Proteus vulgaris</i>	ATCC 13315
	<i>Citrobacter freundii</i>	ATCC 8090	<i>Providencia rettgeri</i>	ATCC 9250
	<i>Enterobacter aerogenes</i>	ATCC 13048	<i>Providencia stuartii</i>	ATCC 29914
	<i>Enterobacter cloacae</i>	ATCC 13047	<i>Pseudomonas aeruginosa</i>	ATCC 27853
	<i>Escherichia coli</i>	ATCC 25922	<i>Pseudomonas fluorescens</i>	ATCC 13525
50	<i>Haemophilus influenzae</i>	ATCC 8907	<i>Salmonella choleraesuis</i>	ATCC 7001
	<i>Haemophilus parahaemolyticus</i>	ATCC 10014	<i>Salmonella typhimurium</i>	ATCC 14028
	<i>Haemophilus parainfluenzae</i>	ATCC 7901	<i>Serratia marcescens</i>	ATCC 8100
	<i>Hafnia alvei</i>	ATCC 13337	<i>Shigella flexneri</i>	ATCC 12022
	<i>Kingella indologenes</i>	ATCC 25869	<i>Shigella sonnei</i>	ATCC 29930
55	<i>Klebsiella oxytoca</i>	ATCC 13182	<i>Stenotrophomonas maltophilia</i>	ATCC 13843
	<i>Klebsiella pneumoniae</i>	ATCC 13883	<i>Yersinia enterocolitica</i>	ATCC 9610
	<i>Moraxella catarrhalis</i>	ATCC 25240		

Table 13. Bacterial species used to test the specificity of the penicillin-resistant *Streptococcus pneumoniae* amplification primers derived from *pbp1a* sequences.

Strain	Reference number	Strain	Reference number
Gram-positive species (n=67)			
<i>Abiotrophia adiacens</i>	ATCC 49175	<i>Staphylococcus hominis</i>	ATCC 27844
<i>Abiotrophia defectiva</i>	ATCC 49176	<i>Staphylococcus lugdunensis</i>	ATCC 43809
<i>Actinomyces pyogenes</i>	ATCC 19411	<i>Staphylococcus saprophyticus</i>	ATCC 15305
<i>Bacillus anthracis</i>	ATCC 4229	<i>Staphylococcus simulans</i>	ATCC 27848
<i>Bacillus cereus</i>	ATCC 14579	<i>Staphylococcus. warneri</i>	ATCC 27836
<i>Bifidobacterium breve</i>	ATCC 15700	<i>Streptococcus acidominimus</i>	ATCC 51726
<i>Clostridium difficile</i>	ATCC 9689	<i>Streptococcus agalactiae</i>	ATCC 12403
<i>Enterococcus avium</i>	ATCC 14025	<i>Streptococcus anginosus</i>	ATCC 33397
<i>Enterococcus casseliflavus</i>	ATCC 25788	<i>Streptococcus bovis</i>	ATCC 33317
<i>Enterococcus dispar</i>	ATCC 51266	<i>Streptococcus constellatus</i>	ATCC 27823
<i>Enterococcus durans</i>	ATCC 19432	<i>Streptococcus cricetus</i>	ATCC 19624
<i>Enterococcus faecalis</i>	ATCC 29212	<i>Streptococcus cristatus</i>	ATCC 51100
<i>Enterococcus faecium</i>	ATCC 19434	<i>Streptococcus downei</i>	ATCC 33748
<i>Enterococcus flavescens</i>	ATCC 49996	<i>Streptococcus dysgalactiae</i>	ATCC 43078
<i>Enterococcus gallinarum</i>	ATCC 49573	<i>Streptococcus equi</i>	ATCC 9528
<i>Enterococcus hirae</i>	ATCC 8043	<i>Streptococcus ferus</i>	ATCC 33477
<i>Enterococcus mundtii</i>	ATCC 43186	<i>Streptococcus gordonii</i>	ATCC 10558
<i>Enterococcus raffinosus</i>	ATCC 49427	<i>Streptococcus intermedius</i>	ATCC 27335
<i>Lactobacillus lactis</i>	ATCC 19435	<i>Streptococcus mitis</i>	ATCC 903
<i>Lactobacillus monocytogenes</i>	ATCC 15313	<i>Streptococcus mitis</i>	LSPQ 2583
<i>Mobiluncus curtisii</i>	ATCC 35242	<i>Streptococcus mitis</i>	ATCC 49456
<i>Peptococcus niger</i>	ATCC 27731	<i>Streptococcus mutans</i>	ATCC 27175
<i>Peptostreptococcus acones</i>	ATCC 6919	<i>Streptococcus oralis</i>	ATCC 10557
<i>Peptostreptococcus anaerobius</i>	ATCC 27337	<i>Streptococcus oralis</i>	ATCC 9811
<i>Peptostreptococcus asaccharolyticus</i>	ATCC 2639	<i>Streptococcus oralis</i>	ATCC 35037
<i>Peptostreptococcus lactolyticus</i>	ATCC 51172	<i>Streptococcus parasanguinis</i>	ATCC 15912
<i>Peptostreptococcus magnus</i>	ATCC 15794	<i>Streptococcus parauberis</i>	ATCC 6631
<i>Peptostreptococcus prevotii</i>	ATCC 9321	<i>Streptococcus rattus</i>	ATCC 15912
<i>Peptostreptococcus tetradius</i>	ATCC 35098	<i>Streptococcus salivarius</i>	ATCC 7073
<i>Staphylococcus aureus</i>	ATCC 25923	<i>Streptococcus sanguinis</i>	ATCC10556
<i>Staphylococcus capitis</i>	ATCC 27840	<i>Streptococcus suis</i>	ATCC 43765
<i>Staphylococcus epidermidis</i>	ATCC 14990	<i>Streptococcus uberis</i>	ATCC 19436
<i>Staphylococcus haemolyticus</i>	ATCC 29970	<i>Streptococcus vestibularis</i>	ATCC 49124
Gram-negative species (n=33)			
<i>Actinetobacter baumannii</i>	ATCC 19606	<i>Moraxella morganii</i>	ATCC 13077
<i>Bordetella pertussis</i>	ATCC 9797	<i>Neisseria gonorrhoeae</i>	ATCC 35201
<i>Citrobacter diversus</i>	ATCC 27028	<i>Neisseria meningitidis</i>	ATCC 13077
<i>Citrobacter freundii</i>	ATCC 8090	<i>Proteus mirabilis</i>	ATCC 25933
<i>Enterobacter aerogenes</i>	ATCC 13048	<i>Proteus vulgaris</i>	ATCC 13315
<i>Enterobacter agglomerans</i>	ATCC 27155	<i>Providencia alcalifaciens</i>	ATCC 9886
<i>Enterobacter cloacae</i>	ATCC 13047	<i>Providencia rettgeri</i>	ATCC 9250
<i>Escherichia coli</i>	ATCC 25922	<i>Providencia rustigianii</i>	ATCC 33673
<i>Haemophilus ducreyi</i>	ATCC 33940	<i>Providencia stuartii</i>	ATCC 33672
<i>Haemophilus haemolyticus</i>	ATCC 33390	<i>Pseudomonas aeruginosa</i>	ATCC 35554
<i>Haemophilus influenzae</i>	ATCC 9007	<i>Pseudomonas fluorescens</i>	ATCC 13525
<i>Haemophilus parainfluenzae</i>	ATCC 7901	<i>Pseudomonas stutzeri</i>	ATCC 17588
<i>Hafnia alvei</i>	ATCC 13337	<i>Salmonella typhimurium</i>	ATCC 14028
<i>Klebsiella oxytoca</i>	ATCC 13182	<i>Serratia marcescens</i>	ATCC 13880
<i>Klebsiella pneumoniae</i>	ATCC 13883	<i>Shigella flexneri</i>	ATCC 12022
<i>Moraxella atlantae</i>	ATCC 29525	<i>Yersina enterocolitica</i>	ATCC 9610
<i>Moraxella catarrhalis</i>	ATCC 43628		

Table 14. Bacterial species (n=104) detected by the platelet contaminants assay. Bold characters indicate the major bacterial contaminants found in platelet concentrates.

5	<i>Abiotrophia adiacens</i>	<i>Klebsiella oxytoca</i>	<i>Staphylococcus simulans</i>
	<i>Abiotrophia defectiva</i>	<i>Klebsiella pneumoniae</i>	<i>Staphylococcus warneri</i>
	<i>Acinetobacter baumannii</i>	<i>Legionella pneumophila</i>	<i>Stenotrophomonas maltophilia</i>
	<i>Acinetobacter Iwoffii</i>	<i>Megamonas hypermegale</i>	80 <i>Streptococcus acidominimus</i>
	<i>Aerococcus viridans</i>	45 <i>Moraxella atlantae</i>	<i>Streptococcus agalactiae</i>
10	<i>Bacillus anthracis</i>	<i>Moraxella catarrhalis</i>	<i>Streptococcus anginosus</i>
	<i>Bacillus cereus</i>	<i>Morganella morganii</i>	<i>Streptococcus bovis</i>
	<i>Bacillus subtilis</i>	<i>Neisseria gonorrhoeae</i>	<i>Streptococcus constellatus</i>
	<i>Brucella abortus</i>	<i>Neisseria meningitidis</i>	85 <i>Streptococcus cricetus</i>
	<i>Burkholderia cepacia</i>	50 <i>Pasteurella aerogenes</i>	<i>Streptococcus cristatus</i>
15	<i>Citrobacter diversus</i>	<i>Pasteurella multocida</i>	<i>Streptococcus dysgalactiae</i>
	<i>Citrobacter freundii</i>	<i>Peptostreptococcus magnus</i>	<i>Streptococcus equi</i>
	<i>Enterobacter aerogenes</i>	<i>Proteus mirabilis</i>	<i>Streptococcus ferus</i>
	<i>Enterobacter agglomerans</i>	<i>Providencia alcalifaciens</i>	90 <i>Streptococcus gordonii</i>
	<i>Enterobacter cloacae</i>	55 <i>Providencia rettgeri</i>	<i>Streptococcus intermedius</i>
20	<i>Enterococcus avium</i>	<i>Providencia rustigianii</i>	<i>Streptococcus macacae</i>
	<i>Enterococcus casseliflavus</i>	<i>Providencia stuartii</i>	<i>Streptococcus mitis</i>
	<i>Enterococcus dispar</i>	<i>Pseudomonas aeruginosa</i>	<i>Streptococcus mutans</i>
	<i>Enterococcus durans</i>	<i>Pseudomonas fluorescens</i>	95 <i>Streptococcus oralis</i>
	<i>Enterococcus faecalis</i>	60 <i>Pseudomonas stutzeri</i>	<i>Streptococcus parasanguinis</i>
25	<i>Enterococcus faecium</i>	<i>Salmonella bongori</i>	<i>Streptococcus parauberis</i>
	<i>Enterococcus flavescens</i>	<i>Salmonella choleraesuis</i>	<i>Streptococcus pneumoniae</i>
	<i>Enterococcus gallinarum</i>	<i>Salmonella enteritidis</i>	<i>Streptococcus pyogenes</i>
	<i>Enterococcus mundtii</i>	<i>Salmonella gallinarum</i>	100 <i>Streptococcus rattus</i>
	<i>Enterococcus raffinosus</i>	65 <i>Salmonella typhimurium</i>	<i>Streptococcus salivarius</i>
30	<i>Enterococcus solitarius</i>	<i>Serratia liquefaciens</i>	<i>Streptococcus sanguinis</i>
	<i>Escherichia coli</i>	<i>Serratia marcescens</i>	<i>Streptococcus sobrinus</i>
	<i>Gemella morbillorum</i>	<i>Shigella flexneri</i>	<i>Streptococcus uberis</i>
	<i>Haemophilus ducreyi</i>	<i>Shigella sonnei</i>	105 <i>Streptococcus vestibularis</i>
	<i>Haemophilus haemolyticus</i>	70 <i>Staphylococcus aureus</i>	<i>Vibrio cholerae</i>
35	<i>Haemophilus influenzae</i>	<i>Staphylococcus capitis</i>	<i>Yersinia enterocolitica</i>
	<i>Haemophilus</i>	<i>Staphylococcus epidermidis</i>	<i>Yersinia pestis</i>
	<i>parahaemolyticus</i>	<i>Staphylococcus haemolyticus</i>	<i>Yersinia pseudotuberculosis</i>
	<i>Haemophilus parainfluenzae</i>	<i>Staphylococcus hominis</i>	
	<i>Hafnia alvei</i>	75 <i>Staphylococcus lugdunensis</i>	
40	<i>Kingella kingae</i>	<i>Staphylococcus saprophyticus</i>	

Table 15. Microorganisms identified by automated systems.

	<i>Abiotrophia adiacens</i> (<i>Streptococcus adiacens</i>)	75	<i>Alcaligenes xylosoxidans</i> subsp. <i>xylosoxidans</i>	150	<i>Brevibacterium</i> species
	<i>Abiotrophia defectiva</i> (<i>Streptococcus defectivus</i>)		<i>Alloiococcus otitis</i>		<i>Brevundimonas</i> (<i>Pseudomonas</i>) <i>diminuta</i>
5	<i>Achromobacter</i> species		<i>Anaerobiospirillum succiniciproducens</i>		<i>Brevundimonas</i> (<i>Pseudomonas</i>) <i>vesicularis</i>
	<i>Acidaminococcus fermentans</i>	80	<i>Anaerovibrio lipolytica</i>		<i>Brevundimonas</i> species
	<i>Acinetobacter alcaligenes</i>		<i>Arachnia propionica</i>	155	<i>Brochothrix thermosphacta</i>
	<i>Acinetobacter anitratus</i>		<i>Arcanobacterium</i> (<i>Actinomyces</i>) <i>bernardiae</i>		<i>Brucella abortus</i>
	<i>Acinetobacter baumannii</i>		<i>Arcanobacterium</i> (<i>Actinomyces</i>) <i>pyogenes</i>		<i>Brucella canis</i>
10	<i>Acinetobacter calcoaceticus</i>		<i>Arcanobacterium haemolyticum</i>		<i>Brucella melitensis</i>
	<i>Acinetobacter calcoaceticus</i> biovar <i>anitratus</i>	85	<i>Arcobacter cryaerophilus</i> (<i>Campylobacter cryaerophila</i>)	160	<i>Brucella ovis</i>
	<i>Acinetobacter calcoaceticus</i> biovar <i>lwoffii</i>		<i>Arthrobacter globiformis</i>		<i>Brucella species</i>
15	<i>Acinetobacter genomospecies</i>		<i>Arthrobacter species</i>		<i>Brucella suis</i>
	<i>Acinetobacter haemolyticus</i>	90	<i>Arxiozyma telluris</i> (<i>Torulopsis pintolopesii</i>)	165	<i>Budvicia aquatica</i>
	<i>Acinetobacter johnsonii</i>		<i>Atopobium minutum</i> (<i>Lactobacillus minutus</i>)		<i>Burkholderia</i> (<i>Pseudomonas</i>) <i>cepacia</i>
	<i>Acinetobacter junii</i>		<i>Aureobacterium</i> species		<i>Burkholderia</i> (<i>Pseudomonas</i>) <i>gladioli</i>
	<i>Acinetobacter lwoffii</i>		<i>Bacillus amyloliquefaciens</i>		<i>Burkholderia</i> (<i>Pseudomonas</i>) <i>mallei</i>
20	<i>Acinetobacter radioresistens</i>	95	<i>Bacillus anthracis</i>		<i>Burkholderia</i> (<i>Pseudomonas</i>) <i>pseudomallei</i>
	<i>Acinetobacter</i> species		<i>Bacillus badius</i>	170	<i>Burkholderia species</i>
	<i>Actinobacillus actinomycetemcomitans</i>		<i>Bacillus cereus</i>		<i>Buttiauxella agrestis</i>
	<i>Actinobacillus capsulatus</i>		<i>Bacillus circulans</i>		<i>Campylobacter coli</i>
25	<i>Actinobacillus equuli</i>	100	<i>Bacillus coagulans</i>		<i>Campylobacter concisus</i>
	<i>Actinobacillus hominis</i>		<i>Bacillus firmus</i>	175	<i>Campylobacter fetus</i>
	<i>Actinobacillus lignieresii</i>		<i>Bacillus lentus</i>		<i>Campylobacter fetus</i> subsp. <i>fetus</i>
	<i>Actinobacillus pleuropneumoniae</i>		<i>Bacillus licheniformis</i>		<i>Campylobacter fetus</i> subsp. <i>venerealis</i>
	<i>Actinobacillus species</i>		<i>Bacillus megaterium</i>		<i>Campylobacter hyointestinalis</i>
30	<i>Actinobacillus suis</i>	105	<i>Bacillus mycoides</i>		<i>Campylobacter jejuni</i> subsp. <i>doylei</i>
	<i>Actinobacillus ureae</i>		<i>Bacillus pantothenticus</i>	180	<i>Campylobacter jejuni</i> subsp. <i>jejuni</i>
	<i>Actinomyces bovis</i>		<i>Bacillus pumilus</i>		<i>Campylobacter lari</i>
	<i>Actinomyces israelii</i>		<i>Bacillus species</i>		<i>Campylobacter lari</i> subsp. <i>UPTC</i>
	<i>Actinomyces meyeri</i>		<i>Bacillus sphaericus</i>		<i>Campylobacter mucosalis</i>
35	<i>Actinomyces naeslundii</i>	110	<i>Bacillus stearothermophilus</i>		<i>Campylobacter species</i>
	<i>Actinomyces neuii</i> subsp. <i>anitratus</i>		<i>Bacillus subtilis</i>	185	<i>Campylobacter sputorum</i>
	<i>Actinomyces neuii</i> subsp. <i>neuii</i>		<i>Bacillus thuringiensis</i>		<i>Campylobacter sputorum</i> subsp. <i>bubulus</i>
	<i>Actinomyces odontolyticus</i>		<i>Bacteroides caccae</i>		<i>Campylobacter sputorum</i> subsp. <i>fecalis</i>
	<i>Actinomyces pyogenes</i>		<i>Bacteroides capillosus</i>		<i>Campylobacter sputorum</i> subsp. <i>sputorum</i>
40	<i>Actinomyces radingae</i>	115	<i>Bacteroides distasonis</i>	190	<i>Campylobacter upsaliensis</i>
	<i>Actinomyces species</i>		<i>Bacteroides eggerthii</i>		<i>Candida</i> (<i>Clavispora</i>) <i>lusitanae</i>
	<i>Actinomyces turicensis</i>		<i>Bacteroides fragilis</i>		<i>Candida</i> (<i>Pichia</i>) <i>guilliermondii</i>
	<i>Actinomyces viscosus</i>		<i>Bacteroides merdae</i>		<i>Candida</i> (<i>Torulopsis</i>) <i>glabrata</i>
	<i>Aerococcus</i> species		<i>Bacteroides ovatus</i>		<i>Candida albicans</i>
45	<i>Aerococcus viridans</i>	120	<i>Bacteroides species</i>	195	<i>Candida boidinii</i>
	<i>Aeromonas caviae</i>		<i>Bacteroides splachnicus</i>		<i>Candida catenulata</i>
	<i>Aeromonas hydrophila</i>		<i>Bacteroides stercoris</i>		<i>Candida ciferrii</i>
	<i>Aeromonas hydrophila</i> group		<i>Bacteroides thetaiotaomicron</i>		<i>Candida colliculosa</i>
	<i>Aeromonas jandaei</i>		<i>Bacteroides uniformis</i>		<i>Candida conglobata</i>
50	<i>Aeromonas salmonicida</i>	125	<i>Bacteroides ureolyticus</i> (<i>B. corrodens</i>)	200	<i>Candida curvata</i> (<i>Cryptococcus curvatus</i>)
	<i>Aeromonas salmonicida</i> subsp. <i>achromogenes</i>		<i>Bacteroides vulgatus</i>		<i>Candida dattila</i>
	<i>Aeromonas salmonicida</i> subsp. <i>masoucida</i>		<i>Bergeyella</i> (<i>Weeksella</i>) <i>zoohelcum</i>		<i>Candida dubliniensis</i>
55	<i>Aeromonas salmonicida</i> subsp. <i>salmonicida</i>		<i>Bifidobacterium adolescentis</i>		<i>Candida famata</i>
	<i>Aeromonas schubertii</i>	130	<i>Bifidobacterium bifidum</i>	205	<i>Candida globosa</i>
	<i>Aeromonas sobria</i>		<i>Bifidobacterium breve</i>		<i>Candida hellenica</i>
	<i>Aeromonas species</i>		<i>Bifidobacterium dentium</i>		<i>Candida holmii</i>
	<i>Aeromonas trota</i>		<i>Bifidobacterium infantis</i>		<i>Candida humicola</i>
60	<i>Aeromonas veronii</i>		<i>Bifidobacterium species</i>		<i>Candida inconspicua</i>
	<i>Aeromonas veronii</i> biovar <i>sobria</i>	135	<i>Blastoschizomyces</i> (<i>Dipodascus</i>) <i>capitatus</i>	210	<i>Candida intermedia</i>
	<i>Aeromonas veronii</i> biovar <i>veronii</i>		<i>Bordetella avium</i>		<i>Candida kefir</i>
	<i>Agrobacterium radiobacter</i>		<i>Bordetella bronchiseptica</i>		<i>Candida krusei</i>
65	<i>Agrobacterium species</i>		<i>Bordetella parapertussis</i>		<i>Candida lambica</i>
	<i>Agrobacterium tumefaciens</i>	140	<i>Bordetella pertussis</i>	215	<i>Candida magnoliae</i>
	<i>Alcaligenes denitrificans</i>		<i>Bordetella species</i>		<i>Candida maris</i>
	<i>Alcaligenes faecalis</i>		<i>Borrelia</i> species		<i>Candida melibiosica</i>
	<i>Alcaligenes odorans</i>		<i>Branhamella</i> (<i>Moraxella</i>) <i>catarrhalis</i>		<i>Candida membranaefaciens</i>
70	<i>Alcaligenes odorans</i> (<i>Alcaligenes faecalis</i>)	145	<i>Branhamella species</i>	220	<i>Candida norvegensis</i>
	<i>Alcaligenes species</i>		<i>Brevibacillus brevis</i>		<i>Candida norvegica</i>
	<i>Alcaligenes xylosoxidans</i>		<i>Brevibacterium laterosporus</i>		<i>Candida parapsilosis</i>
	<i>Alcaligenes xylosoxidans</i> subsp. <i>denitrificans</i>		<i>Brevibacterium casei</i>		<i>Candida paratropicalis</i>
			<i>Brevibacterium epidermidis</i>		<i>Candida pelliculosa</i>
			<i>Brevibacterium linens</i>		

Table 15. Microorganisms identified by automated systems (continued).

<i>Candida pseudotropicalis</i>		<i>Clostridium hastiforme</i>		<i>Corynebacterium urealyticum</i> (group D2)
<i>Candida pulcherrima</i>	80	<i>Clostridium histolyticum</i>		<i>Corynebacterium xerosis</i>
<i>Candida ravautii</i>		<i>Clostridium innocuum</i>	160	<i>Cryptococcus albidus</i>
<i>Candida rugosa</i>		<i>Clostridium limosum</i>		<i>Cryptococcus ater</i>
5 <i>Candida sake</i>		<i>Clostridium novyi</i>		<i>Cryptococcus cereanus</i>
<i>Candida silvicola</i>		<i>Clostridium novyi A</i>		<i>Cryptococcus gastricus</i>
<i>Candida species</i>	85	<i>Clostridium paraputrificum</i>		<i>Cryptococcus humicolus</i>
<i>Candida sphaerica</i>		<i>Clostridium perfringens</i>	165	<i>Cryptococcus lactativorus</i>
10 <i>Candida stellatoidea</i>		<i>Clostridium putrificum</i>		<i>Cryptococcus laurentii</i>
<i>Candida tenuis</i>		<i>Clostridium ramosum</i>		<i>Cryptococcus luteolus</i>
<i>Candida tropicalis</i>		<i>Clostridium septicum</i>		<i>Cryptococcus melibiosum</i>
<i>Candida utilis</i>	90	<i>Clostridium sordellii</i>		<i>Cryptococcus neoformans</i>
<i>Candida valida</i>		<i>Clostridium species</i>	170	<i>Cryptococcus species</i>
<i>Candida vini</i>		<i>Clostridium sphenoides</i>		<i>Cryptococcus terreus</i>
15 <i>Candida viswanathii</i>		<i>Clostridium sporogenes</i>		<i>Cryptococcus uniguttulatus</i>
<i>Candida zeylanoides</i>		<i>Clostridium subterminale</i>		<i>Debaryomyces hansenii</i>
<i>Capnocytophaga gingivalis</i>	95	<i>Clostridium tertium</i>		<i>Debaryomyces marama</i>
<i>Capnocytophaga ochracea</i>		<i>Clostridium tetani</i>	175	<i>Debaryomyces polymorphus</i>
<i>Capnocytophaga species</i>		<i>Clostridium tyrobutyricum</i>		<i>Debaryomyces species</i>
20 <i>Capnocytophaga sputigena</i>		<i>Comamonas (Pseudomonas) acidovorans</i>		<i>Dermabacter hominis</i>
<i>Cardiobacterium hominis</i>		<i>Comamonas (Pseudomonas) testosteroni</i>		<i>Dermacoccus (Micrococcus) nishinomiyaensis</i>
<i>Carnobacterium divergens</i>	100	<i>Comamonas species</i>	180	<i>Dietzia species</i>
<i>Carnobacterium piscicola</i>		<i>Corynebacterium accolens</i>		<i>Edwardsiella hoshinae</i>
CDC group ED-2		<i>Corynebacterium afermentans</i>		<i>Edwardsiella ictaluri</i>
25 CDC group EF4 (<i>Pasteurella</i> sp.)		<i>Corynebacterium amycolatum</i>		<i>Edwardsiella species</i>
CDC group EF-4A		<i>Corynebacterium aquaticum</i>	185	<i>Edwardsiella tarda</i>
CDC group EF-4B	105	<i>Corynebacterium argenteratense</i>		<i>Eikenella corrodens</i>
CDC group EQ-Z		<i>Corynebacterium auris</i>		<i>Empedobacter brevis</i> (<i>Flavobacterium breve</i>)
30 CDC group HB-5		<i>Corynebacterium bovis</i>		<i>Enterobacter aerogenes</i>
CDC group II K-2		<i>Corynebacterium coyleae</i>	190	<i>Enterobacter agglomerans</i>
CDC group IV C-2 (<i>Bordetella</i> -like)	110	<i>Corynebacterium cystitidis</i>		<i>Enterobacter amnigenus</i>
CDC group M5		<i>Corynebacterium diphtheriae</i>		<i>Enterobacter amnigenus asburiae</i> (CDC enteric group 17)
CDC group M6		<i>Corynebacterium diphtheriae</i> biotype belfanti	195	<i>Enterobacter amnigenus biogroup 1</i>
35 <i>Cedecea davisae</i>		<i>Corynebacterium diphtheriae</i> biotype gravis		<i>Enterobacter amnigenus biogroup 2</i>
<i>Cedecea lapagei</i>	115	<i>Corynebacterium diphtheriae</i> biotype intermedius		<i>Enterobacter asburiae</i>
<i>Cedecea neteri</i>		<i>Corynebacterium diphtheriae</i> biotype mitis	200	<i>Enterobacter cancerogenus</i>
<i>Cedecea species</i>		<i>Corynebacterium diphtheriae</i> biotype seminale		<i>Enterobacter cloacae</i>
<i>Cellulomonas (Oerskovia) turbata</i>	120	<i>Corynebacterium flavescens</i>		<i>Enterobacter gergoviae</i>
<i>Cellulomonas species</i>		<i>Corynebacterium glucuronolyticum</i>		<i>Enterobacter hormaechei</i>
40 <i>Chlamydia species</i>		<i>Corynebacterium glucuronolyticum-seminale</i>	205	<i>Enterobacter intermedius</i>
<i>Chromobacterium violaceum</i>	125	<i>Corynebacterium group A</i>		<i>Enterobacter sakazakii</i>
<i>Chryseobacterium (Flavobacterium) indologenes</i>		<i>Corynebacterium group A-4</i>		<i>Enterobacter species</i>
<i>Chryseobacterium (Flavobacterium) meningosepticum</i>		<i>Corynebacterium group A-5</i>	210	<i>Enterobacter taylora</i>
45 <i>Chryseobacterium gleum</i>		<i>Corynebacterium group ANF</i>		<i>Enterobacter taylora</i> (CDC enteric group 19)
<i>Chryseobacterium species</i>		<i>Corynebacterium group B</i>		<i>Enterococcus (Streptococcus) cecorum</i>
<i>Chryseomonas indologenes</i>	130	<i>Corynebacterium group B-3</i>		<i>Enterococcus (Streptococcus) faecalis</i> (Group D)
50 <i>Citeromyces matritensis</i>		<i>Corynebacterium group F</i>		<i>Enterococcus (Streptococcus) faecium</i> (Group D)
<i>Citrobacter amalonaticus</i>		<i>Corynebacterium group F-1</i>		<i>Enterococcus (Streptococcus) saccharolyticus</i>
<i>Citrobacter braakii</i>		<i>Corynebacterium group F-2</i>	215	<i>Enterococcus avium</i> (Group D)
<i>Citrobacter diversus</i>	135	<i>Corynebacterium group G</i>		<i>Enterococcus casseliflavus</i> (<i>Streptococcus faecium</i> subsp. casseliflavus)
<i>Citrobacter farmeri</i>		<i>Corynebacterium group G-1</i>		<i>Enterococcus durans</i> (<i>Streptococcus faecium</i> subsp. durans) (Group D)
<i>Citrobacter freundii</i>		<i>Corynebacterium group G-2</i>	220	<i>Enterococcus gallinarum</i>
55 <i>Citrobacter freundii</i> complex		<i>Corynebacterium group I</i>		<i>Enterococcus hirae</i>
<i>Citrobacter koseri</i>		<i>Corynebacterium group I-2</i>		<i>Enterococcus malodoratus</i>
<i>Citrobacter sedlakii</i>	140	<i>Corynebacterium jeikeium</i> (group JK)		<i>Enterococcus mundtii</i>
<i>Citrobacter species</i>		<i>Corynebacterium kutscheri</i> (C. murium)		<i>Enterococcus raffinosus</i>
<i>Citrobacter werkmanii</i>		<i>Corynebacterium macginleyi</i>	225	<i>Enterococcus species</i>
60 <i>Citrobacter youngae</i>		<i>Corynebacterium minutissimum</i>		<i>Erwinia amylovora</i>
<i>Clostridium acetobutylicum</i>		<i>Corynebacterium pilosum</i>		<i>Erwinia carotovora</i>
<i>Clostridium barati</i>	145	<i>Corynebacterium propinquum</i>		<i>Erwinia carotovora</i> subsp. atroseptica
<i>Clostridium beijerinckii</i>		<i>Corynebacterium pseudodiphtheriticum</i>	230	<i>Erwinia carotovora</i> subsp. betavascularum
<i>Clostridium bifermentans</i>		<i>Corynebacterium pseudotuberculosis</i>		<i>Erwinia carotovora</i> subsp. carotovora
65 <i>Clostridium botulinum</i>		<i>Corynebacterium pyogenes</i>		<i>Erwinia chrysanthemi</i>
<i>Clostridium botulinum</i> (NP) B&F		<i>Corynebacterium renale</i>		<i>Erwinia cypripedii</i>
<i>Clostridium botulinum</i> (NP) E	150	<i>Corynebacterium renale</i> group		<i>Erwinia mallotivora</i>
<i>Clostridium botulinum</i> (P) A&H		<i>Corynebacterium seminale</i>		
<i>Clostridium botulinum</i> (P) F		<i>Corynebacterium species</i>		
70 <i>Clostridium botulinum</i> G1		<i>Corynebacterium striatum</i> (C. flavidum)		
<i>Clostridium botulinum</i> G2	155	<i>Corynebacterium ulcerans</i>		
<i>Clostridium butyricum</i>				
<i>Clostridium cadaveris</i>				
<i>Clostridium chauvoei</i>				
75 <i>Clostridium clostridioforme</i>				
<i>Clostridium difficile</i>				
<i>Clostridium fallax</i>				
<i>Clostridium glycolicum</i>				

Table 15. Microorganisms identified by automated systems (continued).

<i>Erwinia nigrifluens</i>		VII	<i>Lactobacillus paracasei</i> subsp. <i>paracasei</i>
<i>Erwinia quercina</i>	80	<i>Haemophilus parainfluenzae</i> biotype	<i>Lactobacillus pentosus</i>
<i>Erwinia rhapontici</i>		VIII	<i>Lactobacillus plantarum</i>
<i>Erwinia rubrifaciens</i>		<i>Haemophilus paraphrohaemolyticus</i>	<i>Lactobacillus salivarius</i>
5 <i>Erwinia salicis</i>		<i>Haemophilus paraphrophilus</i>	<i>Lactobacillus salivarius</i> var. <i>salicinius</i>
<i>Erwinia species</i>		<i>Haemophilus segnis</i>	<i>Lactobacillus species</i>
<i>Erysipelothrix rhusiopathiae</i>	85	<i>Haemophilus somnus</i>	<i>Lactococcus diacitilactis</i>
<i>Erysipelothrix species</i>		<i>Haemophilus species</i>	<i>Lactococcus garvieae</i>
<i>Escherichia blattae</i>		<i>Hafnia alvei</i>	<i>Lactococcus lactis</i> subsp. <i>cremoris</i>
10 <i>Escherichia coli</i>		<i>Hanseniaspora guilliermondii</i>	<i>Lactococcus lactis</i> subsp. <i>diacitilactis</i>
<i>Escherichia coli</i> A-D		<i>Hanseniaspora uvarum</i>	<i>Lactococcus lactis</i> subsp. <i>hordniae</i>
<i>Escherichia coli</i> O157:H7	90	<i>Hanseniaspora valbyensis</i>	<i>Lactococcus lactis</i> subsp. <i>lactis</i>
<i>Escherichia fergusonii</i>		<i>Hansenula anomala</i>	<i>Lactococcus plantarum</i>
<i>Escherichia hermannii</i>		<i>Hansenula holstii</i>	<i>Lactococcus raffinolactis</i>
15 <i>Escherichia species</i>		<i>Hansenula polymorpha</i>	<i>Leclercia adecarboxylata</i>
<i>Escherichia vulneris</i>		<i>Helicobacter (Campylobacter) cinaedi</i>	<i>Legionella species</i>
<i>Eubacterium aerofaciens</i>	95	<i>Helicobacter (Campylobacter)</i>	<i>Leminorella species</i>
<i>Eubacterium alactolyticum</i>		<i>fennelliae</i>	<i>Leptospira species</i>
<i>Eubacterium lentum</i>		<i>Helicobacter (Campylobacter) pylori</i>	<i>Leptotrichia buccalis</i>
20 <i>Eubacterium limosum</i>		<i>Issatchenkia orientalis</i>	<i>Leuconostoc (Weissella)</i>
<i>Eubacterium species</i>		<i>Kingella denitrificans</i>	<i>paramesenteroides</i>
<i>Ewingella americana</i>	100	<i>Kingella indologenes</i>	<i>Leuconostoc carnosum</i>
<i>Filobasidiella neoformans</i>		<i>Kingella kingae</i>	<i>Leuconostoc citreum</i>
<i>Filobasidium floriforme</i>		<i>Kingella species</i>	<i>Leuconostoc gelidum</i>
25 <i>Filobasidium uniguttulatum</i>		<i>Klebsiella ornithinolytica</i>	<i>Leuconostoc lactis</i>
<i>Flavimonas oryzihabitans</i>		<i>Klebsiella oxytoca</i>	<i>Leuconostoc mesenteroides</i>
<i>Flavobacterium gleum</i>	105	<i>Klebsiella planticola</i>	<i>Leuconostoc mesenteroides</i> subsp. <i>cremoris</i>
<i>Flavobacterium indologenes</i>		<i>Klebsiella pneumoniae</i> subsp. <i>ozaenae</i>	<i>Leuconostoc mesenteroides</i> subsp. <i>dextranicum</i>
<i>Flavobacterium odoratum</i>		<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i>	<i>Leuconostoc mesenteroides</i> subsp. <i>mesenteroides</i>
30 <i>Flavobacterium species</i>		<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	<i>Leuconostoc species</i>
<i>Francisella novicida</i>	110	<i>Klebsiella pneumoniae</i> subsp. <i>rhinoscleromatis</i>	<i>Listeria grayi</i>
<i>Francisella philomiragia</i>		<i>Klebsiella species</i>	<i>Listeria innocua</i>
<i>Francisella tularensis</i>		<i>Klebsiella terrigena</i>	<i>Listeria ivanovii</i>
35 <i>Fusobacterium mortiferum</i>		<i>Kloeckera apiculata</i>	<i>Listeria monocytogenes</i>
<i>Fusobacterium necrogenes</i>		<i>Kloeckera apis</i>	<i>Listeria murrayi</i>
<i>Fusobacterium necrophorum</i>	115	<i>Kloeckera japonica</i>	<i>Listeria seeligeri</i>
<i>Fusobacterium nucleatum</i>		<i>Kloeckera species</i>	<i>Listeria species</i>
<i>Fusobacterium species</i>		<i>Kluyvera ascorbata</i>	<i>Listeria welshimeri</i>
40 <i>Fusobacterium varium</i>		<i>Kluyvera cryocrescens</i>	<i>Megasphaera elsdenii</i>
<i>Gaffkya species</i>		<i>Kluyvera species</i>	<i>Methylobacterium mesophilicum</i>
<i>Gardnerella vaginalis</i>	120	<i>Kluyveromyces lactis</i>	<i>Metschnikowia pulcherrima</i>
<i>Gemella haemolysans</i>		<i>Kluyveromyces marxianus</i>	<i>Microbacterium species</i>
<i>Gemella morbillorum</i>		<i>Kluyveromyces thermotolerans</i>	<i>Micrococcus luteus</i>
45 <i>Gemella species</i>		<i>Kocuria (Micrococcus) kristinae</i>	<i>Micrococcus lylae</i>
<i>Geotrichum candidum</i>		<i>Kocuria (Micrococcus) rosea</i>	<i>Micrococcus species</i>
<i>Geotrichum fermentans</i>	125	<i>Kocuria (Micrococcus) varians</i>	<i>Mobiluncus curtisii</i>
<i>Geotrichum penicillarum</i>		<i>Koserella trabulsii</i>	<i>Mobiluncus mulieris</i>
<i>Geotrichum penicillatum</i>		<i>Kytococcus (Micrococcus) sedentarius</i>	<i>Mobiluncus species</i>
50 <i>Geotrichum species</i>		<i>Lactobacillus (Weissella) viridescens</i>	<i>Moellerella wisconsensis</i>
<i>Gordona species</i>		<i>Lactobacillus A</i>	<i>Moraxella (Branhamella) catarrhalis</i>
<i>Haemophilus aegyptius</i>	130	<i>Lactobacillus acidophilus</i>	<i>Moraxella atlantae</i>
<i>Haemophilus aphrophilus</i>		<i>Lactobacillus B</i>	<i>Moraxella bovis</i>
<i>Haemophilus ducreyi</i>		<i>Lactobacillus brevis</i>	<i>Moraxella lacunata</i>
55 <i>Haemophilus haemoglobinophilus</i>		<i>Lactobacillus buchneri</i>	<i>Moraxella nonliquefaciens</i>
<i>Haemophilus haemolyticus</i>		<i>Lactobacillus casei</i>	<i>Moraxella osloensis</i>
<i>Haemophilus influenzae</i>	135	<i>Lactobacillus casei</i> subsp. <i>casei</i>	<i>Moraxella phenylpyruvica</i>
<i>Haemophilus influenzae</i> biotype I		<i>Lactobacillus casei</i> subsp. <i>lactosus</i>	<i>Moraxella species</i>
<i>Haemophilus influenzae</i> biotype II		<i>Lactobacillus casei</i> subsp. <i>rhamnosus</i>	<i>Morganella morganii</i>
60 <i>Haemophilus influenzae</i> biotype III		<i>Lactobacillus cateniformis</i>	<i>Morganella morganii</i> subsp. <i>morganii</i>
<i>Haemophilus influenzae</i> biotype IV		<i>Lactobacillus cellobiosus</i>	<i>Morganella morganii</i> subsp. <i>sibonii</i>
<i>Haemophilus influenzae</i> biotype V	140	<i>Lactobacillus collinoides</i>	<i>Mycobacterium africanum</i>
<i>Haemophilus influenzae</i> biotype VI		<i>Lactobacillus coprophilus</i>	<i>Mycobacterium asiaticum</i>
<i>Haemophilus influenzae</i> biotype VII		<i>Lactobacillus crispatus</i>	<i>Mycobacterium avium</i>
65 <i>Haemophilus influenzae</i> biotype VIII		<i>Lactobacillus curvatus</i>	<i>Mycobacterium bovis</i>
<i>Haemophilus paragallinarum</i>		<i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i>	<i>Mycobacterium chelonae</i>
<i>Haemophilus parahaemolyticus</i>	145	<i>Lactobacillus delbrueckii</i> subsp. <i>delbrueckii</i>	<i>Mycobacterium fortuitum</i>
<i>Haemophilus parainfluenzae</i>		<i>Lactobacillus delbrueckii</i> subsp. <i>lactis</i>	<i>Mycobacterium gordonae</i>
<i>Haemophilus parainfluenzae</i> biotype I		<i>Lactobacillus fermentum</i>	<i>Mycobacterium kansasii</i>
70 <i>Haemophilus parainfluenzae</i> biotype II		<i>Lactobacillus fructivorans</i>	<i>Mycobacterium malmoeense</i>
<i>Haemophilus parainfluenzae</i> biotype III	150	<i>Lactobacillus helveticus</i>	<i>Mycobacterium marinum</i>
<i>Haemophilus parainfluenzae</i> biotype IV		<i>Lactobacillus helveticus</i> subsp. <i>jugurti</i>	<i>Mycobacterium phlei</i>
75 <i>Haemophilus parainfluenzae</i> biotype V		<i>Lactobacillus jensenii</i>	<i>Mycobacterium scrofulaceum</i>
<i>Haemophilus parainfluenzae</i> biotype VI	155	<i>Lactobacillus lindneri</i>	<i>Mycobacterium smegmatis</i>
<i>Haemophilus parainfluenzae</i> biotype		<i>Lactobacillus minutus</i>	<i>Mycobacterium species</i>

Table 15. Microorganisms identified by automated systems (continued).

<i>Mycobacterium tuberculosis</i>		<i>Pichia fermentans</i>		<i>Saccharomyces exiguus</i>
<i>Mycobacterium ulcerans</i>	80	<i>Pichia membranaefaciens</i>		<i>Saccharomyces kluyverii</i>
<i>Mycobacterium xenopi</i>		<i>Pichia norvegensis</i>	160	<i>Saccharomyces species</i>
5 <i>Mycoplasma fermentans</i>		<i>Pichia ohmeri</i>		<i>Sakaguchia dacryoides</i>
<i>Mycoplasma hominis</i>		<i>Pichia spartinae</i>		(<i>Rhodospiridium dacryoidum</i>)
<i>Mycoplasma orale</i>		<i>Pichia species</i>		<i>Salmonella arizonae</i>
<i>Mycoplasma pneumoniae</i>	85	<i>Plesiomonas shigelloides</i>		<i>Salmonella choleraesuis</i>
<i>Mycoplasma species</i>		<i>Porphyromonas asaccharolytica</i>	165	<i>Salmonella enteritidis</i>
10 <i>Myroides species</i>		<i>Porphyromonas endodontalis</i>		<i>Salmonella gallinarum</i>
<i>Neisseria cinerea</i>		<i>Porphyromonas gingivalis</i>		<i>Salmonella paratyphi A</i>
<i>Neisseria elongata</i> subsp. <i>elongata</i>		<i>Porphyromonas levii</i>		<i>Salmonella paratyphi B</i>
<i>Neisseria flava</i>	90	<i>Prevotella (Bacteroides) buccae</i>		<i>Salmonella pullorum</i>
<i>Neisseria flavescens</i>		<i>Prevotella (Bacteroides) buccalis</i>	170	<i>Salmonella species</i>
<i>Neisseria gonorrhoeae</i>		<i>Prevotella (Bacteroides) corporis</i>		<i>Salmonella typhi</i>
15 <i>Neisseria lactamica</i>		<i>Prevotella (Bacteroides) denticola</i>		<i>Salmonella typhimurium</i>
<i>Neisseria meningitidis</i>		<i>Prevotella (Bacteroides) loeschei</i>		<i>Salmonella typhusuis</i>
<i>Neisseria mucosa</i>	95	<i>Prevotella (Bacteroides) oralis</i>		<i>Salmonella/Arizona</i>
<i>Neisseria perflava</i>		<i>Prevotella (Bacteroides) disiens</i>	175	<i>Serratia ficaria</i>
<i>Neisseria polysaccharea</i>		<i>Prevotella (Bacteroides) oris</i>		<i>Serratia fonticola</i>
20 <i>Neisseria saprophytes</i>		<i>Prevotella bivia (Bacteroides bivius)</i>		<i>Serratia grimesii</i>
<i>Neisseria sicca</i>		<i>Prevotella intermedia (Bacteroides intermedius)</i>		<i>Serratia liquefaciens</i>
<i>Neisseria subflava</i>	100	<i>Prevotella melaninogenica (Bacteroides melaninogenicus)</i>	180	<i>Serratia marcescens</i>
<i>Neisseria weaveri</i>		<i>Prevotella ruminicola</i>		<i>Serratia odorifera</i>
<i>Neisseria weaveri</i> (CDC group M5)		<i>Propionibacterium acnes</i>		<i>Serratia odorifera</i> type 1
25 <i>Nocardia species</i>		<i>Propionibacterium avidum</i>		<i>Serratia odorifera</i> type 2
<i>Ochrobactrum anthropi</i>		<i>Propionibacterium granulosum</i>		<i>Serratia plymuthica</i>
<i>Oerskovia species</i>	105	<i>Propionibacterium propionicum</i>	185	<i>Serratia proteamaculans</i>
<i>Oerskovia xanthineolytica</i>		<i>Propionibacterium species</i>		<i>Serratia proteamaculans</i> subsp.
<i>Oligella (Moraxella) urethralis</i>		<i>Proteus mirabilis</i>		<i>Serratia proteamaculans</i> subsp.
30 <i>Oligella species</i>		<i>Proteus penneri</i>		<i>quinovora</i>
<i>Oligella ureolytica</i>	110	<i>Proteus species</i>		<i>Serratia rubidaea</i>
<i>Paenibacillus alvei</i>		<i>Proteus vulgaris</i>	190	<i>Serratia species</i>
<i>Paenibacillus macerans</i>		<i>Prototheca species</i>		<i>Shewanella (Pseudomonas, Alteromonas) putrefaciens</i>
<i>Paenibacillus polymyxa</i>		<i>Prototheca wickerhamii</i>		<i>Shigella boydii</i>
35 <i>Pantoea agglomerans</i>		<i>Prototheca zopfii</i>		<i>Shigella dysenteriae</i>
<i>Pantoea ananas (Erwinia uredovora)</i>	115	<i>Providencia alcalifaciens</i>	195	<i>Shigella flexneri</i>
<i>Pantoea dispersa</i>		<i>Providencia heimbachae</i>		<i>Shigella sonnei</i>
<i>Pantoea species</i>		<i>Providencia rettgeri</i>		<i>Shigella species</i>
<i>Pantoea stewartii</i>		<i>Providencia rustigianii</i>		<i>Sphingobacterium multivorum</i>
40 <i>Pasteurella (Haemophilus) avium</i>		<i>Providencia species</i>		<i>Sphingobacterium species</i>
<i>Pasteurella aerogenes</i>	120	<i>Providencia stuartii</i>	200	<i>Sphingobacterium spiritivorum</i>
<i>Pasteurella gallinarum</i>		<i>Providencia stuartii</i> urea +		<i>Sphingobacterium thalophilum</i>
<i>Pasteurella haemolytica</i>		<i>Pseudomonas (Chryseomonas) luteola</i>		<i>Sphingomonas (Pseudomonas) paucimobilis</i>
45 <i>Pasteurella haemolyticus</i>		<i>Pseudomonas acidovorans</i>		<i>Sporidiobolus salmonicolor</i>
<i>Pasteurella multocida</i>	125	<i>Pseudomonas aeruginosa</i>	205	<i>Sporobolomyces roseus</i>
<i>Pasteurella multocida</i> SF		<i>Pseudomonas alcaligenes</i>		<i>Sporobolomyces salmonicolor</i>
<i>Pasteurella multocida</i> subsp. <i>multocida</i>		<i>Pseudomonas cepacia</i>		<i>Sporobolomyces species</i>
<i>Pasteurella multocida</i> subsp. <i>septica</i>		<i>Pseudomonas chlororaphis (P. aureofaciens)</i>		<i>Staphylococcus (Peptococcus) saccharolyticus</i>
50 <i>Pasteurella pneumotropica</i>	130	<i>Pseudomonas fluorescens</i>	210	<i>Staphylococcus arlettae</i>
<i>Pasteurella species</i>		<i>Pseudomonas fluorescens</i> group		<i>Staphylococcus aureus</i>
<i>Pasteurella ureae</i>		<i>Pseudomonas mendocina</i>		<i>Staphylococcus aureus</i> (Coagulase-negative)
<i>Pediococcus acidilactici</i>	135	<i>Pseudomonas pseudoalcaligenes</i>		<i>Staphylococcus auricularis</i>
<i>Pediococcus damnosus</i>		<i>Pseudomonas putida</i>	215	<i>Staphylococcus capitis</i>
55 <i>Pediococcus pentosaceus</i>		<i>Pseudomonas species</i>		<i>Staphylococcus capitis</i> subsp. <i>capitis</i>
<i>Pediococcus species</i>		<i>Pseudomonas stutzeri</i>		<i>Staphylococcus capitis</i> subsp. <i>ureolyticus</i>
<i>Peptococcus niger</i>		<i>Pseudomonas testosteroni</i>		<i>Staphylococcus caprae</i>
<i>Peptococcus species</i>		<i>Pseudomonas vesicularis</i>		<i>Staphylococcus carnosus</i>
<i>Peptostreptococcus anaerobius</i>	140	<i>Pseudoramibacter (Eubacterium) alactolyticus</i>	220	<i>Staphylococcus caseolyticus</i>
<i>Peptostreptococcus asaccharolyticus</i>		<i>Psychrobacter (Moraxella) phenylpyruvicus</i>		<i>Staphylococcus chromogenes</i>
<i>Peptostreptococcus indolicus</i>		<i>Rahnella aquatilis</i>		<i>Staphylococcus cohnii</i>
<i>Peptostreptococcus magnus</i>	145	<i>Ralstonia (Pseudomonas, Burkholderia) pickettii</i>	225	<i>Staphylococcus cohnii</i> subsp. <i>cohnii</i>
<i>Peptostreptococcus micros</i>		<i>Rhodococcus (Corynebacterium) equi</i>		<i>Staphylococcus cohnii</i> subsp. <i>urealyticum</i>
<i>Peptostreptococcus parvulus</i>		<i>Rhodococcus species</i>		<i>Staphylococcus epidermidis</i>
65 <i>Peptostreptococcus prevotii</i>		<i>Rhodospiridium toruloides</i>		<i>Staphylococcus equorum</i>
<i>Peptostreptococcus productus</i>	150	<i>Rhodotorula glutinis</i>		<i>Staphylococcus gallinarum</i>
<i>Peptostreptococcus species</i>		<i>Rhodotorula minuta</i>		<i>Staphylococcus haemolyticus</i>
<i>Peptostreptococcus tetradius</i>		<i>Rhodotorula mucilaginosa (R. rubra)</i>	230	<i>Staphylococcus hominis</i>
<i>Phaeococcomyces exophialiae</i>		<i>Rhodotorula species</i>		<i>Staphylococcus hominis</i> subsp. <i>hominis</i>
70 <i>Photobacterium damsela</i>		<i>Rickettsia species</i>		<i>Staphylococcus hominis</i> subsp. <i>novobiosepticus</i>
<i>Pichia (Hansenula) anomala</i>	155	<i>Rothia dentocariosa</i>		
<i>Pichia (Hansenula) jadinii</i>		<i>Saccharomyces cerevisiae</i>		
<i>Pichia (Hansenula) petersonii</i>				
<i>Pichia angusta (Hansenula polymorpha)</i>				
75 <i>Pichia carsonii (P. vini)</i>				
<i>Pichia etchellsii</i>				
<i>Pichia farinosa</i>				

Table 15. Microorganisms identified by automated systems (continued).

5	<i>Staphylococcus hyicus</i>	60	<i>Streptococcus</i> Gamma (non)-hemolytic	120	<i>Tetragenococcus</i> (<i>Pediococcus</i>) <i>halophilus</i>
	<i>Staphylococcus intermedius</i>		<i>Streptococcus gordonii</i>		<i>Torulaspora delbrueckii</i> (<i>Saccharomyces rosei</i>)
	<i>Staphylococcus kloosii</i>		<i>Streptococcus</i> Group B		<i>Torulopsis candida</i>
	<i>Staphylococcus lentus</i>	65	<i>Streptococcus</i> Group C		<i>Torulopsis haemulonii</i>
	<i>Staphylococcus lugdunensis</i>		<i>Streptococcus</i> Group D	125	<i>Torulopsis inconspicua</i>
10	<i>Staphylococcus saprophyticus</i>		<i>Streptococcus</i> Group E		<i>Treponema</i> species
	<i>Staphylococcus schleiferi</i>		<i>Streptococcus</i> Group F		<i>Trichosporon asahii</i>
	<i>Staphylococcus sciuri</i>		<i>Streptococcus</i> Group G		<i>Trichosporon asteroides</i>
	<i>Staphylococcus simulans</i>	70	<i>Streptococcus</i> Group L		<i>Trichosporon beigeli</i>
	<i>Staphylococcus species</i>		<i>Streptococcus</i> Group P	130	<i>Trichosporon cutaneum</i>
15	<i>Staphylococcus warneri</i>		<i>Streptococcus</i> Group U		<i>Trichosporon inkin</i>
	<i>Staphylococcus xylosus</i>		<i>Streptococcus intermedius</i>		<i>Trichosporon mucoides</i>
	<i>Stenotrophomonas</i> (<i>Xanthomonas</i>) <i>maltophilia</i>		<i>Streptococcus intermedius</i> (<i>Streptococcus milleri</i> II)		<i>Trichosporon ovoides</i>
	<i>Stephanoascus ciferrii</i>	75	<i>Streptococcus intermedius</i> (viridans <i>Streptococcus</i>)	135	<i>Trichosporon pullulans</i>
	<i>Stomatococcus mucilaginosus</i>		<i>Streptococcus milleri</i> group		<i>Trichosporon species</i>
20	<i>Streptococcus acidominimus</i>		<i>Streptococcus mitis</i>		<i>Turicella otitidis</i>
	<i>Streptococcus agalactiae</i>		<i>Streptococcus mitis</i> (viridans <i>Streptococcus</i>)		<i>Ureaplasma</i> species
	<i>Streptococcus agalactiae</i> (Group B)	80	<i>Streptococcus mitis</i> group	140	<i>Ureaplasma urealyticum</i>
	<i>Streptococcus agalactiae</i> hemolytic		<i>Streptococcus mutans</i>		<i>Veillonella parvula</i> (<i>V. alcalescens</i>)
	<i>Streptococcus agalactiae</i> non-hemolytic		<i>Streptococcus mutans</i> (viridans <i>Streptococcus</i>)		<i>Veillonella</i> species
25	<i>Streptococcus alactolyticus</i>	85	<i>Streptococcus oralis</i>		<i>Vibrio alginolyticus</i>
	<i>Streptococcus anginosus</i>		<i>Streptococcus parasanguis</i>	145	<i>Vibrio cholerae</i>
	<i>Streptococcus anginosus</i> (Group D, nonenterococci)		<i>Streptococcus pneumoniae</i>		<i>Vibrio damsela</i>
	<i>Streptococcus beta-hemolytic</i> group A		<i>Streptococcus porcinus</i>		<i>Vibrio fluvialis</i>
	<i>Streptococcus beta-hemolytic</i> non-group A or B	90	<i>Streptococcus pyogenes</i>		<i>Vibrio furnissii</i>
30	<i>Streptococcus beta-hemolytic</i> non-group A		<i>Streptococcus pyogenes</i> (Group A)		<i>Vibrio harveyi</i>
	<i>Streptococcus beta-hemolytic</i>		<i>Streptococcus salivarius</i>	150	<i>Vibrio hollisae</i>
	<i>Streptococcus bovis</i> (Group D, nonenterococci)		<i>Streptococcus salivarius</i> (viridans <i>Streptococcus</i>)		<i>Vibrio metschnikovii</i>
	<i>Streptococcus bovis</i> I	95	<i>Streptococcus salivarius</i> subsp. <i>salivarius</i>		<i>Vibrio mimicus</i>
	<i>Streptococcus bovis</i> II		<i>Streptococcus salivarius</i> subsp. <i>thermophilus</i>	155	<i>Vibrio parahaemolyticus</i>
35	<i>Streptococcus canis</i>		<i>Streptococcus sanguis</i>		<i>Vibrio species</i>
	<i>Streptococcus constellatus</i>		<i>Streptococcus sanguis</i> I (viridans <i>Streptococcus</i>)		<i>Vibrio species SF</i>
	<i>Streptococcus constellatus</i> (<i>Streptococcus milleri</i> I)	100	<i>Streptococcus sanguis</i> II		<i>Vibrio vulnificus</i>
	<i>Streptococcus constellatus</i> (viridans <i>Streptococcus</i>)		<i>Streptococcus sanguis</i> II (viridans <i>Streptococcus</i>)	160	<i>Weeksella</i> (<i>Bergeyella</i>) <i>virosa</i>
	<i>Streptococcus downei</i>		<i>Streptococcus sobrinus</i>		<i>Weeksella species</i>
40	<i>Streptococcus dysgalactiae</i> subsp. <i>dysgalactiae</i>	105	<i>Streptococcus species</i>		<i>Weeksella virosa</i>
	<i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i>		<i>Streptococcus suis</i> I		<i>Williopsis</i> (<i>Hansenula</i>) <i>saturnus</i>
	<i>Streptococcus equi</i> (Group C/Group G <i>Streptococcus</i>)		<i>Streptococcus suis</i> II		<i>Xanthomonas campestris</i>
	<i>Streptococcus equi</i> subsp. <i>equi</i>	110	<i>Streptococcus uberis</i>		<i>Xanthomonas</i> species
	<i>Streptococcus equi</i> subsp. <i>zooepidemicus</i>		<i>Streptococcus uberis</i> (viridans <i>Streptococcus</i>)	165	<i>Yarrowia</i> (<i>Candida</i>) <i>lipolytica</i>
45	<i>Streptococcus equinus</i>		<i>Streptococcus vestibularis</i>		<i>Yersinia aldovae</i>
	<i>Streptococcus equinus</i> (Group D, nonenterococci)		<i>Streptococcus zooepidemicus</i>	170	<i>Yersinia enterocolitica</i>
	<i>Streptococcus equisimilis</i>	115	<i>Streptococcus zooepidemicus</i> (Group C)		<i>Yersinia enterocolitica</i> group
	<i>Streptococcus equisimilis</i> (Group C/Group G <i>Streptococcus</i>)		<i>Streptomyces somaliensis</i>		<i>Yersinia frederiksenii</i>
			<i>Streptomyces species</i>		<i>Yersinia intermedia</i>
50			<i>Suttonella</i> (<i>Kingella</i>) <i>indologenes</i>		<i>Yersinia intermedius</i>
			<i>Tatumella ptyseos</i>	175	<i>Yersinia kristensenii</i>
					<i>Yersinia pestis</i>
					<i>Yersinia pseudotuberculosis</i>
					<i>Yersinia pseudotuberculosis</i> SF
55					<i>Yersinia ruckeri</i>
					<i>Yersinia species</i>
					<i>Yokenella regensburgei</i>
					<i>Yokenella regensburgei</i> (<i>Koserella trabulsii</i>)
					<i>Zygoascus hellenicus</i>
					<i>Zygosaccharomyces</i> species

Figure 1: *atpD* sequences databases and main subsets.

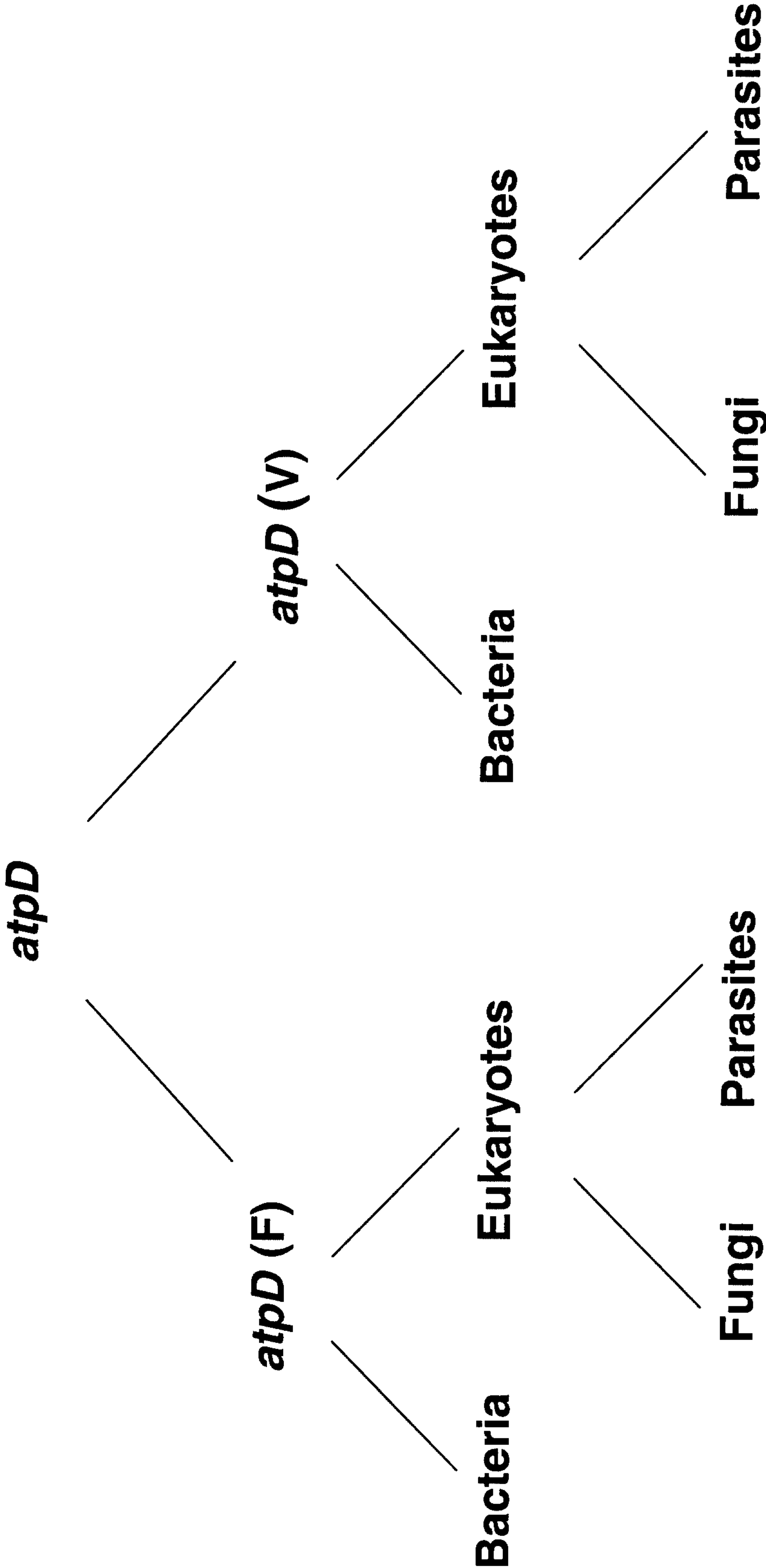
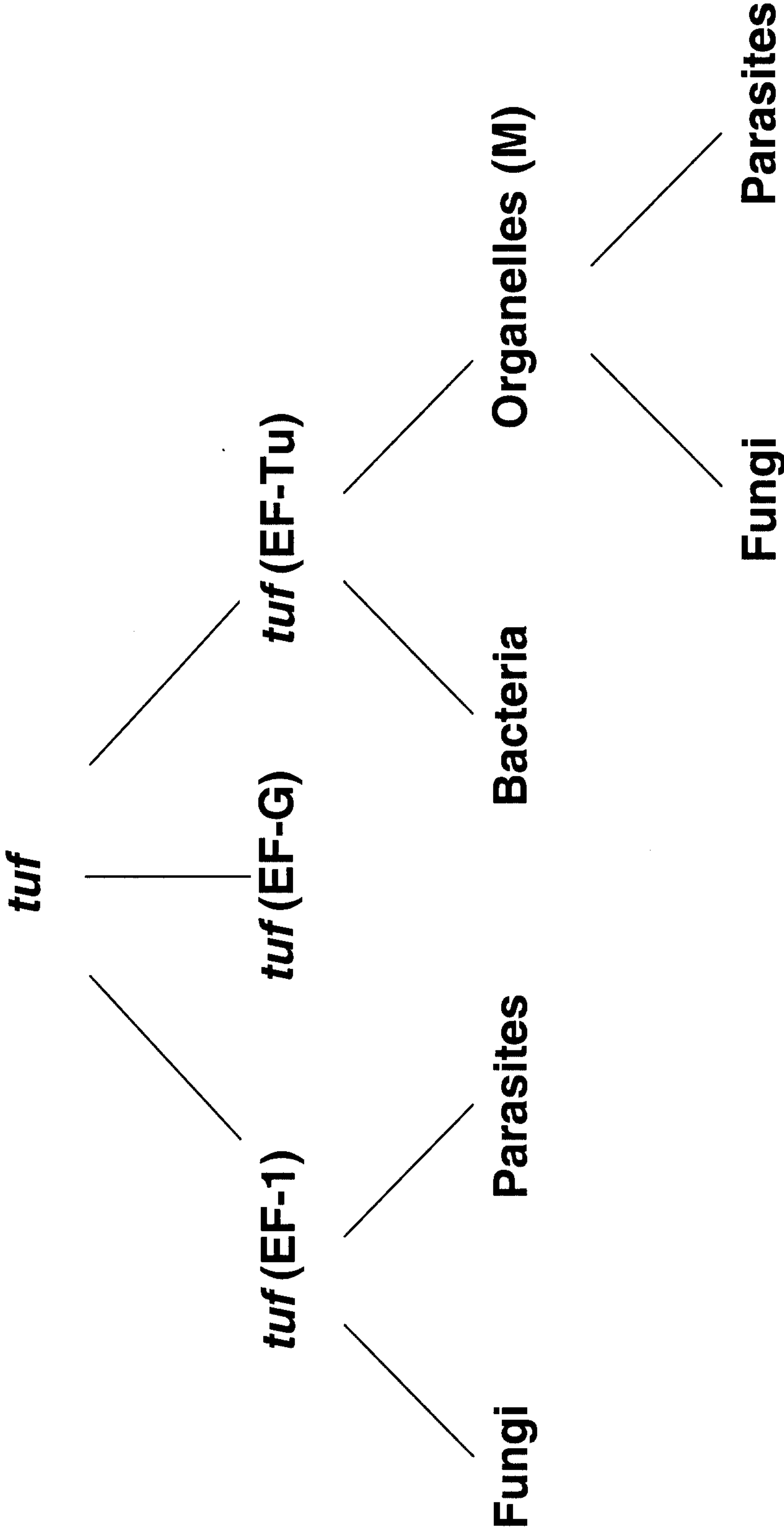


Figure 2: *tuf* sequences databases and main subsets.



Annex I: Specific and ubiquitous primers for nucleic acid amplification (*tuf* sequences).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Bacterial species: <i>Chlamydia pneumoniae</i>			
	630	5'-CGG AGC TAT CCT AGT CGT TTC A	20	2-23
	629 ^a	5'-AAG TTC CAT CTC AAC AAG GTC AAT A	20	146-170
15	Bacterial species: <i>Chlamydia trachomatis</i>			
	554	5'-GTT CCT TAC ATC GTT GTT TTT CTC	22	82-105
	555 ^a	5'-TCT CGA ACT TTC TCT ATG TAT GCA	22	249-272
20	Parasitical species: <i>Cryptosporidium parvum</i>			
	798	5'-TGG TTG TCC CAG CCG ATC GTT T	865	158-179
	804 ^a	5'-CCT GGG ACG GCC TCT GGC AT	865	664-683
25	799	5'-ACC TGT GAA TAC AAG CAA TCT	865	280-300
	805 ^a	5'-CTC TTG TCC ATC TTA GCA GT	865	895-914
	800	5'-GAT GAA ATC TTC AAC GAA GTT GAT	865	307-330
	806 ^a	5'-AGC ATC ACC AGA CTT GAT AAG	865	946-966
30	801	5'-ACA ACA CCG AGA AGA TCC CA	865	353-372
	803 ^a	5'-ACT TCA GTG GTA ACA CCA GC	865	616-635
	802	5'-TTG CCA TTT CTG GTT TCG TT	865	377-396
35	807 ^a	5'-AAA GTG GCT TCA AAG GTT GC	865	981-1000
	Bacterial species: <i>Neisseria gonorrhoeae</i>			
	551	5'-GAA GAA AAA ATC TTC GAA CTG GCT A	126	256-280
40	552 ^a	5'-TAC ACG GCC GGT GAC TAC G	126	378-396
	Bacterial species: <i>Streptococcus agalactiae</i>			
	549	5'-GAA CGT GAT ACT GAC AAA CCT TTA	207-210 ^b	308-331 ^c
45	550 ^a	5'-GAA GAA GAA CAC CAA CGT TG	207-210 ^b	520-539 ^c
	Bacterial species: <i>Streptococcus pyogenes</i>			
	999	5'-TTG ACC TTG TTG ATG ACG AAG AG	1002	143-165
50	1000 ^a	5'-TTA GTG TGT GGG TTG ATT GAA CT	1002	622-644
	1001	5'-AAG AGT TGC TTG AAT TAG TTG AG	1002	161-183
	1000 ^a	5'-TTA GTG TGT GGG TTG ATT GAA CT	1002	622-644

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

^b These sequences were aligned to derive the corresponding primer.

60 ^c The nucleotide positions refer to the *S. agalactiae tuf* sequence fragment (SEQ ID NO. 209).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (*tuf* sequences) (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Parasitical species:</u> <i>Trypanosoma brucei</i>			
	820	5'-GAA GGA GGT GTC TGC TTA CAC	864	513-533
	821 ^a	5'-GGC GCA AAC GTC ACC ACA TCA	864	789-809
15	820	5'-GAA GGA GGT GTC TGC TTA CAC	864	513-533
	822 ^a	5'-CGG CGG ATG TCC TTA ACA GAA	864	909-929
	<u>Parasitical species:</u> <i>Trypanosoma cruzi</i>			
20	794	5'-GAC GAC AAG TCG GTG AAC TT	840-842 ^b	281-300 ^c
	795 ^a	5'-ACT TGC ACG CGA TGT GGC AG	840-842 ^b	874-893 ^c
	<u>Bacterial genus:</u> <i>Bordetella sp.</i>			
25	825	5'-ATG AGC ARC GSA ACC ATC GTT CAG TG	863	1-26
	826	5'-TCG ATC GTG CCG ACC ATG TAG AAC GC	863	1342-1367
	<u>Fungal genus:</u> <i>Candida sp.</i>			
30	576	5'-AAC TTC RTC AAG AAG GTY GGT TAC AA	407-426, 428-432 ^b	332-357 ^d
	632 ^a	5'-CCC TTT GGT GGR TCS TKC TTG GA	407-426, 428-432 ^b	791-813 ^d
35	631	5'-CAG ACC AAC YGA IAA RCC ATT RAG AT	407-426, 428-432 ^b	523-548 ^d
	632 ^a	5'-CCC TTT GGT GGR TCS TKC TTG GA	407-426, 428-432 ^b	791-813 ^d
40	633	5'-CAG ACC AAC YGA IAA RCC ITT RAG AT	407-426, 428-432 ^b	523-548 ^d
	632 ^a	5'-CCC TTT GGT GGR TCS TKC TTG GA	407-426, 428-432 ^b	791-813 ^d

- 45
- a These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.
- b These sequences were aligned to derive the corresponding primer.
- 50 c The nucleotide positions refer to the *T. cruzi tuf* sequence fragment (SEQ ID NO. 842).
- d The nucleotide positions refer to the *C. albicans tuf*(EF-1) sequence fragment (SEQ ID NO. 408).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (*tuf* sequences) (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial genus:</u> <i>Clostridium</i> sp.			
	796	5'-GGT CCA ATG CCW CAA ACW AGA	32,719-724,736 ^a	32-52 ^b
15	797 ^c	5'-CAT TAA GAA TGG YTT ATC TGT SKC TCT	32,719-724,736 ^a	320-346 ^b
	808	5'-GCI TTA IWR GCA TTA GAA RAY CCA	32,719-724,736 ^a	224-247 ^b
	809 ^c	5'-TCT TCC TGT WGC AAC TGT TCC TCT	32,719-724,736 ^a	337-360 ^b
20	810	5'-AGA GMW ACA GAT AAR SCA TTC TTA	32,719-724,736 ^a	320-343 ^b
	811 ^c	5'-TRA ART AGA ATT GTG GTC TRT ATC C	32,719-724,736 ^a	686-710 ^b
25	<u>Bacterial genus:</u> <i>Corynebacterium</i> sp.			
	545	5'-TAC ATC CTB GTY GCI CTI AAC AAG TG	34-44,662 ^a	89-114 ^d
30	546 ^c	5'-CCR CGI CCG GTR ATG GTG AAG AT	34-44,662 ^a	350-372 ^d
	<u>Parasitical genus:</u> <i>Entamoeba</i> sp.			
	703	5'-TAT GGA AAT TCG AAA CAT CT	512	38-57
35	704 ^c	5'-AGT GCT CCA ATT AAT GTT GG	512	442-461
	703	5'-TAT GGA AAT TCG AAA CAT CT	512	38-57
	705 ^c	5'-GTA CAG TTC CAA TAC CTG AA	512	534-553
40	703	5'-TAT GGA AAT TCG AAA CAT CT	512	38-57
	706 ^c	5'-TGA AAT CTT CAC ATC CAA CA	512	768-787
	793	5'-TTA TTG TTG CTG CTG GTA CT	512	149-168
	704 ^c	5'-AGT GCT CCA ATT AAT GTT GG	512	442-461

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^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *C. perfringens tuf* sequence fragment (SEQ ID NO. 32).

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

^d The nucleotide positions refer to the *C. diphtheriae tuf* sequence fragment (SEQ ID NO. 662).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (*tuf* sequences) (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial genus:</u> <i>Enterococcus</i> sp.			
	656	5'-AAT TAA TGG CTG CAG TTG AYG A	58-72 ^a	273-294 ^b
	657 ^c	5'-TTG TCC ACG TTC GAT RTC TTC A	58-72 ^a	556-577 ^b
15	656	5'-AAT TAA TGG CTG CAG TTG AYG A	58-72 ^a	273-294 ^b
	271 ^c	5'-TTG TCC ACG TTG GAT RTC TTC A	58-72 ^a	556-577 ^b
	1137	5'-AAT TAA TGG CTG CWG TTG AYG AA	58-72 ^a	273-295 ^b
20	1136 ^c	5'-ACT TGT CCA CGT TSG ATR TCT	58-72 ^a	559-579 ^b
	<u>Parasitical genus:</u> <i>Giardia</i> sp.			
	816	5'-GCT ACG ACG AGA TCA AGG GC	513	305-324
25	819 ^c	5'-TCG AGC TTC TGG AGG AAG AG	513	895-914
	817	5'-TGG AAG AAG GCC GAG GAG TT	513	355-374
	818 ^c	5'-AGC CGG GCT GGA TCT TCT TC	513	825-844
30	<u>Parasitical genus:</u> <i>Leishmania</i> sp.			
	701	5'-GTG TTC ACG ATC ATC GAT GCG	514-526 ^a	94-114 ^d
	702 ^c	5'-CTC TCG ATA TCC GCG AAG CG	514-526 ^a	913-932 ^d
35	<u>Bacterial genus:</u> <i>Staphylococcus</i> sp.			
	553	5'-GGC CGT GTT GAA CGT GGT CAA ATC A	176-203 ^a	313-337 ^e
	575 ^c	5'-TIA CCA TTT CAG TAC CTT CTG GTA A	176-203 ^a	653-677 ^e
40	553	5'-GGC CGT GTT GAA CGT GGT CAA ATC A	176-203 ^a	313-337 ^e
	707 ^c	5'-TWA CCA TTT CAG TAC CTT CTG GTA A	176-203 ^a	653-677 ^e
	<u>Bacterial genus:</u> <i>Streptococcus</i> sp.			
45	547	5'-GTA CAG TTG CTT CAG GAC GTA TC	206-231 ^a	372-394 ^f
	548 ^c	5'-ACG TTC GAT TTC ATC ACG TTG	206-231 ^a	548-568 ^f

^a These sequences were aligned to derive the corresponding primer.

50 ^b The nucleotide positions refer to the *E. durans tuf* sequence fragment (SEQ ID NO. 61).

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

^d The nucleotide positions refer to the *L. tropica tuf*(EF-1) sequence fragment (SEQ ID NO. 526).

55 ^e The nucleotide positions refer to the *S. aureus tuf* sequence fragment (SEQ ID NO. 179).

^f The nucleotide positions refer to the *S. agalactiae tuf* sequence fragment (SEQ ID NO. 209).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (*tuf* sequences) (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Parasitical genus:</u> <i>Trypanosoma</i> sp.			
	823	5'-GAG CGG TAT GAY GAG ATT GT	529,840-842,864 ^a	493-512 ^b
15	824 ^c	5'-GGC TTC TGC GGC ACC ATG CG	529,840-842,864 ^a	1171-1190 ^b
	<u>Bacterial family:</u> <i>Mycobacteriaceae</i>			
	539	5'-CCI TAC ATC CTB GTY GCI CTI AAC AAG	122	85-111
20	540 ^c	5'-GGD GCI TCY TCR TCG WAI TCC TG	122	181-203
	<u>Bacterial group:</u> <i>Enterobacteriaceae</i> group			
25	933	5'-CAT CAT CGT ITT CMT GAA CAA RTG	78,103,146, 168,238,698 ^a	390-413 ^d
	934 ^c	5'-TCA CGY TTR RTA CCA CGC AGI AGA	78,103,146, 168,238,698 ^a	831-854 ^d
30	<u>Parasitical family:</u> <i>Trypanosomatidae</i> family			
	923	5'-GAC GCI GCC ATC CTG ATG ATC	511,514-526, 529,840-842, 864 ^a	166-188 ^e
35	924 ^c	5'-ACC TCA GTC GTC ACG TTG GCG	511,514-526, 529,840-842, 864 ^a	648-668 ^e
	925	5'-AAG CAG ATG GTT GTG TGC TG	511,514-526, 529,840-842, 864 ^a	274-293 ^e
40	926 ^c	5'-CAG CTG CTC GTG GTG CAT CTC GAT	511,514-526, 529,840-842, 864 ^a	676-699 ^e

- 45
- a These sequences were aligned to derive the corresponding primer.
- b The nucleotide positions refer to the *T. brucei tuf* (EF-1) sequence fragment (SEQ ID NO. 864).
- 50 c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.
- d The nucleotide positions refer to the *E. coli tuf* sequence fragment (SEQ ID NO. 698).
- e The nucleotide positions refer to the *L. tropica tuf* sequence fragment (SEQ ID NO. 526).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (*tuf* sequences) (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Parasitical family:</u> <i>Trypanosomatidae</i> family (continued)			
	927	5'-ACG CGG AGA AGG TGC GCT T	511,514-526, 529,840-842, 864 ^a	389-407 ^b
15	928 ^c	5'-GGT CGT TCT TCG AGT CAC CGC A	511,514-526, 529,840-842, 864 ^a	778-799 ^b
20	<u>Bacterial group:</u> <i>Pseudomonads</i> group			
	541	5'-GTK GAA ATG TTC CGC AAG CTG CT	153-155 ^a	476-498 ^d
	542 ^c	5'-CGG AAR TAG AAC TGS GGA CGG TAG	153-155 ^a	679-702 ^d
	541	5'-GTK GAA ATG TTC CGC AAG CTG CT	153-155 ^a	476-498 ^d
25	544 ^c	5'-AYG TTG TCG CCM GGC ATT MCC AT	153-155 ^a	749-771 ^d
	Universal primers			
30	636	5'-ACT GGY GTT GAI ATG TTC CGY AA	7,54,78, 100,103,159, 209,224,227 ^b	470-492 ^e
	637 ^a	5'-ACG TCA GTI GTA CGG AAR TAG AA	7,54,78, 100,103,159, 209,224,227 ^b	692-714 ^e
35	638	5'-CCA ATG CCA CAA ACI CGT GAR CAC AT	7,54,78, 100,103,159, 209,224,227 ^b	35-60 ^f
40	639 ^a	5'-TTT ACG GAA CAT TTC WAC ACC WGT IAC A	7,54,78, 100,103,159, 209,224,227 ^b	469-496 ^f

^a These sequences were aligned to derive the corresponding primer.

45 ^b The nucleotide positions refer to the *L. tropica tuf* (EF-1) sequence fragment (SEQ ID NO. 526).

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

50 ^d The nucleotide positions refer to the *P. aeruginosa tuf* sequence fragment (SEQ ID NO. 153).

^e The nucleotide positions refer to the *E. coli tuf* sequence fragment (SEQ ID NO. 78).

^f The nucleotide positions refer to the *B. cereus tuf* sequence fragment (SEQ ID NO. 7).

Annex I: Specific and ubiquitous primers for nucleic acid amplification (*tuf* sequences) (continued).

5	SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
			SEQ ID NO.	Nucleotide position
10	643	5'-ACT GGI GTI GAR ATG TTC CGY AA	1,3,4,7,12, 13,16,49,54, 72,78,85,88, 91,94,98,103, 108,112,115, 116,120,121, 126,128,134, 136,146,154, 159,179,186, 205,209,212, 224,238 ^a	470-492 ^b
15				
20	644 ^c	5'-ACG TCI GTI GTI CKG AAR TAG AA	1,3,4,7,12, 13,16,49,54, 72,78,85,88, 91,94,98,103, 108,112,115, 116,120,121, 126,128,134, 136,146,154, 159,179,186, 205,209,212, 224,238 ^a	692-714 ^b
25				
30				

^a These sequences were aligned to derive the corresponding primer.

35 ^b The nucleotide positions refer to the *E. coli tuf* sequence fragment (SEQ ID NO. 78).

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

Annex I: Specific and ubiquitous primers for nucleic acid amplification (*tuf* sequences) (continued).

5	SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
			SEQ ID NO.	Nucleotide position
10	643	5'-ACT GGI GTI GAR ATG TTC CGY AA	1,3,4,7,12, 13,16,49,54, 72,78,85,88, 91,94,98,103, 108,112,115, 116,120,121, 126,128,134, 136,146,154, 159,179,186, 205,209,212, 224,238 ^a	470-492 ^b
15				
20	645 ^c	5'-ACG TCI GTI GTI CKG AAR TAR AA	1,3,4,7,12, 13,16,49,54, 72,78,85,88, 91,94,98,103, 108,112,115, 116,120,121, 126,128,134, 136,146,154, 159,179,186, 205,209,212, 224,238 ^a	692-714 ^b
25				
30				
	646	5'-ATC GAC AAG CCI TTC YTI ATG SC	2,13,82 122,145 ^a	317-339 ^d
35	647 ^c	5'-ACG TCC GTS GTR CGG AAG TAG AAC TG	2,13,82 122,145 ^a	686-711 ^d
	646	5'-ATC GAC AAG CCI TTC YTI ATG SC	2,13,82 122,145 ^a	317-339 ^d
40	648 ^c	5'-ACG TCS GTS GTR CGG AAG TAG AAC TG	2,13,82 122,145 ^a	686-711 ^d

45 ^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *E. coli tuf* sequence fragment (SEQ ID NO. 78).

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

50 ^d The nucleotide positions refer to the *A. meyeri tuf* sequence fragment (SEQ ID NO. 2)

Annex I: Specific and ubiquitous primers for nucleic acid amplification (*tuf* sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Universal primers (continued)			
	649	5'-GTC CTA TGC CTC ARA CWC GIG AGC AC	8,86,141,143 ^a	33-58 ^b
	650 ^c	5'-TTA CGG AAC ATY TCA ACA CCI GT	8,86,141,143 ^a	473-495 ^b
15	636	5'-ACT GGY GTT GAI ATG TTC CGY AA	8,86,141,143 ^a	473-495 ^b
	651 ^c	5'-TGA CGA CCA CCI TCY TCY TTY TTC A	8,86,141,143 ^a	639-663 ^b
	Sequencing primers			
20	556	5'-CGG CGC NAT CYT SGT TGT TGC	668 ^d	306-326
	557 ^c	5'-CCM AGG CAT RAC CAT CTC GGT G	668 ^d	1047-1068
	694	5'-CGG CGC IAT CYT SGT TGT TGC	668 ^d	306-326
	557 ^c	5'-CCM AGG CAT RAC CAT CTC GGT G	668 ^d	1047-1068
25	664	5'-AAY ATG ATI ACI GGI GCI GCI CAR ATG GA	619 ^d	604-632
	652 ^c	5'-CCW AYA GTI YKI CCI CCY TCY CTI ATA	619 ^d	1482-1508
30	664	5'-AAY ATG ATI ACI GGI GCI GCI CAR ATG GA	619 ^d	604-632
	561 ^c	5'-ACI GTI CGG CCR CCC TCA CGG AT	619 ^d	1483-1505
	543	5'-ATC TTA GTA GTT TCT GCT GCT GA	607	8-30
	660 ^c	5'-GTA GAA TTG AGG ACG GTA GTT AG	607	678-700
35	658	5'-GAT YTA GTC GAT GAT GAA GAA TT	621	116-138
	659 ^c	5'-GCT TTT TGI GTT TCW GGT TTR AT	621	443-465
	658	5'-GAT YTA GTC GAT GAT GAA GAA TT	621	116-138
	661 ^c	5'-GTA GAA YTG TGG WCG ATA RTT RT	621	678-700
40	558	5'-TCI TTY AAR TAY GCI TGG GT	665 ^d	157-176
	559 ^c	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^d	1279-1301
45	813	5'-AAT CYG TYG AAA TGC AYC ACG A	665 ^d	687-708
	559 ^c	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^d	1279-1301

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *B. distasonis tuf* sequence fragment (SEQ ID NO. 8).

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

^d Sequences from databases.

Annex I: Specific and ubiquitous primers for nucleic acid amplification (*tuf* sequences) (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Sequencing primers (continued)			
	558	5'-TCI TTY AAR TAY GCI TGG GT	665 ^a	157-176
	815 ^b	5'-TGG TGC ATY TCK ACR GAC TT	665 ^a	686-705
15	560	5'-GAY TTC ATY AAR AAY ATG ATY AC	665 ^a	289-311
	559 ^b	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^a	1279-1301
	653	5'-GAY TTC ATI AAR AAY ATG AT	665 ^a	289-308
	559 ^b	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^a	1279-1301
20	558	5'-TCI TTY AAR TAY GCI TGG GT	665 ^a	157-176
	655 ^b	5'-CCR ATA CCI CMR ATY TTG TA	665 ^a	754-773
	654	5'-TAC AAR ATY KGI GGT ATY GG	665 ^a	754-773
25	559 ^b	5'-CCG ACR GCR AYI GTY TGI CKC AT	665 ^a	1279-1301
	696	5'-ATI GGI CAY RTI GAY CAY GGI AAR AC	698 ^a	52-77
	697 ^b	5'-CCI ACI GTI CKI CCR CCY TCR CG	698 ^a	1132-1154
30	911	5'-GAC GGM KKC ATG CCG CAR AC	853	22-41
	914 ^b	5'-GAA RAG CTG CGG RCG RTA GTG	853	700-720
	912	5'-GAC GGC GKC ATG CCG CAR AC	846	20-39
	914 ^b	5'-GAA RAG CTG CGG RCG RTA GTG	846	692-712
35	913	5'-GAC GGY SYC ATG CCK CAG AC	843	251-270
	915 ^b	5'-AAA CGC CTG AGG RCG GTA GTT	843	905-925
	916	5'-GCC GAG CTG GCC GGC TTC AG	846	422-441
40	561 ^b	5'-ACI GTI CGG CCR CCC TCA CGG AT	619 ^a	1483-1505
	664	5'-AAY ATG ATI ACI GGI GCI GCI CAR ATG GA	619 ^a	604-632
	917 ^b	5'-TCG TGC TAC CCG TYG CCG CCA T	846	593-614

45

^a Sequences from databases.

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

Annex I: Specific and ubiquitous primers for nucleic acid amplification (*tuf* sequences) (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Sequencing primers (continued)			
	1221	5'-GAY ACI CCI GGI CAY GTI GAY TT	1230 ^a	292-314
	1226 ^b	5'-GTI RMR TAI CCR AAC ATY TC	1230 ^a	2014-2033
15	1222	5'-ATY GAY ACI CCI GGI CAY GTI GAY TT	1230 ^a	289-314
	1223 ^b	5'-AYI TCI ARR TGI ARY TCR CCC ATI CC	1230 ^a	1408-1433
	1224	5'-CCI GYI HTI YTI GAR CCI ATI ATG	1230 ^a	1858-1881
	1225 ^b	5'-TAI CCR AAC ATY TCI SMI ARI GGI AC	1230 ^a	2002-2027
20	1227	5'-GTI CCI YTI KCI GAR ATG TTY GGI TA	1230 ^a	2002-2027
	1229 ^b	5'-TCC ATY TGI GCI GCI CCI GTI ATC AT	698 ^a	4-29
	1228	5'-GTI CCI YTI KCI GAR ATG TTY GGI TAY GC	1230 ^a	2002-2030
25	1229 ^b	5'-TCC ATY TGI GCI GCI CCI GTI ATC AT	698 ^a	4-29

^a Sequences from databases.

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

Annex II: Specific and ubiquitous primers for nucleic acid amplification (*atpD* sequences).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial species:</u> <i>Streptococcus agalactiae</i>			
	627	5'-ATT GTC TAT AAA AAT GGC GAT AAG TC	379-383 ^a	42-67 ^b
	625 ^c	5'-CGT TGA AGA CAC GAC CCA AAG TAT CC	379-383 ^a	206-231 ^b
15	628	5'-AAA ATG GCG ATA AGT CAC AAA AAG TA	379-383 ^a	52-77 ^b
	625 ^c	5'-CGT TGA AGA CAC GAC CCA AAG TAT CC	379-383 ^a	206-231 ^b
	627	5'-ATT GTC TAT AAA AAT GGC GAT AAG TC	379-383 ^a	42-67 ^b
20	626 ^c	5'-TAC CAC CTT TTA AGT AAG GTG CTA AT	379-383 ^a	371-396 ^b
	628	5'-AAA ATG GCG ATA AGT CAC AAA AAG TA	379-383 ^a	52-77 ^b
	626 ^c	5'-TAC CAC CTT TTA AGT AAG GTG CTA AT	379-383 ^a	371-396 ^b
25	<u>Bacterial genus:</u> <i>Candida sp.</i>			
	634	5'-AAC ACY GTC AGR RCI ATT GCY ATG GA	460-472, 474-478 ^a	101-126 ^d
	635 ^c	5'-AAA CCR GTI ARR GCR ACT CTI GCT CT	460-472, 474-478 ^a	617-642 ^d
30				

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *S. agalactiae atpD* sequence fragment (SEQ ID NO. 380).

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

^d The nucleotide positions refer to the *C. albicans atpD* sequence fragment (SEQ ID NO. 460).

Annex II: Specific and ubiquitous primers for nucleic acid amplification (*atpD* sequences) (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Universal primers			
15	562	5'-CAR ATG RAY GAR CCI CCI GGI GYI MGI ATG	243,244,262, 264,280,284, 291,297,309, 311,315,317, 324,329,332, 334-336,339, 342,343,351, 356,357,364-366,370,375, 379,393 ^a	528-557 ^b
20	563 ^c	5'-GGY TGR TAI CCI ACI GCI GAI GGC AT	243,244,262, 264,280,284, 291,297,309, 311,315,317, 324,329,332, 334-336,339, 342,343,351, 356,357,364-366,370,375, 379,393 ^a	687-712 ^b
25				
30	564	5'-TAY GGI CAR ATG AAY GAR CCI CCI GGI AA	243,244,262, 264,280,284, 291,297,309, 311,315,317, 324,329,332, 334-336,339, 342,343,351, 356,357,364-366,370,375, 379,393 ^a	522-550 ^b
35				
40				
45	565 ^c	5'-GGY TGR TAI CCI ACI GCI GAI GGD AT	243,244,262, 264,280,284, 291,297,309, 311,315,317, 324,329,332, 334-336,339, 342,343,351, 356,357,364-366,370,375, 379,393 ^a	687-712 ^b
50				

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *K. pneumoniae atpD* sequence fragment (SEQ ID NO. 317).

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

Annex II: Specific and ubiquitous primers for nucleic acid amplification (*atpD* sequences) (continued).

			Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Universal primers (continued)			
	640	5'-TCC ATG GTI TWY GGI CAR ATG AA	248,284,315, 317,343,357, 366,370,379,393 ^a	513-535 ^b
15	641 ^c	5'-TGA TAA CCW ACI GCI GAI GGC ATA CG	248,284,315, 317,343,357, 366,370,379,393 ^a	684-709 ^b
20	642	5'-GGC GTI GGI GAR CGI ACI CGT GA	248,284,315, 317,343,357, 366,370,379,393 ^a	438-460 ^b
	641 ^c	5'-TGA TAA CCW ACI GCI GAI GGC ATA CG	248,284,315, 317,343,357, 366,370,379,393 ^a	684-709 ^b
25	Sequencing primers			
	566	5'-TTY GGI GGI GCI GGI GTI GGI AAR AC	669 ^d	445-470
	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
30	566	5'-TTY GGI GGI GCI GGI GTI GGI AAR AC	669 ^d	445-470
	814	5'-GCI GGC ACG TAC ACI GCC TG	666 ^d	901-920
	568	5'-RTI ATI GGI GCI GTI RTI GAY GT	669 ^d	25-47
35	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
	570	5'-RTI RYI GGI CCI GTI RTI GAY GT	672 ^d	31-53
	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
	572	5'-RTI RTI GGI SCI GTI RTI GA	669 ^d	25-44
40	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
	569	5'-RTI RTI GGI SCI GTI RTI GAT AT	671 ^d	31-53
	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908
45	571	5'-RTI RTI GGI CCI GTI RTI GAT GT	670 ^d	31-53
	567 ^c	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^d	883-908

^a These sequences were aligned to derive the corresponding primer.

50 ^b The nucleotide positions refer to the *K. pneumoniae atpD* sequence fragment (SEQ ID NO. 317).

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

^d Sequences from databases.

Annex II: Specific and ubiquitous primers for nucleic acid amplification (*atpD* sequences) (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Sequencing primers (continued)			
	700	5'-TIR TIG AYG TCG ART TCC CTC ARG	669 ^a	38-61
	567 ^b	5'-TCR TCI GCI GGI ACR TAI AYI GCY TG	669 ^a	883-908
15	568	5'-RTI ATI GGI GCI GTI RTI GAY GT	669 ^a	25-47
	573 ^b	5'-CCI CCI ACC ATR TAR AAI GC	666 ^a	1465-1484
	574	5'-ATI GCI ATG GAY GGI ACI GAR GG	666 ^a	283-305
	573 ^b	5'-CCI CCI ACC ATR TAR AAI GC	666 ^a	1465-1484
20	574	5'-ATI GCI ATG GAY GGI ACI GAR GG	666 ^a	283-305
	708 ^b	5'-TCR TCC ATI CCI ARI ATI GCI ATI AT	666 ^a	1258-1283
	681	5'-GGI SSI TTY GGI ISI GGI AAR AC	685	694-716
25	682 ^b	5'-GTI ACI GGY TCY TCR AAR TTI CCI CC	686	1177-1202
	681	5'-GGI SSI TTY GGI ISI GGI AAR AC	685	694-716
	683 ^b	5'-GTI ACI GGI TCI SWI AWR TCI CCI CC	685	1180-1205
30	681	5'-GGI SSI TTY GGI ISI GGI AAR AC	685	694-716
	699	5'-GTI ACI GGY TCY TYR ARR TTI CCI CC	686	1177-1202
	681	5'-GGI SSI TTY GGI ISI GGI AAR AC	685	694-716
	812 ^b	5'-GTI ACI GGI TCY TYR ARR TTI CCI CC	685	1180-1205
35	1213	5'-AAR GGI GGI ACI GCI GCI ATH CCI GG	714 ^a	697-722
	1212 ^b	5'-CCI CCI RGI GGI GAI ACI GCW CC	714 ^a	1189-1211
	1203	5'-GGI GAR MGI GGI AAY GAR ATG	709 ^a	724-744
40	1207 ^b	5'-CCI TCI TCW CCI GGC ATY TC	709 ^a	985-1004
	1204	5'-GCI AAY AAC ITC IWM YAT GCC	709 ^a	822-842
	1206 ^b	5'-CKI SRI GTI GAR TCI GCC A	709 ^a	926-944
45	1205	5'-AAY ACI TCI AWY ATG CCI GT	709 ^a	826-845
	1207 ^b	5'-CCI TCI TCW CCI GGC ATY TC	709 ^a	985-1004

^a Sequences from databases.

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

Annex III: Internal probes for nucleic acid hybridization and specific detection of *tuf* sequences.

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial species:</u> <i>Candida albicans</i>			
	577	5'-CAT GAT TGA ACC ATC CAC CA	407-411 ^a	406-425 ^b
15	<u>Bacterial species:</u> <i>Candida dubliniensis</i>			
	578	5'-CAT GAT TGA AGC TTC CAC CA	412,414-415 ^a	418-437 ^c
	<u>Bacterial species:</u> <i>Enterococcus faecalis</i>			
20	580	5'-GCT AAA CCA GCT ACA ATC ACT CCA C	62-63,607 ^a	584-608 ^d
	603	5'-GGT ATT AAA GAC GAA ACA TC	62-63,607 ^a	440-459 ^d
	1174	5'-GAA CGT GGT GAA GTT CGC	62-63,607 ^a	398-415 ^d
25	<u>Bacterial species:</u> <i>Enterococcus faecium</i>			
	602	5'-AAG TTG AAG TTG TTG GTA TT	64,608 ^a	426-445 ^e
	<u>Bacterial species:</u> <i>Enterococcus gallinarum</i>			
30	604	5'-GGT GAT GAA GTA GAA ATC GT	66,609 ^a	419-438 ^f
	<u>Bacterial species:</u> <i>Escherichia coli</i>			
35	579	5'-GAA GGC CGT GCT GGT GAG AA	78	503-522

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *C. albicans tuf*(EF-1) sequence fragment (SEQ ID NO. 408).

40 ^c The nucleotide positions refer to the *C. dubliniensis tuf*(EF-1) sequence fragment (SEQ ID NO. 414).

^d The nucleotide positions refer to the *E. faecalis tuf* sequence fragment (SEQ ID NO. 607).

45 ^e The nucleotide positions refer to the *E. faecium tuf* sequence fragment (SEQ ID NO. 608).

^f The nucleotide positions refer to the *E. gallinarum tuf* sequence fragment (SEQ ID NO. 609).

Annex III: Internal probes for nucleic acid hybridization and specific detection of *tuf* sequences (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Bacterial species: <i>Haemophilus influenzae</i>			
	581	5'-ACA TCG GTG CAT TAT TAC GTG G	610 ^a	551-572 ^b
15	Bacterial species: <i>Staphylococcus aureus</i>			
	584	5'-ACA TGA CAC ATC TAA AAC AA	176-180 ^c	369-388 ^d
	585	5'-ACC ACA TAC TGA ATT CAA AG	176-180 ^c	525-544 ^d
	586	5'-CAG AAG TAT ACG TAT TAT CA	176-180 ^c	545-564 ^d
	587	5'-CGT ATT ATC AAA AGA CGA AG	176-180 ^c	555-574 ^d
20	588	5'-TCT TCT CAA ACT ATC GTC CA	176-180 ^c	593-612 ^d
	Bacterial species: <i>Staphylococcus epidermidis</i>			
	589	5'-GCA CGA AAC TTC TAA AAC AA	185,611 ^c	445-464 ^e
25	590	5'-TAT ACG TAT TAT CTA AAG AT	185,611 ^c	627-646 ^e
	591	5'-TCC TGG TTC TAT TAC ACC AC	185,611 ^c	586-605 ^e
	592	5'-CAA AGC TGA AGT ATA CGT AT	185,611 ^c	616-635 ^e
	593	5'-TTC ACT AAC TAT CGC CCA CA	185,611 ^c	671-690 ^e
30	Bacterial species: <i>Staphylococcus haemolyticus</i>			
	594	5'-ATT GGT ATC CAT GAC ACT TC	186,188-190 ^c	437-456 ^f
	595	5'-TTA AAG CAG ACG TAT ACG TT	186,188-190 ^c	615-634 ^f
35	Bacterial species: <i>Staphylococcus hominis</i>			
	596	5'-GAA ATT ATT GGT ATC AAA GA	191,193-196 ^c	431-450 ^g
	597	5'-ATT GGT ATC AAA GAA ACT TC	191,193-196 ^c	437-456 ^g
40	598	5'-AAT TAC ACC TCA CAC AAA AT	191,193-196 ^c	595-614 ^g

^a Sequences from databases.

^b The nucleotide positions refer to the *H. influenzae tuf* sequence fragment (SEQ ID NO. 610).

45 ^c These sequences were aligned to derive the corresponding probe.

^d The nucleotide positions refer to the *S. aureus tuf* sequence fragment (SEQ ID NO. 179).

^e The nucleotide positions refer to the *S. epidermidis tuf* sequence fragment (SEQ ID NO. 611).

50 ^f The nucleotide positions refer to the *S. haemolyticus tuf* sequence fragment (SEQ ID NO. 186).

^g The nucleotide positions refer to the *S. hominis tuf* sequence fragment (SEQ ID NO. 191).

Annex III: Internal probes for nucleic acid hybridization and specific detection of *tuf* sequences (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial species:</u> <i>Staphylococcus saprophyticus</i>			
	599	5'-CGG TGA AGA AAT CGA AAT CA	198-200 ^a	406-425 ^b
	600	5'-ATG CAA GAA GAA TCA AGC AA	198-200 ^a	431-450 ^b
	601	5'-GTT TCA CGT GAT GAT GTA CA	198-200 ^a	536-555 ^b
15	695	5'-GTT TCA CGT GAT GAC GTA CA	198-200 ^a	563-582 ^b
	<u>Bacterial species:</u> <i>Streptococcus agalactiae</i>			
	582 ^c	5'-TTT CAA CTT CGT CGT TGA CAC GAA CAG T	207-210 ^a	404-431 ^d
20	583 ^c	5'-CAA CTG CTT TTT GGA TAT CTT CTT TAA TAC CAA CG	207-210 ^a	433-467 ^d
	1199	5'-GTA TTA AAG AAG ATA TCC AAA AAG C	207-210 ^a	438-462 ^d
	<u>Bacterial species:</u> <i>Streptococcus pneumoniae</i>			
25	1201	5'-TCA AAG AAG AAA CTA AAA AAG CTG T	971,977, 979,986 ^a	513-537 ^e
	<u>Bacterial species:</u> <i>Streptococcus pyogenes</i>			
30	1200	5'-TCA AAG AAG AAA CTA AAA AAG CTG T	1002	473-497
	<u>Bacterial group:</u> <i>Enterococcus casseliflavus-flavescens-gallinarum</i> group			
35	620	5'-ATT GGT GCA TTG CTA CGT	58,65,66 ^a	527-544 ^f
	1122	5'-TGG TGC ATT GCT ACG TGG	58,65,66 ^a	529-546 ^f
	<u>Bacterial genus:</u> <i>Staphylococcus</i> sp.			
40	605	5'-GAA ATG TTC CGT AAA TTA TT	176-203 ^a	403-422 ^g
	606	5'-ATT AGA CTA CGC TGA AGC TG	176-203 ^a	420-439 ^g
	1175	5'-GTT ACT GGT GTA GAA ATG TTC	176-203 ^a	391-411 ^g
	1176	5'-TAC TGG TGT AGA AAT GTT C	176-203 ^a	393-411 ^g

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^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *S. saprophyticus tuf* sequence fragment (SEQ ID NO. 198).

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

^d The nucleotide positions refer to the *S. agalactiae tuf* sequence fragment (SEQ ID NO. 209).

^e The nucleotide positions refer to the *S. pneumoniae tuf* sequence fragment (SEQ ID NO. 986).

55

^f The nucleotide positions refer to the *E. flavescens tuf* sequence fragment (SEQ ID NO. 65).

^g The nucleotide positions refer to the *S. aureus tuf* sequence fragment (SEQ ID NO. 179).

Annex III: Internal probes for nucleic acid hybridization and specific detection of *tuf* sequences.

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial genus:</u> <i>Streptococcus</i> sp.			
	1202	5'-GTG TTG AAA TGT TCC GTA AAC A	206-231,971, 977,979,982-986 ^a	466-487 ^b
15	<u>fungus species:</u> <i>Candida albicans</i>			
	1156	5'-GTT GAA ATG CAT CAC GAA CAA TT	407-412,624 ^a	680-702 ^c
20	<u>fungus species:</u> <i>Candida albicans</i> and <i>tropicalis</i>			
	1160	5'-CGT TTC TGT TAA AGA AAT TAG AAG	407-412, 429,624 ^a	748-771 ^c
25	<u>fungus species:</u> <i>Candida dubliniensis</i>			
	1166	5'-ACG TTA AGA ATG TTT CTG TCA A	414-415 ^a	750-771 ^d
	1168	5'-GAA CAA TTG GTT GAA GGT GT	414-415 ^a	707-726 ^d
30	<u>fungus species:</u> <i>Candida glabrata</i>			
	1158	5'-AAG AGG TAA TGT CTG TGG T	417	781-799
	1159	5'-TGA AGG TTT GCC AGG TGA	417	718-735
35	<u>fungus species:</u> <i>Candida krusei</i>			
	1161	5'-TCC AGG TGA TAA CGT TGG	422	720-737
40	<u>fungus species:</u> <i>Candida lusitaniae</i> and <i>guilliermondii</i>			
	1162	5'-CAA GTC CGT GGA AAT GCA	418,424 ^a	682-699 ^e
45	<u>fungus species:</u> <i>Candida parapsilosis</i>			
	1157	5'-AAG AAC GTT TCA GTT AAG GAA AT	426	749-771
50	<u>fungus species:</u> <i>Candida zeylanoides</i>			
	1165	5'-GGT TTC AAC GTG AAG AAC	432	713-730

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *S. pneumoniae* *tuf* sequence fragment (SEQ ID NO. 986).

^c The nucleotide positions refer to the *C. albicans* *tuf*(EF-1) sequence fragment (SEQ ID NO. 408).

^d The nucleotide positions refer to the *C. dubliniensis* *tuf*(EF-1) sequence fragment (SEQ ID NO. 414).

^e The nucleotide positions refer to the *C. lusitaniae* *tuf*(EF-1) sequence fragment (SEQ ID NO. 424).

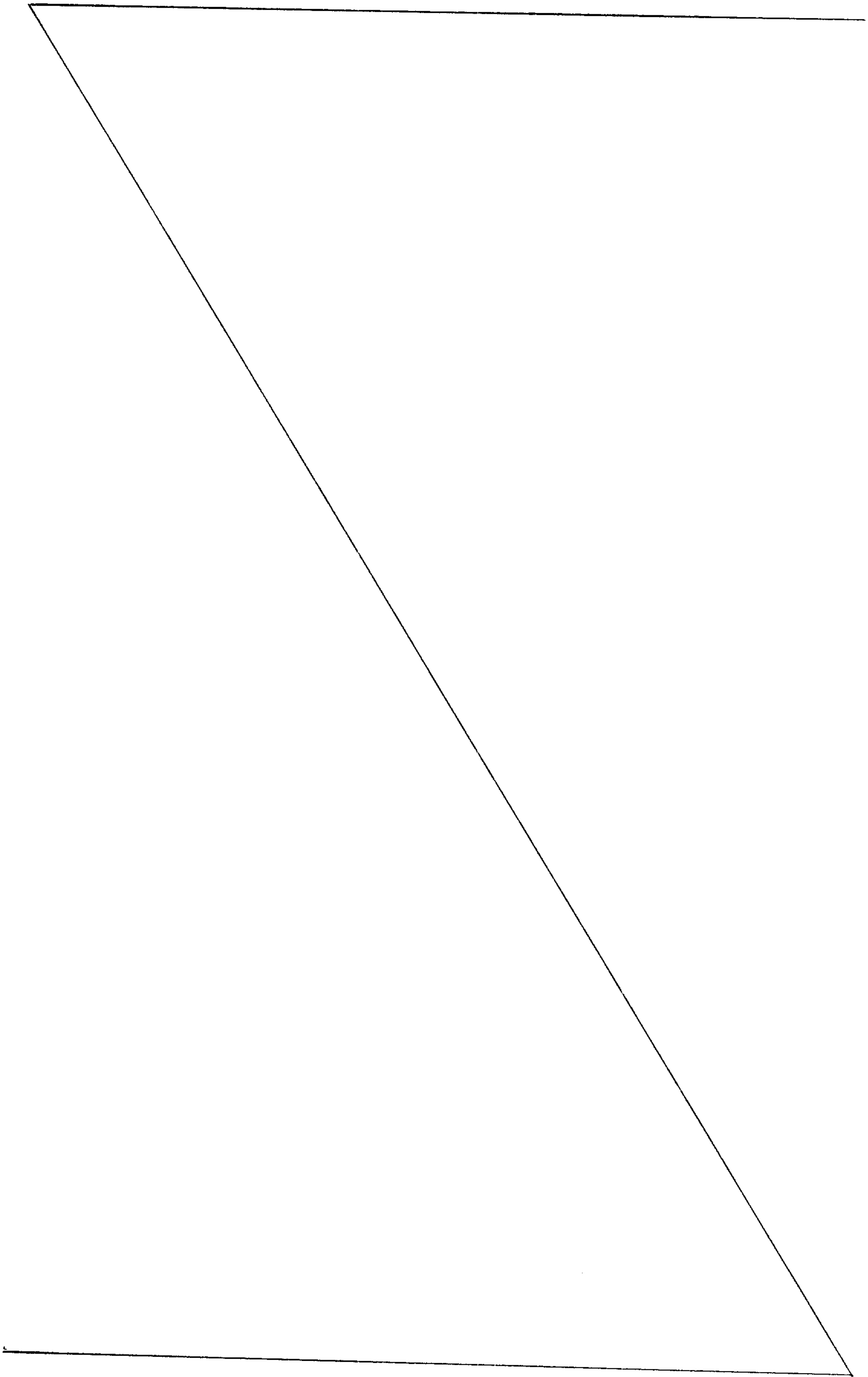
Annex III: Internal probes for nucleic acid hybridization and specific detection of *tuf* sequences (continued).

		Originating DNA fragment	
5	SEQ ID NO.	Nucleotide sequence	SEQ ID NO. Nucleotide position
10	<u>fungal genus:</u> <i>Candida</i> sp.		
	1163	5'-GTT GGT TTC AAC GTT AAG AAC	407-412,414-415,417,418,422,429 ^a 728-748 ^b
15	1164	5'-GGT TTC AAC GTC AAG AAC	413,416,420,421,424,425,426,428,431 ^a 740-757 ^c
20	1167	5'-GTT GGT TTC AAC GT	406-426, 428-432, 624 ^a 728-741 ^b

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *C. albicans tuf*(EF-1) sequence fragment (SEQ ID NO. 408).

^c The nucleotide positions refer to the *C. lusitaniae tuf*(EF-1) sequence fragment (SEQ ID NO. 424).



Annex V: Strategy for the selection of universal amplification/sequencing primers from atpD (V-type) sequences.

5

	691	719	1177	1208	SEQ ID NO.:
<i>E. hirae</i>	CC AGGTCCGTTT	GGTGCAGGGA	AGACAGT...TCTGGTGGAg	ATaTctctGA	ACCAGTGACT CA
<i>H. salinarum</i>	CC GGGCCCGTTC	GGGTCCGGA	AGACGGT...CCCGCGGGG	ACTTctccGA	GCCGGTCACC CA
<i>T. thermophilus</i>	CC TGGGCCCTTC	GGCAGCGGCA	AGACCGT...CCGGCGGCG	ACaTgtccGA	GCCCGTGACC CA
Human	CC TGGGGCCCTTC	GGATGTGGCA	AGACTGT...CCCGGTGGAg	ACTTctcAGA	tCCCCGTGACG AC
<i>T. congolense</i>	CC TGGCGCGTTC	GGATGCCGGA	AGACGGT...CCTGGAGGTg	ACTTTtctGA	cCCAGTGACG TC
<i>P. falciparum</i>	CC TGGTGCAATT	GGTTGTGGAA	AAACTTG...CCAGGTGGTg	ATTTCtctGA	cCCTGTAAC ^a AC
<i>C. pneumoniae</i>	CC AGGACCTTTT	GGTGCAGGGA	AAACAGT...GCAGGAGGAA	ACTTTGAAGA	ACCAGTCACT CA

10

15 Selected sequences for universal primers

GGISSITTY GGIISIGGIA ARAC

681

Selected sequences for universal primers^a

GGIGGIA AYTTYGARGA RCCIGTIAC
GGIGGIG AYWTIWSIGA ICCIGTIAC

682
683

20

The sequence numbering refers to the *Enterococcus hirae atpD* gene fragment (SEQ ID NO. 685). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches for SEQ ID NOs. 681 and 682 are indicated by lower-case letters. Mismatches for SEQ ID NO. 683 are indicated by underlined nucleotides. Dots indicate gaps in the sequences displayed.

25

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

30

^a These sequences are the reverse-complement of the selected primers.

Annex VI: Strategy for the selection of universal amplification/sequencing primers from *tuf* (M) sequences (organelle origin).

	601	635	1479	1511	SEQ ID NO.:	Accession #:
5	<i>C. neoformans</i> ^a	AAGAA CATGATCACC GGTaCctCCC AGgctGACTG...CGCcgtCcGA	GAcAtGcGAC AGAcCgTTGc	CGT	-	U81803
	<i>S. cerevisiae</i> ^a	AAGAA CATGATTACT GGTaCtTtCTC AAgctGACTG...CGCtGtTCAGa	GAcAtGgAGC AAACtGTcGc	TGT	665	X00779
	<i>O. volvulus</i> ^a	AAGAA TATGATCACA GGTaCtTtCTC AGgctGACTG...TGCTgTgTcGt	GAtatGgAGC AAACaGTTGc	GGT	-	M64333
	Human ^a	AAAAA CATGATTACA GGGaCAtCTC AGgctGACTG...TGCTgTtTcGt	GAtatGgAGC AGAcCaGTTGc	TGT	-	X03558
	<i>G. max B1</i> ^b	AAGAA CATGATCACC GGCgCTGCC AGATGGACGG...TGCTATTAGa	GAAGGAGGCA AAACtGTTGG	AGC	-	Y15107
10	<i>G. max B2</i> ^b	AAAAA CATGATCACC GGCgCCGCC AGATGGACGG...TGCTATTAGa	GAAGGAGGCA AAACtGTTGG	AGC	-	Y15108
	<i>E. coli</i> ^c	AAAAA CATGATCACC GGTGCTGCTC AGATGGACGG...CGCaATCcGt	GAAGCGGCC GTACcGTTGG	CGC	78	-
	<i>S. aureofaciens</i> ^c	AAGAA CATGATCACC GGTGCCGCC AGATGGACGG...CGCcATCcGt	GAGGGTGGTc GTACcGTGG	CGC	-	AF007125
	<i>E. tenella</i> ^b	AAAAA TATGATTACA GGAGCAGCAC AAATGGATGG...TGCTATAAGa	GAAGGAGGAA AAACtATAGG	AGC	-	AI755521
	<i>T. gondii</i> ^b	AAGAA TATGATTACT GGAGCCGCAC AAATGGATGG...TGCTATTAGa	GAAGGAGGTC GTACtATAGG	AGC	-	Y11431
15	<i>S. cerevisiae</i> ^b	AAGAA TATGATTACC GGTGCTGCTC AAATGGATGG...CAATATCAGa	GAGGGTGGAA GAAcTGTGG	TAC	619	K00428
	<i>A. thaliana</i> ^b	AAAAA TATGATTACT GGAGCTGCGC AAATGGATGG...TGCCctTAAGG	GAAGGAGGTA GAAcCaGTTGG	AGC	-	X89227

Selected sequence for
universal primer

AA YATGATIACI GGIGCIGCIC ARATGGA

664

Selected sequences
for universal primers

TATIAGR GARGGIGGIM RIACTRTWGG
ATCCGT GAGGGYGGCC GITCIGT

652

561

The sequence numbering refers to the *Saccharomyces cerevisiae tuf* (M) gene (SEQ ID NO. 619). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches for SEQ ID NOS. 652 and 664 are indicated by lower-case letters. Mismatches for SEQ ID NO. 561 are indicated by underlined nucleotides. Dots indicate gaps in the sequences displayed.

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

^a This sequence refers to *tuf*(EF-1) gene.

^b This sequence refers to *tuf* (M) or organelle gene.

^c This sequence refers to *tuf* gene from bacteria.

^d These sequences are the reverse-complement of the selected primers.

Annex VII: Strategy for the selection of eukaryotic sequencing primers from *tuf* (EF-1) sequences.

5		154	179	286	314	SEQ ID NO.:	Accession #:
	<i>S. cerevisiae</i>	GG TTCTTTCAAG	TACGCTTGGG	TTTT...AGAGA	TTTCATCAAG AACATGATTA	665	X00779
	<i>B. hominis</i>	GG CTCCTTCAAG	TACGCGTGGG	TGCT...CGTGA	CTTCATCAAG AACATGATCA	-	D64080
	<i>C. albicans</i>	GG TTCTTTCAAA	TACGCTTGGG	TCTT...AGAGA	TTTCATCAAG AATATGATCA	-	M29934
	<i>C. neoformans</i>	TC TTCTTTCAAG	TACGCTTGGG	TTCT...CGAGA	CTTCATCAAG AACATGATCA	-	U81803
10	<i>E. histolytica</i>	GG ATCATTTCAA	TATGCTTGGG	TCTT...AGAGA	TTTCATTAAG AACATGATTA	-	M92073
	<i>G. lamblia</i>	GG CTCCTTCAAG	TACGCGTGGG	TCCT...CGCGA	CTTCATCAAG AACATGATCA	-	D14342
	<i>H. capsulatum</i>	AA ATCCTTCAA	TATGCGTGGG	TCCT...CGTGA	CTTCATCAAG AACATGATCA	-	U14100
	Human	GG CTCCTTCAAG	TATGCCCTGG	TCTT...AGAGA	CTT ~~E~~ ATCAA AACATGATTA	-	X03558
15	<i>L. braziliensis</i>	GC GTCCTTCAAG	TACGCGTGGG	TGCT...CGCGA	CTTCATCAAG AACATGATCA	-	U72244
	<i>O. volvulus</i>	GG CTCATTTAAA	TATGCTTGGG	TATT...CGTGA	TTTCATTAAG AATATGATCA	-	M64333
	<i>P. berghei</i>	GG TagTTTCAA	TATGCATGGG	TTTT...AAACA	TTT ~~E~~ ATTA AATATGATTA	-	AJ224150
	<i>P. knowlesi</i>	GG AagTTTTAAG	TACGCATGGG	TGTT...AAGGA	TTTCATTA AATATGATTA	-	AJ224153
	<i>S. pombe</i>	GG TTCCCTTCAAG	TACGCCCTGG	TTTT...CGTGA	TTTCATCAAG AACATGATTA	-	U42189
20	<i>T. cruzi</i>	TC TTCTTTCAAG	TACGCGTGGG	TCTT...CGCGA	CTTCATCAAG AACATGATCA	-	L76077
	<i>Y. lipolytica</i>	GG TTCTTTCAAG	TACGCTTGGG	TTCT...CGAGA	TTTCATCAAG AACATGATCA	-	AF054510
	Selected sequences for amplification primers	TCITTYAAR	TAYGCITGGG	T		558	
25				GA YTTCATYAAR	AAAYATGATYA C	560	
				GA YTTCATIAAR	AAAYATGAT	653	

The sequence numbering refers to the *Saccharomyces cerevisiae tuf* (EF-1) gene fragment (SEQ ID NO. 665). Nucleotides in capitals are identical to the selected sequences SEQ ID NOS. 558, 560 or 653, or match those sequences. Mismatches for SEQ ID no. 558 and 560 are indicated by lower-case letters. Mismatches for SEQ ID NO. 653 are indicated by underlined nucleotides. Dots indicate gaps in the sequences displayed.

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

Annex VII: Strategy for the selection of eukaryotic sequencing primers from *tuf* (EF-1) sequences (continued).

5		751	776	1276	1304	SEQ ID NO.:	Accession #:	
	<i>S. cerevisiae</i>	...GTTTACAA	GATCGGTGGT	ATTGGTAC...GACATG	AGACAAACTG	TCGCTGTCGG	TGT	X00779
	<i>B. hominis</i>	...GTGTACAA	GATTGGCGGT	ATTGGTAC...GATATG	AGACAGACTG	TCGCTGTCGG	TAT	D64080
	<i>C. albicans</i>	...GTTTACAA	GATCGGTGGT	ATTGGTAC...GATATG	AGACAAACCG	TTGCTGTtGG	TGT	M29934
	<i>C. neoformans</i>	...GTCTACAA	GATCGGTGGT	ATCGGCAC...GACATG	CGACAGACCG	TTGCCGTtGG	TGT	U81803
10	<i>E. histolytica</i>	...GTTTACAA	GATTTCAGGT	ATTGGAAC...GATATG	AaACAAACCG	TTGCTGTtGG	AGT	M92073
	<i>G. lamblia</i>	...GTCTACAA	GATCTcGGGc	gTCGGGAC...~~~~~	~~~~~	~~~~~	~~~~~	D14342
	<i>H. capsulatum</i>	...GTGTACAA	AATCTcTGGT	ATTGGCAC...GACATG	AGACAAACCG	TCGCTGTCGG	TGT	U14100
	Human	...GTCTACAA	AATTGGTGGT	ATTGGTAC...GATATG	AGACAGACAG	TTGCGgGTgGG	TGT	X03558
	<i>L. braziliensis</i>	...GTGTACAA	GATCGGCGGT	ATCGGCAC...GACATG	CGCagAACGG	TCGCCGTcGG	CAT	U72244
15	<i>O. volvulus</i>	...GTTTACAA	AATTGGAGGT	ATTGGAAC...GATATG	AGACAAACAG	TTGCTGTtGG	CGT	M64333
	<i>P. berghei</i>	...GTATACAA	AATTGGTGGT	ATTGGTAC...GATATG	AGACAAACAA	TTGCTGTcGG	TAT	AJ224150
	<i>P. knowlesi</i>	...GTATACAA	AATCGGTGGT	ATTGGTAC...GATATG	AGACAAACCA	TTGCTGTcGG	TAT	AJ224153
	<i>S. pombe</i>	...GTTTACAA	GATCGGTGGT	ATTGGTAC...GACATG	CGTCAAAACCG	TCGCTGTcGG	TGT	U42189
	<i>T. cruzi</i>	...GTGTACAA	GATCGGCGGT	ATCGGCAC...GACATG	CGCCAGACGG	TCGCCGTcGG	CAT	L76077
20	<i>Y. lipolytica</i>	...GTCTACAA	GATCGGTGGT	ATCGGCAC...GACATG	CGACAGACCG	TTGCTGTcGG	TGT	AF054510

Selected sequence for
amplification primer

TACAA RATYKGIGGT ATYGG

654

Selected sequences for
amplification primers^a

TACAA RATYKGIGGT ATYGG

655

ATG MGICARACIR TYGcYGTcGG

559

The sequence numbering refers to the *Saccharomyces cerevisiae tuf* (EF-1) gene fragment (SEQ ID NO. 665). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. "~" indicate incomplete sequence data. Dots indicate gaps in the sequences displayed.

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

^a This sequences are the reverse-complement of the selected primers.

Annex VIII: Strategy for the selection of *Streptococcus agalactiae*-specific amplification primers from *tuf* sequences.

5	<i>S. agalactiae</i>	305	CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	SEQ ID NO.:	Accession #:
	<i>S. agalactiae</i>		CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	207	-
	<i>S. agalactiae</i>		CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	208	-
	<i>S. agalactiae</i>		CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	209	-
	<i>S. anginosus</i>		CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	210	-
	<i>S. anginosus</i>		CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	211	-
	<i>S. bovis</i>		CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	212	-
	<i>S. gordonii</i>		CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	213	-
	<i>S. mutans</i>		CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	214	-
	<i>S. pneumoniae</i>		CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	215	-
	<i>S. sanguinis</i>		CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	216	-
	<i>S. sobrinus</i>		CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	217	-
	<i>B. cepacia</i>		CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	218	-
	<i>B. fragilis</i>		CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	219	-
	<i>B. subtilis</i>		CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	220	-
	<i>C. diphtheriae</i>		CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	221	-
	<i>C. trachomatis</i>		CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	222	-
	<i>E. coli</i>		CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	223	-
	<i>G. vaginalis</i>		CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	224	-
	<i>S. aureus</i>		CCAGAA	CGTGATACTG	ACAAACCTTT	ACTT...GGAC	AACGTTGGTG	TTCCTCTTCG	542	225	-
10											
15											
20											
25											

Selected sequence for species-specific primer

Selected sequence for species-specific primer^b

The sequence numbering refers to the *Streptococcus agalactiae tuf* gene fragment (SEQ ID NO. 209). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

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

^a The SEQ ID NO. refers to previous patent application WO98/20157.
^b This sequence is the reverse-complement of the selected primer.

Annex IX: Strategy for the selection of *Streptococcus agalactiae*-specific hybridization probes from *tuf* sequences.

5	<i>S. acidominimus</i>	401	GGTACTGT	TaaagTtAAAt	GACGAAGTTG	AAATCGTTGG	TATCAAAAGAC	GAAATCtCtA	AAGCAGTTGT	470	TA	206	Accession #:
	<i>S. agalactiae</i>		GGTACTGT	TCGTGTCAAC	GACGAAGTTG	AAATCGTTGG	TATTAAAGAA	GATATCCAAA	AAGCAGTTGT		TA	209	
	<i>S. agalactiae</i>		GGTACTGT	TCGTGTCAAC	GACGAAGTTG	AAATCGTTGG	TATTAAAGAA	GATATCCAAA	AAGCAGTTGT		TA	144 ^a	
10	<i>S. agalactiae</i>		GGTACTGT	TCGTGTCAAC	GACGAAGTTG	AAATCGTTGG	TATTAAAGAA	GATATCCAAA	AAGCAGTTGT		TA	207	
	<i>S. agalactiae</i>		GGTACTGT	TCGTGTCAAC	GACGAAGTTG	AAATCGTTGG	TATTAAAGAA	GATATCCAAA	AAGCAGTTGT		TA	210	
	<i>S. anginosus</i>		GGTACTGT	TaaagTtCAAC	GACGAAGTTG	AAATCGTTGG	TATTAAAGAA	GATATCCAAA	AAGCAGTTGT		TA	208	
	<i>S. anginosus</i>		GGTACTGT	TaaagTtCAAC	GATGAAGTTG	AAATCGTTGG	TATccgtGAt	GAAATCCAAA	AAGCAGTTGT		TA	211	
	<i>S. bovis</i>		GGTACTGT	TaaagTtCAAC	GACGAAGTTG	AAATCGTTGG	TATccgcGAG	GAAATCCAAA	AAGCAGTTGT		TA	221	
	<i>S. anginosus</i>		GGTACTGT	TaaagTtCAAt	GATGAAGTTG	AAATCGTTGG	TATccgtGAC	GAAATCCAAA	AAGCAGTTGT		TA	212	
	<i>S. cricetus</i>		GGTACTGT	TaaagTtCAAt	GACGAAGTTG	AAATCGTTGG	TATccgtGAC	GAAATCCAAA	AAGCAGTTGT		TA	213	
	<i>S. cristatus</i>		GGTACTGT	TCGTGTCAAC	GATGAaAtCg	AAATCGTTGG	TATCAAGGAC	GAAATCCAAA	AAGCAGTTGT		TA	214	
	<i>S. downei</i>		GGTACTGT	TaaagTtCAAC	GACGAAGTTG	AAATCGTTGG	TATCAAGGAA	GAAATCCAAA	AAGCAGTTGT		TA	215	
	<i>S. dysgalactiae</i>		GGTACTGT	TCGTGTCAAC	GACGAaAtCg	AAATCGTTGG	TATCAAGGAC	GAAATCCAAA	AAGCAGTTGT		TA	216	
20	<i>S. equi equi</i>		GGTACTGT	TCGTGTtAAc	GACGAaAtCg	AAATCGTTGG	TATCAAGGAA	GAAactaAAA	AAGCAGTTGT		TA	217	
	<i>S. ferus</i>		GGTACTGT	aaGaGTCAAC	GATGAAGTTG	AAATCGTTGG	TATCAAGGAC	GAGATCaAAA	AAGCAGTTGT		TA	218	
	<i>S. gordonii</i>		GGTAtcGT	TaaagTtCAAt	GACGAaAtCg	AAATCGTTGG	TATCAAGGAA	GAAATCCactA	AAGCAGTTGT		TA	219	
	<i>S. macacae</i>		GGTACTGT	TaaagTtAAAt	GATGAAGTTG	AAATCGTTGG	TATCAAGGAA	GAAATCCAAA	AAGCAGTTGT		TA	220	
	<i>S. gordonii</i>		GGTAtcGT	TaaagTtCAAC	GACGAaAtCg	AAATCGTTGG	TATCAAGGAA	GATATtCAAA	AAGCAGTTGT		TA	222	
25	<i>S. mutans</i>		GGTACTGT	TaaagTtAAc	GATGAAGTTG	AAATCGTTGG	TATCCgtGAt	GAAactCAAA	AAGCAGTTGT		TA	223	
	<i>S. oralis</i>		GGTACTGT	TCGTGTCAAC	GACGAaAtCg	AAATCGTTGG	TATCCgtGAt	GACATtCAAA	AAGCAGTTGT		TA	224	
	<i>S. parasanguinis</i>		GGTgtTGT	TCGTGTCAAt	GACGAaAtCg	AAATCGTTGG	TATCAAGGAA	GAAactCAAA	AAGCAGTTGT		TA	-	P33170
	<i>S. pneumoniae</i>		GGTAtcGT	TaaagTtCAAC	GATGAaAtCg	AAATCGTTGG	TATCAAGGAA	GAAATCCAAA	AAGCAGTTGT		TA	225	
	<i>S. pyogenes</i>		GGTACTGT	TCGTGTCAAC	GACGAaAtCg	AAATCGTTGG	TATCAAGGAA	GAAactCAAA	AAGCAGTTGT		TA	145 ^a	
30	<i>S. ratti</i>		GGTACTGT	TaaagTtCAAt	GACGAAGTTG	AAATCGTTGG	TATCAAGGAA	GAAactCAAA	AAGCAGTTGT		TA	-	Genome project
	<i>S. salivarius</i>		GGTgtTGT	TCGTGTCAAt	GACGAAGTTG	AAATCGTTGG	TATCCgtGAt	GACATCCAAA	AAGCAGTTGT		TA	226	
	<i>S. sanguinis</i>		GGTAtcGT	TaaagTtCAAC	GACGAaAtCg	AAATCGTTGG	TATCAAGGAA	GAAATCCAAA	AAGCAGTTGT		TA	146 ^a	
	<i>S. sobrinus</i>		GGTACTGT	TaaagTtAAc	GACGAAGTTG	AAATCGTTGG	TATCCgtGAC	GATATCCAAA	AAGCAGTTGT		TA	227	
	<i>S. suis</i>		GGTACTGT	TCGTGTCAAC	GACGAaAtCg	AAATCGTTGG	TCTTCAAGAA	GATAATCCAAA	AAGCAGTTGT		TA	228	
	<i>S. uberis</i>		GGTACTGT	TCGTGTCAAC	GACGAaAtCg	AAATCGTTGG	TCTTCAAGAA	GATAaAtCtA	AAGCAGTTGT		TA	229	
35	<i>S. vestibularis</i>		GGTgtTGT	TCGTGTtAAAt	GACGAAGTTG	AAATCGTTGG	TATCAAGGAA	GAAactaAAA	AAGCAGTTGT		TA	230	
							TCTTAAAGAA	GAAATCCAAA	AAGCAGTTGT		TA	231	

Selected sequences for
species-specific hybri-
dization probes^b

The sequence numbering refers to the *Streptococcus agalactiae* *tuf* gene fragment (SEQ ID NO. 209). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^a The SEQ ID NO. refers to previous patent application WO98/20157.
^b These sequences are the complementary sequences of the sequences in (a).

These sequences are the reverse-complement of the selected probes.

[illegible]

The sequence numbering refers to the *Streptococcus agalactiae* *tuf* gene fragment (SEQ ID NO. 380). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^{a,d,e,f} These sequences were obtained from Genbank and have accession #: a=AB009314, d=AF001955, e=U31170, and f=V00311.

^{b,c} These sequences were obtained from genome sequencing projects.

^g These sequences are the reverse-complement of the selected primers.

Annex XI: Strategy for the selection of *Candida albicans*/*dubliniensis*-specific amplification primers, *Candida albicans*-specific hybridization probe and *Candida dubliniensis*-specific hybridization probe from *tuf* sequences.

5

C. albicans	337	CGTC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	491	SEQ	ID NO.:	Accession #:
C. albicans		CGTC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	624	-		
C. albicans		CGTC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	409	-		
C. albicans		CGTC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	410	-		
C. albicans		CGTC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	407	-		
C. dubliniensis		CGTC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	408	-		
C. dubliniensis		CGTC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	412	-		
C. dubliniensis		CGTC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	414	-		
C. glabrata		CATC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	415	-		
C. guilliermondii		CGTC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	417	-		
C. kefyr		CATC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	418	-		
C. krusei		CATC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	421	-		
C. lusitaniae		CGTC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	422	-		
C. neoformans		CATC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	424	-		
C. parapsilosis		CGTC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	623	-		
C. tropicalis		CGTC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	426	-		
A. fumigatus		CATC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	429	-		
Human		CATC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	404	-		
P. anomala		TATC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	-	X03558		
S. cerevisiae		TATC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	447	-		
S. pombe		CATC	AAGAAGGTTG	GTTACAACCC	AAAGACTG...	CAACATGA	TTGAACCATC	CACCAACT...	C	AAATCCGGTA	AAGTTACTGG	TAAGACCTTG	622	-		
													-	U42189		

Selected sequence

for species-specific

amplification primer^a C AAGAAGGTTG GTTACAACCC AAAGA

30

Selected sequence

for species-specific

amplification primer^{a,b}

35

Selected sequences

for species-specific

hybridization probes

40

CATGA TTGAACCATC CACCA
CATGA TTGAAGCTTC CACCA

577
578

ATCCGGTA AAGTTACTGG TAAGACCT

The sequence numbering refers to the *Candida albicans* *tuf* gene fragment (SEQ ID NO. 408). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches for SEQ ID NO. 577 are indicated by lower-case letters. Mismatches for SEQ ID NO. 578 are indicated by underlined nucleotides. Dots indicate gaps in the sequences displayed.

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

^a *C. albicans* primers have been described in a previous patent (application W098/20157, SEQ ID NOS. 11-12)

^b This sequence is the reverse-complement of the selected primer.

Annex XIII: Strategy for the selection of the *Staphylococcus* genus-specific hybridization probe from *tuf* sequences.

5

		400	425	SEQ ID NO.:	Accession #:
10	<i>S. aureus</i>	G TT GAAATGTT CCGTAAATTA TTAGA	179	-	
	<i>S. aureus</i>	G TT GAAATGTT CCGTAAATTA TTAGA	176	-	
	<i>S. aureus</i>	G TT GAAATGTT CCGTAAATTA TTAGA	177	-	
	<i>S. aureus</i>	G TT GAAATGTT CCGTAAATTA TTAGA	178	-	
	<i>S. aureus aureus</i>	G TT GAAATGTT CCGTAAATTA TTAGA	180	-	
15	<i>S. auricularis</i>	G TAG GAAATGTT CCGTAAATTA TTAGA	181	-	
	<i>S. capitis capitis</i>	G TAG GAAATGTT CCGTAAATTA TTAGA	182	-	
	<i>M. caseolyticus</i>	G TAG GAAATGTT CCGTAAATTA TTAGA	183	-	
	<i>S. cohnii</i>	G TAG GAAATGTT CCGTAAATTA TTAGA	184	-	
	<i>S. epidermidis</i>	G TAG GAAATGTT CCGTAAATTA TTAGA	185	-	
20	<i>S. haemolyticus</i>	G TAG GAAATGTT CCGTAAATTA TTAGA	186	-	
	<i>S. haemolyticus</i>	G TAG GAAATGTT CCGTAAATTA TTAGA	189	-	
	<i>S. haemolyticus</i>	G TAG GAAATGTT CCGTAAATTA TTAGA	190	-	
	<i>S. haemolyticus</i>	G TAG GAAATGTT CCGTAAATTA TTAGA	188	-	
	<i>S. hominis</i>	G TAG GAAATGTT CCGTAAATTA TTAGA	196	-	
25	<i>S. hominis</i>	G TAG GAAATGTT CCGTAAATTA TTAGA	194	-	
	<i>S. hominis hominis</i>	G TAG GAAATGTT CCGTAAATTA TTAGA	191	-	
	<i>S. hominis</i>	G TAG GAAATGTT CCGTAAATTA TTAGA	193	-	
	<i>S. hominis</i>	G TAG GAAATGTT CCGTAAATTA TTAGA	195	-	
	<i>S. lugdunensis</i>	G TAG GAAATGTT CCGTAAATTA TTAGA	197	-	
30	<i>S. saprophyticus</i>	G TAG GAAATGTT CCGTAAATTA TTAGA	198	-	
	<i>S. saprophyticus</i>	G TAG GAAATGTT CCGTAAATTA TTAGA	200	-	
	<i>S. saprophyticus</i>	G TAG GAAATGTT CCGTAAATTA TTAGA	199	-	
	<i>S. sciuri sciuri</i>	G TT GAAATGTT CCGTAAATTA TTAGA	201	-	
	<i>S. warneri</i>	G TAG GAAATGTT CCGTAAgTTA TTAGA	187	-	
35	<i>S. warneri</i>	G TAG GAAATGTT CCGTAAgTTA TTAGA	192	-	
	<i>S. warneri</i>	G TAG GAAATGTT CCGTAAgTTA TTAGA	202	-	
	<i>S. warneri</i>	G TAG GAAATGTT CCGTAAgTTA TTAGA	203	-	
	<i>B. subtilis</i>	G TT GAAATGTT CCGTAAgcTt cTTGA	-	Z99104	
	<i>E. coli</i>	G TT GAAATGTT CCGcAAAcTg cTGGA	78	-	
	<i>L. monocytogenes</i>	G TAG GAAATGTT CCGTAAATTA cTAGA	138 ^a	-	

40

Selected sequence for
genus-specific hybridi-
zation probe

GAAATGTT CCGTAAATTA TT

605

45

The sequence numbering refers to the *Staphylococcus aureus tuf* gene fragment (SEQ ID NO. 179). Nucleotides in capitals are identical to the selected sequence or match that sequence. Mismatches are indicated by lower-case letters.

50 ^a The SEQ ID NO. refers to previous patent application WO98/20157.

Annex XIV: Strategy for the selection of *Staphylococcus saprophyticus*-specific and of *Staphylococcus haemolyticus*-specific hybridization probes from *tuf* sequences.

5

						SEQ ID
						NO.:
10		339			383	
	<i>S. aureus</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACaTC	TAA	179		
	<i>S. aureus</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACaTC	TAA	176		
	<i>S. aureus</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACaTC	TAA	177		
	<i>S. aureus</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACaTC	TAA	178		
15	<i>S. aureus aureus</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACaTC	TAA	180		
	<i>S. auricularis</i>	AG TCGGTGAAGA AgTtGAAATC ATcGGTATga AaGACggTTC	AAA	181		
	<i>S. capitis capitis</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTATCC AcGAaACTTC	TAA	182		
	<i>M. caseolyticus</i>	AG TtGGTGAAGA AgTtGAAATC ATTGGTtTaa cTGAagaacC	AAA	183		
	<i>S. cohnii</i>	AG TCGGTGAAGA AgTtGAAATC ATcGGTATgC AaGAagaTTC	CAA	184		
20	<i>S. epidermidis</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTATgC AcGAaACTTC	TAA	185		
	<i>S. haemolyticus</i>	AG TtGGTGAAGA AgTtGAAATC ATTGGTATCC ATGACACTTC	TAA	186		
	<i>S. haemolyticus</i>	AG TtGGTGAAGA AgTtGAAATC ATTGGTATCC ATGACACTTC	TAA	189		
	<i>S. haemolyticus</i>	AG TtGGTGAAGA AgTtGAAATC ATTGGTATCC ATGACACTTC	TAA	190		
	<i>S. haemolyticus</i>	AG TtGGTGAAGA AgTtGAAATt ATTGGTATCa AaGAaACTTC	TAA	188		
25	<i>S. hominis</i>	AG TtGGTGAAGA AgTtGAAATt ATTGGTATCa AaGAaACTTC	TAA	194		
	<i>S. hominis hominis</i>	AG TtGGTGAAGA AgTtGAAATt ATTGGTATCa AaGAaACTTC	TAA	191		
	<i>S. hominis</i>	AG TtGGTGAAGA AgTtGAAATt ATTGGTATCa AaGAaACTTC	TAA	193		
	<i>S. hominis</i>	AG TtGGTGAAGA AgTtGAAATt ATTGGTATCa AaGAaACTTC	TAA	195		
	<i>S. hominis</i>	AG TtGGTGAAGA AgTtGAAATt ATTGGTATCa AaGAtACTTC	TAA	196		
30	<i>S. lugdunensis</i>	AG TCGGTGAAGA AgTtGAAATt ATTGGTATCC AcGAtACTaC	TAA	197		
	<i>S. saprophyticus</i>	AG TCGGTGAAGA AATCGAAATC ATcGGTATgC AaGAagaATC	CAA	198		
	<i>S. saprophyticus</i>	AG TCGGTGAAGA AATCGAAATC ATcGGTATgC AaGAagaATC	CAA	200		
	<i>S. saprophyticus</i>	AG TCGGTGAAGA AATCGAAATC ATcGGTATgC AaGAagaATC	CAA	199		
	<i>S. sciuri sciuri</i>	TG TtGGTGAAGA AgTtGAAATC ATcGGTtTaa cTGAagaATC	TAA	201		
35	<i>S. warneri</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACTTC	TAA	187		
	<i>S. warneri</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACTTC	TAA	192		
	<i>S. warneri</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACTTC	TAA	202		
	<i>S. warneri</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACTTC	TAA	203		
	<i>B. subtilis</i>	AG TCGGTGAAGA AgTtGAAATC ATcGGTcTtC AaGAagagag	AAA	- ^a		
40	<i>E. coli</i>	AG TtGGTGAAGA AgTtGAAATC gTTGGTATCa AaGAgACTca	GAA	78		
	<i>L. monocytogenes</i>	AG TtGGTGAAGA AgTaGAAGtTt ATcGGTATCg AaGAagaag	AAA	138 ^b		

Selected sequences for
species-specific
hybridization probes

45		CGGTGAAGA AATCGAAATC A	599
		ATTGGTATCC ATGACACTTC	594

The sequence numbering refers to the *Staphylococcus aureus tuf* gene fragment (SEQ ID NO. 179). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters.

50

^a This sequence was obtained from Genbank accession #Z99104.

^b The SEQ ID NO. refers to previous patent application WO98/20157.

Annex XV: Strategy for the selection of *Staphylococcus aureus*-specific and of *Staphylococcus epidermidis*-specific hybridization probes from *tuf* sequences.

5

		521	547	592	617	SEQ ID NO.:
10	<i>S. aureus</i>	TACACCACA TACTGAATTC	AAAGCAG...	TTCTTTcCa	AACTATCGtC CACAATT	179
	<i>S. aureus</i>	TACACCACA TACTGAATTC	AAAGCAG...	TTCTTTcC~	~~~~~	178
	<i>S. aureus</i>	TACACCACA TACTGAATTC	AAAGCAG...	TTCTTTcCa	AACTATCGtC CACAATT	176
	<i>S. aureus</i>	TACACCACA TACTGAATTC	AAAGCAG...	TTCTTTcCa	AACTATCGtC CACAATT	177
	<i>S. aureus aureus</i>	TACACCACA TACTGAATTC	AAAGCAG...	TTCTTTcCa	AACTATCGtC CACAATT	180
15	<i>S. auricularis</i>	TACACCACA cACTaAATTC	ActGCAG...	TTCTTTcCT	AACTAcCGtC CACAATT	181
	<i>S. capitis capitis</i>	CACACCACA cACTaAATTC	AAAGCGG...	TTCTTCAgT	AACTAcCGCC CACAATT	182
	<i>M. caseolyticus</i>	TACtCCACA TACTaAATTC	AAAGCTG...	TTCTTCACT	AACTAcCGCC CtCAGTT	183
	<i>S. cohnii</i>	TACACCACA cACaaAcTTt	AAAGCGG...	TTCTTCAgT	AACTATCGCC CACAATT	184
	<i>S. epidermidis</i>	TACACCACA cACaaAATTC	AAAGCTG...	TTCTTCACT	AACTATCGCC CACAATT	185
20	<i>S. haemolyticus</i>	CACACcCA cACaaAATt	AAAGCAG...	TTCTTCAcCa	AACTATCGtC CACAATT	186
	<i>S. haemolyticus</i>	CACACcCA cACaaAATt	AAAGCAG...	TTCTTCAcCa	AACTATCGtC CACAATT	189
	<i>S. haemolyticus</i>	CACACcCA cACaaAATt	AAAGCAG...	TTCTTCAcCa	AACTATCGtC CACAATT	190
	<i>S. haemolyticus</i>	TACACcCA cACaaAATTC	AAAGCAG...	TTCTTCACT	AACTATCGtC CACAATT	188
	<i>S. hominis</i>	CACACcCA cACaaAATTC	AAAGCAG...	TTCTTCACT	AACTATCGtC CACAATT	195
25	<i>S. hominis</i>	TACACcCA cACaaAATTC	AAAGCAG...	TTCTTCACT	AACTATCGtC CACAATT	196
	<i>S. hominis hominis</i>	TACACcCA cACaaAATTC	AAAGCAG...	TTCTTTcCT	AACTATCGtC CACAATT	191
	<i>S. hominis</i>	TACACcCA cACaaAATTC	AAAGCAG...	TTCTTTcCT	AACTATCGtC CACAATT	193
	<i>S. hominis</i>	TACACcCA cACaaAATTC	AAAGCAG...	TTCTTTcCT	AACTATCGtC CACAATT	194
	<i>S. lugdunensis</i>	TACACcCA cACTaAATt	AAAGCTG...	TTCTTTcCa	AACTAcCGCC CACAATT	197
30	<i>S. saprophyticus</i>	TACACCACA TACaaAATTC	AAAGCGG...	TTCTTCACT	AACTAcCGCC CACAATT	198
	<i>S. saprophyticus</i>	TACACCACA TACaaAATTC	AAAGCGG...	TTCTTCACT	AACTAcCGCC CACAATT	199
	<i>S. saprophyticus</i>	TACACCACA TACaaAATTC	AAAGCGG...	TTCTTCACT	AACTAcCGCC CACAATT	200
	<i>S. sciuri sciuri</i>	CACACcCA cACTaAATTC	AAAGCTG...	TTCTTCAcCa	AACTAcCGCC CACAATT	201
	<i>S. warneri</i>	TACACCACA TACaaAATTC	AAAGCGG...	~~~~~	~~~~~	192
35	<i>S. warneri</i>	TACACCACA TACaaAATTC	AAAGCGG...	TTCTTCAgT	AACTAcCGCC CACAATT	187
	<i>S. warneri</i>	TACACCACA TACaaAATTC	AAAGCGG...	TTCTTCAgT	AACTAcCGCC CACAATT	202
	<i>S. warneri</i>	TACACCACA TACaaAATTC	AAAGCGG...	TTCTTCAgT	AACTAcCGCC CACAATT	203
	<i>B. subtilis</i>	CACtCCACA cAgcaAATTC	AAAGCTG...	TTCTTTcCT	AACTAcCGtC CtCAGTT	- ^a
	<i>E. coli</i>	CAAgCCgCA cACcaAgTTC	gAAtCTG...	TTCTTCAaa	ggCTAcCGtC CgCAGTT	78
40	<i>L. monocytogenes</i>	TACtCCACA cACTaAcTTC	AAAGCTG...	TTCTTCAac	AACTAcCGCC CACAATT	138 ^b

Selected sequences
for species-specific
hybridization
probes

45	ACCACA TACTGAATTC AAAG	585
	TTCaCT AACTATCGCC CACA	593

50 The sequence numbering refers to the *Staphylococcus aureus tuf* gene fragment (SEQ ID NO. 179). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. "~" indicate incomplete sequence data. Dots indicate gaps in the sequences displayed.

^a This sequence was obtained from Genbank accession #Z99104.

^b The SEQ ID NO. refers to previous patent application WO98/20157.

Annex XVI: Strategy for the selection of the *Staphylococcus hominis*-specific hybridization probe from *tuf* sequences.

5					
		358	383	SEQ ID NO.:	
	<i>S. aureus</i>	ATC ATcGGTtTac AtGAcACaTC	TAA	179	
10	<i>S. aureus</i>	ATC ATcGGTtTac AtGAcACaTC	TAA	176	
	<i>S. aureus</i>	ATC ATcGGTtTac AtGAcACaTC	TAA	177	
	<i>S. aureus</i>	ATC ATcGGTtTac AtGAcACaTC	TAA	178	
	<i>S. aureus aureus</i>	ATC ATcGGTtTac AtGAcACaTC	TAA	180	
	<i>S. auricularis</i>	ATC ATcGGTATgA AAGAcggTTC	AAA	181	
15	<i>S. capitis capitis</i>	ATC ATcGGTATCc AcGAAACTTC	TAA	182	
	<i>M. caseolyticus</i>	ATC ATTGGTtTaA ctGAAGaacC	AAA	183	
	<i>S. cohnii</i>	ATC ATcGGTATgc AAGAAgaTTC	CAA	184	
	<i>S. epidermidis</i>	ATC ATcGGTATgc AcGAAACTTC	TAA	185	
	<i>S. haemolyticus</i>	ATC ATTGGTATCc AtGAcACTTC	TAA	186	
20	<i>S. haemolyticus</i>	ATC ATTGGTATCc AtGAcACTTC	TAA	189	
	<i>S. haemolyticus</i>	ATC ATTGGTATCc AtGAcACTTC	TAA	190	
	<i>S. haemolyticus</i>	ATT ATTGGTATCA AAGAAACTTC	TAA	188	
	<i>S. hominis</i>	ATT ATTGGTATCA AAGAtACTTC	TAA	196	
	<i>S. hominis</i>	ATT ATTGGTATCA AAGAAACTTC	TAA	194	
25	<i>S. hominis hominis</i>	ATT ATTGGTATCA AAGAAACTTC	TAA	191	
	<i>S. hominis</i>	ATT ATTGGTATCA AAGAAACTTC	TAA	193	
	<i>S. hominis</i>	ATT ATTGGTATCA AAGAAACTTC	TAA	195	
	<i>S. lugdunensis</i>	ATT ATTGGTATCc AcGAtACTaC	TAA	197	
	<i>S. saprophyticus</i>	ATC ATcGGTATgc AAGAAgaatC	CAA	198	
30	<i>S. saprophyticus</i>	ATC ATcGGTATgc AAGAAgaatC	CAA	200	
	<i>S. saprophyticus</i>	ATC ATcGGTATgc AAGAAgaatC	CAA	199	
	<i>S. sciuri sciuri</i>	ATC ATcGGTtTaA ctGAAGaatC	TAA	201	
	<i>S. warneri</i>	ATC ATcGGTtTac AtGAcACTTC	TAA	187	
	<i>S. warneri</i>	ATC ATcGGTtTac AtGAcACTTC	TAA	192	
35	<i>S. warneri</i>	ATC ATcGGTtTac AtGAcACTTC	TAA	202	
	<i>S. warneri</i>	ATC ATcGGTtTac AtGAcACTTC	TAA	203	
	<i>B. subtilis</i>	ATC ATcGGTcTtc AAGAAgagag	AAA	- ^a	
	<i>E. coli</i>	ATC gTTGGTATCA AAGAgACTca	GAA	78	
40	<i>L. monocytogenes</i>	GTT ATcGGTATCg AAGAAgaaag	AAA	138 ^b	

Selected sequence for
species-specific
hybridization probe

ATTGGTATCA AAGAAACTTC

597

The sequence numbering refers to the *Staphylococcus aureus tuf* gene fragment (SEQ ID NO. 179). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^a This sequence was obtained from Genbank accession #Z99104.

^b The SEQ ID NO. refers to previous patent application WO98/20157.

Annex XVII: Strategy for the selection of the *Enterococcus* genus-specific amplification primers from *tuf* sequences.

	270	298	556	582	SEQ ID NO.:	Accession #			
5	<i>E. avium</i>	TAGAAATTAAT	GGCTGCTGTT	GACGAATAT...TGAA	GATATCCAAC	GTGGACAAAGT	ATT	131 ^a	-
	<i>E. casseliflavus</i>	TGGAATTAAT	GGCTGCAGTT	GACGAATAC...TGAA	GACATCCAAC	GTGGACAAAGT	ATT	58	-
	<i>E. cecorum</i>	TAGAAATTAAT	GGCTGCAGTT	GACGAATAC...TGAA	GATATCCAAC	GTGGTCAAGT	ATT	59	-
	<i>E. dispar</i>	TAGAAATTAAT	GGCTGCAGTT	GACGAATAT...TGAA	GATATCCAAC	GTGGTCAAGT	ATT	60	-
	<i>E. durans</i>	TTGAATTAAT	GGCTGCAGTT	GACGAATAT...TGAA	GACATCCAAC	GTGGACAAAGT	TTT	61	-
10	<i>E. flavescens</i>	TGGAATTAAT	GGCTGCAGTT	GACGAATAC...TGAA	GACATCCAAC	GTGGACAAAGT	ATT	65	-
	<i>E. faecium</i>	TTGAATTAAT	GGCTGCAGTT	GACGAATAC...TGAA	GACATCCAAC	GTGGACAAAGT	TTT	608	-
	<i>E. faecalis</i>	TAGAAATTAAT	GGCTGCAGTT	GACGAATAT...TGAA	GATATCGAAC	GTGGACAAAGT	ATT	607	-
	<i>E. gallinarum</i>	TGGAATTGAT	GGCTGCAGTT	GACGAATAC...TGAA	GACATCCAAC	GTGGACAAAGT	ATT	609	-
	<i>E. hirae</i>	TTGAATTGAT	GGCTGCAGTT	GACGAATAT...TGAA	GACATCCAAC	GTGGACAAAGT	TTT	67	-
15	<i>E. mundtii</i>	TTGAATTGAT	GGCTGCAGTT	GACGAATAT...TGAA	GACATCCAAC	GTGGTCAAGT	TTT	68	-
	<i>E. pseudoavium</i>	TAGAAATTAAT	GSCTGCTGTT	GACGAATAC...TGAA	GACATCCAAC	GTGGACAAAGT	ATT	69	-
	<i>E. raffinosus</i>	TAGAAATTAAT	GGCTGCTGTT	GATGAATAC...TGAA	GACATCCAAC	GTGGACAAAGT	ATT	70	-
	<i>E. saccharolyticus</i>	TCGAATTAAT	GGCTGCAGTT	GACGAATAT...TGAA	GACATCCAAC	GTGGACAAAGT	ATT	71	-
	<i>E. solitarius</i>	TGGACTTAAT	GGAATGCAGTT	GATGACTAC...TGAT	GATATCGAAC	GTGGTCAAGT	ATT	72	-
20	<i>E. coli</i>	TGGAACCTggc	tGgcttccTg	GATcttTAY...TGAA	GAAATCGAAC	GTGGTCAAGT	ACT	78	-
	<i>B. cepacia</i>	TGAGccTggc	cGacGCGcTg	GACacGTAC...TGAA	GACgTgGAGC	GTGGcCAGGT	TCT	16	-
	<i>B. fragilis</i>	TGGAACtGAT	GGaaGCTGTT	GATactTGG...GAAC	GAAATCaAAC	GTGGtatgGT	TCT	-	M22247
	<i>B. subtilis</i>	TCGAACtTAT	GGAATGCgGTT	GATGAGTAC...TGAA	GAAATCCAAC	GTGGTCAAGT	ACT	-	Z99104
	<i>C. diphtheriae</i>	TCGACcTcAT	GcagGCTtgc	KATGATTC...CGAA	GACgTtGAGC	GTGGcCAGGT	TGT	662	-
25	<i>C. trachomatis</i>	GAGAGCTAAT	GcaagCCcGTC	GATGATAAT...GAAC	GATgTgGAAa	GaGGAatgGT	TGT	22	-
	<i>G. vaginalis</i>	AGGAACtCAT	GaagGCTGTT	GACGAGTAC...TACC	GACgTtGAGC	GTGGTCAAGT	TGT	135 ^a	-
	<i>S. aureus</i>	TAGAAATTAAT	GGAAGCTGTa	GATactTAC...TGAA	GACgTaCAAC	GTGGTCAAGT	ATT	179	-
	<i>S. pneumoniae</i>	TGGAATTGAT	GaacaCAGTT	GATGAGTAT...TGAT	GAAATCGAAC	GTGGACAAAGT	TAT	145 ^a	-
	<i>A. adiacens</i>	TAGAAATTAAT	GGCTGCTGTT	GACGAATAC...TGAA	aACATCGAAC	GTGGACAAAGT	TCT	118 ^a	-
30	<i>G. haemolysans</i>	TCGAATTAAT	GGAaaCAGTT	GACGAATAC...TGAA	GACATCGAAC	GTGGACAAAGT	TTT	87	-
	<i>G. morbillorum</i>	TCGAATTAAT	GGAaaCAGTT	GACGAGTAC...TGAA	GATATCGAAC	GTGGACAAAGT	TTT	88	-
	Selected sequence for amplification primer	AAATTAAT	GGCTGCWGT	GAYGAA				1137	
	Selected sequence for amplification primer ^b				A	GAYATCSAAC	GTGGACAAAGT	1136	

The sequence numbering refers to the *Enterococcus durans tuf* gene fragment (SEQ ID NO. 61). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed. "Y" "W" and "S" designate nucleotide positions which are degenerated. "Y" stands for C or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

^a The SEQ ID NO. refers to previous patent application WO98/20157.
^b This sequence is the reverse-complement of the selected primer.

Annex XVIII: Strategy for the selection of the *Enterococcus faecalis*-specific hybridization probe, of the *Enterococcus faecium*-specific hybridization probe and of the *Enterococcus casseliflavus-flavescens-gallinarum* group-specific hybridization probe from *tuf* sequences.

	395	448...526	549	SEQ ID NO.: Accession #:
<i>E. avium</i>	GTTGA ACGTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATcGta GGTATcGCT...CATc GGTGctTTgt TACGTGGTGT			131 ^a -
<i>E. casseliflavus</i>	GTTGA ACGTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATcGTT TGAATcGTT GGTATcGCT...CATc GGTGctTTgt TACGTGGTGT			58 -
<i>E. cecorum</i>	GTTGA ACGTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATcGTT TGAATcGTT GGTATcGCT...CATc GGTGctTTgt TACGTGGTGT			59 -
<i>E. dispar</i>	GTTGA ACGTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATcGTT TGAATcGTT GGTATcGCT...CATc GGTGctTTgt TACGTGGTGT			60 -
<i>E. durans</i>	GTTGA ACGTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATcGTT TGAATcGTT GGTATcGCT...CATc GGTGctTTgt TACGTGGTGT			61 -
<i>E. faecalis</i>	GTTGA ACGTGGTGA GTTCGCGTTG GTGACGAAAGT TGAATcGTT TGAATcGTT GGTATcGCT...CATc GGTGctTTgt TACGTGGTGT			62 -
<i>E. faecium</i>	GTTGA ACGTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATcGTT TGAATcGTT GGTATcGCT...CATc GGTGctTTgt TACGTGGTGT			608 -
<i>E. flavescens</i>	GTTGA ACGTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATcGTT TGAATcGTT GGTATcGCT...CATc GGTGctTTgt TACGTGGTGT			65 -
<i>E. gallinarum</i>	GTTGA ACGTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATcGTT TGAATcGTT GGTATcGCT...CATc GGTGctTTgt TACGTGGTGT			609 -
<i>E. hirae</i>	GTTGA ACGTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATcGTT TGAATcGTT GGTATcGCT...CATc GGTGctTTgt TACGTGGTGT			67 -
<i>E. mundtii</i>	GTTGA ACGTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATcGTT TGAATcGTT GGTATcGCT...CATc GGTGctTTgt TACGTGGTGT			68 -
<i>E. pseudoavium</i>	GTTGA ACGTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATcGTT TGAATcGTT GGTATcGCT...CATc GGTGctTTgt TACGTGGTGT			69 -
<i>E. raffinosus</i>	GTTGA ACGTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATcGTT TGAATcGTT GGTATcGCT...CATc GGTGctTTgt TACGTGGTGT			70 -
<i>E. saccharolyticus</i>	GTTGA ACGTGGACAA GTTCGCGTTG GTGACGAAAGT TGAATcGTT TGAATcGTT GGTATcGCT...CATc GGTGctTTgt TACGTGGTGT			71 -
<i>E. solitarius</i>	GTTGA ACGcGGgact aTcaaaGTcG GCGATGAAGT TGAATcGTT TGAATcGTT GGTATcGCT...CATc GGTGctTTgt TACGTGGTGT			72 -
<i>C. diphtheriae</i>	GTTGA gCGTGGctcc cTgaagGTcA ACGAGGAcGT cGAgatcatc GGTATcGCT...CTGT GGTctgcttc TcCGTGGCCT			662 -
<i>G. vaginalis</i>	GTTGA gCGTGGTaag cTcCcaATcA ACACCCcAGT TGAATcGTT TGAATcGTT GGTATcGCT...CACT GGTcttcttc TcCGcGGTAT			135 ^a -
<i>B. cepacia</i>	GTCGA gCGcGGcatc GTgaagGTcG GCGAAGAAaT cGAAATcGTT GGTATcAAG...CGTT GGTatccctgc TgCGcGGCAC			16 -
<i>S. aureus</i>	GTTGA ACGTGGTcAA aTcaaaGTcG GTgaagAAAGT TGAATcATc GGTtTaCAT...CATc GGTGcATTat TACGTGGTGT			179 -
<i>B. subtilis</i>	GTTGA ACGcGGacAA GTTaaAGTcG GTGACGAAAGT TGAATcATc GGTtTTCAA...CATc GGTGccttc TtCGcGGTGT			- Z99104
<i>S. pneumoniae</i>	ATCGA cCGTGGTatc GTTaaAGTcA ACGACGAAaT cGAAATcGTT GGTATcAAA...CGTa GGTGtcccttc TtCGTGGTGT			145 ^a -
<i>E. coli</i>	GTTGA ACGcGGTatc aTcaaaGTcG GTgaagAAAGT TGAATcGTT GGTATcAAA...CGTa GGTGtccctgc TgCGTGGTAT			78 -
<i>B. fragilis</i>	ATCGA AactGGTgtt aTcCatGTAG GTGATGAAGT cGAAATcctc GGTtTgGGT...CGTa GGTctgtTgc TtCGTGGTGT			- M22247
<i>C. trachomatis</i>	ATTGA gCGTGGaatt GTTaaAGTtT CCGATAAAAGT TcAgTgGtc GGTcTTAGa...CGTT GGattgctcc TcaGagGATAT			22 -

Selected sequences for species-specific or group-specific hybridization probes

1174
602
1122

T GGTGCATTGC TACGTGG

The sequence numbering refers to the *Enterococcus faecium* *tuf* gene fragments (SEQ ID NO. 608). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^a The SEQ ID NO. refers to previous patent application WO98/20157.

Annex XIX: Strategy for the selection of primers for the identification of platelets contaminants from tuf sequences.

5		467		495	689	717	SEQ ID NO.:	Accession #
10	<i>B. cereus</i>	GTA	ACTGGTGTaG	AGATGTTCCG	TAAACT...C	AGTTCTACTTT	CCGTACAAC	7
	<i>B. subtilis</i>	GTT	ACaGGTGTtG	AAATGTTCCG	TAAAGCT...C	AGTTCTACTTT	CCGTACAAC	-
	<i>E. cloacae</i>	TGT	ACTGGCGTTG	AAATGTTCCG	CAAACT...C	AGTTCTACTTT	CCGTACAAC	54
	<i>E. coli</i>	TGT	ACTGGCGTTG	AAATGTTCCG	CAAACT...C	AGTTCTACTTT	CCGTACTACT	78
	<i>K. oxytoca</i>	TGT	ACTGGCGTTG	AAATGTTCCG	CAAACT...C	AGTTCTACTTT	CCGTACAAC	100
15	<i>K. pneumoniae</i>	TGT	ACTGGCGTTG	AAATGTTCCG	CAAACT...C	AGTTCTACTTT	CCGTACTACT	103
	<i>P. aeruginosa</i>	TGC	ACGGCGTTG	AAATGTTCCG	CAAGCT...C	AGTTCTACTTT	CCGTACCACK	153
	<i>S. agalactiae</i>	GTT	ACTGGTGTtG	AAATGTTCCG	TAAACA...C	AATTCTACTTT	CCGTACAAC	209
	<i>S. aureus</i>	GTT	ACaGGTGTtG	AAATGTTCCG	TAAATT...C	AATTCTACTTT	CCGTACTACT	140 ^a
	<i>S. choleraesuis</i>	TGT	ACTGGCGTTG	AAATGTTCCG	CAAACT...C	AGTTCTACTTT	CCGTACTACT	159
20	<i>S. epidermidis</i>	GTT	ACTGGTGTaG	AAATGTTCCG	TAAATT...C	AATTCTACTTT	CCGTACTACT	611
	<i>S. marcescens</i>	TGT	ACTGGCGTTG	AAATGTTCCG	CAAACT...C	AGTTCTACTTT	CCGTACCACK	168
	<i>S. mutans</i>	GTT	ACTGGTGTtG	AAATGTTCCG	TAAACA...C	AATTCTACTTT	CCGTACAAC	224
	<i>S. pyogenes</i>	GTT	ACTGGTGTtG	AAATGTTCCG	TAAACA...C	AATTCTACTTT	CCGTACAAC	-
	<i>S. salivarius</i>	GTT	ACTGGTGTtG	AAATGTTCCG	TAAACA...C	AGTTCTACTTT	CCGTACAAC	146 ^a
20	<i>S. sanguinis</i>	GTT	ACTGGTGTtG	AAATGTTCCG	TAAACA...C	AGTTCTACTTT	CCGTACAAC	227
	<i>Y. enterocolitica</i>	TGT	ACTGGCGTTG	AAATGTTCCG	CAAACT...C	AGTTCTACTTT	CCGTACAAC	235

Selected sequence for amplification primer

ACTGGYGTG AIATGTTCCG YAA

636

Selected sequence for amplification primer^b

TTCTAYTT CCGTACTACT GACGT

637

30 The sequence numbering refers to the *E. coli* tuf gene fragment (SEQ ID NO. 78). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

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

^a The SEQ ID NO. refers to previous patent application WO98/20157.

^b This sequence is the reverse-complement of the selected primer.

Annex XX: Strategy for the selection of the universal amplification primers from *atpD* sequences.

		616	657	781	812	SEQ ID NO.:	Accession #:				
5	<i>C. glutamicum</i>	GTGTTTCGGTC	AGATGGATGA	GCCACCAGGA	GTCCGATATG	CGC...CGTATG	CCTTCCGCCG	TGGGTTACCA	GCCAAC	-	X76875
	<i>M. tuberculosis</i>	GTATTTCGGAC	AGATGGACGA	GCCGCCGGGC	aCCCGTATG	CGT...CGGATG	CCGTCCGCCG	TGGGATACCA	GCCAC	-	Z73419
	<i>E. faecalis</i>	GTGTTTCGGAC	AAATGAACGA	ACCACCAGGT	GCTCGGATG	CGG...CGTATG	CCTTCTGCCG	TTGGTTACCA	ACCAAC	291	-
	<i>S. agalactiae</i>	GTCTTTTGGTC	AAATGAATGA	ACCACCAGGA	GCACGATATG	CGT...CGTATG	CCTTCAGCCG	TTGGTTATCA	ACCAAC	380	-
	<i>B. subtilis</i>	GTATTTCGGAC	AAATGAACGA	GCCGCCGGGC	GCACGATATG	CGT...CGTATG	CCTTCAGCCG	TTGGTTATCA	GCCGAC	-	Z28592
10	<i>L. monocytogenes</i>	GTATTTCGGTC	AAATGAACGA	GCCACCAGGT	GCGCGTATG	CGT...CGTATG	CCATCTGCCG	TAGGTTACCA	ACCAAC	324	-
	<i>S. aureus</i>	GTATTTCGGGC	AAATGAATGA	GCCACCTGGT	GCACGATATG	CGT...CGTATG	CCTTCTGCCG	TAGGTTACCA	ACCAAC	366	-
	<i>A. baumannii</i>	GTCTACGGTC	AGATGAACGA	GCCACCAGGT	aaCCGTTa	CGC...CGTATG	CCATCTGCCG	TAGGTTACCA	ACCTAC	243	-
	<i>N. gonorrhoeae</i>	GTGTATGGCC	AAATGAACGA	ACCTCCAGGC	aaCCGTcTG	CGC...CGTATG	CCTTCTGCCG	TGGGTTACCA	ACCGAC	-	Genome project
	<i>C. freundii</i>	GTATATGGCC	AGATGAACGA	GCCGCTTGA	aaCCGTcTG	CGT...CGTATG	CCATCAGCCG	TAGGCTACCA	GCCGAC	264	-
15	<i>E. cloacae</i>	GTTTACGGCC	AGATGAACGA	GCCACCAGGA	aaCCGTcTG	CGC...CGTATG	CCTTCAGCCG	TAGGTTATCA	GCCTAC	284	-
	<i>E. coli</i>	GTGTATGGCC	AGATGAACGA	GCCGCCGGGA	aaCCGTcTG	CGC...CGTATG	CCTTCAGCCG	TAGGTTATCA	GCCGAC	669	V00267
	<i>S. typhimurium</i>	GTGTATGGCC	AGATGAACGA	GCCGCCGGGA	aaCCGTcTG	CGC...CGTATG	CCTTCCGCCG	TAGGTTACCA	GCCGAC	351	-
	<i>K. pneumoniae</i>	GTGTACGGCC	AGATGAACGA	GCCGCCGGGA	aaCCGTcTG	CGC...CGTATG	CCTTCAGCCG	TAGGTTATCA	GCCGAC	317	-
	<i>S. marcescens</i>	GTTTACGGCC	AGATGAACGA	GCCACCAGGT	aaCCGTcTG	CGC...CGTATG	CCATCCGCCG	TAGGTTATCA	GCCAAC	357	-
20	<i>Y. enterocolitica</i>	GTTTATGGCC	AAATGAATGA	GCCACCAGGT	aaCCGTcTG	CGC...CGTATG	CCATCTGCCG	TAGGTTACCA	GCCAAC	393	-
	<i>B. cepacia</i>	GTGTACGGCC	AGATGAACGA	GCCGCCGGGC	aaCCGTcTG	CGC...CGTATG	CCGTCCGCCG	TGGGCTATCA	GCCGAC	-	X76877
	<i>H. influenzae</i>	GTTTATGGTC	AAATGAACGA	GCCACCAGGT	aaCCGTTa	CGT...CGTATG	CCATCCGCCG	TAGGTTACCA	ACCGAC	-	U32730
	<i>M. pneumoniae</i>	GTGTTTGGTC	AGATGAACGA	ACCCCCAGGA	GCACGGATG	CGG...CGGATG	CCATCAGCCG	TGGGTTACCA	ACCAAC	-	U43738
	<i>H. pylori</i>	TGCTATGGGC	AAATGAATGA	GCCACCAGGT	GCAAGGAat	CGC...CGTATC	CCTTCAGCCG	TGGGGTATCA	GCCAC	670	V00267
25	<i>B. fragilis</i>	GTGTTTCGGAC	AGATGAACGA	ACCTCCTGGA	GCACGTgct	TCA...CGTATg	CCTTCTGCCG	TAGGTTATCA	ACCTAC	-	M22247
	Selected sequences for universal primers		C	ARATGRAYGA	RCCICCIGGI	GYIMGIATG				562	
			TAYGGIC	ARATGAAYGA	RCCICCIGGI	AA				564	
	Selected sequences for universal primers ^a						ATH	CCITCIGCIG	TIGGITAYCA	RCC	565
30							ATG	CCITCIGCIG	TIGGITAYCA	RCC	563

35 The sequence numbering refers to the *Escherichia coli* atpD gene fragment (SEQ ID NO. 669). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches for SEQ ID NOS. 562 and 565 are indicated by lower-case letters. Mismatches for SEQ ID NOS. 564 and 563 are indicated by underlined nucleotides. Dots indicate gaps in the sequences displayed.

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

^a These sequences are the reverse-complement of the selected primers.

Annex XXI: Specific and ubiquitous primers for nucleic acid amplification (*recA* sequences).

5	Originating DNA fragment			
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Universal primers (<i>recA</i>)			
15	919	5'-GGI CCI GAR TCI TMI GGI AAR AC	918 ^a	437-459
	920 ^b	5'-TCI CCV ATI TCI CCI TCI AIY TC	918 ^a	701-723
	921	5'-TIY RTI GAY GCI GAR CAI GC	918 ^a	515-534
	922 ^b	5'-TAR AAY TTI ARI GCI YKI CCI CC	918 ^a	872-894
20	Universal primers (<i>rad51</i>)			
	935	5'-GGI AAR WSI CAR YTI TGY CAY AC	939 ^a	568-590
	936 ^b	5'-TCI SIY TCI GGI ARR CAI GG	939 ^a	1126-1145
25	Universal primers (<i>dmc1</i>)			
	937	5'-ATI ACI GAR GYI TTY GGI GAR TT	940 ^a	1038-1060
	938 ^b	5'-CYI GTI GYI SWI GCR TGI GC	940 ^a	1554-1573
30	^a Sequences from databases. ^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.			
35				

Annex XXII: Specific and ubiquitous primers for nucleic acid amplification (*speA* sequences).

5	Originating DNA fragment			
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Bacterial species:</u> <i>Streptococcus pyogenes</i>			
	994	5'-TGG ACT AAC AAT CTC GCA AGA GG	993 ^a	60-82
	995 ^b	5'-ACA TTC TCG TGA GTA ACA GGG T	993 ^a	173-194
15	996	5'-ACA AAT CAT GAA GGG AAT CAT TTA G	993 ^a	400-424
	997 ^b	5'-CTA ATT CTT GAG CAG TTA CCA TT	993 ^a	504-526
	998	5'-GGA GGG GTA ACA AAT CAT GAA GG	993 ^a	391-413
20	997 ^b	5'-CTA ATT CTT GAG CAG TTA CCA TT	993 ^a	504-526

^a Sequence from databases.

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

Annex XXIII: First strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *speA* sequences.

Accession #	57	85	170	197	SEQ ID NO.:
5 <i>speA</i> X61573	CCTT	GGGCTAACA	cCTCaCAAGA	agTAT...GTGATCCCT.GT	cgtTCATgAG AATGTAAA
<i>speA</i> AF029051	~~~~	GGGCTAACA	cCTCaCAAGA	agTAT...GTGATCCCT.GT	cgtTCATgAG AATGTAAA
<i>speA</i> X61571	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X61570	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X61568	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X61569	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X61572	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X61560	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> U40453	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X61554	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X61557	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X61559	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X61558	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X61556	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X61555	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X61560	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X61561	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X61566	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X61567	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X61562	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X61563	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X61564	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X61565	TCCT	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> AF055698	~~~~	GGACTAACA	TCTCGCAAGA	GGTAT...GTGACCCCT.GT	TACTCACgAG AATGTGAA
<i>speA</i> X03929 ^a	TCCT	GGACTAACA	TCTtGCCaAa	aGGTA...GTGACCCCTGGT	TACTCACgAG AATGTGAA
Selected sequence for species-specific primer	T GGACTAACA TCTCGCAAGA GG				994
Selected sequence for species-specific primer ^b	ACCCCT.GT TACTCACgAG AATGT				995

The sequence numbering refers to the *Streptococcus pyogenes speA* gene fragment (SEQ ID NO. 993). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. "~" indicate incomplete sequence data. Dots indicate gaps in the sequences displayed.

^a The extra G nucleotide introducing a gap in the sequence is probably a sequencing error.

^b This sequence is the reverse-complement of the selected primer.

Annex XXIV: Second strategy for the selection of *Streptococcus pyogenes*-specific amplification primers from *speA* sequences.

	Accession #	388	427	501	529	SEQ ID NO.:
5	<i>speA</i> X61573	TA TGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
	<i>speA</i> AF029051	TA TGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
	<i>speA</i> X61571	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
	<i>speA</i> X61570	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
	<i>speA</i> X61568	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
10	<i>speA</i> X61569	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
	<i>speA</i> X61572	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
	<i>speA</i> X61560	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
	<i>speA</i> U40453	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
	<i>speA</i> X61554	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
15	<i>speA</i> X61557	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
	<i>speA</i> X61559	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
	<i>speA</i> X61558	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
	<i>speA</i> X61556	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
	<i>speA</i> X61555	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
20	<i>speA</i> X61560	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
	<i>speA</i> X61561	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
	<i>speA</i> X61566	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
	<i>speA</i> X61567	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
25	<i>speA</i> X61562	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
	<i>speA</i> X61563	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
	<i>speA</i> X61564	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
	<i>speA</i> X61565	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
	<i>speA</i> AF055698	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAGACT
30	<i>speA</i> X03929	TA CGGAGGGGTA	ACAAATCATG	AAGGGAATCA	TTTAGAAA...AAAATGGT	AACTGCTCAA GAATTAG.CT
	Selected sequences for species-specific primers	GGAGGGGTA	ACAAATCATG	AAGG		998
			ACAAATCATG	AAGGGAATCA	TTTAG	996
35	Selected sequence for species-specific primer ^a			AATGGT	AACTGCTCAA	GAATTAG
						997

The sequence numbering refers to the *Streptococcus pyogenes speA* gene fragment (SEQ ID NO. 993). Dots indicate gaps in the sequences displayed.

^a This sequence is the reverse-complement of the selected primer.

Annex XXV: Strategy for the selection of Streptococcus pyogenes-specific amplification primers from tuf sequences.

		140	186	619	647	SEQ ID NO.:			
5	<i>S. anginosus</i>	A AGTTGACtTg	GTTGACGAtG	AAGAAtTtGCT	TGAATtTgGTT	GAAATG...CC AgGTTCAATt	cAtCCACACA	CTAAATt	211
	<i>S. bovis</i>	A AGTTGACcTt	GTTGATGACG	AAGAAtTtGCT	TGAATtTgGTT	GAAATG...CC AgGTTCAATC	cACCCACACA	CTAAATt	212
	<i>S. dysgalactiae</i>	A AATTGACcTt	GTTGAcGAtG	AAGAAtTtGCT	TGAATtTgGTT	GAAATG...CC AgGTTCAATC	AACCCACACA	CTAAATt	217
	<i>S. pyogenes</i>	A AGTTGACcTt	GTTGATGACG	AAGAGtTtGCT	TGAATtTAGTt	GAGATG...CC AAGTTCAATC	AACCCACACA	CTAAATt	1002
	<i>S. agalactiae</i>	A AGTTGACcTt	GTTGATGAtG	AAGAAtTtGCT	TGAATtTgGTT	GAAATG...CC AgGTTCAATC	AACCCACACA	CTAAATt	144 ^a
10	<i>S. oralis</i>	A AATTGACtTg	GTAGACGACG	AAGAAtTtGCT	TGAATtTgGTT	GAAATG...CC AgGTTCAATC	AACCCACACA	CTAAATt	985
	<i>S. pneumoniae</i>	A AGTTGACtTg	GTTGACGACG	AAGAAtTtGCT	TGAATtTgGTT	GAAATG...CC AgGTTCAATC	AACCCACACA	CTAAATt	145 ^a
	<i>S. cristatus</i>	A GATCGACtTg	GTTGATGACG	AAGAAtTtGCT	TGAATtTgGTT	GAAATG...CC AgGTTCAATC	AACCCACACA	CTAAATt	215
	<i>S. mitis</i>	A GATCGACtTg	GTTGATGACG	AAGAAtTtGCT	TGAATtTgGTT	GAAATG...CC AgGTTCAATC	AACCCACACA	CTAAATt	982
	<i>S. gordonii</i>	A AGTTGACtTg	GTTGAcGAtG	AAGAAtTtGCT	TGAGTtTgGTT	GAAATG...CC AgGTTCAATC	AACCCACACA	CTAAATt	200
15	<i>S. sanguinis</i>	A AGTTGACtTg	GTTGACGAtG	AAGAAtTtGCT	TGAATtTgGTT	GAAATG...CC AgGTTCAATC	AACCCACACA	CTAAATt	227
	<i>S. parasanguinis</i>	A AGTTGACtTg	GTTGATGAtG	AAGAAtTtGCT	TGAATtTgGTT	GAAATG...CC AgGTTCAATC	AACCCACACA	CTAAATt	225
	<i>S. salivarius</i>	A AGTTGACtTg	GTTGACGAtG	AAGAAtTtGCT	TGAATtTgGTT	GAAATG...CC TgGTTCAATC	AACCCACACA	CTAAATt	146 ^a
	<i>S. vestibularis</i>	A AGTTGACtTg	GTTGACGAtG	AAGAAtTtGCT	TGAATtTgGTT	GAAATG...CC TgGTTCAATC	AACCCACACA	CTAAATt	231
	<i>S. suis</i>	A AGTTGACtTg	GTTGACGAtG	AAGAAtTtGCT	TGAGTtTgGTT	GAAATG...CC AgGTTCTAtC	AACCCACACA	CTAAATt	229
20	<i>S. mutans</i>	A AGTTGAttTg	GTTGACGAtG	AAGAAtTtGCT	TGAATtTgGTT	GAAATG...CC AgGTTCAATt	cACCCACACA	CTAAATt	224
	<i>S. rattii</i>	A GGTTGACtTg	GTTGATGAtG	AAGAAtTtGCT	TGAATtTgGTT	GAAATG...CC AgGTTCAATt	cAtCCgCACA	CTAAATt	226
	<i>S. macacae</i>	A AGTTGACtTa	GTTGATGAtG	AAGAAtTtGCT	TGAATtTgGTT	GAAATG...CC AgGATCAATt	cAtCCACACA	CTAAATt	222
	<i>S. cricetus</i>	A GGTTGACtTg	GTTGACGAtG	AAGAAtTtGCT	TGAATtTgGTT	GAAATG...CC TgGTTCAATC	cAtCCACACA	CTAAATt	214
	<i>E. faecalis</i>	A AATgGAtaTg	GTTGATGACG	AAGAAtTtatT	aGAATtTAGTa	GAAATG...CC AgcTaCAATC	ActCCACACA	CaAAATt	607
25	<i>S. aureus</i>	A AGTTGACaTg	GTTGACGAtG	AAGAAtTtatT	aGAATtTAGTa	GAAATG...CC TgGTTCAATt	AcaCCACACA	CTgAAATt	176
	<i>B. cereus</i>	A ATgcGACaTg	GTaGATGACG	AAGAAtTtatT	aGAATtTAGTa	GAAATG...AG CgGTTCTgTa	AAagCtCACg	CTAAATt	7
	<i>E. coli</i>	A ATgcGACaTg	GTTGATGACG	AAGAGcTGCT	gGAActTgGTT	GAAATG...CC GgGCaCcATC	AAGCCgCACA	CcAAAGTt	78
30	Selected sequences for species-specific primers	TTGACcTt	GTTGATGACG	AAGAG	AAGAGtTtGCT	TGAATtTAGTt	GAG		999 1001
	Selected sequence for species-specific primer ^b						AGTTCAATC	AACCCACACA	CTAA

35 The sequence numbering refers to the Streptococcus pyogenes tuf gene fragment (SEQ ID NO. 1002). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^a The SEQ ID NO. refers to previous patent application WO98/20157.

^b This sequence is the reverse-complement of the selected primer.

Annex XXVI: Strategy for the selection of shiga toxin-producing, *Escherichia coli*-specific amplification primers and hybridization probe from *stx*₁ sequences.

	Accession #	230	263	343	375	391	421	SEQ ID NO.:					
5	<i>stx₁</i>	M19473a	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTTACATG	TTTTCACAT	TGCTCTGGTGA	CAGTAGCTAT	ACCA	-
	<i>stx₁</i>	M16625	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTTACATG	TTTTTACAT	TGCTCTGGTGA	CAGTAGCTAT	ACCA	-
	<i>stx₁</i>	M17358	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTTACATG	TTTTTACAT	TGCTCTGGTGA	CAGTAGCTAT	ACCA	-
	<i>stx₁</i>	Z36900	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTTACATG	TTTTTACAT	TGCTCTGGTGA	CAGTAGCTAT	ACCA	-
	<i>stx₁</i>	L04539	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTTACATG	TTTTTACAT	TGCTCTGGTGA	CAGTAGCTAT	ACCA	-
10	<i>stx₁</i>	M19437	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTTACATG	TTTTTACAT	TGCTCTGGTGA	CAGTAGCTAT	ACCA	-
	<i>stx₁</i>	M24352	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTTACATG	TTTTTACAT	TGCTCTGGTGA	CAGTAGCTAT	ACCA	-
	<i>stx₁</i>	X07903	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTTACATG	TTTTTACAT	TGCTCTGGTGA	CAGTAGCTAT	ACCA	-
	<i>stx₁</i>	Z36899	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTTACATG	TTTTTACAT	TGCTCTGGTGA	CAGTAGCTAT	ACCA	-
	<i>stx₁</i>	Z36901	TTGATGTC	AGAGGGATAG	ATCCAGAGGA	AGGGCG...TATCG	CTTTGCTGAT	TTTTTACATG	TTTTTACAT	TGCTCTGGTGA	CAGTAGCTAT	ACCA	1076
15	<i>stx₂</i>	X61283	TGGATaTa	cGAGGGcTtG	ATgtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTaCaCaTa	TatCaGTG...GTTtCca	TGaCaacgGA	CAGcAGtTAT	ACCA	-
	<i>stx₂</i>	L11079	TGGATaTa	cGAGGGcTtG	ATgtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTaCaCaTa	TatCaGTG...GTTtCca	TGaCaacgGA	CAGcAGtTAT	ACCA	-
	<i>stx₂</i>	M21534	TAGgTaTa	cGAGGGcTtG	ATgtttAtca	gGaGCG...TACaG	aTTTtCaGAT	TTTgCaCaTa	TatCaTTG...ATTTcCca	TGaCaacgGA	CAGcAGtTAT	ACCA	-
	<i>stx₂</i>	M36727	TAGgTaTa	cGAGGGcTtG	ATgtttAtca	gGaGCG...TACaG	aTTTtCaGAT	TTTgCaCaTa	TatCaTTG...ATTTcCca	TGaCaacgGA	CAGcAGtTAT	ACCA	-
20	<i>stx₂</i>	X81415	TAGgTaTa	cGAGGGcTtG	ATgtttAtca	gGaGCG...TACaG	aTTTtCaGAT	TTTgCaCaTa	TatCaTTG...ATTTcCca	TGaCaacgGA	CAGcAGtTAT	ACCA	-
	<i>stx₂</i>	X81416	TAGgTaTa	cGAGGGcTtG	ATgtttAtca	gGaGCG...TACaG	aTTTtCaGAT	TTTgCaCaTa	TatCaTTG...ATTTcCca	TGaCaacgGA	CAGcAGtTAT	ACCA	-
	<i>stx₂</i>	X81417	TAGgTaTa	cGAGGGcTtG	ATgtttAtca	gGaGCG...TACaG	aTTTtCaGAT	TTTgCaCaTa	TatCaTTG...ATTTcCca	TGaCaacgGA	CAGcAGtTAT	ACCA	-
	<i>stx₂</i>	X81418	TAGgTaTa	cGAGGGcTtG	ATgtttAtca	gGaGCG...TACaG	aTTTtCaGAT	TTTgCaCaTa	TatCaTTG...ATTTcCca	TGaCaacgGA	CAGcAGtTAT	ACCA	-
25	<i>stx₂</i>	E03962	TGGATaTa	cGAGGGcTtG	ATgtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTaCaCaTa	TatCaGTG...GTTtCca	TGaCaacgGA	CAGcAGtTAT	ACCA	-
	<i>stx₂</i>	E03959	TGGATaTa	cGAGGGcTtG	ATgtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTaCaCaTa	TatCaGTG...GTTtCca	TGaCaacgGA	CAGcAGtTAT	ACCA	-
	<i>stx₂</i>	X07865	TGGATaTa	cGAGGGcTtG	ATgtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTaCaCaTa	TatCaGTG...GTTtCca	TGaCaacgGA	CAGcAGtTAT	ACCA	-
	<i>stx₂</i>	Y10775	TGGATaTa	cGAGGGcTtG	ATgtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTaCaCaTa	TatCaGTG...GTTtCca	TGaCaacgGA	CAGcAGtTAT	ACCA	-
	<i>stx₂</i>	Z37725	TGGATaTa	cGAGGGcTtG	ATgtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTaCaCaTa	TatCaGTG...GTTtCca	TGaCaacgGA	CAGcAGtTAT	ACCA	1077
	<i>stx₂</i>	Z50754	TGGATaTa	cGAGGGcTtG	ATgtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTaCaCaTa	TatCaGTG...GTTtCca	TGaCaacgGA	CAGcAGtTAT	ACCA	-
	<i>stx₂</i>	X67514	TGGATaTa	cGAGGGcTtG	ATgtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTaCaCaTa	TatCaGTG...GTTtCca	TGaCaacgGA	CAGcAGtTAT	ACCA	-
30	<i>stx₂</i>	L11078	TGGATaTa	cGAGGGcTtG	ATgtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTaCaCaTa	TatCaGTG...GTTtCca	TGaCaacgGA	CAGcAGtTAT	ACCA	-
	<i>stx₂</i>	X65949	TGGATaTa	cGAGGGcTtG	ATgtctAtca	gGcGCG...TACCG	tTTTtCaGAT	TTTaCaCaTa	TatCaGTG...GTTtCca	TGaCaacgGA	CAGcAGtTAT	ACCA	-
	<i>stx₂</i>	AF043627	TGGATaTa	cGAGGGcTtG	ATgtctAtca	gGcGCG...TACaG	aTTTtCaGAT	TTTgCaCaTa	TatCaGTG...GTTtCca	TGaCaacgGA	CAGcAGtTAT	ACCA	-

Selected sequence for amplification primer **ATGTC AGAGGGATAG ATCCAGAGGA AGG** 1081

Selected sequence for hybridization probe **CG CTTTGCTGAT TTTTCACATG TTACC** 1084

Selected sequence for amplification primer^a **ACAT TGTCTGGTGA CAGTAGCTAT A** 1080

The sequence numbering refers to the *Escherichia coli stx*₁ gene fragment (SEQ ID NO. 1076). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^a This sequence is the reverse-complement of the selected primer.

Annex XXVII: Strategy for the selection of shiga toxin-producing, *Escherichia coli*-specific amplification primers and hybridization probe from *stx*₂ sequences.

5	Accession #	543	570	614	641	684	708	SEQ ID NO.				
	stx1	M19473	AGCGa	TgtTaCGgTt	TGtTAcTGTG	ACA...CAAC	ACTGgaTGAT	ctcAgTGggc	gTtcTTA...A	AGgtTgAGtA	gCGTcCTgCC	tGAC
	stx1	M16625	AGCGa	TgtTaCGgTt	TGtTAcTGTG	ACA...CAAC	ACTGgaTGAT	ctcAgTGggc	gTtcTTA...A	AGgtTgAGtA	gCGTcCTgCC	tGAC
	stx1	M17358	AGCGa	TgtTaCGgTt	TGtTAcTGTG	ACA...CAAC	ACTGgaTGAT	ctcAgTGggc	gTtcTTA...A	AGgtTgAGtA	gCGTcCTgCC	tGAC
	stx1	Z36900	AGCGa	TgtTaCGgTt	TGtTAcTGTG	ACA...CAAC	ACTGgaTGAT	ctcAgTGggc	gTtcTTA...A	AGgtTgAGtA	gTGTcCTgCC	tGAT
10	stx1	L04539	AGCGa	TgtTaCGgTt	TGtTAcTGTG	ACA...CAAC	ACTGgaTGAT	ctcAgTGggc	gTtcTTA...A	AGgtTgAGtA	gTGTcCTgCC	tGAT
	stx1	M19437	AGCGa	TgtTaCGgTt	TGtTAcTGTG	ACA...CAAC	ACTGgaTGAT	ctcAgTGggc	gTtcTTA...A	AGgtTgAGtA	gTGTcCTgCC	tGAC
	stx1	M24352	AGCGa	TgtTaCGgTt	TGtTAcTGTG	ACA...CAAC	ACTGgaTGAT	ctcAgTGggc	gTtcTTA...A	AGgtTgAGtA	gTGTcCTgCC	tGAC
	stx1	X07903	AGCGa	TgtTaCGgTt	TGtTAcTGTG	ACA...CAAC	ACTGgaTGAT	ctcAgTGggc	gTtcTTA...A	AGgtTgAGtA	gTGTcCTgCC	tGAC
	stx1	Z36899	AGCGa	TgtTaCGgTt	TGtTAcTGTG	ACA...CAAC	ACTGgaTGAT	ctcAgTGggc	gTtcTTA...A	AGgtTgAGtA	gTGTcCTgCC	tGAC
15	stx1	Z36901	AGCGa	TgtTaCGgTt	TGtTAcTGTG	ACA...CAAC	ACTTgaTGAT	ctcAgTGggc	gTtcTTA...A	AGgtTgAGtA	gTGTcCTgCC	tGAC
	stx2	X61283	AGCAG	TTCTGCGTtT	TGTCACtGTC	ACA...AGGC	ACTGTCTGA.	..AACTGCTC	CTGTGTa...G	CGAATCAGCA	ATGTGCTTCC	GGAG
	stx2	L11079	AGCAG	TTCTGCGTtT	TGTCACtGTC	ACA...AGGC	ACTGTCTGA.	..AACTGCTC	CTGTGTa...G	CGAATCAGCA	ATGTGCTTCC	GGAG
	stx2	M21534	AGCAG	TTCTGCGTtT	TGTCACtGTC	ACA...TGGC	ACTGTCTGA.	..AACTGCTC	CTGTtTA...G	AGAATCAGCA	ATGTGCTTCC	GGAG
	stx2	M36727	AGCAG	TTCTGCGTtT	TGTCACtGTC	ACA...TGGC	ACTGTCTGA.	..AACTGCTC	CTGTtTA...G	AGAATCAGCA	ATGTGCTTCC	GGAG
20	stx2	U72191	AGCAG	TTCTGCGTtT	TGTCACtGTC	ACA...TGGC	ACTGTCTGA.	..AACTGCTC	CTGTtTA...G	AGAATCAGCA	ATGTGCTTCC	GGAG
	stx2	X81415	AGCAG	TTCTGCGTtT	TGTCACtGTC	ACA...TGGC	ACTGTCTGA.	..AACTGCTC	CTGTtTA...G	AGAATCAGCA	ATGTGCTTCC	GGAG
	stx2	X81416	AGCAG	TTCTGCGTtT	TGTCACtGTC	ACA...TGGC	ACTGTCTGA.	..AACTGCTC	CTGTtTA...G	AGAATCAGCA	ATGTGCTTCC	GGAG
	stx2	X81417	AGCAG	TTCTGCGTtT	TGTCACtGTC	ACA...TGGC	ACTGTCTGA.	..AACTGCTC	CTGTtTA...G	AGAATCAGCA	ATGTGCTTCC	GGAG
	stx2	X81418	AGCAG	TTCTGCGTtT	TGTCACtGTC	ACA...TGGC	ACTGTCTGA.	..AACTGCTC	CTGTtTA...G	AGAATCAGCA	ATGTGCTTCC	GGAG
25	stx2	E03962	AGCAG	TTCTGCGTtT	TGTCACtGTC	ACA...AGGC	ACTGTCTGA.	..AACTGCTC	CTGTGTa...G	CGAATCAGCA	ATGTGCTTCC	GGAG
	stx2	E03959	AGCAG	TTCTGCGTtT	TGTCACtGTC	ACA...AGGC	ACTGTCTGA.	..AACTGCTC	CTGTGTa...G	CGAATCAGCA	ATGTGCTTCC	GGAG
	stx2	X07865	AGCAG	TTCTGCGTtT	TGTCACtGTC	ACA...AGGC	ACTGTCTGA.	..AACTGCTC	CTGTGTa...G	CGAATCAGCA	ATGTGCTTCC	GGAG
	stx2	Y10775	AGCAG	TTCTGCGTtT	TGTCACtGTC	ACA...AGGC	ACTGTCTGA.	..AACTGCTC	CTGTGTa...G	CGAATCAGCA	ATGTGCTTCC	GGAG
30	stx2	Z37725	AGCAG	TTCTGCGTtT	TGTCACtGTC	ACA...AGGC	ACTGTCTGA.	..AACTGCTC	CTGTGTa...G	CGAATCAGCA	ATGTGCTTCC	GGAG
	stx2	Z50754	AGCAG	TTCTGCGTtT	TGTCACtGTC	ACA...AGGC	ACTGTCTGA.	..AACTGCTC	CTGTGTa...G	CGAATCAGCA	ATGTGCTTCC	GGAG
	stx2	X67514	AGCAG	TTCTGCGTtT	TGTCACtGTC	ACA...AGGC	ACTGTCTGA.	..AACTGCTC	CTGTGTa...G	CGAATCAGCA	ATGTGCTTCC	GGAG
	stx2	L11078	AGCAG	TTCTGCGTtT	TGTCACtGTC	ACA...AGGC	ACTGTCTGA.	..AACTGCTC	CTGTGTa...G	CGAATCAGCA	ATGTGCTTCC	GGAG
	stx2	X65949	AGCAG	TTCTGCGTtT	TGTCACtGTC	ACA...AGGC	ACTGTCTGA.	..AACTGCTC	CTGTGTa...G	CGAATCAGCA	ATGTGCTTCC	GGAG
35	stx2	AF043627	AGCAG	TTCTGCGTtT	TGTCACtGTC	ACA...TGGC	ACTGTCTGA.	..AACTGCTC	CTGTtTA...G	AGAATCAGCA	ATGTGCTTCC	GGAG
	Selected sequence for											
	amplification primer											
			AG	TTCTGCGGTTT	TGTCACtGTC							1078

40	Selected sequence for hybridization probe	C	ACTGTCTGA.	..AACTGCTC	CTGT							1085
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	Selected sequence for amplification primer ^a																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
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45 The sequence numbering refers to the *Escherichia coli* stx₂ gene fragment (SEQ ID NO. 1077). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

^a This sequence is the reverse-complement of the selected primer.

Annex XXVIII: Strategy for the selection of *vanA*-specific amplification primers from *van* sequences.

	Accession #	926	952	1230	1255	SEQ ID NO.:
5	<i>vanA</i>	X56895	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG			1139
	<i>vanA</i>	M97297	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG			1141
	<i>vanA</i>	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG			1051
	<i>vanA</i>	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG			1052
	<i>vanA</i>	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG			1053
10	<i>vanA</i>	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG			1054
	<i>vanA</i>	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG			1055
	<i>vanA</i>	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG			1056
	<i>vanA</i>	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG			1057
	<i>vanA</i>	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG			1049
15	<i>vanA</i>	-	GTCAAT AGCGCGGACG AATTGGACTA C...GT AGAGGTCTAG CCCGTGTGGA TATG			1050
	<i>vanB</i>	U94526	GTAAC gGtaCGGAaG AAcTtaACGC T...GC AGAGGgCTtG CCCGTGTtGA TCTT			1117
	<i>vanB</i>	U94527	GTAAC gGtaCGGAaG AAcTtaACGC T...GC AGAGGgCTtG CtCGTGTtGA TCTT			-
	<i>vanB</i>	U94528	GTAAC gGtaCGGAaG AAcTtaACGC T...GC AGAGGgCTtG CCCGTGTtGA TCTT			-
	<i>vanB</i>	U94529	GTAAC gGtaCGGAaG AAcTtaACGC T...GC AGAGGgCTtG CCCGTGTtGA TCTT			-
20	<i>vanB</i>	U94530	GTAAC gGtaCGGAaG AAcTtaACGC T...GC AGAGGgCTtG CCCGTGTtGA TCTT			-
	<i>vanB</i>	Z83305	GTAAC gGtaCGGAaG AAcTtaACGC T...GC AGAGGgCTtG CCCGTGTtGA TCTT			-
	<i>vanB</i>	U81452	GTAAC gGtaCGGAaG AAcTtaACGC T...GC AGAGGgCTtG CCCGTGTtGA TCTT			-
	<i>vanB</i>	U35369	GTAAC gGtaCGGAaG AAcTtaACGC T...GC AGAGGgCTtG CCCGTGTtGA TCTT			-
	<i>vanB</i>	U72704	GTAAC gGtaCGGAaG AAcTtaACGC T...GC AGAGGgCTtG CCCGTGTtGA TCTT			-
25	<i>vanB</i>	L06138	GTAAC gGtaCGGAaG AAcTtaACGC T...GC AGAGGgCTtG CCCGTGTtGA TCTT			-
	<i>vanB</i>	L15304	GTAAC gGtaCGGAaG AAcTtaACGC T...GC AGAGGgCTtG CCCGTGTtGA TCTT			-
	<i>vanB</i>	U00456	GTAAC gGtaCGGAaG AAcTtaACGC T...GC AGAGGgCTtG CCCGTGTtGA TCTT			-
	<i>vanD</i>	AF130997	GTatgc AagGCaGAaG AAcTGcagGC A...GC AGAGGatTgG CCCGcaTtGA cCTG			-
30	<i>vanE</i>	AF136925	GTAgaA caaaaaagtG AtTtatAtAA A...GC AaAGGatTAG CgaGaaTcGA cTTT			-
	Selected sequence for amplification primer		AAT AGCGCGGACG AATTGGAC			1090
35	Selected sequence for amplification primer ^a		GAGGTCTAG CCCGTGTGGA T			1089

The sequence numbering refers to the *Enterococcus faecium vanA* gene fragment (SEQ ID NO. 1139). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

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

Annex XXIX: Strategy for the selection of vanB-specific amplification primers from van sequences.

	Accession #	470	495	608	633	SEQ ID NO.:
5	vanA	X56895	A CGCaATTgAA tCgGCAaGAC	AAATAT...ACG	GaATCTTTtCG tATTcATcAG	1139
	vanA	M97297	A CGCaATTgAA tCgGCAaGAC	AAATAT...ACG	GaATCTTTtCG tATTcATcAG	1141
	vanA	-	A CGCaATTgAA tCgGCAaGAC	AAATAT...ACG	GaATCTTTtCG tATTcATcAG	1051
	vanA	-	A CGCaATTgAA tCgGCAaGAC	AAATAT...ACG	GaATCTTTtCG tATTcATcAG	1052
	vanA	-	A CGCaATTgAA tCgGCAaGAC	AAATAT...ACG	GaATCTTTtCG tATTcATcAG	1053
10	vanA	-	A CGCaATTgAA tCgGCAaGAC	AAATAT...ACG	GaATCTTTtCG tATTcATcAG	1054
	vanA	-	A CGCaATTgAA tCgGCAaGAC	AAATAT...ACG	GaATCTTTtCG tATTcATcAG	1055
	vanA	-	A CGCaATTgAA tCgGCAaGAC	AAATAT...ACG	GaATCTTTtCG tATTcATcAG	1056
	vanA	-	A CGCaATTgAA tCgGCAaGAC	AAATAT...ACG	GaATCTTTtCG tATTcATcAG	1057
15	vanA	-	A CGCaATTgAA tCgGCAaGAC	AAATAT...ACG	GaATCTTTtCG tATTcATcAG	1049
	vanA	-	A CGCaATTgAA tCgGCAaGAC	AAATAT...ACG	GaATCTTTtCG tATTcATcAG	1050
	vanB	U94526	C TCCGATAGAA GCGGCAGGAC	AAATAT...ACG	GTATCTTTCCG CATCCATcAG	1117
	vanB	U94527	C TCCGATAGAA GCAGCAGGAC	AAATAT...ACG	GTATCTTTCCG CATCCATcAG	-
	vanB	U94528	C TCCGATAGAA GCGGCAGGAC	AAATAT...ACG	GTATCTTTCCG CATCCATcAG	-
20	vanB	U94529	C TCCGATAGAA GCGGCAGGAC	AAATAT...ACG	GTATCTTTCCG CATCCATcAG	-
	vanB	U94530	C TCCGATAGAA GCGGCAGGAC	AAATAT...ACG	GTATCTTTCCG CATCCATcAG	-
	vanB	Z83305	C TCCGATAGAA GCGGCAGGAC	AAATAT...ACG	GTATCTTTCCG CATCCATcAG	-
	vanB	U81452	C TCCGATAGAA GCGGCAGGAC	AAATAT...ACG	GTATCTTTCCG CATCCATcAG	-
	vanB	U35369	C TCCGATAGAA GCAGCAGGAC	AAATAT...ACG	GTATCTTTCCG CATCCATcAG	-
25	vanB	U72704	C TCCGATAGAA GCGGCAGGAC	AAATAT...ATG	GTATCTTTCCG CATCCATcAG	-
	vanB	L06138	C TCCGATAGAA GCAGCAGGAC	AAATAT...ACG	GTATCTTTCCG CATCCATcAG	-
	vanB	L15304	C TCCGATAGAA GCGGCAGGAC	AAATAT...ACG	GTATCTTTCCG CATCCATcAG	-
	vanB	U00456	C TCCGATAGAA GCAGCAGGAC	AAATAT...ACG	GTATCTTTCCG CATCCATcAG	-
	vanD	AF130997	C AGCaATcGAA GaAGCAaGAA	AAATAT...ACG	GctTtTTtaa gATTcATcAG	-
30	vanE	AF136925	A AGCaATAGAc GaAGCttcAA	AAATAT...ATG	GctTtTTcGa CtatgAagAG	-
	Selected sequence for amplification primer					1095
	CGATAGAA GCAGCAGGAC AA					
35	Selected sequence for amplification primer ^a					1096
	GTATCTTTCCG CATCCATcAG					

The sequence numbering refers to the *Enterococcus faecium* vanB gene fragment (SEQ ID NO. 1117). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

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

Annex xxx: Strategy for the selection of vanC-specific amplification primers from vanC sequences.

	Accession #	929	957	1064	1092	SEQ ID NO.:
5	vanC1	-	GT CGACGGCTTTT	TTTGATTTTG AAGAGAA...ACGGGTC	TGGCTCGAAT CGATTTTTTC	1058
	vanC1	-	GT CGACGGCTTTT	TTTGATTTTG AAGAGAA...ACGGGTC	TGGCTCGAAT CGATTTTTTC	1059
	vanC1	M75132	GT CGACGGCTTTT	TTTGATTTTG AAGAGAA...ACGGGTC	TGGCTCGAAT CGATTTTTTC	1138
	vanC2	-	GT AGACGGCTTTT	TTTCGATTTTG AAGAAAA...AAAGGTC	TTGCTCGCAT CGACTTTTTT	1060
	vanC2	-	GT AGACGGCTTTT	TTTCGATTTTG AAGAAAA...AAAGGTC	TTGCTCGCAT CGACTTTTTT	1061
10	vanC2	-	GT AGACGGCTTTT	TTTCGATTTTG AAGAAAA...AAAGGTC	TTGCTCGCAT CGACTTTTTT	1062
	vanC2	-	GT AGACGGCTTTT	TTTCGATTTTG AAGAAAA...AAAGGTC	TTGCTCGCAT CGACTTTTTT	1063
	vanC2	L29638	GT AGACGGCTTTT	TTTCGATTTTG AAGAAAA...AAAGGTC	TTGCTCGCAT CGACTTTTTT	-
	vanC2	L29638	GT AGACGGCTTTT	TTTCGATTTTG AAGAAAA...AAAGGTC	TTGCTCGCAT CGACTTTTTT	-
15	vanC3	-	GT AGACGGCTTTT	TTTCGATTTTG AAGAAAA...AAAGGTC	TTGCTCGCAT CGACTTTTTT	1064
	vanC3	-	GT AGACGGCTTTT	TTTCGATTTTG AAGAAAA...AAAGGTC	TTGCTCGCAT CGACTTTTTT	1065
	vanC3	-	GT AGACGGCTTTT	TTTCGATTTTG AAGAAAA...AAAGGac	TTGCTCGCAT CGACTTTTTT	1066
	vanC3	L29639	GT AGACGGCTTTT	TTTCGATTTTG AAGAAAA...AAAGGTC	TTGCTCGCAT CGACTTTTTT	-
20	Selected sequence for resistance primer		GACGGYTTT	TTYGATTTTG AAGA		1101
	Selected sequence for resistance primer ^a			GGTC	TKGCTCGMAT CGAYTTTTT	1102

25 The sequence numbering refers to the vanC1 gene fragment (SEQ ID NO. 1138). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequence displayed.

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

^a This sequence is the reverse-complement of the selected sequence.

Annex XXXI: Strategy for the selection of *Streptococcus pneumoniae*-specific amplification primers and hybridization probes from *pbp1a* sequences.

	Accession #	453	505	678	706	SEQ ID NO.:
5	<i>pbp1a</i> M90528	A TTGACTATACC AAGCATaCac	TATGctAAtG	CtATTTcAAG	TAATAcAACC	GA...TATATG ATGACaGATA TGATGAAAAC CGT...
	<i>pbp1a</i> X67873	A TCGACTATACC AAGTATtCac	TActCAAAAtG	CcATTTcAAG	TAACAcAACC	GA...TATATG ATGACCGAAA TGATGAAAAC AGT...
	<i>pbp1a</i> AB006868	A TCGACTATACC AAGTATtCac	TActCAAAAtG	CcATTTcAAG	TAACAcAACC	GA...TATATG ATGACCGACA TGATGAAAAC AGT...
	<i>pbp1a</i> AF046234	A TCGACTATACC AAGTATtCac	TActCAAAAtG	CcATTTcAAG	TAACAcAACC	GA...TATATG ATGACCGAAA TGATGAAAAC TGT...
10	<i>pbp1a</i> ...	A TCGACTATACC AAGTATtCac	TActCAAAAtG	CcATTTcAAG	TAACAcAACC	GA...TATATG ATGACCGAAA TGATGAAAAC TGT...
	<i>pbp1a</i> AB006873	A TCGACTATACC AAGTATtCac	TActCAAAAtG	CcATTTcAAG	TAACAcAACC	GA...TATATG ATGACCGACA TGATGAAAAC TGT...
	<i>pbp1a</i> AF139883	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACA	GA...TATATG ATGACCGACA TGATGAAAAC AGT...
	<i>pbp1a</i>	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACA	GA...TATATG ATGACCGACA TGATGAAAAC AGT...
15	<i>pbp1a</i>	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACA	GA...TATATG ATGACCGACA TGATGAAAAC AGT...
	<i>pbp1a</i>	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACA	GA...TATATG ATGACCGACA TGATGAAAAC AGT...
	<i>pbp1a</i>	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACA	GA...TATATG ATGACCGACA TGATGAAAAC AGT...
	<i>pbp1a</i>	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACA	GA...TATATG ATGACCGACA TGATGAAAAC AGT...
	<i>pbp1a</i>	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACA	GA...TATATG ATGACCGACA TGATGAAAAC AGT...
20	<i>pbp1a</i> AF159448	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACA	GA...TATATG ATGACCGACA TGATGAAAAC AGT...
	<i>pbp1a</i>	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACA	GA...TATATG ATGACCGAAA TGATGAAAAC TGT...
	<i>pbp1a</i>	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACA	GA...TATATG ATGACCGAAA TGATGAAAAC TGT...
	<i>pbp1a</i>	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACA	GA...TATATG ATGACCGAAA TGATGAAAAC TGT...
	<i>pbp1a</i>	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACA	GA...TATATG ATGACCGAAA TGATGAAAAC TGT...
25	<i>pbp1a</i> X67867	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACA	GA...TATATG ATGACCGAAA TGATGAAAAC TGT...
	<i>pbp1a</i>	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACC	GA...TATATG ATGACtGAAA TGATGAAAAC TGT...
	<i>pbp1a</i> Z49094	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACC	GA...TATATG ATGACtGAAA TGATGAAAAC TGT...
	<i>pbp1a</i>	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACC	GA...TATATG ATGACtGAAA TGATGAAAAC TGT...
	<i>pbp1a</i>	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACC	GA...TATATG ATGACtGAAA TGATGAAAAC TGT...
30	<i>pbp1a</i> X67870	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACC	GA...TATATG ATGACtGAAA TGATGAAAAC TGT...
	<i>pbp1a</i>	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACC	GA...TATATG ATGACtGAAA TGATGAAAAC TGT...
	<i>pbp1a</i>	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACC	GA...TATATG ATGACtGAAA TGATGAAAAC TGT...
	<i>pbp1a</i>	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACC	GA...TATATG ATGACtGAAA TGATGAAAAC TGT...
	<i>pbp1a</i>	A TCGACTATACC AAGCATGcAT	TATGCAAAACG	CcATTTcAAG	TAATAcAACC	GA...TATATG ATGACtGAAA TGATGAAAAC TGT...
35	Selected sequences for amplification primers	GACTATACC AAGCATGcAT	TATG	ATG ATGACCGAAA	TGATGAAAAC	1130 1129
40	Selected sequence for hybridization probe	CAAAACG CcATTTcAAG	TAATAcAACC			1197

The sequence numbering refers to the *Streptococcus pneumoniae* *pbp1a* gene fragment (SEQ ID NO. 1004). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower- case letters. Dots indicate gaps in the sequences displayed.

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

Annex XXXI: Strategy for the selection of *Streptococcus pneumoniae*-specific amplification primers and hybridization probes from *pbp1a* sequences (continued).

	Accession #	756	783	813	840	SEQ ID NO.:				
5	<i>pbp1a</i>	M90528	...	GCTGGTAA	aActGGTACg	TCaAACTATA...A	ATACgGGTTA	TGTAGCTCCG	GACGAAA	-
	<i>pbp1a</i>	X67873	...	GCTGGTAA	aACAGGaACc	TCTAACTATA...A	CctCTcaaTt	TGTAGCaCct	GATGAAC	-
	<i>pbp1a</i>	AB006868	...	GCTGGTAA	aACAGGaACc	TCTAACTATA...A	CctCTcaaTt	TGTAGCaCct	GACGAAC	-
	<i>pbp1a</i>	AF046234	...	GCAGGTAA	aACAGGTACT	TCTAACTATA...A	ACACTGGTTA	CGTAGCTCCA	GATGAAA	-
	<i>pbp1a</i> ..		...	GCAGGTAA	aACAGGTACT	TCTAACTATA...A	ACACTGGTTA	CGTAGCTCCA	GATGAAA	1014
10	<i>pbp1a</i>		...	GCTGGTAA	GACAGGTACT	TCTAACTACA...A	ACACTGGCTA	TGTAGCTCCA	GATGAAA	1017
	<i>pbp1a</i>	AB006873	...	GCAGGTAA	GACAGGTACT	TCTAACTATA...A	ACACTGGCTA	CGTAGCTCCA	GATGAAA	-
	<i>pbp1a</i>	AF139883	...	GCTGGTAA	aACAGGaACc	TCTAACTATA...A	ACACTGGCTA	TGTAGCTCCA	GATGAAA	1169
	<i>pbp1a</i>		...	GCTGGTAA	aACAGGaACc	TCTAACTATA...A	ACACTGGCTA	TGTAGCTCCA	GATGAAA	1004
	<i>pbp1a</i>		...	GCTGGTAA	aACAGGaACc	TCTAACTATA...A	ACACTGGCTA	TGTAGCTCCA	GATGAAA	1007
15	<i>pbp1a</i>		...	GCTGGTAA	aACAGGaACc	TCTAACTATA...A	ACACTGGCTA	TGTAGCTCCA	GATGAAA	1008
	<i>pbp1a</i>		...	GCTGGTAA	aACAGGaACc	TCTAACTATA...A	ACACTGGCTA	TGTAGCTCCA	GATGAAA	1009
	<i>pbp1a</i>		...	GCTGGTAA	aACAGGaACc	TCTAACTATA...A	ACACTGGCTA	TGTAGCTCCA	GATGAAA	1011
	<i>pbp1a</i>	AF159448	...	GCTGGTAA	aACAGGaACc	TCTAACTATA...A	ACACTGGCTA	TGTAGCTCCA	GATGAAA	-
	<i>pbp1a</i>		...	GCTGGTAA	GACAGGTACT	TCTAACTACA...A	ACACTGGCTA	TGTAGCTCCA	GATGAAA	1005
20	<i>pbp1a</i>		...	GCTGGTAA	GACAGGTACT	TCTAACTACA...A	ACACTGGCTA	TGTAGCTCCA	GATGAAA	1015
	<i>pbp1a</i>		...	GCTGGTAA	GACAGGTACT	TCTAACTACA...A	ACACTGGCTA	TGTAGCTCCA	GATGAAA	1006
	<i>pbp1a</i>		...	GCTGGTAA	GACAGGTACT	TCTAACTACA...A	ACACTGGCTA	TGTAGCTCCA	GATGAAA	1012
	<i>pbp1a</i>	X67867	...	GCTGGTAA	GACAGGTACT	TCTAACTACA...A	ACACTGGCTA	TGTAGCTCCA	GATGAAA	-
	<i>pbp1a</i>		...	GCAGGTAA	GACAGGTACT	TCTAACTATA...A	ACACTGGTTA	CGTAGCTCCA	GATGAAA	1010
25	<i>pbp1a</i>	Z49094	...	GCAGGTAA	GACAGGTACT	TCTAACTATA...A	ACACTGGTTA	CGTAGCTCCA	GATGAAA	-
	<i>pbp1a</i>		...	GCAGGTAA	GACAGGTACT	TCTAACTATA...A	ACACTGGCTA	CGTAGCTCCA	GATGAAA	1013
	<i>pbp1a</i>		...	GCAGGTAA	GACAGGTACT	TCTAACTATA...A	ACACTGGCTA	CGTAGCTCCA	GATGAAA	1016
	<i>pbp1a</i>	X67870	...	GCAGGTAA	GACAGGTACT	TCTAACTATA...A	ACACTGGCTA	CGTAGCTCCA	GATGAAA	-
	<i>pbp1a</i>		...	GCAGGTAA	GACAGGTACT	TCTAACTATA...A	ACACTGGCTA	CGTAGCTCCA	GATGAAA	1018
30	<i>pbp1a</i>	AJ002290	...	GCAGGTAA	GACgGGTACa	TCTAACTACA...A	ACACTGGCTA	C~~~~~	~~~~~	-
	<i>pbp1a</i>	X67871	...	GCTGGTAA	aACAGGTACc	TCTAACTATA...A	ACACTGGTTA	CGTAGCTCCA	GATGAAA	-
	Selected sequence for hybridization probe									
	Selected sequence for amplification primer ^a									
	Selected sequence for hybridization probe									

40 The sequence numbering refers to the *Streptococcus pneumoniae* *pbp1a* gene fragment (SEQ ID NO. 1004). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower- case letters. Dots indicate gaps in the sequences displayed. "R" "Y" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

45 ^a This sequence is the reverse-complement of the selected primer.

Annex XXXII: Specific and ubiquitous primers for nucleic acid amplification (*stx* sequences).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Toxin gene:</u> <i>stx</i>₁			
	1081	5'-ATG TCA GAG GGA TAG ATC CA	1076 ^a	233-252
	1080 ^b	5'-TAT AGC TAC TGT CAC CAG ACA ATG T	1076 ^a	394-418
15	<u>Toxin gene:</u> <i>stx</i>₂			
	1078	5'-AGT TCT GCG TTT TGT CAC TGT C	1077 ^a	546-567
	1079 ^b	5'-CGG AAG CAC ATT GCT GAT T	1077 ^a	687-705
20	<u>Toxin genes:</u> <i>stx</i>₁ and <i>stx</i>₂			
	1082	5'-TTG ARC RAA ATA ATT TAT ATG TG	1076 ^a	287-309
	1083 ^b	5'-TGA TGA TGR CAA TTC AGT AT	1076 ^a	790-809

25

^a Sequences from databases.

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

Annex XXXIII: Molecular beacon internal probes for hybridization and specific detection of toxin sequences.

5	Originating DNA fragment			
	SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
10	<u>Toxin gene:</u> <i>stx₁</i>			
	1084	5'- <u>CCA CGC</u> CGC TTT GCT GAT TTT TCA CAT GTT ACC <u>GCG TGG</u>	1076 ^b	346-372
15	<u>Toxin gene:</u> <i>stx₂</i>			
	1085	5'- <u>CCA CGC</u> CAC TGT CTG AAA CTG CTC CTG TG <u>CGT GG</u>	1077 ^b	617-638
20				

^a Underlined nucleotides indicate the molecular beacon's stem.
^b Sequences from databases.

Annex XXXIV: Specific and ubiquitous primers for nucleic acid amplification (van sequences).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Resistance gene:</u> vanA			
	1086	5'-CTA CTC CCG CCT TTT GGG TT	1049-1057 ^a	513-532 ^b
	1087 ^c	5'-CTC ACA GCC CGA AAC AGC CT	1049-1057 ^a	699-718 ^b
15	1086	5'-CTA CTC CCG CCT TTT GGG TT	1049-1057 ^a	513-532 ^b
	1088 ^c	5'-TGC CGT TTC CTG TAT CCG TC	1049-1057 ^a	885-904 ^b
	1086	5'-CTA CTC CCG CCT TTT GGG TT	1049-1057 ^a	513-532 ^b
20	1089 ^c	5'-ATC CAC ACG GGC TAG ACC TC	1049-1057 ^a	933-952 ^b
	1090	5'-AAT AGC GCG GAC GAA TTG GAC	1049-1057 ^a	629-649 ^b
	1091 ^c	5'-AAC GCG GCA CTG TTT CCC AA	1049-1057 ^a	734-753 ^b
	1090	5'-AAT AGC GCG GAC GAA TTG GAC	1049-1057 ^a	629-649 ^b
25	1089 ^c	5'-ATC CAC ACG GGC TAG ACC TC	1049-1057 ^a	933-952 ^b
	1092	5'-TCG GCA AGA CAA TAT GAC AGC	1049-1057 ^a	662-682 ^b
	1088 ^c	5'-TGC CGT TTC CTG TAT CCG TC	1049-1057 ^a	885-904 ^b
30	<u>Resistance gene:</u> vanB			
	1095	5'-CGA TAG AAG CAG CAG GAC AA	1117 ^d	473-492
	1096 ^c	5'-CTG ATG GAT GCG GAA GAT AC	1117 ^d	611-630
35	<u>Resistance gene:</u> vanAB			
	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057, 1117 ^a	437-456 ^b
	1113 ^c	5'-ACC GAC CTC ACA GCC CGA AA	1049-1057, 1117 ^a	705-724 ^b
40	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057, 1117 ^a	437-456 ^b
	1114 ^c	5'-TCW GAG CCT TTT TCC GGC TCG	1049-1057, 1117 ^a	817-837 ^b
	1115	5'-TTT CGG GCT GTG AGG TCG GBT GHG CG	1049-1057, 1117 ^a	705-730 ^b
45	1114 ^c	5'-TCW GAG CCT TTT TCC GGC TCG	1049-1057, 1117 ^a	817-837 ^b
	1116	5'-TTT CGG GCT GTG AGG TCG GBT GHG CGG	1049-1057, 1117 ^a	705-731 ^b
	1114 ^c	5'-TCW GAG CCT TTT TCC GGC TCG	1049-1057, 1117 ^a	817-837 ^b
	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057, 1117 ^a	437-456 ^b
50	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057, 1117 ^a	817-840 ^b

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the vanA sequence fragment (SEQ ID NO. 1051).

55 ^c These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^d Sequences from databases.

Annex XXXIV: Specific and ubiquitous primers for nucleic acid amplification (van sequences) (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Resistance gene: <i>vanAB</i> (continued)			
	1115	5'-TTT CGG GCT GTG AGG TCG GBT GHG CG	1049-1057,1117 ^a	705-730 ^b
	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-840 ^b
15	1116	5'-TTT CGG GCT GTG AGG TCG GBT GHG CGG	1049-1057,1117 ^a	705-731 ^b
	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-840 ^b
	1119	5'-TTT CGG GCT GTG AGG TCG GBT GHG C	1049-1057,1117 ^a	705-729 ^b
20	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-840 ^b
	1120	5'-TTT CGG GCT GTG AGG TCG GBT GHG	1049-1057,1117 ^a	705-728 ^b
	1118 ^c	5'-TTT TCW GAG CCT TTT TCC GGC TCG	1049-1057,1117 ^a	817-840 ^b
	1121	5'-TGT TTG WAT TGT CYG GYA TCC C	1049-1057,1117 ^a	408-429 ^b
25	1111 ^c	5'-CTT TTT CCG GCT CGW YTT CCT GAT G	1049-1057,1117 ^a	806-830 ^b
	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057,1117 ^a	437-456 ^b
	1111 ^c	5'-CTT TTT CCG GCT CGW YTT CCT GAT G	1049-1057,1117 ^a	806-830 ^b
30	1123	5'-TTT CGG GCT GTG AGG TCG GBT G	1049-1057,1117 ^a	705-726 ^b
	1111 ^c	5'-CTT TTT CCG GCT CGW YTT CCT GAT G	1049-1057,1117 ^a	806-830 ^b
	1112	5'-GGC TGY GAT ATT CAA AGC TC	1049-1057,1117 ^a	437-456 ^b
35	1124 ^c	5'-GAT TTG RTC CAC YTC GCC RAC A	1049-1057,1117 ^a	757-778 ^b
	Resistance gene: <i>vanC1</i>			
	1103	5'-ATC CCG CTA TGA AAA CGA TC	1058-1059 ^a	519-538 ^d
40	1104 ^c	5'-GGA TCA ACA CAG TAG AAC CG	1058-1059 ^a	678-697 ^d
	Resistance gene: <i>vanC1, vanC2, vanC3</i>			
	1097	5'-TCY TCA AAA GGG ATC ACW AAA GTM AC	1058-1066 ^a	607-632 ^d
45	1098 ^c	5'-TCT TCA AAA TCG AAA AAG CCG TC	1058-1066 ^a	787-809 ^d
	1099	5'-TCA AAA GGG ATC ACW AAA GTM AC	1058-1066 ^a	610-632 ^d
	1100 ^c	5'-GTA AAK CCC GGC ATR GTR TTG ATT TC	1058-1066 ^a	976-1001 ^d
	1101	5'-GAC GGY TTT TTY GAT TTT GAA GA	1058-1066 ^a	787-809 ^d
50	1102 ^c	5'-AAA AAR TCG ATK CGA GCM AGA CC	1058-1066 ^a	922-944 ^d
	Resistance gene: <i>vanC2-vanC3</i>			
	1105	5'-CTC CTA CGA TTC TCT TGA YAA ATC A	1060-1066,1140 ^a	487-511 ^e
55	1106 ^c	5'-CAA CCG ATC TCA ACA CCG GCA AT	1060-1066,1140 ^a	690-712 ^e

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *vanA* sequence fragment (SEQ ID NO. 1051).

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

^d The nucleotide positions refer to the *vanC1* sequence fragment (SEQ ID NO. 1058).

^e The nucleotide positions refer to the *vanC2* sequence fragment (SEQ ID NO. 1140).

60

Annex XXXIV: Specific and ubiquitous primers for nucleic acid amplification (*van* sequences) (continued).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID	Nucleotide NO. position
10	Sequencing primers (<i>vanAB</i>)			
	1112	5'-GGC TGY GAT ATT CAA AGC TC	1139 ^a	737-756
	1111 ^b	5'-CTT TTT CCG GCT CGW YTT CCT GAT G	1139 ^a	1106-1130
15	Sequencing primers (<i>vanA</i>, <i>vanX</i>, <i>vanY</i>)			
	1150	5'-TGA TAA TCA CAC CGC ATA CG	1141 ^a	860-879
	1151 ^b	5'-TGC TGT CAT ATT GTC TTG CC	1141 ^a	1549-1568
20	1152	5'-ATA AAG ATG ATA GGC CGG TG	1141 ^a	1422-1441
	1153 ^b	5'-CTC GTA TGT CCC TAC AAT GC	1141 ^a	2114-2133
	1154	5'-GTT TGA AGC ATA TAG CCT CG	1141 ^a	2520-2539
25	1155 ^b	5'-CAG TGC TTC ATT AAC GTA GTC	1141 ^a	3089-3109
	Sequencing primers (<i>vanC1</i>)			
	1110	5'-ACG AGA AAG ACA ACA GGA AGA CC	1138 ^a	122-144
30	1109 ^b	5'-ACA TCG TGA TCG CTA AAA GGA GC	1138 ^a	1315-1337
	Sequencing primers (<i>vanC2-vanC3</i>)			
	1108	5'-GTA AGA ATC GGA AAA GCG GAA GG	1140 ^a	1-23
35	1107 ^b	5'-CTC ATT TGA CTT CCT CCT TTG CT	1140 ^a	1064-1086

^a Sequences from databases.

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

Annex XXXV: Internal probes for nucleic acid hybridization and specific detection of *van* sequences.

5	Originating DNA fragment			
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Resistance gene:</u> <i>vanA</i>			
	1170	5'-ACG AAT TGG ACT ACG CAA TT	1049-1057 ^a	639-658 ^b
15	<u>Resistance gene:</u> <i>vanB</i>			
	1171	5'-ACG AGG ATG ATT TGA TTG TC	1117 ^c	560-579
20	^a These sequences were aligned to derive the corresponding primer. ^b The nucleotide positions refer to the <i>vanA</i> sequence fragment (SEQ ID NO. 1051). ^c Sequences from databases.			

Annex XXXVI: Specific and ubiquitous primers for nucleic acid amplification (pbp sequences).

5			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Resistance gene: <i>pbp1a</i>			
	1129	5'-ATG ATG ACC GAM ATG ATG AAA AC	1004-1018 ^a	681-703 ^b
	1131 ^c	5'-CAT CTG GAG CTA CRT ARC CAG T	1004-1018 ^a	816-837 ^b
15	1130	5'-GAC TAT CCA AGC ATG CAT TAT G	1004-1018 ^a	456-477 ^b
	1131	5'-CAT CTG GAG CTA CRT ARC CAG T	1004-1018 ^a	816-837 ^b
	Sequencing primers (<i>pbp1a</i>)			
20	1125	5'-ACT CAC AAC TGG GAT GGA TG	1169 ^d	873-892
	1126 ^c	5'-TTA TGG TTG TGC TGG TTG AGG	1169 ^d	2140-2160
	1125	5'-ACT CAC AAC TGG GAT GGA TG	1169 ^d	873-892
25	1128 ^c	5'-GAC GAC YTT ATK GAT ATA CA	1169 ^d	1499-1518
	1127	5'-KCA AAY GCC ATT TCA AGT AA	1169 ^d	1384-1403
	1126 ^c	5'-TTA TGG TTG TGC TGG TTG AGG	1169 ^d	2140-2160
	Sequencing primers (<i>pbp2b</i>)			
30	1142	5'-GAT CCT CTA AAT GAT TCT CAG GTG G	1172 ^d	1-25
	1143 ^c	5'-CAA TTA GCT TAG CAA TAG GTG TTG G	1172 ^d	1481-1505
	1142	5'-GAT CCT CTA AAT GAT TCT CAG GTG G	1172 ^d	1-25
35	1145 ^c	5'-AAC ATA TTK GGT TGA TAG GT	1172 ^d	793-812
	1144	5'-TGT YTT CCA AGG TTC AGC TC	1172 ^d	657-676
	1143 ^c	5'-CAA TTA GCT TAG CAA TAG GTG TTG G	1172 ^d	1481-1505
40	Sequencing primers (<i>pbp2x</i>)			
	1146	5'-GGG ATT ACC TAT GCC AAT ATG AT	1173 ^d	219-241
45	1147 ^c	5'-AGC TGT GTT AGC VCG AAC ATC TTG	1173 ^d	1938-1961
	1146	5'-GGG ATT ACC TAT GCC AAT ATG AT	1173 ^d	219-241
	1149 ^c	5'-TCC YAC WAT TTC TTT TTG WG	1173 ^d	1231-1250
	1148	5'-GAC TTT GTT TGG CGT GAT AT	1173 ^d	711-730
50	1147 ^c	5'-AGC TGT GTT AGC VCG AAC ATC TTG	1173 ^d	1938-1961

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *pbp1a* sequence fragment (SEQ ID NO. 1004).

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

^d Sequences from databases.

Annex XXXVII: Internal probes for nucleic acid hybridization and specific detection of *pbp* sequences.

5	Originating DNA fragment			
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	<u>Resistance gene:</u> <i>pbp1a</i>			
15	1132	5'-AGT GAA AAR ATG GCT GCT GC	1004-1018 ^a	531-550 ^b
	1133	5'-CAT CAA GAA CAC TGG CTA YGT AG	1004-1018 ^a	806-828 ^b
	1134	5'-CTA GAT AGA GCT AAA ACC TTC CT	1004-1018 ^a	417-439 ^b
	1135	5'-CAT TAT GCA AAC GCC ATT TCA AG	1004-1018 ^a	471-493 ^b
	1192	5'-GGT AAA ACA GGA ACC TCT AAC T	1004-1018 ^a	759-780 ^b
20	1193	5'-GGT AAG ACA GGT ACT TCT AAC T	1004-1018 ^a	759-780 ^b
	1194	5'-CAT TTC AAG TAA TAC AAC AGA ATC	1004-1018 ^a	485-508 ^b
	1195	5'-CAT TTC AAG TAA CAC AAC TGA ATC	1004-1018 ^a	485-508 ^b
	1196	5'-GCC ATT TCA AGT AAT ACA ACA GAA	1004-1018 ^a	483-506 ^b
	1197	5'-CAA ACG CCA TTT CAA GTA ATA CAA C	1004-1018 ^a	478-502 ^b
25	1094	5'-GGT AAA ACA GGT ACT TCT AAC TA	1004-1018 ^a	759-781 ^b
	1214	5'-GGT AAA ACA GGT ACC TCT AAC TA	1004-1018 ^a	759-781 ^b
	1216	5'-GGT AAG ACT GGT ACA TCA AAC TA	1004-1018 ^a	759-781 ^b
	1217	5'-CAA ATG CCA TTT CAA GTA ACA CAA C	1004-1018 ^a	478-502 ^b
	1218	5'-CAA ACG CCA TTT CAA GTA ACA CAA C	1004-1018 ^a	478-502 ^b
30	1219	5'-CAA ATG CTA TTT CAA GTA ATA CAA C	1004-1018 ^a	478-502 ^b
	1220	5'-CAA ACG CCA TTT CAA GTA ATA CGA C	1004-1018 ^a	478-502 ^b

^a These sequences were aligned to derive the corresponding primer.

^b The nucleotide positions refer to the *pbp1a* sequence fragment (SEQ ID NO. 1004).

Annex XXXVIII: Strategy for the selection of *vanAB*-specific amplification primers and specific hybridization probes *vanA* and *vanB* from *van* sequences.

[illegible]

The sequence numbering refers to the *Enterococcus faecium* vanA gene fragment (SEQ ID NO. 1139). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

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

The sequence numbering refers to the *Enterococcus faecium* vanA gene fragment (SEQ ID NO. 1139). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed.

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

Annex XXXIX: Internal probe for nucleic acid hybridization and specific detection of *mecA*.

5	Originating DNA fragment			
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10	Resistance gene: <i>mecA</i>			
	1177	5'-GCT CAA CAA GTT CCA GAT TA	1178 ^a	1313-1332

15 ^a Sequence from databases.

Annex XL: Specific and ubiquitous primers for nucleic acid amplification (*hexA* sequences).

5				
			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10				
	<u>Bacterial species:</u>		<i>Streptococcus pneumoniae</i>	
15	1179	5'-ATT TGG TGA CGG GTG ACT TT	1183 ^a	431-450
	1181 ^b	5'-AGC AGC TTA CTA GAT GCC GT	1183-1191 ^c	652-671 ^d
	Sequencing primers			
20	1179	5'-ATT TGG TGA CGG GTG ACT TT	1183 ^a	431-450
	1182 ^b	5'-AAC TGC AAG AGA TCC TTT GG	1183 ^a	1045-1064
25	^a Sequences from databases. ^b These sequences are from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing. ^c These sequences were aligned to derive the corresponding primer. ^d The nucleotide positions refer to the <i>hexA</i> sequence fragment (SEQ ID NO. 1183).			

Annex XLI: Internal probe for nucleic acid hybridization and specific detection of *hexA* sequences.

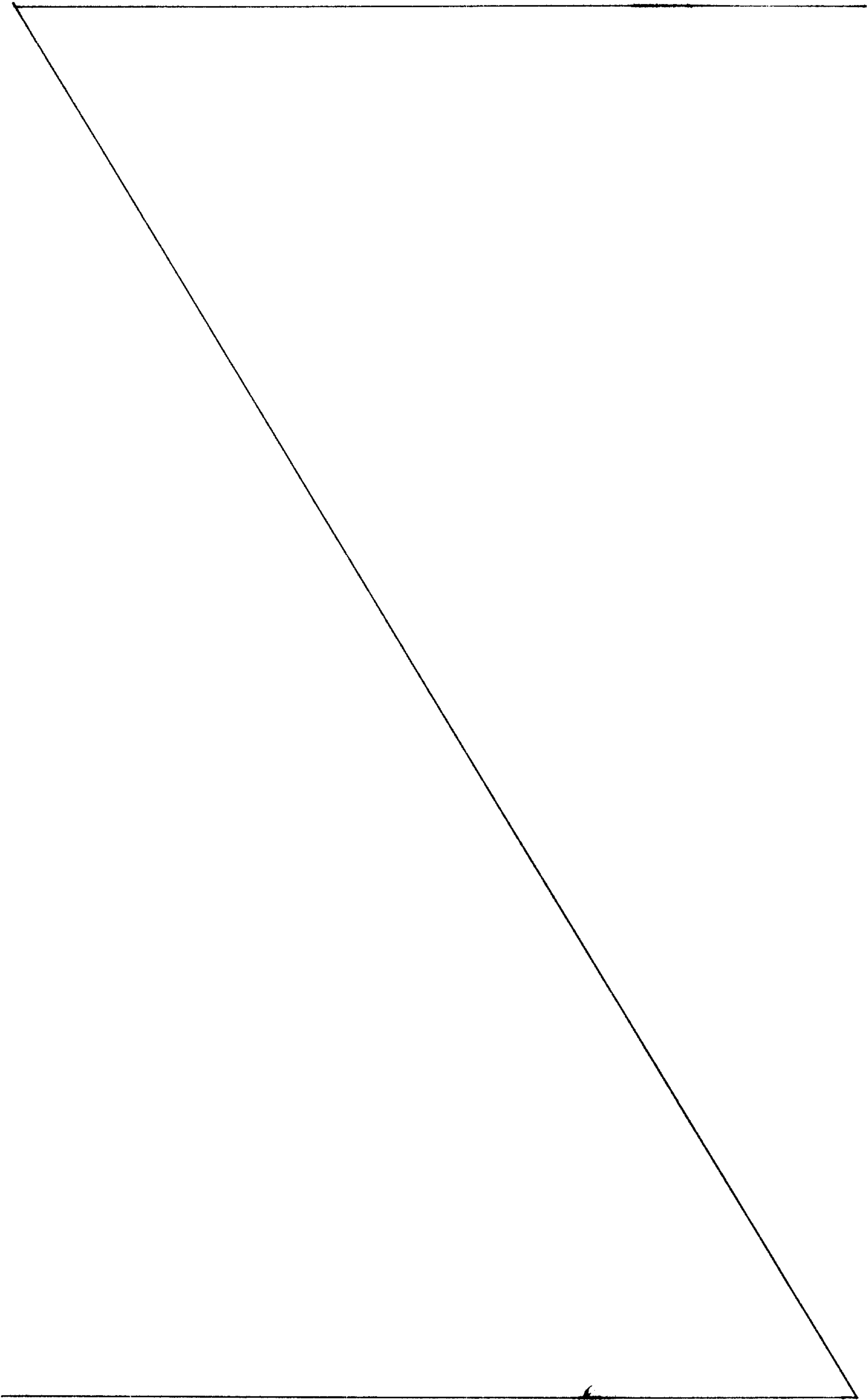
5				
			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
10				
	<u>Bacterial species:</u> <i>Streptococcus pneumoniae</i>			
	1180 ^a	5'-TCC ACC GTT GCC AAT CGC A	1183-1191 ^b	629-647 ^c

15

^a This sequences is from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^b These sequences were aligned to derive the corresponding primer.

20 ^c The nucleotide positions refer to the *hexA* sequence fragment (SEQ ID NO. 1183).



Annex XLII: Strategy for the selection of *Streptococcus pneumoniae* species-specific amplification primers and hybridization probe from hexA sequences.

5

	428	453	626	674	1042	1067	SEQ ID NO.:
<i>S. pneumoniae</i>	TGG ATTTGGTGAC GGGTGACTTTT	TAT...ATTG	CGATTGGCAA	CGGTGGAGCA	AACGGCATCT AGTAAGCTGC	TCCA...AATCCAAAG	GATCTCTTGC AGTTGGC
<i>S. pneumoniae</i>	~~~ ~~~~~TGAC GGGTGACTTTT	TAT...ATTG	CGATTGGCAA	CGGTGGAGCA	AACGGCATCT AGTAAGCTGC	TCCA...AATCCAAAG	GATCTCTTGC ~~~~~
<i>S. pneumoniae</i>	~~~ ~~~~~TGAC GGGTGACTTTT	TAT...ATTG	CGATTGGCAA	CGGTGGAGCA	AACGGCATCT AGTAAGCTGC	TCCA...AATCCAAAG	GATCTCTTGC ~~~~~
<i>S. pneumoniae</i>	~~~ ~~~~~TGAC GGGTGACTTTT	TAT...ATTG	CGATTGGCAA	CGGTGGAGCA	AACGGCATCT AGTAAGCTGC	TCCA...AATCCAAAG	GATCTCTTGC ~~~~~
<i>S. pneumoniae</i>	~~~ ~~~~~TGAC GGGTGACTTTT	TAT...ATTG	CGATTGGCAA	CGGTGGAGCA	AACGGCATCT AGTAAGCTGC	TCCA...AATCCAAAG	GATCTCTTGC ~~~~~
<i>S. pneumoniae</i>	~~~ ~~~~~TGAC GGGTGACTTTT	TAT...ATTG	CGATTGGCAA	CGGTGGAGCA	AACGGCATCT AGTAAGCTGC	TCCA...AATCCAAAG	GATCTCTTGC ~~~~~
<i>S. oralis</i>	~~~ ~~~~~TGAC GGGTGACTTTT	TAT...ATCca	CGACTGGCAG	CtGTGGAGCA	AgCGGCAGCT AGTAAGCTGC	TCCA...~~~~~	~~~~~
<i>S. mitis</i>	~~~ ~~~~~GGTGAC GGGTGACTTTT	TAT...ATTca	CGATTGGCAG	CtGTGGAGCA	AgCGGCATCT AGTAAaCTGC	TTCA...AATCCAAAG	GATCTCTTGC ~~~~~
<i>S. mitis</i>	~~~ ~~~~~TGAC GGGTGACTTTT	CAG...GCGag	gagCTGtCtc	CtaTGGAGCG	TcaGGCAGCa	gGgAAaCTGC	~~~~~
<i>S. mitis</i>	~~~ ~~~~~TGAC GGGTGACTTTT	CAG...GCGag	gaActGtCtc	CtaTGGAGCG	TcaGGCAGCg	gGgAAaTGC	TAGA...AATCCAAAG
							GATCTCTTGC ~~~~~

Selected sequence for
amplification primer

ATTTGGTGAC GGGTGACTTTT

1179

Selected sequences for
amplification primers^a

ACGGCATCT AGTAAGCTGC T

1181

CCAAAG GATCTCTTGC AGTT

1182

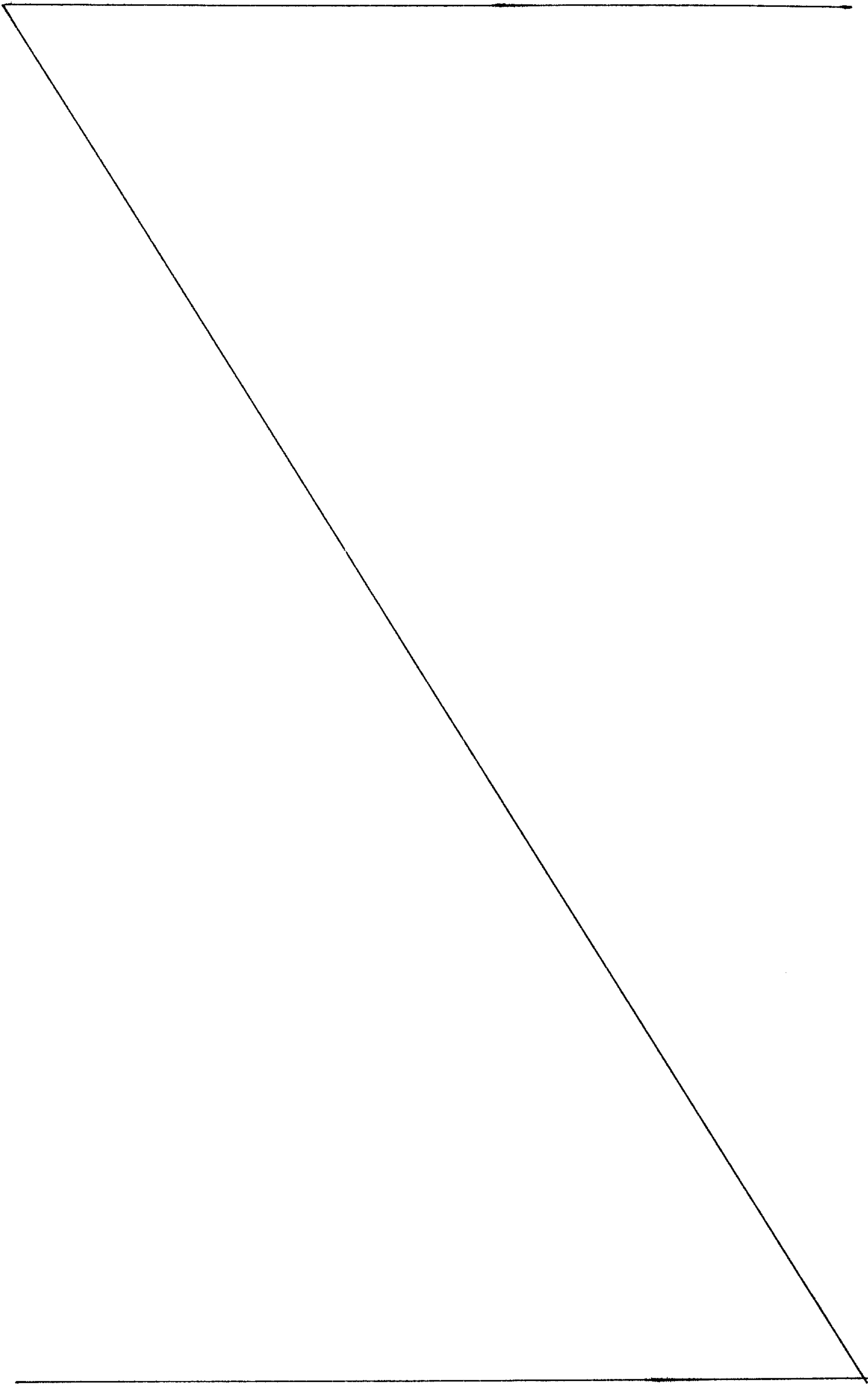
Selected sequence for
hybridization probe^a

TG CGATTGGCAA CGGTGGA

1180

The sequence numbering refers to the *Streptococcus pneumoniae* hexA gene fragment (SEQ ID NO. 1183). Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the sequences displayed. "~" indicate incomplete sequence data.

^a This sequence is the reverse-complement of the selected primer.



Annex XLIII: Specific and ubiquitous primers for nucleic acid amplification (pcp sequence).

5				Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence		SEQ ID NO.	Nucleotide position
10					
	<u>Bacterial species:</u>		<i>Streptococcus pyogenes</i>		
	1211	5'-ATT CTT GTA ACA GGC TTT GAT CCC		1215 ^a	291-314
15	1210 ^b	5'-ACC AGC TTG CCC AAT ACA AAG G		1215 ^a	473-494

^a Sequences from databases.

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

Annex XLIV: Specific and ubiquitous primers for nucleic acid amplification (*S. saprophyticus* unknown gene sequences).

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		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position
<u>Bacterial species:</u> <i>Staphylococcus saprophyticus</i>			
1208	5'-TCA AAA AGT TTT CTA AAA AAT TTA C	74,1093, 1198 ^b	169-193 ^c
1209 ^a	5'-ACG GGC GTC CAC AAA ATC AAT AGG A	74,1093, 1198 ^b	355-379 ^c

^a This sequence is from the complementary DNA strand of the sequence of the originating fragment given in the Sequence Listing.

^b These sequences were aligned to derive the corresponding primer.

^c The nucleotide positions refer to the *S. saprophyticus* unknown gene sequence fragment (SEQ ID NO. 1198).

Annex XLV: Molecular beacon internal probes for hybridization and specific detection of antibiotic resistance gene sequences.

5				
			Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position
10				
	Resistance gene: mecA			
15	1231	5'- <u>GCG</u> <u>AGC</u> CCG AAG ATA AAA AAG AAC CTC TGC TGC TCG C	1178 ^b	1291-1315
	Resistance gene: vanA			
20	1239	5'- <u>GCG</u> <u>AGC</u> GCA GAC CTT TCA GCA GAG GAG <u>GCT</u> <u>CGC</u>	1051	860-880
	1240	5'- <u>GCG</u> <u>AGC</u> CGG CAA GAC AAT ATG ACA GCA AAA TCG CTC GC	1051	663-688
25	Resistance gene: vanB			
	1241	5'- <u>GCG</u> <u>AGC</u> GGG GAA CGA GGA TGA TTT GAT TGG CTC GC	1117	555-577
30				

^a Underlined nucleotides indicate the molecular beacon's stem.
^b Sequence from databases.

Annex XLVI: Molecular beacon internal probe for hybridization and specific detection of an unknown *S. aureus* gene sequence.

5

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence ^a	SEQ ID NO.	Nucleotide position

10

<u>Bacterial species:</u>		<i>S. aureus</i>	
---------------------------	--	-------------------------	--

15

1232	5'- <u>GGA</u> <u>GCC</u> <u>GCG</u> CGA TTT TAT AAA TGA ATG TTG	1244	53-80
	ATA ACC <u>GGC</u> <u>TCC</u>		

^a Underlined nucleotides indicate the molecular beacon's stem.

Annex XLVII: Molecular beacon internal probes for hybridization and specific detection of *tuf* sequences.

5					Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence ^a			SEQ ID NO.	Nucleotide position
10	<u>Bacterial species:</u>		<i>Enterococcus faecalis</i>			
	1236	5'- <u>GCG</u> <u>AGC</u> CGT GGT GAA GTT CGC GTT GGT		883	370-391	
		<u>GGC</u> <u>TCG</u> <u>C</u>				
15	<u>Bacterial species:</u>		<i>Enterococcus faecium</i>			
	1235	5'- <u>GCG</u> <u>AGC</u> CGA AGT TGA AGT TGT TGG TAT		64	412-437	
		<u>TGC</u> <u>TGG</u> <u>CTC</u> <u>GC</u>				
20	<u>Bacterial species:</u>		<i>Staphylococcus</i> sp. other than <i>S. aureus</i>			
	1233	5'- <u>GCG</u> <u>AGC</u> GTT ACT GGT GTA GAA ATG TTC		878	372-394	
		<u>CGG</u> <u>CTC</u> <u>GC</u>				
25						

^a Underlined nucleotides indicate the molecular beacon's stem.

Annex XLVIII: Molecular beacon internal probes for hybridization and specific detection of *ddl* and *mtl* gene sequences.

5						Originating DNA fragment	
	SEQ ID NO.	Nucleotide sequence ^a				SEQ ID NO.	Nucleotide position
10							
	<u>Bacterial species:</u>		<i>E. faecium (ddl)</i>				
15	1237	5'- <u>GCG</u> <u>AGC</u> CGC GAA ATC GAA GTT GCT GTA	1242	334-359			
		TTA GGG <u>CTC</u> <u>GC</u>					
	<u>Bacterial species:</u>		<i>E. faecalis (mtl)</i>				
20	1238	5'- <u>GCG</u> <u>AGC</u> GGC GTT AAT TTT GGC ACC GAA	1243	631-656			
		GAA GAG <u>CTC</u> <u>GC</u>					

^a Underlined nucleotides indicate the molecular beacon's stem.

Annex XLIX: Internal probe for nucleic acid hybridization and specific detection of an unknown *S. aureus* gene sequence.

5

		Originating DNA fragment	
SEQ ID NO.	Nucleotide sequence	SEQ ID NO.	Nucleotide position

10

<u>Bacterial species:</u>		<i>Staphylococcus aureus</i>	
1234	5'-ACT AAA TAA ACG CTC ATT CG	1244	35-54

15

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

5 BERGERON, Michel G. ¹, 1145 des Érables, Québec City,
 Québec, Canada, G2K 1T8
 BOISSINOT, Maurice ¹, 109 Jean-Bruchési, St-Augustin-
 de-Desmaures, Québec, Canada, G3A 2N2
 10 HULETSKY, Ann ¹, 1231 Av des Pins, Sillery, Québec,
 Canada, G1S 4J3
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 15 PICARD, François J. ¹, 1245 de la Sapinière, Cap-Rouge,
 Québec, Canada, G1Y 1A1
 ROY, Paul H. ², 28 Charles Garnier, Loretteville,
 Québec, Canada, G2A 2X8

20 ¹:Canadian citizenship
²:American citizenship

(ii) TITLE OF THE INVENTION: HIGHLY CONSERVED GENES AN THEIR USE
 25 TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC AND UNIVERSAL
 NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY
 DETECT AND IDENTIFY BACTERIAL, FUNGAL AND PARASITICAL
 PATHOGENS FROM CLINICAL SPECIMENS FOR DIAGNOSIS

(iii) NUMBER OF SEQUENCES: 940
 30

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE:
 (B) STREET:
 35 (C) CITY:
 (D) STATE:
 (E) COUNTRY:
 (F) ZIP:

(v) COMPUTER READABLE:

(A) MEDIUM TYPE:
 (B) COMPUTER:
 (C) OPERATING:
 45 (D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION:
 50 (B) FILING DATE:
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

55 (A) APPLICATION:
 (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME:

(B) REGISTRATION NUMBER:

5

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE:

(B) TELEFAX:

2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
 (B) STRAIN: ATCC 19606

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

	CAA	ACT	CGT	G	AGC	ACAT	CCT	TCT	TTCT	CGT	CAG	GTA	GGT	G	TAC	CTT	ACAT	50
	CAT	CGT	ATT	C	TTA	ACAA	AAT	GCG	ACCT	TGT	TGAT	GAC	GAA		GAAT	TACT	TG	100
20	AAT	TAG	TAG	A	AAT	GGA	AGT	CGT	GAA	CTT	TTT	CTA	CTT	A	TGAC	TTCC	CA	150
	GGT	GAT	GAC	A	CTC	CAG	TAA	CCG	TGG	TTCA	GCT	CTT	GCA	G	CGCT	TAA	CGG	200
	TGA	AGC	TGG	T	CCT	TAC	GGT	AAG	AAT	CAGT	TCT	TGCT	CTT		GTA	GCAG	CAC	250
	TTG	ACT	CTT	A	CAT	CCC	CAG	CC	AGAG	CGTG	CAAT	CGA	CAA		AGCA	TTCT	TG	300
	ATG	CCA	AAT	C	AAG	ACG	TAT	CTC	AAT	TTCT	GGT	CGT	GGT	A	CAG	TAG	TAA	350
25	AGG	CCG	TGT	T	GAAG	CTGG	T	TCAT	CAA	AGT	TGGT	GAA	GAA		GTA	GAG	ATC	400
	TTG	GTAT	TAA		AGAT	ACAG	TT	AAA	ACA	ACTG	TAAC	TGG	GCG	T	AGAA	ATGT	T	450
	CGT	AAAC	TTC		TTG	ACGA	AGG	CCG	TGC	AGGT	GAGA	ACT	GTG		GTAT	CTTA	CT	500
	TCG	TGG	TACT		AAG	CGT	GAAG	AAG	TACA	ACG	TGGT	CAAG	T		CTTG	CTAA	AC	550
	CAG	GTACA	AAT		CAAG	CCGC	CAC	ACT	AAAT	TTCG	ACGC	AGA	AGT		ATAC	GTACT	T	600
30	TCT	AAAGA	AAG		AAGG	TGGT	CG	TCAC	ACT	CCA	TTCT	TAA	AATG		GTTA	CCGT	CC	650
	ACAG	TTCT	AC		TTCC	GTACA	A	CTG	ACG	TAA	TGGT	GCR	ATC		CAGT	TGAA	AG	700
	AAGG	CGTT	G		AATG	GTAAT	G	CCAG	G	TGACA	ACGT	TGAA	AAT		GTC	AGTA	GAA	750

35

2) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
 (B) STRAIN: ATCC 35568

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

	CGG	TGCG	ATC	CTC	GTGG	TCG	CCG	CGAC	CGA	CGG	CCCC	CATG	GCC	CAG	ACCC	50		
	GCG	AGC	ACGT	CCT	GCTC	GCC	CGT	CAGG	TCG	GCG	TTCC	CAC	CAT	CCT	CATC	100		
	GCC	CTCA	ACA	AGT	CCG	ACAT	GGT	TGAC	GAC	GAG	GAA	AATGA	TGG	AACT	GGT	150		
55	CGA	GGAG	GAG	TG	CCG	C	GACC	TG	CTGG	AGTC	CC	AGG	ACTT	C	GAT	CGCG	ATG	200
	CCCC	GAT	CGT	CC	AGG	TTT	CC	GCT	CTGA	AAGG	CC	CTC	GAG	GG	CG	ACGC	GGAG	250
	TGG	GTTG	CCA	AG	ATC	GAG	GA	GCT	CATG	GGAG	GCT	GTG	GATT		CCT	ACAT	CCC	300
	CAC	CCCC	CGAG	CG	CAT	ATG	G	ACA	AGC	CCCTT	CCT	CAT	GCCG		ATC	GAG	GACG	350
	TCT	TCAC	GAT	CAC	AGG	TCGT	GG	CAC	G	GTCG	TC	ACG	GGG	CG	TG	TTG	AGCGT	400
60	GGC	AAG	CTGC	CG	ATCA	ACTC	CG	AGG	TCGAG	AT	CCTC	GGTA	TCC	GTG	ATCC	450		

CCAGAAGACC ACGGTCACCG GCATCGAGAT GTTCCACAAG TCGATGGACG 500
 AGGCATGGGC CGGCGAGAAC TGTGGCCTGC TGCTGCGCGG TACCAAGCGC 550
 GATGAGGTTG AGCGCGGCCA GGTGTGGCC ATTCCCGGCT CCATCACGCC 600
 TCACACCGAG TTCGAGGGCC AGGTTTACAT CCTCAAGAAG GAAGAGGGCG 650
 5 GCCGTCACAA CCCGTTCTTC TCGAACTACC GTCCGCAGTT CTACTTCCGT 700
 ACCACGGACG TGACCGGCGT CATCACCTC CCCGAGGGCA CCGACATGGT 750
 CATGCCTGGC GACACCACCG AGATCTCCGT TCAGCTGATC CAGCCCATCG 800
 CCATGGAGCC CGGCTGGGCT TCGCCA 826

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2) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aerococcus viridans*
 (B) STRAIN: ATCC 11563

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

TGGTGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAAACTC 50
 GTGAGCACAT CCTTTTAGCT GGCCAAATCG GTGTTCCCTGC ATTCGTAGTA 100
 30 TTCTTAAACA AAGTTGACCA AGTTGACGAT GAAGAATTAC TAGAATTAGT 150
 TGAAATGGAA GTTCGTGACT TATTATCTGA GTACAACTAC CCAGGTGACG 200
 ATCTACCTGT AATCGCTGGT TCTGCTTTAT TAGCATTACA AGGCGATGAA 250
 GCTCAAGAAG CTAAAATCAT GGAATTAATG GAAGCTGTAG ACTCTTACAT 300
 TCCAGAACCA GAACGTGACA ACGACAAACC ATTCATGATG CCAATTGAGG 350
 35 ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA 400
 CGTGGTGAAG TTCGTACAGG TGACGAAGTT GACATCGTTG GTATTGCTGA 450
 ACAAATCGGT AAATCAGTTG TAACTGGTGT TGAAATGTTC CGTAAAAACT 500
 TAGACTACGC TCAAGCTGGT GACAACATCG GTGCATTATT ACGTGGTGTT 550
 CAACGTGAAG ACATCCAACG TGGTCAAGTA TTGGCTGCTC CTGGTTCAAT 600
 40 CACTCCACAT ACTAAATTTA AAGCGCAAGT TTACGTTTTA TCTAAAGAAG 650
 AAGGTGGACG TCATACACCA TTCTTAACTA ACTACCGTCC ACAATTCTAC 700
 TTCCGTACTA CTGACATTAC TGGTGTTATC ACTTTACCAG AAGACGTAGC 750
 TATGGTTATG CCTGGTGACA ACGTTGATAT GGACGTTGAA TTGATTCACC 800
 CAGTTGCGAT CGAAGATGGT ACTAAATTCT CTATC 835

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2) INFORMATION FOR SEQ ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Achromobacter xylosoxidans* subsp.
 60 *denitrificans*

(B) STRAIN: ATCC 15173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

5	CCTGGTGGTG	TCGGCCGCTG	ACGGCCCGAT	GCCGCAAACG	CGCGAACACA	50
	TCCTGCTGAG	CCGCCAGGTT	GGCGTGCCGT	ACATCATCGT	CTTCCTGAAC	100
	AAGGCCGACA	TGGTTGACGA	CGCCGAGCTG	CTTGAGCTGG	TGGAAATGGA	150
	AGTTCGCGAR	CTGCTGAGCA	AGTACGACTT	CCCGGGCGAC	GACACCCCGA	200
	TCGTGAAGGG	TTCGGCCAAG	CTGGCGCTGG	AAGGCGACAA	GGGCGAACTG	250
10	GGCGAACAGG	CCATCATGGC	GCTGGCCGCT	GCGCTGGACT	CGTACATCCC	300
	GACGCCTGAG	CGTGCCGTTG	ACGGCGCGTT	CCTGATGCCG	GTTGAAGACG	350
	TGTTCTCGAT	CTCGGGTCGC	GGCACCGTGG	TGACCGGCCG	TATCGAACGC	400
	GGCATCATCA	AGGTCGGCGA	GGAAATCGAA	ATCGTCGGTC	TGGTGCCGAC	450
	GGTGAAGACG	ACCTGCACGG	GCGTGAAAT	GTTCCGCAAG	CTGCTGGACC	500
15	AAGGTCAAGC	CGGCGACAAC	GTGGGCATCC	TRCTGCGCGG	CACCAAGCGT	550
	GAAGACGTCC	AGCGCGGCCA	GGTTCTGGCC	AAGCCGGGCT	CGATCACCCC	600
	GCACACGGAC	TTCACGTCCG	AGGTGTACAT	CCTGTCCAAG	GAAGAAGGCG	650
	GCCGTCACAC	TCCGTTCTTC	CAAGGCTATC	GTCCCCAGTT	CTACTTCCGC	700
	ACGACGGACG	TGACGGGCAC	GATCGAGCTG	CCGGCCGACA	AGGAAATGGT	750
20	CCTGCCGGGC	GACAACGTGG	CCATGACGGT	CAAGCTGCTG	GCTCCGATCG	800
	CCATGGAAGA	AGGCCTGCGT	TCGCCAC			827

25 2) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 823 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Anaerorhabdus furcosus</i>
	(B)	STRAIN: ATCC 25662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

40	TGGATCAATC	CTAGTAGTTG	CTGCAACTGA	TGGACCAATG	CCTCAAACCTC	50
	GTGAACATAT	CTTACTTGCT	CGTCAAGTAG	GTGTTCCAAG	AATGGTTGTA	100
	TTCTTGAACA	AATGCGACAT	GGTTGAAGAT	GAAGAATTAA	TCGACCTTGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTAAGTGC	TTACGGTTTC	GAAGGTGATG	200
45	ATACACCAGT	TATCCGTGGT	TCTGCATTAA	AATCTCTTGA	AGGAAATGCT	250
	GATTGGGAAG	CAAAAGTTGC	TGAATTAATG	GATGCAGTTG	ACTCTTGGAT	300
	TCCAACCTCA	ACTCATGAAA	CAGACAAACC	ATTCTTAATG	GCTGTTGAAG	350
	ATGTATTAC	AATTACAGGT	CGTGGTACAG	TTGCTACTGG	ACGTGTTGAA	400
	CGTGGACACT	TAAACCTTAA	CGAAGAAGTT	GAAATCGTTG	GTATTCATGA	450
50	TACTAAGAAA	TCAGTTGTTA	CTGGTATCGA	AATGTTCCGT	AAATTATTAG	500
	ACTATGCTGA	AGCAGGAGAC	AACATTGGTG	CATTATTACG	TGGTGTTTCT	550
	CGTGATGAAA	TCGAACGTGG	ACAATGTCTA	GCTAAACCTG	GATCAGTTAC	600
	TCCACATACA	GCTTTCAAAG	CTCAAGTATA	CGTATTAACT	AAAGAAGAAG	650
	GTGGACGTCA	TACACCATTC	GTAACATACT	ACCGTCCTCA	ATTCTATTTC	700
55	CGTACAACCTG	ACGTAACAGG	AGTTGTTAAA	CTTCCTGAAG	GTACTGAAAT	750
	GGTTATGCCT	GGAGACAACA	TCGAAATGAT	CGTTGAATTA	ATCGCTCCAA	800
	TCGCTGTTGA	ACAAGGAACT	AAG			823

60

2) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

	CGGCGGTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCTCAAACATC	50
	GTGAGCACAT	CCTTCTTTCT	CGTCAAGTAG	GTGTACCTTA	CATCGTTGTA	100
	TTCTTAAACA	AATGCGACAT	GGTAGACGAC	GAAGAATTAT	TAGAATTAGT	150
20	AGAAATGGAA	GTTCGCGACC	TATTATCTGA	ATACGGATTC	CCAGGCGACG	200
	ACATTCCTGT	AATCAAAGGT	TCTGCTCTTA	AAGCTCTTCA	AGGAGAAGCT	250
	GATTGGGAAG	CAAAAATCAT	TGAATTAATG	GCTGAAGTTG	ATGCTTACAT	300
	CCCAACTCCA	GAACGTGAAA	CTGACAAACC	ATTCTTAATG	CCTGTAGAGG	350
	ACGTATTCTC	TATCACAGGT	CGTGGTACAG	TTGCTACTGG	TCGTGTTGAG	400
25	CGCGGTATCG	TTAAAGTTGG	TGACGTAGTA	GAAATCATCG	GTCTTGCTGA	450
	AGAAAATGCT	TCTACAACCTG	TAAGTGGTGT	AGAGATGTTC	CGTAAACTTC	500
	TTGACCAAGC	TCAAGCTGGA	GACAACATCG	GTGCTTTACT	TCGTGGGGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	CTTGCAAAAA	GCGGTTCTGT	600
	AAAAGCTCAC	GCTAAATTCA	AAGCTGAAGT	TTTCGTATTA	TCTAAAGAAG	650
30	AAGGTGGACG	TCACACTCCA	TTCTTCGCTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTATCATC	CAATTACCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGACA	ACATCGAAAT	GACTATCGAA	CTTATCGCTC	800
	CAATCGCTAT	CGAAGAGGGA	ACTAA			825

2) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

	CGGCGGTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCTCAAACAC	50
	GTGAGCACAT	CCTTCTTTCT	CGTCAAGTAG	GTGTTCCTTA	CATCGTTGTA	100
55	TTCTTAAACA	AATGCGACAT	GGTAGATGAC	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCGCGACC	TATTATCTGA	ATACGGATTC	CCAGGCGACG	200
	ACATTCCTGT	AATCAAAGGT	TCTGCTCTTA	AAGCTCTTCA	AGGAGAAGCT	250
	GATTGGGAAG	CAAAAATCAT	TGAATTAATG	GCTGAAGTTG	ATGCTTACAT	300
	CCCAACTCCA	GAACGTGAAA	CTGACAAACC	ATTCTTAATG	CCTGTAGAGG	350
60	ACGTATTCTC	TATCACAGGT	CGTGGTACAG	TTGCTACTGG	TCGTGTTGAG	400

CGCGGTATCG TTAAAGTTGG TGACGTAGTA GAAATCATCG GTCTTGCTGA 450
 AGAAAATGCT TCTACAACTG TAACTGGTGT AGAGATGTTC CGTAAACTTC 500
 TTGACCAAGC TCAAGCTGGA GACAACATCG GTGCTTTACT TCGTGGGGTT 550
 GCTCGTGAAG ACATCCAACG TGGACAAGTA CTTGCAAAAA GCGGTTCTGT 600
 5 AAAAGCTCAC GCTAAATTCA AAGCTGAAGT TTTCGTATTA TCTAAAGAAG 650
 AAGGTGGACG TCACACTCCA TTCTTCGCTA ACTACCGTCC TCAGTTCTAC 700
 TTCCGTACAA CTGACGTAAC TGGTATCATC CAATTACCAG AAGGTACTGA 750
 AATGGTAATG CCTGGTGACA ACATTGAAAT GACTATCGAA CTTATCGCTC 800
 CAATCGCTAT CGAAGAGGGA ACTAAATTC 829
 10

2) INFORMATION FOR SEQ ID NO: 8

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacteroides distasonis*
 25 (B) STRAIN: ATCC 8503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

CGGTGCTATC ATCGTAGTTG CTGCTACTGA TGGTCCTATG CCTCAAACCTC 50
 30 GCGAGCACAT CCTTTTGGCT CGTCAGGTAA ACGTTCCGAG ATTGGTTGTA 100
 TTCATGAACA AGTGTGACAT GGTGACGAC GAGGAAATGT TGGAATTGGT 150
 TGAGATGGAG ATGAGAGAGT TGCTTTCATT CTATCAATTC GACGGTGACA 200
 ACACTCCGAT CATCCGTGGT TCTGCTCTTG GTGCATTGAA CGGTGATGCT 250
 CAATGGGAAG ATAAAGTAAT GGAGTTGATG GAAGCTTGTTG ATACTTGGAT 300
 35 TCCTCTGCCT CCGCGCGAAA TCGACAAGCC GTTCTTGATG CCGGTTGAGG 350
 ACGTATTCTC AATCACGGGT CGTGGTACTG TTGCTACAGG TCGTATCGAG 400
 ACAGGTATTG TTAAGGTTGG TGAGGAAGTT CAGATCATCG GTCTTGCGCG 450
 TGCTGGTAAG AAATCTGTTG TTACAGGTGT TGAGATGTTC CGTAAGTTAT 500
 TGGATCAAGG TGAGGCTGGT GATAACGTTG GTTTGTTGCT TCGCGGTATC 550
 40 GATAAGAATG AGATCAAGCG TGGTATGGTA ATCTGCCACC CGGGTCAGGT 600
 TAAAGAGCAT TCTAAGTTCA AGGCTGAGGT TTATATCTTG AAGAAAGAGG 650
 AAGGTGGTCG TCACACTCCG TTCCACAACA AATATCGTCC TCAGTTCTAT 700
 ATCCGTACAT TGGATGTAAC TGGTGAGATC ACTTTGCCGG AAGGAACTGA 750
 AATGGTAATG CCGGGTGATA ACGTAACGAT CGAGGTTGAG TTGATCTATC 800
 45 CGGTAGCATG TAGCGTAG 818

2) INFORMATION FOR SEQ ID NO: 9

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 639 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

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5  GGTCCTATGC CTCAAACACG TGAACACATC TTGTTATCAC GTAACGTTGG      50
   TGTACCATAC ATCGTTGTTT TCTTAAACAA AATGGATATG GTTGATGACG      100
   AAGAATTACT AGAATTAGTT GAAATGGAAG TTCGTGACTT ATTGTCAGAA      150
   TATGACTTCC CAGGCGACGA TGTTCCTGTA ATCGCTGGTT CTGCTTTGAA      200
   AGCTCTTGAA GCGGATGCTT CATACGAAGA AAAAATCATG GAATTAATGG      250
10 CTGCAGTTGA CGAATACGTT CCAACTCCAG AACGTGACAC TGACAAACCA      300
   TTCATGATGC CAGTCGAAGA CGTATTCTCA ATCACTGGAC GTGGTACTGT      350
   TGCTACAGGC CGTGTTGAAC GTGGACAAGT TCGCGTTGGT GACGAAGTTG      400
   AAATCGTTGG TATTGCTGAA GAACTGCTA AAACAACCTGT AACTGGTGTG      450
   GAAATGTTCC GTAAATTGTT AGACTATGCT GAAGCAGGGG ATAACATTGG      500
15 TGCATTGCTA CGTGGTGTG CTCTGTAAGA CATCCAACGT GGACAAGTAT      550
   TGGCTAAAGC TGGTACAATC ACACCTCATA CAAAATTTAA AGCTGAAGTT      600
   TACGTTTTTAA CAAAAGAAGA AGGTGGACGT CACACACCA      639

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2) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

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25  (A) LENGTH: 692 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

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     (A) ORGANISM: Staphylococcus saprophyticus
     (B) STRAIN: CSG 197

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

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   GAACACATTC TTTTATCACG TAACGTTGGT GTTCCAGCAT TAGTTGTATT      50
   CTTAAACAAA GTTGACATGG TTGACGATGA AGAATTATTA GAATTAGTAG      100
   AAATGGAAGT TCGTGACTTA TTAAGCGAAT ATGACTTCCC AGGTGACGAT      150
40  GTACCTGTAA TCTCTGGTTC TGCATTAAAA GCTTTAGAAG GCGACGCTGA      200
   CTATGAGCAA AAAATCTTAG ACTTAATGCA AGCTGTTGAT GACTTCATTC      250
   CAACACCAGA ACGTGATTCT GACAAACCAT TCATGATGCC AGTTGAGGAC      300
   GTATTCTCAA TCACTGGTCG TGGTACTGTT GCTACAGGCC GTGTTGAACG      350
   TGGTCAAATC AAAGTCGGTG AAGAAATCGA AATCATCGGT ATGCAAGAAG      400
45  AATCAAGCAA AACAACCTGTT ACTGGTGTAG AAATGTTCCG TAAATTATTA      450
   GACTACGCTG AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGT TTC      500
   ACGTGATGAC GTACAACGTG GTCAAGTTTT AGCTGCTCCT GGTACTATTA      550
   CACCACATAC AAAATTCAAA GCGGATGTTT ACGTTTTATC TAAAGATGAA      600
   GGTGGTCGTC ATACACCATT CTTCACTAAC TACCGCCAC AATTCTATTT      650
50  CCGTACTACT GACGTAAC TGTTGTTTAA CTTACCAGAA GG      692

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2) INFORMATION FOR SEQ ID NO: 11

55

(i) SEQUENCE CHARACTERISTICS:

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60  (A) LENGTH: 821 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear

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(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

5 (A) ORGANISM: *Bacteroides ovatus*
(B) STRAIN: ATCC 8483

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 11

10	CGGTGCTATC	ATCGTTTGTG	CTGCAACTGA	TGGTCCGATG	CCTCAAACCTC	50
	GCGAACACAT	TCTGTTAGCT	CGTCAGGTAA	ACGTACCTCG	TCTGGTTGTA	100
	TTCTTGAACA	AATGCGATAT	GGTAGACGAC	GAAGAAATGT	TGGAACCTCGT	150
	TGAAATGGAA	ATGAGAGAAC	TCCTTTCATT	CTATGATTTC	GATGGTGACA	200
	ATACTCCTAT	CATCCGTGGT	TCTGCTCTTG	GCGCATTGAA	CGGTGTTGAA	250
15	AAATGGGAAG	ACAAAGTTAT	GGAAGTGATG	GATGCAGTTG	ATAACTGGAT	300
	TCCACTGCCT	CCGCGCGATG	TTGATAAACC	ATTCTTGATG	CCGGTTGAAG	350
	ACGTGTTCTC	TATCACAGGT	CGTGGTACTG	TAGCAACAGG	TCGTATCGAA	400
	ACAGGTGTCA	TCCACGTTGG	TGATGAAGTC	GAAATTCTTG	GTTTAGGTGA	450
	AGATAAGAAA	TCAGTTGTAA	CTGGTGTTGA	AATGTTCCGT	AAACTGTTGG	500
20	ATCAAGGTGA	AGCTGGTGAC	AACGTAGGTC	TTTTGCTTCG	TGGTATTGAC	550
	AAGAACGAAA	TCAAACGTGG	TATGGTTCCT	TGTAAACCAG	GTCAGATTAA	600
	ACCGCACTCT	AAATTCAAAG	CTGAGGTTTA	TATCTTGAAG	AAAGAAGAAG	650
	GTGGTCGTCA	CACTCCGTTT	CACAACAAAT	ACCGTCCTCA	GTTCTACTTG	700
	CGTACTATGG	ACTGTACAGG	TGAAATCACT	TTGCCGGAAG	GAACAGAAAT	750
25	GGTAATGCCG	GGTGATAACG	TAAGTATTAC	AGTTGAGTTG	ATTTACCCAG	800
	TAGCATTGAA	CCCGGGCTTC	G			821

30 2) INFORMATION FOR SEQ ID NO: 12

(i)SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 838 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

40 (vi)ORIGINAL SOURCE:

(A) ORGANISM: *Bartonella henselae*
(B) STRAIN: ATCC 49882

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 12

45	TGGTGCGATT	TTGGTTGTTT	CAGCTGCTGA	TGGTCCGATG	CCTCAAACAC	50
	GTGAGCATAT	TCTTCTTGCC	CGTCAGGTTG	GTGTTCCAGC	GATTGTTGTT	100
	TTTCTTAATA	AGGTTGATCA	GGTTGATGAT	GCTGAGCTTT	TGGAGCTTGT	150
	TGAGCTTGAA	GTTCGGGAGT	TATTGTCGAA	ATATGATTTT	CCAGGAGACG	200
50	ATATTCCGAT	CGTTAAAGGT	TCTGCTTTTG	CAGCGCTTGA	AGATAAAGAT	250
	AAAAGCATTG	GTGAAGATGC	GGTTCGTCTT	TTGATGAGTG	AAGTTGATAA	300
	TTATATAACG	ACGCCTGAAC	GTCCTGTTGA	TCAGCCGTTT	TTGATGCCAA	350
	TTGAAGATGT	TTTTTTCGATT	TCGGGTCGTG	GAACTGTTGT	GACGGGTCGT	400
	GTTGAGCGTG	GTGTTATTAA	GGTTGGTGAA	GAAGTTGAGA	TTATCGGCAT	450
55	TCGTCCAAC	TCTAAGACAA	CAGTTACAGG	GGTTGAAATG	TTCCGCAAGC	500
	TTTTAGATCA	GGGGCAAGCG	GGTGATAATA	TTGGAGCGCT	GCTTCGTGGT	550
	ATTGATCGTG	AAGGGATTGA	GCGTGGACAA	GTTTTGGCGA	AGCCTGCTTC	600
	GGTTACACCT	CATACGAGAT	TTAAAGCAGA	GGCTTACATT	TTGACGAAAG	650
	ATGAAGGTGG	TCGTCATACT	CCATTTTTC	CGAATTATCG	TCCTCAGTTT	700
60	TATTTCCGTA	CTACGGATGT	AACGGGAATT	GTTACGCTTC	CAGAAGGTAC	750

AGAGATGGTT ATGCCTGGTG ATAATGTTGC TATGGATGTC TCTCTGATTG 800
 TTCCAATTGC CATGGAAGAA AAAC TTCGTT TTGCTATC 838

5

2) INFORMATION FOR SEQ ID NO: 13

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 839 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bifidobacterium adolescentis*
 (B) STRAIN: ATCC 15703

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

TGGCGCCATC CTTGTTGTGG CCGCCACCGA CGGCCCGATG GCTCAGACCC 50
 GCGAGCACGT GCTGCTCGCT CGTCAGGTGG GCGTCCCGAA GATCCTCGTC 100
 GCTCTGAACA AGTGCGATAT GGTCGACGAC GACGAGCTCA TCGAGCTCGT 150
 25 TGAGGAAGAG GTCCGTGACC TCCTCGACGA AAATGGCTTC GATCGCGATT 200
 GCCCGGTCAT CCACGTGTCC GCTTACGGCG CACTGCACGA TGACGCTCCG 250
 GACCACGAGA AGTGGGTTGA GCAGATCAAG AAGCTCATGG ACGCCGTCGA 300
 TGACTACATC CCGACCCCGG TCCACGATCT GGACAAGCCG TTCCTGATGC 350
 CGATCGAAGA TGTCTTCACC ATCTCCGGCC GTGGCACC GTTGACCGGC 400
 30 CGTGTCGAGC GTGGTAAGCT CCCGGTCAAC TCCAACGTCG AGATCGTCGG 450
 CATCCGTCCG ACCCAGACCA CCACCGTCAC CTCCATCGAG ACCTTCCACA 500
 AGCAGATGGA CGAGTGCGAG GCTGGCGACA ACACCGGTCT GCTGCTCCGC 550
 GGCATCAACC GTGACCAGGT CGAGCGTGGC CAGGTTCTGG CTGCTCCGGG 600
 CTCCGTGACC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA 650
 35 AGGACGAAGG CGGCCGTCAC TCGCCGTTCT TCTCCAATA CCGTCCGCAG 700
 TTCTACTTCC GTACCACCGA CGTCACCGGC GTCATCACCC TGCCGGAAGG 750
 CGTTGAGATG GTGCAGCCGG GCGATCACGC TACCTTCGGC GTTGAGCTGA 800
 TCCAGCCGAT CGCTATGGAA GAGGGCCTGA CCTTCGCAG 839

40

2) INFORMATION FOR SEQ ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 839 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bifidobacterium dentium*
 (B) STRAIN: ATCC 27534

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

TGGCGCTATC CTCGTTGTGG CCGCCACCGA CGGCCCGATG GCTCAGACCC 50
 GCGAGCACGT GCTGCTCGCT CGTCAGGTGG GCGTGCCGCG TATCCTCGTC 100
 60 GCCCTGAACA AGTGCGATAT GGTCGACGAC GAAGAGCTCA TCGAGCTCGT 150

```

5  TGAGGAAGAG GTCCGTGACC TCCTCGACGA AAACGGCTTC GATCGCGATT 200
   GCCCGGTCAT CCACACCTCC GCCTACGGCG CGCTGCACGA TGACGCTCCG 250
   GACCACGACA AGTGGGTTGA GTCCGTCAAG GAACTCATGA AGGCCGTCGA 300
   CGAGTACATC CCGACCCCGA CCCACGATCT GGACAAGCCG TTCCTGATGC 350
   CGATCGAAGA TGTGTTTACC ATCTCCGGCC GTGGCACCGT GGTTACCGGC 400
   CGTGTCGAGC GTGGTAAGCT CCCGGTCAAC TCCAACGTTG AGATCGTCGG 450
   CATCCGTCCG ACCCAGACCA CCACCGTCAC CTCCATCGAG ACCTTCCACA 500
   AGCAGATGGA CGAGTGCGAG GCTGGCGACA ACACCGGTCT GCTGCTCCGC 550
   GGCATCAACC GTGACCAGGT CGAGCGTGGC CAGGTTCTGG CTGCTCCGGG 600
10 CTCCGTGACC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA 650
   AGGACGAAGG CGGCCGTCAC TCGCCGTTCT TCTCCAATA CCGTCCGCAG 700
   TTCTACTTCC GTACCACCGA CGTCACCGGC GTCATCACCC TGCCGGAAGG 750
   CGTTGAGATG GTGCAGCCGG GCGATCACGC TACCTTCGGC GTTGAGCTGA 800
   TCCAGCCGAT CGCTATGGAA GAGGGCCTGA CCTTCGCAG 839
15

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2) INFORMATION FOR SEQ ID NO: 15

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20  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 838 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
25
      (ii) MOLECULE TYPE: Genomic DNA

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Brucella abortus
30  (B) STRAIN: S2308

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

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35  TGGCGCGATC CTGGTGGTTT CGGCTGCTGA CGGCCCGATG CCGCAGACCC 50
   GCGAGCACAT CCTGCTTGCC CGTCAGGTTG GCGTTCCGGC GATCGTCGTG 100
   TTCCTCAACA AGTGCGACCA GGTGACGAT GCAGAACTGC TCGAACTGGT 150
   TGAAGTGGAA GTGCGCGAAC TTCTGTCGAA GTACGAATTC CCCGGCGACG 200
   AAATCCCGAT CATCAAGGGC TCGGCTCTTG CTGCTCTGGA AGATTCTTCC 250
   AAGGAAGTGG GCGAAGATGC CATCCGCAAC CTGATGGACG CGGTTGACAG 300
40  CTACATTCCG ACCCCGGAAC GCCCGATCGA CCAGCCGTTT CTGATGCCGA 350
   TCGAAGACGT GTTCTCGATC TCCGGCCGTG GTACGGTTGT GACGGGTCGC 400
   GTTGAGCGCG GTATCGTTAA GGTCGGTGAA GAAGTTGAAA TCGTCGGCAT 450
   CAAGGCGACG ACGAAGACCA CGGTTACCGG CGTTGAAATG TTCCGCAAGC 500
   TGCTCGACCA GGGCCAGGCT GGCACACAACA TTGGCGCGCT GATCCGCGGC 550
45  GTTGGCCGTG AAGACGTTGA ACGCGGCCAG GTTCTCTGCA AGCCGGGTTC 600
   TGTGAAGCCG CACACCAAGT TTAAGGCAGA AGCCTATATT CTGACCAAGG 650
   ACGAAGGTGG CCGTCATACG CCGTTCTTCA CCAACTACCG TCCGCAGTTC 700
   TACTTCCGTA CGACGGACGT GACGGGTGTT GTGACGCTTC CGGCTGGCAC 750
   GGAAATGGTC ATGCCTGGCG ATAACGTCGC CATGGACGTT ACCCTGATCG 800
50  TGCCGATCGC CATGGAAGAG AAGCTTCGCT TCGCTATC 838

```

2) INFORMATION FOR SEQ ID NO: 16

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55
      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 771 bases
          (B) TYPE: Nucleic acid
          (C) STRANDEDNESS: Double
60  (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: *Burkholderia cepacia*
(B) STRAIN: LSPQ 2217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16

10	GGCAGCAGAC	GGCCCGATGC	CGCAAACGCG	TGAGCACATC	CTGCTGGCGC	50
	GTCAGGTTGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	GTGCGACATG	100
	GTGGACGACG	CCGAAGTGT	CGAGCTGGTC	GAGATGGAAG	TTCGCGAACT	150
	CCTGTCTGAAG	TACGACTTCC	CGGGCGACGA	CACGCCGATC	GTGAAGGGTT	200
	CGGCGAAGCT	GGCGCTGGAA	GGCGACACGG	GCGAGCTGGG	CGAAGTGGCG	250
15	ATCATGAGCC	TGGCCGACGC	GCTGGACACG	TACATCCCGA	CGCCGGAGCG	300
	TGCAGTTGAC	GGCGCGTTCC	TGATGCCGGT	GGAAGACGTG	TTCTCGATCT	350
	CGGGCCGCGG	TACGGTGGTG	ACGGGTCGTG	TCGAGCGCGG	CATCGTGAAG	400
	GTCGGCGAAG	AAATCGAAAT	CGTCGGTATC	AAGCCGACGG	TGAAGACGAC	450
	CTGCACGGGC	GTTGAAATGT	TCCGCAAGCT	GCTGGACCAA	GGTCAAGCAG	500
20	GCGACAACGT	TGGTATCCTG	CTGCGCGGCA	CGAAGCGTGA	AGACGTGGAG	550
	CGTGGCCAGG	TTCTGGCGAA	GCCGGGTTCG	ATCACGCCGC	ACACGCACTT	600
	CACGGCTGAA	GTGTACGTGC	TGAGCAAGGA	CGAAGGCGGC	CGTCACACGC	650
	CGTTCTTCAA	CAACTACCGT	CCGCAGTTCT	ACTTCCGTAC	GACGGACGTG	700
	ACGGGCTCGA	TCGAGCTGCC	GAAGGACAAG	GAAATGGTGA	TGCCGGGCGA	750
25	CAACGTGTCG	ATCACGGTGA	A			771

2) INFORMATION FOR SEQ ID NO: 17

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: *Cedecea davisae*
(B) STRAIN: ATCC 33431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

45	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAT	GGCCCAATGC	CACAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTTGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGTGAAGT	TCTGTCCCAG	TACGACTTCC	CGGGCGACGA	200
	TACTCCAATC	GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
50	AGTGGGAAGC	TAAAATCGTT	GAGCTGGCTG	GCTACCTGGA	TTCTTACATC	300
	CCTGAGCCAG	AGCGTGCTAT	CGATAAGCCG	TTCTTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGCC	GTGGTACCGT	TGTTACCGGT	CGTGTAAGAGC	400
	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAT	450
	ACTGCGAAAT	CTACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
55	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCAGG	CTCTATCAAG	600
	CCACACACCA	AGTTCGAATC	TGAAGTGTAC	ATCCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACCTGA	CGTGACCGGC	ACCATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
60	GTAATGCCTG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCAAT	800

CGCGATGGAT GACGGTCTGC GTTTCGCAA

829

5 2) INFORMATION FOR SEQ ID NO: 18

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea neteri*
 (B) STRAIN: ATCC 33855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18

20 CGCTATCCTG GTTGTGCTG CGACTGACGG CCCTATGCCT CAGACCCGTG 50
 AGCACATCCT GCTGGGTCGT CAGGTTGGCG TTCCTTACAT CATCGTGTTT 100
 CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTTGA 150
 AATGGAAGTT CGTGAAC TTC TCTCAGTA CGACTTCCCG GGCGATGACA 200
 25 CTCCAATCAT CCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAAGCAGAG 250
 TGGGAAGCTA AAATYGTGA GCTGGCTGGC TTCCTGGATT CCTACATCCC 300
 AGAACCAGTA CGTGCAATCG AYCTGCCGTT CCTGCTGCCA ATCGAAGACG 350
 TATTCTCCAT CTCCGGCCGT GGTACCGTTG TTACCGGTCTG TGTAGAGCGC 400
 GGTATCGTTA AAGTGGGCGA AGAAGTAGAA ATCGTTGGTA TCAAAGATAC 450
 30 TGCGAATCT ACCTGTACCG GCGTTGAAAT GTTCCGCAA CTGCTGGACG 500
 AAGGCCGTGC TGGTGAGAAC GTTGGTGTTT TGCTGCGTGG TATCAAACGT 550
 GAAGAAATCG AACGTGGTCA GGTCTGGCT AAGCCAGGCT CTATCAAGCC 600
 GCACACCAAG TTCGAATCTG AAGTGTACAT CCTGTCCAAA GACGAAGGCG 650
 GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCACAGTT CTACTTCCGT 700
 35 ACAACTGACG TGACCGGTAC CATCGAACTG CCAGAAGGCG TAGAGATGGT 750
 AATGCCAGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG 800
 CGATGGACGA CGGTCTGCGT TTCG 824

40 2) INFORMATION FOR SEQ ID NO: 19

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea lapagei*
 (B) STRAIN: ATCC 33432

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

60 CGCTATTCTG GTTGTGCTG CAACTGACGG CCCTATGCCT CAGACCCGTG 50
 AGCACATCCT GCTGGGTCGC CAGGTTGGCG TTCCTTACAT CATCGTGTTT 100
 CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTAGA 150
 AATGGAAGTT CGTGAAC TTC TCTCAGTA CGACTTCCCA GGCGATGATA 200

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      CCCC AATCAT CCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAAGCAGAG      250
      TGGGAAGCTA AAATCGTTGA GCTGGCTGGC TTCCTGGATT CCTACATCCC      300
      AGAACCAGTA CGTGCAATCG ACCTGCCGTT CCTGCTGCCA ATCGAAGACG      350
      TATTCTCCAT CTCCGGCCGT GGTACCGTTG TKACCGGTCG TGTAGAGCGC      400
5     GGTATCGTTA AAGTGGGCGA AGAAGTAGAA ATCGTTGGTA TCAAAGATAC      450
      TGC GAAATCT ACCTGTACTG GCGTTGAAAT GTTCCGCAAA CTGCTGGACG      500
      AAGGCCGTGC TGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAACGT      550
      GAAGAAATCG AACGTGGTCA GGTTCCTGGCT AAGCCAGGCT CTATCAAGCC      600
      GCACACCAAG TTCGAATCTG AAGTGTACAT CCTGTCCAAA GACGAAGGCG      650
10    GCCGTCATAC TCCGTTCTTC AARGGCTACC GTCCACAGTT CTACTTCCGT      700
      ACCACTGACG TGACCGGTAC CATCGAACTG CCAGAAGGCG TAGAGATGGT      750
      AATGCCAGGT GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG      800
      CGATGGACGA CGGTCTGCGT TTCGCAA      827

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15

2) INFORMATION FOR SEQ ID NO: 20

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      (i) SEQUENCE CHARACTERISTICS:
20    (A)   LENGTH: 831 bases
      (B)   TYPE: Nucleic acid
      (C)   STRANDEDNESS: Double
      (D)   TOPOLOGY: Linear

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25    (ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

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      (A)   ORGANISM: Chlamydia pneumoniae
      (B)   STRAIN: CWL 029

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30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

```

      GCGGAGCTAT CCTAGTCGTT TCAGCTACAG ACGGAGCTAT GCCACAAACT      50
      AAAGAACATA TCTTGCTAGC TCGCCAGGTT GGAGTTCCTT ATATCGTTGT      100
35    TTTCTTGAAT AAAGTAGATA TGATCTCTCA AGAAGATGCT GAACTTATTG      150
      ACCTTGTTGA GATGGAACCT AGTGAGCTTC TTGAAGAAAA AGGCTACAAA      200
      GGATGCCCTA TTATCCGTGG TTCTGCTTTG AAAGCTCTTG AAGGTGATGC      250
      AAATTATATC GAAAAAGTTC GAGAACTTAT GCAAGCTGTG GATGACAACA      300
      TCCCTACACC AGAAAGAGAA ATTGATAAGC CTTTCTTAAT GCCTATCGAA      350
40    GACGTATTCT CAATCTCTGG TCGTGGTACT GTGGTTACAG GAAGAATCGA      400
      GCGTGGAATC GTTAAAGTTT CTGATAAAGT TCAGCTCGTG GGATTAGGAG      450
      AGACTAAAGA AACAATCGTT ACTGGAGTCG AAATGTTTCAG GAAAGAACTT      500
      CCTGAAGGTC GTGCAGGAGA AAACGTTGGT TTACTCCTCA GAGGTATTGG      550
      AAAGAACGAT GTTGAAAGAG GTATGGTGGT TTGTCAGCCT AACAGCGTGA      600
45    AGCCTCATAC GAAATTTAAG TCAGCTGTTT ACGTTCCTCA GAAAGAAGAA      650
      GGCGGACGTC ATAAGCCTTT CTTCAGCGGA TACAGACCTC AGTTCTTCTT      700
      CCGTACTACA GACGTGACAG GAGTCGTAAC TCTTCCTGAA GGAAGTGAAG      750
      TGGTAATGCC TGGAGATAAC GTTGAGCTTG ATGTTGAGCT CATTGGAACA      800
      GTTGCTCTTG AAGAAGGAAT GAGATTTGCA A      831

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50

2) INFORMATION FOR SEQ ID NO: 21

```

55    (i) SEQUENCE CHARACTERISTICS:
      (A)   LENGTH: 826 bases
      (B)   TYPE: Nucleic acid
      (C)   STRANDEDNESS: Double
      (D)   TOPOLOGY: Linear

```

60

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia psittaci*

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 21

```

5      TGGAGCGATT CTCGTTGTTT CCGCTACTGA CGGTGCGATG CCTCAGACCA      50
      AAGAACATAT TCTTTTGGCG AGACAGGTTG GTGTTCCTTA CATCGTTGTT      100
10     TTCCTTAACA AAATCGATAT GATTTCTCAA GAAGATGCTG AGCTCGTAGA      150
      CTTAGTTGAA ATGGAATTGT CCGAACTTCT AGAAGAAAAA GGTTATAAAG      200
      GTTGCCCAAT TATCCGTGGT TCTGCTTTGA AAGCCTTAGA AGGTGATGCA      250
      AGCTACGTTG AAAAAATTCT CGAGTTAATG CAAGCAGTGG ATGATAACAT      300
      CCCTACTCCA GAGCGTGAAG TTGATAAGCC TTTCTTAATG CCTATCGAAG      350
15     ACGTATTCTC TATTTCTGGT CGTGGTACTG TGGTCACAGG ACGTATCGAG      400
      CGTGGAATCG TTAAAGTGGG TGATAAAGTA CAGATTGTTG GTTTAAGAGA      450
      TACTAGAGAG ACAATTGTTA CCGGTGTGGA AATGTTCAGA AAAGAACTTC      500
      CAGAAGGTCA AGCAGGGGAA AACGTTGGTT TGCTCCTCAG AGGTATCGGT      550
      AAGAATGACG TTGAACGTGG TATGGTTATC TGCCAACCTA ATAGCGTGAA      600
20     ATCTCACACA CAATTTAAAG GTGCTGTCTA CATTCTACAA AAAGAAGAGG      650
      GTGGACGTCA TAAACCTTTC TTTACCGGAT ACAGACCTCA GTTCTTCTTC      700
      CGTACAACAG ATGTTACAGG TGTGTGTAAC CTCCCAGAAG GTACAGAGAT      750
      GGTTATGCCA GGCGATAACG TTGAATTCGA AGTTCAATTA ATTAGCCCAG      800
      TAGCTCTAGA AGAAGGTATG AGATTT      826
25

```

2) INFORMATION FOR SEQ ID NO: 22

(i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia trachomatis*

(B) STRAIN: LGV 12

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 22

```

45     GGGGCTATTC TAGTAGTTTC TGCAACAGAC GGAGCTATGC CTCAAACTAA      50
      AGAGCATATT CTTTTGGCAA GACAAGTTGG GGTTCCTTAC ATCGTTGTTT      100
      TTCTCAATAA AATTGACATG ATTTCCGAAG AAGACGCTGA ATTGGTCGAC      150
      TTGGTTGAGA TGGAGTTGGC TGAGCTTCTT GAAGAGAAAG GATACAAAGG      200
      GTGTCCAATC ATCAGAGGTT CTGCTCTGAA AGCTTTGGAA GGGGATGCTG      250
      CATACATAGA GAAAGTTCGA GAGCTAATGC AAGCCGTCGA TGATAATATC      300
50     CCTACTCCAG AAAGAGAAAT TGACAAGCCT TTCTTAATGC CCATTGAGGA      350
      CGTGTTCTCT ATCTCCGGAC GAGGAACTGT AGTAACTGGA CGTATTGAGC      400
      GTGGAATTGT TAAAGTTTCC GATAAAGTTC AGTTGGTCGG TCTTAGAGAT      450
      ACTAAAGAAA CGATTGTTAC TGGGGTTGAA ATGTTTCAGAA AAGAACTCCC      500
      AGAAGGTCGT GCAGGAGAGA ATGTTGGATT GCTCCTCAGA GGTATTGGTA      550
      AGAACGATGT GGAAAGAGGA ATGGTTGTTT GCTTGCCAAA CAGTGTTAAA      600
      CCTCATACAC GGTTTAAGTG TGCTGTTTAC GTTCTGCAAA AAGAAGAAGG      650
      TGGACGACAT AAGCCTTTCT TCACAGGATA TAGACCTCAA TTCTTCTTCC      700
      GTACAACAGA CGTTACAGGT GTGGTAACTC TGCTTGAGGG AGTTGAGATG      750
      GTCATGCCTG GGGATAACGT TGAGTTTGAA GTGCAGTTGA TTAGCCCTGT      800
60     GGCTTTAGAA GAAGGTATGA GA      822

```

2) INFORMATION FOR SEQ ID NO: 23

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chryseobacterium meningosepticum*
 (B) STRAIN: CDC B7681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23

20	CGGAGCTATC	TTAGTATGTG	CTGCTACAGA	TGGTCCAATG	CCTCAAACCTA	50
	GAGAACACAT	CCTACTTTGC	CGTCAGGTAA	ACGTACCTAG	AATTGTTGTG	100
	TTCATGAACA	AAGTTGACAT	GGTAGATGAT	CCAGAATTGT	TAGAGCTTGT	150
	TGAGCTTGAA	CTTAGAGATC	TATTATCTAC	TTACGAATAT	GATGGTGATA	200
	ACTCTCCAGT	AATTCAAGGT	TCTGCTCTTG	GTGCTCTTAA	CGGTGATGCT	250
25	AAGTGGGTAG	CTACTGTAGA	AGCTCTAATG	GATGCTGTTG	ATACTTGGAT	300
	CGAGCAACCA	GTAAGAGATT	CTGATAAGCC	ATTCCTTATG	CCAATCGAAG	350
	ACGTATTCTC	TATTACAGGT	AGAGGTACTG	TAGCAACTGG	TAGAATCGAG	400
	GCTGGTGTA	TCAACACAGG	TGATCCTGTT	GACATCGTAG	GTATGGGTGA	450
	CGAGAAGTTA	ACTTCTACTA	TTACAGGTGT	TGAGATGTTT	AGAAAAATCC	500
30	TAGACAGAGG	TGAAGCTGGT	GATAACGTAG	GTCTATTGTT	GAGAGGTATT	550
	GAAAAGACTG	ACATCAAGAG	AGGTATGGTT	ATCGCTAAGA	AAGATTCAGT	600
	TAAGCCACAC	AAGAAATTCA	AAGCTGAGGT	TTATATCCTT	TCTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCCACAACA	AATACCGTCC	TCAGTTCTAT	700
	GTAAGAATA	CTGACGTTAC	AGGTGAAATC	TTCTTACCAG	AAGGTGTAGA	750
35	AATGGTAATG	CCTGGTGATA	ACTTAACTAT	CACTGTAGAA	TTGTTACAAC	800
	CAATCGCTCT	TAACGAGGGT	CTTAGATTCG	CGATC		835

2) INFORMATION FOR SEQ ID NO: 24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter amalonaticus*
 (B) STRAIN: ATCC 25405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24

55	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
60	ACACCCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250

	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCC	GGCTTCCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
5	GACTGCCAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCGGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCWCCATCAA	600
	GCCGCACACC	ATGTTTGAAT	CYGAAGTGTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
10	CGTACAACCTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTTGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGG				816

15

2) INFORMATION FOR SEQ ID NO: 25

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 825 bases
20	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Citrobacter braakii</i>
(B)	STRAIN: ATCC 43162

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25

	CGCGATCCTG	GTTGTTGCTG	CAACTGACGG	CCCGATGCCG	CAGACTCGTG	50
	AGCACATCCT	GCTGGGTCGY	CAGGTAGGCG	TTCCGTACAT	CATCGTGTTT	100
	CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTAGA	150
35	AATGGAAGTT	CGTGAACCTT	TGTCTCAGTA	CGATTTCCCG	GGCGACGACA	200
	CGCCGATCGT	TCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGAWGCAGAG	250
	TGGGAAGCGA	AAATCATCGA	ACTGGCTGGC	TTCTTGGATT	CTTACATCCC	300
	GGAACCAGAG	CGTGCGATTG	ACAAGCCGTT	CCTGCTGCCT	ATCGAAGACG	350
	TATTCTCCAT	CTCTGGTCGT	GGTACCGTTG	TTACCGGTCG	TGTAGAGCGC	400
40	GGTATCATCA	AAGTTGGTGA	AGAAGTTGAA	ATCGTTGGTA	TCAARGACAC	450
	TGCTAAGTCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAAA	CTGCTGGACG	500
	AAGGCCGTGC	TGGTGAGAAC	GTTGGTGTTC	TGCTGCGTGG	TATCAAGCGT	550
	GAAGAAATCG	AACGTGGTCA	GGTACTGGCT	AAGCCGGGCT	CTATCAAGCC	600
	GCACACCAAG	TTCGAATCTG	AAGTGACAT	TCTGTCCAAA	GACGAAGGCG	650
45	GCCGTCATAC	TCCGTTCTTC	AARGGCTACC	GTCCGCAGTT	CTACTTCCGT	700
	ACTACTGACG	TGACTGGTAC	CATCGAAGTG	CCGGAAGGCG	TTGAGATGGT	750
	AATGCCGGGC	GACAACATCA	AAATGGTTGT	TACCCTGATC	CACCCAATCG	800
	CGATGGACGA	CGGTCTGCGT	TTCGC			825

50

2) INFORMATION FOR SEQ ID NO: 26

(i) SEQUENCE CHARACTERISTICS:

55	(A)	LENGTH: 829 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter koseri*
 (B) STRAIN: ATCC 27156

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
10	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAGATGGAA	GTGCGTGAAC	TGCTGTCTCA	GTACGATTTT	CCGGGCGACG	200
	ACACGCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAMGCT	250
	GAGTGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTACCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCCCTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATYGTTG	GTATCAAAGA	450
	GACTGCGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GYTCCATCAA	600
20	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATYCTGTCY	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGAGGAC	GACGGTCTGC	GTTTCGCAA			829

25

2) INFORMATION FOR SEQ ID NO: 27

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter farmeri*
 (B) STRAIN: ATCC 51112

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27

	CGCGATCCTG	GTTGTTGCTG	CGACTGACGG	CCCGATGCCG	CAGACTCGTG	50
45	AGCACATCCT	GCTGGGTCGT	CAGGTAGGCG	TTCCGTACAT	CATCGTGTTT	100
	CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTAGA	150
	GATGGAAGTT	CGTGAACCTG	TGTCTCAGTA	CGATTTCCCG	GGCGACGACA	200
	CGCCGATCGT	TCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGACGCAGAG	250
	TGGGAAGCGA	AAATCATCGA	ACTGGCAGGC	TTCCTGGATT	CTTACATCCC	300
50	GGAACCAGAG	CGTGCGATTG	ACAAGCCGTT	CCTGCTGCCG	ATCGAAGACG	350
	TATTCTCCAT	CTCTGGTCGT	GGTACCGTTG	TTACCGGTCG	TGTAGAGCGC	400
	GGTATCATCA	AAGTGGGTGA	AGAAGTTGAA	ATCGTTGGTA	TCAAAGAGAC	450
	TGCCAAGTCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAAA	CTGCTGGACG	500
	AAGGCCGTGC	TGGTGAGAAC	GTAGGTGTTT	TGCTGCGTGG	TATCAAACGT	550
55	GAAGAAATCG	AACGTGGTCA	GGTACTGGCT	AAGCCGGGCW	CCATCAAGCC	600
	RCACACTATG	TTCGAATCTG	AAGTGTACAT	TCTGTCCAAA	GACGAAGGCG	650
	GCCGTCATAC	TCCGTTCTTC	AAAGGCTACC	GTCCGCAGTT	CTACTTCCGT	700
	ACGACTGACG	TGACTGGCAC	CATCGAACTG	CCGGAAGGTG	TTGAGATGGT	750
	TATGCCGGGC	GACAACATCA	AAATGGTTGT	TACCCTGATC	CACCCGATCG	800
60	CGATGGACGA	CGGTCTGCGT	TTGCGCAA			827

2) INFORMATION FOR SEQ ID NO: 28

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter freundii*
 (B) STRAIN: ATCC 8090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28

20	CCTGGTTGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACT	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCGT	ACATCATCGT	G TTCCTGAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGCTG	TAGAAATGGA	150
	AGTTCGTGAA	CTTCTGTCTC	AGTACGATTT	CCCGGGCGAC	GACACTCCGA	200
	TCGTTCTGGG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGAAGC	AGAGTGGGAA	250
25	GCGAAAATCA	TCGAACTGGC	TGGCTTCCTG	GATTCTTACA	TCCCAGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCTATCGAA	GACGTATTCT	350
	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
	ATCAAAGTTG	GTGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTGCTAA	450
	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAGTCTG	GACGAAGGCC	500
30	GTGCTGGTGA	GAACGTTGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCTCTATCA	AGCCGCACAC	600
	CAAGTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGACGAA	GGCGGCCGTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACTACT	700
	GACGTGACTG	GTACCATCGA	ACTGCCGGAA	GGCGTAGAGA	TGGTAATGCC	750
35	GGGCGACAAC	ATCAAAAATGG	TTGTTACCCT	GATCCACCCA	ATCGCGA	797

2) INFORMATION FOR SEQ ID NO: 29

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter sedlakii*
 (B) STRAIN: ATCC 51115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29

55	CGGCGCGATC	CTGGTTGTTG	CCGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGCTGGT	150
	AGAGATGGAA	GTTCGTGAAC	TGCTGTCTCA	GTACGATTTT	CCGGGCGACG	200
	ACACGCCGAT	CGTTCGTGGT	TCAGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
60	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300

	TCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	G TTCCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
5	ACGAAGGCCG	TGCGGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCGAAGCCGG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	TATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAAC TG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
10	GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

15 2) INFORMATION FOR SEQ ID NO: 30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter werkmanii*
 (B) STRAIN: ATCC 51114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30

30	GCGATCCTGG	TTGTTGCTGC	GACTGACGGC	CCGATGCCGC	AGACTCGTGA	50
	GCACATCCTG	CTGGGTCGTC	AGGTAGGCGT	TCCGTACATC	ATCGTGTTCC	100
	TGAACAAATG	CGACATGGTT	GATGACGAAG	AGCTGCTGGA	ACTGGTAGAA	150
	ATGGAAGTTC	GTGAACTTCT	GTCTCAGTAC	GATTTCCCGG	GCGACGACAC	200
35	TCCGATCGTT	CGTGGTTCTG	CTCTGAAAGC	GCTGGAAGGC	GAAGCAGAGT	250
	GGGAAGCGAA	AATCATCGAA	CTGGCTGGCT	TTCTGGATTC	TTACATCCCG	300
	GAACCAGAGC	GTGCGATTGA	CAAGCCGTTT	CTGCTRCCTA	TCGAAGACGT	350
	ATTCTCCATC	TCCGGTCGTG	GTACCGTTGT	TACCGGTCGT	G TAGAGCGCG	400
	GTATCATCAA	AGTTGGTGAA	GAAGTTGAAA	TCGTTGGTAT	CAAAGACACC	450
40	GCTAAGTCTA	CCTGTACCGG	CGTTGAAATG	TTCCGCAAAC	TGCTGGACGA	500
	AGGCCGTGCT	GGTGAGAACG	TTGGTGTTCT	GCTGCGTGGT	ATCAAACGTG	550
	AAGAAATCGA	ACGTGGTCAG	GTACTGGCTA	AGCCGGGCTC	TATCAAGCCG	600
	CACACCAAGT	TCGAATCTGA	AGTGTACATC	CTGTCCAAAG	ACGAAGGCGG	650
	CCGTCATACT	CCGTTCTTCA	AAGGCTACCG	TCCGCAGTTC	TACTTCCGTA	700
45	CTACTGACGT	GACTGGTACC	ATCGAACTGC	CGGAAGGCGT	AGAGATGGTA	750
	ATGCCGGGCG	ACAACATYAA	AATGGTTGTT	ACYCTGATCC	ACCCGATCGC	800
	GATGGACGAC	GGTCTGCGTT	TCG			823

50

2) INFORMATION FOR SEQ ID NO: 31

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter youngae*

(B) STRAIN: ATCC 29935

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

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
10	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTC	CGGGCGACGA	200
	TACGCCGATC	GTTTCGTGGT	CTGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
	AGTGGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATC	300
	CCGGAACCAG	AACGTGCTAT	CGATAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACTGGT	CGTGTAGAAC	400
15	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCCAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCTATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGACGAAGG	650
20	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACGGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
	GTAATGCCGG	GCGACAACAT	CAAATGGTT	GTTACCCTGA	TCCACCCAAT	800
	CGCGATGGAT	GACGGTCTGC	GTTTCG			826

25

2) INFORMATION FOR SEQ ID NO: 32

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium perfringens*

(B) STRAIN: ATCC 13124

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32

	CGGAGCTATA	TTAGTTTGT	CAGCAGCTGA	TGGTCCAATG	CCTCAAACAA	50
	GAGAGCACAT	CTTATTATCA	TCAAGAGTTG	GAGTTGACCA	CATCGTAGTA	100
45	TTCTTAAACA	AAGCAGATAT	GGTTGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTAGAGAGT	TATTAAGCGA	GTACAACCTC	CCAGGAGACG	200
	AYATTCCAGT	AATCAARGGA	TCAGCTTTAG	TAGCATTAGA	AAACCCAACT	250
	GACGAAGCTG	CAACAGCTTG	TATCAGAGAG	TTAATGGATG	CTGTAGATAG	300
	CTACATCCCA	ACACCAGAAA	GAGCAACAGA	TAAGCCATTC	TTAATGCCAG	350
50	TAGAGGACGT	ATTCACAATC	ACTGGTAGAG	GAACAGTTGC	AACAGGAAGA	400
	GTTGAAAGAG	GAGTTCTACA	TGTAGGAGAC	GAAGTAGAAG	TAATCGGATT	450
	AACTGAAGAA	AGAAGAAAAA	CTGTTGTAAC	AGGAATCGAA	ATGTTTCAGAA	500
	AGTTATTAGA	TGAAGCACAA	GCTGGAGATA	ACATCGGAGC	ATTATTAAGA	550
	GGTATCCAAA	GAAGTGAAT	CGAAAGAGGT	CAAGTTTTC	CTCAAGTTGG	600
55	AACAATCAAC	CCACACAAAA	AATTCGTAGG	TCAAGTATAC	GTACTTAAAA	650
	AAGAAGAAGG	TGGAAGACAT	ACTCCATTCT	TCGATGGATA	CAGACCACAA	700
	TTCTACTTCA	GAACAACAGA	CGTTACAGGA	TCAATCAAAT	TACCAGAAGG	750
	AATGGAAATG	GTTATGCCTG	GAGACCACAT	CGACATGGAA	GTTGAATTAA	800
60	TCACAGAAAT	CGCTATGGAY	GAAGGATTAA	GATTCGCTAT	C	841

2) INFORMATION FOR SEQ ID NO: 33

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Comamonas acidovorans*
 15 (B) STRAIN: ATCC 15668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33

20	CGGCGCCATC	CTGGTGTGCT	CGGCCGCTGA	CGGCCCCATG	CCCCAGACCC	50
	GCGAGCACAT	CCTGCTGGCC	CGTCAGGTGG	GCGTGCCCTA	CATCATCGTG	100
	TTCCTGAACA	AGTGCGACAT	GGTGGACGAC	GAAGAGCTGC	TGGAAGTGGT	150
	CGAAATGGAA	GTGCGCGAGC	TGCTTGCCAA	GTACGACTTC	CCCGGCGACG	200
	ACACCCCAT	CATCCGCGGC	TCGGCCAAGC	TGGCCCTGGA	AGGCGACCAG	250
	TCCGACAAGG	GCGAACCTGC	CATCCTGCGC	CTGGCTGAAG	CACTGGACTC	300
25	CTACATCCCC	ACGCCCAGAGC	GCGCTGTGGA	CGGCGCCTTT	GCAATGCCCCG	350
	TGGAAGACGT	GTTCTCGATC	TCTGGCCGTG	GCACCGTGGT	GACTGGCCGT	400
	ATCGAGCGCG	GCATCATCAA	GGTCGGCGAA	GAAATCGAAA	TCGTCGGTAT	450
	CCGCGACACC	CAGAAGACCA	TCGTCACCGG	CGTGGAAATG	TTCCGCAAGC	500
	TGCTGGACCA	AGGTCAAGCT	GGCGACAACG	TGGGTCTGCT	GCTGCGCGGC	550
30	ACCAAGCGTG	AAGACGTGGA	ACGCGGCCAA	GTGCTGTGCA	AGCCCGGCTC	600
	CATCAAGCCC	CACACCCACT	TCACGGCTGA	GGTGTACGTG	CTGTCCAAGG	650
	ACGAAGGTGG	TCGCCACACT	CCGTTCTTCA	ACAAC TACCG	TCCCCAGTTC	700
	TATTTCCGTA	CGACCGACGT	GACCGGCTCC	ATCGAGCTGC	CCGCCGACAA	750
	GGAAATGGTG	ATGCCTGGCG	ACAACGTGTC	GATCACCGTC	AAGCTGATCG	800
35	CCCCCATCGC	CATGGAAGAA	GG			822

2) INFORMATION FOR SEQ ID NO: 34

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 702 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Corynebacterium bovis*
 (B) STRAIN: ATCC 7715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

55	GCCGCAGACC	CGTGAGCACG	TCCTCCTGGC	CCGTCAGGTC	GGTGTGCCCT	50
	ACATCCTCGT	CGCCCTCAAC	AAGTGCGACA	TGGTCGACGA	CGAGGACCTC	100
	ATCGAGCTCG	TCGAGATGGA	GGTCCGTGAG	CTCCTCGCCG	AGCAGGACTA	150
	CGACGAGGAC	GCCCCGATCA	TCCACATCTC	CGCCCTCAAG	GCCCTCGAGG	200
	GTGACCCGGA	GTGGACGCAG	CGCATCGTCG	ACCTCATGAA	GGCCTGCGAC	250
60	GACGCCATCC	CGGATCCGGA	GCGCGAGACG	GACAAGCCGT	TCCTCATGCC	300

5 GATCGAGGAC ATCTTCACGA TCACCGGCCG CGGCACCGTC GTCACGGGGC 350
 GTGTCGAGCG TGGCATCCTC AACGTCAACG AGGAGGTCGA GATCCTGGGT 400
 ATCTGCGAGA ACTCCCAGAA GACGACCGTC ACCTCCATCG AGATGTTCAA 450
 CAAGTTCCTC GACACGGCCG AGGCCGGCGA CAACGCCGCC CTGCTGCTCC 500
 GTGGCCTGAA GCGCGAGGAC GTCGAGCGTG GCCAGATCGT GGCCAAGCCG 550
 GGCGCCTACA CGCCGCACAC CGAGTTCGAG GGCTCCGTGT ACATCCTCTC 600
 CAAGGACGAG GGTGGCCGCC ACACGCCGTT CTTGACAAC TACCGTCCGC 650
 AGTTCTACTT CCGGACGACC GACGTCACCG GCGTCGTCAA GCTGCCGGAG 700
 GG 702

2) INFORMATION FOR SEQ ID NO: 35

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 689 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Corynebacterium cervicis*
 25 (B) STRAIN: NCTC 10604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35

30 GGCTCAGACC CGCGAGCACG TTCTGCTTGC TCGCCAGGTT GCGGTTCCGA 50
 CGATCCTGGT TGCCCTCAAC AAGGCCGATA TGGTCGACGA TGAGGAAATG 100
 CTGGAGCTCG TTGAGGAAGA GTGCCGCGAC CTGCTCGAGT CCCAGGACTT 150
 CGATCGTGAC GCCCCGATCA TCCAGGTTTC CGCGCTGAAG GCTCTCGAAG 200
 GTGATCCGCA GTGGGTGCT AAGGTCGAGG AGCTCATGGA GGCAGTCGAC 250
 ACCTTCGTGC CACTCCTGA GCGCGACATG GACAAGCCGT TCCTCATGCC 300
 35 GATCGAAGAC GTCTTCACCA TCACCGGCCG TGGCACCGTT GTTACCGGTC 350
 GTGTTGAGCG TGGCAAGCTC CCGATCAACT CTGAGGTTGA AATCCTCGGT 400
 ATCCGCGAAC CGCAGAAGAC CACCGTTACC GGTATCGAGA TGTTCACAA 450
 GTCCATGGAT GAAGCATGGG CAGGCGAGAA CTGTGGTCTC CTCCTGCGTG 500
 GCACCAAGCG CGATGAGGTT GAGCGCGGTC AGGTCGTGTC CGTTCCCGGT 550
 40 TCGATCACCC CGCACACCAA CTTACCGGA CAGGTCTACA TCCTCAAGAA 600
 GGAAGAAGGC GGTCGTCACA ACCCGTTCTT CTCGAAGTAC CGTCCGCAGT 650
 TCTACTTCCG CACCACGGAC GTGACCGGCG TCATCACCC 689

45

2) INFORMATION FOR SEQ ID NO: 36

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 804 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 55 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Corynebacterium flavescens*
 (B) STRAIN: ATCC 10340

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

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GGTTGTTGCT GCAACCGATG GTCCTATGCC GCAGACCCGC GAGCACGTTC      50
TTCTGGCTCG CCAGGTTGGC GTTCCTTACA TCCTCGTTGC TCTTAACAAG      100
TGCGACATGG TTGATGATGA GGAAATCATC GAGCTCGTTG AGATGGAAAT      150
5  CCGCGAACTG CTCGCTGAGC AGGACTACGA CGAGGATGCC CCCATCATCC      200
ACATCTCCGC TCTCAAGGCT CTTGAGGGTG ACGAGAAGTG GGTACAGGCC      250
ATCGTCGACC TCATGCAGGC CTGCGATGAC TCCATTCCGG ATCCGGAGCG      300
CGAGACCGAC AAGCCCTTCC TCATGCCTAT CGAGGACATC TTCACCATCA      350
CCGGCCGCGG TACCGTTGTT ACCGGCCGTG TTGAGCGTGG CGTTTTGAAG      400
10 GTCAACGAGG ATGTTGAGAT CATCGGCATC AAGGAGAAGT CCATCTCCAC      450
CACCGTTACC GGTATCGAAA TGTTCGCAA GATGATGGAC TACACCGAGG      500
CTGGCGACAA CTGTGGTCTG CTTCTGCGTG GTACCAAGCG TGAAGAGGTC      550
GAGCGCGGCC AGGTTGTTAT CAAGCCGGGC GCCTACACCC CCCACACCAA      600
GTTCGAGGGT TCCGTCTACG TCCTCAAGAA GGAAGAGGGC GGCCGCCACA      650
15 CCCC GTTCAT GGACA ACTAC CGTCCG CAGT TCTACT TCCG TACCA CTGAC      700
GTGACCGGCG TTGTT CACCT GCCTG AGGGC ACCGAG ATGG TCATG CCTGG      750
CGACAACGTT GATATG ACCG TTGAG CTCAT CCAGCCC GTC GCTAG GATGA      800
GGGC                                                    804

```

20

2) INFORMATION FOR SEQ ID NO: 37

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 692 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium kutscheri*
 (B) STRAIN: ATCC 15677

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

```

TGCCTCAGAC CCGTGAGCAC GTTCTTCTTG CTCGCCAGGT TGGCGTTCCT      50
TACATCCTCG TTGCTCTTAA CAAGTGCGAC ATGGTTGACG ATGAGGAAAT      100
40 CATCGAGCTC GTTGAGATGG AAGTTCGCGA GCTTCTTGCT GAGCAGGAGT      150
ACGATGAAGA GGCTCCAATC ATCCACATCT CTGCTTTGAA GGCTCTTGAG      200
GGCGACGAGA AGTGGACTCA GGCCATCATC GACCTCATGC AGGCTTGTGA      250
TGA CTCCATC CCAGATCCAG AGCGTGAGAC CGACAAGCCA TTCCTCATGC      300
CTATCGAGGA TATCTTCACC ATCACC GGTC GTGGCACC GTTACC GGT      350
45 CGTGTTGAGC GCGGTTCTT GAAGGTGAAT GAGGACGTCG AGATCATCGG      400
CATCAAGGAG AAGTCCACCA CTACTACCGT TACCGGTATC GAAATGTTCC      450
GTAAGCTTCT TGATTACACC GAAGCTGGCG ATA ACTGTGG TCTGCTTCTT      500
CGTGGTATCA AGCGCGAAGA CGTTGAGCGT GGTCAGGTTG TTGTTAAGCC      550
AGGCGCTTAC ACACCTCACA CCGAGTTCGA GGGCTCTGTT TACGTTCTTT      600
50 CCAAGGACGA GGGCGGCCGC CACACCCCAT TCTTCGACAA CTACCGTCCA      650
CAGTTCTACT TCCGCACCAC TGACGTTACC GGTGTTGTGA AG                                                    692

```

55 2) INFORMATION FOR SEQ ID NO: 38

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

60

(D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

5 (vi)ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium minutissimum*

(B) STRAIN: ATCC 23348

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 38

```

10 CCTGGTTGTT GCTGCAACCG ATGGCCCGAT GCCGCAGACC CGCGAGCACG      50
   TTCTTCTGGC CCGCCAGGTT GCGGTTCCGT ACATCCTCGT TGCACCTGAAC      100
   AAGTGTGACA TGGTTGACGA TGAGGAAATC ATCGAGCTCG TTGAGATGGA      150
   GATCCGTGAG CTGCTCGCTG AGCAGGACTA CGACGAGGAA GCTCCGATCG      200
15  TTCACATCTC CGCTCTGAAG GCTCTTGAGG GCGACGAGAA GTGGGCACAG      250
   TCCATCGTTG ACCTGATGCA GGCTTGCGAT GACTCCATCC CGGATCCGGA      300
   GCGCGAGCTG GACAAGCCGT TCCTGATGCC GATCGAGGAC ATCTTCACCA      350
   TTACCGGCCG CGGTACCGTT GTTACCGGCC GTGTTGAGCG TGGCTCCCTG      400
   AACGTTAACG AGGACATCGA GATCATCGGT ATCAAGGACA AGTCCATGTC      450
20  CACCACCGTT ACCGGTATCG AGATGTTCCG CAAGATGATG GACTACACCG      500
   AGGCTGGCGA CAACTGTGGT CTGCTTCTGC GTGGTACCAA GCGTGAAGAG      550
   GTTGAGCGTG GCCAGGTTTG CATCAAGCCG GCGGCTTACA CCCC GCACAC      600
   CAAGTTCGAG GGTTCGCTCT ACGTCCTGAA GAAGGAAGAG GGCGGCCGCC      650
   ACACCCCGTT CATGGACAAC TACCGTCCGC AGTTCTACTT CCGCACCACC      700
25  GACGTCACCG GTGTCATCAA GCTGCCGGAG GGCACCGAGA TGGTCATGCC      750
   GGGCGACAAC GTTGAGATGT CCGTAGAGCT GATCCAGCCG GTCGCTA          797

```

30 2) INFORMATION FOR SEQ ID NO: 39

(i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 702 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

40 (vi)ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium mycetoides*

(B) STRAIN: ATCC 21134

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 39

```

45 GCCGCAGACC CGCGAGCACG TTCTTCTGGC CCGCCAGGTC GGCGTCCCCT      50
   ACATCCTCGT TGCCTGAAC AAGTGCACG TGGTTGATGA TGAGGAGATC      100
   ATCGAGCTCG TGGAGATGGA GGTCCGTGAG CTGCTCGGCG AGCAGGACTA      150
   CGACGAGGAC GCCCCATCA TCCACATCTC CGCTCTGAAG GCTCTCGAGG      200
50  GCGACGAGAA GTGGGTTCAG TCCGTGCTCG ACCTCATGCA GGCGTGCGAC      250
   GACTCCATCC CGGATCCGGT CCGCGAGACC GACCGCGACT TCCTGATGCC      300
   GATCGAGGAC ATCTTCACCA TCTCCGGCCG CCGCACCCTG GTTACCGGTC      350
   GTGTGGAGCG CCGCGTGCTC AACCTCAACG ACGAGGTCGA GATCATCGGC      400
   ATCCGCGACA AGTCCCAGAA GACCACCGTC ACCTCCATCG AGATGTTCAA      450
55  CAAGCTGCTC GATACCGCTG AGGCAGGCGA CAACGCGGCT CTGCTGCTCC      500
   GCGGTCTGAA GCGCGAGGAC GTCGAGCGTG GCCAGGTTGT CATCAAGCCG      550
   GGCGCCTACA CCCC GCACAC CAAGTTCGAG GGTTCGCTCT ACGTCCTGTC      600
   CAAGGACGAG GGCGGCCGCC ACACCCCGTT CTTCGACAAC TACCGTCCGC      650
   AGTTCTACTT CCGCACCACC GACGTGACCG GTGTTGTGAA GCTGCCGGAG      700
60  GG                                702

```

2) INFORMATION FOR SEQ ID NO: 40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudogenitalium*
 (B) STRAIN: ATCC 33038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40

20	GCTCGCCAGG	TTGGCGTTCC	TTACATCCTC	GTTGCGCTGA	ACAAGTGCGA	50
	CATGGTTGAT	GATGAGGAAA	TCATCGAGCT	CGTTGAGATG	GAGATCCGTG	100
	AGCTGCTCGC	AGAGCAGGAT	TACGATGAGG	AAGCTCCTAT	CGTTCACATC	150
	TCCGCTCTGA	AGGCCCTCGA	GGGCGATGAC	AAGTGGGTAC	AGTCCGTCGT	200
	TGATCTGATG	GAAGCCTGCG	ACAACCTCCAT	CCCGGATCCG	GAGCGCGCTA	250
25	CCGACCAGCC	GTTCTTGATG	CCTATCGAGG	ACATCTTCAC	CATTACCGGC	300
	CGCGGTACCG	TTGTTACCGG	CCGTGTTGAG	CGTGGCCGTC	TGAACGTCAA	350
	CGAGGACGTT	GAGATCATCG	GTATCCAGGA	GAAGTCCCAG	ACCACCACCG	400
	TTACCGGTAT	CGAGATGTTT	CGCAAGATGA	TGGACTACAC	CGAGGCTGGC	450
	GACAACTGTG	GTCTGCTTCT	GCGTGGTACC	AAGCGTGAGG	ACGTTGAGCG	500
30	TGGCCAGGTT	GTTATCAAGC	CGGGCGCTTA	CACCCCGCAC	ACCAAGTTCG	550
	AGGGCTCCGT	CTACGTCCTG	AAGAAGGAAG	AGGGCGGCCG	CCACACCCCG	600
	TTCATGAACA	ACTACCGTCC	GCAGTTCTAC	TTCCGTACCA	CGGACGTTAC	650
	CGGTGTTGTT	CACCTGCCAG	AGGG			674

35

2) INFORMATION FOR SEQ ID NO: 41

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium renale*
 (B) STRAIN: ATCC 19412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41

	TGCCTCAGAC	CCGTGAGCAC	GTTCTGCTTG	CTCGTCAGGT	CGGCGTTCCT	50
	TACATCCTCG	TTGCACTGAA	CAAGTGCGAC	ATGGTCGACG	ACGAAGAAAT	100
55	CATCGAGCTC	GTCGAGATGG	AAATCCGTGA	ACTGCTCGCA	GAGCAGGACT	150
	ACGATGAGGA	AGCTCCTATC	GTTCACATCT	CCGCTCTGGG	CGCCCTGAAC	200
	GGCGAGCAGA	AGTGGGTGTA	CTCCATCGTC	GAAGTGATGG	AAGCTTGCGA	250
	CAACTCCATC	CCAGACCCAG	TTCGCGACAT	CGACCACCCA	TTCCTGATGC	300
	CTATCGAGGA	CATCTTCACC	ATTACCGGTC	GCGGTACCGT	TGTTACCGGC	350
60	CGTGTCGAGC	GTGGCCGTCT	CAACGTCAAC	GAAGAAGTTG	AGATCATCGG	400

	TATCAAGGAC	AAGTCCCAGA	AGACCACCGT	CACCGGTATC	GAGATGTTCC	450
	GCAAGATGCT	GGACTACACC	GAAGCTGGCG	ACAACGTGG	TCTGCTGCTC	500
	CGCGGCATCG	GCCGTGAGGA	TGTCGAGCGT	GGCCAGGTTA	TCATCAAGCC	550
	AGGCGCTTAC	ACCCCTCACT	CTGAGTTCGA	GGGCTCTGTC	TACGTCCTGT	600
5	CCAAGGACGA	GGGTGGCCGC	CACACCCCAT	TCTTCGACAA	CTACCGTCCA	650
	CAGTTCTACT	TCCGCACCAC	CGACGTGACC	GGCGTTGTGC	ACCT	694

10 2) INFORMATION FOR SEQ ID NO: 42

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 687 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium ulcerans*
 (B) STRAIN: NCTC 8665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42

25	GCCGCAGACC	CGCGAGCACG	TTCTGCTGGC	TCGCCAGGTT	GGCGTTCCKT	50
	ACATCCTSGT	TGCACTGAAC	AAGTGCGACA	TGGTTGACGA	TGAGGARCTC	100
	CTSGAGCTCG	TCGAGATGGA	GGTCCGCGAG	CTGCTGGCTG	AGCAGGACTA	150
	CGACGAGGAA	GCTCCGRTCG	TTCACATCTC	CGCWCTGAAC	GCCCTGGACG	200
30	GCGACSAGAA	GTGGGCTVAC	TCCATCCTCG	AGCTGATGCA	GGCTTGCGAC	250
	GAGTCCATCC	CGGATCCGGA	GCGCGAGACC	GACAAGCCGT	TCCTGATGCC	300
	GATTGAGGAC	ATCTTCACCA	TTACCGGTCTG	CGGYACCGTT	GTTACCGGCC	350
	GTGTTGAGCG	TGGCDTCCTG	AACGTSAAACG	ACGASGTTGA	GATCATGGGY	400
	ATCCGGGAGA	AGTCCCAGAA	GACCACCGTY	ACCKSCATCG	AGATGTTCAA	450
35	CAAGMTGMTG	GACWCCGCAG	AGGCTGGCGA	CAACGCTGSW	CTGCTGCTGC	500
	GTGGTMTSAA	GCGTGAGGAC	GTTGAGCGTG	GCCAGATCAT	CGYTAAGCCG	550
	GGCGCKTACA	CCCCGCACAC	CGAGTTCGAG	GGCTCCGTCT	ACGTCCTGTC	600
	CAAGGACGAG	GGCGGCCGCC	ACACCCCGTT	CTTCGACAAC	TACCGTCCGC	650
40	AGTTCTACTT	CCGCACCACC	GACGTSACCG	GTGTTGT		687

2) INFORMATION FOR SEQ ID NO: 43

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium urealyticum*
 55 (B) STRAIN: ATCC 43042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43

60	CTGGTTGTTG	CTGCAACCGA	TGGCCCGATG	CCGCAGACCC	GTGAGCACGT	50
	TCTGCTGGCT	CGCCAGGTTG	GCGTTCCGTA	CATCCTCGTT	GCACTGAACA	100

```

AGTGCGACAT GGTGACGAT GAGGAGCTCC TCGAGCTCGT CGAGATGGAG      150
GTCCGCGAGC TTCTGGCTGA GCAGGACTAC GACGAGGAGG CTCCGGTCGT      200
CCCGATCTCC GCACTGGGCG CCCTGGACGG CGATCAGAAG TGGGTCGACT      250
CCATCCTCGA GCTCATGAAG GCTTGCGACG AGTCCATCCC GGACCCGGAG      300
5  CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGAGGACA TCTTCACCAT      350
TACCGGTCGC GGCACCGTCG TTACCGGCCG TGTTGAGCGT GGCGTCCTGA      400
ACCTGAACGA CGAGGTGCGAG ATCCTGGGCA TCCGCGAGAA GTCCACCAAG      450
ACCACCGTCA CCTCCATCGA GATGTTCAAC AAGCTGCTGG ACACCGCAGA      500
GGCTGGCGAC AACGCTGCAC TGCTGCTGCG TGGTCTGAAG CGTGAGGACG      550
10 TCGAGCGAGG CCAGATCATC GCTAAGCCGG GCGCTTACAC CCCGCACACC      600
GAGTTCGAGG GCTCCGTCTA CGTCCTGTCC AAGGACGAGG GCGGCCGTCA      650
CACCCCGTTC TTCGACAACT ACCGTCCGCA GTTCTACTTC CGTACCACCG      700
ACGTCACCGG TGTCGTTACC CTGCCAGAGG GCACCGACAT GGTCATGCCG      750
GGCGACAACG TTGAGATGAG CGTCAAGC      778
15

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2) INFORMATION FOR SEQ ID NO: 44

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20  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 703 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
25
      (ii) MOLECULE TYPE: Genomic DNA

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Corynebacterium xerosis
30  (B) STRAIN: ATCC 373

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44

```

35  CGCAGACCCG TGAGCACGTC CTCCTGGCCC GCCAGGTCGG CGTCCCCTAC      50
ATCCTCGTCG CCCTGAACAA GTGCGACATG GTCGACGATG AGGAGATCAT      100
CGAGCTCGTG GAGATGGAGG TGCGTGAGCT TCTCGCCGAG CAGGACTACG      150
ACGAGGAGGC CCCGATCGTG CACATCTCCG CCCTGGGCGC CCTCAATGGC      200
GAAGAGAAGT GGGTCGACTC CATCGTCGAG CTCATGAACG CCGTCGACGA      250
GAACGTTCCG GACCCGGTCC GCGAGACCGA CAAGCCGTTC CTGATGCCCG      300
40  TCGAGGACAT CTTACCATC ACCGGCCGCG GCACCGTCGC CACCGGTCGC      350
GTGGAGCGCG GCACCCGTGA GGTCAACGAC GAGGTCGAGA TCCTGGGCAT      400
CCAGGAGAAG TCCCAGACCA CCACCGTCAC CGGCATCGAG ATGTTCCGCA      450
AGCTGCTGGA CTCCGCCGAG GCCGGCGACA ACTGTGGCCT GCTGCTCCGC      500
GGCATCAAGC GCGAGGACAT CGAGCGCGGC CAGATCATCG CGAAGCCGGG      550
45  CGCCTACACC CCGCACACCG AGTTCGAGGG CTCCGTCTAC ATCCTGGCCA      600
AGGACGAGGG CGGCCGCCAC ACCCCGTTCT TCGACAATA CCGTCCGCAG      650
TTCTACTTCC GCACCACCGA CGTCACCGGC GTCGTGAAGC TGCCGGAGGG      700
CAC      703
50

```

2) INFORMATION FOR SEQ ID NO: 45

```

55  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 832 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

60  (ii) MOLECULE TYPE: Genomic DNA

```

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coxiella burnetii*
 (B) STRAIN: Nine Mile phase II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45

```

5      GGAGCGATAT TGGTGGTGAG CGCAGCGGAC GGCCCGATGC CGCAAACGCG      50
      GGAACACATT GTATTGGCGA AGCAAGTGGG TGTTCCGAAC ATAGTGGTTT      100
10     ACTTGAACAA AGCGGACATG GTGGATGACA AAGAGCTGTT GGAATTAGTG      150
      GAAATGGAAG TGAGGGATTT ATTGAACAGT TATGATTTCC CTGGGGATGA      200
      GACGCCGATA ATAGTGGGGT CAGCGTTAAA GCGGTTAGAA GGTGACAAGA      250
      GTGAGGTTGG GGAGCCATCG ATAATCAAAT TAGTGGAAC GATGGACACG      300
      TACTTCCCGC AGCCGGAGCG AGCGATAGAC AAACCGTTTT TAATGCCGAT      350
15     CGAAGATGTG TTTTCGATAT CGGGCCGAGG GACGGTGGTG ACGGGACGCG      400
      TAGAGCGAGG GATCATCAAA GTGGGCGACG AGATAGAGAT TGTGGGGATC      450
      AAGGACACGA CGAAGACGAC GTGCACGGGC GTTGAGATGT TTCGCAAATT      500
      ATTGGATGAA GGTCAAGCGG GTGACAACGT AGGAATTTTA TTGAGAGGGA      550
      CGAAACGCGA AGAAGTGGAG CGTGGTCAAG TATTGGCGAA ACCGGGATCG      600
20     ATCACGCCAC ACAAGAAATT TGAGGCGGAG ATTTATGTGT TGTCTGAAGGA      650
      AGAAGGGGGA CGCCACACAC CGTTTTTTACA AGGCTATCGA CCGCAATTTT      700
      ATTTCCGCAC GACGGACGTG ACGGGCCAGT TATTGAGTTT ACCGGAGGGG      750
      ATAGAGATGG TGATGCCGGG AGATAACGTG AAAGTGACGG TTGAATTGAT      800
      TGCGCCGGTA GCGATGGATG AAGGGCTACG AT      832
25

```

2) INFORMATION FOR SEQ ID NO: 46

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella hoshinae*
 (B) STRAIN: ATCC 33379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46

```

45     GCGCTATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG      50
      TGAGCACATC CTGCTGGGTC GCCAGGTAGG CGTTCCGTAC ATCATCGTGT      100
      TCCTGAACAA GTGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT      150
      GAGATGGAAG TTCGCGAACT GCTGTCTCAG TACGATTTCC CGGGCGACGA      200
      TACGCCGGTA ATCCGCGGTT CTGCGCTGAA AGCGCTGGAA GCGGAAGCCG      250
      AGTGGGAAGC GAAGATCATC GAACTGGCTG AAACGCTGGA CTCCTACATT      300
50     CCGGAACCTG AGCGTGACAT CGACAAGCCG TTCTTGCTGC CGATCGAAGA      350
      CGTATTCTCA ATCTCTGGTC GTGGTACCGT TGTTACCGGT CGTGTAAGAGC      400
      GCGGTATCAT CAAGGTAGGC GACGAAGTTG AAATCGTAGG TATCAAGCCG      450
      ACCACCAAGA CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
      CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTACCAAGC      550
      GTGACGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCACT      600
      CCGCACACCA AGTTCGAATC AGAAGTGATC ATCCTGAGCA AGGATGAAGG      650
      CGGCCGTCAT ACTCCGTTCT TCAAAGGTTA CCGTCCGCAG TTCTACTTCC      700
      GTACCACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG      750
      GTAATGCCGG GCGACAACAT CAAGATGGTT GTTACCCTGA TCCACCCGAT      800
60     CGCCATGGAC GATGGT      816

```

2) INFORMATION FOR SEQ ID NO: 47

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella tarda*
 (B) STRAIN: ATCC 15947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47

20	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
	TGAGCACATC	CTGTTGGGTC	GCCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	GTGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
	GAGATGGAAG	TTCGCGAACT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACGCCGGTA	ATCCGCGGTT	CTGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
25	AGTGGAAGC	GAAGATCATC	GAAGTGGCTG	AAACTCTGGA	CTCCTACATC	300
	CCGGAACCTG	AGCGTGACAT	CGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCT	ATCTCTGGCC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAGGTAGGC	GACGAAGTTG	AAATCGTTGG	TATCAAGCCG	450
	ACCACCAAGA	CCACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
30	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTACTAAGC	550
	GTGACGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCACT	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATCCTGAGCA	AGGATGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACTGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
35	GTAATGCCGG	GCGACAACAT	CAAGATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCCATGGAC	GATGGTCTGC	G			821

2) INFORMATION FOR SEQ ID NO: 48

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eikenella corrodens*
 (B) STRAIN: ATCC 23834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48

55	CGGTGCCATC	CTGGTGGTAT	CCGCTGCTGA	CGGCCCCATG	CCTCAGACTC	50
	GCGAACACAT	CCTGTTGGCT	CGTCAGGTAG	GTGTACCCTA	CATCCTCGTA	100
	TTCATGAACA	AATGCGACAT	GGTAGATGAT	GCCGAGCTGC	TTGAGTTGGT	150
	TGAGATGGAA	ATCCGCGACC	TGCTCTCCAG	CTATGACTTC	CCTGGTGACG	200
60	ACTGCCCGAT	CGTACAAGGT	TCCGCTCTCA	AAGCCCTCGA	AGGCGATGCC	250

5 GGTTACAAAG AAAAATCTT CGAACTAGCT GCTGCTTTGG ATAGCTACAT 300
 CCCCACCTCCT CAACGTGCTG TAGACAAACC CTTCTGTGTTG CCGATCGAAG 350
 ACGTATTCTC TATCTCCGGC CGTGGTACCG TAGTAACCGG TCGTGTAGAG 400
 CGCGGCATCA TCAAAGTAGG TGAAGAGATC GAAATCGTTG GTCTGAAGCC 450
 CACTCAGAAA ACTACCTGTA CTGGCGTGGA AATGTTCCGC AAAGTCTGCTGG 500
 ACGAAGGTCA GGCCGGTGAC AACGTAGGCG TACTGCTGCG CGGTACCAAA 550
 CGTGAAGAAG TTGAGCGTGG TCAAGTATTG GCTAAACCCG GCACCATCAC 600
 TCCGCACACC AAGTTCAAAG CCGAAGTATA CGTATTGAGC AAAGAAGAAG 650
 10 GTGGTCGTCA CACCCCGTTC TTTGCCAACT ACCGTCCACA GTTCTACTTC 700
 CGTACTACTG ACGTAACCGG TGCTGTAGAG CTGGAGCCTG GTGTAGAAAT 750
 GGTTATGCCT GGTGAGAACG TAACCATCAC CGTAGAACTG ATTGCTCCGA 800
 TTGCTATGGA AGAAGGTCTG CGCTTTGCGA 830

15

2) INFORMATION FOR SEQ ID NO: 49

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 808 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter aerogenes*
 (B) STRAIN: ATCC 13048

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

GGCGCGATCC TGGTTGTTGC TGC GACTGAC GGCCCGATGC CGCAGACTCG 50
 TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
 TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT 150
 35 GAGATGGAAG TTCGTGAACT GCTGTCTCAG TACGATTTC CCGGCGACGA 200
 CACTCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG 250
 AGTGGGAAGC GAAAATCATC GAACTGGCTG GCTTCCTGGA TTCTTACATC 300
 CCRGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
 CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC 400
 40 GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAC 450
 ACCGCGAAAA CCACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
 CGAAGGCCGT GCTGGTGAGA ACGTAGGYGT TCTGCTGCGT GGTATCAAAC 550
 GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CAGCATCAAG 600
 CCGCACACCA AGTTCGAATC TGAAGTGTAC ATCCTGTCCA AAGACGAAGG 650
 45 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
 GTACTACTGA CGTGACTGGT ACCATCGAAC TGCCGGAAGG CGTAGAGRTG 750
 GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 800
 CGCGATGG 808

50

2) INFORMATION FOR SEQ ID NO: 50

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter agglomerans*
 (B) STRAIN: ATCC 27989

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
10	TTCCTGAACA	AATGTGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ATACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAMGCW	250
	GAGTGGGAAG	CGAAAATCAT	CGARCTGGCT	GGCCACCTGG	ATACCTATAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATCTCCGGT	CGCGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TYAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	TACYGCGAAA	TCAACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
20	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGTCGTCA	CACTCCGTTC	TTCAAAGGCT	ACCGTCCSCA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCGCGATGGA	CGACGGTCTG	CGTTCGCA			828

25

2) INFORMATION FOR SEQ ID NO: 51

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter amnigenus*
 (B) STRAIN: ATCC 33072

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51

	TGGCGCGATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACGC	50
45	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCAGGTGATG	200
	ACACTCCAAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAAGCA	250
	GAGTGGGAAG	CTAAAATCGT	TGAGCTGGCT	GGCTACCTGG	ATTCTTACAT	300
50	CCCGGAACCA	GAACGTGCTA	TCGATAAGCC	ATTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	TATCTCCGGC	CGTGGTACTG	TTGTAACCGG	TCGTGTAGAG	400
	CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCTAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
55	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCAG	GCTCAATCAA	600
	GCCGCACACC	AAATTCGAAT	CTGAAGTTTA	TATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	CACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGCGACAACA	TTCAGATGGT	TGTTACCCTG	ATCCACCCAA	800
60	TCGCGATGGA	TGACGGTCTG	CGTTT			825

2) INFORMATION FOR SEQ ID NO: 52

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter asburiae*
 (B) STRAIN: ATCC 35953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52

20	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTT	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAGATGGAA	GTTTCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ATACTCCAAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
25	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCGA	TTGACAAGCC	ATTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCTAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
30	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCGAAGCCAG	GCTCAATCAA	600
	GCCACACACC	AAGTTCGAAT	CTGAAGTGTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTTGAGAT	750
35	GGTAATGCCA	GGCGACAACA	TCAAGATGGT	TGTGACTCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGTCTG	CG			822

2) INFORMATION FOR SEQ ID NO: 53

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cancerogenus*
 (B) STRAIN: ATCC 35317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53

55	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
	TTCCTGAACA	AGTGCACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTTCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCAGGCGACG	200
60	ACACTCCAAT	CGTTCGTGGT	TCCGCGCTGA	AAGCGCTGGA	AGGCGAAGCT	250

	GAGTGGGAAG	CAAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCGA	TTGACAAGCC	ATTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAAG	400
	CGCGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
5	TACTGCKAAA	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGCGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCGAAGCCAG	GCTCAATCAA	600
	GCCACACACC	AAGTTCGAAT	CTGAAGTGTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
10	CGTACAACTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGCGACAACA	TCAAGATGGT	TGTGACGCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

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2) INFORMATION FOR SEQ ID NO: 54

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 806 bases
20	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Enterobacter cloacae</i>
	(B)	STRAIN: ATCC 13047

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

	GATCCTGGTA	GTAGCTGCGA	CTGACGGCCC	AATGCCTCAG	ACTCGTGAGC	50
	ACATCCTGCT	GGGTCGTCAG	GTAGGCGTTC	CTTACATCAT	CGTGTTCTCTG	100
	AACAAATGCG	ACATGGTTGA	TGACGAAGAG	CTGCTGGAAC	TGGTAGAGAT	150
35	GGAAGTTCGT	GAAGTGCTGT	CTCAGTACGA	TTTCCCAGGC	GACGATACCC	200
	CAATCGTTTCG	TGGTTCTGCT	CTGAAAGCGC	TGGAAGGCGA	CGCAGAGTGG	250
	GAAGMGAAAA	TCATCGAACT	GGCTGGCTAC	CTGGATTCTT	ACATCCCAGA	300
	ACCAGAGCGT	GCGATTGAYA	AGCCATTCCT	GCTGCCAATC	GAAGACGTAT	350
	TCTCCATCTC	CGGTCGTGGT	ACCGTTGTTA	CCGGTCGTGT	AGAGCGCGGT	400
40	ATCATCAAAG	TGGGTGAAGA	AGTTGAAATC	GTTGGTATCA	AAGAGACTGC	450
	GAAGTCTACC	TGTACTGGCG	TTGAAATGTT	CCGCAAACCTG	CTGGACGAAG	500
	GCCGTGCTGG	TGAGAACGTT	GGTGTTCCTG	TGCGTGGTAT	CAAACGTGAA	550
	GAAATCGAAC	GTGGTCAGGT	TCTGGCGAAG	CCAGGCTCAA	TCAAGCCACA	600
	CACCAAGTTC	GAATCTGAAG	TGTACATCCT	GTCCAAAGAC	GAAGGCGGCC	650
45	GTCATACTCC	GTTCTTCAAA	GGCTACCGTC	CACAGTTCTA	CTTCCGTACA	700
	ACTGACGTGA	CCGGTACCAT	CGAACTGCCA	GAAGGCGTAG	AGGTGGTAAT	750
	GCCAGGCGAC	AACATCAAGA	TGGTTGTGAC	TCTGATCCAC	CCAATCGCGA	800
	TGGACG					806

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2) INFORMATION FOR SEQ ID NO: 55

(i) SEQUENCE CHARACTERISTICS:

55	(A)	LENGTH: 826 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter gergoviae*
 (B) STRAIN: ATCC 33028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55

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CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC      50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
10 TTCCTGAACA AGTGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT      150
AGAGATGGAA GTTCGTGAAC TGCTGTCTCA GTACGATTTC CCGGGCGACG      200
ACACCCCGAT CGTTCGCGGT TCTGCGCTGA AAGCGCTGGA AGGCGACGCA      250
GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCCACCTGG ATACCTAYAT      300
CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG      350
15 ACGTATTCTC CATTTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG      400
CGCGGTATCA TCAAGGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
CACCGCGAAA ACCACCTGTA CTGGCGTTGA AATGTTCCGC AAACCTGCTGG      500
ACGAAGGCCG TGCTGGTGAG AACGTCGGCG TTCTGCTGCG TGGTATCAAG      550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCTCCATCAA      600
20 GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATCCTGTCC AAAGACGAAG      650
GCGGCCGTCA CACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
CGTACAACCTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT      750
GGTAATGCCG GCGACAACA TCAAGATGGT TGTTACCCTG ATCCACCCGA      800
TCGCGATGGA CGACGGTCTG CGTTTC      826
25

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2) INFORMATION FOR SEQ ID NO: 56

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter hormaechei*
 (B) STRAIN: ATCC 49162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56

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GGCGCGATCC TGGTTGTTGC TCGGACTGAC GGCCCTATGC CTCAGACCCG      50
45 TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCTTAC ATCATCGTGT      100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTA      150
GAGATGGAAG TTCGTGAACT GCTGTCTCAG TACGATTTC CAGGCGACGA      200
CACCCCAATC GTTCGTGGTT CCGCGCTGAA AGCGCTGGAA GGCGAMGCAG      250
AGTGGGAAGM GAAAATCATC GARCTGGCTG GCTTCCTGGA TTCTTACATC      300
50 CCAGAACCAG AGCGTGCGAT TGACAAGCCA TTCTGCTGCT CAATCGAAGA      350
CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTWGAGC      400
GCGGTATCAT CAAAGTAGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG      450
ACTGCGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAAC      550
55 GTGAAGAAAT CGAACGTGGT CAGGTTCTGG CGAAGCCAGG CTCAATCAAG      600
CCACACACCA AGTTCGAATC TGAAGTGTA ATTCTGTCCA AAGACGAAGG      650
CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC      700
GTACAACCTGA CGTGACCGGT ACCATCGAAC TGCCAGAAGG CGTAGAGATG      750
GTAATGCCAG GCGACAACAT CAAGATGGTT GTGACGCTGA TCCACCCAAT      800
60 CGCGATGGAC GACGGTCTGC GTTTCGCAA      829

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2) INFORMATION FOR SEQ ID NO: 57

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter sakazakii*
 (B) STRAIN: ATCC 29544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57

20	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
	GAGATGGAAG	TGCGCGAGCT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACCCCGATC	GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCTG	250
25	AGTGGGAAGC	GAAAATCATC	GAGCTGGCAG	GTCACCTGGA	TTCTTACATC	300
	CCGGAACCGG	AGCGTGCGAT	TGACAAGCCG	TTCTTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCYGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAAGAGC	400
	GCGGTATCAT	CAAGGTTGGT	GAAGAAGTTG	AAATCGTGGG	CATCAAAGAC	450
	ACCGCGAAAT	CCACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
30	CGAAGGCCGT	GCGGGCGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCCATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGATGAAGG	650
	CGGCCGTCAC	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACRACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTTGAGATG	750
35	GTAATGCCGG	GCGACAACAT	CAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCGATGGAC	GACGGTCTGC	GTTTCGCAAT	C		831

2) INFORMATION FOR SEQ ID NO: 58

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58

55	CGGCGCGATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACAC	50
	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	GTGTACCATA	CATCGTTGTT	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTGTCAGA	ATATGACTTC	CCAGGCGACG	200
60	ATGTTCCCTGT	AATCGCTGGT	TCTGCTTTGA	AAGCTCYTGA	AGGCGATGCT	250

	TCATACGAAG	AAAAAATCAT	GGAATTAATG	GCTGCAGTTG	ACGAATACGT	300
	TCCAACCTCCA	GAACGTGACA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTGCTGA	450
5	AGAAACTGCT	AAAACAACCTG	TAACCTGGTGT	TGAAATGTTC	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGTGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAG	CTGGTACAAT	600
	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	TTACGTTTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCACACACCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
10	TTCCGTACAA	CTGACGTAAC	TGGTGTTGTT	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTAACAAT	CGACGTTGAA	TTGATCCACC	800
	CAATCGCTAT	CGAAGACGGA	ACTCGTTTCT	CAATT		835

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2) INFORMATION FOR SEQ ID NO: 59

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 826 bases
20	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Enterococcus cecorum</i>
(B)	STRAIN: ATCC 43198

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

	GGTGCTATCT	TAGTAGTATC	TGCTGCTGAT	GGTCCTATGC	CACAAACTCG	50
	TGAACACATT	CTTTTATCAC	GTAACGTTGG	TGTTCCATAC	ATCGTTGTTT	100
	TCTTAAACAA	AGTTGATATG	GTTGACGACG	AAGAATTATT	AGAATTAGTT	150
35	GAAATGGAAG	TACGTGACTT	ATTAAC TGAA	TACGACTTCC	CAGGAGACGA	200
	TGTTCCCTGTA	ATCGCTGGTT	CTGCATTAAA	AGCTTTAGAA	GGCGACCCAT	250
	CTTACGAAGA	AAAAATCTTA	GAATTAATGG	CTGCAGTTGA	CGAATACATC	300
	CCAACCTCCAG	AACGTGACAA	CGATAAACCA	TTCATGATGC	CAGTCGAAGA	350
	CGTATTTTCA	ATCACTGGTC	GTGGTACTGT	TGCTACAGGT	CGTGTTGAAC	400
40	GTGGACAAGT	ACGTGTTGGT	GACGAAGTTG	AAATAGTTGG	TATCCATGAT	450
	GAAATTTCTA	AAACAACAGT	TACTGGTGTT	GAAATGTTCC	GTAAATTATT	500
	AGATTACGCT	GAAGCTGGAG	ACAACATCGG	TGCATTATTA	CGTGGTGTGG	550
	CTCGTGAAGA	TATCCAACGT	GGTCAAGTAT	TAGCTAAACC	AGGTTCAATC	600
	ACTCCACATA	CAAAATTCAC	TGCTGAAGTG	TACGTTTTTA	CTAAAGAAGA	650
45	AGGTGGACGT	CATACTCCAT	TCTTCACTAA	CTACCGTCCA	CAATTCTACT	700
	TCCGTACAAC	TGACGTTACA	GGTG TAGTTA	ACTTACCAGA	AGGTACTGAA	750
	ATGGTTATGC	CTGGTGATAA	CGTAAC TATG	GAAGTTGAAT	TAATCCACCC	800
	AATCGCTATC	GAAGACGGAA	CTCGTT			826

50

2) INFORMATION FOR SEQ ID NO: 60

(i) SEQUENCE CHARACTERISTICS:

55	(A)	LENGTH: 835 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*
 (B) STRAIN: ATCC 51266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60

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CGGCGCGATC TTGGTAGTAT CTGCTGCTGA TGGTCCTATG CCTCAAACCTC      50
GTGAACACAT CCTATTGTCA CGTAACGTTG GTGTTTCCTTA CATCGTCGTT      100
10 TTCTTGAACA AAATGGACAT GGTTGATGAC GAAGAATTAT TAGAATTAGT      150
TGAAATGGAA GTTCGTGACT TATTGTCAGA ATACGACTTC CCAGGCGACG      200
ACACTCCAGT TATCGCAGGT TCAGCTTTGA AAGCCTTAGA AGGCGACGCT      250
TCATATGAAG AAAAAATCTT AGAATTAATG GCTGCAGTTG ACGAATATAT      300
CCCAACTCCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG      350
15 ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTTGAA      400
CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATCGCTGA      450
AGAAACTGCT AAAACTACTG TAACAGGTGT TGAAATGTTC CGTAAATTGT      500
TGGATTACGC TGAAGCTGGC GACAACATTG GTGCATTATT ACGTGGTGTG      550
GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTATCAAAAC CAGGTTCAAT      600
20 CACTCCACAT ACAAATTTG CGGCAGAAGT TTACGTTTTA ACTAAAGAAG      650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGCCC ACAATTCTAC      700
TTCCGTACAA CTGACGTAAC AGGTGTTGTT GAATTACCAG AAGGTACTGA      750
AATGGTTATG CCTGGCGATA ACGTTACTAT GGACGTTGAA TTAATCCACC      800
CAATCGCGAT CGAAGACGGT ACTCGTTTCT CAATC      835
25

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2) INFORMATION FOR SEQ ID NO: 61

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus durans*
 (B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61

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CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGCCCTATG CCTCAAACCTC      50
45 GTGAACATAT CCTATTATCT CGTCAAGTTG GTGTTTCCTTA CATCGTYGTA      100
TTCTTGAACA AAGTAGATAT GGTTCGATGAC GAAGAATTAC TAGAATTAGT      150
TGAAATGGAA GTTCGTGACT TATTAACAGA ATACGAATTC CCTGGTGACG      200
ATGTTTCCTGT AATCGCTGGT TCAGCTTTGA AAGCTTTAGA AGGCGACGCT      250
TCATACGAAG AAAAAATCCT TGAATTAATG GCTGCAGTTG ACGAATATAT      300
50 CCCAACTCCA GAACGTGACA ACGACAAACC ATTCATGATG CCAGTTGAAG      350
ATGTATTCTC RATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA      400
CGTGGACAAG TTCGCGTTGG TGACGTTGTA GATATCGTTG GTATCGCAGA      450
AGAAACAGCT CAAACAACAG TTAAGTGGTGT TGAAATGTTC CGTAAATTAT      500
TAGRCTACGC TGAAGCTGGA GACAACATTG GTGCTTTACT ACGTGGTGTG      550
GCACGTGAAG ACATCCAACG TGGACAAGTT TTAGCTAAAC CAGGTACAAT      600
CACKCCTCAT ACAAATTTCT CTGCAGAAGT ATACGTGTTG ACTAAAGAAG      650
AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC      700
TTCCGTACAA CTGACGTAAC AGGTGTTGTT GAATTACCAG AAGGAACTGA      750
AATGGTTATG CCTGGCGACA ACGTAACAAT GGAAGTTGAA TTAATCCACC      800
60 CAATCGCTAT CGAAAATGGT ACTAAATTCT CAATC      835

```

2) INFORMATION FOR SEQ ID NO: 62

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62

20	AGTAGTTTCT	GCTGCTGATG	GTCCTATGCC	TCAAACACGT	GAACATATCT	50
	TATTATCACG	TAACGTTGGT	GTACCATACA	TCGTTGTATT	CTTAAACAAA	100
	ATGGATATGG	TTGATGACGA	AGAATTATTA	GAATTAGTAG	AAATGGAAGT	150
	TCGTGACTTA	TTATCAGAAT	ACGATTTCCT	AGGCGATGAT	GTTCCAGTTA	200
	TCGCAGGTTC	TGCTTTGAAA	GCTTTAGAAG	GCGACGAGTC	TTATGAAGAA	250
25	AAAATCTTAG	AATTAATGGC	TGCAGTTGAC	GAATATATCC	CAACTCCAGA	300
	ACGTGATACT	GACAAACCAT	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	350
	TCACTGGACG	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	TGGTGAAGTT	400
	CGCGTTGGTG	ACGAAGTTGA	AATCGTTGGT	ATTAAAGACG	AAACATCTAA	450
	AACAACGTGT	ACAGGTGTTG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	500
30	AAGCAGGCGA	CAACATCGGT	GCTTTATTAC	GTGGTGTAGC	ACGTGAAGAT	550
	ATCGAACGTG	GACAAGTATT	AGCTAAACCA	GCTACAATCA	CTCCACACAC	600
	AAAATTCAAA	GCTGAAGTAT	ACGTATTATC	AAAAGAAGAA	GGCGGACGTC	650
	AACTCCATT	CTTCACTAAC	TACCGTCCTC			680

35

2) INFORMATION FOR SEQ ID NO: 63

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63

	AGTAGTTTCT	GCTGCTGATG	GTCCTATGCC	TCAAACACGT	GAACATATCT	50
	TATTATCACG	TAACGTTGGT	GTACCATACA	TCGTTGTATT	CTTAAACAAA	100
55	ATGGATATGG	TTGATGACGA	AGAATTATTA	GAATTAGTAG	AAATGGAAGT	150
	TCGTGACTTA	TTATCAGAAT	ACGATTTCCT	AGGCGATGAT	GTTCCAGTTA	200
	TCGCAGGTTC	TGCTTTGAAA	GCTTTAGAAG	GCGACGAGTC	TTATGAAGAA	250
	AAAATCTTAG	AATTAATGGC	TGCAGTTGAC	GAATATATCC	CAACTCCAGA	300
	ACGTGATACT	GACAAACCAT	TCATGATGCC	AGTCGAAGAC	GTATTCTCAA	350
60	TCACTGGACG	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	TGGTGAAGTT	400

	CGCGTTGGTG	ACGAAGTTGA	AATCGTTGGT	ATTAAAGACG	AAACATCTAA	450
	AACAACGTGT	ACAGGTGTTG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	500
	AAGCAGGCGA	CAACATCGGT	GCTTTATTAC	GTGGTGTAGC	ACGTGAAGAT	550
	ATCGAACGTG	GACAAGTATT	AGCTAAACCA	GCTACAATCA	CTCCACACAC	600
5	AAAATTCAAA	GCTGAAGTAT	ACGTATTATC	AAAAGAAGAA	GGCGGACGTC	650
	ACACTCCATT	CTTCACTAAC	TACCGTCCTC			680

10 2) INFORMATION FOR SEQ ID NO: 64

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 685 bases
	(B)	TYPE: Nucleic acid
15	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Enterococcus faecium</i>
	(B)	STRAIN: R482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64

25	AGTAGTTTCT	GCTGCTGACG	GCCCAATGCC	TCAAACCTCGT	GAACACATCC	50
	TATTGTCTCG	TCAAGTTGGT	GTTCCTTACA	TCGTTGTATT	CTTGAACAAA	100
	GTAGACATGG	TTGATGACGA	AGAATTACTA	GAATTAGTTG	AAATGGAAGT	150
	TCGTGACCTA	TTAACAGAAT	ACGAATTCCC	TGGTGACGAT	GTTCTGTAG	200
30	TTGCTGGATC	AGCTTTGAAA	GCTCTAGAAG	GCGACGCTTC	ATACGAAGAA	250
	AAAATTCTTG	AATTAATGGC	TGCAGTTGAC	GAATACATCC	CAACTCCAGA	300
	ACGTGACAAC	GACAAACCAT	TCATGATGCC	AGTTGAAGAC	GTGTTCTCAA	350
	TTACTGGACG	TGGTACTGTT	GCTACAGGTC	GTGTTGAACG	TGGACAAGTT	400
	CGCGTTGGTG	ACGAAGTTGA	AGTTGTTGGT	ATTGCTGAAG	AAACTTCAAA	450
35	AACAACAGTT	ACTGGTGTG	AAATGTTCCG	TAAATTGTTA	GACTACGCTG	500
	AAGCTGGAGA	CAACATTGGT	GCTTTACTAC	GTGGTGTGTC	ACGTGAAGAC	550
	ATCCAACGTG	GACAAGTTTT	AGCTAAACCA	GGTACAATCA	CACCTCATAC	600
	AAAATTCTCT	GCAGAAGTAT	ACGTGTTGAC	AAAAGAAGAA	GGTGGACGTC	650
40	ATACTCCATT	CTTCACTAAC	TACCGTCCTC	AATTT		685

2) INFORMATION FOR SEQ ID NO: 65

45 (i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 825 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
50	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Enterococcus flavescens</i>
55	(B)	STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65

60	CGGCGCGATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCTAYG	CCTCAAACAC	50
	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	GTGTACCATA	CATCGTTGTT	100

	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTGTCAGA	ATATGACTTC	CCAGGCGACG	200
	ATGTTCTGT	AATCGCTGGT	TCTGCTTTGA	AAGCTCTTGA	AGGCGATGCT	250
	TCATACGAAG	AAAAAATCAT	GGAATTAATG	GCTGCAGTTG	ACGAATACGT	300
5	TCCAACCTCCA	GAACGTGACA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTGCTGA	450
	AGAACTGCT	AAAACAACCTG	TAACCTGGTGT	TGAAATGTTC	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGGGTT	550
10	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTAGCTAAAG	CTGGTACAAT	600
	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	TTACGTTTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTGT	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGTGATA	AMGTAACAAT	CGACGTTGAA	TTGATCCACC	800
15	CAATCGCTAT	CGAAGACGGA	ACTCG			825

2) INFORMATION FOR SEQ ID NO: 66

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66

35	TCCTATGCCT	CAAACCTCGTG	AACACATCTT	GTTATCACGT	AACGTTGGCG	50
	TACCATACAT	CGTTGTTTTT	TTGAACAAAA	TGGATATGGT	TGATGACGAA	100
	GAATTGCTAG	AATTAGTTGA	AATGGAAGTT	CGTGACCTAT	TGTCTGAGTA	150
	TGACTTCCCA	GGCGACGATG	TTCCTGTAAT	CGCCGGTTCT	GCTTTGAAAG	200
	CTCTTGAAGG	AGATCCTTCA	TACGAAGAAA	AAATCATGGA	ATTGATGGCT	250
40	GCAGTTGACG	AATACGTTCC	AACTCCAGAA	CGTGATACTG	ACAAACCAT	300
	CATGATGCCA	GTCGAAGACG	TATTCTCAAT	CACTGGACGT	GGTACTGTTG	350
	CTACAGGCCG	TGTTGAACGT	GGACAAGTTC	GCGTTGGTGA	TGAAGTAGAA	400
	ATCGTTGGTA	TTGCTGACGA	AACTGCTAAA	ACAACGTGTA	CAGGTGTTGA	450
	AATGTTCCGT	AAATTGTTAG	ACTATGCTGA	AGCAGGGGAT	AACATTGGTG	500
45	CATTGCTACG	TGGGGTTGCT	CGTGAAGACA	TCCAACGTGG	ACAAGTATTG	550
	GCTAAAGCTG	GTACAATCAC	ACCTCATA	AAATTCAAAG	CTGAAGTTTA	600
	TGTTTTGACA	AAAGAAGAAG	GTGGACGTCA	CACTCC		636

50

2) INFORMATION FOR SEQ ID NO: 67

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus hirae*
 (B) STRAIN: ATCC 8043

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

	CGGAGCTATC	TTAGTAGTTT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACCTC	50
	GTGAACATAT	CCTAYTATCT	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCTTGAACA	AAGTAGATAT	GGTTGACGAC	GAAGAATTAC	TAGAATTAGT	150
10	TGAAATGGAA	GTTCGTGACT	TATTAACAGA	ATACGAATTC	CCTGGTGACG	200
	ATGTTCTGT	AGTTGCTGGT	YCAGCTTTGA	AAGCTTTAGA	AGGCGACGCT	250
	TCATACGAAG	AAAAAATCCT	TGAATTGATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGACA	ACGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
15	CGTGGACAAG	TTCGCGTTGG	TGACGTTGTA	GATATCGTTG	GTATCGCAGA	450
	AGAAACAGCT	CAAACAACAG	TTACTGGTGT	TGAAATGTTC	CGTAAATTAT	500
	TAGACTACGC	TGAAGCTGGA	GACAACATTG	GTGCTTTACT	ACGTGGTGTT	550
	GCACGTGAAG	ACATCCAACG	TGGACAAGTT	TTAGCTAAAC	CAGGTACAAT	600
	CACACCTCAT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACAAAAGAAG	650
20	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACRA	CTGACGTAAC	AGGTGTTGTT	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGCGACA	ACGTAACAAT	GGAAGTTGAA	TTAATCCACC	800
	CAATCGCTAT	CGAAAACGGT	ACTAAATTCT	CAATC		835

25

2) INFORMATION FOR SEQ ID NO: 68

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus mundtii*
 (B) STRAIN: ATCC 43186

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68

	CGGAGCAATC	TTAGTTGTTT	CTGCTGCTGA	CGGCCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CCTATTATCT	CGTCAAGTTG	GTGTACCATA	CATCGTTGTA	100
45	TTCTTGAACA	AAGTAGATAT	GGTTGATGAC	GAAGAATTAC	TTGAATTAGT	150
	TGAAATGGAA	GTTCGTGACC	TATTAACAGA	ATACGAATTC	CCTGGTGACG	200
	ATGTTCTGT	AATCGCTGGT	TCAGCTTTAA	GAGCTTTAGA	AGGCGACGCT	250
	KCATACGAAG	AAAAAATTCT	TGAATTGATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGATA	ACGACAAACC	ATTCATGATG	CCAGTTGAGG	350
50	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	ACGTGTTGAA	400
	CGTGGACAAG	YTCGTGTTGG	TGACGTTATC	GATATCGTTG	GTATCGCAGA	450
	AGAAACAGCT	CAAACAACCTG	TAACCTGGTGT	TGAAATGTTC	CGTAAATTAT	500
	TAGACTACGC	TGAAGCAGGC	GATAACATTG	GTGCGTTACT	ACGTGGTGTT	550
	TCACGTGAAG	ACATCCAACG	TGGTCAAGTT	TTAGCTAAAC	CAGGTACAAT	600
55	CACACCTCAT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
	TTYGTACGA	CTGACGTAAC	TRGTGTTGTY	GAATTACCAG	AAGGAACTGA	750
	AATGGTTATG	CCTGGCGACA	ACGTAACAAT	GGAAGTTGAA	TTAATCCACC	800
	CAATCGCTAT	CGAAAATGGT	ACTAAATTCT	CAATC		835

60

2) INFORMATION FOR SEQ ID NO: 69

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus pseudoavium*
 15 (B) STRAIN: ATCC 49372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69

	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCTATG	CCTCAAACAC	50
20	GTGAACACAT	CTTGTTATCT	CGTAACGTTG	GTGTTCCCTTA	CATCGYTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTGTCAGA	ATACGATTTC	CCAGGCGACG	200
	ACACTCYAGT	TATCGCTGGT	TCAGCYTTGA	AAGCTTTAGA	AGGCGACCCT	250
	TCATACRAAG	AAAAAATCTT	AGAATTAATG	SCTGCTGTTG	ACGAATACAT	300
25	CCCAACACCA	GTTCGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCAACTGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTAG	GTATCGCTGA	450
	AGAAACTGCT	AAAACAACCTG	TTACAGGTGT	TGAAATGTTC	CGTAAATTGT	500
	TAGACTACGC	TGAAGCAGGC	GATAACATCG	GTGCATTATT	ACGTGGTGTT	550
30	GCACGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAC	CAGCTTCAAT	600
	CACTCCACAT	ACAAAATTCT	CTGCAGAAGT	TTACGTTTTA	ACTAAAGAAG	650
	AAGGCGGGCG	TCACACTCCG	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTTGTT	GATCTACCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACAT	GGAAGTTGAA	TTAATCCACC	800
35	CAATCGCGAT	CGAAGACGGA	ACTCGTTTCT	CTATTC		836

2) INFORMATION FOR SEQ ID NO: 70

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus raffinosus*
 50 (B) STRAIN: ATCC 49427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70

55	CGGAGCTRTC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTGTTATCT	CGTAACGTTG	GTGTTCCCTTA	CATCGTTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGACGAT	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGACT	TATTAACCTGA	ATACGACTTC	CCAGGCGACG	200
	ACACTCCAGT	TATCGCAGGT	TCAGCTTTGA	AAGCCTTAGA	AGGCGACGCT	250
60	TCATACGAAG	AAAAAATCTT	AGAATTAATG	GCTGCTGTTG	ATGAATACAT	300

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      CCCAACACCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGYGGAAG      350
      ACGTAYTCTC AATCACTGGT CGTGGAAC TGCAACTGG TCGTGTTGAA      400
      CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATTGCTGA      450
      AGAAACTGCT AAAACAAC TGACAGGTGT TGAAATGTTC CGTAAATTGT      500
5    TGGATTACGC TGAAGCGGGC GACAACATTG GTGCATTATT ACGTGGTGTT      550
      GCACGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAC CAGCTTCAAT      600
      CACTCCACAT ACAAATTTCT CTGCAGAAGT TTACGTTTTA ACTAAAGAAG      650
      AAGGCGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC      700
      TTCCGTACAA CTGACGTAAC TGGTGTAAGT GATCTACCAG AAGGTACTGA      750
10   AATGGTAATG CCTGGTGATA ACGTAACTAT GGAAGTTGAA TTAATCCACC      800
      CAATCGCGAT CGAAGACGGA ACTCGTTTCT CTATT      835

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15 2) INFORMATION FOR SEQ ID NO: 71

(i) SEQUENCE CHARACTERISTICS:

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      (A) LENGTH: 835 bases
      (B) TYPE: Nucleic acid
20   (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

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      (A) ORGANISM: Enterococcus saccharolyticus
      (B) STRAIN: ATCC 43076

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71

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30   CGGCGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCTATG CCTCAAACCTC      50
      GTGAACACAT CTTGTTATCT CGTAACGTAG GTGTTCTTCA CATCGTTGTA      100
      TTCTTAAACA AAATGGATAT GGTGATGAC GAAGAATTAT TAGAATTAGT      150
      AGAAATGGAA GTTCGTGACT TATTATCAGA ATACGATTTC CCAGGCGATG      200
35   ACACTCCAGT TATTGCAGGT TCTGCTTTGA AAGCTTTAGA AGGCGATCCA      250
      GTTTACGAAG AAAAAATCTT CGAATTAATG GCTGCAGTTG ACGAATATAT      300
      CCCAACTCCA GAACGTGATA CTGAAAAACC ATTCATGATG CCAGTTGAGG      350
      ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA      400
      CGTGGACAAG TTCGCGTTGG TGACGTTGTA GAAATCGTTG GTATCGACGA      450
40   AGAAACAGCT CAAACTACTG TAACAGGTGT TGAAATGTTC CGTAAATTAT      500
      TAGACTACGC TGAAGCAGGC GATAACATCG GTGCTTTATT ACGTGGGGTT      550
      GCTCGTGAAG ACATCCAACG TGGACAAGTA TTAGCTAAAC CAGGAACAAT      600
      CACTCCTCAT ACAAATTCG TAGCTGAAGT TTACGTTTTA ACTAAAGAAG      650
      AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC TCAATTCTAC      700
45   TTCCGTACAA CTGACGTAAC TGGTGTTGTA GAATTACGCG AAGGTACTGA      750
      AATGGTAATG CCTGGTGACA ACGTAACTAT CGACGTTGAA TTAATCCACC      800
      CAATCGCTAT CGAAGACGGA ACTCGTTTCT CTATT      835

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50 2) INFORMATION FOR SEQ ID NO: 72

(i) SEQUENCE CHARACTERISTICS:

```

      (A) LENGTH: 823 bases
55   (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus solitarius*
 (B) STRAIN: ATCC 49428

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

	GAGCTATCTT	GGTAGTTTCT	GCAGCTGATG	GCCCAATGCC	ACAAACTCGT	50
	GAACATATTT	TGTTGTCACG	TAATGTAGGT	GTACCTTACA	TCGTTGTGTT	100
	CTTGAACAAA	ATGGATATGG	TTGATGACGA	AGAATTACTT	GAGTTAGTTG	150
10	AAATGGAAGT	ACGTGATCTA	TTATCTGAAT	ACGACTTCCC	AGGAGATGAT	200
	ACTCCAGTTA	TTTCCGGTTC	AGCTTTGAAA	GCTTTAGAAG	GCGACGAAGA	250
	ATATGAACAA	AAAATTATGG	ACTTAATGGA	TGCAGTTGAT	GACTACATTC	300
	CAACTCCTGA	ACGTGACCAT	GACAAACCAT	TCATGATGCC	AATTGAAGAT	350
	GTATTTTCAA	TTACAGGCCG	TGGTACTGTT	GCTACAGGAC	GTGTTGAACG	400
15	CGGGACTATC	AAAGTCGGCG	ATGAAGTTGA	CATTATTGGT	ATTCATGAAG	450
	ACGTTAAAAA	GACAACAGTT	ACTGGTGTAG	AAATGTTCCG	TAAATTGTTG	500
	GACTACGCTG	AAGCAGGCGA	TAACATTGGT	ACTTTGTTAC	GTGGTGTTTC	550
	TCGTGATGAT	ATCGAACGTG	GTCAAGTATT	AGCTAAACCA	GGTTCAATCA	600
	CACCACATAC	AAGATTCTCT	GCTGAAGTTT	ATGTTTTGAC	TAAAGAAGAA	650
20	GGCGGACGTC	ATACTCCATT	CTTCTCAAAC	TATCGTCCTC	AATTCTACTT	700
	CCGTACAAC	GATATCACTG	GTGTCATTGA	ATTGCCAGAA	GGTACTGAAA	750
	TGGTAATGCC	AGGTGATAAT	GTAACAATGG	ATGTTGAATT	AATCCACCCA	800
	GTCGCTATCG	AAGAAGGAAC	TCG			823

25

2) INFORMATION FOR SEQ ID NO: 73

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73

	CGGTGCAATC	TTGGTCGTAT	CAGCGACAGA	TGGCCCAATG	CCACAAACAC	50
	GGGAGCATAT	TTTGCTTTCT	CGTCAAGTGG	GTGTGAAACA	TTTGATCGTC	100
45	TTTTTTGAATA	AGACGGACCT	TGTCGATGAT	GACGAGTTGA	TCGATTTAGT	150
	TGAAATGGAA	GTCAGAGAAT	TGCTGACTGA	ATATGATTTT	CCTGGCGACG	200
	ACATTCCTGT	GATCAAGGGC	TCTGCGTTAA	AAGCCTTGGA	AGGGGACCCA	250
	GATGCTGAAG	CAGCGATCTT	AACGCTGATG	GATACAGTAG	ATGAATATAT	300
	CCCAACGCCA	GAACGTGATA	CTGACAAACC	ATTGTTGTTA	CCGATCGAAG	350
50	ATGTCTTTTC	GATCACAGGA	CGGGGGACCG	TTGCTTCTGG	TCGGATCGAT	400
	CGCGGCATGG	TAAAAGTCGG	GGATGAAGTA	GAAATCGTCG	GAATCAAACC	450
	TGAAACACAA	AAAGCAGTCG	TGACAGGGGT	AGAAATGTTT	CGCAAAACGA	500
	TGGACTTCGG	AGAAGCTGGC	GATAACGTAG	GGGTATTGTT	ACGGGGCATC	550
	ACCCGTGATG	AAATTGAACG	TGGCCAAGTG	TTAGCAAAAC	CAGGTTCTAT	600
55	CACACCGCAT	ACGAAATTCC	AAGCGGAAGT	CTATGTGTTG	ACAAAAGAAG	650
	AAGGCGGTCG	CCATACCCCA	TTCTTTAATA	ATTATCGCCC	ACAATTTTAC	700
	TTCCGTACAA	CGGACGTAAC	TGGGAATATC	GTTTTACCAG	AAGGAACGGA	750
	AATGGTGATG	CCTGGTGACA	ACGTAACGAT	CGATGTGGAA	TTGATCCATC	800
	CGATCGCTGT	AGAAAATGGA	ACGACCTTCT	CGATT		835

60

2) INFORMATION FOR SEQ ID NO: 74

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 15 (B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74

	TAACGGGCGT	CTCGATAGAA	AAACACGTGA	AAATCCCAAT	GATTATAAAC	50
20	AATCAATATA	CGATTTTGCT	GAAGCTGTAA	CAAAAGGTAT	TAAGGAACAA	100
	ACAAATAAAA	ATTAATAGGC	AACTTAACCA	GAATCGTTAA	AACTATATGA	150
	AGATTCTGGT	TTTTTAAATT	CAAAAAGTTT	TCTAAAAAAT	TTACTTGCTT	200
	TTTTAAGTAT	AGGTATAAAA	TACGATTGAT	TAAACAGTA	AAGGAAATGA	250
	ATCATGAAAC	AATTAATACTAA	GCCTTTATAC	TTTTACCTAT	TACTTTTTTAT	300
25	TACAACAACG	CTGATTGGCG	CGTTACTATT	ATATTTGCCA	ATCACAGGTA	350
	AACATCCTAT	TGATTTTGTG	GACGCCCGTT			380

30 2) INFORMATION FOR SEQ ID NO: 75

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75

45	GCAATCTTGG	TCGTATCAGC	GACAGATGGC	CCAATGCCAC	AAACACGGGA	50
	GCATATTTTG	CTTTCTCGTC	AAGTGGGTGT	GAAACATTTG	ATCGTCTTTT	100
	TGAATAAGAC	GGACCTTGTC	GATGATGACG	AGTTGATCGA	TTAGTTGAA	150
	ATGGAAGTCA	GAGAATTGCT	GACTGAATAT	GATTTTCCTG	GCGACGACAT	200
50	TCCTGTGATC	AAGGGCTCTG	CGTTAAAAGC	CTTGGAAGGG	GACCCAGATG	250
	CTGAAGCAGC	GATCTTAACG	CTGATGGATA	CGGTAGATGA	ATATATCCCA	300
	ACGCCAGAAC	GTGATACTGA	CAAACCATTG	TTGTTACCGA	TCGAAGATGT	350
	CTTTTCGATC	ACAGGACGGG	GGACCGTTGC	TTCTGGTCGG	ATCGATCGCG	400
	GCATGGTAAA	AGTCGGGGAT	GAAGTAGAAA	TCGTCGGAAT	CAAACCTGAA	450
55	ACACAAAAAG	CAGTCGTGAC	AGGGGTAGAA	ATGTTCCGCA	AAACGATGGA	500
	CTTCGGAGAA	GCTGGCGATA	ACGTAGGGGT	ATTGTTACGG	GGCATCACCC	550
	GTGATGAAAT	TGAACGTGGC	CAAGTGTTAG	CAAAACCAGG	TTCTATCACA	600
	CCGCATACGA	AATTCCAAGC	GGAAGTCTAT	GTGTTGACAA	AAGAAGAAGG	650
60	CGGTCGCCAT	ACCCCA				666

2) INFORMATION FOR SEQ ID NO: 76

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 15 (B) STRAIN: ATCC 49573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76

20 TGGTGCGATT TTAGTTGTAT CCGCAACAGA TGGTCCAATG CCTCAAACCC 50
 GGGAACATAT CTTGCTTTCG AGACAAGTTG GTGTGAAACA TCTGATTGTT 100
 TTCTTGAACA AAATCGATTT AGTCGATGAC GAAGAATTGA TTGATTTAGT 150
 AGAAATGGAA GTAAGAGAAC TGCTATCTGA ATATAATTTT CCAGGGGATG 200
 ACATTCCTGT TATCAAAGGT TCGGCATTAA AAGCGTTGGA AGGAGACCCT 250
 GATGCAGAAG CTGCCATCAT GGAATTAATG GATACAGTAG ACAGCTATAT 300
 25 CCCAACACCT GAGCGTGATA CAGACAAACC ATTACTCTTG CCAGTTGAAG 350
 ATGTCTTTTC GATTACTGGA CGAGGAACAG TTGCTTCCGG ACGGATCGAT 400
 CGGGGAACAG TTCGGGTAGG CGATGAAGTA GAAATCGTCG GTATCAAACC 450
 TGAAACCCAA AAAGCTGTAG TGACAGGCGT CGAAATGTTC CGCAAGACGA 500
 TGGACTTTGG GGAAGCCGGT GACAATGTAG GTGTCTTGCT GAGAGGGATC 550
 30 ACTCGTGACG AAATTGAACG AGGACAAGTG TTGGCTAAAC CAGGTTTCGAT 600
 CACACCACAT ACAAATTC AAGCAGAAGT TTATGTATTG ACGAAAGAAG 650
 AAGGTGGTCG TCATACACCA TTCTTCAACA ACTATCGTCC ACAATTTTAT 700
 TTCCGTACAA CGGATGTGAC AGGGAACATT ACATTGCCTG AAGGAACAGA 750
 A 751

35

2) INFORMATION FOR SEQ ID NO: 77

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ehrlichia canis*
 50 (B) STRAIN: Florida

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77

55 TGCAGCAATA TTAGTAGTGT CTGCAACTGA TGGAGCAATG CCACAAACAA 50
 GAGAACATAT ATTATTAGCA AAGCAAGTAG GTGTAAAAGA TATAGTAGTG 100
 TGGATGAATA AGTGTGATGT TGTAGATGAT GAAGAAATGT TGTCATTAGT 150
 TGAAATGGAA ATAAGGGAAT TGTTATCAAA ATATGGGTAT CCTGGGGATG 200
 ATATAGATGT AGTTAGAGGA TCTGCAGTTA AAGCATTAGA AGAAGAAACA 250
 GGCTCAGGTG TGTGGAGTGA AAAAATAATG GAATTGATGA ATGCTTTAGA 300
 60 AAAAATAAGT TTACCAGTAA GAGAAAAAGA TAAGCCATTT TTAATGTCAA 350

```

TAGAAGATGT GTTTTCAATA CCTGGAAGAG GTACAGTAGT AACAGGAAGA 400
ATAGAAAGAG GAGTAATTAG AGTAGGGGAT AAAATAGAGA TAGTAGGATT 450
GCGTGAGATA CAAAGTACAG TATGTACAGG TGTTGAAATG TTTCATAAAG 500
CATTAGATGC AGGAGAAGCA GGGGATAATG CTGGAATATT GTTAAGAGGG 550
5 ATAAAAAAG AAGATGTAGA AAGAGGGCAA GTATTGAGTG CACCTGGACA 600
GATACATTCA TATAAGAGAT TTAAGGCAGA GGTATATATA TTGAAAAAAG 650
AAGAAGGAGG AAGACATACT CCATTTTCT CAAATTACCA GCCGCAATTT 700
TATGTTAGAA CAACAGATGT AACAGGGAAT ATAAAGTTAC CAGAAGGAGT 750
AGAAATGGTA ATGCCAGGGG ATAATATAAA TATCGAAGTG AGTTTGGATA 800
10 AGCCTGTTGC TATTGATCAA GGATTGAGAT TTGC 834

```

2) INFORMATION FOR SEQ ID NO: 78

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 23511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78

```

30 CGGCGCGATC CTGGTAGTTG CTGCGACTGA CGGCCCCGATG CCGCAGACTC 50
GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAAGTGGT 150
TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG 200
ACACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA 250
35 GAGTGGGAAG CGAAAATCCT GGAAGTGGCT GGCTTCCTGG ATTCTTAYAT 300
TCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGGTGG 500
40 ACGAAGGCCG TGCTGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA 600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG 650
GCGGCCGTCA TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
CGTACTACTG ACGTGACTGG TACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
45 GGTAATGCCG GCGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA 800
TCGCGATGGA CGACGGT 817

```

50 2) INFORMATION FOR SEQ ID NO: 79

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia fergusonii*
 (B) STRAIN: ATCC 35469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79

```

5      CGATCCTGGT AGTTGCTGCG ACTGACGGCC CGATGCCGCA GACTCGTGAG      50
      CACATCCTGC TGGGTCGTCA GGTAGGCGTT CCGTACATCA TCGTGTTTCCT      100
      GAACAAGTGC GACATGGTTG ATGACGAAGA GCTGCTGGAA CTGGTTGAAA      150
      TGGAAGTTTCG TGAAC TTCTG TCTCAGTACG ACTTCCCGGG CGACGACACT      200
10     CCGATCGTTC GTGGTTCTGC TCTGAAAGCG CTGGAAGGCG ACGCAGAGTG      250
      GGAAGCGAAA ATCCTGGAAC TGGCTGGCTT CCTGGATTCT TACATTCCGG      300
      AACCAGAGCG TGC GATTGAC AAGCCGTTCC TGCTGCCGAT CGAAGACGTG      350
      TTCTCCATCT CCGGTCGTGG TACCGTTGTT ACCGGTCGTG TAGAACGCGG      400
      TATCATCAA GTTGGTGAAG AAGTTGAAAT CGTTGGTATC AAAGAGACTC      450
15     AGAAGTCTAC CTGTACTGGC GTTGAAATGT TCCGCAA ACT GCTGGACGAA      500
      GGCCGTGCTG GTGAGAACGT AGGTGTTCTG CTGCGTGGTA TCAAACGTGA      550
      AGAAATCGAA CGTGGTCAGG TACTGGCTAA GCCGGGCACC ATCAAGCCGC      600
      ACACCAAGTT CGAATCTGAA GTGTACATTC TGTCCAAAGA TGAAGGCGGT      650
      CGTCATACTC CGTTCTTCAA AGGCTACCGT CCGCAGTTCT ACTTCCGTAC      700
20     TACTGACGTG ACTGGTACCA TCGAACTGCC GGAAGGCGTA GAGATGGTAA      750
      TGCCGGGCGA CAACATCAA ATGGTTGTTA CCCTGATCCA CCCGATCGCG      800
      ATGGACGACG GTCTGCGTTT CGCAA      825
  
```

25

2) INFORMATION FOR SEQ ID NO: 80

(i) SEQUENCE CHARACTERISTICS:

```

30     (A) LENGTH: 829 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Escherichia hermannii
      (B) STRAIN: ATCC 33650
  
```

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

```

      GGCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG      50
      TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT      100
      TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT      150
45     GAGATGGAAG TTCGCGAACT GCTGTCCCAG TACGATTTCC CGGGCGACGA      200
      CACCCCGATC GTTCGTGGTT CCGCGCTGAA AGCGCTGGAA GGCGAAGCAG      250
      AGTGGGAAGA GAAAATCATC GAACTGGCTG GCTACCTGGA TTCCTATATC      300
      CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CTATCGAAGA      350
      CGTATTCTCC ATCTCCGGCC GTGGTACCGT TGTTACCGGT CGTG TAGAGC      400
50     GCGGTATCAT CAAAGTGGGT GAAGAAGTTG AAATCGTGGG TATCAAAGAT      450
      ACTGCGAAAT CAACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
      CGAAGGCCGT GCGGGCGAGA ACGTGGGTGT TCTGCTGCGT GGTATCAAAC      550
      GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG TTCCATCAAG      600
      CCKCACACCA AGTTCGAATC TGAAGTGATC ATTCTGTCCA AAGACGAAGG      650
55     CGGCCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC      700
      GTACAACTGA CGTGACTGGC ACCATCGAAC TGCCGGAAGG CGTTGAGATG      750
      GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT      800
      CGCGATGGAC GACGGTCTGC GTTTCGCAA      829
  
```

60

2) INFORMATION FOR SEQ ID NO: 81

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia vulneris*
 (B) STRAIN: ATCC 33821

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

CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC 50
 GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
 20 TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAAGTGGT 150
 TGAGATGGAA GTGCGTGAAC TTCTGTCCCA GTACGACTTC CCGGGCGACG 200
 ACACCCCGAT CATTCGTGGT TCTGCGCTGA AAGCGCTGGA AGGCGAAGCT 250
 GAGTGGGAAG AGAAAATCGT TGAGCTGGCT GGCTACCTGG ATTCCTACAT 300
 CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
 25 ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG 400
 CGCGGTATCA TCAARGTKGG TGAAGAAGTT GAAATCGTGG GTATCAAAGA 450
 TACTGCGAAA TCTACCTGTA CCGGCGTTGA AATGTTCCGC AAAGTCTGCTGG 500
 ACGAAGGTCG TGCAGGCGAG AACTGCGGCG TTCTGCTGCG TGGTATCAAG 550
 CGTGAAGAGA TCCAGCGTGG CCAGGTTCTG GCTAAGCCGG GCTCAATCAA 600
 30 GCCGCACACC AAGTTCGAAT CCGAAGTGTA CATCCTGTCC AAAGACGAAG 650
 GCGGCCGTCA CACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
 CGTACAACCTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
 GGTAATGCCG GGCGACAACA TCAAATGGT TGTACCCTG ATCCATCCGA 800
 TCGCGATGGA CGACGG 816

35

2) INFORMATION FOR SEQ ID NO: 82

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eubacterium lentum*
 50 (B) STRAIN: ATCC 43055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82

CGGCGCCTCC TCGTTATCGC CGCCACCGAC GGCCCGATGG CCCAGACCCG 50
 55 CGAGCACATC CTGCTCGCCC GTCAGGTCGG CGTGCCCTAC ATCGTGGTCT 100
 TCCTGAACAA GTGCGACATG GTCGACGACG AGGAGCTCCT CGAGCTCGTC 150
 GAGATGGAAG TTCGCGAGCT GCTCGACTCT TACGAGTTCC CGGGCGACGA 200
 CACCCCGATC ATCCGCGGCT CCGCTTTGAA GGCCCTCGAG GGCGACAAAG 250
 AGTGGCAGGA GAAGGTCTGG GAGCTCATGG ACGCCGTCGA CTCCTACATC 300
 60 CCGACGCCGG AGCGCATGGT CGACAAGCCG TTCCTGATGG CCGTCGAGGA 350

	CACGATGACC	ATCACCGGCC	GCGGCACCGT	TGCCACCGGT	CGTGTGGAGC	400
	GTGGTACGCT	GCATGTCAAC	GACCCGCTGG	AGATCGTCGG	TATCAAGGAG	450
	ACCCAGAACA	CGGTCTGCAC	CGGTATCGAG	ATGTTCCGCA	AGCTGCTCGA	500
	CGAGGCTCAG	GCCGGCGACA	ACATCGGCTG	CCTGCTCCGC	GGTGTCAAGC	550
5	GCGAGGAGAT	CGTTCGCGGC	CAGGTTCTCT	GCAAGCCCGG	TAGCGTGACC	600
	CCGCACACCG	AGTTCGAGGG	TCAGGTCTAC	ATCCTGACGA	AGGAAGAGGG	650
	CGGCCGCCAC	ACGCCGTTCT	TCGACGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GCACGACGGA	CGTGACGGGT	GTTGCCCACC	TTCCCGAGGG	CACCGAGATG	750
	GTCATGCCGG	GCGACAACGT	GGAGATCAAG	GGCGAGCTCA	TTCACCCGAT	800
10	CGCCAGGAAG	AGGGCTGCGT	TCGCTAAC			828

2) INFORMATION FOR SEQ ID NO: 83

15

(i) SEQUENCE CHARACTERISTICS:

- | | | |
|----|-----|----------------------|
| | (A) | LENGTH: 835 bases |
| | (B) | TYPE: Nucleic acid |
| | (C) | STRANDEDNESS: Double |
| 20 | (D) | TOPOLOGY: Linear |

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- | | | |
|----|-----|--------------------------------------|
| 25 | (A) | ORGANISM: <i>Eubacterium nodatum</i> |
| | (B) | STRAIN: ATCC 33099 |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83

30	GGAGCAATTC	TGGTTTGTGC	AGCAACKGAC	GGACCAATGC	CTCAGACAAG	50
	AGAACATATC	CTTTTGTCAA	GGCAGGTAGG	AGTGCCATAT	ATCATCGTAT	100
	TCCTGAATAA	ATGTGACATG	GTGGATGAYG	AAGAGCTTCT	GGACTTGGTA	150
	GAGATGGAAG	TAAGAGAACT	TCTCAGTGAG	TATGAATTCC	CGGGAGATGA	200
	TACCCCGATA	GTAAGAGGTT	CAGCCCTGAA	GGCACTGGAA	GAACCCAATG	250
35	GAGAATGGGC	AGACAAGATT	GTAGAGCTGA	TGGAGGAAGT	AGATAAATAC	300
	ATTCCTGAAC	CAAAGAGAGA	TAACGACAAA	CCGTTCCCTGA	TGCCTGTAGA	350
	GGACGTATTC	TCAATAACAG	GAAGAGGAAC	AGTAGCGACA	GGAAGRGTG	400
	AAAGAGGAAT	CCTGAAGGTC	GGTGATGAAG	TAGAAATCGT	GGGAATGAGC	450
	GAAGAGAGAA	GAAAGGTAAGT	AGTAACGGGA	GTTGAAATGT	TCAGAAAGCT	500
40	TCTGGATGAA	GCAGAGACAG	GAGACAACAT	CGGAGCACTG	CTGAGAGGAG	550
	TTCAGAGAAC	RGAGATCCAG	AGAGGTCAGG	TATTGGCRGC	ACCTGGAACG	600
	ATCAACCCAC	ATACAAAGTT	CAAGGGTCAG	GTATATGTAC	TGAAGAAGGA	650
	AGAAGGAGGA	AGGCATACGC	CGTTCTTCAA	YGGATACAGW	CCACAGTTCT	700
	ACTTCAGAAC	AACAGACGTA	ACAGGAGATT	TGCAGCTGCC	GGAAGGARCA	750
45	GAGATGTGCA	TGCCGGGAGA	TAATGTGGTA	ATGAACRTCA	GCCTGATCAC	800
	TCCGATTGCT	ATAGAAGAGG	GWCTGAGATT	TGCCA		835

50 2) INFORMATION FOR SEQ ID NO: 84

(i) SEQUENCE CHARACTERISTICS:

- | | | |
|----|-----|----------------------|
| | (A) | LENGTH: 826 bases |
| | (B) | TYPE: Nucleic acid |
| 55 | (C) | STRANDEDNESS: Double |
| | (D) | TOPOLOGY: Linear |

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

DEMANDES OU BREVETS VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET
COMPREND PLUS D'UN TOME.

CECI EST LE TOME 1 DE 4

NOTE: Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE
THAN ONE VOLUME

THIS IS VOLUME 1 OF 4

NOTE: For additional volumes-please contact the Canadian Patent Office

What is claimed is:

1. A repertoire of nucleic acid sequences used for the detection and/or identification of a bacterial, fungal or parasitical species, genus, family or group, which repertoire is created by amplifying the nucleic acids of a plurality of determined bacterial, fungal and parasitical species with any combination of the primer pairs shown in annexes I, II, XXI, XXII, XXXII, XXXIV, XXXVI, XL, XLIII and XLIV.
2. A nucleic acid used for universal detection of any bacterium, fungus or parasite which is derived from the repertoire of claim 1.
3. A nucleic acid used for universal detection as set forth in claim 2, which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with said any bacterium, fungus or parasite and with any one of SEQ ID NOs.: 543, 556-574, 636-655, 658-661, 664, 681-683, 694, 696-697, 699-700, 708, 812-815, 911-917, 919-922, 935-938, 1203-1207, 1212-1213, 1221-1229.
4. A nucleic acid used for the specific and ubiquitous detection and for identification of a bacterial, fungal or parasital species, genus, family or group, which is derived from the repertoire of claim 1.
5. A nucleic acid as set forth in claim 4, which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with the nucleic acids of said bacterial, fungal or parasitical species, genus, family or group and with any one of :

SEQ ID NOs.:

- | | |
|--|--|
| 539, 540 | for the detection and/or identification of <i>Mycobacteriaceae</i> family |
| 541, 542, 544 | for the detection and/or identification of Pseudomonads group |
| 545, 546 | for the detection and/or identification of <i>Corynebacterium</i> sp. |
| 547, 548, 1202 | for the detection and/or identification of <i>Streptococcus</i> sp. |
| 549, 550, 582,
583, 625, 626,
627, 628, 1199 | for the detection and/or identification of <i>Streptococcus agalactiae</i> |
| 551, 552 | for the detection and/or identification of <i>Neisseria gonorrhoeae</i> |
| 553, 575, 605,
606, 707, 1175,
1176, 1233 | for the detection and/or identification of <i>Staphylococcus</i> sp. |
| 554, 555 | for the detection and/or identification of <i>Chlamydia trachomatis</i> |
| 576, 631, 632,
633, 634, 635,
1163, 1164, 1167 | for the detection and/or identification of <i>Candida</i> sp. |
| 577, 1156, 1160 | for the detection and/or identification of <i>Candida albicans</i> |
| 578, 1166, 1168 | for the detection and/or identification of <i>Candida dubliniensis</i> |

	579	for the detection and/or identification of <i>Escherichia coli</i>
	580, 603, 1174, 1236, 1238	for the detection and/or identification of <i>Enterococcus faecalis</i>
	581	for the detection and/or identification of <i>Haemophilus influenzae</i>
5	584, 585, 586, 587, 588, 1232, 1234	for the detection and/or identification of <i>Staphylococcus aureus</i>
	589, 590, 591, 592, 593	for the detection and/or identification of <i>Staphylococcus epidermidis</i>
10	594, 595	for the detection and/or identification of <i>Staphylococcus haemolyticus</i>
	596, 597, 598	for the detection and/or identification of <i>Staphylococcus hominis</i>
	599, 600, 601, 695, 1208, 1209	for the detection and/or identification of <i>Staphylococcus saprophyticus</i>
	602, 1235, 1237	for the detection and/or identification of <i>Enterococcus faecium</i>
15	604	for the detection and/or identification of <i>Enterococcus gallinarum</i>
	620, 1122	for the detection and/or identification of <i>Enterococcus casseliflavus</i> , <i>E. flavescens</i> and <i>E. gallinarum</i>
	629, 630	for the detection and/or identification of <i>Chlamydia pneumoniae</i>
20	656, 657, 271, 1136, 1137	for the detection and/or identification of <i>Enterococcus</i> sp.
	701, 702	for the detection and/or identification of <i>Leishmania</i> sp.
	703, 704, 705, 706, 793	for the detection and/or identification of <i>Entamoeba</i> sp.
	794, 795	for the detection and/or identification of <i>Trypanosoma cruzi</i>
25	796, 797, 808, 809, 810, 811	for the detection and/or identification of <i>Clostridium</i> sp.
	798, 799, 800, 801, 802, 803, 804, 805, 806,	
30	807	for the detection and/or identification of <i>Cryptosporidium parvum</i>
	816, 817, 818, 819	for the detection and/or identification of <i>Giardia</i> sp.
	820, 821, 822	for the detection and/or identification of <i>Trypanosoma brucei</i>
	823, 824	for the detection and/or identification of <i>Trypanosoma</i> sp.
35	825, 826	for the detection and/or identification of <i>Bordetella</i> sp.
	923, 924, 925, 926, 927, 928	for the detection and/or identification of <i>Trypanosomatidae</i> family
	933, 934	for the detection and/or identification of <i>Enterobacteriaceae</i> group
40	935, 938	for the detection and/or identification of platelets contaminants group: <i>Abiotrophia adiacens</i> , <i>Abiotrophia defectiva</i> , <i>Acinetobacter baumannii</i> , <i>Acinetobacter lwoffii</i> , <i>Aerococcus viridans</i> , <i>Bacillus anthracis</i> , <i>Bacillus cereus</i> , <i>Bacillus subtilis</i> , <i>Brucella abortus</i> , <i>Burkholderia cepacia</i> , <i>Citrobacter diversus</i> , <i>Citrobacter freundii</i> , <i>Enterobacter aerogenes</i> , <i>Enterobacter agglomerans</i> , <i>Enterobacter cloacae</i> , <i>Enterococcus avium</i> , <i>Enterococcus casseliflavus</i> , <i>Enterococcus dispar</i> , <i>Enterococcus durans</i> , <i>Enterococcus faecalis</i> , <i>Enterococcus faecium</i> , <i>Enterococcus flavescens</i> , <i>Enterococcus gallinarum</i> ,
45		

- 5 *Enterococcus mundtii*, *Enterococcus raffinosus*, *Enterococcus solitarius*, *Escherichia coli*, *Gemella morbillorum*, *Haemophilus ducreyi*, *Haemophilus haemolyticus*, *Haemophilus influenzae*, *Haemophilus parahaemolyticus*, *Haemophilus parainfluenzae*, *Hafnia alvei*, *Kingella kingae*, *Klebsiella oxytoca*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Megamonas hypermegale*, *Moraxella atlantae*, *Moraxella catarrhalis*, *Morganella morganii*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella aerogenes*, *Pasteurella multocida*, *Peptostreptococcus magnus*, *Proteus mirabilis*, *Providencia alcalifaciens*, *Providencia rettgeri*, *Providencia rustigianii*, *Providencia stuartii*, *Pseudomonas aeruginosa*, *Pseudomonas fluorescens*, *Pseudomonas stutzeri*,
10 *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enteritidis*, *Salmonella gallinarum*, *Salmonella typhimurium*, *Serratia liquefaciens*, *Serratia marcescens*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus capitis*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Staphylococcus hominis*, *Staphylococcus lugdunensis*, *Staphylococcus saprophyticus*, *Staphylococcus simulans*,
15 *Staphylococcus warneri*, *Stenotrophomonas maltophilia*, *Streptococcus acidominimus*, *Streptococcus agalactiae*, *Streptococcus anginosus*, *Streptococcus bovis*, *Streptococcus constellatus*, *Streptococcus cricetus*, *Streptococcus cristatus*, *Streptococcus dysgalactiae*, *Streptococcus equi*, *Streptococcus ferus*, *Streptococcus gordonii*, *Streptococcus intermedius*, *Streptococcus macacae*, *Streptococcus mitis*, *Streptococcus mutans*,
20 *Streptococcus oralis*, *Streptococcus parasanguinis*, *Streptococcus parauberis*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Streptococcus rattii*, *Streptococcus salivarius*, *Streptococcus sanguinis*, *Streptococcus sobrinus*, *Streptococcus uberis*, *Streptococcus vestibularis*, *Vibrio cholerae*, *Yersinia enterocolitica*, *Yersinia pestis*, *Yersinia pseudotuberculosis*.
- 25 994, 995, 996,
997, 998, 999,
1000, 1001, 1200,
1210, 1211 for the detection and/or identification of *Streptococcus pyogenes*
1157 for the detection and/or identification of *Candida parapsilosis*
- 30 1158, 1159 for the detection and/or identification of *Candida glabrata*
1160 for the detection and/or identification of *Candida tropicalis*
1161 for the detection and/or identification of *Candida krusei*
1162 for the detection and/or identification of *Candida guilliermondii*
1162 for the detection and/or identification of *Candida lusitaniae*
- 35 1165 for the detection and/or identification of *Candida zeylanoides*
1201 for the detection and/or identification of *Streptococcus pneumoniae*.
6. A nucleic acid as set forth in claim 4, which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with the nucleic acids of said bacterial, fungal or parasitical species, genus,
40 family, group or universal, and using the former in conjunction with any nucleic acid sequence of at least 12 nucleotides capable of hybridizing with a bacterial antibiotic resistance gene and/or toxin gene respectively listed in Tables 5 and 6.
7. Nucleic acids as set forth in claim 6 where the nucleic acid capable of hybridizing with a bacterial
45 antibiotic resistance gene and/or toxin gene is any one of :

SEQ ID NOs.:

- 1078, 1079, 1085 for the detection and/or identification of the Shiga-like toxin 2 (*stx*₂) gene
 1080, 1081, 1084 for the detection and/or identification of the Shiga-like toxin 1 (*stx*₁) gene
 1082, 1083 for the detection and/or identification of Shiga-like toxins 1 (*stx*₁) and 2 (*stx*₂) genes
- 5 1086, 1087, 1088,
 1089, 1090, 1091,
 1092, 1170, 1239,
 1240 for the detection and/or identification of the *vanA* resistance gene
 1171, 1241 for the detection and/or identification of the *vanB* resistance gene
- 10 1111, 1112, 1113,
 1114, 1115, 1116,
 1118, 1119, 1120,
 1121, 1123, 1124 for the detection and/or identification of the *vanAB* resistance genes
 1103, 1104, 1109,
- 15 1110 for the detection and/or identification of the *vanC1* resistance gene
 1105, 1106, 1107,
 1108 for the detection and/or identification of the *vanC2* and *vanC3* resistance genes
 1097, 1098, 1099,
 1100, 1101, 1102 for the detection and/or identification of the *vanC1*, *vanC2* and *vanC3* resistance genes
- 20 1150, 1153, 1154,
 1155 for the detection and/or identification of the *vanAXY* resistance genes
 1094, 1125, 1126,
 1127, 1128, 1129,
 1130, 1131, 1132,
- 25 1133, 1134, 1135,
 1192, 1193, 1194,
 1195, 1196, 1197,
 1214, 1216, 1217,
 1218, 1219, 1220 for the detection and/or identification of the *S. pneumoniae pbp1a* gene
- 30 1142, 1143, 1144
 1145 for the detection and/or identification of the *S. pneumoniae pbp2b* gene
 1146, 1147, 1148
 1149 for the detection and/or identification of the *S. pneumoniae pbp2x* gene
 1177 for the detection and/or identification of the *mecA* resistance gene.
- 35
8. A method for the specific detection or identification of a bacterial, fungal or parasitical species, genus, family or group in a sample, using a panel of probes or amplification primers or both, each individual probe or primer being derived from a nucleic acid as defined in claim 4, the method comprising the step of contacting the nucleic acids of the sample with said primers or probes under suitable conditions
- 40 of hybridization or of amplification and detecting the presence of hybridized probes or amplified products as an indication of the presence of said specific bacterial, fungal or parasitical species, genus, family or group.
9. A method as set forth in claim 8, which further comprises probes or primers, or both, for the detection
- 45 of at least one of the antibiotic resistance genes listed in Table 5.

10. A method as set forth in claim 8 or 9, which further comprises probes or primers, or both, for the detection of at least one of the toxin genes listed in Table 6.
- 5 11. A method as defined in claim 8, which further comprises the universal detection of any bacterium, fungus or parasite.
12. A nucleic acid having the nucleotide sequence of any one of the *tuf* sequences listed in Table 7 or in Table 11, or a part of thereof and variants thereof, which can be used as target nucleic acids for the
10 detection and identification of microbial species.
13. A nucleic acid having the nucleotide sequence of any one of the *atpD* sequences listed in Table 7 or in Table 11, or a part of thereof and variants thereof, which can be used as target nucleic acids for the detection and identification of microbial species.
- 15 14. A nucleic acid having the nucleotide sequence of any one of the *recA* sequences listed in Table 7 or in Table 11, or a part of thereof and variants thereof, which can be used as target nucleic acids for the detection and identification of microbial species.
- 20 15. A nucleic acid having the nucleotide sequence of any one of the antibiotic resistance genes sequences determined by us which are listed in Table 7, or a part of thereof and variants thereof, which can be used as target nucleic acids for the detection and identification of microbial species.
- 25 16. A nucleic acid having the nucleotide sequence of any one of the antibiotic resistance genes sequences listed in Table 5, or a part of thereof and variants thereof, which can be used as target nucleic acids for the detection and identification of microbial species.
- 30 17. A nucleic acid having the nucleotide sequence of any one of the toxin genes sequences listed in Table 6, a part of thereof and variants thereof, which can be used as target nucleic acids for the detection and identification of toxins in microbial species.
- 35 18. A repertory of *hexA* nucleic acid sequences used for the detection and/or identification of *Streptococcus pneumoniae*, which repertory is created by amplifying the nucleic acid of any streptococcal species with any combination of primers SEQ ID NOs. 1179, 1181 and 1182.
19. A nucleic acid used for the specific and ubiquitous detection and for identification of *Streptococcus pneumoniae*, which is derived from the repertory of claim 18.

20. A nucleic acid used for detection as set forth in claim 19 which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with said any *Streptococcus pneumoniae* and with any one of SEQ ID NOs. 1184 to 1187.
- 5 21. A nucleic acid as set forth in claim 19, which has a nucleic acid sequence of at least 12 nucleotides capable of hybridizing with the nucleic acids of *Streptococcus pneumoniae* and with any one of SEQ ID NOs. 1179, 1180, 1181, 1182.
- 10 22. A peptide sequence derived from the translation of the nucleic acid sequences from the repertory of claim 1.
23. The use of the peptide sequences of claim 22 as part of a vaccine.
- 15 24. The use of the peptide sequences of claim 22 as targets of antimicrobial agents.
25. The use of the peptide sequences of claim 22 to design or improve antimicrobial agents.
26. The use of *tuf* sequences to identify any of the microorganisms listed in table 15.
- 20 27. The use of *atpD* sequences to identify any of the microorganisms listed in table 15.
28. The use of *recA* sequences to identify any of the microorganisms listed in table 15.