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Barry et al.

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(54) **NUCLEIC ACID PROBE-BASED DIAGNOSTIC ASSAYS TARGETING SSRA GENES OF PROKARYOTIC AND EUKARYOTIC ORGANISMS**

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C12Q 1/68 (2006.01)
C12P 19/34 (2006.01)

(52) **U.S. Cl.** **435/6**; 435/91.2

(58) **Field of Classification Search** 435/6, 91.2
See application file for complete search history.

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Primary Examiner — Kenneth R. Horlick

(74) *Attorney, Agent, or Firm* — Birch, Stewart, Kolasch & Birch, LLP.

(57) **ABSTRACT**

Use of the ssrA gene or tmRNA, an RNA transcript of the ssrA gene, or fragments thereof as target regions in a nucleic acid probe assay for the detection and identification of prokaryotic and/or eukaryotic organisms is described. Nucleotide sequence alignment of tmRNA sequences from various organisms can be used to identify regions of homology and non-homology within the sequences which in turn can be used to design both genus specific and species specific oligonucleotide probes. These newly identified regions of homology and non-homology provide the basis of identifying and detecting organisms at the molecular level. Oligonucleotide probes identified in this way can be used to detect tmRNA in samples thereby giving an indication of the viability of non-viral organisms present in various sample types.

29 Claims, 20 Drawing Sheets

```
E.c.    GGGGCTGATTCTGGATTCGACGGGATTTGCGAAACCCAAGGTGCATGCCG
V.c.    GGGGCTGATTCAGGATTCGACGGGAATTTTGCAGTCTGAGGTGCATGCCG
        *********** ************* **  * *  *  ************

E.c.    AGGGGCGGTTGGCCTCGTAAA-AAGCCGCAAAAAA-TAGTCGCAAACGAC
V.c.    AGGTGCGGTAGGCCTCGTTAACAAACCGCAAAAAAATAGTCGCAAACGAC
        *** ***** ******** ** ** ********** **************

E.c.    GAAAACTACGCTTTAGCAGCTTAATAACCTGCTTAGAGCCCTCTCTCCCT
V.c.    GAAAACTACGCACTAGCAGCTTAATACCCTGCTCAGAGCCCTTCCTCCCT
        ***********  ************* ****** ********  ******

E.c.    AGCCTCCGCTCTTAGGACGGGGAT-CAAGAGAGGTCAAACCCAAAAGAGA
V.c.    AGCTTCCGCTTGTAAGACGGGGAAATCAGGAAGGTCAAACCAAATCAAGC
        *** ******  ** ********    **  ********** **   **

E.c.    TCGCGTGGAAGCCCT-GCCTG-GGGTTGAAGCGTTAAAACTTAATCAGGC
V.c.    TGGCGTGGATTCCCCCACCTGAGGGATGAAGCGCGAGATCTAATTCAGGT
        * *******  ***   **** *** *******  * * ** * *****

E.c.    TAGTTTGTTAGTGGCGTGTCCGTCCGCAGCTGGCAAGCGAATGTAAAGAC
V.c.    TAGCCATTCGTTAGCGTGTCGGTTCGCAGGCGGTG-GTGAAATTAAAGAT
        ***    *   * ******* ** *****  **   * ***  ******

E.c.    TGACTAAGCATGTAGTACCGAGGATGTAGGAATTTCGGACGCGGGTTCAA
V.c.    CGACTAAGCATGTAGTACCAAAGATGAATGGTTTTCGGACGGGGGTTCAA
         ****************** * **** * *  ********* ********

E.c.    CTCCCGCCAGCTCCACCAAAATTCTCCA
V.c.    CTCCCCCCAGCTCCACCA----------
        ***** ************
```

FIG. 1

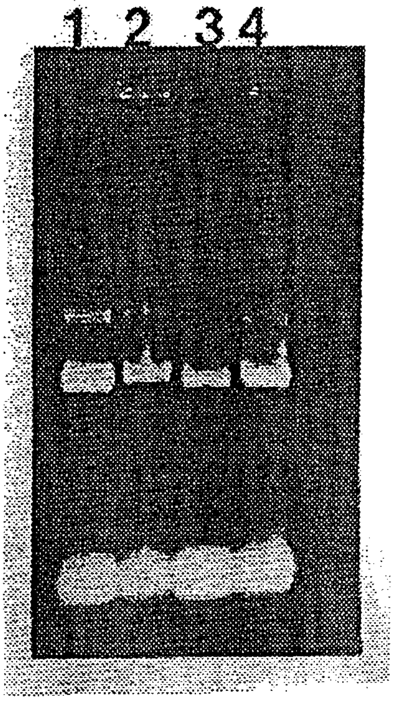

FIG. 2

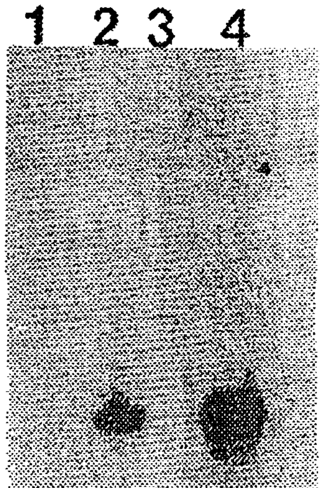

FIG. 3

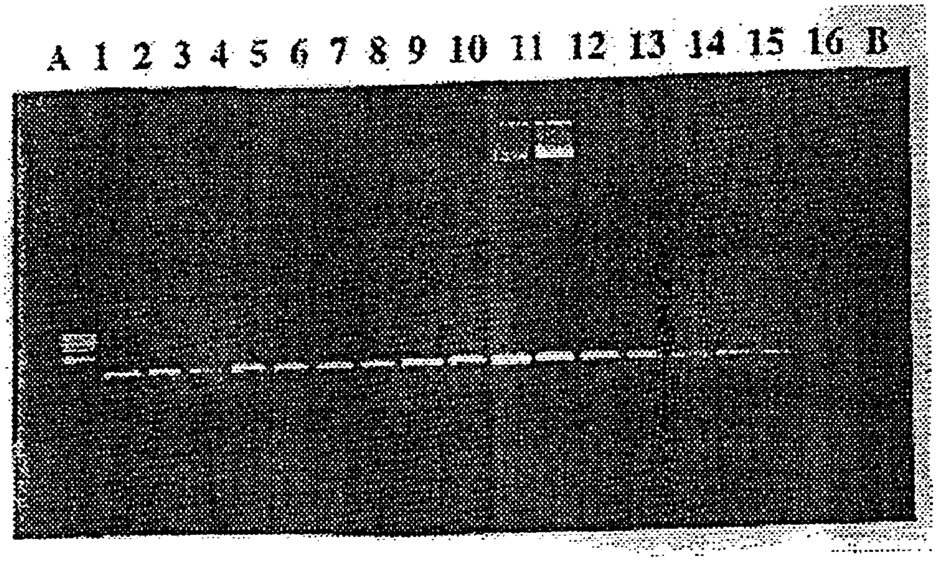

FIG. 4

```
L.m.    ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGATCGTCCTCGTTA
L.i.    ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGATCGTCCTCGTTA
L.mu.   ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGATCGTCCTCGTTA
L.w.    ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGATCGTCCTCGTTA
L.g.    ACAGGGATAGGTCGAGCTTGAGTTGCGAGCCGGGGGGATCGGCC-CGTCA
        ********** ****************** *********** ** *** *

                       Ltm1
L.m.    TCAACGTC|AAAGCCAATAATAACTGG|CAAAGAAAAACAAAACCTAGCTTT
L.i.    TCAACGTC|AAAGCCAATAATAACTGG|CAAAGAAAAACAAAACCTAGCTTT
L.mu.   TCAACGTC|AAAGCCAATAATAACTGG|CAAAGAAAAACAAAACCTAGCTTT
L.w.    TCAACGTC|AAAGCCAATAATAACTGG|CAAAGAAAAACAAAACCTAGCTTT
L.g.    TCAACGTC|AAAGCCAATAATAACTGG|CAAACAAAACAACAATTTAGCTTT
        ******** ****************** **** ****  * **  *******

L.m.    CGCTGCCTAATAAGCAGTA-GCATAGCTGATCCTCCGTGCATCGCCCATG
L.i.    CGCTGCCTAATAAGCAGTA-GCATAGCTGATCCTCCGTGCATCGCCCATG
L.mu.   CGCTGCCTAATAAGCAGTA-GCATAGCTGATCCTCCGTGCATCGCCCATG
L.w.    CGCTGCCTAATAAGCAGTA-GCATAGCTGATCCTCCGTGCATCGCCCATG
L.g.    CGCTGCCTAATA-GCAGTCTGAATAGCTGATCCTCCGTGCATCACCCATG
        ************ *****  * ********************* ******

                 LGtm
L.m.    TG|CTACGGTAAGGGTCTCAC|TCT-AAGTGGGCTACACTAGTTAATCTCCG
L.i.    TG|CTACGGTAAGGGTCTCAC|TCT-AAGTGGGCTACACTAGTTAATCTCCG
L.mu.   TG|CTACGGTAAGGGTCTCAC|TCT-AAGTGGGCTACACTAGTTAATCTCCG
L.w.    TG|CTACGGTAAGGGTCTCAC|TCT-AAGTGGGCTACACTGGCTAATCTCCG
L.g.    TG|CTACGGTAAGGGTCTCAC|TTTTAAGTGGGTTACGCTGGCTTATCTCCG
        ** ****************** * * ******* *** ** * * *******
```

FIG. 5A

```
               LStm
L.m.      TCTGGGGTTAAATAGAAGAGCTTAATCAGACTAGCTGAATGGAAGCCTGT
L.i.      TCTGAGGTTAAATAGAAGAGCTTAATCAGACTAGCTGAATGGAAGCCTGT
L.mu.     TCTGAGGTTAAATAGAAGAGCTTAATGAGACTAGCTGAATGGAAGCCTGT
L.w.      TCTGAGGTTAGTTGGAAGAGCTTAATCAGACTAGCTGAATGGAAGCCTGT
L.g.      TCTGGGGCAAACGAGAAGAGCATAATCAGACTAGCTAGATAGAGCCCTGA
          **** **  *    ******* **** *********  ** **  ****

L.m.      TACCGGGCCGATGTTTATGCGAAATGCTAATACGGTGACTACGCTCGTAG
L.i.      TACCGGGCTGATGTTTATGCGAAATGCTAATACGGTGACTACGCTCGTAG
L.mu.     TACCGGGCTGATGTTTATGCGAAATGCTAATACGGTGACTACGCTCGTAG
L.w.      TACCGGGCCGATGTTTATGCGAAATGCTAATACGGTGACTACGCTCGTAG
L.g.      CGCCGGGCAGACATCTATGCGAAATCCAAATACGGCAACTACGCTCGTAG
            ****** ** * *********** * ******* **************

                         Ltm2
L.m.      ATATTT|AAGTGCCGATATTTCTGG |
L.i.      ATATTC|AAGTGCCGATATTTCTGG |
L.mu.     ATATTC|AAGTGCCGATATTTCTGG |
L.w.      ATATTT|AAGTGCCGATATTTCTGG |
L.g.      ATGCTC|AAGTGCCGATATTTCTGG |
          **  *  ******************
```

FIG. 5B

```
B.s.      ACAGGGATGGATCGAGCTTGAGCTGCGAGCCGAGAGG--CGATCTCGTAA
L.m.      ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGATCGTCCTCGTTA
          ******** * *********** ****** ** * **  **  ***** *

B.s.      ACACGCACTTAAATATAACTGGCAAAACTAACAGTTTTAACCAAAACGTA
L.m.      TCA-ACG-TCAAAGCCAA-TAATA--ACTGGCAAAGAAAAACAAAACCTA
           **  *  * ***   ** *   *  ***  **     ** ****** **

B.s.      GCATTAGCTGCCTAATAAGC-GCAGCGAGACT---CTTCCTGACATTGCC
L.m.      GCTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCTCCGTGCATCGCC
          ** ** ************** * ***    **   * ***   *** ***

B.s.      TATGTGT--CTGTGAAGAGCACA-TCCAAGTAGGCTACGCTTGC--GTTC
L.m.      CATGTGCTACGGTAAGGGTCTCACTCTAAGTGGGCTACACTAGTTAATCT
           *****   * ** * *  * ** ** **** ****** ** *    *

B.s.      CCGTCTGAGAACGTA-AGAAGAGATGAA-CAGACTAGCTCTCGGAAGGCC
L.m.      CCGTCTGGGGTTAAATAGAAGAGCTTAATCAGACTAGCTGAATGGAAGCC
          ******* *     * ******* * ** **********    * * ***

B.s.      CGCCCGCAGGCAAGAAGATGAGTGAAACCATAAATATGCAGGCTACGCTC
L.m.      TGTTACCGGGCCGATGTTTATGCGAAAT-GCTAATACGGTGACTACGCTC
           *    * ***       *  * ****     **** *  * ********

B.s.      G-AGACGCTTAAGTTAATCGATGTTTCTGG
L.m.      GTAGATATTTAAGT--GCCGATATTTCTGG
          * ***   ******    **** *******
```

FIG. 6

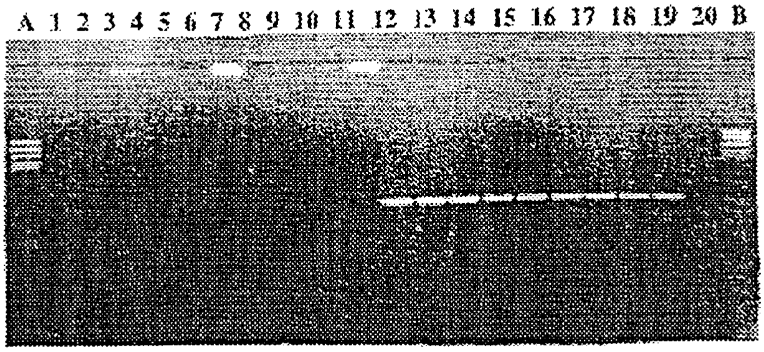

FIG. 7

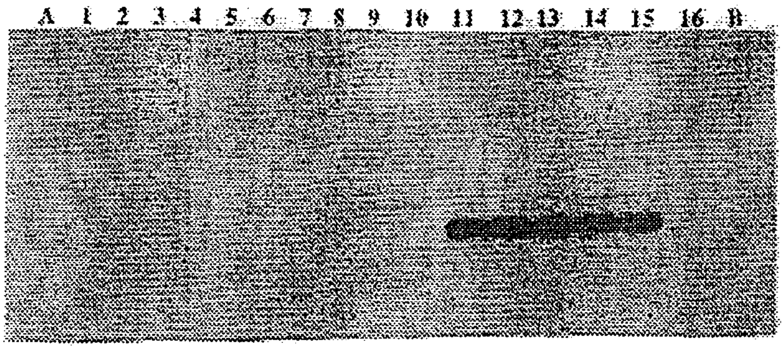

FIG. 8

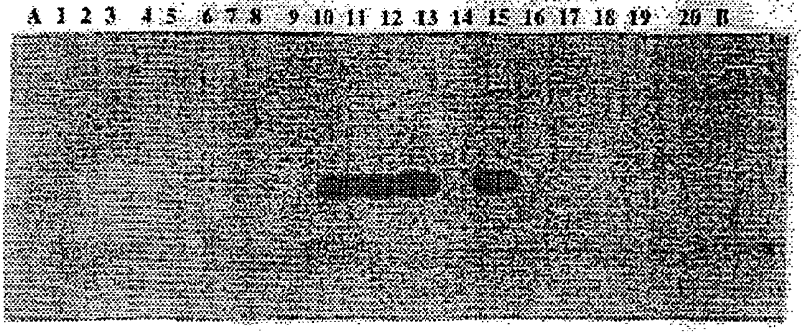

FIG. 9

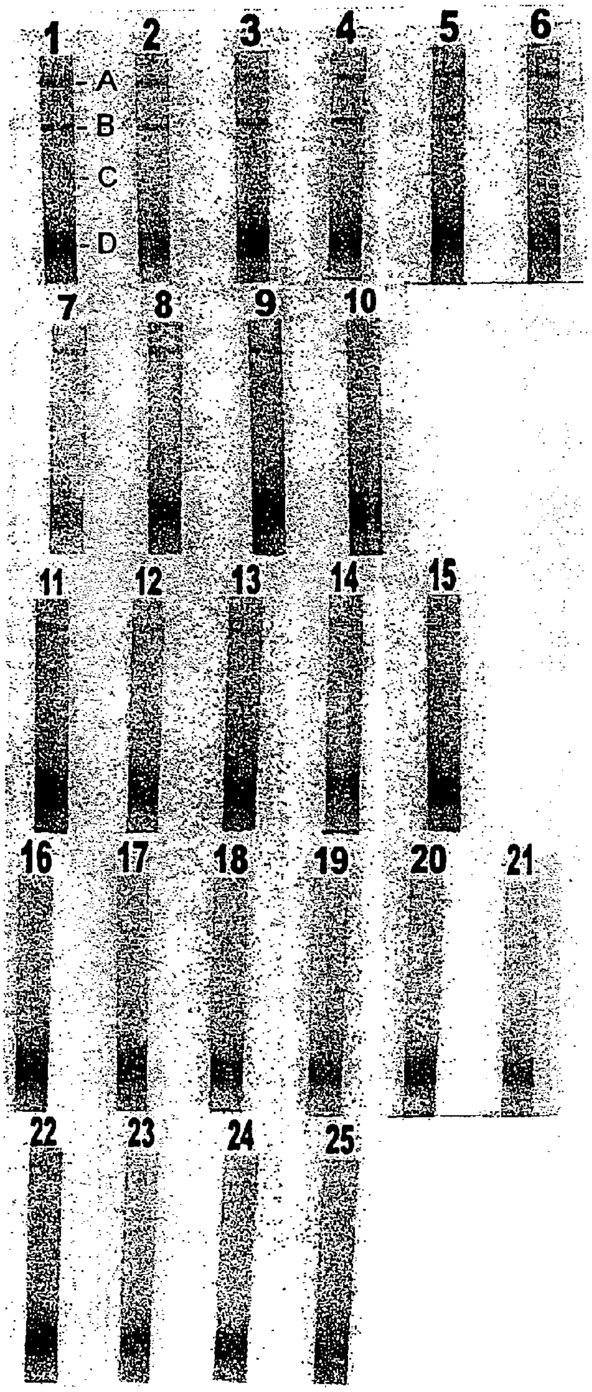

FIG. 10

```
Ct1     GGGGGTGTAAAGGTTTCGACTTAGAAATGAAGCGTTAATTGCATGCGGAG
Ct2     GGGGGTGTAAAGGTTTCGACTTAGAAATGAAGCGTTAATTGCATGCGGAG
        **************************************************

Ct1     GGCGTTGGCTGGCCTCCTAAAAAGCCGACAAAACAATAAATGCCGAACCT
Ct2     GGCGTTGGCTGGCCTCCTAAAAAGCCGACAAAACAATAAATGCCGAACCT
        **************************************************

Ct1     AAGGCTGAATGCGAAATTATCAGCTTCGCTGATCTCGAAGATCTAAGAGT
Ct2     AAGGCTGAATGCGAAATTATCAGCTTCGCTGATCTTAATGATCTAAGAGT
        ***********************************  * ***********

Ct1     AGCTGCTTAATTAGCAAAGTTGTTACCTAAATACGGGTGACCCGGTGTTC
Ct2     TGCTGCTTAATTAGCAAAGTTGTTACCTAAGTACTGGTAACCCGGTGTTC
         ***************************** *** *** ***********

Ct1     GCGAGCTCCACCAGAGGTTTTCGAAACACCGTCATGTATCTGGTTAGAAC
Ct2     GCGAGCTCCACCAGAGGTTTTCGAAACGCCGTCATTTATCTGGTTAGAAT
        *************************** ******* ************* 
```

FIG. 11A

```
Ct1        TTAGGTCCTTTAATTCTCGAGGAAATGAGTTTGAAATTTAATGAGAGTCG
Ct2        TAGGGCCTTTTAACTCTCAAGGGAACTAATTTGAATTTTAATGAGAGTCG
           *  ** * ***** **** *** **  * ****** **************

Ct1        TTAGTCTCTATAGGGGTTTCTAGCTGAGGAGACATAACGTATAGTAC-CT
ct2        TTGGTCTCTATAGAGGTTTCTAGCTGAGGAGATATAACGTAAAATATTCT
           ** ********** ****************** ******** * **  **

Ct1        AGGAACTAAGCATGTAGAGGTTAGCGGGGAGTTTACTAAGGACGAGAGTT
Ct2        AGAAACTAAGCATGTAGAGGTTAGCGGGGAGTTTACTAAGGACGAGAGTT
           ** ***********************************************

Ct1        CGACTCTCTCCACCTCCACCA
Ct2        CGAATCTCTCCACCTCCACCA
           *** *****************
```

FIG. 11B

```
Hpl          AGATTTCTTGTCGCGCAGATAGCATGCCAAGCGCTGCTTGTAAAACAGCA
HP2          AGATTTCTTGTCGCACAGATAGCATGCCAAGCGCTGCTTGTAAAACAGCA
             ************** ***********************************

Hpl          ACAAAAATAACTGTAAACAACACAGATTACGCTCCAGCTTACGCTAAAGC
HP2          ACAAAAATAACTGTAAACAACACAGATTACGCTCCAGCTTACGCTAAAGC
             **************************************************

Hpl          TGCGTGAGTTAATCTCCTTTTGGAGCTGGACTGATTAGAATTTCTAGCGT
HP2          TGCGTGAGTTAATCTCCTTTTGGAGCTGGACTGATTAGAATTTCTAGCGT
             **************************************************

Hpl          TTTAATCGCTCCATAACCTTAAGCTAGACGCTTTTAAAAGGTGGTTCGCC
HP2          TTTAATCGCTCCATAACCTTAAGCTAGACGCTTTTAAAAGGTGGTTCGCC
             **************************************************

Hpl          TTTTAAACTAAGAAACAAGAACTCTTGAAACTATCTTAAGGTTTTAGAAA
HP2          TTTTAAACTAAGAAACAAGAACTCTTGAAACTATCTCAAGGTTTTAGAAA
             ************************************ *************

Hpl          GTTGGACCAGAGCTAGTTTTAAGGCTAAAAACTAACCAATTTTCTAAGC
HP2          GTTGGACCAGAGCTAGTTTTAAGGCTAAAAACCAACCAATTTTCTAAGC
             ******************************** ****************

Hpl          ATTGTAGAAGTTTGTGTTTAGGGCAAGATTTTTGGACTGGGG
HP2          ATTGTAGAAGTTTGTGTTTAGGGCAAGATTTTTGGACTGGGG
             ******************************************
```

FIG. 12

```
Mc1    ACATAATGCTGATAGACAAACAGTAGCATTGGGGTATGCCCCTTACAGCG
Mc2    ACATAATGCTGATAGACAAACAGTAGCATTGGGGTATGCCCCTTACAGCG
       **************************************************

Mc1    CTAGGTTCAATAACCGACAAAGAAAATAACGAAGTGTTGGTAGAACCAAA
Mc2    CTAGGTTCAATAACCGACAAAGAAAATAACGAAGTGTTGGTAGATCCAAA
       ******************************************** *****

Mc1    TTTGATCATTAACCAACAAGCAAGTGTTAACTTTGCTTTTGCATAAGTAG
Mc2    TTTGATCATTAACCAACAAGCAAGTGTTAACTTTGCTTTTGCATAAGTAG
       **************************************************

Mc1    ATACTAAAGCTACAGCTGGTGAATAGTCATAGTTTGCTAGCTGTCATAGT
Mc2    ATACTAAAGCTACAGCTGGTGAATAGTCATAGTTTGCTAGCTGTCATAGT
       **************************************************

Mc1    TTATGACTCGAGGTTAAATCGTTCAATTTAACCTTTAAAAATAGAACTTG
Mc2    TTATGACTCGAGGTTAAATCGTTCAATTTAACCTTTAAAAATAGAACTTG
       **************************************************

Mc1    TTGTTTCCATGATTGTTTTGTGATCAATTGGAAACAAGACAAAAATCCAC
Mc2    TTGTTTCCATGATTGTTTTGTGATCAATTGGAAACAAGACAAAAATCCAC
       **************************************************

Mc1    AAAACTAAAATGTAGAAGCTGTTTGTTGTGTCCTTTATGGAAACGGGTTC
Mc2    AAAACTAAAATGTAGAAGCTGTTTGTTGTGTCCTTTATGGAAACGGGTTC
       **************************************************
```

FIG. 13

```
Ng1                GGGGGTTGCGAAGCAGATGCGGGCATACCGGGGTCTCAGATTCCCGTAAA
Ng2                GGGGGTTGCGAAGCAGATGCGGGCATACCGGGGTCTCAGATTCCCGTAAA
                   **************************************************

Ng1                ACACTGAATTCAAATAGTCGCAAACGACGAAACTTACGCTTTAGCCGCTT
Ng2                ACACTGAATTCAAATAGTCGCAAACGACGAAACTTACGCTTTAGCCGCTT
                   **************************************************

Ng1                AAGGCTAGCCGTTGCAGCAGTCGGTCAATGGGCTGTGTGGCGAAAGCCAC
Ng2                AAGGCTAGCCGTTGCAGCAGTCGGTCAATGGGCTGTGTGGTGAAAGCCAC
                   **************************************** *********

Ng1                CGCAACGTCATCTTACATTGACTGGTTTCCAGCCGGGTTACTTGGCAGGA
Ng2                CGCAACGTCATCTTACATTGACTGGTTTCCAGCCGGGTTACTTGGCAGGA
                   **************************************************

Ng1                AATAAGACTTAAGGTAACTGGTTTCCAAAAGGCCTGTTGGTCGGCATGAT
Ng2                AATAAGACTTAAGGTAACTGGTTTCCAAAAGGCCTGTTGGTCGGCATGAT
                   **************************************************

Ng1                GGAAATAAGATTTTCAAATAGACACAACTAAGTATGTAGAACGCTTTGTA
Ng2                GGAAATAAGATTTTCAAATAGACACAACTAAGTATGTAGAACGCTTTGTA
                   **************************************************

Ng1                GAGGACTTTCGGACGGGGG
Ng2                GAGGACTTTCGGACGGGGG
                   *******************
```

FIG. 14

```
L.m1          CAAAGAAAAACAAAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGC
L.m2          CAAAGAAAAACAAAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGC
              **************************************************

L.m1          TGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGT
L.m2          TGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGT
              **************************************************

L.m1          GGGCTACACTAGTTAATCTCCGTCTGGGGTTAAATAGAAGAGCTTAATCA
L.m2          GGGCTACACTAGTTAATCTCCGTCTGAGGTTAAATAGAAGAGCTTAATCA
              ************************** ***********************

L.m1          GACTAGCTGAATGGAAGCCTGTTACCGGGCCGATGTTTATGCGAAATGCT
L.m2          GACTAGCTGAATGGAAGCCTGTTACCGGGCCGATGTTTATGCGAAATGCT
              **************************************************

L.m1          AATACGGTGACTACGCTCGTAGATATTT
L.m2          AATACGGTGACTACGCTCGTAGATATTT
              ****************************
```

FIG. 15

```
L.m1          CAAAGAAAAACAAAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGC
L.m2          CAAAGAAAAACAAAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGC
L.i           CAAAGAAAAACAAAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGC
              **************************************************

L.m1          TGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGT
L.m2          TGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGT
L.i           TGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGT
              **************************************************

L.m1          GGGCTACACTAGTTAATCTCCGTCTGGGGTTAAATAGAAGAGCTTAATCA
L.m2          GGGCTACACTAGTTAATCTCCGTCTGAGGTTAAATAGAAGAGCTTAATCA
L.i           GGGCTACACTAGTTAATCTCCGTCTGAGGTTAAATAGAAGAGCTTAATCA
              ************************** ***********************

L.m1          GACTAGCTGAATGGAAGCCTGTTACCGGGCCGATGTTTATGCGAAATGCT
L.m2          GACTAGCTGAATGGAAGCCTGTTACCGGGCCGATGTTTATGCGAAATGCT
L.i           GACTAGCTGAATGGAAGCCTGTTACCGGGCTGATGTTTATGCGAAATGCT
              ****************************** *******************

L.m1          AATACGGTGACTACGCTCGTAGATATTT
L.m2          AATACGGTGACTACGCTCGTAGATATTT
L.i           AATACGGTGACTACGCTCGTAGATATTC
              ***************************
```

FIG. 16

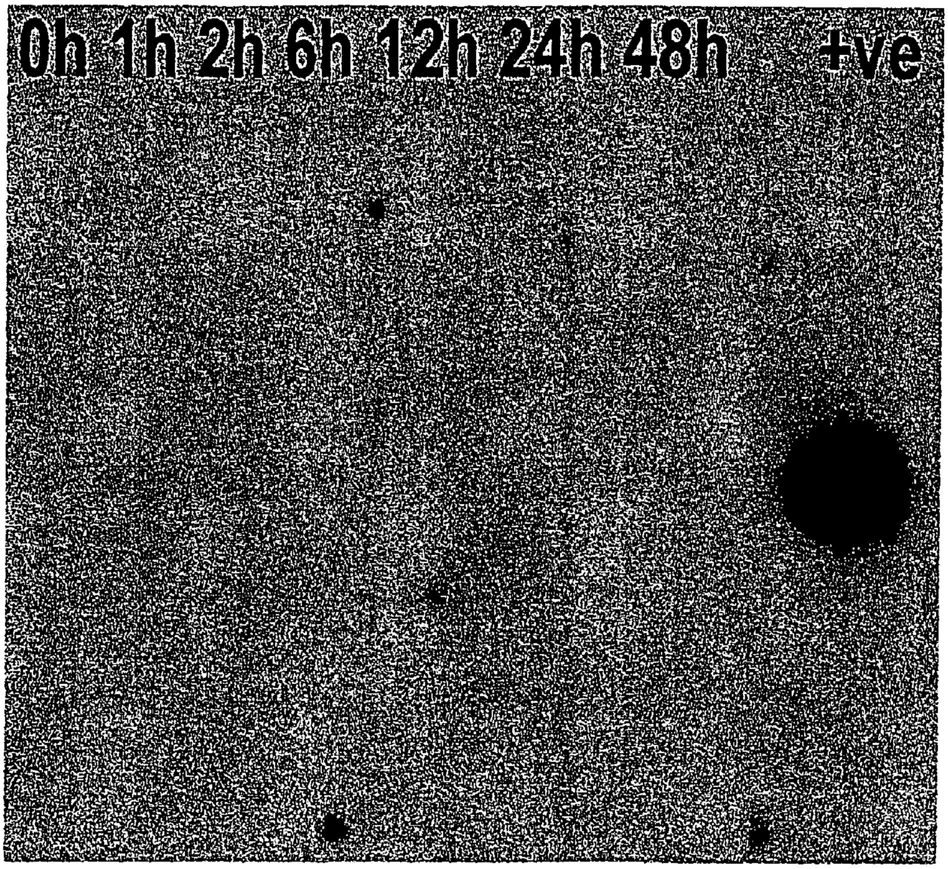

FIG. 17

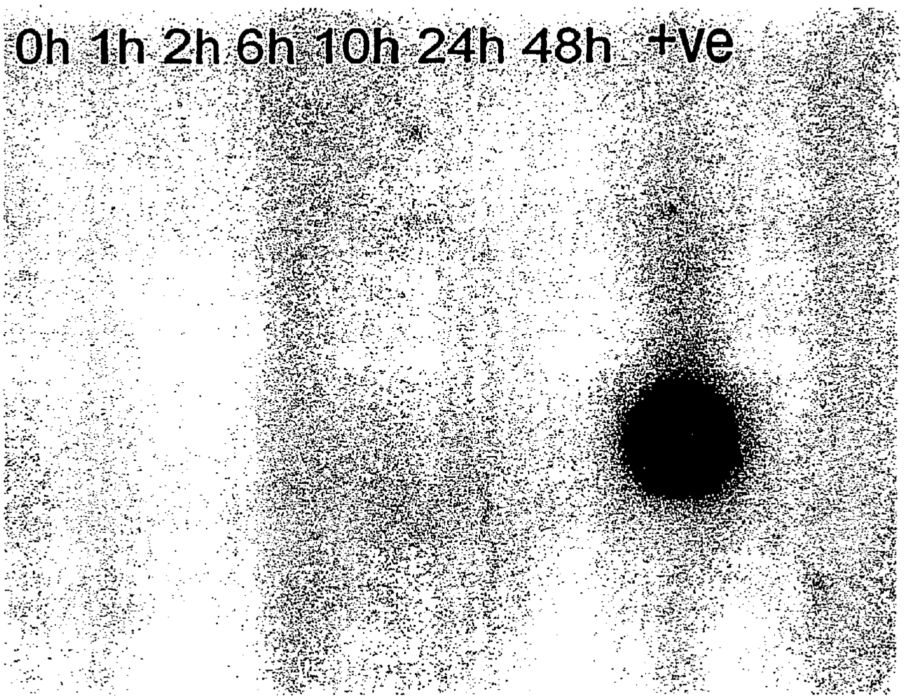

FIG. 18

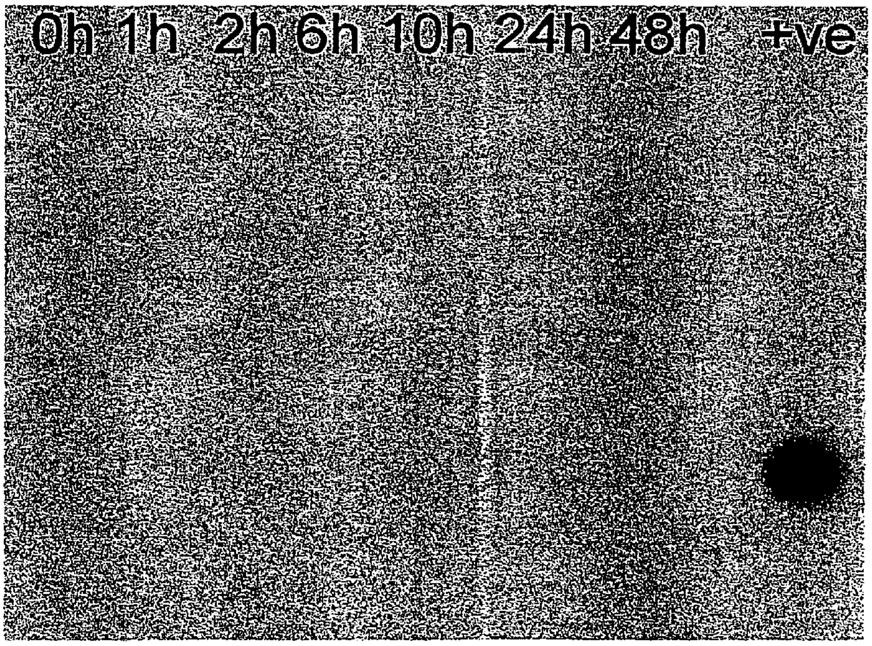

FIG. 19

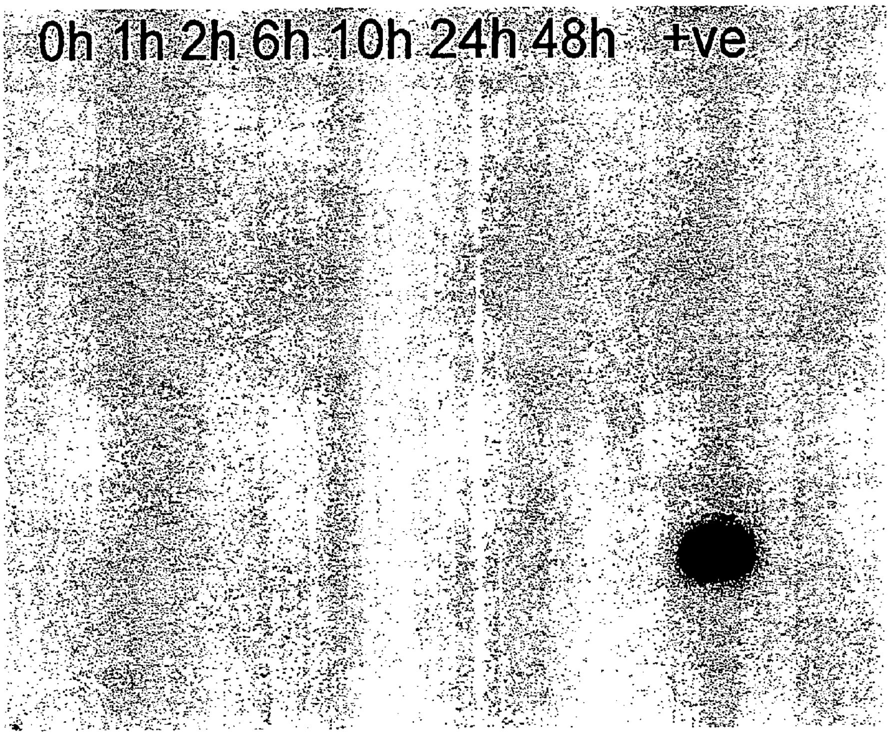

FIG. 20

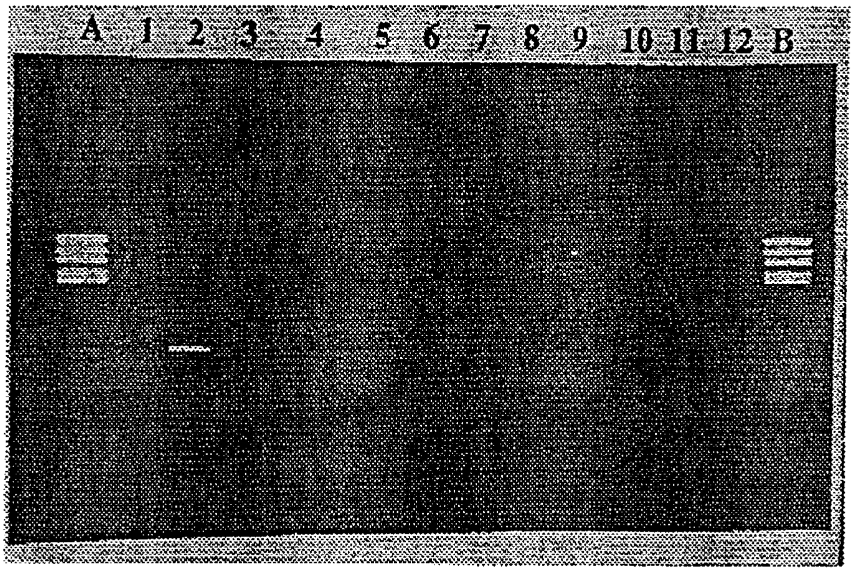

FIG. 21

NUCLEIC ACID PROBE-BASED DIAGNOSTIC ASSAYS TARGETING SSRA GENES OF PROKARYOTIC AND EUKARYOTIC ORGANISMS

This application is the national phase under 35 U.S.C. §371 of PCT International Application No. PCT/IE00/00066 which has an International filing date of May 15, 2000, which designated the United States of America and was published in English.

TECHNICAL FIELD

This invention relates to the identification of target sequences for use in nucleic acid assays for the detection and identification of prokaryotic and/or eukaryotic organisms.

BACKGROUND ART

The ssrA gene, which encodes a small stable high copy number RNA transcript (tmRNA), is found in all bacteria and has recently been identified in chloroplasts and diatoms. It has a dual function both as a tRNA and as an mRNA molecule and is involved in rescuing truncated mRNAs which have lost stop codons, facilitating trans-translation of truncated peptides prior to protease degradation (Keiler, K. C. et al. (1996), Science, 271, 990-993). The unique function of tmRNAs has directed researchers to analyse the relationship of the secondary structure of these molecules with their function. These studies have focussed on the conservation of the secondary structure of tmRNAs from different microorganisms, and on the evolutionary significance and functional relevance of such structural conservation. Studies were carried out by Matveeva, O et al (1998), Vol. 16, No. 13, 1374-1375 to investigate oligonucleotide binding to RNA molecules using tmRNA as a model of RNA containing secondary structure. The studies did not have as their objective the identification of sites in tmRNA with the goal of designing antisense oligonucleotide for therapeutic purposes.

The number of nucleic acid targets/probes for bacterial diagnostics is currently limited. As such, the need to identify and characterise novel DNA and RNA targets for diagnostic purposes is now seen as a priority. Target nucleic acid sequences for the development of probes can be for example, plasmids, ribosomal RNA genes, intergenic regions, genes encoding virulence factors or random genomic DNA fragments. In addition, a number of RNA molecules have been described which are used as targets for RNA-based detection for example, ribosomal RNA and RNase P.

The basis of any nucleic acid-based probe assay is the requirement for well characterised nucleic acid sequences which are present in all prokaryotes and eukaryotes under study. For reliable detection of a prokaryotic or eukaryotic organism, the nucleic acid probes used should be highly specific (i.e. not cross-react with nucleic acids from other organisms) and highly sensitive (i.e. most or all strains of the organism to be detected should react with the probe). Therefore, preferred target sequences would be present in all strains of the organism concerned. Such sequences would have significant sequence variability to allow differentiation of the species concerned from other closely related species but, on the other hand, have sufficient sequence conservation to allow the detection of all strains of the species concerned. In general, the precise identification of a nucleic acid sequence, which could form the basis of a specific nucleic acid probe assay, is tedious, difficult and uncertain. To date there are few general approaches which would facilitate the development of nucleic acid probes for a wide variety of microorganisms. The nucleic acid sequences which have been identified as potentially useful targets for probe development are, for example, rRNA genes and RNA, and the rRNA 16S/23S intergenic region.

The majority of nucleic acid probe/target assays centre on the high copy number ribosomal RNAs (rRNA) and rRNA 16S/23S spacer regions (European Patent No. 0 395 292) of the bacterial cell for the purposes of detection and identification. A number of successful commercial bacterial diagnostic kits have been marketed based on these rRNA probes/targets for the detection of a variety of microrganisms. These include a range of commercial probe kits based on the 16S rRNA gene marketed by Gen-probe Inc. San Diego Calif., and DNA probes based on the 16S/23S spacer region marketed by Innogenetics N.V. Ghent, Belgium. However, many of these diagnostic kits have limitations, including lack of sensitivity due to low copy-number target sequences and lack of specificity due to sequence identity between closely related organisms in many cases.

Nucleic acid-based methods that could be applied directly to samples to give an indication of the viability of any microbes present therein would be of enormous significance for food, industrial, environmental and medical applications.

A disadvantage of DNA-based methods is that they do not distinguish between living and dead organisms. Some studies have focussed on using rRNA and mRNA as indicators of cell viability (Sheridan, G. E. C. et al. (1998) Applied and Environmental Microbiology, 64, 1313-1318). However, these sequences are not satisfactory targets as rRNA and mRNA can be present in bacterial cells up to 48 hours after cell death.

With the advent of nucleic acid based microarray-like formatting, incorporating simultaneous monitoring of multiple nucleic acid targets, there is now a clear requirement to identify and characterise novel nucleic acid sequences for use as probes and/or target regions to detect and identify viable prokaryotic and eukaryotic cells.

DISCLOSURE OF INVENTION

The invention provides use of the ssrA gene or a fragment thereof as a target region in a nucleic acid probe assay for a prokaryotic or eukaryotic organism.

Thus, the invention has application in relation to all organisms other than viruses.

No other nucleic acid probe assay has been reported which uses regions of the ssrA gene as a target region to detect and identify species of prokaryotes and eukaryotes with the attendant advantages.

According to one embodiment of the invention a fragment of the ssrA gene molecule corresponding to a region of high homology from the 5' end of the DNA molecule can be used as a universal target region.

In an alternative embodiment of the invention a fragment of the ssrA gene molecule corresponding to a region of high homology from the 3' end of the DNA molecule can be used as a universal target region.

In a further embodiment of the invention a fragment of the ssrA gene molecule corresponding to a region of low homology can be used as a target region in a nucleic acid probe assay to distinguish between species.

In a still further embodiment of the invention a fragment of the ssrA gene molecule corresponding to a region of low homology can be used as a target region for the generation of a genus specific probe.

As hereinafter described nucleotide sequence alignments of ssrA gene sequences from different organisms show that the 5' and 3' regions of these molecules demonstrate a high degree of homology and are therefore useful as universal target regions. The ssrA genes also demonstrate a more significant degree of nucleotide sequence variability between closely related organisms than any other bacterial high copy number RNA. These variable regions are ideal targets for nucleic acid assays to distinguish between species.

The invention also provides use of tmRNA, an RNA transcript of the ssrA gene, or a fragment thereof as a target region in a nucleic acid probe assay for a prokaryotic or eukaryotic organism.

According to one embodiment of this aspect of the invention a fragment of a tmRNA molecule corresponding to a region of high homology from the 5' end of the tmRNA molecule can be used as a universal target region.

Alternatively, a fragment of a tmRNA molecule corresponding to a region of high homology from the 3' end of the tmRNA molecule can be used as a universal target region.

According to a further embodiment of this aspect of the invention a fragment of a tmRNA molecule corresponding to a region of low homology can be used as a target region in a nucleic acid probe assay to distinguish between species.

According to a still further embodiment a fragment of a tmRNA molecule corresponding to a region of low homology can be used as a target region for the generation of a genus specific probe.

The nucleic acid probe (DNA or RNA) in accordance with the invention typically consists of at least 10 nucleotides of the ssrA gene and/or tmRNA transcript or their complementary sequence and is used in a nucleic acid probe hybridisation assay for a prokaryotic or eukaryotic organism. Probe hybridisation to its complementary sequence is typically revealed by labelling the nucleic acid probe with a radioactive or non-radioactive (e.g. colorimetric or fluorimetric) label.

In preferred embodiments said ssrA gene fragment or said tmRNA fragment can be used as the basis of a primer to be used in an amplification procedure.

Universal oligonucleotide primers directed to the 5' and 3' regions of either the ssrA gene or the tmRNA sequence can be used in accordance with the invention to amplify the ssrA gene or its encoding tmRNA from a wide variety of bacteria, facilitating amplification of a wide range of organisms simultaneously, whilst also enabling specific nucleic acid probe hybridisation and detection.

Preferably, the product of the amplification procedure is used as a target region in a nucleic probe assay.

Further, preferably, a cDNA transcript of a tmRNA molecule is used as a probe in a nucleic acid hybridisation assay.

Such assays can be carried out in vitro or in situ.

The target region as defined herein can be used as the basis of an assay for distinguishing between living and dead prokaryotic or eukaryotic organisms.

In contrast to rRNA and mRNA which can be present in bacterial cells following cell death, tmRNA is rapidly degraded in dead organisms. Thus, tmRNA can be a useful target for distinguishing between living and dead prokaryotic or eukaryotic organisms either directly by nucleic acid probe hybridisation to isolated bacterial RNA, or by combined RNA amplification and nucleic acid probe hybridisation to the amplified product.

Preferably, the target region is used in a multiple probe format for broad scale detection and/or identification of prokaryotic or eukaryotic organisms.

An ssrA gene probe or a tmRNA transcript probe in accordance with the invention can be linked to a microarray gene chip system for the broad scale high throughput detection and identification of prokaryotic or eukaryotic organisms.

A target region in accordance with the invention can also be used as a probe in an assay to detect prokaryotic or eukaryotic organisms in a sample of matter.

Such a sample of matter can include biological samples such as samples of tissue from the respiratory tract, the urogenital tract or the gastrointestinal tract, or body fluids such as blood and blood fractions, sputum or cerebrospinal fluid.

An assay in accordance with the invention can also be carried out on food samples, environmental samples including air, water, marine and soil samples, and plant and animal derived samples.

According to the invention a fragment of the ssrA gene or the tmRNA transcript can also be used in an assay to obtain a DNA profile of a prokaryotic or eukaryotic organism and, thereby, distinguish between strains of the same species.

Nucleic acid sequence alignments have shown that sequence variation occurs in the ssrA gene and the tmRNA transcript within individual species. This intra-species sequence variation can be used to distinguish between strains of the same species for epidemiology, tracing of infectious agents for example, in outbreaks, or for population studies.

Other applications of the invention include the use of the ssrA gene, the tmRNA transcript or a DNA sequence complementary thereto, or a fragment thereof, to design an agent directed against infectious prokaryotic or eukaryotic organisms for therapeutic purposes.

Such agents can include antisense mRNA or oligonucleotides, ribozymes, and antagonistic peptides and are suitable for use in any kind of medical condition.

Thus, the invention can be used for the detection of viable organisms only in biological samples using the tmRNA target. Thus, during and following any anti-infectious agent drug treatment, the tmRNA target can be used to monitor the efficacy of the therapy on those specific infectious agents (e.g. antimicrobial and/or anti-parasitic treatments).

In one embodiment, the target region is used to monitor the efficacy of drug therapies against infectious agents.

In another embodiment, the target region is used to monitor the viability and level of health-promoting organisms in the gastrointestinal tract.

This aspect of the invention relates, for example, to the introduction into the gut flora of health-promoting (probiotic) organisms contained in for example yoghurt or other food to improve health. There is an interest and need to continuously monitor the presence and levels of these organisms to ensure their continued function in promoting health. The tmRNA region can be used as a target to detect viable organisms, for example in faeces, so as to monitor the presence of the health promoting organisms.

In a further embodiment, the assay is used for the quantification of prokaryotic or eukaryotic organisms.

When using probe hybridisation and/or in vitro amplification to detect organisms in a sample it is possible to determine the number of organisms present, based on the signal intensity. Real-time methods of in vitro amplification can also be used to enable the quantification of organisms in a sample. Thus, the ability to quantify the number of organisms in a sample can be important in clinical situations for treatment purposes, for example for antibiotic or other treatments or for monitoring treatment efficacy.

A still further application of the invention is the use of a database of ssrA gene sequences to identify a prokaryotic or eukaryotic organism.

The invention provides a variety of probes for the 5' and 3' homologous regions and the variable regions of the ssrA gene and tmRNA sequences, the probes being derived from these sequences or sequences complementary thereto. Representative sequences are as follows:

Actinobacillus actinomycetemcomitans ssrA

GGGGCTGATTCTGGATTCGACGGGATTAGCGAAGCCCGAAGTGC
ACGTCGAGGTGCGGTAGGCCTCGTAAATAAACCGCAAAAAAATA
GTCGCAAACGACGAACAATACGCTTTAGCAGCTTAATAACCTGC
CTTTAGCCTTCGCTCCCCAGCTTCCGCTCGTAAGACGGGGATAAA
GCGGAGTCAAACCAAAACGAGATCGTGTGGAAGCCACCGTTTGA
GGATCGAAGCATTAAATTAAATCAAAGTAGCTTAATTGTCGCGT
GTCCGTCAGCAGGATTAAGTGAATTTAAAGACCGGACTAAACGT
GTAGTGCTAACGGCAGAGGAATTTCGGACGGGGGTTCAACTCCC
CCCAGCTCCACCA SEQ ID NO: 1

Actinobacillus actinomycetemcomitans tmRNA

GGGGCUGAUUCUGGAUUCGACGGGAUUAGCGAAGCCCGAAGU
GCACGUCGAGGUGCGGUAGGCCUCGUAAAUAAACCGCAAAAAA
AUAGUCGCAAACGACGAACAAUACGCUUUAGCAGCUUAAUAAC
CUGCCUUUAGCCUUCGCUCCCCAGCUUCCGCUCGUAAGACGGG
GAUAAAGCGGAGUCAAACCAAAACGAGAUCGUGUGGAAGCCA
CCGUUUGAGGAUCGAAGCAUUAAAUUAAAUCAAAGUAGCUUA
AUUGUCGCGUGUCCGUCAGCAGGAUUAAGUGAAUUUAAAGAC
CGGACUAAACGUGUAGUGCUAACGGGAGAGGAAUUUCGGACG
GGGGUUCAACUCCCCCCAGCUCCACCA SEQ ID NO: 2

Aeromonas salmonicida ssrA, Internal Partial

AAGATTCACGAAACCCAAGGTGCATGCCGAGGTGCGGTAGGCCT
CGTTAACAAACCGCAAAAAAATAGTCGCAAACGACGAAAACTA
CGCACTAGCAGCtTAATAACCTGCATAGAGCCCTTCTACCCTAGC
TTGCCTGTGTCCTAGGGAATCGGAAGGTCATCCTTCACAGGATC
GTGTGGAAGTCCTGCTCGGGGCGGAAGCATTAAAACCAATCGAG
CTAGTCAATTCGTGGCGTGTCTCTCCGCAGCGGGTTGGCGAATGT
AAAGAGTGACTAAGCATGTAGTACCGAGGATGTAGTAATTTTGG
ACGGGG SEQ ID NO: 3

Aeromonas salmonicida tmRNA, Internal Partial

AAGAUUCACGAAACCCAAGGUGCAUGCCGAGGUGCGGUAGGCC
UCGUUAACAAACCGCAAAAAAAUAGUCGCAAACGACGAAAACU
ACGCACUAGCAGCUUAAUAACCUGCAUAGAGCCCUUCUACCCU
AGCUUGCCUGUGUCCUAGGGAAUCGGAAGGUCAUCCUUCACAG
GAUCGUGUGGAAGUCCUGCUCGGGGCGGAAGCAUUAAAACCA
AUCGAGCUAGUCAAUUCGUGGCGUGUCUCUCCGCAGCGGGUUG
GCGAAUGUAAAGAGUGACUAAGCAUGUAGUACCGAGGAUGUA
GUAAUUUUGGACGGGG SEQ ID NO: 4

Alcaligenes eutrophus ssrA

TGGGCCGACCTGGTTTCGACGTGGTTACAAAGCAGTGAGGCATA
CCGAGGACCCGTCACCTCGTTAATCAATGGAATGCAATAACTGC
TAACGACGAACGTTACGCACTCGCTTAATTGCGGCCGTCCTCGC
ACTGGCTCGCTGACGGGCTAGGGTCGCAAGACCACGCGAGGTAT
TTACGTCAGATAAGCTCCGGAAGGGTCACGAAGCCGGGGACGA
AAACCTAGTGACTCGCCGTCGTAGAGCGTGTTCGTCCGATGCGC
CGGTTAAATCAAATGACAGAACTAAGTATGTAGAACTCTCTGTG
GAGGGCTTACGGACGCGGGTTCGATTCCCGCCGGCTCCACCA
SEQ ID NO: 5

Alcaligenes eutrophus tmRNA

UGGGCCGACCUGGUUUCGACGUGGUUACAAAGCAGUGAGGCA
UACCGAGGACCCGUCACCUCGUUAAUCAAUGGAAUGCAAUAAC
UGCUAACGACGAACGUUACGCACUCGCUUAAUUGCGGCCGUCC
UCGCACUGGCUCGCUGACGGGCUAGGGUCGCAAGACCACGCGA
GGUAUUUACGUCAGAUAAGCUCCGGAAGGGUCACGAAGCCGG
GGACGAAAACCUAGUGACUCGCCGUCGUAGAGCGUGUUCGUCC
GAUGCGCCGGUUAAAUCAAAUGACAGAACUAAGUAUGUAGAA
CUCUCUGUGGAGGGCUUACGGACGCGGGUUCGAUUCCCGCCGG
CUCCACCA SEQ ID NO: 6

Aquifex aeolicus ssrA

GGGGGCGGAAAGGATTCGACGGGGACAGGCGGTCCCCGAGGAG
CAGGCCGGGTGGCTCCCGTAACAGCCGCTAAAACAGCTCCCGAA
GCTGAACTCGCTCTCGCTGCCTAATTAAACGGCAGCGCGTCCCC
GGTAGGTTTGCGGGTGGCCTACCGGAGGGCGTCAGAGACACCCG
CTCGGGCTACTCGGTCGCACGGGGCTGAGTAGCTGACACCTAAC
CCGTGCTACCCTCGGGGAGCTTGCCCGTGGGCGACCCGAGGGGA
AATCCTGAACACGGGCTAAGCCTGTAGAGCCTCGGATGTGGCCG
CCGTCCTCGGACGCGGGTTCGATTCCCGCCGCCTCCACCA
SEQ ID NO: 7

Aquifex aeolicus tmRNA

GGGGGCGGAAAGGAUUCGACGGGGACAGGCGGUCCCCGAGGA
GCAGGCCGGGUGGCUCCCGUAACAGCCGCUAAAACAGCUCCCG
AAGCUGAACUCGCUCUCGCUGCCUAAUUAAACGGCAGCGCGUC
CCCGGUAGGUUUGCGGGUGGCCUACCGGAGGGCGUCAGAGACA
CCCGCUCGGGCUACUCGGUCGCACGGGGCUGAGUAGCUGACAC
CUAACCCGUGCUACCCUCGGGGAGCUUGCCCGUGGGCGACCCG
AGGGGAAAUCCUGAACACGGGCUAAGCCUGUAGAGCCUCGGAU

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GUGGCCGCCGUCCUCGGACGCGGGUUCGAUUCCCGCCGCCUCC
ACCA SEQ ID NO: 8

Bacillus megaterium ssrA, Internal Partial

AGGGTAGTTCGAGCTTAGGTMCGAGTCGAGGAGATGGCCTCGT
TAAAACATCAACGCCAATAATAACTGGCAAATCTAACAATAACT
TCGCTTTAGCTGCATAATAGTAGCTTAGCGTTCCTCCCTCCATCG
CCCATGTGGTAGGGIAAGGGACTCACTTTAAGTGGGCTACGCCG
GAGTTCGCCGTCTGAGGACGAAGGAAGAGAATAATCAGACTAG
CGACTGGGACGCCTGTTGGTAGGCAGAACAGCTCGCGAATGATC
AATATGCCAACTACACTCGTAGACGCTTAAGTGGCCATATTTCTG
GACGTGG SEQ ID NO: 9

Bacillus megaterium tmRNA, Internal Partial

AGGGUAGUUCGAGCUUAGGUUGCGAGUCGAGGAGAUGGCCUC
GUUAAAACAUCAACGCCAAUAAUAACUGGCAAAUCUAACAAU
AACUUCGCUUUAGCUGCAUAAUAGUAGCUUAGCGUUCCUCCCU
CCAUCGCCCAUGUGGUAGGGUAAGGGACUCACUUUAAGUGGGC
UACGCCGGAGUUCGCCGUCUGAGGACGAAGGAAGAGAAUAAU
CAGACUAGCGACUGGGACGCCUGUUGGUAGGCAGAACAGCUCG
CGAAUGAUCAAUAUGCCAACUACACUCGUAGACGCUUAAGUGG
CCAUAUUUCUGGACGUGG SEQ ID NO: 10

Bacillus subtilis ssrA

GGGGACGTTACGGATTCGACAGGGATGGATCGAGCTTGAGCTGC
GAGCCGAGAGGCGATCTCGTAAACACGCACTTAAATATAACTGG
CAAAACTAACAGTTTTAACCAAAACGTAGCATTAGCTGCCTAAT
AAGCGCAGCGAGCTCTTCCTGACATTGCCTATGTGTCTGTGAAG
AGCACATCCAAGTAGGCTACGCTTGCGTTCCCGTCTGAGAACGT
AAGAAGAGATGAACAGACTAGCTCTCGGAAGGCCCGCCCGCAG
GCAAGAAGATGAGTGAAACCATAAATATGCAGGCTACGCTCGTA
GACGCTTAAGTAATCGATGTTTCTGGACGTGGGTTCGACTCCCAC
CGTCTCCACCA SEQ ID NO: 11

Bacillus subtilis tmRNA

GGGGACGUUACGGAUUCGACAGGGAUGGAUCGAGCUUGAGCU
GCGAGCCGAGAGGCGAUCUCGUAAACACGCACUUAAAUAUAAC
UGGCAAAACUAACAGUUUUAACCAAAACGUAGCAUUAGCUGCC
UAAUAAGCGCAGCGAGCUCUUCCUGACAUUGCCUAUGUGUCUG
UGAAGAGCACAUCCAAGUAGGCUACGCUUGCGUUCCCGUCUGA
GAACGUAAGAAGAGAUGAACAGACUAGCUCUCGGAAGGCCCGC
CCGCAGGCAAGAAGAUGAGUGAAACCAUAAAUAUGCAGGCUA

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CGCUCGUAGACGCUUAAGUAAUCGAUGUUUCUGGACGUGGGU
UCGACUCCCACCGUCUCCACCA SEQ ID NO: 12

Bordetella pertussis ssrA

GGGGCCGATCCGGATTCGACGTGGGTCATGAAACAGCTCAGGGC
ATGCCGAGCACCAGTAAGCTCGTTAATCCACTGGAACACTACAA
ACGCCAACGACGAGCGTCTCGCTCTCGCCGCTTAAGCGGTGAGC
CGCTGCACTGATCTGTCCTTGGGTCAGGCGGGGGAAGGCAACTT
CACAGGGGGCAACCCCCGAACCGCAGCAGCGACATTCACAAGGA
ATCGGCCACCGCTGGGGTCACACGGCGTTGGTTTAAATTACGTG
AATCGCCCTGGTCCGGCCCGTCGATCGGCTAAGTCCAGGGTTAA
ATCCAAATAGATCGACTAAGCATGTAGAACTGGTTGCGGAGGGC
TTGCGGACGGGGGTTCAATTCCCCCCGGCTCCACCA
SEQ ID NO: 13

Bordetella pertussis tmRNA

GGGGCCGAUCCGGAUUCGACGUGGGUCAUGAAACAGCUCAGGG
CAUGCCGAGCACCAGUAAGCUCGUUAAUCCACUGGAACACUAC
AAACGCCAACGACGAGCGUCUCGCUCUCGCCGCUUAAGCGGUG
AGCCGCUGCACUGAUCUGUCCUUGGGUCAGGCGGGGGAAGGCA
ACUUCACAGGGGGCAACCCCGAACCGCAGCAGCGACAUUCACA
AGGAAUCGGCCACCGCUGGGGUCACACGGCGUUGGUUUAAAUU
ACGUGAAUCGCCCUGGUCCGGCCCGUCGAUCGGCUAAGUCCAG
GGUUAAAUCCAAAUAGAUCGACUAAGCAUGUAGAACUGGUUG
CGGAGGGCUUGCGGACGGGGGUUCAAUUCCCCCCGGCUCCACC
A SEQ ID NO: 14

Borrelia burgdorferi ssrA

GGGGATGTTTTGGATTTGACTGAAAATGTTAATATTGTAAGTTGC
AGGCAGAGGGAATCTCTTAAAACTTCTAAAATAAATGCAAAAAA
TAATAACTTTACAAGCTCAAATCTTGTAATGGCTGCTTAAGTTAG
CAGAGGGTTTTGTTGAATTTGGCTTTGAGGTTCACTTATACTCTT
TTCGACATCAAAGCTTGCTTAAAAATGTTTTCAAGITGATTTTTA
GGGACTTTTATACTTGAGAGCAATTTGGTGGTTTGCTAGTATTTC
CAAACCATATTGCTTAATAAAATACTAGATAAGCTTGTAGAAGC
TTATAGTATTATTTTTAGGACGCGGGTTCAATTCCCGCCATCTCC
ACCA SEQ ID NO: 15

Borrelia burgdorferi tmRNA

GGGGAUGUUUUGGAUUUGACUGAAAAUGUUAAUAUUGUAAGU
UGCAGGCAGAGGGAAUCUCUUAAAACUUCUAAAAUAAAUGCA

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AAAAAUAAUAACUUUACAAGCUCAAAUCUUGUAAUGGCUGCU
UAAGUUAGCAGAGGGUUUUGUUGAAUUUGGCUUUGAGGUUCA
CUUAUACUCUUUUCGACAUCAAAGCUUGCUUAAAAAUGUUUU
CAAGUUGAUUUUUAGGGACUUUUAUACUUGAGAGCAAUUUGG
UGGUUUGCUAGUAUUUCCAAACCAUAUUGCUUAAUAAAAUAC
UAGAUAAGCUUGUAGAAGCUUAUAGUAUUAUUUUUAGGACGC
GGGUUCAAUUCCCGCCAUCUCCACCA SEQ ID NO: 16

Campylobacter jejuni ssrA

GGGAGCGACTTGGCTTCGACAGGAGTAAGTCTGCTTAGATGGCA
TGTCGCTTTGGGCAAAGCGTAAAAAGCCCAAATAAAATTAAACG
CAAACAACGTTAAATTCGCTCCTGCTTACGCTAAAGCTGCGTAA
GTTCAGTTGAGCCTGAAATTTAAGTCATACTATCTAGCTTAATTT
TCGGTCATTTTTGATAGTGTAGCCTTGCGTTTGACAAGCGTTGAG
GTGAAATAAAGTCTTAGCCTTGCTTTTGAGTTTTGGAAGATGAGC
GAAGTAGGGTGAAGTAGTCATCTTTGCTAAGCATGTAGAGGTCT
TTGTGGGATTATTTTTGGACAGGGGTTCGATTCCCCTCGCTTCCA
CCA SEQ ID NO: 17

Campylobacter jejuni tmRNA

GGGAGCGACUUGGCUUCGACAGGAGUAAGUCUGCUUAGAUGG
CAUGUCGCUUUGGGCAAAGCGUAAAAAGCCCAAAUAAAAUUA
AACGCAAACAACGUUAAAUUCGCUCCUGCUUACGCUAAAGCUG
CGUAAGUUCAGUUGAGCCUGAAAUUUAAGUCAUACUAUCUAG
CUUAAUUUUCGGUCAUUUUUGAUAGUGUAGCCUUGCGUUUGA
CAAGCGUUGAGGUGAAAUAAAGUCUUAGCCUUGCUUUUGAGU
UUUGGAAGAUGAGCGAAGUAGGGUGAAGUAGUCAUCUUUGCU
AAGCAUGUAGAGGUCUUUGUGGGAUUAUUUUUGGACAGGGGU
UCGAUUCCCCUCGCUUCCACCA SEQ ID NO: 18

Chlamydia trachomatis (D/UW-3/CX) ssrA

GGGGGTGTAAAGGTTTCGACTTAGAAATGAAGCGTTAATTGCAT
GCGGAGGGCGTTGGCTGGCCTCCTAAAAAGCCGACAAAACAATA
AATGCCGAACCTAAGGCTGAATGCGAAATTATCAGCTTCGCTGA
TCTCGAAGATCTAAGAGTAGCTGCTTAATTAGCAAAGTTGTTACC
TAAATACGGGTGACCCGGTGTTCGCGAGCTCCACCAGAGGTTTT
CGAAACACCGTCATGTATCTGGTTAGAACTTAGGTCCTTTAATTC
TCGAGGAAATGAGTTTGAAATTTAATGAGAGTCGTTAGTCTCTAT
AGGGGTTTCTAGCTGAGGAGACATAACGTATAGTACCTAGGAAC
TAAGCATGTAGAGGTTAGCGGGGAGTTTACTAAGGACGAGAGTT
CGACTCTCTCCACCTCCACCA SEQ ID NO: 19

Chlamydia trachomatis (D/UW-3/CX) tmRNA

GGGGGUGUAAAGGUUUCGACUUAGAAAUGAAGCGUUAAUUGC
AUGCGGAGGGCGUUGGCUGGCCUCCUAAAAAGCCGACAAAACA
AUAAAUGCCGAACCUAAGGCUGAAUGCGAAAUUAUCAGCUUC
GCUGAUCUCGAAGAUCUAAGAGUAGCUGCUUAAUUAGCAAAG
UUGUUACCUAAAUACGGGUGACCCGGUGUUCGCGAGCUCCACC
AGAGGUUUUCGAAACACCGUCAUGUAUCUGGUUAGAACUUAG
GUCCUUUAAUUCUCGAGGAAAUGAGUUUGAAAUUUAAUGAGA
GUCGUUAGUCUCUAUAGGGGUUUCUAGCUGAGGAGACAUAAC
GUAUAGUACCUAGGAACUAAGCAUGUAGAGGUUAGCGGGGAG
UUUACUAAGGACGAGAGUUCGACUCUCUCCACCUCCACCA
SEQ ID NO: 20

Chlamydia trachomatis (Mouse Pneumonitis) ssrA

GGGGGTGTAAAGGTTTCGACTTAGAAATGAAGCGTTAATTGCAT
GCGGAGGGCGTTGGCTGGCCTCCTAAAAAGCCGACAAAACAATA
AATGCCGAACCTAAGGCTGAATGCGAAATTATCAGCTTCGCTGA
TCTTAATGATCTAAGAGTTGCTGCTTAATTAGCAAAGTTGTTACC
TAAGTACTGGTAACCCGGTGTTCGCGAGCTCCACCAGAGGTTTTC
GAAACGCCGTCATTTATCTGGTTAGAATTAGGGCCTTTTAACTCT
CAAGGGAACTAATTTGAATTTTAATGAGAGTCGTTGGTCTCTATA
GAGGTTTCTAGCTGAGGAGATATAACGTAAAATATTCTAGAAAC
TAAGCATGTAGAGGTTAGCGGGGAGTTTACTAAGGACGAGAGTT
CGAATCTCTCCACCTCCACCA SEQ ID NO: 21

Chlamydia trachomatis (Mouse Pneumonitis) tmRNA

GGGGGUGUAAAGGUUUCGACUUAGAAAUGAAGCGUUAAUUGC
AUGCGGAGGGCGUUGGCUGGCCUCCUAAAAAGCCGACAAAACA
AUAAAUGCCGAACCUAAGGCUGAAUGCGAAAUUAUCAGCUUC
GCUGAUCUUAAUGAUCUAAGAGUUGCUGCUUAAUUAGCAAAG
UUGUUACCUAAGUACUGGUAACCCGGUGUUCGCGAGCUCCACC
AGAGGUUUUCGAAACGCCGUCAUUUAUCUGGUUAGAAUUAGG
GCCUUUUAACUCUCAAGGGAACUAAUUUGAAUUUUAAUGAGA
GUCGUUGGUCUCUAUAGAGGUUUCUAGCUGAGGAGAUAUAAC
GUAAAAUAUUCUAGAAACUAAGCAUGUAGAGGUUAGCGGGGA
GUUUACUAAGGACGAGAGUUCGAAUCUCUCCACCUCCACCA
SEQ ID NO: 22

Chlorobium tepidum ssrA

GGGGATGACAGGCTATCGACAGGATAGGTGTGAGATGTCGTTGC
ACTCCGAGTTTCAGCATGGACGGACTCGTTAAACAAGTCTATGT

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ACCAATAGATGCAGACGATTATTCGTATGCAATGGCTGCCTGAT

TAGCACAAGTTAATTCAGAAGCCATCGTCCTGCGGTGAATGCGC

TTACTCTGAAGCCGCCGGATGGCATAACCCGCGCTTGAGCCTAC

GGGTTCGCGCAAGTAAGCTCCGTACATTCATGCCCGAGGGGGTG

TGCGGGTAACCAATCGGGATAAGGGGACGAACGCTGCTGGCGGT

GTAATCGGACCACGAAAAACCAACCACCAGAGATGAGTGTGGT

AACTGCATCGAGCAGTGTCCTGGACGCGGGTTCAAGTCCCGCCA

TCTCCACCA SEQ ID NO: 23

Chlorobium tepidum tmRNA

GGGGAUGACAGGCUAUCGACAGGAUAGGUGUGAGAUGUCGUU

GCACUCCGAGUUUCAGCAUGGACGGACUCGUUAAACAAGUCUA

UGUACCAAUAGAUGCAGACGAUUAUUCGUAUGCAAUGGCUGC

CUGAUUAGCACAAGUUAAUUCAGAAGCCAUCGUCCUGCGGUGA

AUGCGCUUACUCUGAAGCCGCCGGAUGGCAUAACCCGCGCUUG

AGCCUACGGGUUCGCGCAAGUAAGCUCCGUACAUUCAUGCCCG

AGGGGGUGUGCGGGUAACCAAUCGGGAUAAGGGGACGAACGC

UGCUGGCGGUGUAAUCGGACCACGAAKAACCAACCACCAGAGA

UGAGUGUGGUAACUGCAUCGAGCAGUGUCCUGGACGCGGGUU

CAAGUCCCGCCAUCUCCACCA SEQ ID NO: 24

Cyanophora paradoxa (Alga) Cyanelle ssrA

GGGGCTGTTTAGGTTTCGACGTTTTTTTCTAATTATGTTTGTTAAG

CAAGTCGAGGATTTGTTCTATCTCGAAAATCAAGAACTCTCAAA

ATTTAAACGCAACTAATATTGTACGTTTTAACCGTAAAGCAGCTT

TCGCTGTTTAATAATTACTTTTAATTTAAAAACCTAATTTTTTTAG

GAATTTATTTATTTATTGTTTATCCTGCTTAATGAATTAAAAAAA

GCTATACTTGTGAATAAACGCATAATTTAAAAAAACGGACGTGG

GTTCAAATCCCACCAGCTCCACCA SEQ ID NO: 25

Cyanophora paradoxa (Alga) Cyanelle tmRNA

GGGGCUGUUUAGGUUUCGACGCUUUUUUUCUAAUUAUGUUUGU

UAAGCAAGUCGAGGAUUUGUUCUAUCUCGAAAAUCAAGAACU

CUCAAAAUUUAAACGCAACUAAUAUUGUACGUUUUAACCGUA

AAGCAGCUUUCGCUGUUUAAUAAUUACUUUUAAUUUAAAAAC

CUAAUUUUUUUAGGAAUUUAUUUAUUUAUUGUUUAUCCUGCU

UAAUGAAUUAAAAAAAGCUAUACUUGUGAAUAAACGCAUAAU

UUAAAAAAACGGACGUGGGUUCAAAUCCCACCAGCUCCACCA

SEQ ID NO: 26

Clostridium acetobutylicum ssrA, 3' Partial

AATCTGGCGTCGAGAGCGGGGAAACGAGCCTTACAAAGCTTTGA

GTAAGGAACGGAATTTATGAAGCTACTGAAGTGAAAAGCTTGTT

-continued

TGTAGGCGTTTCATGGAGGGAATGTTAAAATACAAACTGCACTC

GGAGATGCTTAATGAAACCATTTTCGGACAGGGGTTCGATTCCC

CTCGCCTCCACCA SEQ ID NO: 27

Clostridium acetobutylicum tmRNA, 3' Partial

AAUCUGGCGUCGAGAGCGGGGAAACGAGCCUUACAAAGCUUU

GAGUAAGGAACGGAAUUUAUGAAGCUACUGAAGUGAAAAGCU

UGUUUGUAGGCGUUUCAUGGAGGGAAUGUUAAAAUACAAACU

GCACUCGGAGAUGCUUAAUGAAACCAUUUUCGGACAGGGGUU

CGAUUCCCCUCGCCUCCACCA SEQ ID NO: 28

Deinococcus radiodurans ssrA

GGGGGTGACCCGGTTTCGACAGGGGAACTGAAGGTGATGTTGCG

TGTCGAGGTGCCGTTGGCCTCGTAAACAAACGGCAAAGCCATTT

AACTGGCAACCAGAACTACGCTCTCGCTGCTTAAGTGAGATGAC

GACCGTGCAGCCCGGCCTTTGGCGTCGCGGAAGTCACTAAAAAA

GAAGGCTAGCCCAGGCGATTCTCCATAGCCGACGGCGAAACTTT

ATGGAGCTACGGCCTGCGAGAACCTGCCCACTGGTGAGCGCCGG

CCCGACAATCAAACAGTGGGATACACACGTAGACGCACGCTGGA

CGGACCTTTGGACGGCGGTTCGACTCCGCCCACCTCCACCA

SEQ ID NO: 29

Deinococcus radiodurans tmRNA

GGGGGUGACCCGGUUUCGACAGGGGAACUGAAGGUGAUGUUG

CGUGUCGAGGUGCCGUUGGCCUCGUAAACAAACGGCAAAGCCA

UUUAACUGGCAACCAGAACUACGCUCUCGCUGCUUAAGUGAGA

UGACGACCGUGCAGCCCGGCCUUUGGCGUCGCGGAAGUCACUA

AAAAAGAAGGCUAGCCCAGGCGAUUCUCCAUAGCCGACGGCGA

AACUUUAUGGAGCUACGGCCUGCGAGAACCUGCCCACUGGUGA

GCGCCGGCCCGACAAUCAAACAGUGGGAUACACACGUAGACGC

ACGCUGGACGGACCUUUGGACGGCGGUUCGACUCCGCCCACCU

CCACCA SEQ ID NO: 30

Desulfovibrio desulfuricans ssrA, Internal Partial

GGGACTGGAACCGTAGCGGCAGGTCGAGGCGCCGCTGGCCTCGT

AAAAAGCGGCACAAAAGTAATTGCCAACAACGATTACGACTAC

GCTTACGCTGCCTAATAACAGCGAGGCAATGACCGTTTAACGGT

CGCGCCGATCAGGGCCATGCCTGATAACCCTGATTGGCGACACT

TATCAGGCTGGCGAAAACCGGCTCTCGCCGGGGTTTTTCGCGAG

GAGTTTACCGGCGGGATTGCTGCGTTGTGCCTGGTCAGGGGCCA

ACAGCGCGGTGAAATACATACTTGACCTAAACCTGTAATGCTTC

GTGTGGAATGTTCTCGGACGGGG SEQ ID NO: 31

Desulfovibrio desulfuricans tmRNA, Internal Partial

GGGACUGGAACCGUAGCGGCAGGUCGAGGCGCCGCUGGCCUCG

UAAAAAGCGGCACAAAAGUAAUUGCCAACAACGAUUACGACU

ACGCUUACGCUGCCUAAUAACAGCGAGGCAAUGACCGUUUAAC

GGUCGCGCCGAUCAGGGCCAUGCCUGAUAACCCUGAUUGGCGA

CACUUAUCAGGCUGGCGAAAACCGGCUCUCGCCGGGGUUUUUC

GCGAGGAGUUUACCGGCGGGAUUGCUGCGUUGUGCCUGGUCA

GGGGCCAACAGCGCGGUGAAAUACAUACUUGACCUAAACCUGU

AAUGCUUCGUGUGGAAUGUUCUCGGACGGGG SEQ ID NO: 32

Dichelobacter nodosus ssrA, 3 Partial

CTCGAGGTGCATGTCGAGAATGAGAGAATCTCGTTAAATACTTT

CAAAACTTATAGTTGCAAACGACGACAACTACGCTTTAGCGGCT

TAATTCCCGCTTTCGCTTACCTAGATTTGTCTGTGGGTTTACCGTA

AGCGACATTAACACAGAATCGCTGGTTAACGCGTCCGCTGTTAA

TCGGTTAAATTAAGCGGAATCGCTTGTAAAATGCCTGAGCGTTG

GCTGTTTATGAGTTAAACCTAATTAACTGCTCTAAACATGTAGTA

CCAAAAGTTAAGGATTCGCGGACGGGGGTTCAAATCCCCCCGCC

TCCACCA SEQ ID NO: 33

Dichelobacter nodosus tmRNA, 3 Partial

CUCGAGGUGCAUGUCGAGAAUGAGAGAAUCUCGUUAAAUACU

UUCAAAACUUAUAGUUGCAAACGACGACAAGUACGCUUUAGCG

GCUUAAUUCCCGCUUUCGCUUACCUAGAUUUGUCUGUGGGUUU

ACCGUAAGCGACAUUAACACAGAAUCGCUGGUUAACGCGUCCG

CUGUUAAUCGGUUAAAUUAAGCGGAAUCGCUUGUAAAAUGCC

UGAGCGUUGGCUGUUUAUGAGUUAAACCUAAUUAACUGCUCU

AAACAUGUAGUACCAAAAGUUAAGGAUUCGCGGACGGGGGUU

CAAAUCCCCCCGCCUCCACCA SEQ ID NO: 34

Enterococcus faecalis ssrA

GGGGGCGTTACGGATTCGACAGGCATAGTTGAGCTTGAATTGCG

TTTCGTAGGTTACGGCTACGTTAAAACGTTACAGTTAAATATAAC

TGCTAAAAACGAAAACAATTCTTTCGCTTTAGCTGCCTAAAAAC

CAGCTAGCGAAGATCCTCCCGGCATCGCCCATGTGCTCGGGTCA

GGGTCCTAATCGAAGTGGGATACGCTAAATTTTTCCGTCTGTAAA

ATTTAGAGGAGCTTACCAGACTAGCAATACAGAATGCCTGTCAC

TCGGCACGCTGTAAAGCGAACCTTTAAATGAGTGTCTATGAACG

TAGAGATTTAAGTGGCAATATGTTTGGACGCGGGTTCGACTCCC

GCCGTCTCCACCA SEQ ID NO: 35

Enterococcus faecalis tmRNA

GGGGGCGUUACGGAUUCGACAGGCAUAGUUGAGCUUGAAUUG

CGUUUCGUAGGUUACGGCUACGUUAAAACGUUACAGUUAAAU

AUAACUGCUAAAAACGAAAACAAUUCUUUCGCUUUAGCUGCCU

AAAAACCAGCUAGCGAAGAUCCUCCCGGCAUCGCCCAUGUGCU

CGGGUCAGGGUCCUAAUCGAAGUGGGAUACGCUAAAUUUUUC

CGUCUGUAAAAUUUAGAGGAGCUUACCAGACUAGCAAUACAG

AAUGCCUGUCACUCGGCACGCUGUAAAGCGAACCUUUAAAUGA

GUGUCUAUGAACGUAGAGAUUUAAGUGGCAAUAUGUUUGGAC

GCGGGUUCGACUCCCGCCGUCUCCACCA SEQ ID NO: 36

Escherichia coli ssrA

GGGGCTGATTCTGGATTCGACGGGATTTGCGAAACCCAAGGTGC

ATGCCGAGGGGCGGTTGGCCTCGTAAAAAGCCGCAAAAAATAGT

CGCAAACGACGAAAACTACGCTTTAGCAGCTTAATAACCTGCTT

AGAGCCCTCTCTCCCTAGCCTCCGCTCTTAGGACGGGGATCAAG

AGAGGTCAAACCCAAAAGAGATCGCGTGGAAGCCCTGCCTGGG

GTTGAAGCGTTAAAACTTAATCAGGCTAGTTTGTTAGTGGCGTGT

CCGTCCGCAGCTGGCAAGCGAATGTAAAGACTGACTAAGCATGT

AGTACCGAGGATGTAGGAATTTCGGACGCGGGTTCAACTCCCGC

CAGCTCCACCA SEQ ID NO: 37

Escherichia coli tmRNA

GGGGCUGAUUCUGGAUUCGACGGGAUUUGCGAAACCCAAGGU

GCAUGCCGAGGGGCGGUUGGCCUCGUAAAAAGCCGCAAAAAAU

AGUCGCAAACGACGAAAACUACGCUUUAGCAGCUUAAUAACCU

GCUUAGAGCCCUCUCUCCCUAGCCUCCGCUCUUAGGACGGGGA

UCAAGAGAGGUCAAACCCAAAAGAGAUCGCGUGGAAGCCCUGC

CUGGGGUUGAAGCGUUAAAACUUAAUCAGGCUAGUUUGUUAG

UGGCGUGUCCGUCCGCAGCUGGCAAGCGAAUGUAAAGACUGAC

UAAGCAUGUAGUACCGAGGAUGUAGGAAUUUCGGACGCGGGU

UGAACUCCGGCCAG SEQ ID NO: 38

Haemophilus influenzae ssrA

GGGGCTGATTCTGGATTCGACGGGATTAGCGAAGCCCAAGGTGC

ACGTCGAGGTGCGGTAGGCCTCGTAAATAAACCGCAAAAAAATA

GTCGCAAACGACGAACAATACGCTTTAGCAGCTTAATAACCTGC

ATTTAGCCTTCGCGCTCCAGCTTCCGCTCGTAAGACGGGGATAAC

GCGGAGTCAAACCAAAACGAGATCGTGTGGAAGCCACCGTTTGA

GGATCGAAGCACTAAATTGAATCAAACTAGCTTAAGTTTAGCGT

GTCTGTCCGCATGCTTAAGTGAAATTAAAGACGAGACTAAACGT

-continued

GTAGTACTGAAGGTAGAGTAATTTCGGACGGGGGTTCAACTCCC

CCCAGCTCCACCA SEQ ID NO: 39

Haemophilus influenzae tmRNA

GGGGCUGAUUCUGGAUUCGACGGGAUUAGCGAAGCCCAAGGU

GCACGUCGAGGUGCGGUAGGCCUCGUAAAUAAACCGCAAAAAA

AUAGUCGCAAACGACGAACAAUACGCUUUAGCAGCUUAAUAAC

CUGCAUUUAGCCUUCGCGCUCCAGCUUCCGCUCGUAAGACGGG

GAUAACGCGGAGUCAAACCAAAACGAGAUCGUGUGGAAGCCAC

CGUUUGAGGAUCGAAGCACUAAAUUGAAUCAAACUAGCUUAA

GUUUAGCGUGUCUGUCCGCAUGCUUAAGUGAAAUUAAAGACG

AGACUAAACGUGUAGUACUGAAGGUAGAGUAAUUUCGGACGG

GGGUUCAACUCCCCCCAGCUCCACCA SEQ ID NO: 40

Helicobacter pylori (ATCC 43504) ssrA, Internal Partial

SEQ ID NO: 41

AGATTTCTTGTCGCGCAGATAGCATGCCAAGCGCTGCTTGTAAA

ACAGCAACAAAAATAACTGTAAACAACACAGATTACGCTCCAGC

TTACGCTAAAGCTGCGTGAGTTAATCTCCTTTTGGAGCTGGACTG

ATTAGAATTTCTAGCGTTTTAATCGCTCCATAACCTTAAGCTAGA

CGCTTTTAAAAGGTGGTTCGCCTTTTAAACTAAGAAACAAGAAC

TCTTGAAACTATCTTAAGGTTTTAGAAAGTTGGACCAGAGCTAGT

TTTAAGGCTAAAAACTAACCAATTTTCTAAGCATTGTAGAAGTTT

GTGTTTAGGGCAAGATTTTTGGACTGGG

Helicobacter pylori (ATCC 43504) tmRNA, Internal Partial

SEQ ID NO: 42

AGAUUUCUUGUCGCGCAGAUAGCAUGCCAAGCGCUGCUUGUAA

AACAGCAACAAAAAUAACUGUAAACAACACAGAUUACGCUCCA

GCUUACGCUAAAGCUGCGUGAGUUAAUCUCCUUUUGGAGCUG

GACUGAUUAGAAUUUCUAGCGUUUUAAUCGCUCCAUAACCUU

AAGCUAGACGCUUUUAAAAGGUGGUUCGCCUUUUAAACUAAG

AAACAAGAACUCUUGAAACUAUCUUAAGGUUUUAGAAAGUUG

GACCAGAGCUAGUUUUAAGGCUAAAAACUAACCAAUUUUCUA

AGCAUUGUAGAAGUUUGUGUUUAGGGCAAGAUUUUUGGACUG

GG

Helicobacter pylori (strain 26695) ssrA

SEQ ID NO: 43

GGGGCTGACTTGGATTTCGACAGATTTCTTGTCGCACAGATAGC

ATGCCAAGCGCTGCTTGTAAAACAGCAACAAAAATAACTGTAAA

CAACACAGATTACGCTCCAGCTTACGCTAAAGCTGCGTGAGTTA

ATCTCCTTTTGGAGCTGGACTGATTAGAATTTCTAGCGTTTTAAT

-continued

CGCTCCATAACCTTAAGCTAGACGCTTTTAAAAGGTGGTTCGCCT

TTTAAACTAAGAAACAAGAACTCTTGAAACTATCTCAAGGTTTT

AGAAAGTTGGACCAGAGCTAGTTTTAAGGCTAAAAAACCAACCA

ATTTTCTAAGCATTGTAGAAGTTTGTGTTTAGGGCAAGATTTTTG

GACTGGGGTTCGATTCCCCACAGCTCCACCA

Helicobacter pylori (Strain 26695) tmRNA

SEQ ID NO: 44

GGGGCUGACUUGGAUUUCGACAGAUUUCUUGUCGCACAGAUA

GCAUGCCAAGCGCUGCUUGUAAAACAGCAACAAAAAUAACUGU

AAACAACACAGAUUACGCUCCAGCUUACGCUAAAGCUGCGUGA

GUUAAUCUCCUUUUGGAGCUGGACUGAUUAGAAUUUCUAGCG

UUUUAAUCGCUCCAUAACCUUAAGCUAGACGCUUUUAAAAGG

UGGUUCGCCUUUUAAACUAAGAAACAAGAACUCUUGAAACUA

UCUCAAGGUUUUAGAAAGUUGGACCAGAGCUAGUUUUAAGGC

UAAAAAACCAACCAAUUUUCUAAGCAUUGUAGAAGUUUGUGU

UUAGGGCAAGAUUUUUGGACUGGGGUUCGAUUCCCCACAGCUC

CACCA

Klebsiella aerogenes (NCTC 9528) ssrA, Internal Partial

SEQ ID NO: 45

GGGATTCGCGAAACCCAAGGTGCATGCCGAGGGGCGGTTGGCCT

CGTAAAAAGCCGCAAAAAAATAGTCGCAAACGACGAAAACTAC

GCTTTAGCAGCTTAATAACCTGCTAAGAGCCCTCTCTCCCTAGCT

TCCGCTCCTAAGACGGGGAATAAAGAGAGGTCAAACCCAAAAG

AGATCGCGTGGAAGCCCTGCCTGGGGTTGAAGCGTTAAAACTAA

TCAGGCTAGTTTGTCAGTGGCGTGTCCGTCCGCAGCTGGCCAGC

GAATGTAAAGACTGGACTAAGCATGTAGTGCCGAGGATGTAGGA

ATTTC

Klebsiella aerogenes (NCTC 9528) tmRNA, Internal Partial

SEQ ID NO: 46

GGGAUUCGCGAAACCCAAGGUGCAUGCCGAGGGGCGGUUGGCC

UCGUAAAAAGCCGCAAAAAAAUAGUCGCAAACGACGAAAACU

ACGCUUUAGCAGCUUAAUAACCUGCUAAGAGCCCUCUCUCCCU

AGCUUCCGCUCCUAAGACGGGGAAUAAAGAGAGGUCAAACCCA

AAAGAGAUCGCGUGGAAGCCCUGCCUGGGGUUGAAGCGUUAA

AACUAAUCAGGCUAGUUUGUCAGUGGCGUGUCCGUCCGCAGCU

GGCCAGCGAAUGUAAAGACUGGACUAAGCAUGUAGUGCCGAG

GAUGUAGGAAUUUC

Lactobacillus lactis (NCTC 662) ssrA, Internal Partial

SEQ ID NO: 47

AAGCACAGTTCGAGCTTGAATTGCGTTTCGTAGGTTACGTCTACG

TTAAAACGTTACAGTTAAATATAACTGCTAAAAACGAAAACAAC

-continued

TCTTACGCTTTAGCTGCCTAAAAACAGTTAGCGTAGATCCTCTCG

GCATCGCCCATGTGCTCGAGTAAGGGTCTCAAATTTAGTGGGAT

ACGTTAAACTTTTCCGTCTGTAAAGTTTAAAAGAGATCATCAGAC

TAGCGATACAGAATGCCTGTCACTCGGCAAGCTGTAAAGCGAAA

CCTCAAATGAGTTGACTATGAACGTAGATTTTTAAGTGTCGATGT

GTTT

Lactobacillus lactis (NCTC 662) tmRNA, Internal Partial

SEQ ID NO: 48

AAGCACAGUUCGAGCUUGAAUUGCGUUUCGUAGGUUACGUCU

ACGUUAAAACGUUACAGUUAAAUAUAACUGCUAAAAACGAAA

ACAACUCUUACGCUUUAGCUGCCUAAAAACAGUUAGCGUAGAU

CCUCUCGGCAUCGCCCAUGUGCUCGAGUAAGGGUCUCAAAUUU

AGUGGGAUACGUUAAACUUUUCCGUCUGUAAAGUUUAAAAGA

GAUCAUCAGACUAGCGAUACAGAAUGCCUGUCACUCGGCAAGC

UGUAAAGCGAAACCUCAAAUGAGUUGACUAUGAACGUAGAUU

UUUAAGUGUCGAUGUGUUU

Legionella pneumophila ssrA, Internal Partial

SEQ ID NO: 49

GTGGGTTGCAAAACCGGAAGTGCATGCCGAGAAGGAGATCTCTC

GTAAATAAGACTCAATTAAATATAAATGCAAACGATGAAAACTT

TGCTGGTGGGGAAGCTATCGCTGCCTAATAAGCACTTTAGTTAA

ACCATCACTGTGTACTGGCCAATAAACCCAGTATCCCGTTCGACC

GAGCCCGCTTATCGGTATCGAATCAACGGTCATAAGAGATAAGC

TAGCGTCCTAATCTATCCCGGGTTATGGCGCGAAACTCAGGGAA

TCGCTGTGTATCATCCTGCCCGTCGGAGGAGCCACAGTTAAATTC

AAAAGACAAGGCTATGCATGTAGAGCTAAAGGCAGAGGACTTG

CGGACGCGG

Legionella pneumophila tmRNA, Internal Partial

SEQ ID NO: 50

GUGGGUUGCAAAACCGGAAGUGCAUGCCGAGAAGGAGAUCUC

UCGUAAAUAAGACUCAAUUAAAUAUAAAUGCAAACGAUGAAA

ACUUUGCUGGUGGGGAAGCUAUCGCUGCCUAAUAAGCACUUU

AGUUAAACCAUCACUGUGUACUGGCCAAUAAACCCAGUAUCCC

GUUCGACCGAGCCCGCUUAUCGGUAUCGAAUCAACGGUCAUAA

GAGAUAAGCUAGCGUCCUAAUCUAUCCCGGGUUAUGGCGCGAA

ACUCAGGGAAUCGCUGUGUAUCAUCCUGCCCGUCGGAGGAGCC

ACAGUUAAAUUCAAAAGACAAGGCUAUGCAUGUAGAGCUAAA

GGCAGAGGACUUGCGGACGCGG

Listeria grayi ssrA, Internal Partial

SEQ ID NO: 51

ACAGGGATAGGTCGAGCTTGAGTTGCGAGCCGGGGGGATCGGCC

CGTCATCAACGTCAAAGCCAATAATAACTGGCAAACAAAACAAC

AATTTAGCTTTCGCTGCCTAATAGCAGTCTGAATAGCTGATCCTC

CGTGCATCACCCATGTGCTACGGTAAGGGTCTCACTTTTAAGTGG

GTTACGCTGGCTTATCTCCGTCTGGGGCAAACGAGAAGAGCATA

ATCAGACTAGCTAGATAGAGCCCTGACGCCGGGCAGACATCTAT

GCGAAATCCAAATACGGCAACTACGCTCGTAGATGCTCAAGTGC

CGATATTTCTGG

Listeria grayi tmRNA, Internal Partial

SEQ ID NO: 52

ACAGGGAUAGGUCGAGCUUGAGUUGCGAGCCGGGGGGAUCGG

CCCGUCAUCAACGUCAAAGCCAAUAAUAACUGGCAAACAAAAC

AACAAUUUAGCUUUCGCUGCCUAAUAGCAGUCUGAAUAGCUG

AUCCUCCGUGCAUCACCCAUGUGCUACGGUAAGGGUCUCACUU

UUAAGUGGGUUACGCUGGCUUAUCUCCGUCUGGGGCAAACGA

GAAGAGCAUAAUCAGACUAGCUAGAUAGAGCCCUGACGCCGGG

CAGACAUCUAUGCGAAAUCCAAAUACGGCAACUACGCUCGUAG

AUGCUCAAGUGCCGAUAUUUCUGG

Listeria innocua ssrA, Internal Partial

SEQ ID NO: 53

ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGATCGTCC

TCGTTATCAACGTCAAAGCCAATAATAACTGGCAAAGAAAAACA

AAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT

CCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGTG

GGCTACACTAGTTAATCTCCGTCTGAGGTTAAATAGAAGAGCTT

AATCAGACTAGCTGAATGGAAGCCTGTTACCGGGCTGATGTTTA

TGCGAAATGCTAATACGGTGACTACGCTCGTAGATATTCAAGTG

CCGATATTTCTGG

Listeria innocua tmRNA, Internal Partial

SEQ ID NO: 54

ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGGAUCGU

CCUCGUUAUCAACGUCAAAGCCAAUAAUAACUGGCAAAGAAAA

ACAAAACCUAGCUUUCGCUGCCUAAUAAGCAGUAGCAUAGCUG

AUCCUCCGUGCAUCGCCCAUGUGCUACGGUAAGGGUCUCACUC

UAAGUGGGCUACACUAGUUAAUCUCCGUCUGAGGUUAAAUAG

AAGAGCUUAAUCAGACUAGCUGAAUGGAAGCCUGUUACCGGG

CUGAUGUUUAUGCGAAAUGCUAAUACGGUGACUACGCUCGUA

GAUAUUCAAGUGCCGAUAUUUCUGG

Listeria monocytogenes (NCTC 7973) ssrA, Internal Partial

SEQ ID NO: 55

ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGATCGTCC

TCGTTATCAACGTCAAAGCCAATAATAACTGGCAAAGAAAAACA

AAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT

CCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGTG

GGCTACACTAGTTAATCTCCGTCTGGGGTTAAATAGAAGAGCTT

AATCAGACTAGCTGAATGGAAGCCTGTTACCGGGCCGATGTTTA

TGCGAAATGCTAATACGGTGACTACGCTCGTAGATATTTAAGTG

CCGATATTTCTGG

Listeria monocytogenes (NCTC 7973) tmRNA, Internal Partial

ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGGAUCGU

CCUCGUUAUCAACGUCAAAGCCAAUAAUAACUGGCAAAGAAAA

ACAAAACCUAGCUUUCGCUGCCUAAUAAGCAGUAGCAUAGCUG

AUCCUCCGUGCAUCGCCCAUGUGCUACGGUAAGGGUCUCACUC

UAAGUGGGCUACACUAGUUAAUCUCCGUCUGGGGUUAAAUAG

AAGAGCUUAAUCAGACUAGCUGAAUGGAAGCCUGUUACCGGG

CCGAUGUUUAUGCGAAAUGCUAAUACGGUGACUACGCUCGUA

GAUAUUUAAGUGCCGAUAUUUCUGG SEQ ID NO: 56

Listeria monocytogenes (NCTC 11994) ssrA, Internal Partial

CAAAGCCAATAATAACTGGCAAAGAAAAACAAAACCTAGCTTTC

GCTGCCTAATAAGCAGTAGCATAGCTGATCCTCCGTGCATCGCC

CATGTGCTACGGTAAGGGTCTCACTCTAAGTGGGCTACACTAGTT

AATCTCCGTCTGGGGTTAAATAGAAGAGCTTAATCAGACTAGCT

GAATGGAAGCCTGTTACCGGGCCGATGTTTATGCGAAATGCTAA

TACGGTGACTACGCTCGTAGATATTT SEQ ID NO: 57

Listeria monocytogenes (NCTC 11994) tmRNA, Internal Partial

CAAAGCCAAUAAUAACUGGCAAAGAAAAACAAAACCUAGCUU

UCGCUGCCUAAUAAGCAGUAGCAUAGCUGAUCCUCCGUGCAUC

GCCCAUGUGCUACGGUAAGGGUCUCACUCUAAGUGGGCUACAC

UAGUUAAUCUCCGUCUGGGGUUAAAUAGAAGAGCUUAAUCAG

ACUAGCUGAAUGGAAGCCUGUUACCGGGCCGAUGUUUAUGCG

AAAUGCUAAUACGGUGACUACGCUCGUAGAUAUUU

SEQ ID NO: 58

Listeria murrayi ssrA, Internal Partial

ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGATCGTCC

TCGTTATCAACGTCAAAGCCAATAATAACTGGCAAAGAAAAACA

-continued

AAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT

CCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGTG

GGCTACACTAGTTAATCTCCGTCTGAGGTTAAATAGAAGAGCTT

AATGAGACTAGCTGAATGGAAGCCTGTTACCGGGCTGATGTTTA

TGCGAAATGCTAATACGGTGACTACGCTCGTAGATATTCAAGTG

CCGATATTTCTGG SEQ ID NO: 59

Listeria murrayi tmRNA, Internal Partial

ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGGAUCGU

CCUCGUUAUCAACGUCAAAGCCAAUAAUAACUGGCAAAGAAAA

ACAAAACCUAGCUUUCGCUGCCUAAUAAGCAGUAGCAUAGCUG

AUCCUCCGUGCAUCGCCCAUGUGCUACGGUAAGGGUCUCACUC

UAAGUGGGCUACACUAGUUAAUCUCCGUCUGAGGUUAAAUAG

AAGAGCUUAAUGAGACUAGCUGAAUGGAAGCCUGUUACCGGG

CUGAUGUUUAUGCGAAAUGCUAAUACGGUGACUACGCUCGUA

GAUAUUCAAGUGCCGAUAUUUCUGG SEQ ID NO: 60

Listeria welshimeri ssrA, Internal Partial

ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGATCGTCC

TCGTTATCAACGTCAAAGCCAATAATAACTGGGAAAGAAAAACA

AAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT

CCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGTG

GGCTACACTGGCTAATCTCCGTCTGAGGTTAGTTGGAAGAGCTT

AATCAGACTAGCTGAATGGAAGCCTGTTACCGGGCCGATGTTTA

TGCGAAATGCTAATACGGTGACTACGCTCGTAGATATTTAAGTG

CCGATATTTCTGG SEQ ID NO: 61

Listeria welshimeri tmRNA, Internal Partial

ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGGAUCGU

CCUCGUUAUCAACGUCAAAGCCAAUAAUAACUGGCAAAGAAAA

ACAAAACCUAGCUUUCGCUGCCUAAUAAGCAGUAGCAUAGCUG

AUCCUCCGUGCAUCGCCCAUGUGCUACGGUAAGGGUCUCACUC

UAAGUGGGCUACACUGGCUAAUCUCCGUCUGAGGUUAGUUGG

AAGAGCUUAAUCAGACUAGCUGAAUGGAAGCCUGUUACCGGG

CCGAUGUUUAUGCGAAAUGCUAAUACGGUGACUACGCUCGUA

GAUAUUUAAGUGCCGAUAUUUCUGG SEQ ID NO: 62

Marinobacter hydrocarbonoclasticus ssrA, Internal Partial

GCCGGTGACGAACCCTTGGGTGCATGCCGAGATGGCAGCGAATC

TCGTAAATCCAAAGCTGCAACGTAATAGTCGCAAACGACGAAAA

CTACGCACTGGCGGCGTAAGCCGTTCCAGTCGTCCTGGCTGAGG

-continued

CGCCTATAACTCAGTAGCAACATCCCAGGACGTCATCGCTTATA
GGCTGCTCCGTTCACCAGAGCTCACTGGTGTTCGGCTAAGATTAA
AGAGCTCGCCTCTTGCACCCTGACCTTCGGGTCGCTTGAGGTTAA
ATCAATAGAAGGACACTAAGGATGTAGACCTCAAGGCCTAGTGC
TGGCGGACGCGG SEQ ID NO: 63

Marinobacter hydrocarbonoclasticus tmRNA, Internal Partial

GCCGGUGACGAACCCUUGGGUGCAUGCCGAGAUGGCAGCGAAU
CUCGUAAAUCCAAAGCUGCAACGUAAUAGUCGCAAACGACGAA
AACUACGCACUGGCGGCGUAAGCCGUUCCAGUCGUCCUGGCUG
AGGCGCCUAUAACUCAGUAGCAACAUCCCAGGACGUCAUCGCU
UAUAGGCUGCUCCGUUCACCAGAGCUCACUGGUGUUCGGCUAA
GAUUAAAGAGCUCGCCUCUUGCACCCUGACCUUCGGGUCGCUU
GAGGUUAAAUCAAUAGAAGGACACUAAGCAUGUAGACCUCAA
GGCCUAGUGCUGGCGGACGCGG SEQ ID NO: 64

Mycobacterium avium ssrA, Internal Partial

TTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAACTGA
CCACCGTAAGCGTCGTTGCAAATAGATAAGCGCCGATTCACATC
AGCGCGACTTACCTCTCGCTGCCTAAGCGACAGCTAGTCCGTCA
GCCCGGGAACGCCCTCGACCCGGAGCCTGGCGTCAGCTAGAGGG
ATCCACCGATGAGTTCGGTCGCGGGACTCATCGGGACACCAACA
GCGACTGGGATCGTCATCCTGGCTTGTTCGCGTGACCAGGAGAT
CCGAGTAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGAGG
GAATGCCGTAGAACCCGGGTTCGATTCCCAA SEQ ID NO: 65

Mycobacterium avium tmRNA, Internal Partial

UUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAACUG
ACCACCGUAAGCGUCGUUGCAAAUAGAUAAGCGCCGAUUCACA
UCAGCGCGACUUACCUCUCGCUGCCUAAGCGACAGCUAGUCCG
UCAGCCCGGGAACGCCCUCGACCCGGAGCCUGGCGUCAGCUAG
AGGGAUCCACCGAUGAGUUCGGUCGCGGGACUCAUCGGGACAC
CAACAGCGACUGGGAUCGUCAUCCUGGCUUGUUCGCGUGACCA
GGAGAUCCGAGUAGAGGCAUAGCGAACUGCGCACGGAGAAGCC
UUGAGGGAAUGCCGUAGAACCCGGGUUCGAUUCCCAA
SEQ ID NO: 66

Mycobacterium bovis ssrA, Internal Partial

TTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGAG
ACCACCGTAAGCGTCGTTGCGACCAAATAAGCGCCGATTCACAT
CAGCGCGACTACGTCTCGCTGCCTAAGCGACGGCTAGTCTGTCA
GACCGGGAACGCCCTCGGCCCGGACCCTGGCATCAGCTAGAGGG
ATCCACCGATGAGTCCGGTCGCGGGACTCCTCGGGACAACCACA
GCGACTGGGATCGTCATCTCGGCTAGTTCGCGTGACCGGGAGAT
CCGAGCAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGAGG
GAATGCCGTAGG SEQ ID NO: 67

Mycobacterium bovis tmRNA, Internal Partial

UUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAGAG
ACCACCGUAAGCGUCGUUGCGACCAAAUAAGCGCCGAUUCACA
UCAGCGCGACUACGUCUCGCUGCCUAAGCGACGGCUAGUCUGU
CAGACCGGGAACGCCCUCGGCCCGGACCCUGGCAUCAGCUAGA
GGGAUCCACCGAUGAGUCCGGUCGCGGGACUCCUCGGGACAAC
CACAGCGACUGGGAUCGUCAUCUCGGCUAGUUCGCGUGACCGG
GAGAUCCGAGCAGAGGCAUAGCGAACUGCGCACGGAGAAGCCU
UGAGGGAAUGCCGUAGG SEQ ID NO: 68

Mycobacterium leprae ssrA

GGGGCTGAAAGGTTTCGACTTCGCGCATCGAATCAAGGGAAGCG
TGCCGGTGCAGGCAAGAGACCACCGTAAGCGTCGTTGCAGCAAT
ATAAGCGCCGATTCATATCAGCGCGACTATGCTCTCGCTGCCTAA
GCGATGGCTAGTCTGTCAGACCGGGAACGCCCTCGTCCCGGAGC
CTGGCATCAGCTAGAGGGATCTACCGATGGGTTCGGTCGCGGGA
CTCGTCGGGACACCAACCGCGACTGGGATCGTCATCCTGGCTAG
TTCGCGTGATCAGGAGATCCGAGTAGAGGCATAGCGAACTACGC
ACGGAGAAGCCTTGAGGGAAATGCCGTAGGACCCGGGTTCGATT
CCCGGCAGCTCCACCA SEQ ID NO: 69

Mycobacterium leprae tmRNA

GGGGCUGAAAGGUUUCGACUUCGCGCAUCGAAUCAAGGGAAG
CGUGCCGGUGCAGGCAAGAGACCACCGUAAGCGUCGUUGCAGC
AAUAUAAGCGCCGAUUCAUAUCAGCGCGACUAUGCUCUCGCUG
CCUAAGCGAUGGCUAGUCUGUCAGACCGGGAACGCCCUCGUCC
CGGAGCCUGGCAUCAGCUAGAGGGAUCUACCGAUGGGUUCGGU
CGCGGGACUCGUCGGGACACCAACCGCGACUGGGAUCGUCAUC
CUGGCUAGUUCGCGUGAUCAGGAGAUCCGAGUAGAGGCAUAG
CGAACUACGCACGGAGAAGCCUUGAGGGAAAUGCCGUAGGACC
CGGGUUCGAUUCCCGGCAGCUCCACCA SEQ ID NO: 70

Mycobacterium paratuberculosis ssrA, Internal Partial

TTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAACTGA
CCACCGTAAGCGTCGTTGCAAATAGATAAGCGCCGATTCACATC
AGCGCGACTTACCTCTCGCTGCCTAAGCGACAGCTAGTCCGTCA

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GCCCGGGAACGCCCTCGACCCGGAGCCTGGCGTCAGCTAGAGGG

ATCCACCGATGAGTTCGGTCGCGGGACTCATCGGGACACCAACA

GCGACTGGGATCGTCATCCTGGCTTGTTCGCGTGACCAGGAGAT

CCGAGTAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGAGG

GAATGCCGTAGAACCCGGGTTCGATTCCCAA SEQ ID NO: 71

Mycobacterium paratuberculosis tmRNA, Internal Partial

UUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAACUG

ACCACCGUAAGCGUCGUUGCAAAUAGAUAAGCGCCGAUUCACA

UCAGCGCGACUUACCUCUCGCUGCCUAAGCGACAGCUAGUCCG

UCAGCCCGGGAACGCCCUCGACCCGGAGCCUGGCGUCAGCUAG

AGGGAUCCACCGAUGAGUUCGGUCGCGGGACUCAUCGGGACAC

CAACAGCGACUGGGAUCGUCAUCCUGGCUUGUUCGCGUGACCA

GGAGAUCCGAGUAGAGGCAUAGCGAACUGCGCACGGAGAAGCC

UUGAGGGAAUGCCGUAGAACCCGGGUUCGAUUCCCAA

SEQ ID NO: 72

Mycobacterium tuberculosis ssrA

GGGGCTGAACGGTITCGACITCGCGCATCGAATCAAGGGAAGCG

TGCCGGTGCAGGCAAGAGACCACCGTAAGCGTCGTTGCGACCAA

ATAAGCGCCGATTCACATCAGCGCGACTACGCTCTCGCTGCCTA

AGCGACGGCTAGTCTGTCAGACCGGGAACGCCCTCGGCCCGGAC

CCTGGCATCAGCTAGAGGGATCCACCGATGAGTCCGGTCGCGGG

ACTCCTCGGGACAACCACAGCGACTGGGATCGTCATCTCGGCTA

GTTCGCGTGACCGGGAGATCCGAGCAGAGGCATAGCGAACTGCG

CACGGAGAAGCCTTGAGGGAATGCCGTAGGACCCGGGTTCGATT

CCCGGCAGCTCCACCA SEQ ID NO: 73

Mycobacterium tuberculosis tmRNA

GGGGCUGAACGGUUUCGACUUCGCGCAUCGAAUCAAGGGAAGC

GUGCCGGUGCAGGCAAGAGACCACCGUAAGCGUCGUUGCGACC

AAAUAAGCGCCGAUUCACAUCAGCGCGACUACGCUCUCGCUGC

CUAAGCGACGGCUAGUCUGUCAGACCGGGAACGCCCUCGGCCC

GGACCCUGGCAUCAGCUAGAGGGAUCCACCGAUGAGUCCGGUC

GCGGGACUCCUCGGGACAACCACAGCGACUGGGAUCGUCAUCU

CGGCUAGUUCGCGUGACCGGGAGAUCCGAGCAGAGGCAUAGCG

AACUGCGCACGGAGAAGCCUUGAGGGAAUGCCGUAGGACCCGG

GUUCGAUUCCCGGCAGCUCCACCA SEQ ID NO: 74

Mycoplasma capricolumn ssrA

GGGGATGTCATGGATTTGACAGGATATCTTTAGTACATATAAGC

AGTAGTGTTGTAGACTATAAATACTACTAGGITIAAAAAAACGC

-continued

AAATAAAAACGAAGAAACTTTTGAAATGCCAGCATTTATGATGA

ATAATGCATCAGCTGGAGCAAACTTTATUTTTGCTTAATAACTAC

TAGTTTAGTTATAGTATTTCACGAATTATAGATATTTTAAGCTTT

ATTTATAACCGTATTACCCAAGCTTAATAGAATATATGATTGCAA

TAAATATATTTGAAATCTAATTGCAAATGATATTTAACCTTTAGT

TAATTTTAGTTAAATATTTTAATTAGAAAATTAACTAAACTGTAG

AAAGTATGTATTAATATATCTTGGACGCGAGTTCGATTCTCGCCA

TCTCCACCA SEQ ID NO: 75

Mycoplasma capricolumn tmRNA

GGGGAUGUCAUGGAUUUGACAGGAUAUCUUUAGUACAUAUAA

GCAGUAGUGUUGUAGACUAUAAAUACUACUAGGUUUAAAAAA

ACGCAAAUAAAAACGAAGAAACUUUUGAAAUGCCAGCAUUUA

UGAUGAAUAAUGCAUCAGCUGGAGCAAACUUUAUGUUUGCUU

AAUAACUACUAGUUUAGUUAUAGUAUUUCACGAAUUAUAGAU

AUUUUAAGCUUUAUUUAUAACCGUALTUACCCAAGCUUAAUAG

AAUAUAUGAUUGCAAUAAAUAUAUUUGAAAUCUAAUUGCAAA

UGAUAUUUAACCUUUAGUUAAUUUUAGUUAAAUAUUUUAAUU

AGAAAAUUAACUAAACUGUAGAAAGUAUGUAUUAAUAUAUCU

UGGACGCGAGUUCGAUUCUCGCCAUCUCCACCA SEQ ID NO: 76

Mycoplasma genitalium (ATTC 33530, #1) ssrA

GGGGATGTTTTGGGTTTGACATAATGCTGATAGACAAACAGTAG

CATTGGGGTATGCCCCTTACAGCGCTAGGTTCAATAACCGACAA

AGAAAATAACGAAGTGTTGGTAGAACCAAATITGATCATTAACC

AACAAGCAAGTGTTAAGCTTTGCTTTTGCATAAGTAGATACTAAA

GCTACAGCTGGTGAATAGTCATAGTTTGCTAGCTGTCATAGTTTA

TGACTCGAGGTTAAATCGTTCAATTTAACCTTTAAAAATAGAACT

TGTTGTTTCCATGATTGTTTTGTGATCAATTGGAAACAAGACAAA

AATCCACAAAACTAAAATGTAGAAGCTGTTTGTTGTGTCCTTTAT

GGAAACGGGTTCGATTCCCGTCATCTCCACCA SEQ ID NO: 77

Mycoplasma genitalium (ATTC 33530, #1) tmRNA

GGGGAUGUUUUGGGUUUGACAUAAUGCUGAUAGACAAACAGU

AGCAUUGGGGUAUGCCCCUUACAGCGCUAGGUUCAAUAACCGA

CAAAGAAAAUAACGAAGUGUUGGUAGAACCAAAUUUGAUCAU

UAACCAACAAGCAAGUGUUAACUUUGCUUUUGCAUAAGUAGA

UACUAAAGCUACAGCUGGUGAAUAGUCAUAGUUUGCUAGCUG

UCAUAGLTUUAUGACUCGAGGUUAAAUCGUUCAAUUUAACCUU

UAAAAAUAGAACUUGUUGUUUCCAUGAUUGUUUUGUGAUCAA

UUGGAAACAAGACAAAAAUCCACAAAACUAAAAUGUAGAAGC

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UGUUUGUUGUGUCCUUUAUGGAAACGGGUUCGAUUCCCGUCA

UCUCCACCA SEQ ID NO: 78

Mycoplasma genitalium (ATTC 33530, ≯2) tmRNA, Internal Partial

ACATAATGCTGATAGACAAACAGTAGCATTGGGGTATGCCCCTT

ACAGCGCTAGGTTCAATAACCGACAAAGAAAATAACGAAGTGTT

GGTAGATCCAAATTTGATCATTAACCAACAAGCAAGTGTTAACT

TTGCTTTTGCATAAGTAGATACTAAAGCTACAGCTGGTGAATAGT

CATAGTTTGCTAGCTGTCATAGTTTATGACTCGAGGTTAAATCGT

TCAATTTAACCTTTAAAAATAGAACTTGTTGTTTCCATGATTGTT

TTGTGATCAATTGGAAACAAGACAAAAATCCACAAAACTAAAAT

GTAGAAGCTGTTTGTTGTGTCCTTTATGGAAACGGGTTC

SEQ ID NO: 79

Mycoplasma genitalium (ATTC 33530, #2) tmRNA, Internal Partial

ACAUAAUGCUGAUAGACAAACAGUAGCAUUGGGGUAUGCCCC

UUACAGCGCUAGGUUCAAUAACCGACAAAGAAAAUAACGAAG

UGUUGGUAGAUCCAAAUUUGAUCAUUAACCAACAAGCAAGUG

UUAACUUUGCUUUUGCAUAAGUAGAUACUAAAGCUACAGCUG

GUGAAUAGUCAUAGUUUGCUAGCUGUCAUAGUUUAUGACUCG

AGGUUAAAUCGUUCAAUUUAACCUUUAAAAAUAGAACUUGUU

GUUUCCAUGAUUGUUUUGUGAUCAAUUGGAAACAAGACAAAA

AUCCACAAAACUAAAAUGUAGAAGCUGUUUGUUGUGUCCUUU

AUGGAAACGGGUUC SEQ ID NO: 80

Mycoplasma Pneumophila ssrA

GGGGATGTAGAGGTTTTGACATAATGTTGAAAGGAAAACAGTTG

CAGTGGGGTATGCCCCTTACAGCTCTAGGTATAATAACCGACAA

AAATAACGACGAAGTTTTGGTAGATCCAATGTTGATCGCTAACC

AACAAGCAAGTATCAACTACGCTTTCGCTTAGAACATACTAAAG

CTACACGAATTGAATCGCCATAGTTTGGTTCGTGTCACAGTTTAT

GGCTCGGGGTTAACTGGTTCAACTTAATCCTTAAATTATGAACTT

ATCGTITACTTGTITGTCTTATGATCTAAAGTAAGCGAGACATTA

AAACATAAGACTAAACTGTAGAAGCTGTTTTACCAATCCTTTATG

GAAACGGGITCGATTCCCGTCATCTCCACCA SEQ ID NO: 81

Mycoplasma pneumophila tmRNA

GGGGAUGUAGAGGUUUUGACAUAAUGUUGAAAGGAAAACAGU

UGCAGUGGGGUAUGCCCCUUACAGCUCUAGGUAUAAUAACCGA

CAAAAAUAACGACGAAGUUUUGGUAGAUCCAAUGUUGAUCGC

UAACCAACAAGCAAGUAUCAACUACGCUUUCGCUUAGAACAUA

CUAAAGCUACACGAAUUGAAUCGCCAUAGUUUGGUUCGUGUC

-continued

ACAGUUUAUGGCUCGGGGUUAACUGGUUCAACUUAAUCCUUA

AAUUAUGAACUUAUCGUUUACUUGUUUGUCUUAUGAUCUAAA

GUAAGCGAGACAUUAAAACAUAAGACUAAACUGUAGAAGCUG

UUUUACCAAUCCUUUAUGGAAACGGGUUCGAUUCCCGUCAUCU

CCACCA SEQ ID NO: 82

Neisseria gonorrhoeae (ATCC 19424) ssrA, Internal Partial

GGGGGTTGCGAAGCAGATGCGGGCATACCGGGGTCTCAGATTCC

CGTAAAACACTGAATTCAAATAGTCGCAAACGACGAAACTTACG

CTTTAGCCGCTTAAGGCTAGCCGTTGCAGCAGTCGGTCAATGGG

CTGTGTGGCGAAAGCCACCGCAACGTCATCTTACATTGACTGGTT

TCCAGCCGGGTTACTTGGCAGGAAATAAGACTTAAGGTAACTGG

TTTCCAAAAGGCCTGTIGGTCGGCATGATGGAAATAAGATTTTC

AAATAGACACAACTAAGTATGTAGAACGCTTTGTAGAGGACTTT

CGGACGGGG SEQ ID NO: 83

Neisseria gonorrhoeae (ATCC 19424) tmRNA, Internal Partial

GGGGGUUGCGAAGCAGAUGCGGGCAUACCGGGGUCUCAGAUU

CCCGUAAAACACUGAAUUCAAAUAGUCGCAAACGACGAAACUU

ACGCUUUAGCCGCUUAAGGCUAGCCGUUGCAGCAGUCGGUCAA

UGGGCUGUGUGGCGAAAGCCACCGCAACGUCAUCUUACAUUGA

CUGGUUUCCAGCCGGGUUACUUGGCAGGAAAUAAGACUUAAG

GUAACUGGUUUCCAAAAGGCCUGUUGGUCGGCAUGAUGGAAA

UAAGAUUUUCAAAUAGACACAACUAAGUAUGUAGAACGCUUU

GUAGAGGACUUUCGGACGGGG SEQ ID NO: 84

Neisseria gonorrhoeae (FA 1090) ssrA

GGGGGCGACCTTGGTTTCGACGGGGGTTGCGAAGCAGATGCGGG

CATACCGGGGTCTCAGATTCCCGTAAAACACTGAATTCAAATAG

TCGCAAACGACGAAACTTACGCTTTAGCCGCTTAAGGCTAGCCG

TTGCAGCAGTCGGTCAATGGGCTGTGTGGTGAAAGCCACCGCAA

CGTCATCTTACATTGACTGGTTTCCAGCCGGGTTACTTGGCAGGA

AATAAGACTTAAGGTAACTGGTTTCCAAAAGGCCTGTTGGTCGG

CATGATGGAAATAAGATTTTCAAATAGACACAACTAAGTATGTA

GAACGCTTTGTAGAGGACTTTCGGACGGGGGTTCGATTCCCCCC

GCCTCCACCA SEQ ID NO: 85

Neisseria gonorrhoeae (FA 1090) tmRNA

SEQ ID NO: 86

GGGGGCGACCUUGGUUUCGACGGGGGUUGCGAAGCAGAUGCG

GGCAUACCGGGGUCUCAGAUUCCCGUAAAACACUGAAUUCAA

-continued

AUAGUCGCAAACGACGAAACUUACGCUUUAGCCGCUUAAGGC

UAGCCGUUGCAGCAGUCGGUCAAUGGGCUQUGUGGUGAAAGC

CACCGCAACGUCAUCUUACAUUGACUGGUUUCCAGCCGGGUU

ACUUGGCAGGAAAUAAGACUUAAGGUAACUGGUUUCCAAAAG

GCCUGUUGGUCGGCAUGAUGGAAAUAAGAUUUUCAAAUAGAC

ACAACUAAGUAUGUAGAACGCUUUGUAGAGGACUUUCGGACG

GGGGUUCGAUUCCCCCCGCCUCCACCA

Neisseria meningitidis ssrA

SEQ ID NO: 87

GGGGGCGACCTTGGTTTCGACGGGGGTTGCGAAGCAGATGCGGG

CATACCGGGGTCTCAGATTCCCGTAAAACACTGAATTCAAATAG

TCGCAAACGACGAAACTTACGCTTTAGCCGCTTAAGGCTAGCCG

TTGCAGCAGTCGGTCAATGGGCTGTGTGGCGAAAGCCACCGCAA

CGTCATCTTACATTGACTGGTTTCCTGCCGGGTTATTTGGCAGG

AAATGAGATTTAAGGTAACTGGTTTCCAAAAGGCCTGTTGGTCG

GCATGATGGAAATAAGATTTTCAAATAGACACAACTAAGTATGT

AGAACGCTTTGTAGAGGACTTTCGGACGGGGGTTCGATTCCCCC

CGCCTCCACCA

Neisseria meningitidis tmRNA

SEQ ID NO: 88

GGGGGCGACCUUGGUUUCGACGGGGGUUGCGAAGCAGAUGCG

GGCAUACCGGGGUCUCAGAUUCCCGUAAAACACUGAAUUCAA

AUAGUCGCAAACGACGAAACUUACGCUUUAGCCGCUUAAGGC

UAGCCGUUGCAGCAGUCGGUCAAUGGGCUGUGUGGCGAAAGC

CACCGCAACGUCAUCUUACAUUGACUGGUUUCCUGCCGGGUU

AUUUGGCAGGAAAUGAGAUUUAAGGUAACUGGUUUCCAAAAG

GCCUGUUGGUCGGCAUGAUGGAAAUAAGAUUUUCAAAUAGAC

ACAACUAAGUAUGUAGAACGCUUUGUAGAGGACUUUCGGACG

GGGGUUCGAUUCCCCCCGCCUCCACCA

Nostoc muscorum PCC7120 ssrA

SEQ ID NO: 89

GGGTCCGTCGGTTTCGACAGGTTGGCGAACGCTACTCTGTGATT

CAGGTCGAGAGTGAGTCTCCTCTGCAAATCAAGGCTCAAAACAA

AAGTAAATGCGAATAACATCGTTAAATTTGCTCGTAAGGACGCT

CTAGTAGCTGCCTAAATAGCCTCTTTCAGGTTCGAGCGTCTTCG

GTTTGACTCCGTTAAGGACTGAAGACCAACCCCCAACGGATGCT

CTAGCAATGTTCTCTGGTTGGCTTGCTAGCTAAGATTTAATCAG

AGCATCCTACGTTCGGGATAATGAACGATTCCCGCCTTGAGGGT

CAGAAAGGCTAAACCTGTGAATGAGCGGGGGGTCAATACCCAAT

TTGGACAGCAGTTCGACTCTGCTCGATCCACCA

Nostoc muscorum PCC7120 tmRNA

SEQ ID NO: 90

GGGUCCGUCGGUUUCGACAGGUUGGCGAACGCUACUCUGUGA

UUCAGGUCGAGAGUGAGUCUCCUCUGCAAAUCAAGGCUCAAA

ACAAAAGUAAAUGCGAAUAACAUCGUUAAAUUUGCUCGUAAG

GACGUCUAGUAGCUGCCUAAAUAGCCUCUUUCAGGUUCGAGC

GUCUUCGGULTUGACUCCGUUAAGGACUGAAGACCAACCCCC

AACGGAUGCUCUAGCAAUGUUCUCUGGUUGGCUUGCUAGCUA

AGAUUUAAUCAGAGCAUCCUACGUUCGGGAUAAUGAACGAUU

CCCGCCUUGAGGGUCAGAAAGGCUAAACCUGUGAAUGAGCGG

CGGGGUAAUACCCAAUUUGGACAGCAGUUCGACUCUGCUCGA

UCCACCA

Odontella sinensis (diatom) Chloroplast ssrA

SEQ ID NO: 91

GGGGCTGACTTGGTTTCGACATTTAAAAATTGTTACAGTATGA

TGCAGGTCGAAGTTTCTAATCTTCGTAAAAAAAGAGAAATTTA

TAATAAATGCTAATAATTTAATTTCTTCTGTGTTTAAAAGTTT

ATCAACTAAGCAAAATAGTTTAAATTTAAGTTTTGCTGTTTAA

GTTTTATGCACATTTAATGATCTAGTAAATAACTTTGTTCGCT

ATAATTTATATTTATAACTAGACTTTTGTCTTTITTATAGTTT

AGAATAACTTTATCATTTCAAACCTCGTTCCATCTAGTTGAAC

TAAACCTGTGAACGAATACTATAATAAAATTTTAGATGGACGT

GGGTTCGACTCCCATCAGCTCCACCA

Odontella sinensis (Diatom) Chloroplast tmRNA

SEQ ID NO: 92

GGGGCUGACUUGGUUUCGACALTUUAAAAAUUGUUACAGUAUG

AUGCAGGUCGAAGUUUCUAAUCUUCGUAAAAAAAGAGAAAUTU

UAUAAUAAAUGCUAAUAAUUUAAUUUCUTUCUGUGUUTUAAAA

GUUUAUCAACUAAGCAAAAUAGUTUUAAAUUUAAGUTTUTGGC

UGUUUAAGUUUUAUGCACAUUUAAUGAUCUAGUAAAUAACUUU

GUUCGCUAUAAUUUAUAUUUAUAACUAGACUUUUGUCUUUUUU

AUAGUUUAGAAUAACULTUAUCAUUUCAAACCUCGUTUCCAUC

UAGUUGAACUAAACCUGUGAACGAAUACUAUAAUAAAAUUUTU

UAGAUGGACGUGGGUUCGACUCCCAUCAGCUCCACCA

Porphyra purpureum (Red Alga) Chloroplast ssrA

SEQ ID NO: 93

GGGGCTGCAAGGTTTCTAGATTGTGAAAAAACAAATATATGAAA

GTAAAACGAGCTCATTAITAGAGCTTTTAGTTAAATAAATGCAG

AAAATAATATTATTGCTTTTTCTCGAAAATTAGCTGTTGCATAA

ATAGTCTCAATTTTTGTAATTCGAAGTGATAGACTCTTATACAC

-continued

TACGAATATTCTGTTAGAGTTGCTCTTAATAAAAGAAAAGTAAA

AAAATACAAATTCTTATGTTTTTTACCTGAATTGATTCAATTTA

AGGTTAGTATTTTTTGATTTTTACAATGGACGTGGGTTCAAGTC

CCACCAGCTCCACCA

Porphyra purpureum (Red Alga) Chloroplast tmRNA

SEQ ID NO: 94

GGGGCUGCAAGGUUUCUACAUUGUGAAAAAACAAAUAUAUGA

AAGUAAAACGAGCUCAUUAUUAGAGCUUUUAGUUAAAUAAAU

GCAGAAAAUAAUAUUAUUGCUUUUUCUCGAAAAUUAGCUGUU

GCAUAAAUAGUCUCAAUUUUUGUAAUUCGAAGUGAUAGACUC

UUAUACACUACGAAUAUUCUGUUAGAGUUGCUCUUAAUAAAA

GAAAAGUAAAAAAAUACAAAUUCUUAUGUUUUUUACCUGAAU

UGAUUCAAUUUAAGGUUAGUAUUUUUUGAUUUUUACAAUGGA

CGUGGGUUCAAGUCCCACCAGCUCCACCA

Porphyromonas gingivalis ssrA

SEQ ID NO: 95

GGGGCTGACCGGCTTTGACAGCGTGATGAAGCGGTATGTAAGCA

TGTAGTGCGTGGGTGGCTTGCACTATAATCTCAGACATCAAAAG

TTTAATTGGCGAAAATAACTACGCTCTCGCTGCGTAATCGAAGA

ATAGTAGATTAGACGCTTCATCGCCGCCAAAGTGGCAGCGACGA

GACATCGCCCGAGCAGCTTTTTCCCGAAGTAGCTCGATGGTGCG

GTGCTGACAAATCGGGAACCGCTACAGGATGCTTCCTGCCTGTG

GTCAGATCGAACGGAAGATAAGGATCGTGCATTGGGTCGTTTCA

GCCTCCGCTCGCTCACGAAAATTCCAACTGAAACTAAACATGTA

GAAAGCATATTGATTCCATGTTTGGACGAGGGTTCAATTCCCTC

CAGCTCCACCA

Porphyromonas gingivalis tmRNA

SEQ ID NO: 96

GGGGCUGACCGGCUUUGACAGCGUGAUGAAGCGGUAUGUAAG

CAUGUAGUGCGUGGGUGGCUUGCACUAUAAUCUCAGACAUCA

AAAGUUUAAUUGGCGAAAAUAACUACGCUCUCGCUGCGUAAU

CGAAGAAUAGUAGAUUAGACGCUUCAUCGCCGCCAAAGUGGC

AGCGACGAGACAUCGCCCGAGCAGCUUUUUCCCGAAGUAGCU

CGAUGGUGCGGUGCUGACAAAUCGGGAACCGCUACAGGAUGC

UUCCUGCCUGUGGUCAGAUCGAACGGAAGAUAAGGAUCGUGC

AUUGGGUCGUUUCAGCCUCCGCUCGCUCACGAAAAUUCCAAC

UGAAACUAAACAUGUAGAAAGCAUAUUGAUUCCAUGUUUGGA

CGAGGGUUCAAUUCCCUCCAGCUCCACCA

Proteus rettgeri ssrA (NCTC 10975), Internal Partial

SEQ ID NO: 97

GGGATTTGCGAAACCCAAGGTGCATGCCGAGGGGCGGTTGGCC

TCGTAAAAAGCCGCAAAAAAATAGTCGCAAACGACGAAAACTA

CGCTTTAGCAGCTTAATAACCTGCTTAGAGCCCTCTCTCCCTA

GCCTCCGCTCTTGGACGGGGATCAAGAGAGGTCAAACCCAAAA

GAGATCGCGTGGATGCCTTGCCTGGGGTTGAAGCGTTAAACTT

AATCAGGATAGTTTGTTGGTGGCGTGTCTGTCCGCAGCTGGCA

AAATGATTCAAAGACTAGACTAAGCATGTAGTACCGAGGATGT

AGAAATTTC

Proteus rettgeri tmRNA (NCTC 10975), Internal Partial

SEQ ID NO: 98

GGGAUUUGCGAAACCCAAGGUGCAUGCCGAGGGGCGGUUGGC

CUCGUAAAAAGCCGCAAAAAAAUAGUCGCAAACGACGAAAAC

UACGCUUUAGCAGCUUAAUAACCUGCUUAGAGCCCUCUCUCC

CUAGCCUCCGCUCUUGGACGGGGAUCAAGAGAGGUCAAACCC

AAAAGAGAUCGCGUGGAUGCCUUGCCUGGGGUUGAAGCGUUA

AACUUAAUCAGGAUAGUUUGUUGGUGGCGUGUCUGUCCGCAG

CUGGCAAAUGAAUUCAAAGACUAGACUAAGCAUGUAGUACCG

AGGAUGUAGAAAUUUC

Pseudoalteromonas haloplanktoni ssrA, Internal Partial

SEQ ID NO: 99

GGAATTCAAGAAGCCCGAGGTGCATGTCGAGGTGCGGTTTGCCT

CGTAAAAAAGCCGCAATTTAAAGTAATCGCAAACGACGATAACT

ACTCTCTAGCAGCTTAGGCTGGCTAGCGCTCCTTCCATGTATTC

TTGTGGACTGGATTTTGGAGTGTCACCCTAACACCTGATCGCGA

CGGAAACCCTGGCCGGGGTTGAAGCGTTAAAACTAAGCGGCCTC

GCCTTTATCTACCGTGTTTGTCCGGGATTTAAAGGTTAATTAAA

TGACAATACTAAACATGTAGTACCGACGGTCGAGGCTTTTCGGA

CGGGG

Pseudoalteromonas haloplanktoni tmRNA, Internal Partial

SEQ ID NO: 100

GGAAUUCAAGAAGCCCGAGGUGCAUGUCGAGGUGCGGUUUGC

CUCGUAAAAAAGCCGCAAUUUAAAGUAAUCGCAAACGACGAU

AACUACUCUCUAGCAGCUUAGGCUGGCUAGCGCUCCUUCCAU

GUAUUCUUGUGGACUGGAUUUUGGAGUGUCACCCUAACACCU

GAUCGCGACGGAAACCCUGGCCGGGGUUGAAGCGUUAAAACU

AAGCGGCCUCGCCUUUAUCUACCGUGUUUGUCCGGGAUUUAA

AGGUUAAUUAAAUGACAAUACUAAACAUGUAGUACCGACGGU

CGAGGCUUUUCGGACGGGG

Pseudomonas aeruginosa ssrA

SEQ ID NO: 101

GGGGCCGATTAGGATTCGACGCCGGTAACAAAAGTTGAGGGGCA

TGCCGAGTTGGTAGCAGAACTCGTAAATTCGCTGCTGCAAACTT

ATAGTTGCCAACGACGACAACTACGCTCTAGCTGCTTAATGCGG

CTAGCAGTCGCTAGGGGATGCCTGTAAACCCGAAACGACTGTCA

GATAGAACAGGATCGCCGCCAAGTTCGCTGTAGACGTAACGGCT

AAAACTCATACAGCTCGCTCCAAGCACCCTGCCACTCGGGCGGC

GCGGAGTTAACTCAGTAGAGCTGGCTAAGCATGTAAAACCGATA

GCGGAAAGCTGGCGGACGGGGGTTCAAATCCCCCCGGTTCCACC

A

Pseudomonas aeruginosa tmRNA

SEQ ID NO: 102

GGGGCCGAUUAGGAUUCGACGCCGGUAACAAAAGUUGAGGGGCA

UGCCGAGUUGGUAGCAGAACUCGUAAAUUCGCUGCUGCAAACUU

AUAGUUGCCAACGACGACAACUACGCUCUAGCUGCUUAAUGCGG

CUAGCAGUCGCUAGGGGAUGCCUGUAAACCCGAAACGACUGUCA

GAUAGAAGAGGAUCGCCGCCAAGUUCGCUGUAGACGUAACGGCU

AAAACUCAUACAGCUCGCUCCKAGCACCCUGCCACUCGGGCGGC

GCGGAGUUAACUCAGUAGAGCUGGCUAAGCAUGUAAAACCGAUA

GCGGAAAGCUGGCGGACGGGGGUUCAAAUCCCCCCGGUUCCACC

A

Salmonella typhimurium ssrA

SEQ ID NO: 103

GGGGCTGATTCTGGATTCGACGGGATTTGCGAAACCCAAGGTGC

ATGCCGAGGGGCGGTTGGCCTCGTAAAAAGCCGCAAAAAAATAG

TCGCAAACGACGAAACCTACGCTTTAGCAGCTTAATAACCTGCT

TAGAGCCCTCTCTCCCTAGCCTCCGCTCTTAGGACGGGGATCAA

GAGAGGTCAAACCCAAAAGAGATCGCGCGGATGCCCTGCCTGGG

GTTGAAGCGTTAAAACGAATCAGGCTAGTCTGGTAGTGGCGTGT

CCGTCCGCAGGTGCCAGGCGAATGTAAAGACTGACTAAGCATGT

AGTACCGAGGATGTAGGAATTTCGGACGCGGGTTCAACTCCCGC

CAGCTCCACCA

Salmonella typhimurium tmRNA

SEQ ID NO: 104

GGGGCUGAUUCUGGAUUCGACGGGAUUUGCGAAACCCAAGGUGC

AUGCCGAGGGGCGGUUGGCCUCGUAAAAAGCCGCAAAAAAAUAG

UCGCAAACGACGAAACCUACGCUUUAGCAGCUUAAUAACCUGCU

UAGAGCCCUCUCUCCCUAGCCUCCGCUCUUAGGACGGGGAUCAA

GAGAGGUCAAACCCAAAAGAGAUCGCGCGGAUGCCCUGCCUGGG

GUUGAAGCGUUAAAACGAAUCAGGCUAGUCUGGUAGUGGCGUGU

-continued

CCGUCCGCAGGUGCCAGGCGAAUGUAAAGACUGACUAAGCAUGU

AGUACCGAGGAUGUAGGAAUUUCGGACGCGGGUUCAACUCCCGC

CAGCUCCACCA

Shewanella putrefaciens ssrA

SEQ ID NO: 105

GGGGGCGATTCTGGATTCGACAGGATTCACGAAACCCTGGGAGC

ATGCCGAGGGGCGGTTGGCCTCGTAAAAAGCCGCAAAGTTATAG

TTGCAAACGACGATAACTACGCTCTAGCCGCTTAATGCCGCTAG

CCATCTACCACACGCTTTGCACATGGGCAGTGGATTTGATGGTC

ATCTCACATCGTGCTAGCGAGGGAACCCTGTCTGGGGGTGAACC

GCGAAACAGTACCGGACTCACCGTGTGGGATCCTGTCTTTCGGA

GTTCAAACGGTTAAACAATAGAAAGACTAAGCATGTAGCGCCTT

GGATGTAGGTTTTCTGGACGCGGGTTCAAGTCCCGCCGCCTCCA

CCA

Shewanella putrefaciens tmRNA

SEQ ID NO: 106

GGGGGCGAUUCUGGAUUCGACAGGAUUCACGAAACCCUGGGAGC

AUGCCGAGGGGCGGUUGGCCUCGUAAAAAGCCGCAAAGUUAUAG

UUGCAAACGACGAUAACUACGCUCUAGCCGCUUAAUGCCGCUAG

CCAUCUACCACACGCUUUGCACAUGGGCAGUGGAUUUGAUGGUC

AUCUCACAUCGUGCUAGCGAGGGAACCCUGUCUGGGGGUGAACC

GCGAAACAGUACCGGACUCACCGUGUGGGAUCCUGUCUUUCGGA

GUUCAAACGGUUTAAACAAUAGAAAGACUAAGCAUGUAGCGCCU

UGGAUGUAGGUUUUCUGGACGCGGGUUCAAGUCCCGCCGCCUCC

ACCA

Staphylococcus aureus ssrA

SEQ ID NO: 107

GGGGACGTTCATGGATTCGACAGGGGTCCCCCGAGCTCATTAAG

CGTGTCGGAGGGTTGTCTTCGTCATCAACACACACAGTTTATAA

TAACTGGCAAATCAAACAATAATTTCGCAGTAGCTGCCTAATCG

CACTCTGCATCGCCTAACAGCATTTCCTATGTGCTGTTAACGCG

ATTCAACCTTAATAGGATATGCTAAACACTGCCGTTTGAAGTCT

GTTTAGAAGAAACTTAATCAAACTAGCATCATGTTGGTTGTTTA

TCACTTTTCATGATGCGAAACCTATCGATAAACTACACACGTAG

AAAGATGTGTATCAGGACCTTTGGACGCGGGTTCAAATCCCGCC

GTCTCCACCA

Staphylococcus aureus tmRNA

SEQ ID NO: 108

GGGGACGUUCAUGGAUUCGACAGGGGUCCCCCGAGCUCAUUAAG

CGUGUCGGAGGGUUGUCUUCGUCAUCAACACACACAGUUUAUAA

UAACUGGCAAAUCAAACAAUAAUUUCGCAGUAGCUGCCUAAUCG

-continued

CACUCUGCAUCGCCUAACAGCAUUUCCUAUGUGCUGUUAACGCG

AUUCAACCUUAAUAGGAUAUGCUAAACACUGCCGUUUGAAGUCU

GUUUAGAAGAAACUUAAUCAAACUAGCAUCAUGUUGGUUGUUUA

UCACUUUUCAUGAUGCGAAACCUAUCGAUAAACUACACACGUAG

AAAGAUGUGUAUCAGGACCUUUGGACGCGGGUUCAAAUCCCGCC

GUCUCCACCA

Streptococcus gordonii ssrA

SEQ ID NO: 109

GGGGTCGTTACGGATTCGACAGGCATTATGAGGCATATTTTGCG

ACTCATCTAGCGGATGTAAAACGCCAGTTAAATATAACTGCAAA

AAATAATACTTCTTACGCTTTAGCTGCCTAAAAACCAGCGGGCG

TGACCCGATTCGGATTGCTTGTGTCTGATGACAGGTCTTATTAT

TAGCAAGCTACGGTAGAATCTTGTCTAGTGATTTTACAAGAGAT

TGATAGACTCGCTTGATTTGGGCTTGAGTTATGTGTCAAAATCA

AGTTAAAACAATACATAGCCTATGGTTGTAGACAAATGTGTTGG

CAGATGTTTGGACGTGGGTTCGACTCCCACCGGCTCCACCA

Streptococcus gordonii tmRNA

SEQ ID NO: 110

GGGGUCGUUACGGAUUCGACAGGCAUUAUGAGGCAUAUUUUGCG

ACUCAUCUAGCGGAUGUAAAACGCCAGUUAAAUAUAACUGCAAA

AAAUAAUACUUCUUACGCUUUAGCUGCCUAAAAACCAGCGGGCG

UGACCCGAUUCGGAUUGCUUGUGUCUGAUGACAGGUCUUAUUAU

UAGCAAGCUACGGUAGAAUCUUGUCUAGUGAUUUUACAAGAGAU

UGAUAGACUCGCUUGAUUUGGGCUUGAGUUAUGUGUCAAAAUCA

AGUUAAAACAAUACAUAGCCUAUGGUUGUAGACAAAUGUGUUGG

CAGAUGUUUGGACGUGGGUUCGACUCCCACCGGCUCCACCA

Streptococcus mutans ssrA

SEQ ID NO: 111

GGGGTCGTTACGGATTCGACAGGCATTATGAGACCTATTTTGCG

ACTCATCTAGCGGATGTAAAACGCCAGTTAAATATAACTGCAAA

AAATACAAATTCTTACGCAGTAGCTGCCTAAAAACCAGCCTGTG

TGATCAATAACAAATTGCTTGTGTTTGTTGATTGGTCTTATTGT

TAACAAGCTACGTTAGAACTGAGTCAGGCTGTTCTAAAAGAGTT

CTACTGACTCGCATCGTTAGAGTTTGAGTTATGTATTGTAACGG

TGTTAAATAAACACATAACCTATAGTTGTAGACAAATGGGTTAG

CAGATGTTTGGACGTGGGTTCGACTCCCACCGGCTCCACCA

Streptococcus mutans tmRNA

SEQ ID NO: 112

GGGGUCGUUACGGAUUCGACAGGCAUUAUGAGACCUAUUUUGCG

ACUCAUCUAGCGGAUGUAAAACGCCAGUUAAAUAUAACUGCAAA

-continued

AAAUACAAAUUCUUACGCAGUAGCUGCCUAAAAACCAGCCUGUG

UGAUCAAUAACAAAUUGCUUGUGUUUGUUGAUUGGUCUUAUUGU

UAACAAGCUACGUUAGAACUGAGUCAGGCUGUUCUAAAAGAGUU

CUACUGACUCGCAUCGUUAGAGUUUGAGUUAUGUAUUGUAACGG

UGUUAAAUAAACACAUAACCUAUAGUUGUAGACAAAUGGGUUAG

CAGAUGUUUGGACGUGGGUUCGACUCCCACCGGCUCCACCA

Streptococcus pneumoniae ssrA

SEQ ID NO: 113

GGGGTCGTTACGGATTCGACAGGCATTATGAGGCATATTTTGCG

ACTCGTGTGGCGACGTAAACGCTCAGTTAAATATAACTGCAAAA

AATAACACTTCTTACGCTCTAGCTGCCTAAAAACCAGCAGGCGT

GACCCGATTTGGATTGCTCGTGTTCAATGACAGGTCTTATTATT

AGCGAGATACGATTAAGCCTTGTCTAGCGGTTTGATAAGAGATT

GATAGACTCGCAGTTTCTAGACTTGAGTTATGTGTCGAGGGGCT

GTTAAAATAATACATAACCTATGGTTGTAGACAAATATGTTGGC

AGGTGTTTGGACGTGGGTTCGACTCCCACCGGCTCCACCA

Streptococcus pneumoniae tmRNA

SEQ ID NO: 114

GGGGUCGUUACGGAUUCGACAGGCAUUAUGAGGCAUAUUUUGCG

ACUCGUGUGGCGACGUAAACGCUCAGUUAAAUAUAACUGCAAAA

AAUAACACUUCUUACGCUCUAGCUGCCUAAAAACCAGCAGGCGU

GACCCGAUUUGGAUUGCUCGUGUUCAAUGACAGGUCUUAUUAUU

AGCGAGAUACGAUUAAGCCUUGUCUAGCGGUUUGAUAAGAGAUU

GAUAGACUCGCAGUUUCUAGACUUGAGUUAUGUGUCGAGGGGCU

GUUAAAAUAAUACAUAACCUAUGGUUGUAGACAAAUAUGUUGGC

AGGUGUUUGGACGUGGGUUCGACUCCCACCGGCUCCACCA

Streptococcus pyogenes ssrA

SEQ ID NO: 115

GGGGTTGTTACGGATTCGACAGGCATTATGAGGCATGTTTTGCG

TCCCATCGGCAGATGTAAATTGCCAGTTAAATATAACTGCAAAA

AATACAAACTCTTACGCTTTAGCTGCCTAAAAACCAGCTAGCGT

GACTTCTACAAGATTGCTTGTGTCCTGTTAGAAGTCTCAAAATA

GCAAGCTACGGTTACGAAATTGTCTAGTTTCGTGACAAGAGATT

GATAGACTCGCAAACTAATGGCTTGAGTTATGTGTCTTTAGTTT

GTTAAATGAAGACATAACCTATGGACGTAGACAAATATGTTGGC

AGGTGTTTGGACGTGGGTTCGACTCCCACCAGCTCCACCA

Streptococcus pyogenes tmRNA

SEQ ID NO: 116

GGGGUUGUUACGGAUUCGACAGGCAUUAUGAGGCAUGUUUUGCGUCCCAUC

GGCAGAUGUAAAUUGCCAGUUAAAUAUAACUGCAAAAAAUACAAACUCUUA

-continued

CGCUUUAGCUGCCUAAAAACCAGCUAGCGUGACUUCUACAAGAUUGCUUGU

GUCCUGUUAGAAGUCUCAAAAUAGCAAGCUACGGUUACGAAAUUGUCUAGU

UUCGUGACAAGAGAUUGAUAGACUCGCAAACUAAUGGCUUGAGUUAUGUGU

CUUUAGUUUGUUAAAUGAAGACAUAACCUAUGGACGUAGACAAAUAUGUUG

GCAGGUGUUUGGACGUGGGUUCGACUCCCACCAGCUCCACCA

Synechococcus sp. PCC6301 ssrA

SEQ ID NO: 117

GGGGCTGTAATGGTTTCGACGTGTTGGTGAATCCTTCACCGTGATTCAGGC

CGAGAGGGAGTCCACTCTCGTAAATCCAGGCTCAACCAAAAGTAACTGCGA

ACAACATCGTTCCTTTCGCTCGTAAGGCTGCTCCTGTAGCTGCTTAAACGC

CACAAACTTTCTGGCTCGAGCGTCTAGTCGTAGACTCCGTTAATACGCCTA

GACTTAAACCCCCAACGGATGCTCGAGTGGCGGCCTCAGGTCCGTCCTCTC

GCTAAGCAAAAACCTGAGCATCCCGCCACGGGGATAATCGTTGGCTCCCGC

ACAGTGGGTCAACCGTGCTAAGCCTGTGAACGAGCGGAAAGTTACTAGTCA

ATGCGGACAGCGGTTCGATTCCGCTCAGCTCCACCA

Synechococcus sp. PCC6301 tmRNA

SEQ ID NO: 118

GGGGCUGUAAUGGUUUCGACGUGUUGGUGAAUCCUUCACCGUGAUUCAGGC

CGAGAGGGAGUCCACUCUCGUAAAUCCAGGCUCAACCAAAAGUAACUGCGA

ACAACAUCGUUCCUUUCGCUCGUAAGGCUGCUCCUGUAGCUGCUUAAACGC

CACAAACUUUCUGGCUCGAGCGUCUAGUCGUAGACUCCGUUAAUACGCCUA

GACUUAAACCCCCAACGGAUGCUCGAGUGGCGGCCUCAGGUCCGUCCUCUC

GCUAAGCAAAAACCUGAGCAUCCCGCCAACGGGGAUAAUCGUUGGCUCCCG

CACAGUGGGUCAACCGUGCUAAGCCUGUGAACGAGCGGAAAGUUACUAGUC

AAUGCGGACAGCGGUUCGAUUCCGCUCAGCUCCACCA

Synechocystis sp. PCC6803 ssrA

SEQ ID NO: 119

GGGGCCGCAATGGTTTCGACAGGTTGGCGAAAGCTTGCCCGTGATACAGGT

CGAGAGTGAGTCTCCTCTCGCAAATCAAAGGCTCAAAAAAAAGTAACTGCG

AATAACATCGTCAGCTTCAAACGGGTAGCCATAGCAGCCTAGTCTGTAAAA

GCTACATTTTCTTGTCAAAGACCGTTTACTTCTTTTCTGACTCCGTTAAGG

ATTAGAGGTTAACCCCAACGGATGCTTTGTTTGGCTCTTCTCTAGTTAGCT

AAACAATCAAGACTCAGACTAGAGCATCCCACCATCAGGGATAATCGATGG

TCCCCGTCCTAGGGCTAGAAGGACTAAACCTGTGAATGAGCGGAAAGTTAA

TACCCAGTTTGGACAGCAGTTCAATTCTGCTCGGCTCCACCA

Synechocystis sp. PCC6803 tmRNA

SEQ ID NO: 120

GGGGCCGCAAUGGUUUCGACAGGUUGGCGAAAGCUUGCCCGUGAUACAGGU

CGAGAGUGAGUCUCCUCUCGCAAAUCAAAGGCUCAAAAAAAAGUAACUGCG

-continued

AAUAACAUCGUCAGCUUCAAACGGGUAGCCAUAGCAGCCUAGUCUGUAAAA

GCUACAUUUUCUUGUCAAAGACCGUUUACUUCUUUUCUGACUCCGUUAAGG

AUUAGAGGUUAACCCCAACGGAUGCUUUGUUUGGCUCUUCUCUAGUUAGCU

AAACAAUCAAGACUCAGACUAGAGCAUCCCACCAUCAGGGAUAAUCGAUGG

UCCCCGUCCUAGGGCUAGAAGGACUAAACCUGUGAAUGAGCGGAAAGUUAA

UACCCAGUUUGGACAGCAGUUCAAUUCUGCUCGCUCCACCA

Thermotoga maritima ssrA

SEQ ID NO: 121

GGGGGCGAACGGGTTCGACGGGGATGGAGTCCCCTGGGAAGCGAGCCGAGG

TCCCCACCTCCTCGTAAAAAAGGTGGGACAAAGAATAAGTGCCAACGAACC

TGTTGCTGTTGCCGCTTAATAGATAAGCGGCCGTCCTCTCCGAAGTTGGCT

GGGCTTCGGAAGAGGGCGTGAGAGATCCAGCCTACCGATTCAGCTTCGCCT

TCCGGCCTGAATCGGGAAAACTCAGGAAGGCTGTGGGAGAGGACACCCTGC

CCGTGGGAGGTCCCTCCCGAGAGCGAAAACACGGGCTGCGCTCGGAGAAGC

CCAGGGGCCTCCATCTTCGGACGGGGGTTCGAATCCCCCCGCCTCCACCA

Thermotoga maritima tmRNA

SEQ ID NO: 122

GGGGGCGAACGGGUUCGACGGGGAUGGAGUCCCCUGGGAAGCGAGCCGAGG

UCCCCACCUCCUCGUAAAAAAGGUGGGACAAAGAAUAAGUGCCAACGAACC

UGUUGCUGLTUGCCGCUUAAUAGAUAAGCGGCCGUCCUCUCCGAAGUUGGC

UGGGCUUCGGAAGAGGGCGUGAGAGAUCCAGCCUACCGAUUCAGCUUCGCC

UUCCGGCCUGAAUCGGGAAAACUCAGGAAGGCUGUGGGAGAGGACACCCUG

CCCGUGGGAGGUCCCUCCCGAGAGCGAAAACACGGGCUGCGCUCGGAGAAG

CCCAGGGGCCUCCAUCUUCGGACGGGGGUUCGAAUCCCCCCGCCUCCACCA

Thermus thermophilus ssrA

SEQ ID NO: 123

GGGGGTGAAACGGTCTCGACGGGGGTCGCCGAGGGCGTGGCTGCGCGCCGA

GGTGCGGGTGGCCTCGTAAAAACCCGCAACGGCATAACTGCCAACACCAAC

TACGCTCTCGCGGCTTAATGACCGCGACCTCGCCCGGTAGCCCTGCCGGGG

GCTCACCGGAAGCGGGGACACAAACCCGGCTAGCCCGGGGCCACGCCCTCT

AACCCCGGGCGAAGCTTGAAGGGGGCTCGCTCCTGGCCGCCCGTCCGCGGG

CCAAGCCAGGAGGACACGCGAAACGCGGACTACGCGCGTAGAGGCCCGCCG

TAGAGACCTTCGGACGGGGGTTCGACTCCCCCCACCTCCACCA

Thermus thermophilus tmRNA

SEQ ID NO: 124

GGGGGUGAAACGGUCUCGACGGGGGUCGCCGAGGGCGUGGCUGCGCGCCGA

GGUGCGGGUGGCCUCGUAAAAACCCGCAACGGCAUAACUGCCAACACCAAC

UACGCUCUCGCGGCUUAAUGACCGCGACCUCGCCCGGUAGCCCUGCCGGGG

GCUCACCGGAAGCGGGGACACAAACCCGGCUAGCCCGGGGCCACGCCCUCU

AACCCCGGGCGAAGCUUGAAGGGGGCUCGCUCCUGGCCGCCCGUCCGCGGG

-continued

CCAAGCCAGGAGGACACGCGAAACGCGGACUACGCGCGUAGAGGCCCGCCG

UAGAGACCUUCGGACGGGGGUUCGACUCCCCCCACCUCCACCA

Treponema pallidum ssrA

SEQ ID NO: 125

GGGGATGACTAGGTTTCGACTAGGGATGTGGGGTGTTGCGCTGCAGGTGGA

GTGTCGATCTCCTGATTCGGCGCCTTTATAACTGCCAATTCTGACAGTTTC

GACTACGCGCTCGCCGCGTAATCGCGGGCCTGTGTTTGCGCTGCTCTGAGC

GAACATATCGGCCCGACGCCAAACGGAGCTTGCTCTTACGTTGTGCACGGC

GGACGTAGGGGGACTTTTGTCTGTGCTAAGACTCTGGCGCGTGCGGTGCAG

GCCTAGCAGAGTCCGACAAACGCAGTACGCACCGCTAAACCTGTAGGCGCG

CAGCACTCGCGCTTTAGGACGGGGGTTCGATTCCCCCCATCTCCACCA

Treponema pallidum tmRNA

SEQ ID NO: 126

GGGGAUGACUAGGUUUCGACUAGGGAUGUGGGGUGUUGCGCUGCAGGUGGA

GUGUCGAUCUCCUGAUUCGGCGCCUUUUAUAACUGCCAAUUCUGACAGUUU

CGACUACGCGCUCGCCGCGUAAUCGCGGGCCUGUGUUUGCGCUGCUCUGAG

CGAACAUAUCGGCCCGACGCCAAACGGAGCUUGCUCUUACGUUGUGCACGG

CGGACGUAGGGGGACUUUUGUCUGUGCUAAGACUCUGGCGCGUGCGGUGCA

GGCCUAGCAGAGUCCGACAAACGCAGUACGCACCGCUAAACCUGUAGGCGC

GCAGCACUCGCUCUUUAGGACGGGGGUUCGAUUCCCCCCAUCUCCACCA

Vibrio cholerae ssrA

SEQ ID NO: 127

GGGGCTGATTCAGGATTCGACGGGAATTTTGCAGTCTGAGGTGCATGCCGA

GGTGCGGTAGGCCTCGTTAACAAACCGCAAAAAAATAGTCGCAAACGACGA

AAACTACGCACTAGCAGCTTAATACCCTGCTCAGAGCCCTTCCTCCCTAGC

TTCCGCTTGTAAGACGGGGAAATCAGGAAGGTCAAACCAAATCAAGCTGGC

GTGGATTCCCCCACCTGAGGATGAAGCGCGAGATCTAATTCAGGTTAGCCA

TTAGCGTGTCGGTTCGCAGGCGGTGGTGAAATTAAAGATCGACTAAGCATG

TAGTACCAAAGATGAATGGTTTTCGGACGGGGGTTCAACTCCCCCCAGCTC

CACCA

Vibrio cholerae tmRNA

SEQ ID NO: 128

GGGGCUGAUUCAGGAUUCGACGGGAAUUUUGCAGUCUGAGGUGCAUGCCGA

GGUGCGGUAGGCCUCGUUAACAAACCGCAAAAAAAUAGUCGCAAACGACGA

AAACUACGCACUAGCAGCUUAAUACCCUGCUCAGAGCCCUUCCUCCCUAGC

UUCCGCUUGUAAGACGGGGAAAUCAGGAAGGUCAAACCAAAUCAAGCUGGC

GUGGAUUCCCCCACCUGAGGGAUGAAGCGCGAGAUCUAAUUCAGGUUAGCC

AUUCGUUAGCGUGUCGGUUCGCAGGCGGUGGUGAAAUUAAAGAUCGACUAA

GCAUGUAGUACCAAAGAUGAAUGGUUUUCGGACGGGGGUUCAACUCCCCCC

AGCUCCACCA

Yersinia pestis ssrA

SEQ ID NO: 129

GGGGCTGATTCTGGATTCGACGGGATTCGCGAAACCCAAGGTGCATGCCGA

GGTGCGGTGGCCTCGTAAAAAACCGCAAAAAAAATAGTTGCAAACGACGAA

AACTACGCACTAGCAGCTTAATAACCTGCTTAGAGCCCTCTCTGCCTAGCC

TCCGCTCTTAGGACGGGGATCAAGAGAGGTCAAACCTAAAAGAGCTCGTGT

GGAAACCTTGCCTGGGGTGGAAGCATTAAAACTAATSAGGATAGTTTGTCA

GTAGCGTGTCCATCCGCAGCTGGCCGGCGAATGTAATGATTGGACTAAGCA

TGTAGTGCCGACGGTGTAGTAATTTCGGACGGGGGTTCAAATCCCCCCAGC

TCCACCA

Yersinia pestis tmRNA

SEQ ID NO: 130

GGGGCUGAUUCUGGAUUCGACGGGAUUCGCGAAACCCAAGGUGCAUGCCGA

GGUGCGGUGGCCUCGUAAAAAACCGCAAAAAAAAUAGUUGCAAACGACGAA

AACUACGCACUAGCAGCUUAAUAACCUGCUUAGAGCCCUCUCUGCCUAGCC

UCCGCUCUUAGGACGGGGAUCAAGAGAGGUCAAACCUAAAAGAGCUCGUGU

GGAAACCUUGCCUGGGGUGGAAGCAUUAAAACUAAUCAGGAUAGUUUGUCA

GUAGCGUGUCCAUCCGCAGCUGGCCGGCGAAUGUAAUGAUUGGACUAAGCA

UGUAGUGCCGACGGUGUAGUAAUUUCGGACGGGGGUUCAAAUCCCCCCAGC

UCCACCA

Campylobacter fetus ssrA, Internal Partial

SEQ ID NO: 131

AGGAGTAAGTCTGCTTAGATGGCATGTCGCTTTGGGCAAAGCGTAAAAAGC

CCAAATAAAATTAAACGCAAACAACGTTAAATTCGCTCCTGCTTACGCTAA

AGCTGCGTAAGTTCAGTTGAGCCTGAAATTTAAGTCATACTATCTAGCTTA

ATTTTCGGTCATCTTTGATAGTGTAGCCTTGCGTTTGACAAGCGTTGAGGT

GAAATAAAGTCTTAGCCTTGCTTTTGAGTTTTGGAAGATGAGCGAAGTAGG

GTGAAGTAGTCATCTTTGCTAAGCATGTAGAGGTCTTTGTGGGATTATTTT

TGG

Campylobacter fetus tmRNA, Internal Partial

SEQ ID NO: 132

AGGAGUAAGUCUGCUUAGAUGGCAUGUCGCUUUGGGCAAAGCGUAAAAAGC

CCAAAUAAAAUUAAACGCAAACAACGUUAAAUUCGCUCCUGCUUACGCUAA

AGCUGCGUAAGUUCAGUUGAGCCUGAAAUUUAAGUCAUACUAUCUAGCUUA

AUUUUCGGUCAUCUUTGAUAGUGUAGCCUUGCGUUUGACAAGCGUUUGAG

GUGAAAUAAAGUCUUAGCCUUGCUUUUGAGUUUUGGAAGAUGAGCGAAGUA

GGGUGAAGUAGUCAUCUUUGCUAAGCAUGUAGAGGUCUUUGUGGGAUUAUU

UUUGG

Campylobacter coli (BM2509) ssrA, Internal Partial

SEQ ID NO: 133

AGGAGTAAGTCTGCTTAGATGGCATGTCGCTTTGGACAAAGCGTAAAAAGT
CCAAATTAAAATTAAACGCAAATAACGTTAAATTTGCTCCTGCTTACGCTA
AAGCTGCGTAAGTTCAGTTGAGCCCGAAACTCAAGTGATGCTATCTAGCTT
GAATTTTGGTCATCTTTGATAGTGTAGATTGAAAATTGACAACTTTTAATC
GAAGTTAAAGTCTTAGTCTAGCTTGAAATTTTGGAAGGTGAGTTTAGCCAG
ATGAAGTTTTCACCTTTGCTAAACATGTAGAAGTCTTTGTGGGGTTATTTT
TGG

Campylobacter coli (BM2509) tmRNA, Internal Partial

SEQ ID NO: 134

AGGAGUAAGUCUGCUUAGAUGGCAUGUCGCUUUGGACAAAGCGUAAAAAG
UCCAAAUUAAAAUUAAACGCAAAUAACGUUAAAUUUGCUCCUGCUUACGCU
AAAGCUGCGUAAGUUCAGUUGAGCCCGAAACUCAAGUGAUGCUAUCUAGCU
UGAAUUUUGGUCAUCUUUGAUAGUGUAGAUUGAAAAUUGACAACUUUUAAU
CGAAGUUAAAGUCUUAGUCUAGCUUGAAAUUUUGGAAGGUGAGUUUAGCCA
GAUGAAGUUUUCACCUUUGCUAAACAUGUAGAAGUCUUUGUGGGGUUAUUU
UUGG

Camplyobacter Chicken Isolate ssrA, Internal Partial

SEQ ID NO: 135

ACAGGAGTAAGTCTGCTTAGATGGCATGTCGCTTTGGGCAAAGCGTAAAAA
GCCCAAATAAAATTAAACGCAAACAACGTTAAATTCGCTCCTGCTTACGCT
AAAGCTGCGTAAGTTCAGTTGAGCCTGAAATTTAAGTCATACTATCTAGCT
TAATTTTCGGTCATTTTTGATAGTGTAGCCTTGCGTTTGACAAGCGTTGAG
GTGAAATAAGGTCTTAGCCTTGCTTTTGAGTTTTGGAAGATGAGCGAAGTA
GGGTGAAGTAGTCATCTTTGCTAAGCATGTAGAGGTCTTTGTGGGATTATT
TTTGG

Camplyobacter Chicken Isolate tmRNA, Internal Partial

SEQ ID NO: 136

ACAGGAGUAAGUCUGCUUAGAUGGCAUGUCGCUUUGGGCAAAGCGUAAAAA
GCCCAAAUAAAAUUAAACGCAAACAACGUUAAAUUCGCUCCUGCUUACGCU
AAAGCUGCGUAAGUUCAGUUGAGCCUGAAAUUUAAGUCAUACUAUCUAGCU
UAAUUUTUCGGUCAUUUUUGAUAGUGUAGCCUUGCGUUUGACAAGCGUUGA
GGUGAAAUAAGGUCUUAGCCUUGCUUUUGAGUUUUUGGAAGAUGAGCGAAG
UAGGGUGAAGUAGUCAUCUUUGCUAAGCAUGUAGAGGUCUUUGUGGGAUUA
UUUUUGG

Clostridium perfringens ssrA, Internal Partial

SEQ ID NO: 137

ACGGGGGTAGGATGGGTTTGATAAGCGAGTCGAGGGAAGCATGGTGCCTCG
ATAATAAAGTATGCATTAAAGATAAACGCACGAGATAATTTTGCATTAGCA

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GCTTAAGTTAGCGCTGCTCATCCTTCCTCAATTGCCCACGGTTGAGAGTAA
GGGTGTCATTTAAAAGTGGGGAACCGAGCCTAGCAAAGCTTTGAGCTAGGA
ACGGAATTTATGAAGCTTACCAAAGAGGAAGTTTGTCTGTGGACGTTCTCT
GAGGGAATTTTAAAACACAAGACTACACTCGTAGAAAGTCTTACTGGTCTG
CTTTCGG

Clostridium perfringens tmRNA, Internal Partial

SEQ ID NO: 138

ACGGGGGUAGGAUGGGUUUGAUAAGCGAGUCGAGGGAAGCAUGGUGCCUCG
AUAAUAAAGUAUGCAUUAAAGAUAAACGCACGAGAUAAUUUUGCAUUAGCA
GCUUAAGUUAGCGCUGCUCAUCCUUCCUCAAUUGCCCACGGUUGAGAGUAA
GGGUGUCAUUUAAAAGUGGGGAACCGAGCCUAGCAAAGCUUUGAGCUAGGA
ACGGAAUUUAUGAAGCUUACCAAAGAGGAAGUUUGUCUGUGGACGUUCUCU
GAGGGAAUUUUAAAACACAAGACUACACUCGUAGAAAGUCUUACUGGUCUG
CUUUCGG

Haemophilus ducreyi (NCTC 10945) ssrA, Internal Partial

SEQ ID NO: 139

ACGGGATTAGCGAAGTCCAAGGTGCACGTCGAGGTGCGGTAGGCCTCGTAA
CAAACCGCAAAAAAATAGTCGCAAACGACGAACAATACGCTTTAGCAGCTT
AATAACCTGCATTTAGCCTTCGCGCCCTAGCTTTCGCTCGTAAGACGGGGA
GCACGCGGAGTCAAACCAAAACGAGATCGTGTGGACGCTTCCGCTTGTAGA
TGAAACACTAAATTGAATCAAGCTAGTTTATTTCTTGCGTGTCTGTCCGCT
GGAGATAAGCGAAATTAAAGACCAGACTAAACGTGTAGTACTGAAGATAGA
GTAATTTCGGACCCGGGTTCGACTC

Haemophilus ducreyi (NCTC 10945) tmRNA, Internal Partial

SEQ ID NO: 140

ACGGGAUUAGCGAAGUCCAAGGUGCACGUCGAGGUGCGGUAGGCCUCGUAA
CAAACCGCAAAAAAAUAGUCGCAAACGACGAACAAUACGCUUUAGCAGCUU
AAUAACCUGCAUUUAGCCUUCGCGCCCUAGCUUUCGCUCGUAAGACGGGG
AGCACGCGGAGUCAAACCAAAACGAGAUCGUGUGGACGCUUCCGCUUGUAG
AUGAAACACUAAAUUGAAUCAAGCUAGUUUAUUUCUUUGCGUGUCUGUCCG
CUGGAGAUAAGCGAAAUUAAAGACCAGACUAAACGUGUAGUACUGAAGAUA
UAGUAAUUUCGGACCCGGGUUCGACUC

Listeria innocua (Food Isolate #1) ssrA, Internal Partial

SEQ ID NO: 141

GGCAAAGAAAAACAAAACCTAGCTTTCGCTGCCTAATAACCAGTAGCATAG
CTGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGT
GGGCTACACTAGTTAATCTCCGTCTGAGGTAAATAGAAGAGCTTAATCAGA
CTAGCTGAATGGAAGCCTGTTACCGGGCTGATGTTTATGCGAAATGCTAAT
ACGGTGACTACGCTCGTAGATATTCAA

Listeria innocua (Food Isolate #1) tmRNA, Internal Partial

SEQ ID NO: 142

GGCAAAGAAAAACAAAACCUAGCUUUCGCUGCCUAAUAACCAGUAGCAUAG

CUGAUCCUCCGUGCAUCGCCCAUGUGCUACGGUAAGGGUCUCACUCUAAGU

GGGCUACACUAGUUAAUCUCCGUCUGAGGUUAAAUAGAAGAGCUUAAUCAG

ACUAGCUGAAUGGAAGCCUGUUACCGGGCUGAUGUUUAUGCGAAAUGCUAA

UACGGUGACUACGCUCGUAGAUAUUCAA

Listeria innocua (Food Isolate #2) ssrA, Internal Partial

SEQ ID NO: 143

GGCAAAGAAAAACAAAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAG

CTGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGT

GGGCTACACTAGTTAATCTCCGTCTGAGGTTAAATAGAAGAGCTTAATCAG

ACTAGCTGAATGGAAGCCTGTTACCGGGCCGATGTTTATGCGAAATGCTAA

TACGGTGACTACGCTCGTAGATATTTAA

Listeria innocua (Food Isolate #2) tmRNA, Internal Partial

SEQ ID NO: 144

GGCAAAGAAAAACAAAACCUAGCUUUCGCUGCCUAAUAAGCAGUAGCAUAG

CUGAUCCUCCGUGCAUCGCCCAUGUGCUACGGUAAGGGUCUCACUCUAAGU

GGGCUACACUAGUUAAUCUCCGUCUGAGGUUAAAUAGAAGAGCUUAAUCAG

ACUAGCUGAAUGGAAGCC

Listeria innocua (Food Isolate #3) ssrA, Internal Partial

SEQ ID NO: 145

GGCAAAGAAAAACAAAACCTAGCTTTCGCTGCCTAATAAGCAGTAGAATAG

CTGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTCTAAGT

GGGCTACACTAGTTAATCTCCGTCTGAGGTTAAATAGAAGAGCTTAATCGG

ACTAGCTGAATGGAAGCCTGTTACCGGGCCGATGTTTATGCGAAATGCTAA

TACGGTGACTACGCTCGTAGATATTTAA

Listeria innocua (Food Isolate #3) tmRNA, Internal Partial

GGCAAAGAAAAACAAAACCUAGCUUUCGCUGCCUAAUAAGCAG

UAGAAUAGCUGAUCCUCCGUGCAUCGCCCAUGUGCUACGGUAA

GGGUCUCACUCUAAGUGGGCUACACUAGUUAAUCUCCGUCUGA

GGUUAAAUAGAAGAGCUUAAUCGGACUAGCUGAAUGGAAGCC

UGUUACCGGGCCGAUGUUUAUGCGAAAUGCUAAUACGGUGAC

UACGCUCGUAGAUAUUUAA SEQ ID NO: 146

Listeria innocua (ATCC 12210) ssrA, Internal Partial

GGCAAAGAAAAACAAAACCTAGCCGCTGCCTAATAAGCAGT

AGCATAGCTGATCCTCCGTGCATCGCCCATGTGCTACGGTAAGG

GTCTCACTCTAAGTGGGCTACACTAGTTAATCTCCGTCTGGGGTT

AAATAGAAGAGCTTAATCAGACTAGCTGAATGGAAGCCTGTTAC

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TGGGCCGATGTTTATGCGAAATGCTAATACGGTGACTACGCTCG

TAGATATTTA SEQ ID NO: 147

Listeria innocua (ATCC 12210) tmRNA, Internal Partial

GGCAAAGAAAAACAAAACCUAGCUUUCGCUGCCUAAUAAGCAG

UAGCAUAGCUGAUCCUCCGUGCAUCGCCCAUGUGCUACGGUAA

GGGUCUCACUCUAAGUGGGCUACACUAGUUAAUCUCCGUCUGG

GGUUAAAUAGAAGAGCUUAAUCAGACUAGCUGAAUGGAAGCC

UGUUACUGGGCCGAUGUUUAUGCGAAAUGCUAAUACGGUGAC

UACGCUCGUAGAUAUUUAA SEQ ID NO: 148

Listeria ivanovii (NCTC 11846) ssrA, Internal Partial

ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGATCGTCC

TCGTTATTAACGTCAAAGCCAATAATAACTGGCAAAGAAAAACA

AAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT

CCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTTTAAGTGG

GCTACACTAAATAATCTCCGTCTGGGGTTAGTTAGAAGAGCTTA

ATCAGACTAGCTGAATGGAAGCCTGTTACCGGGCTGATGTTTAT

GCGAAATGCTAATACGGTGACTACGCTCGTAGATATTTAAGTGC

CGATATTTCTGG SEQ ID NO: 149

Listeria ivanovii (NCTC 11846) tmRNA, Internal Partial

ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGGAUCGU

CCUCGUUAUUAACGUCAAAGCCAAUAAUAACUGGCAAAGAAA

AACAAAACCUAGCUUUCGCUGCCUAAUAAGCAGUAGCAUAGCU

GAUCCUCCGUGCAUCGCCCAUGUGCUACGGUAAGGGUCUCACU

UUAAGUGGGCUACACUAAAUAAUCUCCGUCUGGGGUUAGUUA

GAAGAGCUUAAUCAGACUAGCUGAAUGGAAGCCUGUUACCGG

GCUGAUGUUUAUGCGAAAUGCUAAUACGGUGACUCGCUCGUA

GAUAUUUAAGUGCCGAUAUUUCUGG SEQ ID NO: 150

Listeria seeligeri (NCTC 11856) ssrA, Internal Partial

ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGATCGTCC

TCGTTATCAACGTCAAAGCCAATAATAACTGGCAAAGAAAAACA

AAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT

CCGTGCATCGCCCATGTGCTACGGAAAGGGTCTCACTTTAAGTG

GGCTACACTAAATAATCTCCGTCTGGGGTTAGTTAGAAGAGCTT

AATCAGACTAGCTGAATGGAAGCCTUTTACCGGGCTGATGTTTA

TGCGAAATACTAATACGGTGACTACGCTCGTAGATATTTAAGTG

CCCATATTTCTGG SEQ ID NO: 151

Listeria seeligeri (NCTC 11856) tmRNA, Internal Partial

ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGGAUCGU
CCUCGUUAUCAACGUCAAAGCCAAUAAUAACUGGCAAAGAAAA
ACAAAACCUAGCUUUCGCUGCCUAAUAAGCAGUAGCAUAGCUG
AUCCUCCGUGCAUCGCCCAUGUGCUACGGAAAGGGUCUCACUU
UAAGUGGGCUACACUAAAUAAUCUCCGUCUGGGGUUAGUUAG
AAGAGCUUAAUCAGACUAGCUGAAUGGAAGCCUGUUACCGGG
CUGAUGUUUAUGCGAAAUACUAAUACGGUGACUACGCUCGUA
GAUAUUUAAGUGCCCAUAUUUCUGG SEQ ID NO: 152

Salmonella enteritidis ssrA, Internal Partial

ACGGGATTTGCGAAACCCAAGGTGCATGCCGAGGGGCGGTTGGC
CTCGTAAAAAGCCGCAAAAAAATAGTCGCAAACGACGAAACCT
ACGCTTTAGCAGCTTAATAACCTGCTTAGAGCCCTCTCTCCCTAG
CCTCCGCTCTTAGGACGGGGATCAAGAGAGGTCAAACCCAAAAG
AGATCGCGTGGATGCCCTGCCTGGGGTTGAAGCGTTAAAACGAA
TCAGGCTAGTCTGGTAGTGGCGTGTCCGTCCGCAGGTGCCAGGC
GAATGTAAAGACTGACTAAGCATGTAGTACCGAGGATGTAGGAA
TTTCGG SEQ ID NO: 153

Salmonella enteritidis tmRNA, Internal Partial

ACGGGAUUUGCGAAACCCAAGGUGCAUGCCGAGGGGCGGUUG
GCCUCGUAAAAAGCCGCAAAAAAAUAGUCGCAAACGACGAAAC
CUACGCUUUAGCAGCUUAAUAACCUGCUUAGAGCCCUCUCUCC
CUAGCCUCCGCUCUUAGGACGGGGAUCAAGAGAGGUCAAACCC
AAAAGAGAUCGCGUGGAUGCCCUGCCUGGGGUUGAAGCGUUA
AAACGAAUCAGGCUAGUCUGGUAGUGGCGUGUCCGUCCGCAGG
UGCCAGGCGAAUGUAAAGACUGACUAAGCAUGUAGUACCGAG
GAUGUAGGAAUUUCGG SEQ ID NO: 154

Staphylococcus epidermidis (NCTC 11047) ssrA, Internal Partial

ACAGGGGTCCCCCGAGCTTATTAAGCGTGTCGGAGGGTTGGCTC
CGTCATCAACACATTTCGGTTAAATATAACTGACAAATCAAACA
ATAATTTCGCAGTAGCTGCGTAATAGCCACTGCATCGCCTAACA
GCATCTCCTACGTGCTGTTAACGCGATTCAACCCTAGTAGGATAT
GCTAAACACTGCCGCTTGAAGTCTGTTTAGATGAAATATAATCA
HGCTAGTATC+TGTTGGTTGTTTATTGCTTAGCATGATGCGAAAA
TTATCAATAAACTACACACGTAGAAAGATTTGTATCAGGACCTC
TGG SEQ ID NO: 155

Staphylococcus epidermidis (NCTC 11047) tmRNA, Internal Partial

ACAGGGGUCCCCCGAGCUUAUUAAGCGUGUCGGAGGGUUGGCU
CCGUCAUCAACACAUUUCGGUUAAAUAUAACUGACAAAUCAAA
4AAUAAUUUCJ3CAGUAGCUGCGUAAUAGCCACUGCAUCGCCUA
ACAGCAUCUCCUACGUGCUGUUAACGCGAUUCAACCCUAGUAG
GAUAUGCUAAACACUGCCGCUUGAAGUCUGUUUAGAUGAAAU
AUAAUCAAGCUAGUAUCAUGUUGGUUGUUUALnjGCUUAGCAU
GAUGCGAAAAUUAUCAAUAAACUACACACGUAGAAAGAUUUG
UAUCAGGACCUCUGG SEQ ID NO: 156

Streptococcus agalactiae (NCTC 8181) ssrA, Internal Partial

ACAGGCATTATGAGGTATATTTTGCGACTCATCGGCAGATGTAA
AATGCCAGTTAAATATAACTGCAAAAAATACAAATTCTTACGCA
TTAGCTGCCTAAAAAACAGCCTGCGTGATCTTCACAAGATTGTTT
GCGTTTTGCTAGAAGGTCTTATTTATCAGCAAACTACGTTTGGCT
ACTGTCTAGTTAGTTAAAAAGAGATTTATAGACTCGCTATGTGA
GGGCTTGAGTTATGTGTCATCACCTAGTTAAATCAATACATAACC
TATAGTTGTAGACAAATATATTAGCAGATGTTTGG
SEQ ID NO: 157

Streptococcus agalactiae (NCTC 8181) tmRNA, Internal Partial

ACAGGCAUUAUGAGGUAUAUUUUGCGACUCAUCGGCAGAUGU
AAAAUGCCAGUUAAAUAUAACUGCAAAAAAUACAAAUUCUUA
CGCAUUAGCUCCUAAAAAACAGCCUGCGUGAUCUUCACAAGA
UUGUUUGCGUUUUGCUAGAAGGUCUUAUUUAUCAGCAAACUA
CGUUUGGCUACUGUCUAGUUAGUUAAAAAGAGAUUUAUAGAC
UCGCUAUGUGAGGGCUUGAGUUAUGUGUCAUCACCUAGUUAA
AUCAAUACAUAACCUAUAGUUGUAGACAAAUAUAUUAGCAGA
UGUUUGG SEQ ID NO: 158

Bordetella bronchiseptica ssrA

GGGGCCGATCCGGATTCGACGTGGGTCATGAAACAGCTCAAGGC
ATGCCGAGCACCAGTAAGCTCGTTAATCCACTGGAACACTACAA
ACGCCAACGACGAGCGITICGCTCTCGCCGCTTAAGCGGTGAGC
CGCTGCACTGATCTGTCCTTGGGTCACGCGGGGGAA
SEQ ID NO: 159

Bordetella bronchiseptica tmRNA

GGGGCCGAUCCGGAUUCGACGUGGGUCAUGAAACAGCUCAAGGC
AUGCCGAGCACCAGUAAGCUCGUUAAUCCACUGGAACACUACAA

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ACGCCAACGACGAGCGUUUCGCUCUCGCCGCUUAAGCGGUGAGC

CGCUGCACUGAUCUGUCCUUGGGUCACGCGGGGGAA

SEQ ID NO: 160

Chlamydia pneumoniae (CWL029), ssrA

GGGGGTGTATAGGTTTCGACTTGAAAATGAAGTGTTAATTGCAT

GCGGAGGGCGTTGGCTGGCCTCCTAAAAAGCCAACAAAACAATA

AATGCCGAACCTAAGGCTGAATGCGAAATTATTAGCTTGTTTGA

CTCAGTAGAGGAAAGACTAGCTGCTTAATTAGCAAAAGTTGTTA

GCTAGATAATCTCTAGGTAACCCGGTATCTGCGAGCTCCACCAG

AGGCTTGCAAAATACCGTCATTTATCTGGTTGGAACTTACTTTCT

CTAATTCTCAAGGAAGTTCGTTCGAGATTTTTGAGAGTCATTGGC

TGCTATAGAGGCTTCTAGCTAAGGGAGTCCAATGTAAACAATTC

TAGAAGATAAGCATGTAGAGGTTAGCAGGGAGTTTGTCAAGGAC

GAGAGTTCGAGTCTCTCCACCTCCACCA SEQ ID NO: 161

Chlamydia pneumoniae (CWL029) tmRNA

GGGGGUGUAUAGGUUUCGACUUGAAAAUGAAGUGUUAAUUGC

AUGCGGAGGGCGUUGGCUGGCCUCCUAAAAAGCCAACAAAACA

AUAAAUGCCGAACCUAAGGCUGAAUGCGAAAUUAUUAGCUUG

UUUGACUCAGUAGAGGAAAGACUAGCUGCUUAAUUAGCAAAA

GUUGUUAGCUAGAUAAUCUCUAGGUAACCCGGUAUCUGCGAG

CUCCACCAGAGGCUUGCAAAAUACCGUCAUUUAUCUGGUUGGA

ACUUACUUUCUCUAAUUCUCAAGGAAGUUCGUUCGAGAUUUU

UGAGAGUCAUUGGCUGCUAUAGAGGCUUCUAGCUAAGGGAGU

CCAAUGUAAACAAUUCUAGAAGAUAAGCAUGUAGAGGUUAGC

AGGGAGUUUGUCAAGGACGAGAGUUCGAGUCUCUCCACCUCCA

CCA SEQ ID NO: 162

Francisella tularensis ssrA

GGGGGCGAATATGGTTTCGACATGAATGTCAAAATCTAAGGTGC

ATGCCGAGGAAGTACCGTAACCTCGTTAATAACAGTACAAATGC

CAATAATAACTGGCAACAAAAAAGCAAACCGCGTAGCGGCTAA

CGACAGCAACTTTGCTGCTGTTGCTAAAGCTGCCTAGTCTAGCTT

AATAATCTAGATGCGCACGGATATGATAGTCTTTCTTATGACACT

ATCTATACATCCGTTCATATTCCGCATAAGACGGTCTTTGCTTTTT

GTCTGGGAGTTAAGGCTGTATTTAACAGACTCGCTAACTATTACC

CTGGCTAATTGGGGAATAGTCAAGCTAAACTCAAATAGATTAGC

CTAAGCATGTAGATCCAAAGATCTAGAGTTTGTGGACGCGGGTT

CAAATCCCGCCGCCTCCACCA SEQ ID NO: 163

Francisella tularensis tmRNA

GGGGGCGAAUAUGGUUUCGACAUGAAUGUCAAAAUCUAAGGU

GCAUGCCGAGGAAGUACCGUAACCUCGUUAAUAACAGUACAAA

UGCCAAUAAUAACUGGCAACAAAAAAGCAAACCGCGUAGCGGC

UAACGACAGCAACUUUGCUGCUGUUGCUAAAGCUGCCUAGUCU

AGCUUAAUAAUCUAGAUGCGCACGGAUAUGAUAGUCUUUCUU

AUGACACUAUCUAUACAUCCGUUCAUAUUCCGCAUAAGACGGU

CUUUGCUUUUUGUCUGGGAGUUAAGGCUGUAUUUAACAGACU

CGCUAACUAUUACCCUGGCUAAUUGGGGAAUAGUCAAGCUAA

ACUCAAAUAGAUUAGCCUAAGCAUGUAGAUCCAAAGAUCUAG

AGUUUGUGGACGCGGGUUCAAAUCCCGCCGCCUCCACCA

SEQ ID NO: 164

Guillardia theta (Plastid) ssrA

GGGGCTGATTTGGATTCGACATATAAATTTGCGTGTTTCATTATG

AAGCAAGTCAAGTTTAATGATCTTGTAAAAAACATTAAAGTACA

AATAAATGCAAGCAATATAGTTTCATTTAGTTCAAAACGTTTAGT

CTCTTTTGCATAAGCAAAATGTGTTAATAACTTTCTTAGTAGAAA

TTGGAGAAGTTTACTAAGATTTATATTTACTCCATAATTATTTTA

AAGATGGTAAAAAGGTGATTCATCATTTGTATGTTTCTAAACTTT

GTGAAAGAATAGTGGGCTCCATTTATAATGAACGTGGGTTCAAA

TCCCACCAGCTCCACCA SEQ ID NO: 165

Guillardia theta (Plastid) tmRNA

GGGGCUGAUUUGGAUUCGACAUAUAAAUUUGCGUGUUUCAUU

AUGAAGCAAGUCAAGUUUAAUGAUCUUGUAAAAAACAUUAAA

GUACAAAUAAAUGCAAGCAAUAUAGUUUCAUUUAGUUCAAAA

CGUUUAGUCUCUUUUGCAUAAGCAAAAUGUGUUAAUAACUUU

CUUAGUAGAAAUUGGAGAAGUUUACUAAGAUUUAUAUUUACU

CCAUAAUUAUUUUAAAGAUGGUAAAAAGGUGAUUCAUCAUUU

GUAUGUUUCUAAACUUUGUGAAAGAAUAGUGGGCUCCAUUUA

UAAUGAACGUGGGUUCAAAUCCCACCAGCUCCACCA

SEQ ID NO: 166

Thalassiosira Weissflogii (Plastid) ssrA

GGGGCTGATTTGGTTTCGACATTTAAAACTTCTTTCTATGTGTCA

GGTCAAAGTTTGTATTCTTTGTAAAAAAATACTAAAATACTAATA

AATGCTAATAATATAATACCGTTTATTTTTAAAGCAGTAAAAAC

AAAAAAAGAAGCAATGGCTTTAAATTTTGCTGTATAGTTCATTA

ACTTAGGTTATTAAATATTTTTTCATTATAACTGGACTTTTCTCTA

GTTTATAGTTTAGAATAAATTTAAATTTTGCAAAACTCGTTCGAA

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AATTTTCGGGCTAAACCTGTAAACGCAAATACTAAGAAATTTTA
GATGGACATGGGTTCAATTCCCATCAGTTCCACCA
SEQ ID NO: 167

Thalassiosira Weissflogii (Plastid) tmRNA

GGGGCUGAUUUGGUUUCGACAUUUAAAACUUCUUUCUAUGUG
UCAGGUCAAAGUUUGUAUUCUUUGUAAAAAAAUACUAAAAUA
CUAAUAAAUGCUAAUAAUAUAAUACCGUUUAUUUUUAAAGCA
GUAAAAACAAAAAAAGAAGCAAUGGCUUUAAAUUUUGCUGUA
UAGUUCAUUAACUUAGGUUAUUAAAUAUUUUUUCAUUAUAAC
UGGACUUUUCUCUAGUUUAUAGUUUAGAAUAAAUUUAAAUUU
UGCAAAACUCGUUCGAAAAUUUUCGGGCUAAACCUGUAAACGC
AAAUACUAAGAAAUUUUAGAUGGACAUGGGUUCAAUUCCCAU
CAGUUCCACCA SEQ ID NO: 168

Helicobacter pylori ssrA, (Clinical Isolate 1), Internal Partial

TGGGGATGTTACGGTTTCGACAGGGGTAGTTCGAGCTTAGGTGG
CGAGTCGAGGGGATCGGCCTCGTTAAAACGTCAAAGCCTATAAC
TGGCAAACAACAAAACAACTTCGCTTTAGCAGCTTAATAAGCTC
TTAGCGGTTCCTCCCTCCATCGCCCATGTGGTAGGGTAAGGGACT
CAAATTAAGTGGGCTACGCTGGATTCCACCGTCTGAGGATGAAA
GAAGAGAACAACCAGACTAGCTACCCGGACGCCCGTCGATAGG
CAGATGGAGTAGCGAATCGCGAATATATCGACTACACTCGTAGA
AGCTTAAGTGCCGATATTCTTGGACGTGGGTTCGACTCCC
SEQ ID NO: 176

Helicobacter pylori tmRNA, (Clinical Isolate 1), Internal Partial

UGGGGAUGUUACGGUUUCGACAGGGGUAGUUCGAGCUUAGGU
GGCGAGUCGAGGGGAUCGGCCUCGUUAAAACGUCAAAGCCUAU
AACUGGCAAACAACAAAACAACUUCGCUUUAGCAGCUUAAUAA
GCUCUUAGCGGUUCCUCCCUCCAUCGCCCAUGUGGUAGGGUAA
GGGACUCAAAUUAAGUGGGCUACGCUGGAUUCCACCGUCUGAG
GAUGAAAGAAGAGAACAACCAGACUAGCUACCCGGACGCCCGU
CGAUAGGCAGAUGGAGUAGCGAAUCGCGAAUAUAUCGACUAC
ACUCGUAGAAGCUUAAGUGCCGAUAUUCUUGGACGUGGGUUC
GACUCCC SEQ ID NO: 177

Helicobacter pylori ssrA, (Clinical Isolate 2), Internal Partial

TGGGGACGTTACGGTTTCGACAGGGATAGTTCGAGCTTAGGTTG
CGAGTCGAGGGGATCGGCCTCGTTAAAACGTCAAAGCCTATAAT
TGGCAAACAAAACAATCTTTCTTTAGCTGCTTAATTGCACTAAAG
GTTCCTCCCTCCATCGTCCATGTGGTAGGGTAAGGGACTCAAACT
AAGTGGACTACGCCGGAGTTCGCCGTCTGAGGACAAAGGAAGA
GAACAACCAGACTAGCAACTTGGAAGCCTGTCGATAGGCCGAAG
AGTTCGCGAAATGCTAATATATCGACTACACTCGTAGAAGCTTA
AGTGCCGATATTTTTGGACGTGGGTTCGATTCCCT SEQ ID
NO: 178

Helicobacter pylori tmRNA, (Clinical Isolate 2), Internal Partial

UGGGGACGUUACGGUUUCGACAGGGAUAGUUCGAGCUUAGGU
UGCGAGUCGAGGGGAUCGGCCUCGUUAAAACGUCAAAGCCUAU
AAUUGGCAAACAAAACAAUCUUUCUUUAGCUGCUUAAUUGCA
CUAAAGGUUCCUCCCUCCAUCGUCCAUGUGGUAGGGUAAGGGA
CUCAAACUAAGUGGACUACGCCGGAGUUCGCCGUCUGAGGACA
AAGGAAGAGAACAACCAGACUAGCAACUUGGAAGCCUGUCGA
UAGGCCGAAGAGUUCGCGAAAUGCUAAUAUAUCGACUACACUC
GUAGAAGCUUAAGUGCCGAUAUUUUUGGACGUGGGUUCGAUU
CCCU SEQ ID NO: 179

Listeria seeligeri (NCTC 11856) ssrA, Internal Partial

ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGATCGTCC
TCGTTATCAACGTCAAAGCCAATAATAACTGGCAAAGAAAAACA
AAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT
CCGTGCATCGCCCATGTGCTACGGAAAGGGTCTCACTTTAAGTG
GGCTACACTAAATAATCTCCGTCTGGGGTTAGTTAGAAGAGCTT
AATCAGACTAGCTGAATGGAAGCCTGTTACCGGGCTGATGTTTA
TGCGAAATACTAATACGGTGACTACGCTCGTAGATATTTAAGTG
CCCATATTTCTGG SEQ ID NO: 180

Listeria seeligeri (NCTC 11856) tmRNA, Internal Partial

ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGGAUCGU
CCUCGUUAUCAACGUCAAAGCCAAUAAUAACUGGCAAAGAAAA
ACAAAACCUAGCUUUCGCUGCCUAAUAAGCAGUAGCAUAGCUG
AUCCUCCGUGCAUCGCCCAUGUGCUACGGAAAGGGUCUCACUU
UAAGUGGGCUACACUAAAUAAUCUCCGUCUGGGGUUAGUUAG
AAGAGCUUAAUCAGACUAGCUGAAUGGAAGCCUGUUACCGGG
CUGAUGUUUAUGCGAAAUACUAAUACGGUGACUACGCUCGUA
GAUAUUUAAGUGCCCAUAUUUCUGG SEQ ID NO: 181

Listeria ivanovii (NCTC 11846) ssrA, Internal Partial

ACAGGGATAGTTCGAGCTTGAGTTGCGAGTCGGGGGGATCGTCC
TCGTTATTAACGTCAAAGCCAATAATAACTGGCAAAGAAAAACA

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AAACCTAGCTTTCGCTGCCTAATAAGCAGTAGCATAGCTGATCCT

CCGTGCATCGCCCATGTGCTACGGTAAGGGTCTCACTTTAAGTGG

GCTACACTAAATAATCTCCGTCTGGGGTTAGTTAGAAGAGCTTA

ATCAGACTAGCTGAATGGAAGCCTGTTACCGGGCTGATGTTTAT

GCGAAATGCTAATACGGTGACTACGCTCGTAGATATTTAAGTGC

CGATATTTCTGG SEQ ID NO: 182

Listeria ivanovii (NCTC 11846) tmRNA, Internal Partial

ACAGGGAUAGUUCGAGCUUGAGUUGCGAGUCGGGGGGAUCGU

CCUCGUUAUUAACGUCAAAGCCAAUAAUAACUGGCAAAGAAA

AACAAAACCUAGCUUUCGCUGCCUAAUAAGCAGUAGCAUAGCU

GAUCCUCCGUGCAUCGCCCAUGUGCUACGGUAAGGGUCUCACU

UUAAGUGGGCUACACUAAAUAAUCUCCGUCUGGGGUUAGUUA

GAAGAGCUUAAUCAGACUAGCUGAAUGGAAGCCUGUUACCGG

GCUGAUGUUUAUGCGAAAUGCUAAUACGGUGACUCGCUCGUA

GAUAUUUAAGUGCCGAUAUUUCUGG SEQ ID NO: 183

Mycobacterium africanum (Clinical Isolate) ssrA, Internal Partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA

GACCACCGTAAGCGTCGTTGCGACCAAATAAGCGCCGATTCACA

TCAGCGCGACTACGCTCTCGCTGCCTAAGCGACGGCTAGTCTGTC

AGACCGGGAACGCCCTCGGCCCGGACCCTGGCATCAGCTAGAGG

GATCCACCGATGAGTCCGGTCGCGGGACTCCTCGGGACAACCAC

AGCGACTGGGATCGTCATCTCGGCTAGTTCGCGTGACCGGGAGA

TCCGAGCAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGAG

GGAATGCCGTA SEQ ID NO: 184

Mycobacterium africanum (Clinical Isolate) tmRNA, Internal Partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG

AGACCACCGUAAGCGUCGUUGCGACCAAAUAAGCGCCGAUUCA

CAUCAGCGCGACUACGCUCUCGCUGCCUAAGCGACGGCUAGUC

UGUCAGACCGGGAACGCCCUCGGCCCGGACCCUGGCAUCAGCU

AGAGGGAUCCACCGAUGAGUCCGGUCGCGGGACUCCUCGGGAC

AACCACAGCGACUGGGAUCGUCAUCUCGGCUAGUUCGCGUGAC

CGGGAGAUCCGAGCAGAGGCAUAGCGAACUGCGCACGGAGAAG

CCUUGAGGGAAUGCCGUA SEQ ID NO: 185

Mycobacterium gordonae(Clinical Isolate) ssrA, Internal Partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGIGCAGGCAAGA

GACCACCGTAAGCGTCGTTGCAACCATATAAGCGCCGATTCACA

-continued

TCAGCGCGACTACGCTCTCGCTGCCTAAGCGACGGCTAGTCTGTC

GGACCGGGAACGCCCTCGCCCCGGACCCCGGCATCAGCTAGAGG

GATCAACCGATGAGTTCGGTCGCGGGACTCATCGGGACACCAAC

AGCGACTGGGATCGTCATCCTGGCTAGTCCGTGTGACCAGGAGA

TCCGAGCAGAGACATAGCGGACTGCGCACGGAGAAGCCTTGAG

GGAATGCCGTA SEQ ID NO: 186

Mycobacterium gordonae(Clinical Isolate) tmRNA, Internal Partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG

AGACCACCGUAAGCGUCGUUGCAACCAUAUAAGCGCCGAUUCA

CAUCAGCGCGACUACGCUCUCGCUGCCUAAGCGACGGCUAGUC

UGUCGGACCGGGAACGCCCUCGCCCCGGACCCCGGCAUCAGCU

AGAGGGAUCAACCGAUGAGUUCGGUCGCGGGACUCAUCGGGAC

ACCAACAGCGACUGGGAUCGUCAUCCUGGCUAGUCCGUGUGAC

CAGGAGAUCCGAGCAGAGACAUAGCGGACUGCGCACGGAGAAG

CCUUGAGGGAAUGCCGUA SEQ ID NO: 187

Mycobacterium kansasii (Clinical Isolate) ssrA, Internal Partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA

GACCACCGTAAGCGTCGTTGCAACCAAATAAGCGCCGATTCACA

TCAGCGCGACTACGCTCTCGCTGCCTAAGCGACGGCTAGTCTGTC

AGACCGGGACCGCCCTCGACCCGGACTCTGGCATCAGCTAGAGG

GATCAACCGATGAGTTCGGTCGCGGGACTCGTCGGGACACCAAC

AGCGACTGGGATCGTCATCCTGGCTAGTTCGCGTGACCAGGAGA

TCCGAGCAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGAG

GGAATGCCGTA SEQ ID NO: 188

Mycobacterium kansasii (Clinical Isolate) tmRNA, Internal Partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG

AGACCACCGUAAGCGUCGUUGCAACCAAAUAAGCGCCGAUUCA

CAUCAGCGCGACUACGCUCUCGCUGCCUAAGCGACGGCUAGUC

UGUCAGACCGGGACCGCCCUCGACCCGGACUCUGGCAUCAGCU

AGAGGGAUCAACCGAUGAGUUCGGUCGCGGGACUCGUCGGGAC

ACCAACAGCGACUGGGAUCGUCAUCCUGGCUAGUUCGCGUGAC

CAGGAGAUCCGAGCAGAGGCAUAGCGAACUGCGCACGGAGAAG

CCUUGAGGGAAUGCCGUA SEQ ID NO: 189

Mycobacterium chelonae ssrA, Internal Partial

ACAGCGAGTCTCGACTTAAGGGAAGCGTGCCGGTGCAGGCAAG

AGACCACCGTAAGCGTCATTGCAACCAATTAAGCGCCGATTCTC

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ATCAGCGCGACTACGCACTCGCTGCCTAAGCGACTGCGTGTCTG
TCAGACCGGGAGCGCCCTCAGCCCGGACCCTGGCATCAGCTAGA
GGGACAAACTACGGGTTCGGTCGCGGGACCCGTAGGGACATCAA
ACAGCGACTGGGATCGTCATCTCGGCTTGTTCGCGGGACCGAGA
GATCCAAGTAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTA
ATGAACGGCCGTTG SEQ ID NO: 190

Mycobacterium chelonae tmRNA, Internal Partial

ACAGCGAGUCUCGACUUAAGGGAAGCGUGCCGGUGCAGGCAAG
AGACCACCGUAAGCGUCAUUGCAACCAAUUAAGCGCCGAUUCU
CAUCAGCGCGACUACGCACUCGCUGCCUAAGCGACUGCGUGUC
UGUCAGACCGGGAGCGCCCUCAGCCCGGACCCUGGCAUCAGCU
AGAGGGACAAACUACGGGUUCGGUCGCGGGACCCGUAGGGACA
UCAAACAGCGACUGGGAUCGUCAUCUCGGCUUGUUCGCGGGAC
CGAGAGAUCCAAGUAGAGGCAUAGCGAACUGCGCACGGAGAA
GCCUUAAUGAACGGCCGUUG SEQ ID NO: 191

Mycobacterium szulgai (ATCC 35799) ssrA, Internal Partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA
GACCACCGTAAGCGTCGTTGCAACCAATTAAGCGCCGAGAACAC
TCAGCGCGACTTCGCTCTCGCTGCCTAAGCGACAGCAAGTCCGT
CAGACCGGGAAAGCCCTCGACCCGGACCCTGGCGTCATCTAGAG
GGATCCACCGGTGAGTTCGGTCGCGGGACTCATCGGGACACCAA
CAGCGACTGGGATCGTCATCCTGGCTAGTTCGCGTGACCAGGAG
ATCCGAGTAGAGACATAGCGAACTGCGCACGGAGAAGCCTTGA
GGGAATGCCGTAG SEQ ID NO: 192

Mycobacterium szulgai (ATCC 35799) tmRNA, Internal Partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG
AGACCACCGUAAGCGUCGUUGCAACCAAUUAAGCGCCGAGAAC
ACUCAGCGCGACUUCGCUCUCGCUGCCUAAGCGACAGCAAGUC
CGUCAGACCGGGAAAGCCCUCGACCCGGACCCUGGCGUCAUCU
AGAGGGAUCCACCGGUGAGUUCGGUCGCGGGACUCAUCGGGAC
ACCAACAGCGACUGGGAUCGUCAUCCUGGCUAGUUCGCGUGAC
CAGGAGAUCCGAGUAGAGACAUAGCGAACUGCGCACGGAGAA
GCCUUGAGGGAAUGCCGUAG SEQ ID NO: 193

Mycobacterium malmoense (Clinical Isolate) ssrA, Internal Partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA
GACCACCGTAAGCGTCGTTGCAACCATATAAGCGCCGTTTCAAC

-continued

ACAGCGCGACTACGCTCTCGCTGCCTAAGCGACAGCTAGTCCGT
CAGACCGGGAACGCCCTCGACCCGGAGCCTGGCGTCAGCTGGAG
GGATCCACCGGTGAGTCCGGTCGCGGGACTCATCGGGACATACA
CAGCGACTGGGATCGTCATCCTGGCTGGTTCGCGTGACCGGGAG
ATCCGAGCAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGA
GGGAATGCCGTAG SEQ ID NO: 194

Mycobacterium malmoense (Clinical Isolate) tmRNA, Internal Partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG
AGACCACCGUAAGCGUCGUUGCAACCAUAUAAGCGCCGUUUCA
ACACAGCGCGACUACGCUCUCGCUGCCUAAGCGACAGCUAGUC
CGUCAGACCGGGAACGCCCUCGACCCGGAGCCUGGCGUCAGCU
GGAGGGAUCCACCGGUGAGUCCGGUCGCGGGACUCAUCGGGAC
AUACACAGCGACUGGGAUCGUCAUCCUGGCUGGUUCGCGUGAC
CGGGAGAUCCGAGCAGAGGCAUAGCGAACUGCGCACGGAGAAG
CCUUGAGGGAAUGCCGUAG SEQ ID NO: 195

Mycobacterium flavescens ssrA, Internal Partial

ACTTCGAGCGTCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAG
AGACCACCGTAAGCGTCGTTGCAACCAATTAAGCGCCGATTCCA
ATCAGCGCGACTACGCACTCGCTGCCTAAGCGACTGCGTGTCTG
TCAGCCCGGGAGAGCCCTCGACCCGGTGTCTGGCATCAGCTAGA
GGGATAAACCGGTGGGTCCGGTCGCGGGACTCATCGGGACATCA
AACAGCGACTGGGATCGTCATCCTGACTTGTTCGCGTGATCAGG
AGATCCGAGTAGAGACATAGCGAACTGCGCACGGAGAAGCCTT
GAGGGAACGCCGTAG SEQ ID NO: 196

Mycobacterium flavescens tmRNA, Internal Partial

ACUUCGAGCGUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG
AGACCACCGUAAGCGUCGUUGCAACCAAUUAAGCGCCGAUUCC
AAUCAGCGCGACUACGCACUCGCUGCCUAAGCGACUGCGUGUC
UGUCAGCCCGGGAGAGCCCUCGACCCGGUGUCUGGCAUCAGCU
AGAGGGAUAAACCGGUGGGUCCGGUCGCGGGACUCAUCGGGAC
AUCAAACAGCGACUGGGAUCGUCAUCCUGACUUGUUCGCGUGA
UCAGGAGAUCCGAGUAGAGACAUAGCGAACUGCGCACGGAGA
AGCCUUGAGGGAACGCCGUAG SEQ ID NO: 197

Mycobacterium marinum ssrA, Internal Partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA
GACCACCGTAAGCGTCGATGCAACTAGATAAGCGCCGATTCACA
TCAGCGCGACTACGCTCTCGCTGCCTAAGCGACGGCTAGTCTGTC

-continued

GGACCGGGAACGCCCTCGCCCCGGACCCCGGCATCAGCTAGAGG

GATCAACCGATGAGTTCGGTCGCGGGGCTCATCGGGACATCAAC

AGCGACTGGGATCGTCATCCTGGCTAGTTCGCGTGACCAGGAGA

TCCGAGCAGAGACCTAGCGGACTGCGCACGGAGAAGCCTTGAG

GGAATGCCGTAG SEQ ID NO: 198

Mycobacterium marinum tmRNA, Internal Partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG

AGACCACCGUAAGCGUCGAUGCAACUAGAUAAGCGCCGAUUCA

CAUCAGCGCGACUACGCUCUCGCUGCCUAAGCGACGGCUAGUC

UGUCGGACCGGGAACGCCCUCGCCCCGGACCCCGGCAUCAGCU

AGAGGGAUCAACCGAUGAGUUCGGUCGCGGGGCUCAUCGGGAC

AUCAACAGCGACUGGGAUCGUCAUCCUGGCUAGUUCGCGUGAC

CAGGAGAUCCGAGCAGAGACCUAGCGGACUGCGCACGGAGAAG

CCUUGAGGGAAUGCCGUAG SEQ ID NO: 199

Mycobacterium microti (Environmental Isolate) ssrA, Internal Partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA

GACCACCGTAAGCGTCGTTGCGACCAAATAAGCGCCGATTCACA

TCAGCGCGACTACGCTCTCGCTGCCTAAGCGACGGCTAGTCTGTC

AGACCGGGAACGCCCTCGGCCCGGACCCTGGCATCAGCTAGAGG

GATCCACCGATGAGTCCGGTCGCGGGACTCCTCGGGACAGCCAC

AGCGACTGGGATCGTCATCTCGGCTAGTTCGCGTGACCGGGAGA

TCCGAGCAGAGGCATAGCGAACTGCGCACGGAGAAGCCTTGAG

GGAATGCCGTA SEQ ID NO: 200

Mycobacterium microti (Environmental Isolate) tmRNA, Internal Partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG

AGACCACCGUAAGCGUCGUUGCGACCAAAUAAGCGCCGAUUCA

CAUCAGCGCGACUACGCUCUCGCUGCCUAAGCGACGGCUAGUC

UGUCAGACCGGGAACGCCCUCGGCCCGGACCCUGGCAUCAGCU

AGAGGGAUCCACCGAUGAGUCCGGUCGCGGGACUCCUCGGGAC

AGCCACAGCGACUGGGAUCGUCAUCUCGGCUAGUUCGCGUGAC

CGGGAGAUCCGAGCAGAGGCAUAGCGAACUGCGCACGGAGAAG

CCUUGAGGGAAUGCCGUA SEQ ID NO: 201

Mycobacterium smegmatis (ATCC 10143) ssrA, Internal Partial

ACTTCGAGCATCGAATCCAGGGAAGCGTGCCGGTGCAGGCAAGA

GACCACCGTAAGCGTCGTTGCAACCAATTAAGCGCCGATTCCAA

-continued

TCAGCGCGACTACGCCCTCGCTGCCTAAGCGACGGCTGGTCTGT

CAGACCGGGAGTGCCCTCGGCCCGGATCCTGGCATCAGCTAGAG

GGACCCACCCACGGGTTCGGTCGCGGGACCTGTGGGGACATCAA

ACAGCGACTGGGATCGTCATCTCGGCTTGTTCGTGTGACCGGGA

GATCCGAGTAGAGACATAGCGAACTGCGCACGGAGAAGCCTCG

AGGACATGCCGTAG SEQ ID NO: 202

Mycobacterium smegmatis (ATCC 10143) ssrA, Internal Partial

ACUUCGAGCAUCGAAUCCAGGGAAGCGUGCCGGUGCAGGCAAG

AGACCACCGUAAGCGUCGUUGCAACCAAUUAAGCGCCGAUUCC

AAUCAGCGCGACUACGCCCUCGCUGCCUAAGCGACGGCUGGUC

UGUCAGACCGGGAGUGCCCUCGGCCCGGAUCCUGGCAUCAGCU

AGAGGGACCCACCCACGGGUUCGGUCGCGGGACCUGUGGGGAC

AUCAAACAGCGACUGGGAUCGUCAUCUCGGCUUGUUCGUGUGA

CCGGGAGAUCCGAGUAGAGACAUAGCGAACUGCGCACGGAGAA

GCCUCGAGGACAUGCCGUAG SEQ ID NO: 203

Mycobacterium xenopi (Clinical Isolate) ssrA, Internal Partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAGA

GACCACCGTAAGCGTCGTTGCAACTAAATAAGCGCCGATTCACA

TCAGCGCGACTACGCTCTCGCTGCCTAAGCGACAGCTAGTCCGT

CAGGCCGGGAGTTCCCTCGACCCGGATCCTGGCGTCAGCTAGAG

GGATCCACCGATGGGTTCGGTCGCGGGACCCATCGGGACACCAC

ACAGCGACTGGGATCGCCGTCCCGGCTAGTTCGCGAGACCGGGA

GATCCGAGTAAGGGCAAAGCGAACTGCGCACGGAGAAGCCTTG

AGGGTATGCCGTA SEQ ID NO: 204

Mycobacterium xenopi (Clinical Isolate) tmRNA, Internal Partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG

AGACCACCGUAAGCGUCGUUGCAACUAAAUAAGCGCCGAUUCA

CAUCAGCGCGACUACGCUCUCGCUGCCUAAGCGACAGCUAGUC

CGUCAGGCCGGGAGUUCCCUCGACCCGGAUCCUGGCGUCAGCU

AGAGGGAUCCACCGAUGGGUUCGGUCGCGGGACCCAUCGGGAC

ACCACACAGCGACUGGGAUCGCCGUCCCGGCUAGUUCGCGAGA

CCGGGAGAUCCGAGUAAGGGCAAAGCGAACUGCGCACGGAGAA

GCCUUGAGGGUAUGCCGUA SEQ ID NO: 205

Mycobacterium intracellulare (NCTC 10425) ssrA, Internal Partial

ACTTCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAACC

GACCACCGTAAGCGTCGTTGCAAACAGATAAGCGCCGATTCACA

-continued

TCAGCGCGACTACGCTCTCGCTGCCTAAGCGACAGCTAGTCCGT
CAGACCGGGAACGCCCTCGACCCGGAGCCTGGCGTCAGCTAGAG
GGATCCACCGATGAGTCCGGTCGCGGGACTTATCGGGACACCAA
CAGCGACTGGGATCGTCATCTCGGCTTGTTCGCGTGACCGGGAG
ATCCGAGTAGAGGCATAGCGAACTGCGCACGGAGAAGTCTTGAG
GGAATGCCGTAG SEQ ID NO: 206

Mycobacterium intracellulare (NCTC 10425) tmRNA, Internal Partial

ACUUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAC
CGACCACCGUAAGCGUCGUUGCAAACAGAUAAGCGCCGAUUCA
CAUCAGCGCGACUACGCUCUCGCUGCCUAAGCGACAGCUAGUC
CGUCAGACCGGGAACGCCCUCGACCCGGAGCCUGGCGUCAGCU
AGAGGGAUCCACCGAUGAGUCCGGUCGCGGGACUUAUCGGGAC
ACCAACAGCGACUGGGAUCGUCAUCUCGGCUUGUUCGCGUGAC
CGGGAGAUCCGAGUAGAGGCAUAGCGAACUGCGCACGGAGAA
GUCUUGAGGGAAUGCCGUAG SEQ ID NO: 207

Mycobacterium scrofulaceum (NCTC 10803) ssrA, Internal Partial

ACATCGCGCATCGAATCAAGGGAAGCGTGCCGGTGCAGGCAAG
AGACCACCGTAAGCGTCGTTGCAACCAATTAAGCGCCGATTCAC
ATCAGCGCGACTACGCTCTCGCTGCCTAAGCGACAGCTAGTCCG
TCAGACCGGGAAAGCCCTCGACCCGGAGCCTGGCGTCAGCTAGA
GGGATCAACCGATGAGTTCGGTCGCGGGACTCATCGGGACACCA
ACAGCGACTGGGATCGTCATCCTGGCTAGTCCGCGTGACCAGGA
GATCCGAGCAGAGGCATAGCGGACTGCGCACGGAGAAGTCTTG
AGGGAATGCCGTTG SEQ ID NO: 208

Mycobacterium scrofulaceum (NCTC 10803) tmRNA, Internal Partial

ACAUCGCGCAUCGAAUCAAGGGAAGCGUGCCGGUGCAGGCAAG
AGACCACCGUAAGCGUCGUUGCAACCAAUUAAGCGCCGAUUCA
CAUCAGCGCGACUACGCUCUCGCUGCCUAAGCGACAGCUAGUC
CGUCAGACCGGGAAAGCCCUCGACCCGGAGCCUGGCGUCAGCU
AGAGGGAUCAACCGAUGAGUUCGGUCGCGGGACUCAUCGGGAC
ACCAACAGCGACUGGGAUCGUCAUCCUGGCUAGUCCGCGUGAC
CAGGAGAUCCGAGCAGAGGCAUAGCGGACUGCGCACGGAGAAG
UCUUGAGGGAAUGCCGUUG SEQ ID NO: 209

Nocardia asteroides ssrA, Internal Partial

ACTGTGTGCGCCGAGGTAGGGGAAGCGTGTCGGTGCAGGCTGGA
GACCACCGTTAAGCGTCGCGGCAACCAATTAAGCGCCGATTCCA

-continued

ATCAGCGCGACTACGCCCTCGCTGCCTGATCAGCGACGGCTAGC
TGTCGGCCCGGGTTGTGTTCCCGAACCCGGATGCCGGCATCATCT
CAGGGAACTCACCGTGTTCGCCGGTCGCGGACGGACACGGGACA
GCAAACAGCGACTGGGATCGTCATCTCGGCTTGTTCGCGTGACC
GGGAGATCCAAGTAGAGACATAGCGGACTGCACACGGAGAAGC
CCTACTGACTCGACACAG SEQ ID NO: 210

Nocardia asteroides tmRNA, Internal Partial

ACUGUGUGCGCCGAGGUAGGGGAAGCGUGUCGGUGCAGGCUG
GAGACCACCGUUAAGCGUCGCGGCAACCAAUUAAGCGCCGAUU
CCAAUCAGCGCGACUACGCCCUCGCUGCCUGAUCAGCGACGGC
UAGCUGUCGGCCCGGGUUGUGUUCCCGAACCCGGAUGCCGGCA
UCAUCUCAGGGAACUCACCGUGUUCGCCGGUCGCGGACGGACA
CGGGACAGCAAACAGCGACUGGGAUCGUCAUCUCGGCUUGUUC
GCGUGACCGGGAGAUCCAAGUAGAGACAUAGCGGCUGCACACG
GAGAAGCCCUACUGACUCGACACAG SEQ ID NO: 211

Salmonella enteritidis ssrA, Internal Partial

ACGGGATTTGCGAAACCCAAGGTGCATGCCGAGGGGCGGTTGGC
CTCGTAAAAAGCCGCAAAAAAATAGTCGCAAACGACGAAACCT
ACGCTTTAGCAGCTTAATAACCTGCTTAGAGCCCTCTCTCCCTAG
CCTCCGCTCTTAGGACGGGGATCAAGAGAGGTCAAACCCAAAAG
AGATCGCGTGGATGCCCTGCCTGGGGTTGAAGCGTTAAAACGAA
TCAGGCTAGTCTGGTAGTGGCGTGTCCGTCCGCAGGTGCCAGGC
GAATGTAAAGACTGACTAAGCATGTAGTACCGAGGATGTAGGAA
TTTCGG SEQ ID NO: 212

Salmonella enteritidis tmRNA, Internal Partial

ACGGGAUUUGCGAAACCCAAGGUGCAUGCCGAGGGGCGGUUG
GCCUCGUAAAAAGCCGCAAAAAAAUAGUCGCAAACGACGAAAC
CUACGCUUUAGCAGCUUAAUAACCUGCUUAGAGCCCUCUCUCC
CUAGCCUCCGCUCUUAGGACGGGGAUCAAGAGAGGUCAAACCC
AAAAGAGAUCGCGUGGAUGCCCUGCCUGGGGUUGAAGCGUUA
AAACGAAUCAGGCUAGUCUGGUAGUGGCGUGUCCGUCCGCAGG
UGCCAGGCGAAUGUAAAGACUGACUAAGCAUGUAGUACCGAG
GAUGUAGGAAUUUCGG SEQ ID No: 213

Staphylococcus epidermidis (NCTC 11047) ssrA, Internal Partial

ACAGGGGTCCCCCGAGCTTATTAAGCGTGTCGGAGGGTTGGCTC
CGTCATCAACACATTTCGGTTAAATATAACTGACAAATCAAACA

-continued

ATAATTTCGCAGTAGCTGCGTAATAGCCACTGCATCGCCTAACA

GCATCTCCTACGTGCTGTTAACGCGATTCAACCCTAGTAGGATAT

GCTAAACACTGCCGCTTGAAGTCTGTTTAGATGAAATATAATCA

AGCTAGTATCATGTTGGTTGTTTATTGCTTAGCATGATGCGAAAA

TTATCAATAAACTACACACGTAGAAAGATTTGTATCAGGACCTC

TGG SEQ ID NO: 214

Staphylococcus epidermidis (NCTC 11047) tmRNA, Internal Partial

ACAGGGGUCCCCCGAGCUUAUUAAGCGUGUCGGAGGGUUGGCU

CCGUCAUCAACACAUUUCGGUUAAAUAUAACUGACAAAUCAAA

CAAUAAUUUCGCAGUAGCUGCGUAAUAGCCACUGCAUCGCCUA

ACAGCAUCUCCUACGUGCUGUUAACGCGAUUCAACCCUAGUAG

GAUAUGCUAAACACUGCCGCUUGAAGUCUGUUUAGAUGAAAU

AUAAUCAAGCUAGUAUCAUGUUGGUUGUUUAUUGCUUAGCAU

GAUGCGAAAAUUAUCAAUAAACUACACACGUAGAAAGAUUUG

UAUCAGGACCUCUGG SEQ ID NO: 215

Streptococcus agalactiae (NCTC 8181) ssrA, Internal Partial

ACAGGCATTATGAGGTATATTTTGCGACTCATCGGCAGATGTAA

AATGCCAGTTAAATATAACTGCAAAAAATACAAATTCTTACGCA

TTAGCTGCCTAAAAAACAGCCTGCGTGATCTTCACAAGATTGTTT

GCGTTTTGCTAGAAGGTCTTATTTATCAGCAAACTACGTTTGGCT

ACTGTCTAGTTAGTTAAAAAGAGATTTATAGACTCGCTATGTGA

GGGCTTGAGTTATGTGTCATCACCTAGTTAAATCAATACATAACC

TATAGITGTAGACAAATATATTAGCAGATGTTTGG SEQ ID

NO: 216

Streptococcus agalactiae (NCTC 8181) tmRNA, Internal Partial

ACAGGCAUUAUGAGGUAUAUUUUGCGACUCAUCGGCAGAUGU

AAAAUGCCAGUUAAAUAUAACUGCAAAAAAUACAAAUUCUUA

CGCAUUAGCUGCCUAAAAAACAGCCUGCGUGAUCUUCACAAGA

LTUGUUUGCGUUUUGCUAGAAGGUCUUAUUUAUCAGCAAACUA

CGUUUGGCUACUGUCUAGUUAGUUAAAAAGAGAUUUAUAGAC

UCGCUAUGUGAGGGCUUGAGUUAUGUGUCAUCACCUAGUUAA

AUCAAUACAUAACCUAUAGUUGUAGACAAAUAUAUUAGCAGA

UGUUUGG SEQ ID NO: 217

Of the above sequences SEQ ID NOs 47 to 62, 65 to 68, 71 and 72, and 99, 159 to 168 and 176-217 are novel sequences.

The above mentioned sequences can be used to form a database of ssrA gene sequences which can be used to identify a bacterial species, or for the generation of nucleic acid diagnostic assays.

Representative probes identified in accordance with the invention are as follows:

Salmonella:

1) Genius specific probe:

5'-CGAATCAGGCTAGTCTGGTAG-3' SEQ ID NO: 218

Mycobacteria:

2) Oligonucleotide probe for detection of tuberculosis complex

SEQ ID NO: 219

TB01

5'-ACTCCTCGGACA (A/G) CCACAGCGA-3'

3) Oligonucleotide probes for detection of *M. avium* and *M. paratuberculosis* Sequences

Probe 1:

PAV1-5'-GTTGCAAATAGATAAGCGCC-3' SEQ ID NO: 220

Probe 2:

PAV2-5'-TCCGTCAGCCCGGGAACGCC-3' SEQ ID NO: 221

Listeria:

4) Oligonucleotide probe used in the determination of tmRNA integrity after heat killing treatment of cells:

LVtm: 5'-TTTTGTTTTTCTTTGCCA-3' SEQ ID NO: 222

Escherichia coli:

5) Oligonucleotide probe used in the determination of tmRNA integrity after heat killing treatment of cells:

Evtm: 5'-AGTTTTCGTCGTTTGCGA-3' SEQ ID NO: 223

Further representative primers identified in accordance with the invention are as follows:

Mycobacteria:

1) Degenerative oligonucleotide primers for the amplification of all mycobacterial sequences

5' Primer

SEQ ID NO: 224

10SAAM3-5'-CAGGCAA (G/C) (A/T/C) GACCACCGTAA-3'

3' Primer

SEQ ID NO: 225

10SAAM4-5'GGATCTCC(C/T)G(A/G)TC(A/T)C(A/G)CG

(A/G)AC(A/T)A-3'

2) Oligonucleotide primers for the amplification of *M. avium* and *M. paratuberculosis*

SEQ ID NO: 226

5'Primer: API for-5'-TGCCGGTGCAGGCAACTG-3'

SEQ ID NO: 227

3'Primer: AP2rev-5'-CACGCGAACAAGCCAGGA-3'

BRIEF DESCRIPTION OF THE DRAWINGS

In the accompanying drawings:

FIG. **1** is a clustal alignment of *E. coli* and *V. cholerae* ssrA gene sequences;

FIG. **2** is a photograph of an agarose gel of total cellular RNA prepared from *E. coli* and *V. cholerae* cells;

FIG. **3** is a photograph of an autoradiogram of hybridisation of a *V. cholerae* oligonucleotide probe to tmRNA transcripts of *E. coli* and *V. cholerae;*

FIG. **4** is a photograph of an agarose gel of the amplified products of universal ssrA gene amplification primers from a panel of organisms;

FIG. **5** is a clustal alignment of the ssrA gene sequences from the *Listeria* species;

FIG. **6** is a clustal alignment of the *L. monocytogenes* and *B. subtilus* ssrA/tmRNA gene sequences;

FIG. **7** is a photograph of an agarose gel of the amplified products of *Listeria* genus specific PCR amplification primers from a panel of organisms;

FIG. **8** is a photograph of an autoradiogram of hybridised *Listeria* genus specific oligonucleotide probe to a panel of organisms as prepared in Example 4;

FIG. **9** is a photograph of an autoradiogram of hybridised *L. monocytogenes* species specific probe to a panel of organisms as prepared in Example 7;

FIG. **10** is a computer scanned image of a nylon membrane strip used in the multiple colorimetric probe detection of *Listeria* ssrA gene sequences as described in Example 6.

FIG. **11** is a clustal alignment of ssrA gene sequences from *C. trachomatis* strains;

FIG. **12** is a clustal alignment of ssrA gene sequences from *H. pylori* strains;

FIG. **13** is a clustal alignment of ssrA gene sequences from *M. genitalium* strains;

FIG. **14** is a clustal alignment of ssrA gene sequences from *N. gonorrhoeae* strains;

FIG. **15** is a clustal alignment of ssrA gene sequences from *L. monocytogenes* strains;

FIG. **16** is a clustal alignment of ssrA gene sequences from *L. monocytogenes* strains and the *L. innocua* strain;

FIG. **17** is a photograph of an autoradiogram hybridised *Listeria* oligonucleotide probe (Evtm) to total RNA samples isolated after medium heat treatment of *E. coli* cells;

FIG. **18** is a photograph of an autoradiogram hybridised *Listeria* oligonucleotide probe (Evtm) to total RNA samples isolated after extreme heat treatment of *E. coli* cells;

FIG. **19** is a photograph of an autoradiogram hybridised *Listeria* oligonucleotide probe (Lvtm) to total RNA samples isolated after medium heat treatment of *L. monocytogenes* cells;

FIG. **20** is a photograph of an autoradiogram hybridised *Listeria* oligonucleotide probe (Lvtm) to total RNA samples isolated after extreme heat treatment of *L. monocytogenes* cells; and

FIG. **21** is a photograph of an agarose gel of RT-PCR generated tmRNA products at various time points post heat treatment.

The invention will be further illustrated by the following Examples.

MODES FOR CARRYING OUT THE INVENTION

Example 1

Examination of the Primary Nucleotide Sequences of Available tmRNA Sequences

A comparative primary nucleotide sequence alignment of available tmRNA sequences using the Clustal W nucleic acid alignment programme demonstrated that tmRNA sequences from prokaryotes show a more significant degree of nucleotide sequence variability and non-homology than other bacterial high copy number RNA, as demonstrated in Table 1.

TABLE 1

Percentage nucleotide sequence homology between RNA molecules from different bacteria.

	Escherichia coli vs. *Vibrio cholerae*	*Bacillus subtilus* vs. *Mycobacterium tuberculosis*
rRNA % homology	88	66
tmRNA % homology	68	25

These regions of non-homology between tmRNA sequences from different bacteria are located in the middle of the molecule, and the extent of nucleotide sequence non-homology within the tmRNA molecule indicated that genus as well as species specific probes could be generated to distinguish between and/or detect bacteria.

Nucleotide sequence alignments had previously shown that the 5' and 3' flanking regions of the tmRNA molecules share a high degree of homology both within species and within genus. This observation indicated that universal oligonucleotide primers could be generated to amplify the ssrA gene or its encoding tmRNA from a wide variety of bacteria.

We have now demonstrated that these regions of homology and non-homology within the nucleotide sequence of tmRNA molecules from different organisms can be used as the basis of identifying and detecting organisms at the molecular level.

Example 2

Development of a *V. cholerae* tmRNA Specific Probe

A nucleotide sequence alignment of the *E. coli* (SEQ ID NO. 37) and *V. cholerae* (SEQ ID NO. 127) ssrA sequences as depicted in FIG. **1**, shows that these two bacterial species are phylogenetically closely related. There are however, regions of non-homology between the sequences as evidenced by the absence of asterix marks. An oligonucleotide probe, complementary to the variable region of the *V. cholerae* ssrA nucleotide sequence underlined in FIG. **1**, was synthesised.

The sequence of the *V. cholerae* tmRNA specific probe is

```
                                    SEQ ID NO. 169
            5'-AACGAATGGCTAACCTGAA-3'
```

Total RNA was isolated from liquid cultures of *E. coli* and *V. cholerae* at the mid-exponential phase and the stationary phase of growth. Equivalent amounts of the isolated total RNA were electrophoresed on a denaturing formaldehyde agarose gel and blotted onto HYBOND-N nylon membrane as shown in FIG. **2** in which the Lanes 1-4 represent the following:

Lane 1: Total *E. coli* RNA mid-log phase
Lane 2: Total *V. cholerae* RNA mid-log phase
Lane 3: Total *E. coli* RNA stationary phase
Lane 4: Total *V. cholerae* RNA stationary phase

The resulting Northern blot was then hybridised with the *V. cholerae* tmRNA specific probe end-labelled with γP^{32}. The results of the hybridisation experiment shown in FIG. **3** demonstrate the specificity of the probe as only *V. cholerae* tmRNAs were detected. Moreover, a greater degree of hybridisation signal intensity was observed with the *V. cholerae* tmRNA isolated from cultures during the stationary phase of growth, indicating that a higher copy number of the tmRNA molecule is present in *V. cholerae* cells during this phase.

Example 3

Generation of Universal ssrA/tmRNA Oligonucleotide Amplification Primers for the Characterisation of Unknown ssrA Gene and tmRNA Sequences

Clustal W alignment of all available ssrA gene and tmRNA sequences indicated that degenerate oligonucleotide primers could be designed to amplify ssrA gene and tmRNA nucleotide sequences for a wide variety of organisms.

Degenerate oligonucleotide primers were synthesised to PCR amplify ssrA gene sequences from total genomic DNA preparations from a broad range of bacteria.

The sequences of the synthesised degenerate oligonucleotides are as follows:

(a)	tmU5':	5' in vitro PCR amplification primer 5'- GGG(A/C)(C/T)TACGG(A/T)TTCGAC- 3' SEQ ID NO: 170
(b)	tmU3':	3' in vitro PCR amplification primer 5'- GGGA(A/G)TCGAACC(A/G)(C/G)GTCC- 3' SEQ ID NO: 171

Degenerate base positions are in parentheses.

The products of PCR reactions were electrophoresed on an agarose gel and a 350 base pair (approx.) PCR product was amplified in all cases, as shown in FIG. **4**, demonstrating the "universality" of the degenerate tmRNA primers.

In FIG. **4** the lanes represent the following:

Lane A: Molecular weight marker V
Lane 1: *Escherichia coli*
Lane 2: *Salmonella poona*
Lane 3: *Klebsiella aerogenes*
Lane 4: *Proteus mirabilis*
Lane 5: *Proteus rettgeri*
Lane 6: *Aeromonas hydrophilia*
Lane 7: *Staphyloccus aureus*
Lane 8: *Enterococcus faecalis*
Lane 9: *Lactobacillus lactis*
Lane 10: *Bacillus subtilus*
Lane 11: *Listeria monocytogenes*
Lane 12: *Listeria innocua*
Lane 13: *Listeria murrayi*
Lane 14: *Listeria welshimeri*
Lane 15: *Listeria grayi*
Lane 16: *Mycobacterium bovis*
Lane B: Molecular weight marker V

The universal primers amplified the ssrA gene from both Gram positive and Gram negative bacteria, as shown in Table 2.

TABLE 2

Bacterial species tested with universal amplification primers.

		PCR Product
Gram Negative Bacteria	*Escherichia coli*	+
	Salmonella poona	+
	Klebsiella aerogenes	+
	Proteus mirabilis	+
	Proteus rettgeri	+
	Aeromonas hydrophilia	+
Gram Positive Bacteria	*Staphyloccus aureus*	+
	Enterococcus faecalis	+
	Lactobacillus lactis	+
	Bacillus subtilus	+
	Listeria monocytogenes	+
	Listeria innocua	+
	Listeria murrayi	+
	Listeria welshimeri	+
	Listeria grayi	+
	Mycobacterium bovis	+

Example 4

Isolation and Characterisation of Previously Unknown Bacterial ssrA/tmRNA Nucleotide Sequences

The PCR products amplified from genomic DNA from the *Listeria* species of bacteria and that from the *M. bovis* bacterium, from Example 2, were subcloned into a T-tailed plasmid vector for the purposes of DNA sequencing. Three recombinant clones were selected for each species and sequenced by the di-deoxy sequencing method. The sequence of both DNA strands for each subclone was determined.

The nucleotide sequence determined for the *M. bovis* ssrA gene shared 100% homology with the *Mycobacterium tuberculosis* ssrA gene sequence.

A clustal W alignment of the novel ssrA gene sequences obtained for the *Listeria* species (SEQ ID NOS 51, 53, 55, 59 and 61) is shown in FIG. **5**. This analysis indicated that genus-specific probes and oligonucleotide amplification primers can be generated for *Listeria* bacteria. Furthermore, the alignment also indicated that a species specific oligonucleotide probe can be generated which will distinguish *L. monocytogenes* from the other *Listeria* species.

In FIG. **5** the proposed genus specific oligonucleotide primers, Ltm 1 and Ltm 2, are boxed, as is the genus specific *Listeria* oligonucleotide probe, LGtm. The proposed *L. monocytogenes* species specific oligonucleotide probe sequence, LStm, is underlined and italicised.

To further illustrate that the ssrA gene/tmRNA nucleic acid target is a suitable target for bacterial diagnostics, a comparative alignment of the *L. monocytogenes* ssrA gene nucleotide sequence (SEQ ID NO. 55) with the available *B. subtilis* ssrA gene nucleotide sequence (SEQ ID NO. 11) (a phylogenetically closely related bacteria to *Listeria*) was carried out as shown in FIG. **6**. Analysis of the sequence alignment showed a percentage nucleotide sequence homology of 41%, whereas the corresponding 16S rRNA alignment exhibits a nucleotide sequence percentage homology of 87%, (data not shown).

Example 5

Generation and Application of ssrA Gene/tmRNA Genus-Specific Amplification Primers, Genus-Specific and Species-Specific Probes for the *Listeria* Bacterial Species

Using the *Listeria* genus ssrA gene/tmRNA nucleotide sequence alignment of Example 4, regions of the ssrA gene/tmRNA nucleotide sequence were analysed to determine their suitability for the generation of genus-specific amplification primers, and genus-specific and species-specific oligonucleotide probes. In this analysis, regions which demonstrated the greatest sequence differences to *B. subtilis*, were selected in the design of these amplification primers and probes.

The sequences of the synthesised oligonucleotides are as follows:

(a)	Ltm1:	5' *Listeria* genus specific amplification primer 5'-AAAGCCAATAATAACTGG- 3' SEQ ID NO: 172
(b)	Ltm2:	3' *Listeria* genus specific amplification primer 5'-CCAGAAATATCGGCACTT- 3' SEQ ID NO: 173
(c)	LGtm:	*Listeria* genus specific hybridisation probe 5'-GTGAGACCCTTACCGTAG- 3' SEQ ID NO: 174
(d)	LStm:	*L. monocytogenes* species specific hybridisation probe 5'-TCTATTTAACCCCAGACG- 3' SEQ ID NO: 175

The genus specific amplification primers Ltm1 and Ltm2 were used in a series of PCR reactions with total genomic DNA from twenty different strains as the template in each case. Only ssrA gene sequences from the *Listeria* species were amplified (260 base pair product) with these primers (FIG. **7** and Table 3) demonstrating that the ssrA gene/tmRNA is a suitable target for specific in vitro amplification of a bacterial genus. No amplification products were observed for any other bacterial species tested, although PCR products were obtained from the DNA from these bacterial species using the universal primers (tmU5' and tmU3') described in Example 2.

In FIG. **7** the lanes represent the following:

Lane A: Molecular weight marker V
Lane 1: *E. coli*
Lane 2: *S. poona*
Lane 3: *K. aerogenes*
Lane 4: *P. mirabilis*
Lane 5: *P. rettgeri*
Lane 6: *A. hydrophilia*
Lane 7: *S. aureus*
Lane 8: *E. faecalis*
Lane 9: *L. lactis*
Lane 10: *B. subtilus*
Lane 11: *L. monocytogenes* strain 1
Lane 12: *L. monocytogenes* strain 2
Lane 13: *L. monocytogenes* strain 3
Lane 14: *L. monocytogenes* strain 4
Lane 15: *L. monocytogenes* clinical isolate
Lane 16: *L. innocua*
Lane 17: *L. murrayi*
Lane 18: *L. welshimeri*
Lane 19: *L. grayi*
Lane 20: *M. bovis*
Lane B: Molecular weight marker V

TABLE 3

Bacterial species tested with *Listeria* specific amplification primers.

		PCR Product
Gram Negative Bacteria	*Escherichia coli*	–
	Salmonella poona	–
	Klebsiella aerogenes	–
	Proteus mirabilis	–
	Proteus rettgeri	–
	Aeromonas hydrophilia	–
Gram positive bacteria	*Staphyloccus aureus*	–
	Entrococcus faecalis	–
	Lactobacillus lacus	–
	Bacillus subtilus	–
	Listeria monocytogenes strain 1	+
	Listeria monocytogenes strain 2	+
	Listeria monocytogenes strain 3	+
	Listeria monocytogenes strain 4	+
	Listeria monocytogenes clinical isolate	+
	Listeria innocua	+
	Listeria murrayi	+
	Listeria welshimeri	+
	Listeria grayi	+
	Mycobacterium bovis	–

The *Listeria* genus specific oligonucleotide probe, LGtm, was hybridised to the Southern blot depicted in FIG. **4**. Positive hybridisation signals were observed only with *Listeria* species as shown in FIG. **8** and Table 4, demonstrating the utility of the tmRNA sequence as a target in detecting a specific genus.

In FIG. **8** the lanes represent the following:

Lane A: Molecular weight marker V
Lane 1: *Escherichia coli*
Lane 2: *Salmonella poona*
Lane 3: *Klebsiella aerogenes*
Lane 4: *Proteus mirabilis*
Lane 5: *Proteus rettgeri*
Lane 6: *Aeromonas hydrophilia*
Lane 7: *Staphyloccus aureus*
Lane 8: *Enterococcus faecalis*
Lane 9: *Lactobacillus lactis*
Lane 10: *Bacillus subtilus*
Lane 11: *Listeria monocytogenes*
Lane 12: *Listeria innocua*
Lane 13: *Listeria murrayi*
Lane 14: *Listeria welshimeri*
Lane 15: *Listeria grayi*
Lane 16: *Mycobacterium bovis*
Lane B: Molecular weight marker V

The PCR products generated using the genus-specific amplification described in this Example, and shown in FIG. **7**, were Southern blotted and hybridised to the *L. monocytogenes* species-specific oligonucleotide probe. A positive hybridisation signal was observed with three of the four typed strains and the clinical isolate of *L. monocytogenes* as shown in FIG. **9** and Table 4.

In FIG. **9** the lanes represent the following:

Lane A: Molecular weight marker V
Lane 1: *E. coli*
Lane 2: *S. poona*
Lane 3: *K. aerogenes*
Lane 4: *P. mirabilis*
Lane 5: *P. rettgeri*
Lane 6: *A. hydrophilia*
Lane 7: *S. aureus*
Lane 8: *E. faecalis*
Lane 9: *L. lactis*
Lane 10: *B. subtilus*
Lane 11: *L. monocytogenes* strain 1
Lane 12: *L. monocytogenes* strain 2
Lane 13: *L. monocytogenes* strain 3
Lane 14: *L. monocytogenes* strain 4

Lane 15: *L. monocytogenes* clinical isolate
Lane 16: *L. innocua*
Lane 17: *L. murrayi*
Lane 18: *L. welshimeri*
Lane 19: *L. grayi*
Lane 20: *M. bovis*
Lane B: Molecular weight marker V

TABLE 4

Specificity of the *Listeria* genus-specific probe and the *L. monocytogenes* species-specific probe.

		LGtm Genus-specific probe	LStm Species-specific probe
Gram negative bacteria	*Escherichia coli*	−	−
	Salmonella poona	−	−
	Klebsiella aerogenes	−	−
	Proteus mirabilis	−	−
	Proteus rettgeri	−	−
	Aeromonas hydrophilia	−	−
Gram positive bacteria	*Staphyloccus aureus*	−	−
	Entrococcus aecalis	−	−
	Lactobacillus lactis	−	−
	Bacillus subtilus	−	−
	Listeria monocytogenes strain 1	+	+
	Listeria monocytogenes strain 2	+	+
	Listeria monocytogenes strain 3	+	+
	Listeria monocytogenes strain 4	+	−
	Listeria monocytogenes clinical isolate	+	+
	Listeria innocua	+	−
	Listeria murrayi	+	−
	Listeria welshimeri	+	−
	Listeria grayi	+	−
	Mycobacterium bovis	−	−

One of the typed *L. monocytogenes* strains, strain 4, failed to generate a positive signal with this probe. DNA sequencing of the PCR amplified ssrA gene from this strain demonstrated that it contained a probe target region identical to *L. innocua*. It should be noted however that the ssrA gene from this strain contains other regions where the sequence is identical to the previously characterised *L. monocytogenes* strain and that these sequences are different to the *L. innocua* sequence, as shown in FIG. **15**. Therefore a species specific oligonucleotide directed to one of these variable regions can be synthesised which would recognise each strain type (isolate) within the species, for example *L. monocytogenes.*

Example 6

Multiple Colorimetric Probe Detection of *Listeria* ssrA Gene Sequences

LGTm (A), LStm (B) and a *Campylobacter upsaliensis* 16S-23S rRNA spacer (C-5' CATTAAACTTTAGCAAGGAAGTG 3') SEQ ID NO: 228 oligonucleotide probe were irreversibly bound to nylon membrane strips and hybridised to with amplified ssrA PCR product, using the genus specific primers Ltm1 and Ltm2 (Ltm1 was labelled with biotin at the 5' end), from *L. monocytogenes* (1-6), *L. innocua* (7-10), *Z. ivanovii* (11), *L. murrayi* (12), *L. seeligeri* (13), *L. welshmeri* (14) and *L. grayii* (15). The ssrA amplified PCR products, using tmU5' and tmU3' (tmU5' was labelled with biotin at the 5' end), were also hybridised to the nylon membrane strips from the Gram-positive bacteria, *B. subtilus, L. lactis, S. aureus, S. epidermis, E. faecalis, C. perfringins* (16-21) and the Gram-negative bacteria *E. coli, S. enteritidis, P. Rettgeri, K. aerogenes* (22-25). As shown in FIG. **10** after hybridisation, development of the colorimetric assay to biotin revealed the following: Strips 1-6 demonstrates that the ssrA amplified PCR product originated from *L. monocytogenes* combined with the confirmation that the PCR product amplified is from the genus *Listeria*—A and B give colour detection; Strips 7-15 demonstrate that these PCR products originated from the genus *Listeria*—only A gives colour detection; and Strips 16-25 demonstrate that the PCR products are not from the genus *Listeria*—no colour detection. C is a negative oligonucleotide control probe and D is a positive control colorimetric detection assay for all samples.

Example 7

Use of ssrA/tmRNA Sequences to Distinguish Between Species of Organisms

Clustal W alignments as shown in FIGS. **11** (SEQ ID NOS:19 and 21), **12** (SEQ ID NOS:41 and 43), **13** (SEQ ID NOS:77 and 79), **14** (SEQ ID NOS:83 and 85), **15** (SEQ ID NOS: 229 (L.m.2) and 57, residues 20-247 (L.m.1)), and **16** (SEQ ID NOS:53 (L.i.=Res. Nos. 77 to 304), 229 (L.m.2), and 57 (L.m1), indicate that there are nucleotide differences within the ssrA/tmRNA sequences of different strains of the same bacteria. This suggests that the ssrA/tmRNA sequences could potentially be used to discriminate between individual and/or groups of strains within a bacterial species. This may have useful applications in epidemiology and bacterial population analysis.

Example 8

tmRNA Integrity Analysis After Medium and Extreme Heat Treatment of Bacterial Cells

E. coli and *L. monocytogenes* cultures were heat treated at 80° C., for 20 min. in the case of *E. coli* and 40 min. in the case of *L. monocytogenes* and at 120° C. for 15 min. (autoclaving) after overnight growth and tested for viability at 0 h, 1 h, 2 h, 6 h, 12 h, 24 h and 48 h after heat treatment. No viability was observed at each time period tested. Total RNA was also isolated at these time periods and electrophoresed on denaturing 1.2% agarose gels and Northern blotted. Each blot was hybridised to, in the case of *E. coli* (FIGS. **17** and **18**) with a radioactively labelled oligonucleotide probe Evtm and in the case of *L. monocytogenes* (FIGS. **19** and **20**) with a radiolabelled LVtm. No tmRNA transcript was detected with each sample tested, demonstrating that tmRNA transcript is degraded after heat treatment. The lanes represented with the notation +ve is a positive control total RNA sample.

Example 9

Use of the tmRNA Transcript in Distinguishing Between Viable and Non-Viable Bacteria

A 100 ml culture of *L. monocytogenes* was grown overnight in liquid culture. After growth, serial dilutions of the cells were carried out and viability was determined by spread plating on nutrient agar plates. Simultaneously, total RNA was isolated from a 1 ml aliquot of these cells. The remainder of the cells were heated at 65° C. for 20 min. Cells were then removed for both viability analysis and total RNA isolation. Samples were taken for viability and RNA isolation at time periods of 0 h, 2 h, 6 h and 24 h after treatment.

Spread plating on nutrient agar plates indicated that heat treatment killed *L. monocytogenes* cells, with no viable colony forming units observed. Each RNA sample isolated was then treated with DNase to remove any contaminating DNA and total RNA samples (100 ng) were subjected to Reverse Transcriptase-PCR amplification using the *Listeria* genus specific ssrA/tmRNA oligonucleotide primers Ltm1 and Ltm2. Negative control amplification reactions included primers, target, and Tag polymerase, but no Reverse Transcriptase. The results of the amplification reactions are shown in FIG. **12**.

Amplified tmRNA RT-PCR products were only observed with the RNA sample which was not heat treated. All other samples gave no RT-PCR product indicating that the tmRNA molecules in these samples may have been degraded in the non-viable heat treated cells.

In FIG. **21** the lanes represent the following:

Lane A:	Molecular weight marker V;
Lane 1:	PCR amplification of RNA (no heat treatment treatment of cells) −Reverse Transcriptase (RT), +Taq polymerase (TP);
Lane 2:	RT-PCR of RNA (no heat treatment of cells), +RT, +TP;
Lane 3:	PCR amplification of RNA (at 0 time after heat treatment), −RT, +TP;
Lane 4:	RT-PCR of RNA (at 0 time after heat treatment), +RT, +TP;
Lane 5:	PCR amplification of RNA (at 1 h time after heat treatment), −RT, +TP;
Lane 6:	RT-PCR of RNA (at 1 h time after heat treatment), +RT, +TP;
Lane 7:	PCR amplification of RNA (at 2 h time after heat treatment), −RT, +TP;
Lane 8:	RT,PCR of RNA (at 2 h time after heat treatment) +RT, +TP;
Lane 9:	PCR amplification of RNA (at 6 h time after heat treatment), −RT, +TP;
Lane 10:	RT-PCR of RNA (at 6 h time after heat treatment), +RT, +TP;
Lane 11:	PCR amplification of RNA (at 24 h time after heat treatment), −RT, +TP;
Lane 12:	RT-PCR of RNA (at 24 h time after heat treatment), +RT, +TP;
Lane B:	Molecular weight marker V.

SEQUENCE LISTING

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ggccguccuc gcacuggcuc gcugacgggc uagggucgca agaccacgcg agguauuuac    180

gucagauaag cuccggaagg gucacgaagc cggggacgaa aaccuaguga cucgccgucg    240

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ugcccguggg cgacccgagg ggaaauccug aacacgggcu aagccuguag agccucggau    300

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tcgacatcaa agcttgctta aaaatgtttt caagttgatt tttagggact tttatacttg 240

agagcaattt ggtggtttgc tagtatttcc aaaccatatt gcttaataaa atactagata 300

agcttgtaga agcttatagt attattttta ggacgcgggt tcaattcccg ccatctccac 360

ca 362

<210> SEQ ID NO 16
<211> LENGTH: 362
<212> TYPE: RNA
<213> ORGANISM: Borrelia burgdorferi

<400> SEQUENCE: 16

ggggauguuu uggauuugac ugaaaauguu aauauuguaa guugcaggca gagggaaucu 60

cuuaaaacuu cuaaaauaaa ugcaaaaaau aauaacuuua caagcucaaa ucuuguaaug 120

gcugcuuaag uuagcagagg guuuuguuga auuuggcuuu gagguucacu uauacucuuu 180

ucgacaucaa agcuugcuua aaaauguuuu caaguugauu uuuagggacu uuuauacuug 240

agagcaauuu ggugguuugc uaguauuucc aaaccauauu gcuuaauaaa auacuagaua 300

agcuuguaga agcuuauagu auuauuuuua ggacgcgggu ucaauucccg ccaucuccac 360

ca 362

<210> SEQ ID NO 17
<211> LENGTH: 359
<212> TYPE: DNA
<213> ORGANISM: Campylobacter jejuni

<400> SEQUENCE: 17

gggagcgact tggcttcgac aggagtaagt ctgcttagat ggcatgtcgc tttgggcaaa 60

gcgtaaaaag cccaaataaa attaaacgca aacaacgtta aattcgctcc tgcttacgct 120

aaagctgcgt aagttcagtt gagcctgaaa tttaagtcat actatctagc ttaattttcg 180

gtcatttttg atagtgtagc cttgcgtttg acaagcgttg aggtgaaata aagtcttagc 240

cttgcttttg agttttggaa gatgagcgaa gtagggtgaa gtagtcatct ttgctaagca 300

tgtagaggtc tttgtgggat tatttttgga caggggttcg attcccctcg cttccacca 359

<210> SEQ ID NO 18
<211> LENGTH: 359
<212> TYPE: RNA
<213> ORGANISM: Campylobacter jejuni

<400> SEQUENCE: 18

gggagcgacu uggcuucgac aggaguaagu cugcuuagau ggcaugucgc uuugggcaaa 60

gcguaaaaag cccaaauaaa auuaaacgca aacaacguua aauucgcucc ugcuuacgcu 120 aaagcugcgu aaguucaguu gagccugaaa uuuaagucau acuaucuagc uuaauuuucg   180

gucauuuuug auaguguagc cuugcguuug acaagcguug aggugaaaua aagucuuagc   240

cuugcuuuug aguuuuggaa gaugagcgaa guagggugaa guagucaucu uugcuaagca   300

uguagagguc uuugugggau uauuuuugga cagggguucg auuccccucg cuuccacca   359

<210> SEQ ID NO 19
<211> LENGTH: 420
<212> TYPE: DNA
<213> ORGANISM: Chlamydia trachomatis (D/UW-3/CX)

<400> SEQUENCE: 19

gggggtgtaa aggtttcgac ttagaaatga agcgttaatt gcatgcggag ggcgttggct   60

ggcctcctaa aaagccgaca aaacaataaa tgccgaacct aaggctgaat gcgaaattat   120

cagcttcgct gatctcgaag atctaagagt agctgcttaa ttagcaaagt tgttacctaa   180

atacgggtga cccggtgttc gcgagctcca ccagaggttt tcgaaacacc gtcatgtatc   240

tggttagaac ttaggtcctt taattctcga ggaaatgagt ttgaaattta atgagagtcg   300

ttagtctcta taggggtttc tagctgagga gacataacgt atagtaccta ggaactaagc   360

atgtagaggt tagcggggag tttactaagg acgagagttc gactctctcc acctccacca   420

<210> SEQ ID NO 20
<211> LENGTH: 420
<212> TYPE: RNA
<213> ORGANISM: Chlamydia trachomatis (D/UW-3/CX)

<400> SEQUENCE: 20

gggggugua a agguuucgac uuagaaauga agcguuaauu gcaugcggag ggcguuggcu   60

ggccuccuaa aaagccgaca aaacaauaaa ugccgaaccu aaggcugaau gcgaaauuau   120

cagcuucgcu gaucucgaag aucuaagagu agcugcuuaa uuagcaaagu uguuaccuaa   180

auacggguga cccgguguuc gcgagcucca ccagagguuu ucgaaacacc gucauguauc   240

ugguuagaac uuagguccuu uaauucucga ggaaaugagu uugaaauuua augagagucg   300

uuagucucua uagggguuuc uagcugagga gacauaacgu auaguaccua ggaacuaagc   360

auguagaggu uagcggggag uuuacuaagg acgagaguuc gacucucucc accuccacca   420

<210> SEQ ID NO 21
<211> LENGTH: 421
<212> TYPE: DNA
<213> ORGANISM: Chlamydia trachomatis (mouse pneumonitis)

<400> SEQUENCE: 21

gggggtgtaa aggtttcgac ttagaaatga agcgttaatt gcatgcggag ggcgttggct   60

ggcctcctaa aaagccgaca aaacaataaa tgccgaacct aaggctgaat gcgaaattat   120

cagcttcgct gatcttaatg atctaagagt tgctgcttaa ttagcaaagt tgttacctaa   180

gtactggtaa cccggtgttc gcgagctcca ccagaggttt tcgaaacgcc gtcatttatc   240

tggttagaat tagggccttt taactctcaa gggaactaat ttgaatttta atgagagtcg   300

ttggtctcta tagaggtttc tagctgagga gatataacgt aaaatattct agaaactaag   360

catgtagagg ttagcgggga gtttactaag gacgagagtt cgaatctctc cacctccacc   420

a   421

<210> SEQ ID NO 22
<211> LENGTH: 421

<212> TYPE: RNA
<213> ORGANISM: Chlamydia trachomatis (mouse pneumonitis)

<400> SEQUENCE: 22

gggggguguaa agguuucgac uuagaaauga agcguuaauu gcaugcggag ggcguuggcu 60

ggccuccuaa aaagccgaca aaacaauaaa ugccgaaccu aaggcugaau gcgaaauuau 120

cagcuucgcu gaucuuaaug aucuaagagu ugcugcuuaa uuagcaaagu uguuaccuaa 180

guacugguaa cccgguguuc gcgagcucca ccagagguuu ucgaaacgcc gucauuuauc 240

ugguuagaau uagggccuuu uaacucucaa gggaacuaau uugaauuuua augagagucg 300

uuggucucua uagagguuuc uagcugagga gauauaacgu aaaauauucu agaaacuaag 360

cauguagagg uuagcgggga guuuacuaag gacgagaguu cgaaucucuc caccuccacc 420

a 421

<210> SEQ ID NO 23
<211> LENGTH: 404
<212> TYPE: DNA
<213> ORGANISM: Chlorobium tepidum

<400> SEQUENCE: 23

ggggatgaca ggctatcgac aggataggtg tgagatgtcg ttgcactccg agtttcagca 60

tggacggact cgttaaacaa gtctatgtac caatagatgc agacgattat tcgtatgcaa 120

tggctgcctg attagcacaa gttaattcag aagccatcgt cctgcggtga atgcgcttac 180

tctgaagccg ccggatggca taacccgcgc ttgagcctac gggttcgcgc aagtaagctc 240

cgtacattca tgcccgaggg ggtgtgcggg taaccaatcg ggataagggg acgaacgctg 300

ctggcggtgt aatcggacca cgaaaaacca accaccagag atgagtgtgg taactgcatc 360

gagcagtgtc ctggacgcgg gttcaagtcc cgccatctcc acca 404

<210> SEQ ID NO 24
<211> LENGTH: 404
<212> TYPE: RNA
<213> ORGANISM: Chlorobium tepidum

<400> SEQUENCE: 24

ggggaugaca ggcuaucgac aggauaggug ugagaugucg uugcacuccg aguuucagca 60

uggacggacu cguuaaacaa gucuauguac caauagaugc agacgauuau ucguaugcaa 120

uggcugccug auuagcacaa guuaauucag aagccaucgu ccugcgguga augcgcuuac 180

ucugaagccg ccggauggca uaacccgcgc uugagccuac ggguucgcgc aaguaagcuc 240

cguacauuca ugcccgaggg ggugugcggg uaaccaaucg ggauaagggg acgaacgcug 300

cuggcggugu aaucggacca cgaaaaacca accaccagag augaguguggg uaacugcauc 360

gagcaguguc cuggacgcgg guucaagucc cgccaucucc acca 404

<210> SEQ ID NO 25
<211> LENGTH: 294
<212> TYPE: DNA
<213> ORGANISM: Cyanophora paradoxa (alga) cyanelle

<400> SEQUENCE: 25

ggggctgttt aggtttcgac gtttttttct aattatgttt gttaagcaag tcgaggattt 60

gttctatctc gaaaatcaag aactctcaaa atttaaacgc aactaatatt gtacgtttta 120

accgtaaagc agctttcgct gtttaataat tacttttaat ttaaaaacct aattttttta 180

ggaatttatt tatttattgt ttatcctgct taatgaatta aaaaaagcta tacttgtgaa 240

```
taaacgcata atttaaaaaa acggacgtgg gttcaaatcc caccagctcc acca         294


<210> SEQ ID NO 26
<211> LENGTH: 294
<212> TYPE: RNA
<213> ORGANISM: Cyanophora paradoxa (alga) cyanelle

<400> SEQUENCE: 26

ggggcuguuu agguuucgac guuuuuuucu aauuauguuu guuaagcaag ucgaggauuu     60

guucuaucuc gaaaaucaag aacucucaaa auuuaaacgc aacuaauauu guacguuuua    120

accguaaagc agcuuucgcu guuuaauaau uacuuuuaau uuaaaaaccu aauuuuuuua    180

ggaauuuauu uauuuauugu uuauccugcu uaaugaauua aaaaaagcua uacuugugaa    240

uaaacgcaua auuuaaaaaa acggacgugg guucaaaucc caccagcucc acca         294


<210> SEQ ID NO 27
<211> LENGTH: 189
<212> TYPE: DNA
<213> ORGANISM: Clostridium acetobutylicum

<400> SEQUENCE: 27

aatctggcgt cgagagcggg gaaacgagcc ttacaaagct ttgagtaagg aacggaattt     60

atgaagctac tgaagtgaaa agcttgtttg taggcgtttc atggagggaa tgttaaaata    120

caaactgcac tcggagatgc ttaatgaaac cattttcgga caggggttcg attcccctcg    180

cctccacca                                                            189


<210> SEQ ID NO 28
<211> LENGTH: 189
<212> TYPE: RNA
<213> ORGANISM: Clostridium acetobutylicum

<400> SEQUENCE: 28

aaucuggcgu cgagagcggg gaaacgagcc uuacaaagcu uugaguaagg aacggaauuu     60

augaagcuac ugaagugaaa agcuuguuug uaggcguuuc auggagggaa uguuaaaaua    120

caaacugcac ucggagaugc uuaaugaaac cauuuucgga cagggguucg auuccccucg    180

ccuccacca                                                            189


<210> SEQ ID NO 29
<211> LENGTH: 349
<212> TYPE: DNA
<213> ORGANISM: Deinococcus radiodurans

<400> SEQUENCE: 29

gggggtgacc cggtttcgac aggggaactg aaggtgatgt tgcgtgtcga ggtgccgttg     60

gcctcgtaaa caaacggcaa agccatttaa ctggcaacca gaactacgct ctcgctgctt    120

aagtgagatg acgaccgtgc agcccggcct ttggcgtcgc ggaagtcact aaaaaagaag    180

gctagcccag gcgattctcc atagccgacg gcgaaacttt atggagctac ggcctgcgag    240

aacctgccca ctggtgagcg ccggcccgac aatcaaacag tgggatacac acgtagacgc    300

acgctggacg gacctttgga cggcggttcg actccgccca cctccacca               349


<210> SEQ ID NO 30
<211> LENGTH: 349
<212> TYPE: RNA
<213> ORGANISM: Deinococcus radiodurans

<400> SEQUENCE: 30
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-continued

gggggugacc cgguuucgac aggggaacug aaggugaugu ugcgugucga ggugccguug 60

gccucguaaa caaacggcaa agccauuuaa cuggcaacca gaacuacgcu cucgcugcuu 120

aagugagaug acgaccgugc agcccggccu uuggcgucgc ggaagucacu aaaaaagaag 180

gcuagcccag gcgauucucc auagccgacg gcgaaacuuu auggagcuac ggccugcgag 240

aaccugccca cuggugagcg ccggcccgac aaucaaacag ugggauacac acguagacgc 300

acgcuggacg gaccuuugga cggcgguucg acuccgccca ccuccacca 349

<210> SEQ ID NO 31
<211> LENGTH: 330
<212> TYPE: DNA
<213> ORGANISM: Desulfovibrio desulfuricans

<400> SEQUENCE: 31

gggactggaa ccgtagcggc aggtcgaggc gccgctggcc tcgtaaaaag cggcacaaaa 60

gtaattgcca acaacgatta cgactacgct tacgctgcct aataacagcg aggcaatgac 120

cgtttaacgg tcgcgccgat cagggccatg cctgataacc ctgattggcg acacttatca 180

ggctggcgaa aaccggctct cgccggggtt tttcgcgagg agtttaccgg cgggattgct 240

gcgttgtgcc tggtcagggg ccaacagcgc ggtgaaatac atacttgacc taaacctgta 300

atgcttcgtg tggaatgttc tcggacgggg 330

<210> SEQ ID NO 32
<211> LENGTH: 330
<212> TYPE: RNA
<213> ORGANISM: Desulfovibrio desulfuricans

<400> SEQUENCE: 32

gggacuggaa ccguagcggc aggucgaggc gccgcuggcc ucguaaaaag cggcacaaaa 60

guaauugcca acaacgauua cgacuacgcu uacgcugccu aauaacagcg aggcaaugac 120

cguuuaacgg ucgcgccgau cagggccaug ccugauaacc cugauuggcg acacuuauca 180

ggcuggcgaa aaccggcucu cgccgggguu uuucgcgagg aguuuaccgg cgggauugcu 240

gcguugugcc uggucagggg ccaacagcgc ggugaaauac auacuugacc uaaaccugua 300

augcuucgug uggaauguuc ucggacgggg 330

<210> SEQ ID NO 33
<211> LENGTH: 318
<212> TYPE: DNA
<213> ORGANISM: Dichelobacter nodosus

<400> SEQUENCE: 33

ctcgaggtgc atgtcgagaa tgagagaatc tcgttaaata ctttcaaaac ttatagttgc 60

aaacgacgac aactacgctt tagcggctta attcccgctt tcgcttacct agatttgtct 120

gtgggtttac cgtaagcgac attaacacag aatcgctggt taacgcgtcc gctgttaatc 180

ggttaaatta agcggaatcg cttgtaaaat gcctgagcgt tggctgttta tgagttaaac 240

ctaattaact gctctaaaca tgtagtacca aaagttaagg attcgcggac gggggttcaa 300

atccccccgc ctccacca 318

<210> SEQ ID NO 34
<211> LENGTH: 318
<212> TYPE: RNA
<213> ORGANISM: Dichelobacter nodosus

<400> SEQUENCE: 34

```
cucgaggugc augucgagaa ugagagaauc ucguuaaaua cuuucaaaac uuauaguugc     60

aaacgacgac aacuacgcuu uagcggcuua auucccgcuu ucgcuuaccu agauuugucu    120

gugggguuac cguaagcgac auuaacacag aaucgcuggu uaacgcgucc gcuguuaauc    180

gguuaaauua agcggaaucg cuuguaaaau gccugagcgu uggcuguuua ugaguuaaac    240

cuaauuaacu gcucuaaaca uguaguacca aaaguuaagg auucgcggac gggggguucaa    300

aucccccccgc cuccacca                                                 318


<210> SEQ ID NO 35
<211> LENGTH: 367
<212> TYPE: DNA
<213> ORGANISM: Enterococcus faecalis

<400> SEQUENCE: 35

gggggcgtta cggattcgac aggcatagtt gagcttgaat tgcgtttcgt aggttacggc     60

tacgttaaaa cgttacagtt aaatataact gctaaaaacg aaaacaattc tttcgcttta    120

gctgcctaaa aaccagctag cgaagatcct cccggcatcg cccatgtgct cgggtcaggg    180

tcctaatcga agtgggatac gctaaatttt tccgtctgta aaatttagag gagcttacca    240

gactagcaat acagaatgcc tgtcactcgg cacgctgtaa agcgaacctt taaatgagtg    300

tctatgaacg tagagattta agtggcaata tgtttggacg cgggttcgac tcccgccgtc    360

tccacca                                                              367


<210> SEQ ID NO 36
<211> LENGTH: 367
<212> TYPE: RNA
<213> ORGANISM: Enterococcus faecalis

<400> SEQUENCE: 36

gggggcguua cggauucgac aggcauaguu gagcuugaau ugcguuucgu agguuacggc     60

uacguuaaaa cguuacaguu aaauauaacu gcuaaaaacg aaaacaauuc uuucgcuuua    120

gcugccuaaa aaccagcuag cgaagauccu cccggcaucg cccaugugcu cgggucaggg    180

uccuaaucga agugggauac gcuaaauuuu uccgucugua aaauuuagag gagcuuacca    240

gacuagcaau acagaaugcc ugucacucgg cacgcuguaa agcgaaccuu uaaaugagug    300

ucuaugaacg uagagauuua aguggcaaua uguuuggacg cggguucgac ucccgccguc    360

uccacca                                                              367


<210> SEQ ID NO 37
<211> LENGTH: 363
<212> TYPE: DNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 37

ggggctgatt ctggattcga cgggatttgc gaaacccaag gtgcatgccg aggggcggtt     60

ggcctcgtaa aaagccgcaa aaaatagtcg caaacgacga aaactacgct ttagcagctt    120

aataacctgc ttagagccct ctctccctag cctccgctct taggacgggg atcaagagag    180

gtcaaaccca aaagagatcg cgtggaagcc ctgcctgggg ttgaagcgtt aaaacttaat    240

caggctagtt tgttagtggc gtgtccgtcc gcagctggca agcgaatgta aagactgact    300

aagcatgtag taccgaggat gtaggaattt cggacgcggg ttcaactccc gccagctcca    360

cca                                                                  363
```

<210> SEQ ID NO 38
<211> LENGTH: 363
<212> TYPE: RNA
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 38

ggggcugauu cuggauucga cgggauuugc gaaacccaag gugcaugccg aggggcgguu 60

ggccucguaa aaagccgcaa aaaauagucg caaacgacga aacuacgcu uuagcagcuu 120

aauaaccugc uuagagcccu cucucccuag ccuccgcucu uaggacgggg aucaagagag 180

gucaaaccca aaagagaucg cguggaagcc cugccugggg uugaagcguu aaaacuuaau 240

caggcuaguu uguuaguggc guguccgucc gcagcuggca agcgaaugua aagacugacu 300

aagcauguag uaccgaggau guaggaauuu cggacgcggg uucaacuccc gccagcucca 360

cca 363

<210> SEQ ID NO 39
<211> LENGTH: 366
<212> TYPE: DNA
<213> ORGANISM: Haemophilus influenzae

<400> SEQUENCE: 39

ggggctgatt ctggattcga cgggattagc gaagcccaag gtgcacgtcg aggtgcggta 60

ggcctcgtaa ataaaccgca aaaaaatagt cgcaaacgac gaacaatacg ctttagcagc 120

ttaataacct gcatttagcc ttcgcgctcc agcttccgct cgtaagacgg ggataacgcg 180

gagtcaaacc aaaacgagat cgtgtggaag ccaccgtttg aggatcgaag cactaaattg 240

aatcaaacta gcttaagttt agcgtgtctg tccgcatgct taagtgaaat taaagacgag 300

actaaacgtg tagtactgaa ggtagagtaa tttcggacgg gggttcaact ccccccagct 360

ccacca 366

<210> SEQ ID NO 40
<211> LENGTH: 366
<212> TYPE: RNA
<213> ORGANISM: Haemophilus influenzae

<400> SEQUENCE: 40

ggggcugauu cuggauucga cgggauuagc gaagcccaag gugcacgucg aggugcggua 60

ggccucguaa auaaaccgca aaaaaauagu cgcaaacgac gaacaauacg cuuuagcagc 120

uuaauaaccu gcauuuagcc uucgcgcucc agcuuccgcu cguaagacgg ggauaacgcg 180

gagucaaacc aaaacgagau cguguggaag ccaccguuug aggaucgaag cacuaaauug 240

aaucaaacua gcuuaaguuu agcgugucug uccgcaugcu uaagugaaau uaaagacgag 300

acuaaacgug uaguacugaa gguagaguaa uuucggacgg ggguucaacu ccccccagcu 360

ccacca 366

<210> SEQ ID NO 41
<211> LENGTH: 340
<212> TYPE: DNA
<213> ORGANISM: Helicobacter pylori (ATC 43504)

<400> SEQUENCE: 41

agatttcttg tcgcgcagat agcatgccaa gcgctgcttg taaaacagca acaaaaataa 60

ctgtaaacaa cacagattac gctccagctt acgctaaagc tgcgtgagtt aatctccttt 120

tggagctgga ctgattagaa tttctagcgt tttaatcgct ccataacctt aagctagacg 180

cttttaaaag gtggttcgcc ttttaaacta agaaacaaga actcttgaaa ctatcttaag 240 gttttagaaa gttggaccag agctagtttt aaggctaaaa actaaccaat tttctaagca 300

ttgtagaagt ttgtgtttag ggcaagattt ttggactggg 340

<210> SEQ ID NO 42
<211> LENGTH: 340
<212> TYPE: RNA
<213> ORGANISM: Helicobacter pylori (ATC 43504)

<400> SEQUENCE: 42

agauuucuug ucgcgcagau agcaugccaa gcgcugcuug uaaaacagca acaaaaauaa 60

cuguaaacaa cacagauuac gcuccagcuu acgcuaaagc ugcgugaguu aaucuccuuu 120

uggagcugga cugauuagaa uuucuagcgu uuuaaucgcu ccauaaccuu aagcuagacg 180

cuuuuaaaag gugguucgcc uuuuaaacua agaaacaaga acucuugaaa cuaucuuaag 240

guuuuagaaa guuggaccag agcuaguuuu aaggcuaaaa acuaaccaau uuucuaagca 300

uuguagaagu uuguguuuag ggcaagauuu uuggacuggg 340

<210> SEQ ID NO 43
<211> LENGTH: 386
<212> TYPE: DNA
<213> ORGANISM: Helicobacter pylori (strain 26695)

<400> SEQUENCE: 43

ggggctgact tggatttcga cagatttctt gtcgcacaga tagcatgcca agcgctgctt 60

gtaaaacagc aacaaaaata actgtaaaca acacagatta cgctccagct tacgctaaag 120

ctgcgtgagt taatctcctt ttggagctgg actgattaga atttctagcg ttttaatcgc 180

tccataacct taagctagac gcttttaaaa ggtggttcgc cttttaaact aagaaacaag 240

aactcttgaa actatctcaa ggttttagaa agttggacca gagctagttt taaggctaaa 300

aaaccaacca attttctaag cattgtagaa gtttgtgttt agggcaagat ttttggactg 360

gggttcgatt ccccacagct ccacca 386

<210> SEQ ID NO 44
<211> LENGTH: 386
<212> TYPE: RNA
<213> ORGANISM: Helicobacter pylori (strain 26695)

<400> SEQUENCE: 44

ggggcugacu uggauuucga cagauuucuu gucgcacaga uagcaugcca agcgcugcuu 60

guaaaacagc aacaaaaaua acuguaaaca acacagauua cgcuccagcu uacgcuaaag 120

cugcgugagu uaaucuccuu uuggagcugg acugauuaga auuucuagcg uuuuaaucgc 180

uccauaaccu uaagcuagac gcuuuuaaaa ggugguucgc cuuuuaaacu aagaaacaag 240

aacucuugaa acuaucucaa gguuuuagaa aguuggacca gagcuaguuu uaaggcuaaa 300

aaaccaacca auuuucuaag cauuguagaa guuuguguuu agggcaagau uuuuggacug 360

ggguucgauu ccccacagcu ccacca 386

<210> SEQ ID NO 45
<211> LENGTH: 312
<212> TYPE: DNA
<213> ORGANISM: Klebsiella aerogenes (NCTC 9528)

<400> SEQUENCE: 45

gggattcgcg aaacccaagg tgcatgccga ggggcggttg gcctcgtaaa aagccgcaaa 60

aaaatagtcg caaacgacga aaactacgct ttagcagctt aataacctgc taagagccct 120 ctctccctag cttccgctcc taagacgggg aataaagaga ggtcaaaccc aaaagagatc 180

gcgtggaagc cctgcctggg gttgaagcgt taaaactaat caggctagtt tgtcagtggc 240

gtgtccgtcc gcagctggcc agcgaatgta aagactggac taagcatgta gtgccgagga 300

tgtaggaatt tc 312

<210> SEQ ID NO 46
<211> LENGTH: 312
<212> TYPE: RNA
<213> ORGANISM: Klebsiella aerogenes (NCTC 9528)

<400> SEQUENCE: 46

gggauucgcg aaacccaagg ugcaugccga ggggcgguug gccucguaaa aagccgcaaa 60

aaaauagucg caaacgacga aaacuacgcu uuagcagcuu aauaaccugc uaagagcccu 120

cucucccuag cuuccgcucc uaagacgggg aauaaagaga ggucaaaccc aaaagagauc 180

gcguggaagc ccugccuggg guugaagcgu uaaaacuaau caggcuaguu ugucaguggc 240

guguccgucc gcagcuggcc agcgaaugua aagacuggac uaagcaugua gugccgagga 300

uguaggaauu uc 312

<210> SEQ ID NO 47
<211> LENGTH: 316
<212> TYPE: DNA
<213> ORGANISM: Lactobacillus lactis (NCTC 662)

<400> SEQUENCE: 47

aagcacagtt cgagcttgaa ttgcgtttcg taggttacgt ctacgttaaa acgttacagt 60

taaatataac tgctaaaaac gaaaacaact cttacgcttt agctgcctaa aaacagttag 120

cgtagatcct ctcggcatcg cccatgtgct cgagtaaggg tctcaaattt agtgggatac 180

gttaaacttt tccgtctgta aagtttaaaa gagatcatca gactagcgat acagaatgcc 240

tgtcactcgg caagctgtaa agcgaaacct caaatgagtt gactatgaac gtagattttt 300

aagtgtcgat gtgttt 316

<210> SEQ ID NO 48
<211> LENGTH: 316
<212> TYPE: RNA
<213> ORGANISM: Lactobacillus lactis (NCTC 662)

<400> SEQUENCE: 48

aagcacaguu cgagcuugaa uugcguuucg uagguuacgu cuacguuaaa acguuacagu 60

uaaauauaac ugcuaaaaac gaaaacaacu cuuacgcuuu agcugccuaa aaacaguuag 120

cguagauccu cucggcaucg cccaugugcu cgaguaaggg ucucaaauuu agugggauac 180

guuaaacuuu uccgucugua aaguuuaaaa gagaucauca gacuagcgau acagaaugcc 240

ugucacucgg caagcuguaa agcgaaaccu caaaugaguu gacuaugaac guagauuuuu 300

aagugucgau guguuu 316

<210> SEQ ID NO 49
<211> LENGTH: 362
<212> TYPE: DNA
<213> ORGANISM: Legionella pneumophila

<400> SEQUENCE: 49

gtgggttgca aaaccggaag tgcatgccga gaaggagatc tctcgtaaat aagactcaat 60

taaatataaa tgcaaacgat gaaaactttg ctggtgggga agctatcgct gcctaataag 120

```
cactttagtt aaaccatcac tgtgtactgg ccaataaacc cagtatcccg ttcgaccgag    180

cccgcttatc ggtatcgaat caacggtcat aagagataag ctagcgtcct aatctatccc    240

gggttatggc gcgaaactca gggaatcgct gtgtatcatc ctgcccgtcg gaggagccac    300

agttaaattc aaaagacaag gctatgcatg tagagctaaa ggcagaggac ttgcggacgc    360

gg                                                                    362


<210> SEQ ID NO 50
<211> LENGTH: 362
<212> TYPE: RNA
<213> ORGANISM: Legionella pneumophila

<400> SEQUENCE: 50

gugggguugca aaaccggaag ugcaugccga gaaggagauc ucucguaaau aagacucaau     60

uaaauauaaa ugcaaacgau gaaaacuuug cuggugggga agcuaucgcu gccuaauaag    120

cacuuuaguu aaaccaucac uguguacugg ccaauaaacc caguaucccg uucgaccgag    180

cccgcuuauc gguaucgaau caacggucau aagagauaag cuagcguccu aaucuauccc    240

ggguuauggc gcgaaacuca gggaaucgcu guguaucauc cugcccgucg gaggagccac    300

aguuaaauuc aaaagacaag gcuaugcaug uagagcuaaa ggcagaggac uugcggacgc    360

gg                                                                    362


<210> SEQ ID NO 51
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Listeria grayi

<400> SEQUENCE: 51

acagggatag gtcgagcttg agttgcgagc cgggggggatc ggcccgtcat caacgtcaaa     60

gccaataata actggcaaac aaaacaacaa tttagctttc gctgcctaat agcagtctga    120

atagctgatc ctccgtgcat cacccatgtg ctacggtaag ggtctcactt ttaagtgggt    180

tacgctggct tatctccgtc tggggcaaac gagaagagca taatcagact agctagatag    240

agccctgacg ccgggcagac atctatgcga aatccaaata cggcaactac gctcgtagat    300

gctcaagtgc cgatatttct gg                                              322


<210> SEQ ID NO 52
<211> LENGTH: 322
<212> TYPE: RNA
<213> ORGANISM: Listeria grayi

<400> SEQUENCE: 52

acagggauag gucgagcuug aguugcgagc cggggggauc ggcccgucau caacgucaaa     60

gccaauaaua acuggcaaac aaaacaacaa uuuagcuuuc gcugccuaau agcagucuga    120

auagcugauc cuccgugcau cacccaugug cuacgguaag ggucucacuu uuaagugggu    180

uacgcuggcu uaucuccguc uggggcaaac gagaagagca uaaucagacu agcuagauag    240

agcccugacg ccgggcagac aucuaugcga aauccaaaua cggcaacuac gcucguagau    300

gcucaagugc cgauauuucu gg                                              322


<210> SEQ ID NO 53
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Listeria innocua

<400> SEQUENCE: 53
```

acagggatag ttcgagcttg agttgcgagt cggggggatc gtcctcgtta tcaacgtcaa 60

agccaataat aactggcaaa gaaaaacaaa acctagcttt cgctgcctaa taagcagtag 120

catagctgat cctccgtgca tcgcccatgt gctacggtaa gggtctcact ctaagtgggc 180

tacactagtt aatctccgtc tgaggttaaa tagaagagct taatcagact agctgaatgg 240

aagcctgtta ccgggctgat gtttatgcga aatgctaata cggtgactac gctcgtagat 300

attcaagtgc cgatatttct gg 322

<210> SEQ ID NO 54
<211> LENGTH: 322
<212> TYPE: RNA
<213> ORGANISM: Listeria innocua

<400> SEQUENCE: 54

acagggauag uucgagcuug aguugcgagu cggggggauc guccucguua ucaacgucaa 60

agccaauaau aacuggcaaa gaaaaacaaa accuagcuuu cgcugccuaa uaagcaguag 120

cauagcugau ccuccgugca ucgcccaugu gcuacgguaa gggucucacu cuaagugggc 180

uacacuaguu aaucuccguc ugagguuaaa uagaagagcu uaaucagacu agcugaaugg 240

aagccuguua ccgggcugau guuuaugcga aaugcuaaua cggugacuac gcucguagau 300

auucaagugc cgauauuucu gg 322

<210> SEQ ID NO 55
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Listeria monocytogenes (NCTC 7973)

<400> SEQUENCE: 55

acagggatag ttcgagcttg agttgcgagt cggggggatc gtcctcgtta tcaacgtcaa 60

agccaataat aactggcaaa gaaaaacaaa acctagcttt cgctgcctaa taagcagtag 120

catagctgat cctccgtgca tcgcccatgt gctacggtaa gggtctcact ctaagtgggc 180

tacactagtt aatctccgtc tggggttaaa tagaagagct taatcagact agctgaatgg 240

aagcctgtta ccgggccgat gtttatgcga aatgctaata cggtgactac gctcgtagat 300

atttaagtgc cgatatttct gg 322

<210> SEQ ID NO 56
<211> LENGTH: 322
<212> TYPE: RNA
<213> ORGANISM: Listeria monocytogenes (NCTC 7973)

<400> SEQUENCE: 56

acagggauag uucgagcuug aguugcgagu cggggggauc guccucguua ucaacgucaa 60

agccaauaau aacuggcaaa gaaaaacaaa accuagcuuu cgcugccuaa uaagcaguag 120

cauagcugau ccuccgugca ucgcccaugu gcuacgguaa gggucucacu cuaagugggc 180

uacacuaguu aaucuccguc ugggguuaaa uagaagagcu uaaucagacu agcugaaugg 240

aagccuguua ccgggccgau guuuaugcga aaugcuaaua cggugacuac gcucguagau 300

auuuaagugc cgauauuucu gg 322

<210> SEQ ID NO 57
<211> LENGTH: 247
<212> TYPE: DNA
<213> ORGANISM: Listeria monocytogenes (NCTC 11994)

<400> SEQUENCE: 57

caaagccaat aataactggc aaagaaaaac aaaacctagc tttcgctgcc taataagcag 60

tagcatagct gatcctccgt gcatcgccca tgtgctacgg taagggtctc actctaagtg 120

ggctacacta gttaatctcc gtctggggtt aaatagaaga gcttaatcag actagctgaa 180

tggaagcctg ttaccgggcc gatgtttatg cgaaatgcta atacggtgac tacgctcgta 240

gatattt 247

<210> SEQ ID NO 58
<211> LENGTH: 247
<212> TYPE: RNA
<213> ORGANISM: Listeria monocytogenes (NCTC 11994)

<400> SEQUENCE: 58

caaagccaau aauaacuggc aaagaaaaac aaaaccuagc uuucgcugcc uaauaagcag 60

uagcauagcu gauccuccgu gcaucgccca ugugcuacgg uaagggucuc acucuaagug 120

ggcuacacua guuaaucucc gucugggguu aaauagaaga gcuuaaucag acuagcugaa 180

uggaagccug uuaccgggcc gauguuuaug cgaaaugcua auacggugac uacgcucgua 240

gauauuu 247

<210> SEQ ID NO 59
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Listeria murrayi

<400> SEQUENCE: 59

acagggatag ttcgagcttg agttgcgagt cgggggggatc gtcctcgtta tcaacgtcaa 60

agccaataat aactggcaaa gaaaaacaaa acctagcttt cgctgcctaa taagcagtag 120

catagctgat cctccgtgca tcgcccatgt gctacggtaa gggtctcact ctaagtgggc 180

tacactagtt aatctccgtc tgaggttaaa tagaagagct taatgagact agctgaatgg 240

aagcctgtta ccgggctgat gtttatgcga aatgctaata cggtgactac gctcgtagat 300

attcaagtgc cgatatttct gg 322

<210> SEQ ID NO 60
<211> LENGTH: 322
<212> TYPE: RNA
<213> ORGANISM: Listeria murrayi

<400> SEQUENCE: 60

acagggauag uucgagcuug aguugcgagu cgggggggauc guccucguua ucaacgucaa 60

agccaauaau aacuggcaaa gaaaaacaaa accuagcuuu cgcugccuaa uaagcaguag 120

cauagcugau ccuccgugca ucgcccaugu gcuacgguaa gggucucacu cuaagugggc 180

uacacuaguu aaucuccguc ugagguuaaa uagaagagcu uaaugagacu agcugaaugg 240

aagccuguua ccgggcugau guuuaugcga aaugcuaaua cggugacuac gcucguagau 300

auucaagugc cgauauuucu gg 322

<210> SEQ ID NO 61
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Listeria welshimeri

<400> SEQUENCE: 61

acagggatag ttcgagcttg agttgcgagt cgggggggatc gtcctcgtta tcaacgtcaa 60

agccaataat aactggcaaa gaaaaacaaa acctagcttt cgctgcctaa taagcagtag 120 catagctgat cctccgtgca tcgcccatgt gctacggtaa gggtctcact ctaagtgggc 180

tacactggct aatctccgtc tgaggttagt tggaagagct taatcagact agctgaatgg 240

aagcctgtta ccgggccgat gtttatgcga aatgctaata cggtgactac gctcgtagat 300

atttaagtgc cgatatttct gg 322

<210> SEQ ID NO 62
<211> LENGTH: 322
<212> TYPE: RNA
<213> ORGANISM: Listeria welshimeri

<400> SEQUENCE: 62

acagggauag uucgagcuug aguugcgagu cggggggauc guccucguua ucaacgucaa 60

agccaauaau aacuggcaaa gaaaaacaaa accuagcuuu cgcugccuaa uaagcaguag 120

cauagcugau ccuccgugca ucgcccaugu gcuacgguaa gggucucacu cuaagugggc 180

uacacuggcu aaucuccguc ugagguuagu uggaagagcu uaaucagacu agcugaaugg 240

aagccuguua ccgggccgau guuuaugcga aaugcuaaua cggugacuac gcucguagau 300

auuuaagugc cgauauuucu gg 322

<210> SEQ ID NO 63
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Marinobacter hydrocarbonoclasticus

<400> SEQUENCE: 63

gccggtgacg aacccttggg tgcatgccga gatggcagcg aatctcgtaa atccaaagct 60

gcaacgtaat agtcgcaaac gacgaaaact acgcactggc ggcgtaagcc gttccagtcg 120

tcctggctga ggcgcctata actcagtagc aacatcccag gacgtcatcg cttataggct 180

gctccgttca ccagagctca ctggtgttcg gctaagatta aagagctcgc ctcttgcacc 240

ctgaccttcg ggtcgcttga ggttaaatca atagaaggac actaagcatg tagacctcaa 300

ggcctagtgc tggcggacgc gg 322

<210> SEQ ID NO 64
<211> LENGTH: 322
<212> TYPE: RNA
<213> ORGANISM: Marinobacter hydrocarbonoclasticus

<400> SEQUENCE: 64

gccggugacg aacccuuggg ugcaugccga gauggcagcg aaucucguaa auccaaagcu 60

gcaacguaau agucgcaaac gacgaaaacu acgcacuggc ggcguaagcc guuccagucg 120

uccuggcuga ggcgccuaua acucaguagc aacaucccag gacgucaucg cuuauaggcu 180

gcuccguuca ccagagcuca cugguguucg gcuaagauua aagagcucgc cucuugcacc 240

cugaccuucg ggucgcuuga gguuaaauca auagaaggac acuaagcaug uagaccucaa 300

ggccuagugc uggcggacgc gg 322

<210> SEQ ID NO 65
<211> LENGTH: 338
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium avium

<400> SEQUENCE: 65

ttcgcgcatc gaatcaaggg aagcgtgccg gtgcaggcaa ctgaccaccg taagcgtcgt 60

tgcaaataga taagcgccga ttcacatcag cgcgacttac ctctcgctgc ctaagcgaca 120 gctagtccgt cagcccggga acgccctcga cccggagcct ggcgtcagct agagggatcc 180

accgatgagt tcggtcgcgg gactcatcgg gacaccaaca gcgactggga tcgtcatcct 240

ggcttgttcg cgtgaccagg agatccgagt agaggcatag cgaactgcgc acggagaagc 300

cttgagggaa tgccgtagaa cccgggttcg attcccaa 338

<210> SEQ ID NO 66
<211> LENGTH: 338
<212> TYPE: RNA
<213> ORGANISM: Mycobacterium avium

<400> SEQUENCE: 66

uucgcgcauc gaaucaaggg aagcgugccg gugcaggcaa cugaccaccg uaagcgucgu 60

ugcaaauaga uaagcgccga uucacaucag cgcgacuuac cucucgcugc cuaagcgaca 120

gcuaguccgu cagcccggga acgcccucga cccggagccu ggcgucagcu agagggaucc 180

accgaugagu ucggucgcgg gacucaucgg gacaccaaca gcgacuggga ucgucauccu 240

ggcuuguucg cgugaccagg agauccgagu agaggcauag cgaacugcgc acggagaagc 300

cuugagggaa ugccguagaa cccggguucg auucccaa 338

<210> SEQ ID NO 67
<211> LENGTH: 318
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium bovis

<400> SEQUENCE: 67

ttcgcgcatc gaatcaaggg aagcgtgccg gtgcaggcaa gagaccaccg taagcgtcgt 60

tgcgaccaaa taagcgccga ttcacatcag cgcgactacg tctcgctgcc taagcgacgg 120

ctagtctgtc agaccgggaa cgccctcggc ccggaccctg gcatcagcta gagggatcca 180

ccgatgagtc cggtcgcggg actcctcggg acaaccacag cgactgggat cgtcatctcg 240

gctagttcgc gtgaccggga gatccgagca gaggcatagc gaactgcgca cggagaagcc 300

ttgagggaat gccgtagg 318

<210> SEQ ID NO 68
<211> LENGTH: 318
<212> TYPE: RNA
<213> ORGANISM: Mycobacterium bovis

<400> SEQUENCE: 68

uucgcgcauc gaaucaaggg aagcgugccg gugcaggcaa gagaccaccg uaagcgucgu 60

ugcgaccaaa uaagcgccga uucacaucag cgcgacuacg ucucgcugcc uaagcgacgg 120

cuagucuguc agaccgggaa cgcccucggc ccggacccug gcaucagcua gagggaucca 180

ccgaugaguc cggucgcggg acuccucggg acaaccacag cgacugggau cgucaucucg 240

gcuaguucgc gugaccggga gauccgagca gaggcauagc gaacugcgca cggagaagcc 300

uugagggaau gccguagg 318

<210> SEQ ID NO 69
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium leprae

<400> SEQUENCE: 69

ggggctgaaa ggtttcgact tcgcgcatcg aatcaaggga agcgtgccgg tgcaggcaag 60

agaccaccgt aagcgtcgtt gcagcaatat aagcgccgat tcatatcagc gcgactatgc 120 tctcgctgcc taagcgatgg ctagtctgtc agaccgggaa cgccctcgtc ccggagcctg 180

gcatcagcta gagggatcta ccgatgggtt cggtcgcggg actcgtcggg acaccaaccg 240

cgactgggat cgtcatcctg gctagttcgc gtgatcagga gatccgagta gaggcatagc 300

gaactacgca cggagaagcc ttgagggaaa tgccgtagga cccgggttcg attcccggca 360

gctccacca 369

<210> SEQ ID NO 70
<211> LENGTH: 369
<212> TYPE: RNA
<213> ORGANISM: Mycobacterium leprae

<400> SEQUENCE: 70

ggggcugaaa gguuucgacu ucgcgcaucg aaucaaggga agcgugccgg ugcaggcaag 60

agaccaccgu aagcgucguu gcagcaauau aagcgccgau ucauaucagc gcgacuaugc 120

ucucgcugcc uaagcgaugg cuagucuguc agaccgggaa cgcccucguc ccggagccug 180

gcaucagcua gagggaucua ccgaugggguu cggucgcggg acucgucggg acaccaaccg 240

cgacugggau cgucauccug gcuaguucgc gugaucagga gauccgagua gaggcauagc 300

gaacuacgca cggagaagcc uugagggaaa ugccguagga cccggguucg auucccggca 360

gcuccacca 369

<210> SEQ ID NO 71
<211> LENGTH: 338
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium paratuberculosis

<400> SEQUENCE: 71

ttcgcgcatc gaatcaaggg aagcgtgccg gtgcaggcaa ctgaccaccg taagcgtcgt 60

tgcaaataga taagcgccga ttcacatcag cgcgacttac ctctcgctgc ctaagcgaca 120

gctagtccgt cagcccggga acgccctcga cccggagcct ggcgtcagct agagggatcc 180

accgatgagt tcggtcgcgg gactcatcgg gacaccaaca gcgactggga tcgtcatcct 240

ggcttgttcg cgtgaccagg agatccgagt agaggcatag cgaactgcgc acggagaagc 300

cttgagggaa tgccgtagaa cccgggttcg attcccaa 338

<210> SEQ ID NO 72
<211> LENGTH: 338
<212> TYPE: RNA
<213> ORGANISM: Mycobacterium paratuberculosis

<400> SEQUENCE: 72

uucgcgcauc gaaucaaggg aagcgugccg gugcaggcaa cugaccaccg uaagcgucgu 60

ugcaaauaga uaagcgccga uucacaucag cgcgacuuac cucucgcugc cuaagcgaca 120

gcuaguccgu cagcccggga acgcccucga cccggagccu ggcgucagcu agagggaucc 180

accgaugagu ucggucgcgg gacucaucgg gacaccaaca gcgacuggga ucgucauccu 240

ggcuuguucg cgugaccagg agauccgagu agaggcauag cgaacugcgc acggagaagc 300

cuugagggaa ugccguagaa cccggguucg auucccaa 338

<210> SEQ ID NO 73
<211> LENGTH: 368
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium tuberculosis

<400> SEQUENCE: 73

ggggctgaac ggtttcgact tcgcgcatcg aatcaaggga agcgtgccgg tgcaggcaag 60

agaccaccgt aagcgtcgtt gcgaccaaat aagcgccgat tcacatcagc gcgactacgc 120

tctcgctgcc taagcgacgg ctagtctgtc agaccgggaa cgccctcggc ccggaccctg 180

gcatcagcta gagggatcca ccgatgagtc cggtcgcggg actcctcggg acaaccacag 240

cgactgggat cgtcatctcg gctagttcgc gtgaccggga gatccgagca gaggcatagc 300

gaactgcgca cggagaagcc ttgagggaat gccgtaggac ccgggttcga ttcccggcag 360

ctccacca 368

<210> SEQ ID NO 74
<211> LENGTH: 368
<212> TYPE: RNA
<213> ORGANISM: Mycobacterium tuberculosis

<400> SEQUENCE: 74

ggggcugaac gguuucgacu ucgcgcaucg aaucaaggga agcgugccgg ugcaggcaag 60

agaccaccgu aagcgucguu gcgaccaaau aagcgccgau ucacaucagc gcgacuacgc 120

ucucgcugcc uaagcgacgg cuagucuguc agaccgggaa cgcccucggc ccggacccug 180

gcaucagcua gagggaucca ccgaugaguc cggucgcggg acuccucggg acaaccacag 240

cgacugggau cgucaucucg gcuaguucgc gugaccggga gauccgagca gaggcauagc 300

gaacugcgca cggagaagcc uugagggaau gccguaggac ccggguucga uucccggcag 360

cuccacca 368

<210> SEQ ID NO 75
<211> LENGTH: 411
<212> TYPE: DNA
<213> ORGANISM: Mycoplasma capricolum

<400> SEQUENCE: 75

ggggatgtca tggatttgac aggatatctt tagtacatat aagcagtagt gttgtagact 60

ataaatacta ctaggtttaa aaaaacgcaa ataaaaacga agaaactttt gaaatgccag 120

catttatgat gaataatgca tcagctggag caaactttat gtttgcttaa taactactag 180

tttagttata gtatttcacg aattatagat attttaagct ttatttataa ccgtattacc 240

caagcttaat agaatatatg attgcaataa atatatttga aatctaattg caaatgatat 300

ttaaccttta gttaatttta gttaaatatt ttaattagaa aattaactaa actgtagaaa 360

gtatgtatta atatatcttg gacgcgagtt cgattctcgc catctccacc a 411

<210> SEQ ID NO 76
<211> LENGTH: 411
<212> TYPE: RNA
<213> ORGANISM: Mycoplasma capricolum

<400> SEQUENCE: 76

ggggauguca uggauuugac aggauaucuu uaguacauau aagcaguagu guuguagacu 60

auaaauacua cuagguuuaa aaaaacgcaa auaaaaacga agaaacuuuu gaaaugccag 120

cauuuaugau gaauaaugca ucagcuggag caaacuuuau guuugcuuaa uaacuacuag 180

uuuaguuaua guauuucacg aauuauagau auuuuaagcu uuauuuauaa ccguauuacc 240

caagcuuaau agaauauaug auugcaauaa auauauuuga aaucuaauug caaaugauau 300

uuaaccuuua guuaauuuua guuaaauauu uuaauuagaa aauuaacuaa acuguagaaa 360

guauguauua auauaucuug gacgcgaguu cgauucucgc caucuccacc a 411

<210> SEQ ID NO 77
<211> LENGTH: 388
<212> TYPE: DNA
<213> ORGANISM: Mycoplasma genitalium (ATTC 33530, #1)

<400> SEQUENCE: 77

ggggatgttt tgggtttgac ataatgctga tagacaaaca gtagcattgg ggtatgcccc 60

ttacagcgct aggttcaata accgacaaag aaaataacga agtgttggta gaaccaaatt 120

tgatcattaa ccaacaagca agtgttaact ttgcttttgc ataagtagat actaaagcta 180

cagctggtga atagtcatag tttgctagct gtcatagttt atgactcgag gttaaatcgt 240

tcaatttaac ctttaaaaat agaacttgtt gtttccatga ttgttttgtg atcaattgga 300

aacaagacaa aaatccacaa aactaaaatg tagaagctgt ttgttgtgtc ctttatggaa 360

acgggttcga ttcccgtcat ctccacca 388

<210> SEQ ID NO 78
<211> LENGTH: 388
<212> TYPE: RNA
<213> ORGANISM: Mycoplasma genitalium (ATTC 33530, #1)

<400> SEQUENCE: 78

ggggauguuu uggguuugac auaaugcuga uagacaaaca guagcauugg gguaugcccc 60

uuacagcgcu agguucaaua accgacaaag aaaauaacga aguguuggua gaaccaaauu 120

ugaucauuaa ccaacaagca aguguuaacu uugcuuuugc auaaguagau acuaaagcua 180

cagcugguga auagucauag uuugcuagcu gucauaguuu augacucgag guuaaaucgu 240

ucaauuuaac cuuuaaaaau agaacuuguu guuuccauga uuguuuugug aucaauugga 300

aacaagacaa aaauccacaa aacuaaaaug uagaagcugu uuguuguguc cuuuauggaa 360

acggguucga uucccgucau cuccacca 388

<210> SEQ ID NO 79
<211> LENGTH: 243
<212> TYPE: RNA
<213> ORGANISM: Mycoplasma genitalium (ATTC 33530, #2)

<400> SEQUENCE: 79

acaaagcgaa gacaaacaga gcaggggagc cccacagcgc aggcaaaacc gacaaagaaa 60

aaacgaaggg gagaccaaag acaaaccaac aagcaaggaa cgcgcaaaga gaacaaagca 120

cagcgggaaa gcaaggcagc gcaagagacc gaggaaacgc aaaaccaaaa aagaacggcc 180

agagggacaa ggaaacaaga caaaaaccac aaaacaaaag agaagcgggg ccaggaaacg 240

ggc 243

<210> SEQ ID NO 80
<211> LENGTH: 350
<212> TYPE: RNA
<213> ORGANISM: Mycoplasma genitalium (ATTC 33530, #2)

<400> SEQUENCE: 80

acauaaugcu gauagacaaa caguagcauu gggguaugcc ccuuacagcg cuagguucaa 60

uaaccgacaa agaaaauaac gaaguguugg uagaaccaaa uuugaucauu aaccaacaag 120

caaguguuaa cuuugcuuuu gcauaaguag auacuaaagc uacagcuggu gaauagucau 180

aguuugcuag cugucauagu uuaugacucg agguuaaauc guucaauuua accuuuaaaa 240

auagaacuug uuguuuccau gauuguuuug ugaucaauug gaaacaagac aaaaauccac 300 aaaacuaaaa uguagaagcu guuuguugug uccuuuaugg aaacggguuc 350

<210> SEQ ID NO 81
<211> LENGTH: 387
<212> TYPE: DNA
<213> ORGANISM: Mycoplasma pneumophila

<400> SEQUENCE: 81

ggggatgtag aggttttgac ataatgttga aaggaaaaca gttgcagtgg ggtatgcccc 60

ttacagctct aggtataata accgacaaaa ataacgacga agttttggta gatccaatgt 120

tgatcgctaa ccaacaagca agtatcaact acgctttcgc ttagaacata ctaaagctac 180

acgaattgaa tcgccatagt ttggttcgtg tcacagttta tggctcgggg ttaactggtt 240

caacttaatc cttaaattat gaacttatcg tttacttgtt tgtcttatga tctaaagtaa 300

gcgagacatt aaaacataag actaaactgt agaagctgtt ttaccaatcc tttatggaaa 360

cgggttcgat tcccgtcatc tccacca 387

<210> SEQ ID NO 82
<211> LENGTH: 387
<212> TYPE: RNA
<213> ORGANISM: Mycoplasma pneumophila

<400> SEQUENCE: 82

ggggauguag agguuuugac auaauguuga aaggaaaaca guugcagugg gguaugcccc 60

uuacagcucu agguauaaua accgacaaaa auaacgacga aguuuuggua gauccaaugu 120

ugaucgcuaa ccaacaagca aguaucaacu acgcuuucgc uuagaacaua cuaaagcuac 180

acgaauugaa ucgccauagu uugguucgug ucacaguuua uggcucgggg uuaacugguu 240

caacuuaauc cuuaaauuau gaacuuaucg uuuacuuguu ugucuuauga ucuaaaguaa 300

gcgagacauu aaaacauaag acuaaacugu agaagcuguu uuaccaaucc uuuauggaaa 360

cggguucgau ucccgucauc uccacca 387

<210> SEQ ID NO 83
<211> LENGTH: 318
<212> TYPE: DNA
<213> ORGANISM: Neisseria gonorrhoeae (ATCC 19424)

<400> SEQUENCE: 83

gggggttgcg aagcagatgc gggcataccg gggtctcaga ttcccgtaaa acactgaatt 60

caaatagtcg caaacgacga aacttacgct ttagccgctt aaggctagcc gttgcagcag 120

tcggtcaatg ggctgtgtgg cgaaagccac cgcaacgtca tcttacattg actggtttcc 180

agccgggtta cttggcagga aataagactt aaggtaactg gtttccaaaa ggcctgttgg 240

tcggcatgat ggaaataaga ttttcaaata gacacaacta agtatgtaga acgctttgta 300

gaggactttc ggacgggg 318

<210> SEQ ID NO 84
<211> LENGTH: 318
<212> TYPE: RNA
<213> ORGANISM: Neisseria gonorrhoeae (ATCC 19424)

<400> SEQUENCE: 84

ggggguugcg aagcagaugc gggcauaccg gggucucaga uucccguaaa acacugaauu 60

caaauagucg caaacgacga aacuuacgcu uuagccgcuu aaggcuagcc guugcagcag 120

ucggucaaug ggcugugugg cgaaagccac cgcaacguca ucuuacauug acugguuucc 180 agccggguua cuuggcagga aauaagacuu aagguaacug guuuccaaaa ggccuguugg 240

ucggcaugau ggaaauaaga uuuucaaaua gacacaacua aguauguaga acgcuuugua 300

gaggacuuuc ggacgggg 318

<210> SEQ ID NO 85
<211> LENGTH: 363
<212> TYPE: DNA
<213> ORGANISM: Neisseria gonorrhoeae (FA 1090)

<400> SEQUENCE: 85

gggggcgacc ttggtttcga cgggggttgc gaagcagatg cgggcatacc ggggtctcag 60

attcccgtaa aacactgaat tcaaatagtc gcaaacgacg aaacttacgc tttagccgct 120

taaggctagc cgttgcagca gtcggtcaat gggctgtgtg gtgaaagcca ccgcaacgtc 180

atcttacatt gactggtttc cagccgggtt acttggcagg aaataagact taaggtaact 240

ggtttccaaa aggcctgttg gtcggcatga tggaaataag attttcaaat agacacaact 300

aagtatgtag aacgctttgt agaggacttt cggacggggg ttcgattccc cccgcctcca 360

cca 363

<210> SEQ ID NO 86
<211> LENGTH: 363
<212> TYPE: RNA
<213> ORGANISM: Neisseria gonorrhoeae (FA 1090)

<400> SEQUENCE: 86

gggggcgacc uugguuucga cgggggguugc gaagcagaug cgggcauacc ggggucucag 60

auucccguaa aacacugaau ucaaauaguc gcaaacgacg aaacuuacgc uuuagccgcu 120

uaaggcuagc cguugcagca gucggucaau gggcugugug gugaaagcca ccgcaacguc 180

aucuuacauu gacugguuuc cagccggguu acuuggcagg aaauaagacu uaagguaacu 240

gguuuccaaa aggccuguug gucggcauga uggaaauaag auuuucaaau agacacaacu 300

aaguauguag aacgcuuugu agaggacuuu cggacggggg uucgauuccc cccgccucca 360

cca 363

<210> SEQ ID NO 87
<211> LENGTH: 363
<212> TYPE: DNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 87

gggggcgacc ttggtttcga cgggggttgc gaagcagatg cgggcatacc ggggtctcag 60

attcccgtaa aacactgaat tcaaatagtc gcaaacgacg aaacttacgc tttagccgct 120

taaggctagc cgttgcagca gtcggtcaat gggctgtgtg gcgaaagcca ccgcaacgtc 180

atcttacatt gactggtttc ctgccgggtt atttggcagg aaatgagatt taaggtaact 240

ggtttccaaa aggcctgttg gtcggcatga tggaaataag attttcaaat agacacaact 300

aagtatgtag aacgctttgt agaggacttt cggacggggg ttcgattccc cccgcctcca 360

cca 363

<210> SEQ ID NO 88
<211> LENGTH: 363
<212> TYPE: RNA
<213> ORGANISM: Neisseria meningitidis

<400> SEQUENCE: 88

```
gggggcgacc uugguuucga cggggguugc gaagcagaug cgggcauacc ggggucucag     60

auucccguaa aacacugaau ucaaauaguc gcaaacgacg aaacuuacgc uuuagccgcu    120

uaaggcuagc cguugcagca gucggucaau gggcugugug gcgaaagcca ccgcaacguc    180

aucuuacauu gacugguuuc cugccggguu auuuggcagg aaaugagauu uaagguaacu    240

gguuuccaaa aggccuguug gucggcauga uggaaauaag auuuucaaau agacacaacu    300

aaguauguag aacgcuuugu agaggacuuu cggacggggg uucgauuccc cccgccucca    360

cca                                                                  363


<210> SEQ ID NO 89
<211> LENGTH: 385
<212> TYPE: DNA
<213> ORGANISM: Nostoc muscorum PCC7120

<400> SEQUENCE: 89

gggtccgtcg gtttcgacag gttggcgaac gctactctgt gattcaggtc gagagtgagt     60

ctcctctgca aatcaaggct caaaacaaaa gtaaatgcga ataacatcgt taaatttgct    120

cgtaaggacg ctctagtagc tgcctaaata gcctctttca ggttcgagcg tcttcggttt    180

gactccgtta aggactgaag accaaccccc aacggatgct ctagcaatgt tctctggttg    240

gcttgctagc taagatttaa tcagagcatc ctacgttcgg gataatgaac gattcccgcc    300

ttgagggtca gaaaggctaa acctgtgaat gagcgggggg tcaataccca atttggacag    360

cagttcgact ctgctcgatc cacca                                          385


<210> SEQ ID NO 90
<211> LENGTH: 385
<212> TYPE: RNA
<213> ORGANISM: Nostoc muscorum PCC7120

<400> SEQUENCE: 90

ggguccgucg guuucgacag guuggcgaac gcuacucugu gauucagguc gagagugagu     60

cuccucugca aaucaaggcu caaaacaaaa guaaaugcga auaacaucgu uaaauuugcu    120

cguaaggacg cucuaguagc ugccuaaaua gccucuuuca gguucgagcg ucuucgguuu    180

gacuccguua aggacugaag accaaccccc aacggaugcu cuagcaaugu ucucugguug    240

gcuugcuagc uaagauuuaa ucagagcauc cuacguucgg gauaaugaac gauucccgcc    300

uugaggguca gaaaggcuaa accugugaau gagcgggggg ucaauaccca auuuggacag    360

caguucgacu cugcucgauc cacca                                          385


<210> SEQ ID NO 91
<211> LENGTH: 371
<212> TYPE: DNA
<213> ORGANISM: Odontella sinensis (diatom) chloroplast

<400> SEQUENCE: 91

ggggctgact tggtttcgac atttaaaaat tgttacagta tgatgcaggt cgaagtttct     60

aatcttcgta aaaaaagaga aatttataat aaatgctaat aatttaattt cttctgtgtt    120

taaaagttta tcaactaagc aaaatagttt aaatttaagt tttgctgttt aagttttatg    180

cacatttaat gatctagtaa ataactttgt tcgctataat ttatatttat aactagactt    240

ttgtcttttt tatagtttag aataacttta tcatttcaaa cctcgttcca tctagttgaa    300

ctaaacctgt gaacgaatac tataataaaa tttttagatg gacgtgggtt cgactcccat    360

cagctccacc a                                                         371
```

<210> SEQ ID NO 92
<211> LENGTH: 371
<212> TYPE: RNA
<213> ORGANISM: Odontella sinensis (diatom) chloroplast

<400> SEQUENCE: 92

ggggcugacu ugguuucgac auuuaaaaau uguuacagua ugaugcaggu cgaaguuucu 60

aaucuucgua aaaaaagaga aauuuauaau aaaugcuaau aauuuaauuu cuucuguguu 120

uaaaaguuua ucaacuaagc aaaauaguuu aaauuuaagu uuugcuguuu aaguuuuaug 180

cacauuuaau gaucuaguaa auaacuuugu ucgcuauaau uuauauuuau aacuagacuu 240

uugucuuuuu uauaguuuag aauaacuuua ucauuucaaa ccucguucca ucuaguugaa 300

cuaaaccugu gaacgaauac uauaauaaaa uuuuuagaug gacgugggu cgacucccau 360

cagcuccacc a 371

<210> SEQ ID NO 93
<211> LENGTH: 323
<212> TYPE: DNA
<213> ORGANISM: Porphyra purpureum (red alga) chloroplast

<400> SEQUENCE: 93

ggggctgcaa ggtttctaca ttgtgaaaaa acaaatatat gaaagtaaaa cgagctcatt 60

attagagctt ttagttaaat aaatgcagaa aataatatta ttgctttttc tcgaaaatta 120

gctgttgcat aaatagtctc aatttttgta attcgaagtg atagactctt atacactacg 180

aatattctgt tagagttgct cttaataaaa gaaaagtaaa aaaatacaaa ttcttatgtt 240

ttttacctga attgattcaa tttaaggtta gtatttttg atttttacaa tggacgtggg 300

ttcaagtccc accagctcca cca 323

<210> SEQ ID NO 94
<211> LENGTH: 323
<212> TYPE: RNA
<213> ORGANISM: Porphyra purpureum (red alga) chloroplast

<400> SEQUENCE: 94

ggggcugcaa gguuucuaca uugugaaaaa acaaauauau gaaaguaaaa cgagcucauu 60

auuagagcuu uuaguuaaau aaaugcagaa aauaauauua uugcuuuuuc ucgaaaauua 120

gcuguugcau aaauagucuc aauuuuugua auucgaagug auagacucuu auacacuacg 180

aauauucugu uagaguugcu cuuaauaaaa gaaaaguaaa aaaauacaaa uucuuauguu 240

uuuuaccuga auugauucaa uuuaagguua guauuuuug auuuuuacaa uggacguggg 300

uucaaguccc accagcucca cca 323

<210> SEQ ID NO 95
<211> LENGTH: 407
<212> TYPE: DNA
<213> ORGANISM: Porphyromonas gingivalis

<400> SEQUENCE: 95

ggggctgacc ggctttgaca gcgtgatgaa gcggtatgta agcatgtagt gcgtgggtgg 60

cttgcactat aatctcagac atcaaaagtt taattggcga aaataactac gctctcgctg 120

cgtaatcgaa gaatagtaga ttagacgctt catcgccgcc aaagtggcag cgacgagaca 180

tcgcccgagc agctttttcc cgaagtagct cgatggtgcg gtgctgacaa atcgggaacc 240

gctacaggat gcttcctgcc tgtggtcaga tcgaacggaa gataaggatc gtgcattggg 300 tcgtttcagc ctccgctcgc tcacgaaaat tccaactgaa actaaacatg tagaaagcat 360

attgattcca tgtttggacg agggttcaat tccctccagc tccacca 407

<210> SEQ ID NO 96
<211> LENGTH: 407
<212> TYPE: RNA
<213> ORGANISM: Porphyromonas gingivalis

<400> SEQUENCE: 96

ggggcugacc ggcuuugaca gcgugaugaa gcgguaugua agcauguagu gcgugggugg 60

cuugcacuau aaucucagac aucaaaaguu uaauuggcga aaauaaacuac gcucucgcug 120

cguaaucgaa gaauaguaga uuagacgcuu caucgccgcc aaaguggcag cgacgagaca 180

ucgcccgagc agcuuuuucc cgaaguagcu cgauggugcg gugcugacaa aucgggaacc 240

gcuacaggau gcuuccugcc uguggucaga ucgaacggaa gauaaggauc gugcauuggg 300

ucguuucagc cuccgcucgc ucacgaaaau uccaacugaa acuaaacaug uagaaagcau 360

auugauucca uguuuggacg aggguucaau ucccuccagc uccacca 407

<210> SEQ ID NO 97
<211> LENGTH: 310
<212> TYPE: DNA
<213> ORGANISM: Proteus rettgeri (NCTC 10975)

<400> SEQUENCE: 97

gggatttgcg aaacccaagg tgcatgccga ggggcggttg gcctcgtaaa aagccgcaaa 60

aaaatagtcg caaacgacga aaactacgct ttagcagctt aataacctgc ttagagccct 120

ctctccctag cctccgctct tggacgggga tcaagagagg tcaaacccaa aagagatcgc 180

gtggatgcct tgcctggggt tgaagcgtta aacttaatca ggatagtttg ttggtggcgt 240

gtctgtccgc agctggcaaa tgaattcaaa gactagacta agcatgtagt accgaggatg 300

tagaaatttc 310

<210> SEQ ID NO 98
<211> LENGTH: 310
<212> TYPE: RNA
<213> ORGANISM: Proteus rettgeri (NCTC 10975)

<400> SEQUENCE: 98

gggauuugcg aaacccaagg ugcaugccga ggggcgguug gccucguaaa aagccgcaaa 60

aaaauagucg caaacgacga aaacuacgcu uuagcagcuu aauaaccugc uuagagcccu 120

cucucccuag ccuccgcucu uggacgggga ucaagagagg ucaaacccaa aagagaucgc 180

guggaugccu ugccuggggu ugaagcguua aacuuaauca ggauaguuug uugguggcgu 240

gucuguccgc agcuggcaaa ugaauucaaa gacuagacua agcauguagu accgaggaug 300

uagaaauuuc 310

<210> SEQ ID NO 99
<211> LENGTH: 241
<212> TYPE: DNA
<213> ORGANISM: Pseudoalteromonas haloplanktis

<400> SEQUENCE: 99

gggagcgaaa cccaagggca gccgaggggc ggggcccgaa aaagccgcaa aaaaaagcgc 60

aaacgacgaa aacacgcagc agcaaaaccg cagagccccc cccagccccg ccggacgggg 120

acaagagagg caaacccaaa agagacgcgg gagccgccgg gggaagcgaa acaacaggaa 180 gggggcggc gccgcagcgg caaagaacaa agacagacaa gcagagaccg aggagagaaa 240

c 241

<210> SEQ ID NO 100
<211> LENGTH: 313
<212> TYPE: RNA
<213> ORGANISM: Pseudoalteromonas haloplanktis

<400> SEQUENCE: 100

ggaauucaag aagcccgagg ugcaugucga ggugcgguuu gccucguaaa aaagccgcaa 60

uuuaaaguaa ucgcaaacga cgauaacuac ucucuagcag cuuaggcugg cuagcgcucc 120

uuccauguau ucuuguggac uggauuuugg agugucaccc uaacaccuga ucgcgacgga 180

aacccuggcc gggguugaag cguuaaaacu aagcggccuc gccuuuaucu accguguuug 240

uccgggauuu aaagguuaau uaaaugacaa uacuaaacau guaguaccga cggucgaggc 300

uuuucggacg ggg 313

<210> SEQ ID NO 101
<211> LENGTH: 353
<212> TYPE: DNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 101

ggggccgatt aggattcgac gccggtaaca aaagttgagg ggcatgccga gttggtagca 60

gaactcgtaa attcgctgct gcaaacttat agttgccaac gacgacaact acgctctagc 120

tgcttaatgc ggctagcagt cgctagggga tgcctgtaaa cccgaaacga ctgtcagata 180

gaacaggatc gccgccaagt tcgctgtaga cgtaacggct aaaactcata cagctcgctc 240

caagcaccct gccactcggg cggcgcggag ttaactcagt agagctggct aagcatgtaa 300

aaccgatagc ggaaagctgg cggacggggg ttcaaatccc cccggatcca cca 353

<210> SEQ ID NO 102
<211> LENGTH: 353
<212> TYPE: RNA
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 102

ggggccgauu aggauucgac gccgguaaca aaaguugagg ggcaugccga guugguagca 60

gaacucguaa auucgcugcu gcaaacuuau aguugccaac gacgacaacu acgcucuagc 120

ugcuuaaugc ggcuagcagu cgcuagggga ugccuguaaa cccgaaacga cugucagaua 180

gaacaggauc gccgccaagu ucgcuguaga cguaacggcu aaaacucaua cagcucgcuc 240

caagcacccu gccacucggg cggcgcggag uuaacucagu agagcuggcu aagcauguaa 300

aaccgauagc ggaaagcugg cggacggggg uucaaauccc cccggcucca cca 353

<210> SEQ ID NO 103
<211> LENGTH: 363
<212> TYPE: DNA
<213> ORGANISM: Salmonella typhimurium

<400> SEQUENCE: 103

ggggctgatt ctggattcga cgggatttgc gaaacccaag gtgcatgccg aggggcggtt 60

ggcctcgtaa aaagccgcaa aaaaatagtc gcaaacgacg aaacctacgc tttagcagct 120

taataacctg cttagagccc tctctcccta gcctccgctc ttaggacggg gatcaagaga 180

ggtcaaaccc aaaagagatc gcgcggatgc cctgcctggg gttgaagcgt taaaacgaat 240 caggctagtc tggtagtggc gtgtccgtcc gcaggtgcca ggcgaatgta aagactgact 300

aagcatgtag taccgaggat gtaggaattt cggacgcggg ttcaactccc gccagctcca 360

cca 363

<210> SEQ ID NO 104
<211> LENGTH: 363
<212> TYPE: RNA
<213> ORGANISM: Salmonella typhimurium

<400> SEQUENCE: 104

ggggcugauu cuggauucga cgggauuugc gaaacccaag gugcaugccg aggggcgguu 60

ggccucguaa aaagccgcaa aaaaauaguc gcaaacgacg aaaccuacgc uuuagcagcu 120

uaauaaccug cuuagagccc ucucucccua gccuccgcuc uuaggacggg gaucaagaga 180

ggucaaaccc aaaagagauc gcgcggaugc ccugccuggg guugaagcgu uaaaacgaau 240

caggcuaguc ugguaguggc guguccgucc gcaggugcca ggcgaaugua aagacugacu 300

aagcauguag uaccgaggau guaggaauuu cggacgcggg uucaacuccc gccagcucca 360

cca 363

<210> SEQ ID NO 105
<211> LENGTH: 355
<212> TYPE: DNA
<213> ORGANISM: Shewanella putrefaciens

<400> SEQUENCE: 105

gggggcgatt ctggattcga caggattcac gaaaccctgg gagcatgccg aggggcggtt 60

ggcctcgtaa aaagccgcaa agttatagtt gcaaacgacg ataactacgc tctagccgct 120

taatgccgct agccatctac cacacgcttt gcacatgggc agtggatttg atggtcatct 180

cacatcgtgc tagcgaggga accctgtctg gggtgaacc gcgaaacagt accggactca 240

ccgtgtggga tcctgtcttt cggagttcaa acggttaaac aatagaaaga ctaagcatgt 300

agcgccttgg atgtaggttt tctggacgcg ggttcaagtc ccgccgcctc cacca 355

<210> SEQ ID NO 106
<211> LENGTH: 355
<212> TYPE: RNA
<213> ORGANISM: Shewanella putrefaciens

<400> SEQUENCE: 106

gggggcgauu cuggauucga caggauucac gaaacccugg gagcaugccg aggggcgguu 60

ggccucguaa aaagccgcaa aguuauaguu gcaaacgacg auaacuacgc ucuagccgcu 120

uaaugccgcu agccaucuac cacacgcuuu gcacaugggc aguggauuug auggucaucu 180

cacaucgugc uagcgaggga acccugucug gggugaacc gcgaaacagu accggacuca 240

ccguguggga uccugucuuu cggaguucaa acgguuaaac aauagaaaga cuaagcaugu 300

agcgccuugg auguagguuu ucuggacgcg gguucaaguc ccgccgccuc cacca 355

<210> SEQ ID NO 107
<211> LENGTH: 362
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 107

ggggacgttc atggattcga caggggtccc ccgagctcat taagcgtgtc ggagggttgt 60

cttcgtcatc aacacacaca gtttataata actggcaaat caaacaataa tttcgcagta 120 gctgcctaat cgcactctgc atcgcctaac agcatttcct atgtgctgtt aacgcgattc 180

aaccttaata ggatatgcta aacactgccg tttgaagtct gtttagaaga aacttaatca 240

aactagcatc atgttggttg tttatcactt ttcatgatgc gaaacctatc gataaactac 300

acacgtagaa agatgtgtat caggaccttt ggacgcgggt tcaaatcccg ccgtctccac 360

ca 362

<210> SEQ ID NO 108
<211> LENGTH: 362
<212> TYPE: RNA
<213> ORGANISM: Staphylococcus aureus

<400> SEQUENCE: 108

ggggacguuc auggauucga caggggucccc ccgagcucau uaagcguguc ggaggguugu 60

cuucgucauc aacacacaca guuuauaaua acuggcaaau caaacaauaa uuucgcagua 120

gcugccuaau cgcacucugc aucgccuaac agcauuuccu augugcuguu aacgcgauuc 180

aaccuuaaua ggauaugcua aacacugccg uuugaagucu guuuagaaga aacuuaauca 240

aacuagcauc auguugguug uuuaucacuu uucaugaugc gaaaccuauc gauaaacuac 300

acacguagaa agauguguau caggaccuuu ggacgcgggu ucaaaucccg ccgucuccac 360

ca 362

<210> SEQ ID NO 109
<211> LENGTH: 349
<212> TYPE: DNA
<213> ORGANISM: Streptococcus gordonii

<400> SEQUENCE: 109

ggggtcgtta cggattcgac aggcattatg aggcatattt tgcgactcat ctagcggatg 60

taaaacgcca gttaaatata actgcaaaaa ataatacttc ttacgcttta gctgcctaaa 120

aaccagcggg cgtgacccga ttcggattgc ttgtgtctga tgacaggtct tattattagc 180

aagctacggt agaatcttgt ctagtgattt tacaagagat tgatagactc gcttgatttg 240

ggcttgagtt atgtgtcaaa atcaagttaa aacaatacat agcctatggt tgtagacaaa 300

tgtgttggca gatgtttgga cgtgggttcg actcccaccg gctccacca 349

<210> SEQ ID NO 110
<211> LENGTH: 349
<212> TYPE: RNA
<213> ORGANISM: Streptococcus gordonii

<400> SEQUENCE: 110

ggggucguua cggauucgac aggcauuaug aggcauauuu ugcgacucau cuagcggaug 60

uaaaacgcca guuaaauaua acugcaaaaa auaauacuuc uuacgcuuua gcugccuaaa 120

aaccagcggg cgugacccga uucggauugc uugugucuga ugacaggucu uauuauuagc 180

aagcuacggu agaaucuugu cuagugauuu uacaagagau ugauagacuc gcuugauuug 240

ggcuugaguu augugucaaa aucaaguuaa aacaauacau agccuauggu uguagacaaa 300

uguguuggca gauguuugga cgugggguucg acucccaccg gcuccacca 349

<210> SEQ ID NO 111
<211> LENGTH: 349
<212> TYPE: DNA
<213> ORGANISM: Streptococcus mutans

<400> SEQUENCE: 111

ggggtcgtta cggattcgac aggcattatg agacctattt tgcgactcat ctagcggatg 60

taaaacgcca gttaaatata actgcaaaaa atacaaattc ttacgcagta gctgcctaaa 120

aaccagcctg tgtgatcaat aacaaattgc ttgtgtttgt tgattggtct tattgttaac 180

aagctacgtt agaactgagt caggctgttc taaaagagtt ctactgactc gcatcgttag 240

agtttgagtt atgtattgta acggtgttaa ataaacacat aacctatagt tgtagacaaa 300

tgggttagca gatgtttgga cgtgggttcg actcccaccg gctccacca 349

<210> SEQ ID NO 112
<211> LENGTH: 349
<212> TYPE: RNA
<213> ORGANISM: Streptococcus mutans

<400> SEQUENCE: 112

ggggucguua cggauucgac aggcauuaug agaccuauuu ugcgacucau cuagcggaug 60

uaaaacgcca guuaaauaua acugcaaaaa auacaaauuc uuacgcagua gcugccuaaa 120

aaccagccug ugugaucaau aacaaauugc uuguguuugu ugauuggucu uauuguuaac 180

aagcuacguu agaacugagu caggcuguuc uaaaagaguu cuacugacuc gcaucguuag 240

aguuugaguu auguauugua acgguguuaa auaaacacau aaccuauagu uguagacaaa 300

uggguuagca gauguuugga cguggguucg acucccaccg gcuccacca 349

<210> SEQ ID NO 113
<211> LENGTH: 348
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 113

ggggtcgtta cggattcgac aggcattatg aggcatattt tgcgactcgt gtggcgacgt 60

aaacgctcag ttaaatataa ctgcaaaaaa taacacttct tacgctctag ctgcctaaaa 120

accagcaggc gtgacccgat ttggattgct cgtgttcaat gacaggtctt attattagcg 180

agatacgatt aagccttgtc tagcggtttg ataagagatt gatagactcg cagtttctag 240

acttgagtta tgtgtcgagg ggctgttaaa ataatacata acctatggtt gtagacaaat 300

atgttggcag gtgtttggac gtgggttcga ctcccaccgg ctccacca 348

<210> SEQ ID NO 114
<211> LENGTH: 348
<212> TYPE: RNA
<213> ORGANISM: Streptococcus pneumoniae

<400> SEQUENCE: 114

ggggucguua cggauucgac aggcauuaug aggcauauuu ugcgacucgu guggcgacgu 60

aaacgcucag uuaaauauaa cugcaaaaaa uaacacuucu uacgcucuag cugccuaaaa 120

accagcaggc gugacccgau uuggauugcu cguguucaau gacaggucuu auuauuagcg 180

agauacgauu aagccuuguc uagcgguuug auaagagauu gauagacucg caguuucuag 240

acuugaguua ugugucgagg ggcuguuaaa auaauacaua accuaugguu guagacaaau 300

auguuggcag guguuuggac guggguucga cucccaccgg cuccacca 348

<210> SEQ ID NO 115
<211> LENGTH: 348
<212> TYPE: DNA
<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 115

ggggttgtta cggattcgac aggcattatg aggcatgttt tgcgtcccat cggcagatgt 60

aaattgccag ttaaatataa ctgcaaaaaa tacaaactct tacgctttag ctgcctaaaa 120

accagctagc gtgacttcta caagattgct tgtgtcctgt tagaagtctc aaaatagcaa 180

gctacggtta cgaaattgtc tagtttcgtg acaagagatt gatagactcg caaactaatg 240

gcttgagtta tgtgtcttta gtttgttaaa tgaagacata acctatggac gtagacaaat 300

atgttggcag gtgtttggac gtgggttcga ctcccaccag ctccacca 348

<210> SEQ ID NO 116
<211> LENGTH: 348
<212> TYPE: RNA
<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 116

gggguuguua cggauucgac aggcauuaug aggcauguuu ugcgucccau cggcagaugu 60

aaauugccag uuaaauauaa cugcaaaaaa uacaaacucu uacgcuuuag cugccuaaaa 120

accagcuagc gugacuucua caagauugcu uguguccugu uagaagucuc aaaauagcaa 180

gcuacgguua cgaaauuguc uaguuucgug acaagagauu gauagacucg caaacuaaug 240

gcuugaguua ugugucuuua guuuguuaaa ugaagacaua accuauggac guagacaaau 300

auguuggcag guguuuggac guggguucga cucccaccag cuccacca 348

<210> SEQ ID NO 117
<211> LENGTH: 394
<212> TYPE: DNA
<213> ORGANISM: Synechococcus sp. PCC6301

<400> SEQUENCE: 117

ggggctgtaa tggtttcgac gtgttggtga atccttcacc gtgattcagg ccgagaggga 60

gtccactctc gtaaatccag gctcaaccaa aagtaactgc gaacaacatc gttcctttcg 120

ctcgtaaggc tgctcctgta gctgcttaaa cgccacaaac tttctggctc gagcgtctag 180

tcgtagactc cgttaatacg cctagactta aacccccaac ggatgctcga gtggcggcct 240

caggtccgtc ctctcgctaa gcaaaaacct gagcatcccg ccaacgggga taatcgttgg 300

ctcccgcaca gtgggtcaac cgtgctaagc ctgtgaacga gcggaaagtt actagtcaat 360

gcggacagcg gttcgattcc gctcagctcc acca 394

<210> SEQ ID NO 118
<211> LENGTH: 394
<212> TYPE: RNA
<213> ORGANISM: Synechococcus sp. PCC6301

<400> SEQUENCE: 118

ggggcuguaa ugguuucgac guguuggUga auccuucacc gugauucagg ccgagaggga 60

guccacucuc guaaauccag gcucaaccaa aaguaacugc gaacaacauc guuccuuucg 120

cucguaaggc ugcuccugua gcugcuuaaa cgccacaaac uuucuggcuc gagcgucuag 180

ucguagacuc cguuaauacg ccuagacuua aacccccaac ggaugcucga guggcggccu 240

cagguccguc cucucgcuaa gcaaaaaccu gagcaucccg ccaacgggga uaaucguugg 300

cucccgcaca gugggucaac cgugcuaagc cugugaacga gcggaaaguu acuagucaau 360

gcggacagcg guucgauucc gcucagcucc acca 394

<210> SEQ ID NO 119
<211> LENGTH: 399

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<212> TYPE: DNA
<213> ORGANISM: Synechocystis PCC6803

<400> SEQUENCE: 119

gggccgcaa tggtttcgac aggttggcga aagcttgccc gtgatacagg tcgagagtga 60

gtctcctctc gcaaatcaaa ggctcaaaaa aaagtaactg cgaataacat cgtcagcttc 120

aaacgggtag ccatagcagc ctagtctgta aaagctacat tttcttgtca aagaccgttt 180

acttcttttc tgactccgtt aaggattaga ggttaacccc aacggatgct ttgtttggct 240

cttctctagt tagctaaaca atcaagactc agactagagc atcccaccat cagggataat 300

cgatggtccc cgtcctaggg ctagaaggac taaacctgtg aatgagcgga aagttaatac 360

ccagtttgga cagcagttca attctgctcg gctccacca 399

<210> SEQ ID NO 120
<211> LENGTH: 399
<212> TYPE: RNA
<213> ORGANISM: Synechocystis PCC6803

<400> SEQUENCE: 120

ggggccgcaa ugguuucgac agguuggcga aagcuugccc gugauacagg ucgagaguga 60

gucuccucuc gcaaaucaaa ggcucaaaaa aaaguaacug cgaauaacau cgucagcuuc 120

aaacggguag ccauagcagc cuagucugua aaagcuacau uuucuuguca aagaccguuu 180

acuucuuuuc ugacuccguu aaggauuaga gguuaacccc aacggaugcu uuguuuggcu 240

cuucucuagu uagcuaaaca aucaagacuc agacuagagc aucccaccau cagggauaau 300

cgauggaccc cguccuaggg cuagaaggac uaaaccugug aaugagcgga aaguuaauac 360

ccaguuugga cagcaguuca auucugcucg gcuccacca 399

<210> SEQ ID NO 121
<211> LENGTH: 356
<212> TYPE: DNA
<213> ORGANISM: Thermotoga maritima

<400> SEQUENCE: 121

gggggcgaac gggttcgacg gggatggagt cccctgggaa gcgagccgag gtccccacct 60

cctcgtaaaa aaggtgggac aaagaataag tgccaacgaa cctgttgctg ttgccgctta 120

atagataagc ggccgtcctc tccgaagttg gctgggcttc ggaagagggc gtgagagatc 180

cagcctaccg attcagcttc gccttccggc ctgaatcggg aaaactcagg aaggctgtgg 240

gagaggacac cctgcccgtg ggaggtccct cccgagagcg aaaacacggg ctgcgctcgg 300

agaagcccag gggcctccat cttcggacgg gggttcgaat ccccccgcct ccacca 356

<210> SEQ ID NO 122
<211> LENGTH: 356
<212> TYPE: RNA
<213> ORGANISM: Thermotoga maritima

<400> SEQUENCE: 122

gggggcgaac ggguucgacg gggauggagu ccccugggaa gcgagccgag guccccaccu 60

ccucguaaaa aaggugggac aaagaauaag ugccaacgaa ccuguugcug uugccgcuua 120

auagauaagc ggccguccuc uccgaaguug gcugggcuuc ggaagagggc gugagagauc 180

cagccuaccg auucagcuuc gccuuccggc cugaaucggg aaaacucagg aaggcugugg 240

gagaggacac ccugcccgug ggaggucccu cccgagagcg aaaacacggg cugcgcucgg 300

agaagcccag gggccuccau cuucggacgg ggguucgaau ccccccgccu ccacca 356

<210> SEQ ID NO 123
<211> LENGTH: 349
<212> TYPE: DNA
<213> ORGANISM: Thermus thermophilus

<400> SEQUENCE: 123

gggggtgaaa cggtctcgac gggggtcgcc gagggcgtgg ctgcgcgccg aggtgcgggt 60

ggcctcgtaa aaacccgcaa cggcataact gccaacacca actacgctct cgcggcttaa 120

tgaccgcgac ctcgcccggt agccctgccg ggggctcacc ggaagcgggg acacaaaccc 180

ggctagcccg gggccacgcc ctctaacccc gggcgaagct tgaagggggc tcgctcctgg 240

ccgcccgtcc gcgggccaag ccaggaggac acgcgaaacg cggactacgc gcgtagaggc 300

ccgccgtaga gaccttcgga cgggggttcg actcccccca cctccacca 349

<210> SEQ ID NO 124
<211> LENGTH: 349
<212> TYPE: RNA
<213> ORGANISM: Thermus thermophilus

<400> SEQUENCE: 124

gggggugaaa cggucucgac gggggucgcc gagggcgugg cugcgcgccg aggugcgggu 60

ggccucguaa aaacccgcaa cggcauaacu gccaacacca acuacgcucu cgcggcuuaa 120

ugaccgcgac cucgcccggu agcccugccg ggggcucacc ggaagcgggg acacaaaccc 180

ggcuagcccg gggccacgcc cucuaacccc gggcgaagcu ugaagggggc ucgcuccugg 240

ccgcccgucc gcgggccaag ccaggaggac acgcgaaacg cggacuacgc gcguagaggc 300

ccgccguaga gaccuucgga cggggguucg acucccccca ccuccacca 349

<210> SEQ ID NO 125
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Treponema pallidum

<400> SEQUENCE: 125

ggggatgact aggtttcgac tagggatgtg gggtgttgcg ctgcaggtgg agtgtcgatc 60

tcctgattcg gcgcctttat aactgccaat tctgacagtt tcgactacgc gctcgccgcg 120

taatcgcggg cctgtgtttg cgctgctctg agcgaacata tcggcccgac gccaaacgga 180

gcttgctctt acgttgtgca cggcggacgt agggggactt ttgtctgtgc taagactctg 240

gcgcgtgcgg tgcaggccta gcagagtccg acaaacgcag tacgcaccgc taaacctgta 300

ggcgcgcagc actcgctctt taggacgggg gttcgattcc ccccatctcc acca 354

<210> SEQ ID NO 126
<211> LENGTH: 354
<212> TYPE: RNA
<213> ORGANISM: Treponema pallidum

<400> SEQUENCE: 126

ggggaugacu agguuucgac uagggaugug ggguguugcg cugcaggugg agugucgauc 60

uccugauucg gcgccuuuau aacugccaau ucugacaguu ucgacuacgc gcucgccgcg 120

uaaucgcggg ccuguguuug cgcugcucug agcgaacaua ucggcccgac gccaaacgga 180

gcuugcucuu acguugugca cggcggacgu agggggacuu uugucugugc uaagacucug 240

gcgcgugcgg ugcaggccua gcagaguccg acaaacgcag uacgcaccgc uaaaccugua 300

ggcgcgcagc acucgcucuu uaggacgggg guucgauucc ccccaucucc acca 354

<210> SEQ ID NO 127
<211> LENGTH: 367
<212> TYPE: DNA
<213> ORGANISM: Vibrio cholerae

<400> SEQUENCE: 127

ggggctgatt caggattcga cgggaatttt gcagtctgag gtgcatgccg aggtgcggta 60

ggcctcgtta acaaaccgca aaaaaatagt cgcaaacgac gaaaactacg cactagcagc 120

ttaataccct gctcagagcc cttcctccct agcttccgct tgtaagacgg ggaaatcagg 180

aaggtcaaac caaatcaagc tggcgtggat tcccccacct gagggatgaa gcgcgagatc 240

taattcaggt tagccattcg ttagcgtgtc ggttcgcagg cggtggtgaa attaaagatc 300

gactaagcat gtagtaccaa agatgaatgg ttttcggacg gggttcaac tccccccagc 360

tccacca 367

<210> SEQ ID NO 128
<211> LENGTH: 367
<212> TYPE: RNA
<213> ORGANISM: Vibrio cholerae

<400> SEQUENCE: 128

ggggcugauu caggauucga cgggaauuuu gcagucugag gugcaugccg aggugcggua 60

ggccucguua acaaaccgca aaaaaauagu cgcaaacgac gaaaacuacg cacuagcagc 120

uuaauacccu gcucagagcc cuuccucccu agcuuccgcu uguaagacgg ggaaaucagg 180

aaggucaaac caaaucaagc uggcguggau ucccccaccu gagggaugaa gcgcgagauc 240

uaauucaggu uagccauucg uuagcguguc gguucgcagg cgguggugaa auuaaagauc 300

gacuaagcau guaguaccaa agaugaaugg uuuucggacg gggguucaac ucccccagc 360

uccacca 367

<210> SEQ ID NO 129
<211> LENGTH: 364
<212> TYPE: DNA
<213> ORGANISM: Yersinia pestis

<400> SEQUENCE: 129

ggggctgatt ctggattcga cgggattcgc gaaacccaag gtgcatgccg aggtgcggtg 60

gcctcgtaaa aaaccgcaaa aaaaatagtt gcaaacgacg aaaactacgc actagcagct 120

taataacctg cttagagccc tctctgccta gcctccgctc ttaggacggg gatcaagaga 180

ggtcaaacct aaaagagctc gtgtggaaac cttgcctggg gtggaagcat taaaactaat 240

caggatagtt tgtcagtagc gtgtccatcc gcagctggcc ggcgaatgta atgattggac 300

taagcatgta gtgccgacgg tgtagtaatt tcggacgggg gttcaaatcc ccccagctcc 360

acca 364

<210> SEQ ID NO 130
<211> LENGTH: 364
<212> TYPE: RNA
<213> ORGANISM: Yersinia pestis

<400> SEQUENCE: 130

ggggcugauu cuggauucga cgggauucgc gaaacccaag gugcaugccg aggugcggug 60

gccucguaaa aaaccgcaaa aaaaauaguu gcaaacgacg aaaacuacgc acuagcagcu 120

uaauaaccug cuuagagccc ucucugccua gccuccgcuc uuaggacggg gaucaagaga 180 ggucaaaccu aaaagagcuc guguggaaac cuugccuggg guggaagcau uaaaacuaau 240

caggauaguu ugucaguagc guguccaucc gcagcuggcc ggcgaaugua augauuggac 300

uaagcaugua gugccgacgg uguaguaauu ucggacgggg guucaaaucc ccccagcucc 360

acca 364

<210> SEQ ID NO 131
<211> LENGTH: 309
<212> TYPE: DNA
<213> ORGANISM: Campylobacter fetus

<400> SEQUENCE: 131

aggagtaagt ctgcttagat ggcatgtcgc tttgggcaaa gcgtaaaaag cccaaataaa 60

attaaacgca aacaacgtta aattcgctcc tgcttacgct aaagctgcgt aagttcagtt 120

gagcctgaaa tttaagtcat actatctagc ttaattttcg gtcatctttg atagtgtagc 180

cttgcgtttg acaagcgttg aggtgaaata aagtcttagc cttgcttttg agttttggaa 240

gatgagcgaa gtagggtgaa gtagtcatct ttgctaagca tgtagaggtc tttgtgggat 300

tatttttgg 309

<210> SEQ ID NO 132
<211> LENGTH: 309
<212> TYPE: RNA
<213> ORGANISM: Campylobacter fetus

<400> SEQUENCE: 132

aggaguaagu cugcuuagau ggcaugucgc uuugggcaaa gcguaaaaag cccaaauaaa 60

auuaaacgca aacaacguua aauucgcucc ugcuuacgcu aaagcugcgu aaguucaguu 120

gagccugaaa uuuaagucau acuaucuagc uuaauuuucg gucaucuuug auaguguagc 180

cuugcguuug acaagcguug aggugaaaua aagucuuagc cuugcuuuug aguuuuggaa 240

gaugagcgaa guagggugaa guagucaucu uugcuaagca uguagagguc uuugugggau 300

uauuuuugg 309

<210> SEQ ID NO 133
<211> LENGTH: 309
<212> TYPE: DNA
<213> ORGANISM: Campylobacter coli (BM2509)

<400> SEQUENCE: 133

aggagtaagt ctgcttagat ggcatgtcgc tttggacaaa gcgtaaaaag tccaaattaa 60

aattaaacgc aaataacgtt aaatttgctc ctgcttacgc taaagctgcg taagttcagt 120

tgagcccgaa actcaagtga tgctatctag cttgaatttt ggtcatcttt gatagtgtag 180

attgaaaatt gacaactttt aatcgaagtt aaagtcttag tctagcttga aattttggaa 240

ggtgagttta gccagatgaa gttttcacct ttgctaaaca tgtagaagtc tttgtggggt 300

tatttttgg 309

<210> SEQ ID NO 134
<211> LENGTH: 309
<212> TYPE: RNA
<213> ORGANISM: Campylobacter coli (BM2509)

<400> SEQUENCE: 134

aggaguaagu cugcuuagau ggcaugucgc uuuggacaaa gcguaaaaag uccaaauuaa 60

aauuaaacgc aaauaacguu aaauuugcuc cugcuuacgc uaaagcugcg uaaguucagu 120 ugagcccgaa acucaaguga ugcuaucuag cuugaauuuu ggucaucuuu gauaguguag 180

auugaaaauu gacaacuuuu aaucgaaguu aaagucuuag ucuagcuuga aauuuuggaa 240

ggugaguuua gccagaugaa guuuucaccu uugcuaaaca uguagaaguc uuuguggggu 300

uauuuuugg 309

<210> SEQ ID NO 135
<211> LENGTH: 311
<212> TYPE: DNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown Organism:Campylobacter
chicken isolate

<400> SEQUENCE: 135

acaggagtaa gtctgcttag atggcatgtc gctttgggca aagcgtaaaa agcccaaata 60

aaattaaacg caaacaacgt taaattcgct cctgcttacg ctaaagctgc gtaagttcag 120

ttgagcctga aatttaagtc atactatcta gcttaatttt cggtcatttt tgatagtgta 180

gccttgcgtt tgacaagcgt tgaggtgaaa taaggtctta gccttgcttt tgagttttgg 240

aagatgagcg aagtagggtg aagtagtcat ctttgctaag catgtagagg tctttgtggg 300

attattttg g 311

<210> SEQ ID NO 136
<211> LENGTH: 311
<212> TYPE: RNA
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown Organism:Campylobacter
chicken isolate

<400> SEQUENCE: 136

acaggaguaa gucugcuuag auggcauguc gcuuugggca aagcguaaaa agcccaaaua 60

aaauuaaacg caaacaacgu uaaauucgcu ccugcuuacg cuaaagcugc guaaguucag 120

uugagccuga aauuuaaguc auacuaucua gcuuaauuuu cggucauuuu ugauagugua 180

gccuugcguu ugacaagcgu ugaggugaaa uaaggucuua gccuugcuuu ugaguuuugg 240

aagaugagcg aaguagggug aaguagucau cuuugcuaag cauguagagg ucuuuguggg 300

auuauuuug g 311

<210> SEQ ID NO 137
<211> LENGTH: 313
<212> TYPE: DNA
<213> ORGANISM: Clostridium perfringens

<400> SEQUENCE: 137

acgggggtag gatgggtttg ataagcgagt cgagggaagc atggtgcctc gataataaag 60

tatgcattaa agataaacgc acgagataat tttgcattag cagcttaagt tagcgctgct 120

catccttcct caattgccca cggttgagag taagggtgtc atttaaaagt ggggaaccga 180

gcctagcaaa gctttgagct aggaacggaa tttatgaagc ttaccaaaga ggaagtttgt 240

ctgtggacgt tctctgaggg aattttaaaa cacaagacta cactcgtaga aagtcttact 300

ggtctgcttt cgg 313

<210> SEQ ID NO 138
<211> LENGTH: 313
<212> TYPE: RNA
<213> ORGANISM: Clostridium perfringens

-continued

<400> SEQUENCE: 138

acggggguag gaugggguuug auaagcgagu cgagggaagc auggugccuc gauaauaaag 60

uaugcauuaa agauaaacgc acgagauaau uuugcauuag cagcuuaagu uagcgcugcu 120

cauccuuccu caauugccca cgguugagag uaagggugu c auuuaaaagu ggggaaccga 180

gccuagcaaa gcuuugagcu aggaacggaa uuuaugaagc uuaccaaaga ggaaguuugu 240

cuguggacgu ucucugaggg aauuuuaaaa cacaagacua cacucguaga aagucuuacu 300

ggucugcuuu cgg 313

<210> SEQ ID NO 139
<211> LENGTH: 331
<212> TYPE: DNA
<213> ORGANISM: Haemophilus ducreyi (NCTC 10945)

<400> SEQUENCE: 139

acgggattag cgaagtccaa ggtgcacgtc gaggtgcggt aggcctcgta acaaaccgca 60

aaaaaatagt cgcaaacgac gaacaatacg ctttagcagc ttaataacct gcatttagcc 120

ttcgcgccct agctttcgct cgtaagacgg ggagcacgcg gagtcaaacc aaaacgagat 180

cgtgtggacg cttccgcttg tagatgaaac actaaattga atcaagctag tttatttctt 240

gcgtgtctgt ccgctggaga taagcgaaat taaagaccag actaaacgtg tagtactgaa 300

gatagagtaa tttcggaccc gggttcgact c 331

<210> SEQ ID NO 140
<211> LENGTH: 331
<212> TYPE: RNA
<213> ORGANISM: Haemophilus ducreyi (NCTC 10945)

<400> SEQUENCE: 140

acgggauuag cgaaguccaa ggugcacguc gaggugcggu aggccucgua acaaaccgca 60

aaaaaauagu cgcaaacgac gaacaauacg cuuuagcagc uuaauaaccu gcauuuagcc 120

uucgcgcccu agcuuucgcu cguaagacgg ggagcacgcg gagucaaacc aaaacgagau 180

cguguggacg cuuccgcuug uagaugaaac acuaaauuga aucaagcuag uuuauuucuu 240

gcgugucugu ccgcuggaga uaagcgaaau uaaagaccag acuaaacgug uaguacugaa 300

gauagaguaa uuucggaccc ggguucgacu c 331

<210> SEQ ID NO 141
<211> LENGTH: 232
<212> TYPE: DNA
<213> ORGANISM: Listeria innocua (food isolate #1)

<400> SEQUENCE: 141

ggcaaagaaa aacaaaacct agctttcgct gcctaataac cagtagcata gctgatcctc 60

cgtgcatcgc ccatgtgcta cggtaagggt ctcactctaa gtgggctaca ctagttaatc 120

tccgtctgag gttaaataga agagcttaat cagactagct gaatggaagc ctgttaccgg 180

gctgatgttt atgcgaaatg ctaatacggt gactacgctc gtagatattc aa 232

<210> SEQ ID NO 142
<211> LENGTH: 232
<212> TYPE: RNA
<213> ORGANISM: Listeria innocua (food isolate #1)

<400> SEQUENCE: 142

ggcaaagaaa aacaaaaccu agcuuucgcu gccuaauaac caguagcaua gcugauccuc 60 cgugcaucgc ccaugugcua cgguaagggu cucacucuaa gugggcuaca cuaguuaauc 120

uccgucugag guuaaauaga agagcuuaau cagacuagcu gaauggaagc cuguuaccgg 180

gcugauguuu augcgaaaug cuaauacggu gacuacgcuc guagauauuc aa 232

<210> SEQ ID NO 143
<211> LENGTH: 232
<212> TYPE: DNA
<213> ORGANISM: Listeria innocua (food isolate #2)

<400> SEQUENCE: 143

ggcaaagaaa aacaaaacct agctttcgct gcctaataag cagtagcata gctgatcctc 60

cgtgcatcgc ccatgtgcta cggtaagggt ctcactctaa gtgggctaca ctagttaatc 120

tccgtctgag gttaaataga agagcttaat cagactagct gaatggaagc ctgttaccgg 180

gccgatgttt atgcgaaatg ctaatacggt gactacgctc gtagatattt aa 232

<210> SEQ ID NO 144
<211> LENGTH: 232
<212> TYPE: RNA
<213> ORGANISM: Listeria innocua (food isolate #2)

<400> SEQUENCE: 144

ggcaaagaaa aacaaaaccu agcuuucgcu gccuaauaag caguagcaua gcugauccuc 60

cgugcaucgc ccaugugcua cgguaagggu cucacucuaa gugggcuaca cuaguuaauc 120

uccgucugag guuaaauaga agagcuuaau cagacuagcu gaauggaagc cuguuaccgg 180

gccgauguuu augcgaaaug cuaauacggu gacuacgcuc guagauauuu aa 232

<210> SEQ ID NO 145
<211> LENGTH: 232
<212> TYPE: DNA
<213> ORGANISM: Listeria innocua (food isolate #3)

<400> SEQUENCE: 145

ggcaaagaaa aacaaaacct agctttcgct gcctaataag cagtagaata gctgatcctc 60

cgtgcatcgc ccatgtgcta cggtaagggt ctcactctaa gtgggctaca ctagttaatc 120

tccgtctgag gttaaataga agagcttaat cggactagct gaatggaagc ctgttaccgg 180

gccgatgttt atgcgaaatg ctaatacggt gactacgctc gtagatattt aa 232

<210> SEQ ID NO 146
<211> LENGTH: 232
<212> TYPE: RNA
<213> ORGANISM: Listeria innocua (food isolate #3)

<400> SEQUENCE: 146

ggcaaagaaa aacaaaaccu agcuuucgcu gccuaauaag caguagaaua gcugauccuc 60

cgugcaucgc ccaugugcua cgguaagggu cucacucuaa gugggcuaca cuaguuaauc 120

uccgucugag guuaaauaga agagcuuaau cggacuagcu gaauggaagc cuguuaccgg 180

gccgauguuu augcgaaaug cuaauacggu gacuacgcuc guagauauuu aa 232

<210> SEQ ID NO 147
<211> LENGTH: 232
<212> TYPE: DNA
<213> ORGANISM: Listeria innocua (ATCC 12210)

<400> SEQUENCE: 147

ggcaaagaaa aacaaaacct agctttcgct gcctaataag cagtagcata gctgatcctc 60 cgtgcatcgc ccatgtgcta cggtaagggt ctcactctaa gtgggctaca ctagttaatc 120

tccgtctggg gttaaataga agagcttaat cagactagct gaatggaagc ctgttactgg 180

gccgatgttt atgcgaaatg ctaatacggt gactacgctc gtagatattt aa 232

<210> SEQ ID NO 148
<211> LENGTH: 232
<212> TYPE: RNA
<213> ORGANISM: Listeria innocua (ATCC 12210)

<400> SEQUENCE: 148

ggcaaagaaa aacaaaaccu agcuuucgcu gccuaauaag caguagcaua gcugauccuc 60

cgugcaucgc ccaugugcua cgguaagggu cucacucuaa gugggcuaca cuaguuaauc 120

uccgucuggg guuaaauaga agagcuuaau cagacuagcu gaauggaagc cuguuacugg 180

gccgauguuu augcgaaaug cuaauacggu gacuacgcuc guagauauuu aa 232

<210> SEQ ID NO 149
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Listeria ivanovii (NCTC 11846)

<400> SEQUENCE: 149

acagggatag ttcgagcttg agttgcgagt cggggggatc gtcctcgtta ttaacgtcaa 60

agccaataat aactggcaaa gaaaaacaaa acctagcttt cgctgcctaa taagcagtag 120

catagctgat cctccgtgca tcgcccatgt gctacggtaa gggtctcact ttaagtgggc 180

tacactaaat aatctccgtc tggggttagt tagaagagct taatcagact agctgaatgg 240

aagcctgtta ccgggctgat gtttatgcga aatgctaata cggtgactac gctcgtagat 300

atttaagtgc cgatatttct gg 322

<210> SEQ ID NO 150
<211> LENGTH: 321
<212> TYPE: RNA
<213> ORGANISM: Listeria ivanovii (NCTC 11846)

<400> SEQUENCE: 150

acagggauag uucgagcuug aguugcgagu cggggggauc guccucguua uuaacgucaa 60

agccaauaau aacuggcaaa gaaaaacaaa accuagcuuu cgcugccuaa uaagcaguag 120

cauagcugau ccuccgugca ucgcccaugu gcuacgguaa gggucucacu uuaagugggc 180

uacacuaaau aaucuccguc ugggguuagu uagaagagcu uaaucagacu agcugaaugg 240

aagccuguua ccgggcugau guuuaugcga aaugcuaaua cggugacucg cucguagaua 300

uuuaagugcc gauauuucug g 321

<210> SEQ ID NO 151
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Listeria seeligeri (NCTC 11856)

<400> SEQUENCE: 151

acagggatag ttcgagcttg agttgcgagt cggggggatc gtcctcgtta tcaacgtcaa 60

agccaataat aactggcaaa gaaaaacaaa acctagcttt cgctgcctaa taagcagtag 120

catagctgat cctccgtgca tcgcccatgt gctacggaaa gggtctcact ttaagtgggc 180

tacactaaat aatctccgtc tggggttagt tagaagagct taatcagact agctgaatgg 240

aagcctgtta ccgggctgat gtttatgcga aatactaata cggtgactac gctcgtagat 300 atttaagtgc ccatatttct gg 322

<210> SEQ ID NO 152
<211> LENGTH: 322
<212> TYPE: RNA
<213> ORGANISM: Listeria seeligeri (NCTC 11856)

<400> SEQUENCE: 152

acagggauag uucgagcuug aguugcgagu cggggggauc guccucguua ucaacgucaa 60

agccaauaau aacuggcaaa gaaaaacaaa accuagcuuu cgcugccuaa uaagcaguag 120

cauagcugau ccuccgugca ucgcccaugu gcuacggaaa gggucucacu uuaagugggc 180

uacacuaaau aaucuccguc ugggguuagu uagaagagcu uaaucagacu agcugaaugg 240

aagccuguua ccgggcugau guuuaugcga aauacuaaua cggugacuac gcucguagau 300

auuuaagugc ccauauuucu gg 322

<210> SEQ ID NO 153
<211> LENGTH: 314
<212> TYPE: DNA
<213> ORGANISM: Salmonella enteritidis

<400> SEQUENCE: 153

acgggatttg cgaaacccaa ggtgcatgcc gaggggcggt tggcctcgta aaaagccgca 60

aaaaaatagt cgcaaacgac gaaacctacg ctttagcagc ttaataacct gcttagagcc 120

ctctctccct agcctccgct cttaggacgg ggatcaagag aggtcaaacc caaaagagat 180

cgcgtggatg ccctgcctgg ggttgaagcg ttaaaacgaa tcaggctagt ctggtagtgg 240

cgtgtccgtc cgcaggtgcc aggcgaatgt aaagactgac taagcatgta gtaccgagga 300

tgtaggaatt tcgg 314

<210> SEQ ID NO 154
<211> LENGTH: 314
<212> TYPE: RNA
<213> ORGANISM: Salmonella enteritidis

<400> SEQUENCE: 154

acgggauuug cgaaacccaa ggugcaugcc gaggggcggu uggccucgua aaaagccgca 60

aaaaaauagu cgcaaacgac gaaaccuacg cuuuagcagc uuaauaaccu gcuuagagcc 120

cucucucccu agccuccgcu cuuaggacgg ggaucaagag aggucaaacc caaaagagau 180

cgcguggaug cccugccugg gguugaagcg uuaaaacgaa ucaggcuagu cugguagugg 240

cguguccguc cgcaggugcc aggcgaaugu aaagacugac uaagcaugua guaccgagga 300

uguaggaauu ucgg 314

<210> SEQ ID NO 155
<211> LENGTH: 313
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus epidermidis (NCTC 11047)

<400> SEQUENCE: 155

acaggggtcc cccgagctta ttaagcgtgt cggagggttg gctccgtcat caacacattt 60

cggttaaata taactgacaa atcaaacaat aatttcgcag tagctgcgta atagccactg 120

catcgcctaa cagcatctcc tacgtgctgt taacgcgatt caaccctagt aggatatgct 180

aaacactgcc gcttgaagtc tgtttagatg aaatataatc aagctagtat catgttggtt 240

gtttattgct tagcatgatg cgaaaattat caataaacta cacacgtaga aagatttgta 300

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tcaggacctc tgg                                                    313


<210> SEQ ID NO 156
<211> LENGTH: 313
<212> TYPE: RNA
<213> ORGANISM: Staphylococcus epidermidis (NCTC 11047)

<400> SEQUENCE: 156

acaggggucc cccgagcuua uuaagcgugu cggaggguug gcuccgucau caacacauuu    60

cgguuaaaua uaacugacaa aucaaacaau aauuucgcag uagcugcgua auagccacug   120

caucgccuaa cagcaucucc uacgugcugu uaacgcgauu caacccuagu aggauaugcu   180

aaacacugcc gcuugaaguc uguuuagaug aaauauaauc aagcuaguau cauguugguu   240

guuuauugcu uagcaugaug cgaaaauuau caauaaacua cacacguaga aagauuugua   300

ucaggaccuc ugg                                                    313


<210> SEQ ID NO 157
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Streptococcus agalactiae (NCTC 8181)

<400> SEQUENCE: 157

acaggcatta tgaggtatat tttgcgactc atcggcagat gtaaaatgcc agttaaatat    60

aactgcaaaa aatacaaatt cttacgcatt agctgcctaa aaaacagcct gcgtgatctt   120

cacaagattg tttgcgtttt gctagaaggt cttatttatc agcaaactac gtttggctac   180

tgtctagtta gttaaaaaga gatttataga ctcgctatgt gagggcttga gttatgtgtc   240

atcacctagt taaatcaata cataacctat agttgtagac aaatatatta gcagatgttt   300

gg                                                                302


<210> SEQ ID NO 158
<211> LENGTH: 302
<212> TYPE: RNA
<213> ORGANISM: Streptococcus agalactiae (NCTC 8181)

<400> SEQUENCE: 158

acaggcauua ugagguauau uuugcgacuc aucggcagau guaaaaugcc aguuaaauau    60

aacugcaaaa aauacaaauu cuuacgcauu agcugccuaa aaaacagccu gcgugaucuu   120

cacaagauug uuugcguuuu gcuagaaggu cuuauuuauc agcaaacuac guuuggcuac   180

ugucuaguua guuaaaaaga gauuuauaga cucgcuaugu gagggcuuga guuaugugue   240

aucaccuagu uaaaucaaua cauaaccuau aguuguagac aaauauauua gcagauguuu   300

gg                                                                302


<210> SEQ ID NO 159
<211> LENGTH: 168
<212> TYPE: DNA
<213> ORGANISM: Bordetella bronchiseptica

<400> SEQUENCE: 159

ggggccgatc cggattcgac gtgggtcatg aaacagctca aggcatgccg agcaccagta    60

agctcgttaa tccactggaa cactacaaac gccaacgacg agcgtttcgc tctcgccgct   120

taagcggtga gccgctgcac tgatctgtcc ttgggtcacg cgggggaa              168


<210> SEQ ID NO 160
<211> LENGTH: 168
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<212> TYPE: RNA
<213> ORGANISM: Bordetella bronchiseptica

<400> SEQUENCE: 160

ggggccgauc cggauucgac gugggucaug aaacagcuca aggcaugccg agcaccagua 60

agcucguuaa uccacuggaa cacuacaaac gccaacgacg agcguuucgc ucucgccgcu 120

uaagcgguga gccgcugcac ugaucugucc uugggucacg cgggggaa 168

<210> SEQ ID NO 161
<211> LENGTH: 426
<212> TYPE: DNA
<213> ORGANISM: Chlamydia pneumoniae (CWL029)

<400> SEQUENCE: 161

gggggtgtat aggtttcgac ttgaaaatga agtgttaatt gcatgcggag ggcgttggct 60

ggcctcctaa aaagccaaca aaacaataaa tgccgaacct aaggctgaat gcgaaattat 120

tagcttgttt gactcagtag aggaaagact agctgcttaa ttagcaaaag ttgttagcta 180

gataatctct aggtaacccg gtatctgcga gctccaccag aggcttgcaa aataccgtca 240

tttatctggt tggaacttac tttctctaat tctcaaggaa gttcgttcga gatttttgag 300

agtcattggc tgctatagag gcttctagct aagggagtcc aatgtaaaca attctagaag 360

ataagcatgt agaggttagc agggagtttg tcaaggacga gagttcgagt ctctccacct 420

ccacca 426

<210> SEQ ID NO 162
<211> LENGTH: 426
<212> TYPE: RNA
<213> ORGANISM: Chlamydia pneumoniae (CWL029)

<400> SEQUENCE: 162

gggggugguau agguuucgac uugaaaauga aguguuaauu gcaugcggag ggcguuggcu 60

ggccuccuaa aaagccaaca aaacaauaaa ugccgaaccu aaggcugaau gcgaaauuau 120

uagcuuguuu gacucaguag aggaaagacu agcugcuuaa uuagcaaaag uuguuagcua 180

gauaaucucu agguaacccg guaucugcga gcuccaccag aggcuugcaa aauaccguca 240

uuuaucuggu uggaacuuac uuucucuaau ucucaaggaa guucguucga gauuuuugag 300

agucauuggc ugcuauagag gcuucuagcu aagggagucc aauguaaaca auucuagaag 360

auaagcaugu agagguuagc agggaguuug ucaaggacga gaguucgagu cucuccaccu 420

ccacca 426

<210> SEQ ID NO 163
<211> LENGTH: 421
<212> TYPE: DNA
<213> ORGANISM: Francisella tularensis

<400> SEQUENCE: 163

gggggcgaat atggtttcga catgaatgtc aaaatctaag gtgcatgccg aggaagtacc 60

gtaacctcgt taataacagt acaaatgcca ataataactg gcaacaaaaa agcaaaccgc 120

gtagcggcta acgacagcaa ctttgctgct gttgctaaag ctgcctagtc tagcttaata 180

atctagatgc gcacggatat gatagtcttt cttatgacac tatctataca tccgttcata 240

ttccgcataa gacggtcttt gctttttgtc tgggagttaa ggctgtattt aacagactcg 300

ctaactatta ccctggctaa ttggggaata gtcaagctaa actcaaatag attagcctaa 360

gcatgtagat ccaaagatct agagtttgtg gacgcgggtt caaatcccgc cgcctccacc 420

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a                                                                   421


<210> SEQ ID NO 164
<211> LENGTH: 421
<212> TYPE: RNA
<213> ORGANISM: Francisella tularensis

<400> SEQUENCE: 164

gggggcgaau augguuucga caugaauguc aaaaucuaag gugcaugccg aggaaguacc    60

guaaccucgu uaauaacagu acaaaugcca auaauaacug gcaacaaaaa agcaaaccgc   120

guagcggcua acgacagcaa cuuugcugcu guugcuaaag cugccuaguc uagcuuaaua   180

aucuagaugc gcacggauau gauagucuuu cuuaugacac uaucuauaca uccguucaua   240

uuccgcauaa gacggucuuu gcuuuuuguc ugggaguuaa ggcuguauuu aacagacucg   300

cuaacuauua cccuggcuaa uuggggaaua gucaagcuaa acucaaauag auuagccuaa   360

gcauguagau ccaaagaucu agaguuugug gacgcggguu caaaucccgc cgccuccacc   420

a                                                                   421


<210> SEQ ID NO 165
<211> LENGTH: 330
<212> TYPE: DNA
<213> ORGANISM: Guillardia theta (plastid)

<400> SEQUENCE: 165

ggggctgatt tggattcgac atataaattt gcgtgtttca ttatgaagca agtcaagttt    60

aatgatcttg taaaaaacat taaagtacaa ataaatgcaa gcaatatagt ttcatttagt   120

tcaaaacgtt tagtctcttt tgcataagca aaatgtgtta ataactttct tagtagaaat   180

tggagaagtt tactaagatt tatatttact ccataattat tttaaagatg gtaaaaaggt   240

gattcatcat ttgtatgttt ctaaactttg tgaaagaata gtgggctcca tttataatga   300

acgtgggttc aaatcccacc agctccacca                                    330


<210> SEQ ID NO 166
<211> LENGTH: 330
<212> TYPE: RNA
<213> ORGANISM: Guillardia theta (plastid)

<400> SEQUENCE: 166

ggggcugauu uggauucgac auauaaauuu gcguguuuca uuaugaagca agucaaguuu    60

aaugaucuug uaaaaaacau uaaaguacaa auaaaugcaa gcaauauagu uucauuuagu   120

ucaaaacguu uagucucuuu ugcauaagca aaauguguua auaacuuucu uaguagaaau   180

uggagaaguu uacuaagauu uauauuuacu ccauaauuau uuuaaagaug guaaaaaggu   240

gauucaucau uuguauguuu cuaaacuuug ugaaagaaua gugggcucca uuuauaauga   300

acgugggguuc aaaucccacc agcuccacca                                   330


<210> SEQ ID NO 167
<211> LENGTH: 348
<212> TYPE: DNA
<213> ORGANISM: Thalassiosira Weissflogii (plastid)

<400> SEQUENCE: 167

ggggctgatt tggtttcgac atttaaaact tctttctatg tgtcaggtca aagtttgtat    60

tctttgtaaa aaaatactaa aatactaata aatgctaata atataatacc gtttattttt   120

aaagcagtaa aaacaaaaaa agaagcaatg gctttaaatt ttgctgtata gttcattaac   180
```

```
ttaggttatt aaatattttt tcattataac tggacttttc tctagtttat agtttagaat    240

aaatttaaat tttgcaaaac tcgttcgaaa attttcgggc taaacctgta aacgcaaata    300

ctaagaaatt ttagatggac atgggttcaa ttcccatcag ttccacca                 348


<210> SEQ ID NO 168
<211> LENGTH: 348
<212> TYPE: RNA
<213> ORGANISM: Thalassiosira Weissflogii (plastid)

<400> SEQUENCE: 168

ggggcugauu ugguuucgac auuuaaaacu ucuuucuaug ugucagguca aaguuuguau     60

ucuuuguaaa aaaauacuaa aauacuaaua aaugcuaaua auauaauacc guuuauuuuu    120

aaagcaguaa aaacaaaaaa agaagcaaug gcuuuaaauu uugcuguaua guucauuaac    180

uuagguuauu aaauauuuuu ucauuauaac uggacuuuuc ucuaguuuau aguuuagaau    240

aaauuuaaau uuugcaaaac ucguucgaaa auuuucgggc uaaaccugua aacgcaaaua    300

cuaagaaauu uuagauggac augguucaa uucccaucag uuccacca                  348


<210> SEQ ID NO 169
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:V. cholerae
      tmRNA specific probe

<400> SEQUENCE: 169

aacgaatggc taacctgaa                                                  19


<210> SEQ ID NO 170
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:Universal
      ssrA/tmRNA 5'  in vitro amplification primer

<400> SEQUENCE: 170

gggmytacgg wttcgac                                                    17


<210> SEQ ID NO 171
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:Universal
      ssrA/tmRNA 3' in vitro amplification primer

<400> SEQUENCE: 171

gggartcgaa ccrsgtcc                                                   18


<210> SEQ ID NO 172
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:5' Listeria
      genus specific PCR amplification primer

<400> SEQUENCE: 172

aaagccaata ataactgg                                                   18
```

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<210> SEQ ID NO 173
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:3' Listeria
      genus specific amplification primer

<400> SEQUENCE: 173

ccagaaatat cggcactt                                                   18


<210> SEQ ID NO 174
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:Listeria
      genus specific hybridisation probe

<400> SEQUENCE: 174

gtgagaccct taccgtag                                                   18


<210> SEQ ID NO 175
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:Listeria
      monocytogenes species specific hybridisation probe

<400> SEQUENCE: 175

tctatttaac cccagacg                                                   18


<210> SEQ ID NO 176
<211> LENGTH: 348
<212> TYPE: DNA
<213> ORGANISM: Helicobacter pylori

<400> SEQUENCE: 176

tggggatgtt acggtttcga caggggtagt tcgagcttag gtggcgagtc gaggggatcg     60

gcctcgttaa aacgtcaaag cctataactg gcaaacaaca aaacaacttc gctttagcag    120

cttaataagc tcttagcggt tcctccctcc atcgcccatg tggtagggta agggactcaa    180

attaagtggg ctacgctgga ttccaccgtc tgaggatgaa agaagagaac aaccagacta    240

gctacccgga cgcccgtcga taggcagatg gagtagcgaa tcgcgaatat atcgactaca    300

ctcgtagaag cttaagtgcc gatattcttg gacgtgggtt cgactccc                 348


<210> SEQ ID NO 177
<211> LENGTH: 348
<212> TYPE: RNA
<213> ORGANISM: Helicobacter pylori

<400> SEQUENCE: 177

uggggauguu acgguuucga cagggguagu ucgagcuuag guggcgaguc gaggggaucg     60

gccucguuaa aacgucaaag ccuauaacug gcaaacaaca aaacaacuuc gcuuuagcag    120

cuuaauaagc ucuuagcggu uccucccucc aucgcccaug ugguagggua agggacucaa    180

auuaaguggg cuacgcugga uuccaccguc ugaggaugaa agaagagaac aaccagacua    240

gcuacccgga cgcccgucga uaggcagaug gaguagcgaa ucgcgaauau aucgacuaca    300

cucguagaag cuuaagugcc gauauucuug gacgugggguu cgacuccc                348


<210> SEQ ID NO 178
```

<211> LENGTH: 344
<212> TYPE: DNA
<213> ORGANISM: Helicobacter pylori

<400> SEQUENCE: 178

tggggacgtt acggtttcga cagggatagt tcgagcttag gttgcgagtc gaggggatcg 60

gcctcgttaa aacgtcaaag cctataattg gcaaacaaaa caatctttct ttagctgctt 120

aattgcacta aaggttcctc cctccatcgt ccatgtggta gggtaaggga ctcaaactaa 180

gtggactacg ccggagttcg ccgtctgagg acaaaggaag agaacaacca gactagcaac 240

ttggaagcct gtcgataggc cgaagagttc gcgaaatgct aatatatcga ctacactcgt 300

agaagcttaa gtgccgatat ttttggacgt gggttcgatt ccct 344

<210> SEQ ID NO 179
<211> LENGTH: 344
<212> TYPE: RNA
<213> ORGANISM: Helicobacter pylori

<400> SEQUENCE: 179

uggggacguu acgguuucga cagggauagu ucgagcuuag guugcgaguc gaggggaucg 60

gccucguuaa aacgucaaag ccuauaauug gcaaacaaaa caaucuuucu uuagcugcuu 120

aauugcacua aagguuccuc ccuccaucgu ccauguggua ggguaaggga cucaaacuaa 180

guggacuacg ccggaguucg ccgucugagg acaaaggaag agaacaacca gacuagcaac 240

uuggaagccu gucgauaggc cgaagaguuc gcgaaaugcu aauauaucga cuacacucgu 300

agaagcuuaa gugccgauau uuuuggacgu ggguucgauu cccu 344

<210> SEQ ID NO 180
<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Listeria seeligeri (NCTC 11856)

<400> SEQUENCE: 180

acagggatag ttcgagcttg agttgcgagt cggggggatc gtcctcgtta tcaacgtcaa 60

agccaataat aactggcaaa gaaaaacaaa acctagcttt cgctgcctaa taagcagtag 120

catagctgat cctccgtgca tcgcccatgt gctacggaaa gggtctcact ttaagtgggc 180

tacactaaat aatctccgtc tggggttagt tagaagagct taatcagact agctgaatgg 240

aagcctgtta ccgggctgat gtttatgcga aatactaata cggtgactac gctcgtagat 300

atttaagtgc ccatatttct gg 322

<210> SEQ ID NO 181
<211> LENGTH: 322
<212> TYPE: RNA
<213> ORGANISM: Listeria seeligeri (NCTC 11856)

<400> SEQUENCE: 181

acagggauag uucgagcuug aguugcgagu cggggggauc guccucguua ucaacgucaa 60

agccaauaau aacuggcaaa gaaaaacaaa accuagcuuu cgcugccuaa uaagcaguag 120

cauagcugau ccuccgugca ucgcccaugu gcuacggaaa gggucucacu uuaagugggc 180

uacacuaaau aaucuccguc ugggguuagu uagaagagcu uaaucagacu agcugaaugg 240

aagccuguua ccgggcugau guuuaugcga aauacuaaua cggugacuac gcucguagau 300

auuuaagugc ccauauuucu gg 322

<210> SEQ ID NO 182

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<211> LENGTH: 322
<212> TYPE: DNA
<213> ORGANISM: Listeria ivanovii (NCTC 11846)

<400> SEQUENCE: 182

acagggatag ttcgagcttg agttgcgagt cggggggatc gtcctcgtta ttaacgtcaa     60

agccaataat aactggcaaa gaaaaacaaa acctagcttt cgctgcctaa taagcagtag    120

catagctgat cctccgtgca tcgcccatgt gctacggtaa gggtctcact ttaagtgggc    180

tacactaaat aatctccgtc tggggttagt tagaagagct taatcagact agctgaatgg    240

aagcctgtta ccgggctgat gtttatgcga aatgctaata cggtgactac gctcgtagat    300

atttaagtgc cgatatttct gg                                             322


<210> SEQ ID NO 183
<211> LENGTH: 321
<212> TYPE: RNA
<213> ORGANISM: Listeria ivanovii (NCTC 11846)

<400> SEQUENCE: 183

acagggauag uucgagcuug aguugcgagu cggggggauc guccucguua uuaacgucaa     60

agccaauaau aacuggcaaa gaaaaacaaa accuagcuuu cgcugccuaa uaagcaguag    120

cauagcugau ccuccgugca ucgcccaugu gcuacgguaa gggucucacu uuaagugggc    180

uacacuaaau aaucuccguc ugggguuagu uagaagagcu uaaucagacu agcugaaugg    240

aagccuguua ccgggcugau guuuaugcga aaugcuaaua cggugacucg cucguagaua    300

uuuaagugcc gauauuucug g                                              321


<210> SEQ ID NO 184
<211> LENGTH: 319
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium africanum

<400> SEQUENCE: 184

acttcgcgca tcgaatcaag ggaagcgtgc cggtgcaggc aagagaccac cgtaagcgtc     60

gttgcgacca aataagcgcc gattcacatc agcgcgacta cgctctcgct gcctaagcga    120

cggctagtct gtcagaccgg gaacgccctc ggcccggacc ctggcatcag ctagagggat    180

ccaccgatga gtccggtcgc gggactcctc gggacaacca cagcgactgg gatcgtcatc    240

tcggctagtt cgcgtgaccg ggagatccga gcagaggcat agcgaactgc gcacggagaa    300

gccttgaggg aatgccgta                                                 319


<210> SEQ ID NO 185
<211> LENGTH: 319
<212> TYPE: RNA
<213> ORGANISM: Mycobacterium africanum

<400> SEQUENCE: 185

acuucgcgca ucgaaucaag ggaagcgugc cggugcaggc aagagaccac cguaagcguc     60

guugcgacca aauaagcgcc gauucacauc agcgcgacua cgcucucgcu gccuaagcga    120

cggcuagucu gucagaccgg gaacgcccuc ggcccggacc cuggcaucag cuagagggau    180

ccaccgauga guccggucgc gggacuccuc gggacaacca cagcgacugg gaucgucauc    240

ucggcuaguu cgcgugaccg ggagauccga gcagaggcau agcgaacugc gcacggagaa    300

gccuugaggg aaugccgua                                                 319


<210> SEQ ID NO 186
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-continued

<211> LENGTH: 319
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium gordonae

<400> SEQUENCE: 186

acttcgcgca tcgaatcaag ggaagcgtgc cggtgcaggc aagagaccac cgtaagcgtc 60

gttgcaacca tataagcgcc gattcacatc agcgcgacta cgctctcgct gcctaagcga 120

cggctagtct gtcggaccgg gaacgccctc gccccggacc ccggcatcag ctagagggat 180

caaccgatga gttcggtcgc gggactcatc gggacaccaa cagcgactgg gatcgtcatc 240

ctggctagtc cgtgtgacca ggagatccga gcagagacat agcggactgc gcacggagaa 300

gccttgaggg aatgccgta 319

<210> SEQ ID NO 187
<211> LENGTH: 319
<212> TYPE: RNA
<213> ORGANISM: Mycobacterium gordonae

<400> SEQUENCE: 187

acuucgcgca ucgaaucaag ggaagcgugc cggugcaggc aagagaccac cguaagcguc 60

guugcaacca uauaagcgcc gauucacauc agcgcgacua cgcucucgcu gccuaagcga 120

cggcuagucu gucggaccgg gaacgcccuc gccccggacc ccggcaucag cuagagggau 180

caaccgauga guucggucgc gggacucauc gggacaccaa cagcgacugg gaucgucauc 240

cuggcuaguc cgugugacca ggagauccga gcagagacau agcggacugc gcacggagaa 300

gccuugaggg aaugccgua 319

<210> SEQ ID NO 188
<211> LENGTH: 319
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium kansasii

<400> SEQUENCE: 188

acttcgcgca tcgaatcaag ggaagcgtgc cggtgcaggc aagagaccac cgtaagcgtc 60

gttgcaacca aataagcgcc gattcacatc agcgcgacta cgctctcgct gcctaagcga 120

cggctagtct gtcagaccgg gaccgccctc gacccggact ctggcatcag ctagagggat 180

caaccgatga gttcggtcgc gggactcgtc gggacaccaa cagcgactgg gatcgtcatc 240

ctggctagtt cgcgtgacca ggagatccga gcagaggcat agcgaactgc gcacggagaa 300

gccttgaggg aatgccgta 319

<210> SEQ ID NO 189
<211> LENGTH: 319
<212> TYPE: RNA
<213> ORGANISM: Mycobacterium kansasii

<400> SEQUENCE: 189

acuucgcgca ucgaaucaag ggaagcgugc cggugcaggc aagagaccac cguaagcguc 60

guugcaacca aauaagcgcc gauucacauc agcgcgacua cgcucucgcu gccuaagcga 120

cggcuagucu gucagaccgg gaccgcccuc gacccggacu cuggcaucag cuagagggau 180

caaccgauga guucggucgc gggacucguc gggacaccaa cagcgacugg gaucgucauc 240

cuggcuaguu cgcgugacca ggagauccga gcagaggcau agcgaacugc gcacggagaa 300

gccuugaggg aaugccgua 319

<210> SEQ ID NO 190

<211> LENGTH: 320
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium chelonae

<400> SEQUENCE: 190

acagcgagtc tcgacttaag ggaagcgtgc cggtgcaggc aagagaccac cgtaagcgtc 60

attgcaacca attaagcgcc gattctcatc agcgcgacta cgcactcgct gcctaagcga 120

ctgcgtgtct gtcagaccgg gagcgccctc agcccggacc ctggcatcag ctagagggac 180

aaactacggg ttcggtcgcg ggacccgtag ggacatcaaa cagcgactgg gatcgtcatc 240

tcggcttgtt cgcgggaccg agagatccaa gtagaggcat agcgaactgc gcacggagaa 300

gccttaatga acggccgttg 320

<210> SEQ ID NO 191
<211> LENGTH: 320
<212> TYPE: RNA
<213> ORGANISM: Mycobacterium chelonae

<400> SEQUENCE: 191

acagcgaguc ucgacuuaag ggaagcgugc cggugcaggc aagagaccac cguaagcguc 60

auugcaacca auuaagcgcc gauucucauc agcgcgacua cgcacucgcu gccuaagcga 120

cugcgugucu gucagaccgg gagcgcccuc agcccggacc cuggcaucag cuagagggac 180

aaacuacggg uucggucgcg ggacccguag ggacaucaaa cagcgacugg gaucgucauc 240

ucggcuuguu cgcgggaccg agagauccaa guagaggcau agcgaacugc gcacggagaa 300

gccuuaauga acggccguug 320

<210> SEQ ID NO 192
<211> LENGTH: 320
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium szulgai

<400> SEQUENCE: 192

acttcgcgca tcgaatcaag ggaagcgtgc cggtgcaggc aagagaccac cgtaagcgtc 60

gttgcaacca attaagcgcc gagaacactc agcgcgactt cgctctcgct gcctaagcga 120

cagcaagtcc gtcagaccgg gaaagccctc gacccggacc ctggcgtcat ctagagggat 180

ccaccggtga gttcggtcgc gggactcatc gggacaccaa cagcgactgg gatcgtcatc 240

ctggctagtt cgcgtgacca ggagatccga gtagagacat agcgaactgc gcacggagaa 300

gccttgaggg aatgccgtag 320

<210> SEQ ID NO 193
<211> LENGTH: 320
<212> TYPE: RNA
<213> ORGANISM: Mycobacterium szulgai

<400> SEQUENCE: 193

acuucgcgca ucgaaucaag ggaagcgugc cggugcaggc aagagaccac cguaagcguc 60

guugcaacca auuaagcgcc gagaacacuc agcgcgacuu cgcucucgcu gccuaagcga 120

cagcaagucc gucagaccgg gaaagcccuc gacccggacc cuggcgucau cuagagggau 180

ccaccgguga guucggucgc gggacucauc gggacaccaa cagcgacugg gaucgucauc 240

cuggcuaguu cgcgugacca ggagauccga guagagacau agcgaacugc gcacggagaa 300

gccuugaggg aaugccguag 320

<210> SEQ ID NO 194

<211> LENGTH: 320
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium malmoense

<400> SEQUENCE: 194

acttcgcgca tcgaatcaag ggaagcgtgc cggtgcaggc aagagaccac cgtaagcgtc 60

gttgcaacca tataagcgcc gtttcaacac agcgcgacta cgctctcgct gcctaagcga 120

cagctagtcc gtcagaccgg gaacgccctc gacccggagc ctggcgtcag ctggagggat 180

ccaccggtga gtccggtcgc gggactcatc gggacataca cagcgactgg gatcgtcatc 240

ctggctggtt cgcgtgaccg ggagatccga gcagaggcat agcgaactgc gcacggagaa 300

gccttgaggg aatgccgtag 320

<210> SEQ ID NO 195
<211> LENGTH: 320
<212> TYPE: RNA
<213> ORGANISM: Mycobacterium malmoense

<400> SEQUENCE: 195

acuucgcgca ucgaaucaag ggaagcgugc cggugcaggc aagagaccac cguaagcguc 60

guugcaacca uauaagcgcc guuucaacac agcgcgacua cgcucucgcu gccuaagcga 120

cagcuagucc gucagaccgg gaacgcccuc gacccggagc cuggcgucag cuggagggau 180

ccaccgguga guccggucgc gggacucauc gggacauaca cagcgacugg gaucgucauc 240

cuggcugguu cgcgugaccg ggagauccga gcagaggcau agcgaacugc gcacggagaa 300

gccuugaggg aaugccguag 320

<210> SEQ ID NO 196
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium flavescens

<400> SEQUENCE: 196

acttcgagcg tcgaatcaag ggaagcgtgc cggtgcaggc aagagaccac cgtaagcgtc 60

gttgcaacca attaagcgcc gattccaatc agcgcgacta cgcactcgct gcctaagcga 120

ctgcgtgtct gtcagcccgg gagagccctc gacccggtgt ctggcatcag ctagagggat 180

aaaccggtgg gtccggtcgc gggactcatc gggacatcaa acagcgactg ggatcgtcat 240

cctgacttgt tcgcgtgatc aggagatccg agtagagaca tagcgaactg cgcacggaga 300

agccttgagg gaacgccgta g 321

<210> SEQ ID NO 197
<211> LENGTH: 321
<212> TYPE: RNA
<213> ORGANISM: Mycobacterium flavescens

<400> SEQUENCE: 197

acuucgagcg ucgaaucaag ggaagcgugc cggugcaggc aagagaccac cguaagcguc 60

guugcaacca auuaagcgcc gauuccaauc agcgcgacua cgcacucgcu gccuaagcga 120

cugcgugucu gucagcccgg gagagcccuc gacccggugu cuggcaucag cuagagggau 180

aaaccggugg guccggucgc gggacucauc gggacaucaa acagcgacug ggaucgucau 240

ccugacuugu ucgcgugauc aggagauccg aguagagaca uagcgaacug cgcacggaga 300

agccuugagg gaacgccgua g 321

<210> SEQ ID NO 198

<211> LENGTH: 320
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium marinum

<400> SEQUENCE: 198

acttcgcgca tcgaatcaag ggaagcgtgc cggtgcaggc aagagaccac cgtaagcgtc 60

gatgcaacta gataagcgcc gattcacatc agcgcgacta cgctctcgct gcctaagcga 120

cggctagtct gtcggaccgg gaacgccctc gccccggacc ccggcatcag ctagagggat 180

caaccgatga gttcggtcgc ggggctcatc gggacatcaa cagcgactgg gatcgtcatc 240

ctggctagtt cgcgtgacca ggagatccga gcagagacct agcggactgc gcacggagaa 300

gccttgaggg aatgccgtag 320

<210> SEQ ID NO 199
<211> LENGTH: 320
<212> TYPE: RNA
<213> ORGANISM: Mycobacterium marinum

<400> SEQUENCE: 199

acuucgcgca ucgaaucaag ggaagcgugc cggugcaggc aagagaccac cguaagcguc 60

gaugcaacua gauaagcgcc gauucacauc agcgcgacua cgcucucgcu gccuaagcga 120

cggcuagucu gucggaccgg gaacgcccuc gccccggacc ccggcaucag cuagagggau 180

caaccgauga guucggucgc ggggcucauc gggacaucaa cagcgacugg gaucgucauc 240

cuggcuaguu cgcgugacca ggagauccga gcagagaccu agcggacugc gcacggagaa 300

gccuugaggg aaugccguag 320

<210> SEQ ID NO 200
<211> LENGTH: 319
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium microti

<400> SEQUENCE: 200

acttcgcgca tcgaatcaag ggaagcgtgc cggtgcaggc aagagaccac cgtaagcgtc 60

gttgcgacca aataagcgcc gattcacatc agcgcgacta cgctctcgct gcctaagcga 120

cggctagtct gtcagaccgg gaacgccctc ggcccggacc ctggcatcag ctagagggat 180

ccaccgatga gtccggtcgc gggactcctc gggacagcca cagcgactgg gatcgtcatc 240

tcggctagtt cgcgtgaccg ggagatccga gcagaggcat agcgaactgc gcacggagaa 300

gccttgaggg aatgccgta 319

<210> SEQ ID NO 201
<211> LENGTH: 319
<212> TYPE: RNA
<213> ORGANISM: Mycobacterium microti

<400> SEQUENCE: 201

acuucgcgca ucgaaucaag ggaagcgugc cggugcaggc aagagaccac cguaagcguc 60

guugcgacca aauaagcgcc gauucacauc agcgcgacua cgcucucgcu gccuaagcga 120

cggcuagucu gucagaccgg gaacgcccuc ggcccggacc cuggcaucag cuagagggau 180

ccaccgauga guccggucgc gggacuccuc gggacagcca cagcgacugg gaucgucauc 240

ucggcuaguu cgcgugaccg ggagauccga gcagaggcau agcgaacugc gcacggagaa 300

gccuugaggg aaugccgua 319

<210> SEQ ID NO 202

<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium smegmatis

<400> SEQUENCE: 202

acttcgagca tcgaatccag ggaagcgtgc cggtgcaggc aagagaccac cgtaagcgtc 60

gttgcaacca attaagcgcc gattccaatc agcgcgacta cgccctcgct gcctaagcga 120

cggctggtct gtcagaccgg gagtgccctc ggcccggatc ctggcatcag ctagagggac 180

ccacccacgg gttcggtcgc gggacctgtg gggacatcaa acagcgactg ggatcgtcat 240

ctcggcttgt tcgtgtgacc gggagatccg agtagagaca tagcgaactg cgcacggaga 300

agcctcgagg acatgccgta g 321

<210> SEQ ID NO 203
<211> LENGTH: 321
<212> TYPE: RNA
<213> ORGANISM: Mycobacterium smegmatis

<400> SEQUENCE: 203

acuucgagca ucgaauccag ggaagcgugc cggugcaggc aagagaccac cguaagcguc 60

guugcaacca auuaagcgcc gauuccaauc agcgcgacua cgcccucgcu gccuaagcga 120

cggcuggucu gucagaccgg gagugcccuc ggcccggauc cuggcaucag cuagagggac 180

ccacccacgg guucggucgc gggaccugug gggacaucaa acagcgacug ggaucgucau 240

cucggcuugu ucgugugacc gggagauccg aguagagaca uagcgaacug cgcacggaga 300

agccucgagg acaugccgua g 321

<210> SEQ ID NO 204
<211> LENGTH: 320
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium xenopi

<400> SEQUENCE: 204

acttcgcgca tcgaatcaag ggaagcgtgc cggtgcaggc aagagaccac cgtaagcgtc 60

gttgcaacta aataagcgcc gattcacatc agcgcgacta cgctctcgct gcctaagcga 120

cagctagtcc gtcaggccgg gagttccctc gacccggatc ctggcgtcag ctagagggat 180

ccaccgatgg gttcggtcgc gggacccatc gggacaccac acagcgactg ggatcgccgt 240

cccggctagt tcgcgagacc gggagatccg agtaagggca aagcgaactg cgcacggaga 300

agccttgagg gtatgccgta 320

<210> SEQ ID NO 205
<211> LENGTH: 320
<212> TYPE: RNA
<213> ORGANISM: Mycobacterium xenopi

<400> SEQUENCE: 205

acuucgcgca ucgaaucaag ggaagcgugc cggugcaggc aagagaccac cguaagcguc 60

guugcaacua aauaagcgcc gauucacauc agcgcgacua cgcucucgcu gccuaagcga 120

cagcuagucc gucaggccgg gaguucccuc gacccggauc cuggcgucag cuagagggau 180

ccaccgaugg guucggucgc gggacccauc gggacaccac acagcgacug ggaucgccgu 240

cccggcuagu ucgcgagacc gggagauccg aguaagggca aagcgaacug cgcacggaga 300

agccuugagg guaugccgua 320

<210> SEQ ID NO 206

<211> LENGTH: 320
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium intracellulare

<400> SEQUENCE: 206

acttcgcgca tcgaatcaag ggaagcgtgc cggtgcaggc aaccgaccac cgtaagcgtc 60

gttgcaaaca gataagcgcc gattcacatc agcgcgacta cgctctcgct gcctaagcga 120

cagctagtcc gtcagaccgg gaacgccctc gacccggagc ctggcgtcag ctagagggat 180

ccaccgatga gtccggtcgc gggacttatc gggacaccaa cagcgactgg gatcgtcatc 240

tcggcttgtt cgcgtgaccg ggagatccga gtagaggcat agcgaactgc gcacggagaa 300

gtcttgaggg aatgccgtag 320

<210> SEQ ID NO 207
<211> LENGTH: 320
<212> TYPE: RNA
<213> ORGANISM: Mycobacterium intracellulare

<400> SEQUENCE: 207

acuucgcgca ucgaaucaag ggaagcgugc cggugcaggc aaccgaccac cguaagcguc 60

guugcaaaca gauaagcgcc gauucacauc agcgcgacua cgcucucgcu gccuaagcga 120

cagcuagucc gucagaccgg gaacgcccuc gacccggagc cuggcgucag cuagagggau 180

ccaccgauga guccggucgc gggacuuauc gggacaccaa cagcgacugg gaucgucauc 240

ucggcuuguu cgcgugaccg ggagauccga guagaggcau agcgaacugc gcacggagaa 300

gucuugaggg aaugccguag 320

<210> SEQ ID NO 208
<211> LENGTH: 320
<212> TYPE: DNA
<213> ORGANISM: Mycobacterium scrofulaceum

<400> SEQUENCE: 208

acatcgcgca tcgaatcaag ggaagcgtgc cggtgcaggc aagagaccac cgtaagcgtc 60

gttgcaacca attaagcgcc gattcacatc agcgcgacta cgctctcgct gcctaagcga 120

cagctagtcc gtcagaccgg gaaagccctc gacccggagc ctggcgtcag ctagagggat 180

caaccgatga gttcggtcgc gggactcatc gggacaccaa cagcgactgg gatcgtcatc 240

ctggctagtc cgcgtgacca ggagatccga gcagaggcat agcggactgc gcacggagaa 300

gtcttgaggg aatgccgttg 320

<210> SEQ ID NO 209
<211> LENGTH: 320
<212> TYPE: RNA
<213> ORGANISM: Mycobacterium scrofulaceum

<400> SEQUENCE: 209

acaucgcgca ucgaaucaag ggaagcgugc cggugcaggc aagagaccac cguaagcguc 60

guugcaacca auuaagcgcc gauucacauc agcgcgacua cgcucucgcu gccuaagcga 120

cagcuagucc gucagaccgg gaaagcccuc gacccggagc cuggcgucag cuagagggau 180

caaccgauga guucggucgc gggacucauc gggacaccaa cagcgacugg gaucgucauc 240

cuggcuaguc cgcgugacca ggagauccga gcagaggcau agcggacugc gcacggagaa 300

gucuugaggg aaugccguug 320

<210> SEQ ID NO 210

<211> LENGTH: 326
<212> TYPE: DNA
<213> ORGANISM: Nocardia asteroides

<400> SEQUENCE: 210

actgtgtgcg ccgaggtagg ggaagcgtgt cggtgcaggc tggagaccac cgttaagcgt 60

cgcggcaacc aattaagcgc cgattccaat cagcgcgact acgccctcgc tgcctgatca 120

gcgacggcta gctgtcggcc cgggttgtgt tcccgaaccc ggatgccggc atcatctcag 180

ggaactcacc gtgttcgccg gtcgcggacg gacacgggac agcaaacagc gactgggatc 240

gtcatctcgg cttgttcgcg tgaccgggag atccaagtag agacatagcg gactgcacac 300

ggagaagccc tactgactcg acacag 326

<210> SEQ ID NO 211
<211> LENGTH: 325
<212> TYPE: RNA
<213> ORGANISM: Nocardia asteroides

<400> SEQUENCE: 211

acugugugcg ccgagguagg ggaagcgugu cggugcaggc uggagaccac cguuaagcgu 60

cgcggcaacc aauuaagcgc cgauuccaau cagcgcgacu acgcccucgc ugccugauca 120

gcgacggcua gcugucggcc cggguugugu ucccgaaccc ggaugccggc aucaucucag 180

ggaacucacc guguucgccg gucgcggacg gacacgggac agcaaacagc gacugggauc 240

gucaucucgg cuuguucgcg ugaccgggag auccaaguag agacauagcg gcugcacacg 300

gagaagcccu acugacucga cacag 325

<210> SEQ ID NO 212
<211> LENGTH: 314
<212> TYPE: DNA
<213> ORGANISM: Salmonella enteritidis

<400> SEQUENCE: 212

acgggatttg cgaaacccaa ggtgcatgcc gaggggcggt tggcctcgta aaaagccgca 60

aaaaaatagt cgcaaacgac gaaacctacg ctttagcagc ttaataacct gcttagagcc 120

ctctctccct agcctccgct cttaggacgg ggatcaagag aggtcaaacc caaaagagat 180

cgcgtggatg ccctgcctgg ggttgaagcg ttaaaacgaa tcaggctagt ctggtagtgg 240

cgtgtccgtc cgcaggtgcc aggcgaatgt aaagactgac taagcatgta gtaccgagga 300

tgtaggaatt tcgg 314

<210> SEQ ID NO 213
<211> LENGTH: 314
<212> TYPE: RNA
<213> ORGANISM: Salmonella enteritidis

<400> SEQUENCE: 213

acgggauuug cgaaacccaa ggugcaugcc gaggggcggu uggccucgua aaaagccgca 60

aaaaaauagu cgcaaacgac gaaaccuacg cuuuagcagc uuaauaaccu gcuuagagcc 120

cucucucccu agccuccgcu cuuaggacgg ggaucaagag aggucaaacc caaaagagau 180

cgcguggaug cccugccugg gguugaagcg uuaaaacgaa ucaggcuagu cugguagugg 240

cguguccguc cgcaggugcc aggcgaaugu aaagacugac uaagcaugua guaccgagga 300

uguaggaauu ucgg 314

<210> SEQ ID NO 214

<211> LENGTH: 313
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus epidermidis (NCTC 11047)

<400> SEQUENCE: 214

acaggggtcc cccgagctta ttaagcgtgt cggagggttg gctccgtcat caacacattt 60

cggttaaata taactgacaa atcaaacaat aatttcgcag tagctgcgta atagccactg 120

catcgcctaa cagcatctcc tacgtgctgt taacgcgatt caaccctagt aggatatgct 180

aaacactgcc gcttgaagtc tgtttagatg aaatataatc aagctagtat catgttggtt 240

gtttattgct tagcatgatg cgaaaattat caataaacta cacacgtaga aagatttgta 300

tcaggacctc tgg 313

<210> SEQ ID NO 215
<211> LENGTH: 313
<212> TYPE: RNA
<213> ORGANISM: Staphylococcus epidermidis (NCTC 11047)

<400> SEQUENCE: 215

acaggggucc cccgagcuua uuaagcgugu cggaggguug gcuccgucau caacacauuu 60

cgguuaaaua uaacugacaa aucaaacaau aauuucgcag uagcugcgua auagccacug 120

caucgccuaa cagcaucucc uacgugcugu uaacgcgauu caacccuagu aggauaugcu 180

aaacacugcc gcuugaaguc uguuuagaug aaauauaauc aagcuaguau cauguugguu 240

guuuauugcu uagcaugaug cgaaaauuau caauaaacua cacacguaga aagauuugua 300

ucaggaccuc ugg 313

<210> SEQ ID NO 216
<211> LENGTH: 302
<212> TYPE: DNA
<213> ORGANISM: Streptococcus agalactiae (NCTC 8181)

<400> SEQUENCE: 216

acaggcatta tgaggtatat tttgcgactc atcggcagat gtaaaatgcc agttaaatat 60

aactgcaaaa aatacaaatt cttacgcatt agctgcctaa aaaacagcct gcgtgatctt 120

cacaagattg tttgcgtttt gctagaaggt cttatttatc agcaaactac gtttggctac 180

tgtctagtta gttaaaaaga gatttataga ctcgctatgt gagggcttga gttatgtgtc 240

atcacctagt taaatcaata cataacctat agttgtagac aaatatatta gcagatgttt 300

gg 302

<210> SEQ ID NO 217
<211> LENGTH: 302
<212> TYPE: RNA
<213> ORGANISM: Streptococcus agalactiae (NCTC 8181)

<400> SEQUENCE: 217

acaggcauua ugagguauau uuugcgacuc aucggcagau guaaaaugcc aguuaaauau 60

aacugcaaaa aauacaaauu cuuacgcauu agcugccuaa aaaacagccu gcgugaucuu 120

cacaagauug uuugcguuuu gcuagaaggu cuuauuuauc agcaaacuac guuuggcuac 180

ugucuaguua guuaaaaaga gauuuauaga cucgcuaugu gagggcuuga guuauguguc 240

aucaccuagu uaaaucaaua cauaaccuau aguuguagac aaauauauua gcagauguuu 300

gg 302

<210> SEQ ID NO 218

<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Salmonella genus specificic probe

<400> SEQUENCE: 218

cgaatcaggc tagtctggta g 21

<210> SEQ ID NO 219
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide probe for detection of tuberculosis complex

<400> SEQUENCE: 219

actcctcggg acarccacag cga 23

<210> SEQ ID NO 220
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide probes for detection of M.avium and M. paratuberculosis sequences

<400> SEQUENCE: 220

gttgcaaata gataagcgcc 20

<210> SEQ ID NO 221
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide probe for detection of M. avium and M. paratuberculosis sequences

<400> SEQUENCE: 221

tccgtcagcc cgggaacgcc 20

<210> SEQ ID NO 222
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide probe used in determination of tmRNA integrity after heat killing treatment of Listeria cells

<400> SEQUENCE: 222

ttttgttttt ctttgcca 18

<210> SEQ ID NO 223
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide probe used in determination of tmRNA integrity after heat killing treatment of Escherichia coli cells

<400> SEQUENCE: 223

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agttttcgtc gtttgcga                                                     18


<210> SEQ ID NO 224
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
      Degenerative oligonucleotide primer for amplification of all
      mycobacterial sequences

<400> SEQUENCE: 224

caggcaashg accaccgtaa                                                   20


<210> SEQ ID NO 225
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
      Degenerative oligonucleotide primers for amplification of all
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<400> SEQUENCE: 225

ggatctccyg rtcwcrcgra cwa                                               23


<210> SEQ ID NO 226
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
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      avium and M. paratuberculosis sequences

<400> SEQUENCE: 226

tgccggtgca ggcaactg                                                     18


<210> SEQ ID NO 227
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
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      avium and M. paratuberculosis sequences

<400> SEQUENCE: 227

cacgcgaaca agccagga                                                     18


<210> SEQ ID NO 228
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence:
      Oligonucleotide probe for the detection of
      Listeria ssrA gene sequences

<400> SEQUENCE: 228

cattaaactt tagcaaggaa gtg                                               23


<210> SEQ ID NO 229
<211> LENGTH: 228
<212> TYPE: DNA
<213> ORGANISM: Listeria monocytogenes

<400> SEQUENCE: 229
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caaagaaaaa caaaacctag ctttcgctgc ctaataagca gtagcatagc tgatcctccg 60

tgcatcgccc atgtgctacg gtaagggtct cactctaagt gggctacact agttaatctc 120

cgtctgaggt taaatagaag agcttaatca gactagctga atggaagcct gttaccgggc 180

cgatgtttat gcgaaatgct aatacggtga ctacgctcgt agatattt 228

<210> SEQ ID NO 230
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide primer
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: n is a or c
<220> FEATURE:
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<223> OTHER INFORMATION: n is c or t
<220> FEATURE:
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<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: n is a or t

<400> SEQUENCE: 230

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<210> SEQ ID NO 231
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: n is a or g
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<221> NAME/KEY: misc_feature
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: n is a or g
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: n is c or g

<400> SEQUENCE: 231

gggantcgaa ccnngtcc 18

<210> SEQ ID NO 232
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
oligonucleotide primer

<400> SEQUENCE: 232

ggggctgatt ctggattcga c 21

<210> SEQ ID NO 233
<211> LENGTH: 19
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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<210> SEQ ID NO 234
<211> LENGTH: 15
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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<400> SEQUENCE: 234

tggtggagcc ggggg                                                    15


<210> SEQ ID NO 235
<211> LENGTH: 14
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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<400> SEQUENCE: 235

agcgacttgg cttc                                                     14


<210> SEQ ID NO 236
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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<400> SEQUENCE: 236

tacatgctta gcaaagatga                                               20


<210> SEQ ID NO 237
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (9)..(9)
<223> OTHER INFORMATION: n is c or g
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<223> OTHER INFORMATION: n is c or t

<400> SEQUENCE: 237

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<210> SEQ ID NO 238
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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<400> SEQUENCE: 238

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<210> SEQ ID NO 239
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<211> LENGTH: 18
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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<400> SEQUENCE: 239

ggggatgtag aggttttg                                                   18
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The invention claimed is:

1. A method of assaying a sample for a prokaryotic or eukaryotic organism which comprises contacting the sample with a nucleic acid sequence which is complementary to a target region of an ssrA gene or a fragment thereof;

detecting and identifying nucleic acid sequences in the sample that bind to the complementary nucleic acid sequence; and

correlating the nucleic acid sequences in the sample that bind to the complementary nucleic acid sequence to the presence and/or amount of one or more prokaryotic or eukaryotic organisms by comparing the detected nucleic acid sequences to one or more sequences contained in a database of known ssrA genes that includes the gene of the nucleic acid to be detected or by comparing the binding of the nucleic acids in the sample to the binding of one or more known control nucleic acid sequences to the complementary nucleic acid sequence.

2. The method according to claim **1**, wherein a fragment of the ssrA gene molecule corresponding to a region of high homology from the 5' end of the ssrA gene is used as a universal target region.

3. The method according to claim **1**, wherein a fragment of the ssrA gene molecule corresponding to a region of high homology from the 3' end of ssrA gene is used as a universal target region.

4. The method according to claim **1**, wherein a fragment of the ssrA gene molecule corresponding to a region of low homology is used as a target region in a nucleic acid probe assay to distinguish between species.

5. The method according to claim **1**, wherein a fragment of the ssrA gene molecule corresponding to a region of low homology is used as a target region for the generation of a genus specific probe.

6. A method of assaying for a prokaryotic or eukaryotic organism which comprises

contacting the sample with a nucleic acid sequence which is complementary to a target region of a tmRNA, an RNA transcript of the ssrA gene, or a fragment thereof;

detecting and identifying nucleic acid sequences in the sample that bind to the complementary nucleic acid sequence; and

correlating the nucleic acid sequences in the sample that bind to the complementary nucleic acid sequence to one or more prokaryotic or eukaryotic organisms by comparing the detected nucleic acid sequences to one or more sequences contained in a database of known ssrA genes that includes the gene of the nucleic acid sequences detected or by comparing the binding of the nucleic acids in the sample to the binding of one or more known control nucleic acid sequences to the complementary nucleic acid sequence.

7. The method according to claim **6**, wherein a fragment of a tmRNA molecule corresponding to a region of high homology from the 5' end of the tmRNA is used as a universal target region.

8. The method according to claim **6**, wherein a fragment of a tmRNA molecule corresponding to a region of high homology from the 3' end of the tmRNA is used as a universal target region.

9. The method according to claim **6**, wherein a fragment of a tmRNA corresponding to a region of low homology is used as a target region in a nucleic acid probe assay to distinguish between species.

10. The method according to claim **6**, wherein a fragment of a tmRNA corresponding to a region of low homology is used as a target region for the generation of a genus specific probe.

11. The method according to claim **1** or **6**, wherein said complementary nucleic acid sequence is a primer to be used in an amplification procedure.

12. The method according to claim **11**, wherein a product of the amplification procedure is used as a target region in a nucleic acid probe assay.

13. The method according to claim **6**, wherein a cDNA transcript of a tmRNA molecule is used as a probe in a nucleic acid hybridisation assay.

14. The method according to claim **1** or **6**, where the assay is carried out in vitro.

15. The method according to claim **1** or **6**, where the assay is carried out in situ.

16. A method of distinguishing between living and dead prokaryotic or eukaryotic organisms with the method of claim **6**, further comprising analyzing binding activity of the complementary nucleic acid sequence to target region in the sample wherein a decrease in binding activity indicates a loss of organism viability.

17. The method according to claim **1** or **6**, wherein the assay has a multiple probe format for broad scale detection and/or identification of prokaryotic or eukaryotic organisms.

18. The method according to claim **17**, wherein an ssrA gene probe or a tmRNA transcript probe is linked to a microarray gene chip system for the broad scale high throughput detection and identification of prokaryotic or eukaryotic organisms.

19. The method according to claim **1** or **6**, wherein the complementary nucleic acid is used as a probe or primers in an assay to detect prokaryotic or eukaryotic organisms in a sample of matter.

20. The method according to claim **1** or **6**, wherein a fragment of the ssrA gene or the tmRNA transcript is used in an assay to obtain a DNA profile of a prokaryotic or eukaryotic organism and, thereby, distinguish between strains of the same species.

21. A method of designing an agent directed against infectious prokaryotic or eukaryotic organisms for therapeutic purposes which comprises

identifying an ssrA gene or tmRNA sequence with the assay of claim **1** or claim **6** and designing a therapeutic agent which inhibits the function of the ssrA gene or tmRNA based on the identified sequence.

22. A method of monitoring a drug therapy against infections agents which comprises

comparing the amount or presence of the ssrA gene or fragment thereof, tmRNA, RNA transcript of the ssrA gene, or fragment thereof detected and identified in the assay of claim **1** or claim **6**, which is performed prior to administration of the drug therapy to the amount or presence the ssrA gene or fragment thereof, tmRNA, RNA transcript of the ssrA gene, or fragment thereof detected and identified in the assay of claim **1** or claim **6**, which is performed after administration of the drug therapy.

23. A method of monitoring the viability and level of health-promoting organisms in the gastrointestinal tract, which comprises

obtaining a sample from the gastrointestinal tract

determining the presence or amount of one or more health-promoting organisms in the sample with the method of claim **1** or claim **6**.

24. The method according to claim **1** or **6**, which further comprises quantifying the amount of prokaryotic or eukaryotic organisms detected and identified in the sample.

25. The method according to claim **1** or **6**, wherein a database of ssrA gene sequences is used to identify a prokaryotic or eukaryotic organism.

26. A method of assaying a sample for a prokaryotic or eukaryotic organism which comprises

contacting the sample with a nucleic acid sequence which is complementary to a target region of an ssrA gene or a fragment thereof;

detecting and identifying nucleic acid sequences in the sample that bind to the complementary nucleic acid sequence; and

correlating the nucleic acid sequences in the sample that bind to the complementary nucleic acid sequence to the presence and/or amount of one or more prokaryotic or eukaryotic organisms,

wherein said sample is selected from the group consisting of food samples, environmental samples, plant samples and animal samples.

27. The assay according to claim **26**, wherein said environmental sample is selected from the group consisting of air, water, marine, and soil.

28. The method according to claim **26**, wherein said sample is a human or animal sample and is a tissue sample from the respiratory tract, the uro-genital tract, the gastrointestinal tract or is a body fluid sample.

29. The method according to claim **28**, wherein the body fluid sample is blood, a blood fraction, sputum or cerebrospinal fluid.

* * * * *

专利名称(译)	基于核酸探针的诊断测定，靶向原核和真核生物的ssrA基因		
公开(公告)号	US7972777	公开(公告)日	2011-07-05
申请号	US09/959964	申请日	2000-05-15
[标]申请(专利权)人(译)	爱尔兰国立大学,戈尔韦		
申请(专利权)人(译)	爱尔兰企业局 爱尔兰国立高威大学		
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[标]发明人	BARRY THOMAS GERARD SMITH TERENCE JAMES		
发明人	BARRY, THOMAS GERARD SMITH, TERENCE JAMES		
IPC分类号	C12Q1/68 C12P19/34 G01N33/50 A61K31/7088 A61K38/00 A61K48/00 A61P31/04 A61P33/00 C12N15/09 C12Q1/689 G01N33/15 G01N33/53 G01N37/00		
CPC分类号	C12N15/113 C12Q1/689 A61P31/04 A61P33/00 C12Q2600/158		
审查员(译)	霍利克，肯尼斯R.		
优先权	PCT/IE1999/000043 1999-05-14 WO		
外部链接	Espacenet USPTO		

摘要(译)

描述了ssrA基因或tmRNA，ssrA基因的RNA转录物或其片段在核酸探针测定中作为靶区域用于检测和鉴定原核和/或真核生物的用途。来自各种生物的tmRNA序列的核苷酸序列比对可用于鉴定序列内的同源性和非同源性区域，其又可用于设计属特异性和物种特异性寡核苷酸探针。这些新鉴定的同源和非同源区域提供了在分子水平上鉴定和检测生物的基础。以这种方式鉴定的寡核苷酸探针可用于检测样品中的tmRNA，从而给出各种样品类型中存在的非病毒生物的存活力的指示。